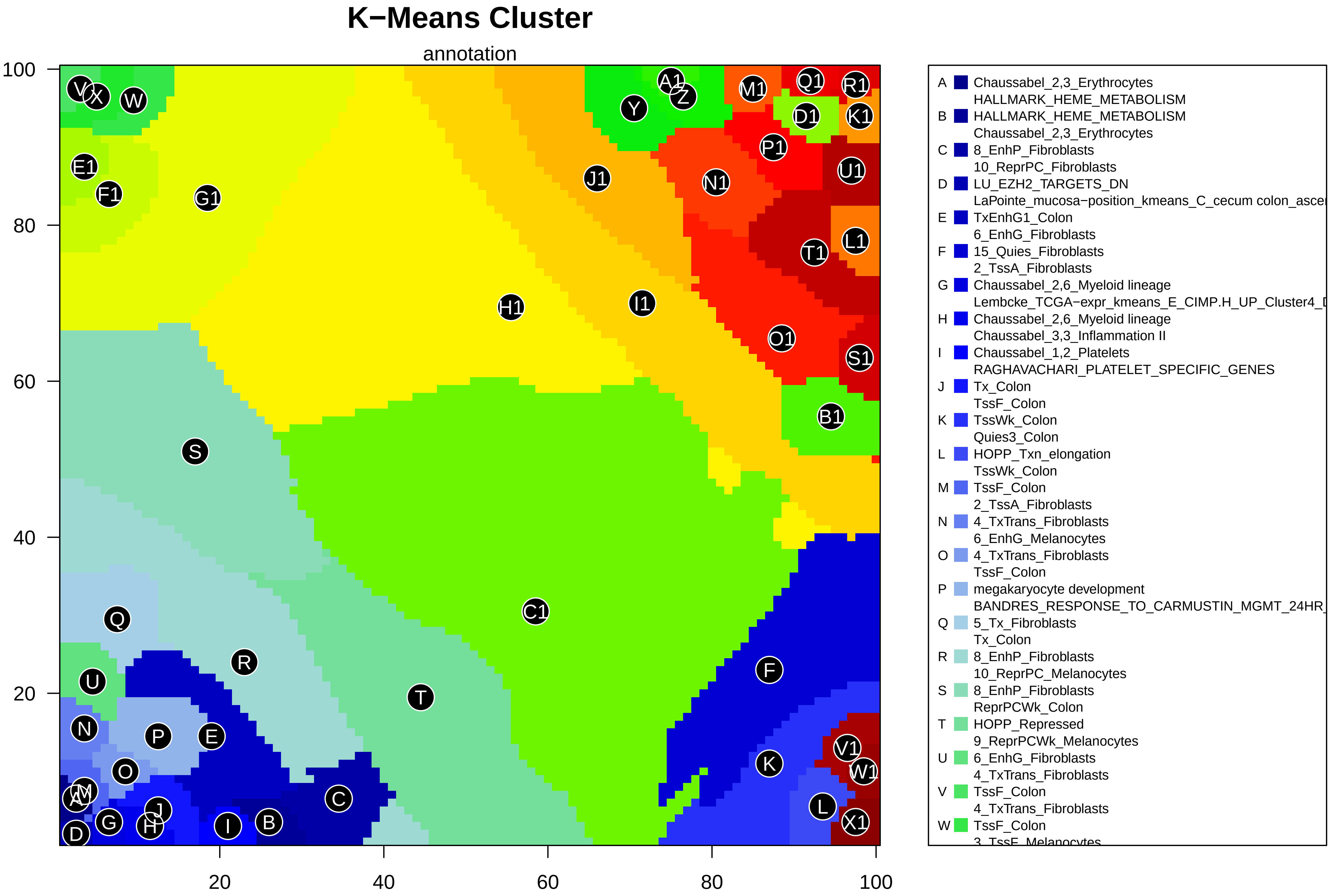
K−Means Cluster
annotation
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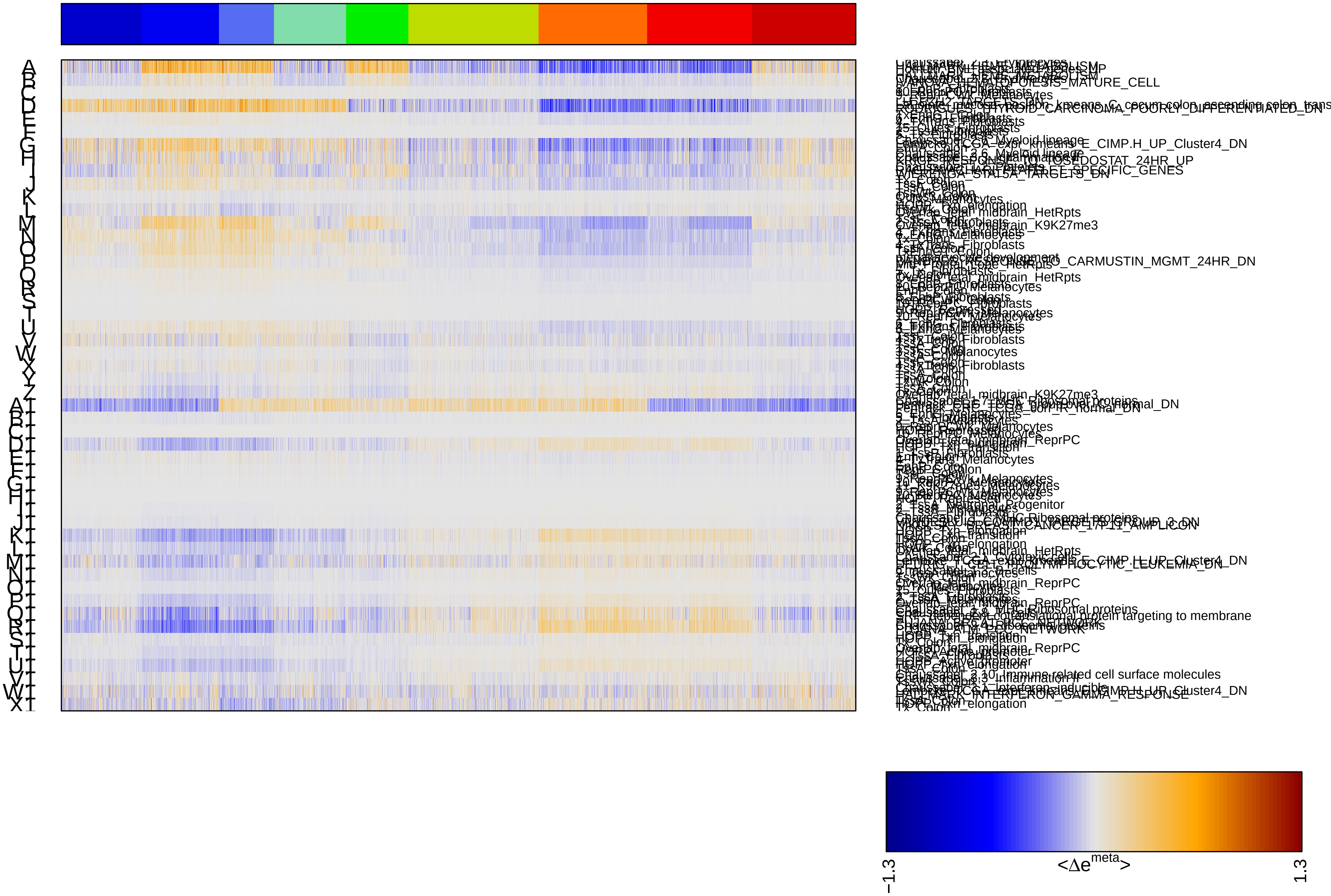
D
A 🟦 Chaussabel_2,3_Erythrocytes
HALLMARK_HEME_METABOLISM
B 🟦 HALLMARK_HEME_METABOLISM
Chaussabel_2,3_Erythrocytes
C 🟦 8_EnhP_Fibroblasts
10_ReprPC_Fibroblasts
D 🟦 LU_EZH2_TARGETS_DN
LaPointe_mucosa−position_kmeans_C_cecum colon_asce
E 🟦 TxEnhG1_Colon
6_EnhG_Fibroblasts
F 🟦 15_Quies_Fibroblasts
2_TssA_Fibroblasts
G 🟦 Chaussabel_2,6_Myeloid lineage
Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_
H 🟦 Chaussabel_2,6_Myeloid lineage
Chaussabel_3,3_Inflammation II
I 🟦 Chaussabel_1,2_Platelets
RAGHAVACHARI_PLATELET_SPECIFIC_GENES
J 🟦 Tx_Colon
TssF_Colon
K 🟦 TssWk_Colon
Quies3_Colon
L 🟦 HOPP_Txn_elongation
TssWk_Colon
M 🟦 TssF_Colon
2_TssA_Fibroblasts
N 🟦 4_TxTrans_Fibroblasts
6_EnhG_Melanocytes
O 🟦 4_TxTrans_Fibroblasts
TssF_Colon
P 🟦 megakaryocyte development
BANDRES_RESPONSE_TO_CARMUSTIN_MGMT_24HR_
Q 🟦 5_Tx_Fibroblasts
Tx_Colon
R 🟩 8_EnhP_Fibroblasts
10_ReprPC_Melanocytes
S 🟩 8_EnhP_Fibroblasts
ReprPCWk_Colon
T 🟩 HOPP_Repressed
9_ReprPCWk_Melanocytes
U 🟩 6_EnhG_Fibroblasts
4_TxTrans_Fibroblasts
V 🟩 TssF_Colon
4_TxTrans_Fibroblasts
W 🟩 TssF_Colon
3_TssF_Melanocytes



A
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O1
P1
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V1
W1
X1
VANOVA_HEMATOPOIESIS_MATURE_CELL
CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_DN
RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_DN
E_CIMP.H_UP_Cluster4_DN
DOSTAT_24HR_UP
WIERENGA_STAT5A_TARGETS_DN
Overlap_fetal_midbrain_HetRpts
Overlap_fetal_midbrain_K9K27me3
_CARMUSTIN_MGMT_24HR_DN
Overlap_fetal_midbrain_HetRpts
Overlap_fetal_midbrain_K9K27me3
Overlap_fetal_midbrain_ReprPC
2_TssA_Neuronal_Progenitor
NIKOLSKY_BREAST_CANCER_17P11_AMPLICON
Overlap_fetal_midbrain_HetRpts
E_CIMP.H_UP_Cluster4_DN
Overlap_fetal_midbrain_ReprPC
SRP-dependent cotranslational protein targeting to membrane
Overlap_fetal_midbrain_ReprPC
Chaussabel_3.10_Immune-related cell surface molecules
HALLMARK_INTERFERON_GAMMA_RESPONSE
HOPP_Txn_elongation
Tx_Colon
−1.3
<Δe^meta>
1.3

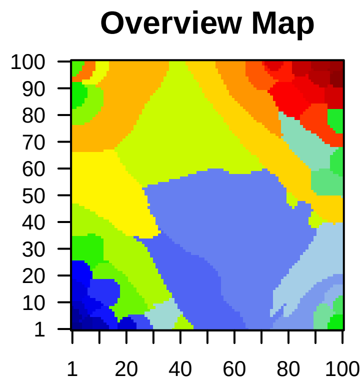
K−Means Cluster

Spot Summary: A

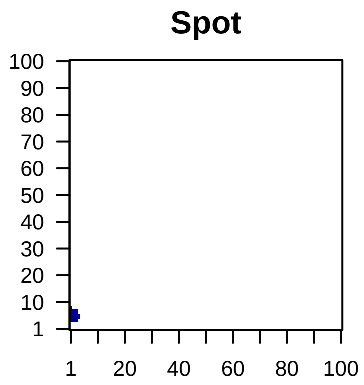
metagenes = 18
genes = 291

<r> metagenes = 0.98
<r> genes = 0.64
beta: r2= 227.12 / log p= −Inf

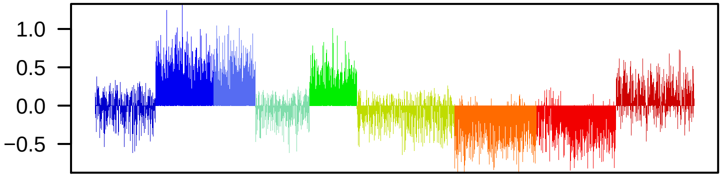
samples with spot = 1234 (36.4 %)
A * : 84 (24.4 %)
A C * : 321 (97.9 %)
A C F * : 230 (97.9 %)
A F * : 49 (15.9 %)
C F * : 261 (98.5 %)
F * : 59 (10.6 %)
F J * : 5 (1.1 %)
J * : 8 (1.8 %)
N * : 217 (49 %)



Overview Map



Spot

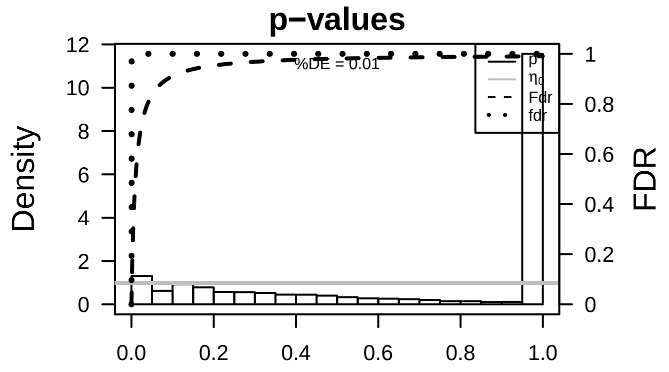


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_169326	3.22	−2.11	0.51		
2	ILMN_167935	3.21	−3.04	0.47	DEFA1B	defensin alpha 1 [Source:HGNC Symbol;Acc:HGNC:2761]
3	ILMN_177651	3.13	−1.1	0.44	RAP1GAP	RAP1 GTPase activating protein [Source:HGNC Symbol;Acc:
4	ILMN_219321	3.07	−2.61	0.46	DEFA1B	defensin alpha 1 [Source:HGNC Symbol;Acc:HGNC:2761]
5	ILMN_216528	3.02	−1.93	0.45	DEFA1B	defensin alpha 1 [Source:HGNC Symbol;Acc:HGNC:2761]
6	ILMN_172566	2.96	−2.08	0.45	DEFA1B	defensin alpha 1 [Source:HGNC Symbol;Acc:HGNC:2761]
7	ILMN_211687	2.86	−1.31	0.39	OLFM4	olfactomedin 4 [Source:HGNC Symbol;Acc:HGNC:17190]
8	ILMN_170832	2.82	−1.91	0.84	ALAS2	5'−aminolevulinate synthase 2 [Source:HGNC Symbol;Acc:H
9	ILMN_165243	2.79	−1.83	0.82	CA1	carbonic anhydrase 1 [Source:HGNC Symbol;Acc:HGNC:13
10	ILMN_168858	2.54	−1.91	0.52	CAMP	cathelicidin antimicrobial peptide [Source:HGNC Symbol;Acc:
11	ILMN_174983	2.5	−1.99	0.5	SMIM1	small integral membrane protein 1 (Vel blood group) [Source:
12	ILMN_175334	2.49	−1.4	0.41		
13	ILMN_176616	2.48	−2.2	0.85	SNCA	synuclein alpha [Source:HGNC Symbol;Acc:HGNC:11138]
14	ILMN_171345	2.47	−1.33	0.38	HBZ	hemoglobin subunit zeta [Source:HGNC Symbol;Acc:HGNC:
15	ILMN_328576	2.47	−2.05	0.9	SLC4A1	solute carrier family 4 member 1 (Diego blood group) [Source
16	ILMN_169651	2.44	−2.23	0.92	AHSP	alpha hemoglobin stabilizing protein [Source:HGNC Symbol;
17	ILMN_169222	2.41	−1.48	0.56		
18	ILMN_173571	2.39	−1.48	0.66	KRT1	keratin 1 [Source:HGNC Symbol;Acc:HGNC:6412]
19	ILMN_168065	2.38	−1.7	0.94	SELENBP1	selenium binding protein 1 [Source:HGNC Symbol;Acc:HGN
20	ILMN_170663	2.3	−1.37	0.46	ELANE	elastase, neutrophil expressed [Source:HGNC Symbol;Acc:H

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	5e−87	57 / 111	Refer	Chaussabel_2,3_Erythrocytes
2	1e−60	51 / 185	HM	HALLMARK_HEME_METABOLISM
3	8e−19	21 / 147	Lifest	Homuth_BMI−associated−genes_UP
4	9e−19	26 / 267	GSE	IVANOVA_HEMATOPOIESIS_MATURE_CELL
5	3e−18	23 / 202	GSE	JAATINEN_HEMATOPOIETIC_STEM_CELL_DN
6	4e−18	12 / 26	GSE	VALK_AML_CLUSTER_7
7	2e−17	10 / 15	Lifest	DUMEAUX_Red blood cells in non smokers literature genes up
8	3e−17	13 / 39	Refer	Chaussabel_2,2_Neutrophils
9	2e−14	10 / 25	GSE	VALK_AML_CLUSTER_8
10	3e−13	157 / 10779	Colon	Enh_Colon
11	2e−12	25 / 451	GSE	PILON_KLF1_TARGETS_UP
12	5e−12	120 / 7354	Colon	TssF_Colon
13	3e−11	64 / 2845	Colon	TxEnhG1_Colon
14	1e−09	162 / 12298	Chro	2_TssA_Melanocytes
15	1e−09	49 / 2028	Chro	4_TxTrans_Melanocytes
16	1e−09	7 / 23	CC	cortical cytoskeleton
17	2e−09	95 / 5699	Chro	6_EnhG_Melanocytes
18	3e−09	84 / 4795	Chro	6_EnhG_Fibroblasts
19	5e−09	61 / 2979	CC	cytosol
20	5e−09	99 / 6138	Colon	TssD2_Colon
21	9e−09	7 / 29	Refer	JONGENEEL_Bone Marrow
22	1e−08	165 / 12983	Chro	2_TssA_Neuronal_Progenitor
23	3e−08	65 / 3450	Chro	4_TxTrans_Fibroblasts
24	3e−08	5 / 11	MF	oxygen transporter activity
25	4e−08	132 / 9555	Colon	TssA_Colon
26	4e−08	127 / 9054	Colon	Tx_Colon
27	6e−08	5 / 12	BP	oxygen transport
28	6e−08	153 / 11836	Chro	3_TssF_Melanocytes
29	1e−07	131 / 9635	Chro	3_TssF_Fibroblasts
30	2e−07	5 / 15	GSE	STEINER_ERYTHROCYTE_MEMBRANE_GENES
31	3e−07	59 / 3164	Brain	Mid_Frontal_Lobe_ZNF
32	5e−07	121 / 8818	MF	protein binding
33	7e−07	9 / 103	GSE	ACOSTA_PROLIFERATION_INDEPENDENT_MYC_TARGETS_DN
34	9e−07	136 / 10430	Brain	Overlap_fetal_midbrain_Quies
35	1e−06	90 / 5956	Chro	3_TssF_Neuronal_Progenitor
36	1e−06	5 / 20	GSE	VANDESLUIS_NORMAL_EMBRYOS_DN
37	1e−06	141 / 10999	Colon	TssWk_Colon
38	1e−06	24 / 818	Brain	Mid_Frontal_Lobe_Het
39	1e−06	83 / 5373	Colon	EnhWk1_Colon
40	2e−06	4 / 10	GSE	BIOCARTA_AHSP_PATHWAY



p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.7	1 / 111	HORVATH_aging_genes meth DOWN
2	1.0	0 / 142	HORVATH_aging_genes meth UP
3	1.0	0 / 58	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	6e−08	5 / 12	oxygen transport
2	2e−05	15 / 435	negative regulation of apoptotic process
3	4e−05	4 / 20	heme biosynthetic process
4	2e−04	4 / 29	mitophagy
5	2e−04	3 / 12	regulation of proteasomal protein catabolic process
6	2e−04	5 / 56	cellular response to oxidative stress
7	4e−04	5 / 64	negative regulation of cysteine−type endopeptidase activity involved in apoptc
8	4e−04	7 / 140	ubiquitin−dependent protein catabolic process
9	4e−04	3 / 16	erythrocyte development
10	6e−04	4 / 40	erythrocyte differentiation
11	1e−03	3 / 21	regulation of reactive oxygen species metabolic process
12	1e−03	3 / 21	skeletal muscle fiber development
13	1e−03	7 / 163	protein polyubiquitination
14	1e−03	10 / 330	protein ubiquitination
15	2e−03	3 / 24	regulation of RNA splicing

Brain

Rank	p−value	#in/all	Geneset
1	3e−07	59 / 3164	Mid_Frontal_Lobe_ZNF
2	9e−07	136 / 10430	Overlap_fetal_midbrain_Quies
3	1e−06	24 / 818	Mid_Frontal_Lobe_Het
4	3e−06	125 / 9504	Overlap_fetal_midbrain_K9K27me3
5	8e−06	49 / 2709	Mid_Frontal_Lobe_HetRpts
6	2e−03	17 / 796	Overlap_fetal_midbrain_ZNF
7	2e−03	29 / 1728	Fetal_ReprPCWk
8	3e−03	56 / 4112	Mid_Frontal_Lobe_ReprPC
9	7e−03	113 / 9815	Overlap_fetal_midbrain_ReprPC
10	2e−02	111 / 9917	Overlap_fetal_midbrain_ReprPCWk
11	2e−02	71 / 5936	Overlap_fetal_midbrain_HetRpts
12	2e−02	30 / 2127	Mid_Frontal_Lobe_K9K27me3
13	3e−02	15 / 924	Mid_Frontal_Lobe_TssF
14	2e−01	5 / 304	Mid_Frontal_Lobe_TssA
15	2e−01	14 / 1119	Overlap_fetal_midbrain_TssA

Cancer

Rank	p−value	#in/all	Geneset
1	0.03	3 / 73	SHAUGHNESSY_MM high risk
2	0.07	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
3	0.12	1 / 13	RHODES_CANCER_META_SIGNATURE
4	0.12	1 / 13	GENTLES_modul2
5	0.12	1 / 13	GENTLES_modul12
6	0.13	1 / 14	GENTLES_modul1
7	0.13	1 / 15	WANG_ER_UP
8	0.14	1 / 16	GENTLES_modul7
9	0.14	1 / 16	GENTLES_modul11
10	0.17	8 / 554	Lembcke_Colonic Inflammation
11	0.20	0 / 14	LIU_PROSTATE_CANCER_UP
12	0.27	0 / 13	LIU_LIVER_CANCER
13	0.33	4 / 301	SPANG_BCL6−index2
14	0.34	2 / 125	PanCan_CC+Apop_geneset_nanostring
15	0.36	1 / 46	PanCan_DNARepair_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	1e−09	7 / 23	cortical cytoskeleton
2	5e−09	61 / 2979	cytosol
3	1e−04	3 / 11	TORC2 complex
4	2e−04	69 / 4822	cytoplasm
5	9e−04	10 / 310	dendrite
6	1e−03	33 / 1979	membrane
7	2e−03	5 / 93	blood microparticle
8	4e−03	3 / 34	polysome
9	6e−03	4 / 74	mitochondrial membrane
10	6e−03	2 / 12	specific granule
11	7e−03	62 / 4828	nucleus
12	8e−03	2 / 14	Cul4−RING E3 ubiquitin ligase complex
13	1e−02	7 / 249	axon
14	1e−02	3 / 49	transcriptional repressor complex
15	1e−02	8 / 330	cytoskeleton

Chr

Rank	p−value	#in/all	Geneset
1	0.03	10 / 536	Chr 22
2	0.04	21 / 1467	Chr 19
3	0.04	15 / 959	Chr 16
4	0.08	18 / 1318	Chr 17
5	0.09	29 / 2323	Chr 1
6	0.11	12 / 836	Chr 8
7	0.36	11 / 994	Chr X
8	0.45	12 / 1170	Chr 7
9	0.46	8 / 768	Chr 14
10	0.55	6 / 619	Chr 20
11	0.60	13 / 1411	Chr 11
12	0.64	3 / 342	Chr 18
13	0.68	10 / 1160	Chr 12
14	0.74	10 / 1217	Chr 3
15	0.78	12 / 1492	Chr 2

Chromatin states

Rank	p−value	#in/all	Geneset
1	1e−09	162 / 12298	2_TssA_Melanocytes
2	1e−09	49 / 2028	4_TxTrans_Melanocytes
3	2e−09	95 / 5699	6_EnhG_Melanocytes
4	3e−09	84 / 4795	6_EnhG_Fibroblasts
5	1e−08	165 / 12983	2_TssA_Neuronal_Progenitor
6	3e−08	65 / 3450	4_TxTrans_Fibroblasts
7	6e−08	153 / 11836	3_TssF_Melanocytes
8	1e−07	131 / 9635	3_TssF_Fibroblasts
9	1e−06	90 / 5956	3_TssF_Neuronal_Progenitor
10	3e−06	156 / 12741	7_Enh_Melanocytes
11	5e−06	117 / 8771	5_Tx_Melanocytes
12	5e−06	143 / 11455	2_TssA_Fibroblasts
13	8e−06	146 / 11847	7_Enh_Neuronal_Progenitor
14	1e−03	142 / 12393	15_Quies_Neuronal_Progenitor
15	1e−03	23 / 1206	6_EnhG_Neuronal_Progenitor

Colon Cancer

Rank	p−value	#in/all	Geneset
1	3e−13	157 / 10779	Enh_Colon
2	5e−12	120 / 7354	TssF_Colon
3	3e−11	64 / 2845	TxEnhG1_Colon
4	5e−09	99 / 6138	TssD2_Colon
5	4e−08	132 / 9555	TssA_Colon
6	4e−08	127 / 9054	Tx_Colon
7	1e−06	141 / 10999	TssWk_Colon
8	1e−06	83 / 5373	EnhWk1_Colon
9	2e−06	18 / 505	Pentrack_CRC_TCGA_corr_C_normal_UP
10	5e−06	51 / 2810	EnhA_Colon
11	2e−05	113 / 8568	TxWk_Colon
12	6e−05	112 / 8678	Quies3_Colon
13	9e−04	27 / 1470	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
14	4e−03	26 / 1547	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
15	9e−03	15 / 789	TxEnhG2_Colon

Glio

Rank	p−value	#in/all	Geneset
1	5e−04	12 / 401	Down_b
2	3e−03	5 / 98	WILLSCHER_GBM_proteomics_wtOnly_SpotB
3	9e−03	3 / 44	WILLSCHER_GBM_Verhaak−PNwt_up
4	2e−02	9 / 419	Down_a
5	3e−02	39 / 2988	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
6	3e−02	21 / 1417	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
7	4e−02	2 / 33	Shaw_responders_down_in_oligo_glioma
8	4e−02	2 / 35	Colman_survival_associated
9	5e−02	3 / 84	GIEZELT_GBM_STS_up_VS_LTS
10	5e−02	3 / 84	Weller_LGG_gradeII−vs−III_UP
11	5e−02	2 / 37	WILLSCHER_GBM_proteomics_wtOnly_SpotH
12	7e−02	1 / 8	Donson−migration tethering and rolling−associated with LTS in HGA
13	8e−02	3 / 104	WIRTH_Normal Brain
14	8e−02	1 / 9	Colman_survival_robust
15	1e−01	2 / 55	Stuehler_Proteins_up_in_STS

GSEA C2

Rank	p−value	#in/all	Geneset
1	9e−19	26 / 267	IVANOVA_HEMATOPOIESIS_MATURE_CELL
2	3e−18	23 / 202	JAATINEN_HEMATOPOIETIC_STEM_CELL_DN
3	4e−18	12 / 26	VALK_AML_CLUSTER_7
4	2e−14	10 / 25	VALK_AML_CLUSTER_8
5	2e−12	25 / 451	PILON_KLF1_TARGETS_UP
6	2e−07	5 / 15	STEINER_ERYTHROCYTE_MEMBRANE_GENES
7	7e−07	9 / 103	ACOSTA_PROLIFERATION_INDEPENDENT_MYC_TARGETS_DN
8	1e−06	5 / 20	VANDESLUIS_NORMAL_EMBRYOS_DN
9	2e−06	4 / 10	BIOCARTA_AHSP_PATHWAY
10	6e−06	10 / 169	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_HSC_DN
11	6e−06	11 / 210	CHYLA_CBFA2T3_TARGETS_DN
12	9e−06	26 / 1043	GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_UP
13	1e−05	29 / 1265	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
14	2e−05	4 / 17	WELCH_GATA1_TARGETS
15	2e−05	18 / 594	KIM_BIPOLAR_DISORDER_OLIGODENDROCYTE_DENSITY_CORR_UP

HM

Rank	p−value	#in/all	Geneset
1	1e−60	51 / 185	HALLMARK_HEME_METABOLISM
2	5e−04	8 / 189	HALLMARK_HYPOXIA
3	2e−03	7 / 175	HALLMARK_XENOBIOTIC_METABOLISM
4	2e−03	6 / 137	HALLMARK_UV_RESPONSE_UP
5	2e−02	4 / 103	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
6	3e−02	5 / 176	HALLMARK_ADIPOGENESIS
7	3e−02	5 / 186	HALLMARK_ESTROGEN_RESPONSE_EARLY
8	6e−02	4 / 151	HALLMARK_APOPTOSIS
9	9e−02	4 / 176	HALLMARK_KRAS_SIGNALING_UP
10	9e−02	4 / 177	HALLMARK_KRAS_SIGNALING_DN
11	1e−01	4 / 185	HALLMARK_MTORC1_SIGNALING
12	1e−01	4 / 186	HALLMARK_ESTROGEN_RESPONSE_LATE
13	1e−01	4 / 186	HALLMARK_IL2_STAT5_SIGNALING
14	3e−01	3 / 183	HALLMARK_GLYCOLYSIS
15	3e−01	3 / 185	HALLMARK_TNFA_SIGNALING_VIA_NFKB

Lifestyle

Rank	p−value	#in/all	Geneset
1	8e−19	21 / 147	Homuth_BMI−associated−genes_UP
2	2e−17	10 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
3	1e−02	2 / 17	DUMEAUX_High bmi enriched genes
4	7e−02	1 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
5	2e−01	1 / 18	Huan_blood−pressure_SBP−signature
6	2e−01	2 / 94	DUMEAUX_Smoking enriched genes
7	1e+00	0 / 10	DUMEAUX_Smoking literature genes up
8	1e+00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
9	1e+00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
10	1e+00	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
11	1e+00	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
12	1e+00	0 / 10	DUMEAUX_Women normal BMI literature genes up
13	1e+00	0 / 31	DUMEAUX_Fasting enriched genes
14	1e+00	0 / 211	Homuth_BMI−associated−genes_DN
15	1e+00	0 / 16	Huan_blood−pressure_DBP−signature

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.003	70 / 5356	HOPP_Txn_transition
2	0.005	90 / 7448	HOPP_Strong_enhancer
3	0.012	8 / 318	Hopp_June14_MMML937 tumors+controls_group.overexpression_H_GC−B−
4	0.015	8 / 331	WIRTH_lymphoma937_spot H
5	0.017	4 / 103	Hopp_June14_MMML937 tumors+controls_group.overexpression_MM_MM_
6	0.018	19 / 1169	SPANG_BCR DN
7	0.019	4 / 105	WIRTH_lymphoma937_spot MM
8	0.024	2 / 25	SPANG_BAFF 9hrs UP
9	0.025	84 / 7275	HOPP_Txn_elongation
10	0.029	4 / 121	SPANG_LPS 6hrs UP
11	0.074	1 / 8	YAMANE_AICDA_targets_nonrecruited
12	0.132	2 / 66	TARTE_Plasma cell signature
13	0.149	7 / 455	SPANG_CD40 6hrs DN
14	0.152	2 / 72	Hopp_June14_MMML937 tumors+controls_group.overexpression_IM_mBL_
15	0.159	2 / 74	WIRTH_lymphoma937_spot IM

Melanoma

Rank	p−value	#in/all	Geneset
1	0.3	1 / 30	Hugo_melanoma−all−MET_UP
2	0.3	1 / 43	Hugo_melanoma−BRAFmut−MET_UP
3	1.0	0 / 54	Hugo_melanoma−all−MET_DN
4	1.0	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
5	1.0	0 / 27	Hugo_melanoma−all−LEF1_UP
6	1.0	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

MF

Rank	p−value	#in/all	Geneset
1	3e−08	5 / 11	oxygen transporter activity
2	5e−07	121 / 8818	protein binding
3	3e−05	5 / 38	oxygen binding
4	1e−04	7 / 112	heme binding
5	2e−04	11 / 301	ubiquitin−protein transferase activity
6	1e−03	6 / 121	iron ion binding
7	2e−03	8 / 232	ligase activity
8	2e−03	4 / 58	core promoter binding
9	4e−03	2 / 10	proteasome binding
10	4e−03	13 / 580	identical protein binding
11	7e−03	2 / 13	neutral amino acid transmembrane transporter activity
12	9e−03	2 / 15	protein kinase A regulatory subunit binding
13	1e−02	7 / 256	ubiquitin protein ligase binding
14	1e−02	2 / 19	cysteine−type endopeptidase inhibitor activity involved in apoptotic process
15	2e−02	2 / 20	2 iron, 2 sulfur cluster binding

miRNA Disease

Rank	p−value	#in/all	Geneset
1	0.2	1 / 17	Thyroid carcinoma, follicular
2	0.2	1 / 18	Hodgkin lymphoma
3	0.2	1 / 29	Myelofibrosis, idiopathic
4	0.4	1 / 47	Cervical cancer, somatic
5	0.4	1 / 48	Gastric cancer
6	0.4	1 / 57	Cardiomyopathy, dilated
7	0.5	1 / 65	Hepatocellular carcinoma
8	0.5	1 / 68	Glioblastoma multiforme, somatic
9	0.5	1 / 73	Stroke, susceptibility to
10	0.6	1 / 95	Colorectal cancer
11	0.6	1 / 102	Leukemia
12	0.7	1 / 113	Ovarian cancer
13	0.7	1 / 116	Cancer
14	0.7	1 / 120	Hematological
15	0.7	1 / 123	Pancreatic cancer

miRNA target

Rank	p−value	#in/all	Geneset
1	0.004	3 / 32	hsa−miR−342−5p
2	0.006	4 / 75	hsa−miR−651
3	0.010	8 / 308	hsa−miR−302b
4	0.010	2 / 16	hsa−miR−891a
5	0.012	8 / 316	hsa−miR−302c
6	0.012	8 / 317	hsa−miR−520c−3p
7	0.012	3 / 50	hsa−miR−337−3p
8	0.012	4 / 93	hsa−miR−216a
9	0.015	5 / 149	hsa−miR−142−3p
10	0.016	8 / 336	hsa−miR−520d−3p
11	0.017	7 / 273	hsa−miR−520b
12	0.017	4 / 103	hsa−miR−377
13	0.017	4 / 103	hsa−miR−146b−5p
14	0.018	3 / 58	hsa−miR−187
15	0.019	6 / 217	hsa−miR−185

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.1	1 / 15	GUSTAFSON_PI3K_DN
2	1.0	0 / 14	GUSTAFSON_PI3K_UP
3	1.0	0 / 13	BENTINK_e2f3.1
4	1.0	0 / 13	BENTINK_e2f3.2
5	1.0	0 / 13	BENTINK_myc.1
6	1.0	0 / 12	BENTINK_ras.1
7	1.0	0 / 11	BENTINK_ras.4
8	1.0	0 / 14	BENTINK_ras.6
9	1.0	0 / 13	BENTINK_src.10
10	1.0	0 / 12	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Reference Signatures

Rank	p−value	#in/all	Geneset
1	5e−87	57 / 111	Chaussabel_2,3_Erythrocytes
2	3e−17	13 / 39	Chaussabel_2,2_Neutrophils
3	9e−09	7 / 29	JONGENEEL_Bone Marrow
4	3e−06	4 / 11	WIRTH_Prim. lymphoid organs
5	6e−06	4 / 13	WIRTH_Bone marrow
6	3e−03	5 / 102	Chaussabel_1,2_Platelets
7	8e−03	14 / 695	PROTEINATLAS_bone marrow
8	1e−02	2 / 19	VAQUERIZAS_Bone marrow_TF
9	2e−02	12 / 639	PROTEINATLAS_breast
10	7e−02	1 / 8	VAQUERIZAS_Tongue_TF
11	7e−02	1 / 8	JONGENEEL_Fetal Brain
12	8e−02	5 / 242	Chaussabel_3,2_Inflammation I
13	9e−02	1 / 10	VAQUERIZAS_Skeletal muscle_TF
14	9e−02	1 / 10	JONGENEEL_Pituitary Gland
15	9e−02	2 / 53	JONGENEEL_Kidney

Telomeres

Rank	p−value	#in/all	Geneset
1	0.03	2 / 27	Nabetani_alt len telomeres_genes_ko
2	1.00	0 / 13	Alternative lengthening of telomeres
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	2e−05	69 / 4468	ICGC_Egr1_targets
2	1e−04	83 / 5984	ICGC_Mta3_targets
3	1e−04	89 / 6578	ICGC_Pou2_targets
4	1e−04	92 / 6868	ICGC_Elf1_targets
5	1e−04	76 / 5383	ICGC_Sp1_targets
6	2e−04	64 / 4345	ICGC_Zeb1_targets
7	2e−04	64 / 4362	ICGC_Creb1_targets
8	2e−04	73 / 5188	ICGC_Ebfsc137065_targets
9	3e−04	71 / 5067	ICGC_Taf1_targets
10	3e−04	94 / 7247	ICGC_Runx3_targets
11	4e−04	84 / 6322	ICGC_Tcf3_targets
12	8e−04	17 / 733	ICGC_Atf3_targets
13	8e−04	82 / 6267	ICGC_Yy1_targets
14	8e−04	74 / 5518	ICGC_Stat5_targets
15	9e−04	67 / 4890	ICGC_Bclaf101388_targets

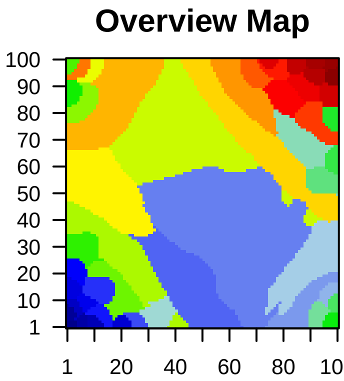
K−Means Cluster

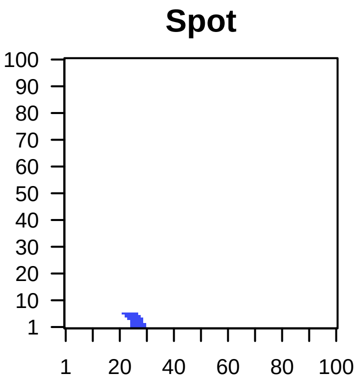
Spot Summary: B

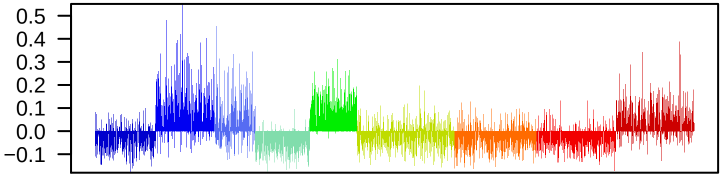
metagenes = 35
genes = 240

<r> metagenes = 0.94
<r> genes = 0.3
beta: r2= 15.96 / log p= −Inf

samples with spot = 332 (9.8 %)
A C * : 106 (32.3 %)
A C F * : 47 (20 %)
C F * : 104 (39.2 %)
F * : 4 (0.7 %)
F J * : 2 (0.4 %)
J * : 3 (0.7 %)
N * : 66 (14.9 %)





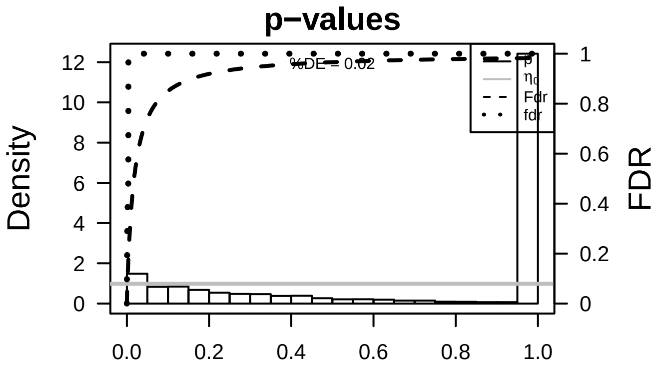


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_324311	1.66	−0.52	0.38	RNF182	ring finger protein 182 [Source:HGNC Symbol;Acc:HGNC:28
2	ILMN_171896	1.46	−0.99	0.83	BNIP3L	BCL2 interacting protein 3 like [Source:HGNC Symbol;Acc:H
3	ILMN_172470	1.33	−1.03	0.83	RIOK3	RIO kinase 3 [Source:HGNC Symbol;Acc:HGNC:11451]
4	ILMN_169716	1.22	−0.82	0.68	C9orf78	chromosome 9 open reading frame 78 [Source:HGNC Symb
5	ILMN_211798	1.19	−0.76	0.78	TFDP1	transcription factor Dp−1 [Source:HGNC Symbol;Acc:HGNC:
6	ILMN_181502	1.16	−0.97	0.64	PIM1	Pim−1 proto−oncogene, serine/threonine kinase [Source:HG
7	ILMN_166171	1.16	−0.67	0.82	TFDP1	transcription factor Dp−1 [Source:HGNC Symbol;Acc:HGNC:
8	ILMN_166740	1.08	−0.67	0.73	EPB41	erythrocyte membrane protein band 4.1 [Source:HGNC Sym
9	ILMN_180255	1.07	−0.77	0.43	HEBP1	heme binding protein 1 [Source:HGNC Symbol;Acc:HGNC:1
10	ILMN_324314	1.07	−0.85	0.66	KAT2B	lysine acetyltransferase 2B [Source:HGNC Symbol;Acc:HGN
11	ILMN_168062	1.05	−0.72	0.6	CREG1	cellular repressor of E1A stimulated genes 1 [Source:HGNC
12	ILMN_237239	1.03	−0.67	0.73	ALDH5A1	aldehyde dehydrogenase 5 family member A1 [Source:HGNC
13	ILMN_323663	1.02	−0.69	0.72	PIP4K2A	phosphatidylinositol−5−phosphate 4−kinase type 2 alpha [So
14	ILMN_171934	1.01	−0.76	0.73	WDR26	WD repeat domain 26 [Source:HGNC Symbol;Acc:HGNC:21
15	ILMN_178169	1	−0.51	0.52	TRAK2	trafficking kinesin protein 2 [Source:HGNC Symbol;Acc:HGN
16	ILMN_232342	1	−0.56	0.71	EPB41	erythrocyte membrane protein band 4.1 [Source:HGNC Sym
17	ILMN_167932	0.96	−0.65	0.77		
18	ILMN_238189	0.95	−0.77	0.69	OPTN	optineurin [Source:HGNC Symbol;Acc:HGNC:17142]
19	ILMN_166942	0.95	−0.83	0.52		Y−box binding protein 1 pseudogene 2 [Source:HGNC Symb
20	ILMN_174323	0.94	−0.46	0.68	MICALCL	MICAL C−terminal like [Source:HGNC Symbol;Acc:HGNC:25

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	1e−33	32 / 185	HM	HALLMARK_HEME_METABOLISM
2	8e−19	18 / 111	Refer	Chaussabel_2,3_Erythrocytes
3	2e−17	23 / 267	GSEA	IVANOVA_HEMATOPOIESIS_MATURE_CELL
4	3e−15	17 / 147	Lifest	Homuth_BMI−associated−genes_UP
5	2e−13	9 / 25	GSEA	VALK_AML_CLUSTER_8
6	9e−13	38 / 1265	GSEA	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
7	1e−12	123 / 9555	Colon	TssA_Colon
8	5e−11	101 / 7354	Colon	TssF_Colon
9	4e−10	111 / 8771	Chror	5_Tx_Melanocytes
10	1e−09	6 / 15	GSEA	STEINER_ERYTHROCYTE_MEMBRANE_GENES
11	2e−08	35 / 1547	Colon	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP
12	2e−08	94 / 7275	Lympl	HOPP_Txn_elongation
13	2e−08	106 / 8678	Colon	Quies3_Colon
14	2e−08	109 / 9054	Colon	Tx_Colon
15	5e−08	6 / 26	GSEA	VALK_AML_CLUSTER_7
16	7e−08	78 / 5699	Chror	6_EnhG_Melanocytes
17	8e−08	12 / 202	GSEA	JAATINEN_HEMATOPOIETIC_STEM_CELL_DN
18	1e−07	103 / 8568	Colon	TxWk_Colon
19	1e−07	89 / 6970	Chror	5_Tx_Neuronal_Progenitor
20	1e−07	12 / 210	GSEA	CHYLA_CBFA2T3_TARGETS_DN
21	1e−07	132 / 12298	Chror	2_TssA_Melanocytes
22	1e−07	9 / 103	GSEA	ACOSTA_PROLIFERATION_INDEPENDENT_MYC_TARGETS_DN
23	3e−07	136 / 12983	Chror	2_TssA_Neuronal_Progenitor
24	3e−07	73 / 5356	Lympl	HOPP_Txn_transition
25	7e−07	67 / 4822	CC	cytoplasm
26	1e−06	27 / 1206	Chror	6_EnhG_Neuronal_Progenitor
27	2e−06	107 / 9504	Brain	Overlap_fetal_midbrain_K9K27me3
28	2e−06	132 / 12741	Chror	7_Enh_Melanocytes
29	2e−06	76 / 5936	Brain	Overlap_fetal_midbrain_HetRpts
30	2e−06	96 / 8226	Lympl	HOPP_Active_promoter
31	2e−06	122 / 11455	Chror	2_TssA_Fibroblasts
32	2e−06	109 / 9815	Brain	Overlap_fetal_midbrain_ReprPC
33	4e−06	92 / 7854	Chror	5_Tx_Fibroblasts
34	4e−06	124 / 11836	Chror	3_TssF_Melanocytes
35	5e−06	4 / 15	Lifest	DUMEAUX_Red blood cells in non smokers literature genes up
36	6e−06	101 / 8990	Chror	15_Quies_Fibroblasts
37	6e−06	117 / 10999	Colon	TssWk_Colon
38	7e−06	6 / 59	GSEA	GUO_HEX_TARGETS_DN
39	8e−06	15 / 483	GSEA	MARTORIATI_MDM4_TARGETS_FETAL_LIVER_DN
40	8e−06	4 / 17	GSEA	WELCH_GATA1_TARGETS



Aging

Rank	p−value	#in/all	Geneset
1	0.2	2 / 111	HORVATH_aging_genes meth DOWN
2	1.0	0 / 142	HORVATH_aging_genes meth UP
3	1.0	0 / 58	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	2e−04	3 / 14	glutamate metabolic process
2	2e−04	3 / 14	organic cation transport
3	4e−04	3 / 19	apoptotic mitochondrial changes
4	5e−04	3 / 20	heme biosynthetic process
5	7e−04	3 / 22	response to light stimulus
6	2e−03	3 / 32	chaperone−mediated protein folding
7	2e−03	4 / 70	macroautophagy
8	3e−03	3 / 37	autophagosome assembly
9	4e−03	2 / 12	response to arsenic−containing substance
10	5e−03	2 / 13	motile cilium assembly
11	5e−03	2 / 13	regulation of TOR signaling
12	5e−03	6 / 197	in utero embryonic development
13	5e−03	2 / 14	cellular glucose homeostasis
14	6e−03	3 / 46	regulation of autophagy
15	7e−03	2 / 16	erythrocyte development

Brain

Rank	p−value	#in/all	Geneset
1	2e−06	107 / 9504	Overlap_fetal_midbrain_K9K27me3
2	2e−06	76 / 5936	Overlap_fetal_midbrain_HetRpts
3	2e−06	109 / 9815	Overlap_fetal_midbrain_ReprPC
4	8e−06	108 / 9917	Overlap_fetal_midbrain_ReprPCWk
5	3e−05	110 / 10430	Overlap_fetal_midbrain_Quies
6	5e−04	42 / 3164	Mid_Frontal_Lobe_ZNF
7	3e−02	12 / 818	Mid_Frontal_Lobe_Het
8	3e−02	21 / 1728	Fetal_ReprPCWk
9	5e−02	6 / 328	Fetal_Het
10	6e−02	29 / 2709	Mid_Frontal_Lobe_HetRpts
11	1e−01	10 / 796	Overlap_fetal_midbrain_ZNF
12	1e−01	13 / 1162	Fetal_Enh
13	2e−01	3 / 180	Overlap_fetal_midbrain_Het
14	2e−01	8 / 681	Overlap_fetal_midbrain_EnhP
15	2e−01	10 / 906	Fetal_HetRpts

Cancer

Rank	p−value	#in/all	Geneset
1	0.005	2 / 13	GENTLES_modul12
2	0.006	1 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
3	0.010	7 / 301	SPANG_BCL6−index2
4	0.027	3 / 82	PanCan_JAK−ST_geneset_nanostring
5	0.031	0 / 14	LIU_PROSTATE_CANCER_UP
6	0.053	4 / 178	SPANG_LPS−index2
7	0.077	3 / 125	PanCan_CC+Apop_geneset_nanostring
8	0.098	1 / 13	GENTLES_modul2
9	0.112	1 / 15	GENTLES_modul17
10	0.120	1 / 16	GENTLES_modul14
11	0.162	2 / 91	PanCan_TXmisReg_geneset_nanostring
12	0.174	1 / 24	PanCan_Notch_geneset_nanostring
13	0.273	0 / 15	LIU_PROSTATE_CANCER_DN
14	0.276	6 / 554	Lembcke_Colonic Inflammation
15	0.293	2 / 136	PanCan_RAS_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	7e−07	67 / 4822	cytoplasm
2	8e−05	5 / 56	autophagosome
3	1e−04	24 / 1304	mitochondrion
4	4e−04	58 / 4828	nucleus
5	8e−04	6 / 138	mitochondrial outer membrane
6	2e−03	8 / 287	mitochondrial matrix
7	4e−03	6 / 185	transcription factor complex
8	4e−03	3 / 40	cytoplasmic side of plasma membrane
9	5e−03	2 / 13	A band
10	6e−03	36 / 2979	cytosol
11	7e−03	2 / 16	sperm principal piece
12	9e−03	31 / 2535	nucleoplasm
13	1e−02	2 / 20	histone acetyltransferase complex
14	1e−02	2 / 21	autophagosome membrane
15	1e−02	2 / 23	cortical cytoskeleton

Chr

Rank	p−value	#in/all	Geneset
1	0.04	26 / 2323	Chr 1
2	0.06	6 / 342	Chr 18
3	0.06	12 / 902	Chr 4
4	0.23	10 / 959	Chr 16
5	0.29	9 / 904	Chr 10
6	0.31	11 / 1160	Chr 12
7	0.42	5 / 536	Chr 22
8	0.45	10 / 1170	Chr 7
9	0.49	8 / 954	Chr 9
10	0.55	5 / 619	Chr 20
11	0.60	10 / 1318	Chr 17
12	0.65	3 / 422	Chr 13
13	0.73	5 / 768	Chr 14
14	0.75	8 / 1211	Chr 6
15	0.75	10 / 1492	Chr 2

Chromatin states

Rank	p−value	#in/all	Geneset
1	4e−10	111 / 8771	5_Tx_Melanocytes
2	7e−08	78 / 5699	6_EnhG_Melanocytes
3	1e−07	89 / 6970	5_Tx_Neuronal_Progenitor
4	1e−07	132 / 12298	2_TssA_Melanocytes
5	3e−07	136 / 12983	2_TssA_Neuronal_Progenitor
6	1e−06	27 / 1206	6_EnhG_Neuronal_Progenitor
7	2e−06	132 / 12741	7_Enh_Melanocytes
8	2e−06	122 / 11455	2_TssA_Fibroblasts
9	4e−06	92 / 7854	5_Tx_Fibroblasts
10	4e−06	124 / 11836	3_TssF_Melanocytes
11	6e−06	101 / 8990	15_Quies_Fibroblasts
12	3e−05	121 / 11847	7_Enh_Neuronal_Progenitor
13	4e−05	95 / 8613	7_Enh_Fibroblasts
14	5e−05	103 / 9635	3_TssF_Fibroblasts
15	7e−05	124 / 12393	15_Quies_Neuronal_Progenitor

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−12	123 / 9555	TssA_Colon
2	5e−11	101 / 7354	TssF_Colon
3	2e−08	35 / 1547	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
4	2e−08	106 / 8678	Quies3_Colon
5	2e−08	109 / 9054	Tx_Colon
6	1e−07	103 / 8568	TxWk_Colon
7	6e−06	117 / 10999	TssWk_Colon
8	1e−05	114 / 10779	Enh_Colon
9	3e−05	74 / 6138	TssD2_Colon
10	3e−05	67 / 5373	EnhWk1_Colon
11	3e−04	20 / 1069	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
12	1e−03	49 / 4018	EnhWk2_Colon
13	1e−03	23 / 1468	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
14	2e−03	8 / 278	Kosinski_top−crypt−long−list
15	3e−03	36 / 2845	TxEnhG1_Colon

Glio

Rank	p−value	#in/all	Geneset
1	9e−04	4 / 55	Stuehler_Proteins_up_in_STS
2	6e−03	14 / 820	Sturm_GBM_Meth_overexpression_E_G34_UP
3	6e−03	2 / 15	WILLSCHER_GBM_STSwt_proteomics−O_UP
4	8e−03	2 / 17	Christensen_hypomethylated_in_grade2_astrocytoma
5	2e−02	22 / 1777	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
6	3e−02	2 / 37	Christensen_hypomethylated_in_ependymoma
7	4e−02	4 / 157	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
8	7e−02	2 / 56	Christensen_hypomethylated_in_primary_glioblastoma
9	8e−02	1 / 11	VERHAAK_Brain
10	8e−02	1 / 11	KIM amplified & overexpressed in LTS
11	9e−02	22 / 2043	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
12	1e−01	1 / 13	Donson−immune cell intra signaling−associated with LTS in HGA
13	1e−01	2 / 68	Christensen_hypomethylated_in_secondary_glioblastoma
14	1e−01	1 / 14	astrocytes_glio
15	1e−01	5 / 316	WILLSCHER_GBM_Verhaak−PNwt & CL_up

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−17	23 / 267	IVANOVA_HEMATOPOIESIS_MATURE_CELL
2	2e−13	9 / 25	VALK_AML_CLUSTER_8
3	9e−13	38 / 1265	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
4	1e−09	6 / 15	STEINER_ERYTHROCYTE_MEMBRANE_GENES
5	5e−08	6 / 26	VALK_AML_CLUSTER_7
6	8e−08	12 / 202	JAATINEN_HEMATOPOIETIC_STEM_CELL_DN
7	1e−07	12 / 210	CHYLA_CBFA2T3_TARGETS_DN
8	1e−07	9 / 103	ACOSTA_PROLIFERATION_INDEPENDENT_MYC_TARGETS_DN
9	7e−06	6 / 59	GUO_HEX_TARGETS_DN
10	8e−06	15 / 483	MARTORIATI_MDM4_TARGETS_FETAL_LIVER_DN
11	8e−06	4 / 17	WELCH_GATA1_TARGETS
12	1e−05	8 / 131	LINDGREN_BLADDER_CANCER_CLUSTER_2A_DN
13	1e−05	29 / 1535	BLALOCK_ALZHEIMERS_DISEASE_UP
14	1e−05	4 / 19	OUYANG_PROSTATE_CANCER_PROGRESSION_DN
15	2e−05	4 / 20	SCHURINGA_STAT5A_TARGETS_UP

HM

Rank	p−value	#in/all	Geneset
1	1e−33	32 / 185	HALLMARK_HEME_METABOLISM
2	1e−02	5 / 175	HALLMARK_XENOBIOTIC_METABOLISM
3	1e−02	5 / 176	HALLMARK_ADIPOGENESIS
4	2e−02	5 / 189	HALLMARK_HYPOXIA
5	3e−02	4 / 151	HALLMARK_APOPTOSIS
6	4e−02	2 / 41	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
7	5e−02	4 / 172	HALLMARK_INTERFERON_GAMMA_RESPONSE
8	6e−02	4 / 185	HALLMARK_MTORC1_SIGNALING
9	6e−02	4 / 185	HALLMARK_P53_PATHWAY
10	6e−02	4 / 186	HALLMARK_IL2_STAT5_SIGNALING
11	1e−01	3 / 137	HALLMARK_UV_RESPONSE_UP
12	2e−01	3 / 170	HALLMARK_MYC_TARGETS_V1
13	2e−01	2 / 91	HALLMARK_ANDROGEN_RESPONSE
14	2e−01	3 / 177	HALLMARK_MITOTIC_SPINDLE
15	2e−01	2 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING

Lifestyle

Rank	p−value	#in/all	Geneset
1	3e−15	17 / 147	Homuth_BMI−associated−genes_UP
2	5e−06	4 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
3	1e−01	1 / 17	DUMEAUX_High bmi enriched genes
4	1e+00	0 / 94	DUMEAUX_Smoking enriched genes
5	1e+00	0 / 10	DUMEAUX_Smoking literature genes up
6	1e+00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
7	1e+00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
8	1e+00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
9	1e+00	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
10	1e+00	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
11	1e+00	0 / 10	DUMEAUX_Women normal BMI literature genes up
12	1e+00	0 / 31	DUMEAUX_Fasting enriched genes
13	1e+00	0 / 211	Homuth_BMI−associated−genes_DN
14	1e+00	0 / 18	Huan_blood−pressure_SBP−signature
15	1e+00	0 / 16	Huan_blood−pressure_DBP−signature

Lymphnoma

Rank	p−value	#in/all	Geneset
1	2e−08	94 / 7275	HOPP_Txn_elongation
2	3e−07	73 / 5356	HOPP_Txn_transition
3	2e−06	96 / 8226	HOPP_Active_promoter
4	9e−06	12 / 318	Hopp_June14_MMML937 tumors+controls_group.overexpression_H_GC−B−
5	1e−05	12 / 331	WIRTH_lymphoma937_spot H
6	2e−04	88 / 8098	HOPP_Weak_promoter
7	2e−04	82 / 7448	HOPP_Strong_enhancer
8	2e−03	2 / 8	YAMANE_AICDA_targets_nonrecruited
9	3e−03	4 / 77	Aukema_BCL2 DN_BCL6 UP
10	5e−03	72 / 6959	HOPP_Weak_enhancer
11	5e−03	18 / 1169	SPANG_BCR DN
12	1e−02	67 / 6559	HOPP_Weak_txn
13	2e−02	4 / 121	SPANG_LPS 6hrs UP
14	5e−02	6 / 331	SPANG_CD40 6hrs UP
15	6e−02	1 / 8	MASCQUE_ABC UP

Melanoma

Rank	p−value	#in/all	Geneset
1	1	0 / 30	Hugo_melanoma−all−MET_UP
2	1	0 / 54	Hugo_melanoma−all−MET_DN
3	1	0 / 43	Hugo_melanoma−BRAFmut−MET_UP
4	1	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
5	1	0 / 27	Hugo_melanoma−all−LEF1_UP
6	1	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

MF

Rank	p−value	#in/all	Geneset
1	2e−05	4 / 20	2 iron, 2 sulfur cluster binding
2	7e−05	10 / 274	transcription factor binding
3	6e−04	3 / 21	ferrous iron binding
4	7e−04	9 / 301	ubiquitin−protein transferase activity
5	1e−03	3 / 25	spectrin binding
6	2e−03	90 / 8818	protein binding
7	3e−03	7 / 232	ligase activity
8	3e−03	3 / 35	4 iron, 4 sulfur cluster binding
9	3e−03	2 / 11	acetyltransferase activity
10	3e−03	2 / 11	ribosomal small subunit binding
11	4e−03	3 / 42	manganese ion binding
12	5e−03	2 / 13	GABA receptor binding
13	6e−03	9 / 413	protein heterodimerization activity
14	1e−02	2 / 22	polyubiquitin binding
15	1e−02	4 / 115	actin filament binding

miRNA Disease

Rank	p−value	#in/all	Geneset
1	1	0 / 7	Thyroid carcinoma, papillary
2	1	0 / 123	Pancreatic cancer
3	1	0 / 68	Glioblastoma multiforme, somatic
4	1	0 / 63	Gastrointestinal
5	1	0 / 3	Pituitary adenoma
6	1	0 / 116	Cancer
7	1	0 / 95	Colorectal cancer
8	1	0 / 2	Adenomas, multiple colorectal
9	1	0 / 124	Prostate cancer
10	1	0 / 48	Alzheimer disease, susceptibility to
11	1	0 / 7	Schizophrenia, susceptibility to
12	1	0 / 20	Parkinson disease
13	1	0 / 65	Hepatocellular carcinoma
14	1	0 / 3	Down syndrome, risk of
15	1	0 / 127	Melanoma and neural system tumor syndrome

miRNA target

Rank	p−value	#in/all	Geneset
1	3e−05	6 / 75	hsa−miR−375
2	2e−04	7 / 155	hsa−miR−450b−5p
3	4e−04	6 / 119	hsa−miR−105
4	5e−04	4 / 47	hsa−miR−370
5	9e−04	6 / 141	hsa−miR−522
6	2e−03	4 / 64	hsa−miR−9*
7	2e−03	7 / 216	hsa−miR−548m
8	2e−03	6 / 160	hsa−miR−512−3p
9	3e−03	11 / 516	hsa−miR−15a
10	3e−03	6 / 177	hsa−miR−374a
11	3e−03	7 / 239	hsa−miR−214
12	3e−03	4 / 76	hsa−miR−513c
13	4e−03	5 / 128	hsa−miR−335
14	4e−03	3 / 39	hsa−miR−1308
15	4e−03	3 / 40	hsa−miR−450a

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.09	1 / 12	BENTINK_src.2
2	1.00	0 / 14	GUSTAFSON_PI3K_UP
3	1.00	0 / 15	GUSTAFSON_PI3K_DN
4	1.00	0 / 13	BENTINK_e2f3.1
5	1.00	0 / 13	BENTINK_e2f3.2
6	1.00	0 / 13	BENTINK_myc.1
7	1.00	0 / 12	BENTINK_ras.1
8	1.00	0 / 11	BENTINK_ras.4
9	1.00	0 / 14	BENTINK_ras.6
10	1.00	0 / 13	BENTINK_src.10
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Reference Signatures

Rank	p−value	#in/all	Geneset
1	8e−19	18 / 111	Chaussabel_2,3_Erythrocytes
2	9e−06	25 / 1194	PROTEINATLAS_stomach
3	1e−05	5 / 39	Chaussabel_2,2_Neutrophils
4	3e−05	23 / 1118	PROTEINATLAS_placenta
5	4e−05	20 / 912	PROTEINATLAS_urinary bladder
6	6e−05	14 / 514	PROTEINATLAS_vagina
7	1e−04	16 / 695	PROTEINATLAS_bone marrow
8	2e−04	22 / 1176	PROTEINATLAS_duodenum
9	7e−04	11 / 429	PROTEINATLAS_soft tissue
10	7e−04	13 / 571	PROTEINATLAS_oral mucosa
11	1e−03	11 / 465	PROTEINATLAS_liver
12	2e−03	13 / 640	PROTEINATLAS_parathyroid gland
13	2e−03	14 / 740	PROTEINATLAS_esophagus
14	3e−03	12 / 598	PROTEINATLAS_prostate
15	3e−03	7 / 242	Chaussabel_3,2_Inflammation I

Telomeres

Rank	p−value	#in/all	Geneset
1	1	0 / 13	Alternative lengthening of telomeres
2	1	0 / 27	Nabetani_alt len telomeres_genes_ko
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	1e−05	42 / 2704	ICGC_Pbx3_targets
2	2e−05	58 / 4362	ICGC_Creb1_targets
3	5e−05	27 / 1498	ICGC_Ets1_targets
4	1e−04	76 / 6578	ICGC_Pou2_targets
5	1e−04	66 / 5466	ICGC_Nficsc81335_targets
6	1e−04	76 / 6616	ICGC_Pax5_targets
7	1e−04	70 / 5961	ICGC_Pol24_targets
8	1e−04	33 / 2133	ICGC_Mef2_targets
9	2e−04	55 / 4345	ICGC_Zeb1_targets
10	2e−04	60 / 4890	ICGC_Bclaf101388_targets
11	2e−04	61 / 5067	ICGC_Taf1_targets
12	3e−04	65 / 5518	ICGC_Stat5_targets
13	3e−04	64 / 5442	ICGC_Pmlsc71910_targets
14	3e−04	55 / 4468	ICGC_Egr1_targets
15	4e−04	63 / 5383	ICGC_Sp1_targets

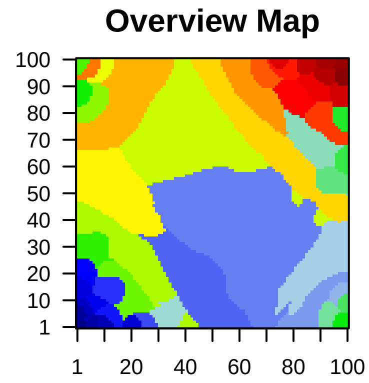
K−Means Cluster

Spot Summary: C

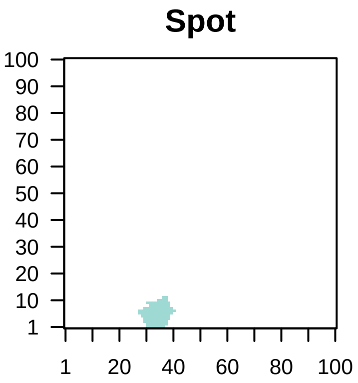
metagenes = 106
genes = 611

<r> metagenes = 0.97
<r> genes = 0.16
beta: r2= 2.12 / log p= −Inf

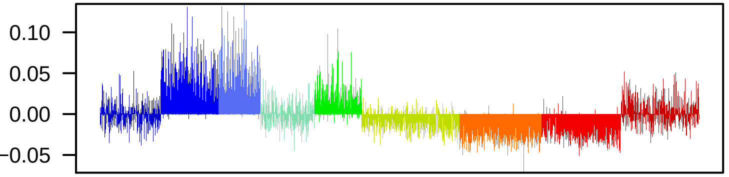
samples with spot = 7 (0.2 %)
A C * : 2 (0.6 %)
A C F * : 5 (2.1 %)



Overview Map



Spot

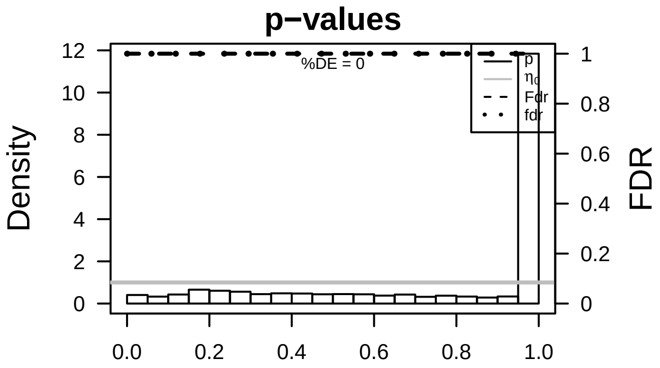


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_323504	0.62	−0.31	0.19		
2	ILMN_325034	0.51	−0.43	0.15		
3	ILMN_175558	0.48	−0.26	0.41		
4	ILMN_206143	0.42	−0.21	0.23	MEG3	maternally expressed 3 (non−protein coding) [Source:HGNC
5	ILMN_174062	0.42	−0.23	0.43		golgin A6 family−like 17, pseudogene [Source:HGNC Symbol
6	ILMN_172696	0.42	−0.23	0.47	OR51S1	olfactory receptor family 51 subfamily S member 1 [Source:H
7	ILMN_169560	0.38	−0.26	0.42	GOLGA6L4	golgin A6 family−like 4 [Source:HGNC Symbol;Acc:HGNC:27
8	ILMN_209927	0.38	−0.24	0.31	HTRA4	HtrA serine peptidase 4 [Source:HGNC Symbol;Acc:HGNC:2
9	ILMN_172728	0.38	−0.21	0.47	EVPL	envoplakin [Source:HGNC Symbol;Acc:HGNC:3503]
10	ILMN_180377	0.38	−0.29	0.31	STK16	serine/threonine kinase 16 [Source:HGNC Symbol;Acc:HGN
11	ILMN_176502	0.37	−0.27	0.44	TOP3B	topoisomerase (DNA) III beta [Source:HGNC Symbol;Acc:HG
12	ILMN_240653	0.37	−0.22	0.39		
13	ILMN_324082	0.37	−0.24	0.31		
14	ILMN_204294	0.37	−0.23	0.34	TMEM159	transmembrane protein 159 [Source:HGNC Symbol;Acc:HGN
15	ILMN_165731	0.36	−0.25	0.2	POLR2J	RNA polymerase II subunit J [Source:HGNC Symbol;Acc:HG
16	ILMN_169347	0.36	−0.21	0.23	KLHL35	kelch like family member 35 [Source:HGNC Symbol;Acc:HGN
17	ILMN_235909	0.35	−0.25	0.34	SS18	SS18, nBAF chromatin remodeling complex subunit [Source:
18	ILMN_239949	0.35	−0.31	0.32		
19	ILMN_223360	0.35	−0.26	0.51	ECSIT	ECSIT signalling integrator [Source:HGNC Symbol;Acc:HGN
20	ILMN_330945	0.34	−0.21	0.32	RNU4−1	RNA, U4 small nuclear 1 [Source:HGNC Symbol;Acc:HGNC:

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	7e−08	84 / 3068	Chror	8_EnhP_Fibroblasts
2	7e−08	105 / 4169	Chror	10_ReprPC_Fibroblasts
3	2e−07	106 / 4304	Chror	9_ReprPCWk_Melanocytes
4	8e−07	100 / 4107	Chror	9_ReprPCWk_Fibroblasts
5	1e−06	91 / 3639	Chror	1_TssP_Fibroblasts
6	2e−06	71 / 2660	Chror	8_EnhP_Melanocytes
7	6e−06	74 / 2894	Colon	TssP_Colon
8	6e−06	71 / 2740	Colon	ReprPCWk_Colon
9	1e−05	78 / 3173	Colon	ReprPC_Colon
10	2e−05	84 / 3523	Chror	1_TssP_Melanocytes
11	2e−05	82 / 3438	Chror	10_ReprPC_Melanocytes
12	4e−05	72 / 2939	Lympl	HOPP_Poised_promoter
13	5e−05	115 / 5384	Lympl	HOPP_Repressed
14	7e−05	15 / 302	GSEA	SHEN_SMARCA2_TARGETS_DN
15	1e−04	7 / 72	MF	protein binding, bridging
16	1e−04	62 / 2516	Chror	11_K9K27me3_Melanocytes
17	1e−04	9 / 125	GSEA	MIKKELSEN_ES_ICP_WITH_H3K4ME3_AND_H3K27ME3
18	5e−04	3 / 11	BP	organic anion transport
19	8e−04	47 / 1893	Brain	Overlap_fetal_midbrain_TssF
20	1e−03	3 / 14	MF	organic anion transmembrane transporter activity
21	1e−03	6 / 77	GSEA	LEE_TARGETS_OF_PTCH1_AND_SUFU_DN
22	1e−03	86 / 4112	Brain	Mid_Frontal_Lobe_ReprPC
23	2e−03	4 / 34	GSEA	DACOSTA_ERCC3_ALLELE_XPCS_VS_TTD_DN
24	2e−03	3 / 17	CC	cell−cell contact zone
25	2e−03	7 / 117	GSEA	MIKKELSEN_IPS_ICP_WITH_H3K4ME3_AND_H327ME3
26	2e−03	66 / 3046	Brain	Fetal_TssA
27	4e−03	36 / 1476	Brain	Overlap_fetal_midbrain_TxTrans
28	4e−03	57 / 2620	Chror	1_TssP_Neuronal_Progenitor
29	4e−03	5 / 70	GSEA	NAKAYAMA_SOFT_TISSUE_TUMORS_PCA1_DN
30	5e−03	13 / 366	Colon	K9K27me3_Colon
31	5e−03	15 / 453	GSEA	BROWNE_HCMV_INFECTION_48HR_DN
32	5e−03	6 / 101	GSEA	ROPERO_HDAC2_TARGETS
33	5e−03	4 / 46	BP	cardiac conduction
34	5e−03	4 / 46	BP	peptide cross−linking
35	5e−03	4 / 46	GSEA	PID_ARF6_TRAFFICKING_PATHWAY
36	6e−03	3 / 24	GSEA	PID_INTEGRIN_A9B1_PATHWAY
37	6e−03	29 / 1143	GSEA	YOSHIMURA_MAPK8_TARGETS_UP
38	6e−03	21 / 746	GSEA	MARTENS_TRETINOIN_RESPONSE_UP
39	6e−03	2 / 8	GSEA	SIMBULAN_UV_RESPONSE_NORMAL_UP
40	6e−03	5 / 76	BP	integrin−mediated signaling pathway



p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.2	3 / 111	HORVATH_aging_genes meth DOWN
2	0.6	1 / 58	TESCHENDORFF_age_hypermethylated
3	0.6	2 / 142	HORVATH_aging_genes meth UP
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	5e−04	3 / 11	organic anion transport
2	5e−03	4 / 46	cardiac conduction
3	5e−03	4 / 46	peptide cross−linking
4	6e−03	5 / 76	integrin−mediated signaling pathway
5	7e−03	4 / 49	regulation of protein localization
6	8e−03	5 / 80	wound healing
7	8e−03	3 / 27	positive regulation of vasodilation
8	1e−02	2 / 10	auditory receptor cell stereocilium organization
9	1e−02	3 / 29	negative regulation of blood pressure
10	1e−02	2 / 11	arachidonic acid secretion
11	1e−02	5 / 90	negative regulation of cell migration
12	1e−02	3 / 32	embryonic forelimb morphogenesis
13	2e−02	2 / 13	cell communication by electrical coupling involved in cardiac conduction
14	2e−02	2 / 13	endothelial cell differentiation
15	2e−02	2 / 13	negative regulation of protein secretion

Brain

Rank	p−value	#in/all	Geneset
1	8e−04	47 / 1893	Overlap_fetal_midbrain_TssF
2	1e−03	86 / 4112	Mid_Frontal_Lobe_ReprPC
3	2e−03	66 / 3046	Fetal_TssA
4	4e−03	36 / 1476	Overlap_fetal_midbrain_TxTrans
5	8e−03	22 / 819	Overlap_fetal_midbrain_TssP
6	1e−02	46 / 2127	Mid_Frontal_Lobe_K9K27me3
7	2e−02	16 / 578	Fetal_Tx
8	2e−02	26 / 1119	Overlap_fetal_midbrain_TssA
9	6e−02	12 / 465	Mid_Frontal_Lobe_TxTrans
10	7e−02	28 / 1360	Mid_Frontal_Lobe_TssP
11	9e−02	4 / 110	Overlap_fetal_midbrain_Tx
12	1e−01	19 / 924	Mid_Frontal_Lobe_TssF
13	2e−01	7 / 307	Fetal_ReprPC
14	2e−01	18 / 937	Fetal_EnhG
15	2e−01	47 / 2700	Fetal_TxTrans

Cancer

Rank	p−value	#in/all	Geneset
1	0.02	2 / 15	LIU_PROSTATE_CANCER_DN
2	0.08	0 / 14	LIU_COMMON_CANCER_GENES
3	0.10	3 / 73	SHAUGHNESSY_MM high risk
4	0.15	0 / 14	LIU_PROSTATE_CANCER_UP
5	0.19	1 / 14	GENTLES_modul13
6	0.20	4 / 150	PanCan_MAPK_geneset_nanostring
7	0.21	1 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
8	0.21	1 / 15	GENTLES_modul17
9	0.22	1 / 16	BEN−PORATH_DN
10	0.22	1 / 16	GENTLES_modul16
11	0.33	2 / 76	PanCan_Wnt_geneset_nanostring
12	0.35	1 / 28	PanCan_HH_geneset_nanostring
13	0.48	9 / 554	Lembcke_Colonic Inflammation
14	0.51	1 / 46	PanCan_DNARepair_geneset_nanostring
15	0.54	2 / 117	PanCan_Driver_Gene_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	0.002	3 / 17	cell−cell contact zone
2	0.007	4 / 49	platelet alpha granule lumen
3	0.007	9 / 220	synapse
4	0.009	3 / 28	voltage−gated calcium channel complex
5	0.013	4 / 59	presynaptic membrane
6	0.015	72 / 3662	plasma membrane
7	0.016	2 / 13	basal part of cell
8	0.030	4 / 76	extrinsic component of membrane
9	0.031	12 / 423	cell junction
10	0.032	4 / 78	Golgi lumen
11	0.035	3 / 47	adherens junction
12	0.038	4 / 82	apical part of cell
13	0.048	27 / 1252	integral component of plasma membrane
14	0.052	2 / 24	integrin complex
15	0.055	4 / 93	blood microparticle

Chr

Rank	p−value	#in/all	Geneset
1	0.07	29 / 1411	Chr 11
2	0.10	20 / 959	Chr 16
3	0.16	13 / 619	Chr 20
4	0.18	23 / 1217	Chr 3
5	0.25	21 / 1160	Chr 12
6	0.27	7 / 342	Chr 18
7	0.29	6 / 289	Chr 21
8	0.38	22 / 1318	Chr 17
9	0.40	13 / 769	Chr 15
10	0.40	20 / 1211	Chr 6
11	0.44	9 / 536	Chr 22
12	0.47	7 / 422	Chr 13
13	0.53	18 / 1170	Chr 7
14	0.66	21 / 1467	Chr 19
15	0.69	21 / 1492	Chr 2

Chromatin states

Rank	p−value	#in/all	Geneset
1	7e−08	84 / 3068	8_EnhP_Fibroblasts
2	7e−08	105 / 4169	10_ReprPC_Fibroblasts
3	2e−07	106 / 4304	9_ReprPCWk_Melanocytes
4	8e−07	100 / 4107	9_ReprPCWk_Fibroblasts
5	1e−06	91 / 3639	1_TssP_Fibroblasts
6	2e−06	71 / 2660	8_EnhP_Melanocytes
7	2e−05	84 / 3523	1_TssP_Melanocytes
8	2e−05	82 / 3438	10_ReprPC_Melanocytes
9	1e−04	62 / 2516	11_K9K27me3_Melanocytes
10	4e−03	57 / 2620	1_TssP_Neuronal_Progenitor
11	1e−02	49 / 2297	10_ReprPC_Neuronal_Progenitor
12	2e−02	72 / 3691	9_ReprPCWk_Neuronal_Progenitor
13	3e−02	38 / 1789	8_EnhP_Neuronal_Progenitor
14	3e−02	42 / 2031	12_Het_Melanocytes
15	4e−02	29 / 1324	13_HetRpts_Fibroblasts

Colon Cancer

Rank	p−value	#in/all	Geneset
1	6e−06	74 / 2894	TssP_Colon
2	6e−06	71 / 2740	ReprPCWk_Colon
3	1e−05	78 / 3173	ReprPC_Colon
4	5e−03	13 / 366	K9K27me3_Colon
5	7e−03	43 / 1895	EnhP_Colon
6	2e−02	5 / 104	Marisa_CRC−cluster−h
7	3e−02	11 / 377	Lembcke_TCGA_meth_kmeans_H_CIMP.L_UP_CIMP.H_DN
8	7e−02	53 / 2810	EnhA_Colon
9	7e−02	12 / 479	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_
10	1e−01	158 / 9530	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP_
11	1e−01	6 / 217	Lembcke_TCGA_meth_kmeans_B_Cluster4_DN
12	1e−01	10 / 425	Lembcke_TCGA_meth_kmeans_E_CIMP.H_UP_
13	1e−01	24 / 1216	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_
14	1e−01	1 / 9	Marisa_CRC−C4
15	1e−01	13 / 599	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN

Glio

Rank	p−value	#in/all	Geneset
1	0.009	7 / 150	Hopp_Sturm_GBM_Epi3_E_G34_UP
2	0.009	15 / 487	Hopp_Sturm_GBM_Epi3_B_adult_UP_G34_DN
3	0.019	32 / 1417	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
4	0.022	2 / 15	VERHAAK_CL subtype
5	0.025	59 / 2988	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
6	0.041	4 / 84	Weller_LGG_gradeII−vs−III_UP
7	0.044	20 / 859	Hopp_Sturm_GBM_Epi3_A_adult_fetus_UP_G34_DN
8	0.078	6 / 193	Hopp_Sturm_GBM_Epi3_F_RTK II_UP_adult_fetus_K27_DN
9	0.078	3 / 65	cultured astroglia vs. in vivo astrocytes
10	0.086	2 / 32	WILLSCHER_GBM_proteomics_wtOnly_SpotC
11	0.101	2 / 35	Colman_survival_associated
12	0.113	5 / 166	Sturm_GBM_Meth_overexpression_B_adult_UP
13	0.130	1 / 9	Colman_survival_robust
14	0.130	1 / 9	WILLSCHER_GBM_LTSmut_proteomics−A_UP
15	0.157	1 / 11	Mukasa_UP_in_Oligodendroglioma_with_1intact

GSEA C2

Rank	p−value	#in/all	Geneset
1	7e−05	15 / 302	SHEN_SMARCA2_TARGETS_DN
2	1e−04	9 / 125	MIKKELSEN_ES_ICP_WITH_H3K4ME3_AND_H3K27ME3
3	1e−03	6 / 77	LEE_TARGETS_OF_PTCH1_AND_SUFU_DN
4	2e−03	4 / 34	DACOSTA_ERCC3_ALLELE_XPCS_VS_TTD_DN
5	2e−03	7 / 117	MIKKELSEN_IPS_ICP_WITH_H3K4ME3_AND_H327ME3
6	4e−03	5 / 70	NAKAYAMA_SOFT_TISSUE_TUMORS_PCA1_DN
7	5e−03	15 / 453	BROWNE_HCMV_INFECTION_48HR_DN
8	5e−03	6 / 101	ROPERO_HDAC2_TARGETS
9	5e−03	4 / 46	PID_ARF6_TRAFFICKING_PATHWAY
10	6e−03	3 / 24	PID_INTEGRIN_A9B1_PATHWAY
11	6e−03	29 / 1143	YOSHIMURA_MAPK8_TARGETS_UP
12	6e−03	21 / 746	MARTENS_TRETINOIN_RESPONSE_UP
13	6e−03	2 / 8	SIMBULAN_UV_RESPONSE_NORMAL_UP
14	8e−03	7 / 147	NIKOLSKY_BREAST_CANCER_11Q12_Q14_AMPLICON
15	8e−03	2 / 9	REACTOME_RECYCLING_OF_BILE_ACIDS_AND_SALTS

HM

Rank	p−value	#in/all	Geneset
1	0.02	7 / 177	HALLMARK_KRAS_SIGNALING_DN
2	0.02	7 / 183	HALLMARK_APICAL_JUNCTION
3	0.07	6 / 186	HALLMARK_MYOGENESIS
4	0.26	3 / 116	HALLMARK_SPERMATOGENESIS
5	0.29	4 / 177	HALLMARK_MITOTIC_SPINDLE
6	0.33	4 / 189	HALLMARK_HYPOXIA
7	0.44	1 / 37	HALLMARK_PANCREAS_BETA_CELLS
8	0.46	1 / 40	HALLMARK_WNT_BETA_CATENIN_SIGNALING
9	0.47	1 / 41	HALLMARK_APICAL_SURFACE
10	0.51	3 / 176	HALLMARK_ADIPOGENESIS
11	0.51	3 / 176	HALLMARK_KRAS_SIGNALING_UP
12	0.54	3 / 185	HALLMARK_P53_PATHWAY
13	0.55	3 / 186	HALLMARK_ESTROGEN_RESPONSE_EARLY
14	0.56	3 / 191	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
15	0.58	2 / 127	HALLMARK_COAGULATION

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.4	1 / 31	DUMEAUX_Fasting enriched genes
2	0.4	1 / 32	Marjolein_ageing−genes_DN
3	0.4	2 / 94	DUMEAUX_Smoking enriched genes
4	0.7	2 / 147	Homuth_BMI−associated−genes_UP
5	0.8	2 / 211	Homuth_BMI−associated−genes_DN
6	1.0	0 / 10	DUMEAUX_Smoking literature genes up
7	1.0	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
8	1.0	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
9	1.0	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
10	1.0	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
11	1.0	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
12	1.0	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
13	1.0	0 / 10	DUMEAUX_Women normal BMI literature genes up
14	1.0	0 / 17	DUMEAUX_High bmi enriched genes
15	1.0	0 / 18	Huan_blood−pressure_SBP−signature

Lymphoma

Rank	p−value	#in/all	Geneset
1	4e−05	72 / 2939	HOPP_Poised_promoter
2	5e−05	115 / 5384	HOPP_Repressed
3	1e−02	2 / 11	DAVE_BL UP
4	5e−02	7 / 220	Hopp_June14_MMML937 tumors+controls_group.overexpression_B_cell line_
5	6e−02	3 / 57	LENZ_Stromal signature 2
6	7e−02	7 / 232	WIRTH_lymphoma937_spot B
7	7e−02	51 / 2701	HOPP_Repetitive
8	9e−02	3 / 70	LEE_Developmental_regulators
9	2e−01	4 / 137	Hopp_June14_MMML937 tumors+controls_group.overexpression_G_tonsil_U
10	2e−01	4 / 138	WIRTH_lymphoma937_spot G
11	2e−01	2 / 60	SPANG_BAFF 9hrs DN
12	2e−01	3 / 109	ROSOLOWSKI_blue total
13	3e−01	1 / 19	DAVE_Immune response 2
14	3e−01	9 / 450	Hopp_June14_MMML937 tumors+controls_group.overexpression_I_MM_GC-
15	3e−01	9 / 464	WIRTH_lymphoma937_spot I

Melanoma

Rank	p−value	#in/all	Geneset
1	0.1	1 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
2	0.3	1 / 27	Hugo_melanoma−all−LEF1_UP
3	0.4	1 / 30	Hugo_melanoma−all−MET_UP
4	0.5	1 / 43	Hugo_melanoma−BRAFmut−MET_UP
5	0.6	1 / 54	Hugo_melanoma−all−MET_DN
6	1.0	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

MF

Rank	p−value	#in/all	Geneset
1	1e−04	7 / 72	protein binding, bridging
2	1e−03	3 / 14	organic anion transmembrane transporter activity
3	1e−02	2 / 10	GDP−dissociation inhibitor activity
4	2e−02	2 / 13	GTPase regulator activity
5	2e−02	2 / 13	Rac guanyl−nucleotide exchange factor activity
6	2e−02	2 / 13	transmembrane receptor protein tyrosine phosphatase activity
7	3e−02	2 / 18	DNA helicase activity
8	3e−02	3 / 45	cytoskeletal protein binding
9	3e−02	2 / 19	cyclin binding
10	3e−02	2 / 19	sodium−independent organic anion transmembrane transporter activity
11	4e−02	3 / 48	protein kinase inhibitor activity
12	5e−02	2 / 23	laminin binding
13	6e−02	11 / 413	protein heterodimerization activity
14	6e−02	2 / 25	protein phosphatase inhibitor activity
15	6e−02	3 / 57	collagen binding

miRNA Disease

Rank	p−value	#in/all	Geneset
1	0.4	1 / 29	Neuroblastoma
2	0.5	1 / 48	Alzheimer disease, susceptibility to
3	0.5	1 / 48	Gastric cancer
4	0.5	1 / 48	Multiple myeloma
5	0.5	2 / 116	Cancer
6	0.6	2 / 120	Hematological
7	0.6	2 / 123	Pancreatic cancer
8	0.6	2 / 124	Prostate cancer
9	0.6	2 / 127	Squamous cell carcinoma, head and neck
10	0.6	2 / 142	Lung cancer
11	0.7	1 / 73	Stroke, susceptibility to
12	0.7	1 / 76	Muscular
13	0.7	2 / 156	Breast cancer
14	0.8	1 / 95	Colorectal cancer
15	0.8	1 / 102	Leukemia

miRNA target

Rank	p−value	#in/all	Geneset
1	0.02	4 / 63	hsa−miR−371−5p
2	0.04	4 / 85	hsa−miR−510
3	0.05	2 / 24	hsa−miR−99b
4	0.06	2 / 25	hsa−miR−941
5	0.06	3 / 58	hsa−miR−187
6	0.06	2 / 27	hsa−miR−1292
7	0.06	3 / 60	hsa−miR−492
8	0.07	4 / 100	hsa−miR−150
9	0.07	5 / 143	hsa−miR−548f
10	0.07	5 / 144	hsa−miR−24
11	0.08	3 / 64	hsa−miR−1826
12	0.09	2 / 33	hsa−miR−1296
13	0.10	4 / 113	hsa−miR−498
14	0.10	3 / 72	hsa−miR−361−3p
15	0.11	5 / 164	hsa−miR−548g

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.2	1 / 13	BENTINK_e2f3.1
2	1.0	0 / 14	GUSTAFSON_PI3K_UP
3	1.0	0 / 15	GUSTAFSON_PI3K_DN
4	1.0	0 / 13	BENTINK_e2f3.2
5	1.0	0 / 13	BENTINK_myc.1
6	1.0	0 / 12	BENTINK_ras.1
7	1.0	0 / 11	BENTINK_ras.4
8	1.0	0 / 14	BENTINK_ras.6
9	1.0	0 / 13	BENTINK_src.10
10	1.0	0 / 12	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Reference Signatures

Rank	p−value	#in/all	Geneset
1	0.007	15 / 478	WIRTH_Nervous System
2	0.016	2 / 13	WIRTH_Sec. lymphoid organs
3	0.019	2 / 14	WIRTH_Telencephalon
4	0.079	8 / 289	JONGENEEL_Testis
5	0.157	1 / 11	WIRTH_Tonsil
6	0.168	2 / 48	WIRTH_Pancreas
7	0.170	1 / 12	VAQUERIZAS_Kidney_TF
8	0.170	1 / 12	Chaussabel_3,5_Hemoglobin genes
9	0.195	1 / 14	WIRTH_B−cells
10	0.195	1 / 14	WIRTH_Thalamus
11	0.195	1 / 14	WIRTH_Thyroid gland
12	0.227	3 / 107	WIRTH_Liver
13	0.232	1 / 17	VAQUERIZAS_Adrenal gland_TF
14	0.255	1 / 19	JONGENEEL_Small Intestine
15	0.278	1 / 21	JONGENEEL_Adrenal Gland

Telomeres

Rank	p−value	#in/all	Geneset
1	1	0 / 13	Alternative lengthening of telomeres
2	1	0 / 27	Nabetani_alt len telomeres_genes_ko
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	0.03	37 / 1753	HEBENSTREIT_low expression TF
2	0.07	30 / 1466	ICGC_NrsfPcr1_targets
3	0.12	16 / 747	ICGC_NrsfPcr2_targets
4	0.19	1 / 14	NOWICK_TF
5	0.21	30 / 1669	ICGC_P300_targets
6	0.22	104 / 6322	ICGC_Tcf3_targets
7	0.23	89 / 5383	ICGC_Sp1_targets
8	0.25	47 / 2759	ICGC_Bcl3_targets
9	0.25	46 / 2704	ICGC_Pbx3_targets
10	0.28	107 / 6616	ICGC_Pax5_targets
11	0.29	58 / 3507	ICGC_Rad21_targets
12	0.35	52 / 3194	ICGC_Irf4_targets
13	0.35	85 / 5312	ICGC_Tcf12_targets
14	0.36	109 / 6868	ICGC_Elf1_targets
15	0.37	54 / 3348	ICGC_BatfPcr1_targets

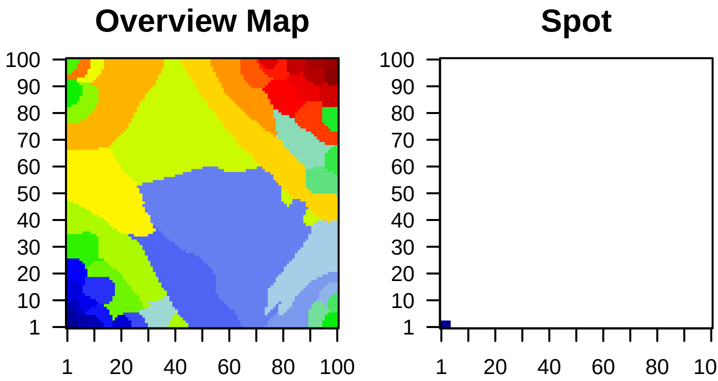
K−Means Cluster

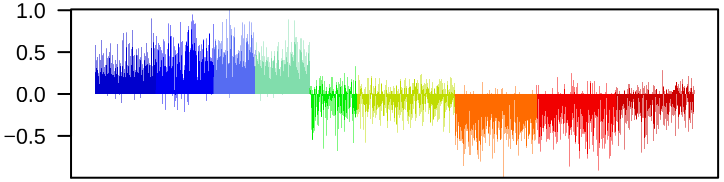
Spot Summary: D

metagenes = 12
genes = 297

<r> metagenes = 0.97
<r> genes = 0.82
beta: r2= 247.08 / log p= −Inf

samples with spot = 1173 (34.6 %)
A * : 286 (83.1 %)
A C * : 269 (82 %)
A C F * : 230 (97.9 %)
A F * : 285 (92.5 %)
C F * : 24 (9.1 %)
F * : 52 (9.4 %)
F J * : 1 (0.2 %)
J * : 11 (2.5 %)
N * : 15 (3.4 %)



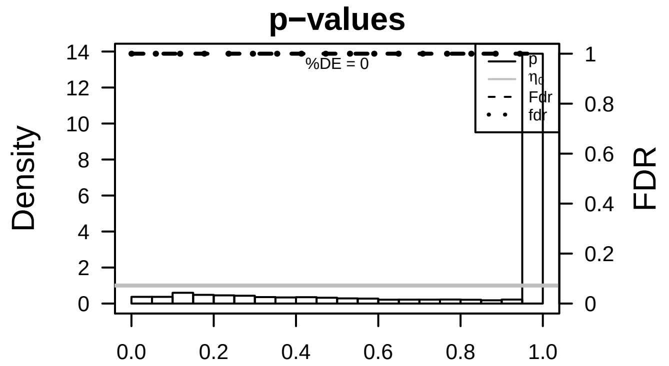


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_323194	1.5	−1.58	0.96		
2	ILMN_167769	1.49	−1.31	0.97		
3	ILMN_323717	1.48	−1.61	0.96	FAM175A	family with sequence similarity 175 member A [Source:HGNC
4	ILMN_323740	1.46	−1.46	0.97		
5	ILMN_318148	1.44	−1.46	0.94	LOC102723623	golgin A6 family−like 1 [Source:HGNC Symbol;Acc:HGNC:37
6	ILMN_327479	1.42	−1.12	0.95	ACTG1P17	actin gamma 1 pseudogene 17 [Source:HGNC Symbol;Acc:H
7	ILMN_172134	1.41	−1.5	0.97		
8	ILMN_218811	1.41	−1.53	0.95	ARL16	ADP ribosylation factor like GTPase 16 [Source:HGNC Symb
9	ILMN_228601	1.4	−1.5	0.95	CATSPER2	cation channel sperm associated 2 [Source:HGNC Symbol;A
10	ILMN_187241	1.4	−1.22	0.92		
11	ILMN_329421	1.39	−1.29	0.98		
12	ILMN_212355	1.38	−1.32	0.97		
13	ILMN_205455	1.38	−1.41	0.96	DTWD2	DTW domain containing 2 [Source:HGNC Symbol;Acc:HGNC
14	ILMN_329841	1.38	−1.2	0.96		
15	ILMN_212251	1.37	−1.45	0.93	CCBE1	collagen and calcium binding EGF domains 1 [Source:HGNC
16	ILMN_215029	1.37	−1.43	0.94	FKBP14	FK506 binding protein 14 [Source:HGNC Symbol;Acc:HGNC:
17	ILMN_207354	1.35	−1.37	0.97	SERF2	small EDRK−rich factor 2 [Source:HGNC Symbol;Acc:HGNC:
18	ILMN_321318	1.35	−1.43	0.97		
19	ILMN_215046	1.35	−1.28	0.84	TMEM267	transmembrane protein 267 [Source:HGNC Symbol;Acc:HGN
20	ILMN_207579	1.34	−1.33	0.94	NLRP8	NLR family pyrin domain containing 8 [Source:HGNC Symbol

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	2e−52	55 / 360	GSEA	LU_EZH2_TARGETS_DN
2	9e−09	25 / 740	Colon	LaPointe_mucosa−position_kmeans_C_cecum colon_ascending colon_tra
3	5e−06	20 / 708	GSEA	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_DN
4	5e−06	5 / 29	Refer	Chaussabel_2,7_Unknown function
5	1e−05	25 / 1083	Colon	ZNF_Colon
6	3e−05	4 / 20	MF	endodeoxyribonuclease activity
7	8e−05	5 / 50	BP	response to ionizing radiation
8	8e−05	3 / 10	BP	mitotic recombination
9	1e−04	17 / 681	Brain	Overlap_fetal_midbrain_EnhP
10	2e−04	3 / 13	BP	cellular response to hepatocyte growth factor stimulus
11	2e−04	3 / 14	MF	four−way junction DNA binding
12	2e−04	1 / 14	Cance	LIU_COMMON_CANCER_GENES
13	3e−04	34 / 2073	Colon	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP
14	3e−04	4 / 38	BP	response to activity
15	4e−04	31 / 1846	Chror	14_ZNF_Melanocytes
16	4e−04	101 / 8771	Chror	5_Tx_Melanocytes
17	5e−04	5 / 73	GSEA	GINESTIER_BREAST_CANCER_ZNF217_AMPLIFIED_UP
18	5e−04	15 / 630	Chror	14_ZNF_Fibroblasts
19	7e−04	83 / 6970	Chror	5_Tx_Neuronal_Progenitor
20	9e−04	12 / 464	Lympl	WIRTH_lymphoma937_spot I
21	1e−03	11 / 416	GSEA	FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN
22	1e−03	16 / 769	Chr	Chr 15
23	1e−03	3 / 25	BP	sprouting angiogenesis
24	1e−03	5 / 94	MF	double−stranded DNA binding
25	1e−03	3 / 26	BP	meiotic nuclear division
26	1e−03	3 / 26	BP	reciprocal meiotic recombination
27	2e−03	21 / 1168	Colon	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_
28	2e−03	10 / 368	GSEA	OSMAN_BLADDER_CANCER_UP
29	2e−03	96 / 8568	Colon	TxWk_Colon
30	2e−03	22 / 1272	BP	regulation of transcription, DNA−templated
31	2e−03	7 / 200	GSEA	KAUFFMANN_DNA_REPAIR_GENES
32	2e−03	71 / 5936	Brain	Overlap_fetal_midbrain_HetRpts
33	2e−03	9 / 319	GSEA	WANG_RESPONSE_TO_GSK3_INHIBITOR_SB216763_UP
34	2e−03	4 / 62	BP	nucleic acid phosphodiester bond hydrolysis
35	2e−03	16 / 812	GSEA	GEORGES_TARGETS_OF_MIR192_AND_MIR215
36	2e−03	5 / 104	BP	tumor necrosis factor−mediated signaling pathway
37	3e−03	6 / 155	GSEA	GARCIA_TARGETS_OF_FLI1_AND_DAX1_DN
38	3e−03	117 / 10999	Colon	TssWk_Colon
39	3e−03	5 / 107	GSEA	BHATI_G2M_ARREST_BY_2METHOXYESTRADIOL_UP
40	3e−03	23 / 1404	Colon	LaPointe_mucosa−position_kmeans_D_transverse colon_UP_



Aging

Rank	p−value	#in/all	Geneset
1	0.4	1 / 58	TESCHENDORFF_age_hypermethylated
2	0.6	1 / 111	HORVATH_aging_genes meth DOWN
3	0.7	1 / 142	HORVATH_aging_genes meth UP
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Cancer

Rank	p−value	#in/all	Geneset
1	2e−04	1 / 14	LIU_COMMON_CANCER_GENES
2	8e−02	2 / 54	KUIPER_MM poor survival
3	1e−01	1 / 12	LIU_BREAST_CANCER
4	1e−01	1 / 13	LIU_LIVER_CANCER
5	1e−01	1 / 15	WANG_ER_UP
6	1e−01	2 / 73	SHAUGHNESSY_MM high risk
7	2e−01	2 / 82	PanCan_JAK−ST_geneset_nanostring
8	2e−01	7 / 527	Lembcke_Normal vs Adenoma
9	3e−01	1 / 36	PanCan_HK_geneset_nanostring
10	3e−01	1 / 38	KUIPER_MM good survival
11	3e−01	0 / 12	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
12	3e−01	1 / 46	PanCan_DNARepair_geneset_nanostring
13	3e−01	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
14	4e−01	0 / 14	RHODES_UNDIFFERENTIATED_CANCER
15	5e−01	5 / 554	Lembcke_Colonic Inflammation

Chromatin states

Rank	p−value	#in/all	Geneset
1	4e−04	31 / 1846	14_ZNF_Melanocytes
2	4e−04	101 / 8771	5_Tx_Melanocytes
3	5e−04	15 / 630	14_ZNF_Fibroblasts
4	7e−04	83 / 6970	5_Tx_Neuronal_Progenitor
5	4e−03	53 / 4237	14_ZNF_Neuronal_Progenitor
6	1e−02	125 / 12298	2_TssA_Melanocytes
7	2e−02	83 / 7854	5_Tx_Fibroblasts
8	4e−02	122 / 12393	15_Quies_Neuronal_Progenitor
9	4e−02	127 / 12983	2_TssA_Neuronal_Progenitor
10	4e−02	32 / 2682	12_Het_Neuronal_Progenitor
11	5e−02	113 / 11455	2_TssA_Fibroblasts
12	1e−01	88 / 8990	15_Quies_Fibroblasts
13	1e−01	16 / 1324	13_HetRpts_Fibroblasts
14	1e−01	35 / 3272	13_HetRpts_Neuronal_Progenitor
15	2e−01	105 / 11130	15_Quies_Melanocytes

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−52	55 / 360	LU_EZH2_TARGETS_DN
2	5e−06	20 / 708	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_DN
3	2e−04	1 / 14	LIU_COMMON_CANCER_GENES
4	5e−04	5 / 73	GINESTIER_BREAST_CANCER_ZNF217_AMPLIFIED_UP
5	1e−03	11 / 416	FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN
6	2e−03	10 / 368	OSMAN_BLADDER_CANCER_UP
7	2e−03	7 / 200	KAUFFMANN_DNA_REPAIR_GENES
8	2e−03	9 / 319	WANG_RESPONSE_TO_GSK3_INHIBITOR_SB216763_UP
9	2e−03	16 / 812	GEORGES_TARGETS_OF_MIR192_AND_MIR215
10	3e−03	6 / 155	GARCIA_TARGETS_OF_FLI1_AND_DAX1_DN
11	3e−03	5 / 107	BHATI_G2M_ARREST_BY_2METHOXYESTRADIOL_UP
12	4e−03	6 / 168	LEE_DIFFERENTIATING_T_LYMPHOCYTE
13	4e−03	2 / 11	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_3
14	5e−03	10 / 425	ZHOU_INFLAMMATORY_RESPONSE_LIVE_UP
15	5e−03	5 / 126	NOUZOVA_TRETINOIN_AND_H4_ACETYLATION

Lymphoma

Rank	p−value	#in/all	Geneset
1	9e−04	12 / 464	WIRTH_lymphoma937_spot I
2	7e−03	10 / 450	Hopp_June14_MMML937 tumors+controls_group.overexpression_I_MM_GC
3	9e−03	10 / 472	Hopp_June14_MMML937 tumors+controls_group.overexpression_J_GC−B−
4	1e−02	80 / 7275	HOPP_Txn_elongation
5	2e−02	4 / 109	ROSOLOWSKI_blue total
6	3e−02	86 / 8226	HOPP_Active_promoter
7	3e−02	7 / 331	WIRTH_lymphoma937_spot H
8	3e−02	59 / 5356	HOPP_Txn_transition
9	3e−02	9 / 493	WIRTH_lymphoma937_spot J
10	5e−02	16 / 1169	SPANG_BCR DN
11	6e−02	6 / 318	Hopp_June14_MMML937 tumors+controls_group.overexpression_H_GC−B−
12	1e−01	1 / 12	WRIGHT_GCB UP
13	1e−01	1 / 14	Subero_T−ALL_hypo_meth
14	1e−01	5 / 300	Hopp_June14_MMML937 tumors+controls_group.overexpression_E_GC−B−
15	1e−01	69 / 6959	HOPP_Weak_enhancer

miRNA Disease

Rank	p−value	#in/all	Geneset
1	1	0 / 7	Thyroid carcinoma, papillary
2	1	0 / 123	Pancreatic cancer
3	1	0 / 68	Glioblastoma multiforme, somatic
4	1	0 / 63	Gastrointestinal
5	1	0 / 3	Pituitary adenoma
6	1	0 / 116	Cancer
7	1	0 / 95	Colorectal cancer
8	1	0 / 2	Adenomas, multiple colorectal
9	1	0 / 124	Prostate cancer
10	1	0 / 48	Alzheimer disease, susceptibility to
11	1	0 / 7	Schizophrenia, susceptibility to
12	1	0 / 20	Parkinson disease
13	1	0 / 65	Hepatocellular carcinoma
14	1	0 / 3	Down syndrome, risk of
15	1	0 / 127	Melanoma and neural system tumor syndrome

Reference Signatures

Rank	p−value	#in/all	Geneset
1	5e−06	5 / 29	Chaussabel_2,7_Unknown function
2	1e−02	5 / 150	Chaussabel_2,6_Myeloid lineage
3	2e−02	2 / 24	Chaussabel_1,6_Signaling molecules
4	4e−02	1 / 5	VAQUERIZAS_Appendix_TF
5	7e−02	7 / 412	WIRTH_Immune system
6	8e−02	1 / 10	JONGENEEL_Colon
7	1e−01	5 / 275	Chaussabel_3,7_Spliceosome
8	1e−01	1 / 13	JONGENEEL_Thyroid
9	1e−01	2 / 66	VAQUERIZAS_Whole blood_TF
10	1e−01	4 / 221	Chaussabel_3,8_Enzymes
11	2e−01	2 / 84	Chaussabel_2,10_Immune related cell surface molecules
12	2e−01	4 / 248	Chaussabel_3,6_Mitochondrial ribosomal proteins
13	2e−01	1 / 24	JONGENEEL_Prostate
14	2e−01	2 / 96	Chaussabel_3,1_Interferon−inducible
15	2e−01	1 / 29	JONGENEEL_Bone Marrow

BP

Rank	p−value	#in/all	Geneset
1	8e−05	5 / 50	response to ionizing radiation
2	8e−05	3 / 10	mitotic recombination
3	2e−04	3 / 13	cellular response to hepatocyte growth factor stimulus
4	3e−04	4 / 38	response to activity
5	1e−03	3 / 25	sprouting angiogenesis
6	1e−03	3 / 26	meiotic nuclear division
7	1e−03	3 / 26	reciprocal meiotic recombination
8	2e−03	22 / 1272	regulation of transcription, DNA−templated
9	2e−03	4 / 62	nucleic acid phosphodiester bond hydrolysis
10	2e−03	5 / 104	tumor necrosis factor−mediated signaling pathway
11	3e−03	2 / 10	positive regulation of T cell chemotaxis
12	4e−03	2 / 11	positive regulation of long−term synaptic potentiation
13	5e−03	2 / 12	axoneme assembly
14	8e−03	2 / 16	female gamete generation
15	8e−03	2 / 16	mitochondrion morphogenesis

CC

Rank	p−value	#in/all	Geneset
1	0.04	2 / 36	condensed nuclear chromosome
2	0.04	3 / 90	chromatin
3	0.06	3 / 104	endomembrane system
4	0.07	2 / 50	SNARE complex
5	0.08	1 / 10	cytosolic ribosome
6	0.08	1 / 10	MKS complex
7	0.09	1 / 11	lateral element
8	0.09	1 / 11	P granule
9	0.10	1 / 12	chromatoid body
10	0.10	1 / 12	proteasome regulatory particle
11	0.11	1 / 13	A band
12	0.11	1 / 13	Golgi−associated vesicle
13	0.11	1 / 13	HOPS complex
14	0.11	2 / 66	mitochondrial intermembrane space
15	0.12	1 / 14	BLOC−1 complex

Colon Cancer

Rank	p−value	#in/all	Geneset
1	9e−09	25 / 740	LaPointe_mucosa−position_kmeans_C_cecum colon_ascending colon_trans
2	1e−05	25 / 1083	ZNF_Colon
3	3e−04	34 / 2073	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
4	2e−03	21 / 1168	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_
5	2e−03	96 / 8568	TxWk_Colon
6	3e−03	117 / 10999	TssWk_Colon
7	3e−03	23 / 1404	LaPointe_mucosa−position_kmeans_D_transverse colon_UP_
8	4e−03	103 / 9530	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP_
9	7e−03	2 / 14	Hewish_dMMR−secondary−mutations_DNA−repair
10	8e−03	97 / 9054	Tx_Colon
11	2e−02	13 / 799	LaPointe_mucosa−position_kmeans_B_ascending colon_transverse colon_U
12	3e−02	98 / 9555	TssA_Colon
13	5e−02	88 / 8678	Quies3_Colon
14	6e−02	3 / 103	Marisa_CRC−cluster−d
15	7e−02	44 / 4034	TssD1_Colon

HM

Rank	p−value	#in/all	Geneset
1	0.02	5 / 176	HALLMARK_KRAS_SIGNALING_UP
2	0.12	3 / 137	HALLMARK_UV_RESPONSE_UP
3	0.23	2 / 103	HALLMARK_BILE_ACID_METABOLISM
4	0.24	3 / 191	HALLMARK_INFLAMMATORY_RESPONSE
5	0.30	1 / 40	HALLMARK_WNT_BETA_CATENIN_SIGNALING
6	0.30	1 / 41	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
7	0.42	2 / 162	HALLMARK_ALLOGRAFT_REJECTION
8	0.45	2 / 172	HALLMARK_INTERFERON_GAMMA_RESPONSE
9	0.46	1 / 69	HALLMARK_CHOLESTEROL_HOMEOSTASIS
10	0.46	2 / 176	HALLMARK_ADIPOGENESIS
11	0.48	2 / 185	HALLMARK_TNFA_SIGNALING_VIA_NFKB
12	0.48	2 / 185	HALLMARK_MTORC1_SIGNALING
13	0.48	2 / 185	HALLMARK_HEME_METABOLISM
14	0.49	2 / 187	HALLMARK_COMPLEMENT
15	0.52	1 / 82	HALLMARK_IL6_JAK_STAT3_SIGNALING

Melanoma

Rank	p−value	#in/all	Geneset
1	0.4	1 / 54	Hugo_melanoma−all−MET_DN
2	1.0	0 / 30	Hugo_melanoma−all−MET_UP
3	1.0	0 / 43	Hugo_melanoma−BRAFmut−MET_UP
4	1.0	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
5	1.0	0 / 27	Hugo_melanoma−all−LEF1_UP
6	1.0	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

miRNA target

Rank	p−value	#in/all	Geneset
1	0.003	3 / 34	hsa−miR−1178
2	0.025	3 / 71	hsa−miR−628−3p
3	0.035	4 / 140	hsa−miR−136
4	0.046	2 / 39	hsa−miR−593
5	0.053	2 / 42	hsa−miR−129−3p
6	0.055	5 / 233	hsa−miR−1252
7	0.060	3 / 101	hsa−miR−574−5p
8	0.064	2 / 47	hsa−miR−553
9	0.065	3 / 105	hsa−miR−605
10	0.073	3 / 110	hsa−miR−190b
11	0.092	1 / 11	hsa−miR−604
12	0.095	4 / 196	hsa−miR−206
13	0.106	2 / 63	hsa−miR−659
14	0.106	2 / 63	hsa−miR−618
15	0.109	2 / 64	hsa−miR−1278

Telomeres

Rank	p−value	#in/all	Geneset
1	0.1	1 / 13	Alternative lengthening of telomeres
2	0.2	1 / 27	Nabetani_alt len telomeres_genes_ko
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Brain

Rank	p−value	#in/all	Geneset
1	1e−04	17 / 681	Overlap_fetal_midbrain_EnhP
2	2e−03	71 / 5936	Overlap_fetal_midbrain_HetRpts
3	7e−03	19 / 1162	Fetal_Enh
4	9e−03	35 / 2654	Fetal_Quies
5	2e−02	102 / 9815	Overlap_fetal_midbrain_ReprPC
6	2e−02	17 / 1115	Overlap_fetal_midbrain_EnhG
7	2e−02	11 / 630	Mid_Frontal_Lobe_EnhP
8	3e−02	20 / 1436	Fetal_K9K27me3
9	3e−02	23 / 1728	Fetal_ReprPCWk
10	5e−02	99 / 9917	Overlap_fetal_midbrain_ReprPCWk
11	5e−02	6 / 307	Fetal_ReprPC
12	9e−02	11 / 796	Overlap_fetal_midbrain_ZNF
13	1e−01	6 / 386	Fetal_ZNF
14	2e−01	11 / 906	Fetal_HetRpts
15	2e−01	15 / 1329	Overlap_fetal_midbrain_Enh

Chr

Rank	p−value	#in/all	Geneset
1	0.001	16 / 769	Chr 15
2	0.007	19 / 1170	Chr 7
3	0.019	21 / 1467	Chr 19
4	0.042	18 / 1318	Chr 17
5	0.140	10 / 768	Chr 14
6	0.329	11 / 1060	Chr 5
7	0.461	9 / 954	Chr 9
8	0.478	21 / 2323	Chr 1
9	0.509	5 / 536	Chr 22
10	0.539	8 / 902	Chr 4
11	0.665	12 / 1492	Chr 2
12	0.685	7 / 904	Chr 10
13	0.724	2 / 289	Chr 21
14	0.742	7 / 959	Chr 16
15	0.805	2 / 342	Chr 18

Glio

Rank	p−value	#in/all	Geneset
1	0.007	2 / 15	Donson−chemokines/cytokines−associated with LTS in HGA
2	0.038	3 / 84	GIEZELT_GBM_STS_up_VS_LTS
3	0.055	2 / 43	Noushmehr_Pron_GCIMP_hypermeth_DN
4	0.076	2 / 52	Hopp_Sturm_GBM_Epi3_B1_G34_DN
5	0.108	1 / 13	WILLSCHER_GBM_Verhaak−PNmut_up (M)
6	0.123	2 / 69	WILLSCHER_GBM_Verhaak−PNwt & MES_up
7	0.187	2 / 90	GIEZELT_GBM_STSwt_down_VS_LTSwt
8	0.198	1 / 25	Sturm_GBM_Meth_overexpression_H_K27_UP
9	0.205	1 / 26	Gorovets_LGG_NB_subclass
10	0.258	6 / 487	Hopp_Sturm_GBM_Epi3_B_adult_UP_G34_DN
11	0.299	18 / 1777	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
12	0.302	4 / 316	WILLSCHER_GBM_Verhaak−PNwt & CL_up
13	0.323	2 / 132	WILLSCHER_GBM_Verhaak−CL_up (C)
14	0.368	1 / 52	Sturm_GBM_Meth_overexpression_F_IDH_UP
15	0.371	2 / 147	Christensen_hypermethylated_in_grade2_oligodendroglioma

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.04	5 / 211	Homuth_BMI−associated−genes_DN
2	1.00	0 / 94	DUMEAUX_Smoking enriched genes
3	1.00	0 / 10	DUMEAUX_Smoking literature genes up
4	1.00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
5	1.00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
6	1.00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
7	1.00	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
8	1.00	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
9	1.00	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
10	1.00	0 / 10	DUMEAUX_Women normal BMI literature genes up
11	1.00	0 / 17	DUMEAUX_High bmi enriched genes
12	1.00	0 / 31	DUMEAUX_Fasting enriched genes
13	1.00	0 / 147	Homuth_BMI−associated−genes_UP
14	1.00	0 / 18	Huan_blood−pressure_SBP−signature
15	1.00	0 / 16	Huan_blood−pressure_DBP−signature

MF

Rank	p−value	#in/all	Geneset
1	3e−05	4 / 20	endodeoxyribonuclease activity
2	2e−04	3 / 14	four−way junction DNA binding
3	1e−03	5 / 94	double−stranded DNA binding
4	4e−03	4 / 72	single−stranded DNA binding
5	1e−02	2 / 19	neuropeptide binding
6	2e−02	3 / 60	metallopeptidase activity
7	2e−02	2 / 25	aminopeptidase activity
8	2e−02	2 / 28	DNA−dependent ATPase activity
9	2e−02	2 / 28	tumor necrosis factor receptor binding
10	3e−02	2 / 29	Hsp70 protein binding
11	3e−02	2 / 33	endonuclease activity
12	4e−02	20 / 1475	DNA binding
13	4e−02	2 / 35	4 iron, 4 sulfur cluster binding
14	5e−02	10 / 627	molecular_function
15	5e−02	4 / 161	cytokine activity

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.1	1 / 15	GUSTAFSON_PI3K_DN
2	1.0	0 / 14	GUSTAFSON_PI3K_UP
3	1.0	0 / 13	BENTINK_e2f3.1
4	1.0	0 / 13	BENTINK_e2f3.2
5	1.0	0 / 13	BENTINK_myc.1
6	1.0	0 / 12	BENTINK_ras.1
7	1.0	0 / 11	BENTINK_ras.4
8	1.0	0 / 14	BENTINK_ras.6
9	1.0	0 / 13	BENTINK_src.10
10	1.0	0 / 12	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	0.007	36 / 2704	ICGC_Pbx3_targets
2	0.010	62 / 5383	ICGC_Sp1_targets
3	0.024	11 / 631	ICGC_RxraPcr1_targets
4	0.072	52 / 4890	ICGC_Bclaf101388_targets
5	0.077	62 / 5984	ICGC_Mta3_targets
6	0.080	70 / 6868	ICGC_Elf1_targets
7	0.081	37 / 3348	ICGC_BatfPcr1_targets
8	0.094	56 / 5410	ICGC_Foxm1_targets
9	0.096	51 / 4881	ICGC_Atf2_targets
10	0.100	46 / 4362	ICGC_Creb1_targets
11	0.100	18 / 1478	ICGC_Myc_targets
12	0.116	1 / 14	NOWICK_TF
13	0.119	63 / 6267	ICGC_Yy1_targets
14	0.123	56 / 5518	ICGC_Stat5_targets
15	0.125	24 / 2133	ICGC_Mef2_targets

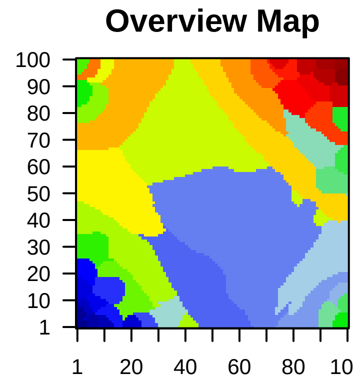
K−Means Cluster

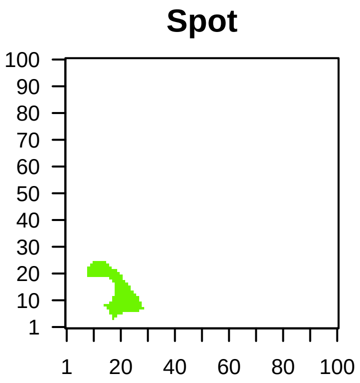
Spot Summary: E

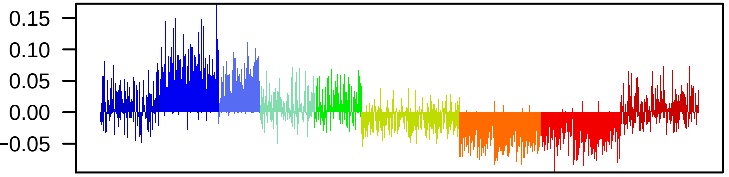
metagenes = 178
genes = 141

<r> metagenes = 0.93
<r> genes = 0.16
beta: r2= 5.6 / log p= −Inf

samples with spot = 19 (0.6 %)
A C * : 16 (4.9 %)
A C F * : 3 (1.3 %)


Overview Map


Spot

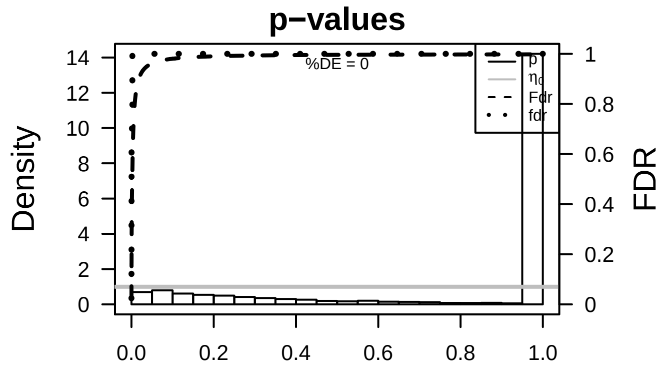


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_174244	0.95	−0.42	0.18		
2	ILMN_220957	0.81	−0.71	0.32	AGAP6	ArfGAP with GTPase domain, ankyrin repeat and PH domain
3	ILMN_176992	0.6	−0.42	0.44	DBN1	drebrin 1 [Source:HGNC Symbol;Acc:HGNC:2695]
4	ILMN_181142	0.58	−0.36	0.29	TMTC1	transmembrane and tetratricopeptide repeat containing 1 [So
5	ILMN_227114	0.56	−0.3	0.23	PGM5	phosphoglucomutase 5 [Source:HGNC Symbol;Acc:HGNC:8
6	ILMN_170529	0.52	−0.29	0.4	MYBPH	myosin binding protein H [Source:HGNC Symbol;Acc:HGNC:
7	ILMN_173942	0.52	−0.25	0.27		
8	ILMN_171207	0.51	−0.35	0.13	SYNM	synemin [Source:HGNC Symbol;Acc:HGNC:24466]
9	ILMN_170199	0.51	−0.44	0.16	AFAP1	actin filament associated protein 1 [Source:HGNC Symbol;Ac
10	ILMN_165905	0.48	−0.43	0.43		
11	ILMN_175341	0.47	−0.35	0.41		
12	ILMN_216597	0.47	−0.25	0.37	CES3	carboxylesterase 3 [Source:HGNC Symbol;Acc:HGNC:1865]
13	ILMN_172678	0.46	−0.35	0.27	TNRC6B	trinucleotide repeat containing 6B [Source:HGNC Symbol;Ac
14	ILMN_170406	0.46	−0.32	0.28	KCNH3	potassium voltage−gated channel subfamily H member 3 [So
15	ILMN_173739	0.46	−0.29	0.39	LMNA	lamin A/C [Source:HGNC Symbol;Acc:HGNC:6636]
16	ILMN_238850	0.46	−0.45	0.4	AKT1	AKT serine/threonine kinase 1 [Source:HGNC Symbol;Acc:H
17	ILMN_165625	0.45	−0.36	0.37		
18	ILMN_179001	0.44	−0.29	0.37	METRNL	meteorin like, glial cell differentiation regulator [Source:HGNC
19	ILMN_180773	0.43	−0.41	0.32	AKAP17A	A−kinase anchoring protein 17A [Source:HGNC Symbol;Acc:
20	ILMN_324187	0.43	−0.38	0.29	FRMD8	FERM domain containing 8 [Source:HGNC Symbol;Acc:HGN

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	4e−06	33 / 2845	Colon	TxEnhG1_Colon
2	5e−06	46 / 4795	Chror	6_EnhG_Fibroblasts
3	1e−05	36 / 3450	Chror	4_TxTrans_Fibroblasts
4	2e−05	60 / 7354	Colon	TssF_Colon
5	2e−05	47 / 5188	TF	ICGC_Ebfsc137065_targets
6	5e−05	47 / 5373	Colon	EnhWk1_Colon
7	6e−05	30 / 2810	Colon	EnhA_Colon
8	8e−05	3 / 17	BP	negative regulation of release of cytochrome c from mitochondria
9	9e−05	76 / 10779	Colon	Enh_Colon
10	1e−04	49 / 5956	Chror	3_TssF_Neuronal_Progenitor
11	2e−04	28 / 2709	Brain	Mid_Frontal_Lobe_HetRpts
12	2e−04	56 / 7247	TF	ICGC_Runx3_targets
13	5e−04	79 / 11836	Chror	3_TssF_Melanocytes
14	5e−04	44 / 5410	TF	ICGC_Foxm1_targets
15	6e−04	32 / 3507	TF	ICGC_Rad21_targets
16	7e−04	49 / 6322	TF	ICGC_Tcf3_targets
17	8e−04	37 / 4345	TF	ICGC_Zeb1_targets
18	8e−04	50 / 6552	TF	ICGC_Pol2_targets
19	9e−04	3 / 37	GSEA	LEE_CALORIE_RESTRICTION_MUSCLE_UP
20	1e−03	4 / 85	GSEA	GAVIN_FOXP3_TARGETS_CLUSTER_P7
21	1e−03	8 / 394	miRN	hsa−miR−301b
22	1e−03	48 / 6267	TF	ICGC_Yy1_targets
23	1e−03	4 / 87	Lympl	Hopp_Lymphoma_Epi1_with_zentr_v_B.cell_DN
24	1e−03	3 / 40	BP	regulation of G−protein coupled receptor protein signaling pathway
25	1e−03	16 / 1318	Chr	Chr 17
26	1e−03	2 / 10	BP	neural precursor cell proliferation
27	1e−03	43 / 5442	TF	ICGC_Pmlsc71910_targets
28	1e−03	51 / 6868	TF	ICGC_Elf1_targets
29	1e−03	3 / 43	BP	cellular response to starvation
30	1e−03	66 / 9635	Chror	3_TssF_Fibroblasts
31	2e−03	44 / 5699	Chror	6_EnhG_Melanocytes
32	2e−03	2 / 12	GSEA	KYNG_DNA_DAMAGE_BY_4NQO_OR_GAMMA_RADIATION
33	2e−03	5 / 167	GSEA	KEGG_CHEMOKINE_SIGNALING_PATHWAY
34	2e−03	11 / 763	GSEA	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP
35	2e−03	2 / 13	BP	regulation of autophagosome assembly
36	2e−03	2 / 13	GSEA	BIOCARTA_EXTRINSIC_PATHWAY
37	2e−03	2 / 13	GSEA	ZHANG_ADIPOGENESIS_BY_BMP7
38	2e−03	15 / 1268	Refer	PROTEINATLAS_colon
39	2e−03	9 / 552	GSEA	MARTINEZ_TP53_TARGETS_UP
40	2e−03	7 / 352	CC	focal adhesion


p−values

Aging

Rank	p−value	#in/all	Geneset
1	1	0 / 111	HORVATH_aging_genes meth DOWN
2	1	0 / 142	HORVATH_aging_genes meth UP
3	1	0 / 58	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	8e−05	3 / 17	negative regulation of release of cytochrome c from mitochondria
2	1e−03	3 / 40	regulation of G−protein coupled receptor protein signaling pathway
3	1e−03	2 / 10	neural precursor cell proliferation
4	1e−03	3 / 43	cellular response to starvation
5	2e−03	2 / 13	regulation of autophagosome assembly
6	2e−03	2 / 14	insulin−like growth factor receptor signaling pathway
7	2e−03	2 / 14	positive regulation of blood coagulation
8	3e−03	2 / 17	positive regulation of blood vessel endothelial cell migration
9	4e−03	2 / 19	positive regulation of receptor internalization
10	5e−03	3 / 65	positive regulation of peptidyl−serine phosphorylation
11	5e−03	2 / 20	regulation of blood coagulation
12	5e−03	3 / 68	negative regulation of protein phosphorylation
13	6e−03	2 / 22	positive regulation of calcium ion transport
14	6e−03	2 / 22	regulation of mitotic nuclear division
15	6e−03	2 / 23	regulation of neuron projection development

Brain

Rank	p−value	#in/all	Geneset
1	2e−04	28 / 2709	Mid_Frontal_Lobe_HetRpts
2	2e−03	34 / 4112	Mid_Frontal_Lobe_ReprPC
3	5e−03	68 / 10430	Overlap_fetal_midbrain_Quies
4	9e−03	62 / 9504	Overlap_fetal_midbrain_K9K27me3
5	9e−03	26 / 3164	Mid_Frontal_Lobe_ZNF
6	2e−02	5 / 304	Mid_Frontal_Lobe_TssA
7	2e−02	9 / 796	Overlap_fetal_midbrain_ZNF
8	6e−02	14 / 1728	Fetal_ReprPCWk
9	6e−02	8 / 818	Mid_Frontal_Lobe_Het
10	9e−02	19 / 2700	Fetal_TxTrans
11	1e−01	4 / 383	Mid_Frontal_Lobe_Tx
12	2e−01	4 / 465	Mid_Frontal_Lobe_TxTrans
13	2e−01	2 / 180	Overlap_fetal_midbrain_Het
14	3e−01	34 / 5936	Overlap_fetal_midbrain_HetRpts
15	3e−01	16 / 2630	Fetal_TssF

Cancer

Rank	p−value	#in/all	Geneset
1	0.02	7 / 554	Lembcke_Colonic Inflammation
2	0.15	2 / 136	PanCan_RAS_geneset_nanostring
3	0.19	0 / 15	LIU_PROSTATE_CANCER_DN
4	0.26	2 / 193	PanCan_PI3K_geneset_nanostring
5	0.31	1 / 73	SHAUGHNESSY_MM high risk
6	0.34	1 / 82	PanCan_JAK−ST_geneset_nanostring
7	0.45	1 / 117	PanCan_Driver_Gene_geneset_nanostring
8	0.46	2 / 301	SPANG_BCL6−index2
9	0.47	1 / 125	PanCan_CC+Apop_geneset_nanostring
10	0.54	1 / 150	PanCan_MAPK_geneset_nanostring
11	0.60	1 / 178	SPANG_LPS−index2
12	0.76	2 / 527	Lembcke_Normal vs Adenoma
13	1.00	0 / 13	RHODES_CANCER_META_SIGNATURE
14	1.00	0 / 14	RHODES_UNDIFFERENTIATED_CANCER
15	1.00	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN

CC

Rank	p−value	#in/all	Geneset
1	0.002	7 / 352	focal adhesion
2	0.004	2 / 19	costamere
3	0.006	7 / 422	protein complex
4	0.018	7 / 524	intracellular
5	0.029	2 / 52	microvillus
6	0.044	2 / 65	caveola
7	0.050	1 / 10	methylosome
8	0.055	1 / 11	actomyosin
9	0.057	3 / 170	cell−cell junction
10	0.060	1 / 12	clathrin adaptor complex
11	0.069	2 / 84	sarcolemma
12	0.069	1 / 14	integral component of peroxisomal membrane
13	0.069	1 / 14	microtubule plus−end
14	0.069	1 / 14	myosin filament
15	0.071	2 / 85	ciliary basal body

Chr

Rank	p−value	#in/all	Geneset
1	0.001	16 / 1318	Chr 17
2	0.017	9 / 768	Chr 14
3	0.020	11 / 1060	Chr 5
4	0.219	10 / 1467	Chr 19
5	0.221	7 / 959	Chr 16
6	0.384	7 / 1160	Chr 12
7	0.495	5 / 904	Chr 10
8	0.520	3 / 536	Chr 22
9	0.558	6 / 1170	Chr 7
10	0.725	4 / 954	Chr 9
11	0.737	6 / 1411	Chr 11
12	0.749	5 / 1211	Chr 6
13	0.830	2 / 619	Chr 20
14	0.853	9 / 2323	Chr 1
15	0.876	4 / 1217	Chr 3

Chromatin states

Rank	p−value	#in/all	Geneset
1	5e−06	46 / 4795	6_EnhG_Fibroblasts
2	1e−05	36 / 3450	4_TxTrans_Fibroblasts
3	1e−04	49 / 5956	3_TssF_Neuronal_Progenitor
4	5e−04	79 / 11836	3_TssF_Melanocytes
5	1e−03	66 / 9635	3_TssF_Fibroblasts
6	2e−03	44 / 5699	6_EnhG_Melanocytes
7	3e−03	14 / 1206	6_EnhG_Neuronal_Progenitor
8	4e−03	78 / 12298	2_TssA_Melanocytes
9	7e−03	79 / 12741	7_Enh_Melanocytes
10	7e−03	19 / 2028	4_TxTrans_Melanocytes
11	9e−03	58 / 8771	5_Tx_Melanocytes
12	1e−02	79 / 12983	2_TssA_Neuronal_Progenitor
13	1e−02	73 / 11847	7_Enh_Neuronal_Progenitor
14	2e−02	51 / 7854	5_Tx_Fibroblasts
15	5e−02	26 / 3639	1_TssP_Fibroblasts

Colon Cancer

Rank	p−value	#in/all	Geneset
1	4e−06	33 / 2845	TxEnhG1_Colon
2	2e−05	60 / 7354	TssF_Colon
3	5e−05	47 / 5373	EnhWk1_Colon
4	6e−05	30 / 2810	EnhA_Colon
5	9e−05	76 / 10779	Enh_Colon
6	2e−03	46 / 6138	TssD2_Colon
7	4e−03	64 / 9555	TssA_Colon
8	5e−03	71 / 10999	TssWk_Colon
9	7e−03	6 / 328	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
10	7e−03	60 / 9054	Tx_Colon
11	7e−03	10 / 789	TxEnhG2_Colon
12	8e−03	15 / 1470	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
13	1e−02	13 / 1281	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv
14	2e−02	1 / 4	Budinska_C_CIMP−H−like_DOWN
15	2e−02	12 / 1216	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_

Glio

Rank	p−value	#in/all	Geneset
1	0.01	5 / 267	WILLSCHER_GBM_Verhaak−CL & MES_up
2	0.02	3 / 113	GIEZELT_GBM_WT_up_VS_mut
3	0.02	3 / 115	Christensen_hypermethylated_in_grade3_astrocytoma
4	0.02	3 / 117	Christensen_hypermethylated_in_grade2_oligoastrocytoma
5	0.03	3 / 134	Christensen_hypermethylated_in_grade3_oligoastrocytoma
6	0.04	2 / 59	Christensen_hypermethylated_in_primary_glioblastoma
7	0.04	3 / 147	Christensen_hypermethylated_in_grade2_oligodendroglioma
8	0.04	2 / 65	cultured astroglia vs. in vivo astrocytes
9	0.05	2 / 68	Christensen_hypermethylated_in_grade2_astrocytoma
10	0.05	1 / 11	KIM amplified & overexpressed in LTS
11	0.07	8 / 839	Hopp_Sturm_GBM_Epi3_no_zentr_1_G34_DN
12	0.09	2 / 96	Weller_LGG_1p19qDel−vs−intact_DOWN
13	0.11	2 / 110	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
14	0.13	1 / 28	KIM prognostic signature LTS vs. STS
15	0.16	1 / 33	Shaw_responders_down_in_oligo_glioma

GSEA C2

Rank	p−value	#in/all	Geneset
1	9e−04	3 / 37	LEE_CALORIE_RESTRICTION_MUSCLE_UP
2	1e−03	4 / 85	GAVIN_FOXP3_TARGETS_CLUSTER_P7
3	2e−03	2 / 12	KYNG_DNA_DAMAGE_BY_4NQO_OR_GAMMA_RADIATION
4	2e−03	5 / 167	KEGG_CHEMOKINE_SIGNALING_PATHWAY
5	2e−03	11 / 763	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP
6	2e−03	2 / 13	BIOCARTA_EXTRINSIC_PATHWAY
7	2e−03	2 / 13	ZHANG_ADIPOGENESIS_BY_BMP7
8	2e−03	9 / 552	MARTINEZ_TP53_TARGETS_UP
9	3e−03	3 / 53	WANG_PROSTATE_CANCER_ANDROGEN_INDEPENDENT
10	3e−03	8 / 466	BONOME_OVARIAN_CANCER_SURVIVAL_SUBOPTIMAL_DEBULKING
11	3e−03	3 / 56	BILD_SRC_ONCOGENIC_SIGNATURE
12	3e−03	5 / 194	MANALO_HYPOXIA_UP
13	3e−03	2 / 17	BANDRES_RESPONSE_TO_CARMUSTIN_WITHOUT_MGMT_48HR_UP
14	4e−03	3 / 60	KEGG_COMPLEMENT_AND_COAGULATION_CASCADES
15	4e−03	7 / 387	SWEET_LUNG_CANCER_KRAS_DN

HM

Rank	p−value	#in/all	Geneset
1	0.02	4 / 185	HALLMARK_HEME_METABOLISM
2	0.06	3 / 176	HALLMARK_ADIPOGENESIS
3	0.10	2 / 103	HALLMARK_BILE_ACID_METABOLISM
4	0.15	2 / 132	HALLMARK_UV_RESPONSE_DN
5	0.16	2 / 138	HALLMARK_FATTY_ACID_METABOLISM
6	0.18	2 / 151	HALLMARK_APOPTOSIS
7	0.20	2 / 162	HALLMARK_ALLOGRAFT_REJECTION
8	0.24	2 / 183	HALLMARK_GLYCOLYSIS
9	0.25	2 / 186	HALLMARK_ESTROGEN_RESPONSE_EARLY
10	0.25	2 / 186	HALLMARK_ESTROGEN_RESPONSE_LATE
11	0.35	1 / 85	HALLMARK_INTERFERON_ALPHA_RESPONSE
12	0.36	1 / 87	HALLMARK_PROTEIN_SECRETION
13	0.37	1 / 91	HALLMARK_ANDROGEN_RESPONSE
14	0.37	1 / 91	HALLMARK_PEROXISOME
15	0.39	1 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.03	1 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
2	0.53	1 / 147	Homuth_BMI−associated−genes_UP
3	0.66	1 / 211	Homuth_BMI−associated−genes_DN
4	1.00	0 / 94	DUMEAUX_Smoking enriched genes
5	1.00	0 / 10	DUMEAUX_Smoking literature genes up
6	1.00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
7	1.00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
8	1.00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
9	1.00	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
10	1.00	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
11	1.00	0 / 10	DUMEAUX_Women normal BMI literature genes up
12	1.00	0 / 17	DUMEAUX_High bmi enriched genes
13	1.00	0 / 31	DUMEAUX_Fasting enriched genes
14	1.00	0 / 18	Huan_blood−pressure_SBP−signature
15	1.00	0 / 16	Huan_blood−pressure_DBP−signature

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.001	4 / 87	Hopp_Lymphoma_Epi1_with_zentr_v_B.cell_DN
2	0.003	3 / 57	LENZ_Stromal signature 2
3	0.009	5 / 244	LENZ_Stromal signature 1
4	0.009	51 / 7448	HOPP_Strong_enhancer
5	0.024	5 / 318	Hopp_June14_MMML937 tumors+controls_group.overexpression_H_GC−B−
6	0.028	5 / 331	WIRTH_lymphoma937_spot H
7	0.035	3 / 139	Hopp_June14_MMML937 tumors+controls_group.overexpression_F_FL_tons
8	0.036	3 / 141	WIRTH_lymphoma937_spot F
9	0.043	22 / 2939	HOPP_Poised_promoter
10	0.065	35 / 5356	HOPP_Txn_transition
11	0.069	4 / 300	Hopp_June14_MMML937 tumors+controls_group.overexpression_E_GC−B−
12	0.093	1 / 19	DAVE_BL Inter
13	0.096	5 / 472	Hopp_June14_MMML937 tumors+controls_group.overexpression_J_GC−B−
14	0.123	2 / 118	Subero_INT_hyper_meth
15	0.169	1 / 36	Subero_MM_hyper_meth

Melanoma

Rank	p−value	#in/all	Geneset
1	1	0 / 30	Hugo_melanoma−all−MET_UP
2	1	0 / 54	Hugo_melanoma−all−MET_DN
3	1	0 / 43	Hugo_melanoma−BRAFmut−MET_UP
4	1	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
5	1	0 / 27	Hugo_melanoma−all−LEF1_UP
6	1	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

MF

Rank	p−value	#in/all	Geneset
1	0.005	2 / 20	phosphatidylinositol−3,4−bisphosphate binding
2	0.005	2 / 21	14−3−3 protein binding
3	0.013	2 / 34	phosphatidylinositol−3,4,5−trisphosphate binding
4	0.015	2 / 36	protein complex scaffold
5	0.015	2 / 37	structural constituent of muscle
6	0.022	2 / 45	protein kinase C binding
7	0.024	2 / 47	scaffold protein binding
8	0.040	55 / 8818	protein binding
9	0.050	1 / 10	cyclin−dependent protein serine/threonine kinase inhibitor activity
10	0.050	1 / 10	microtubule plus−end binding
11	0.050	1 / 10	type 1 angiotensin receptor binding
12	0.050	1 / 10	vinculin binding
13	0.055	1 / 11	misfolded protein binding
14	0.055	1 / 11	phosphatidylinositol−3,5−bisphosphate 3−phosphatase activity
15	0.060	1 / 12	protein kinase B binding

miRNA Disease

Rank	p−value	#in/all	Geneset
1	1	0 / 7	Thyroid carcinoma, papillary
2	1	0 / 123	Pancreatic cancer
3	1	0 / 68	Glioblastoma multiforme, somatic
4	1	0 / 63	Gastrointestinal
5	1	0 / 3	Pituitary adenoma
6	1	0 / 116	Cancer
7	1	0 / 95	Colorectal cancer
8	1	0 / 2	Adenomas, multiple colorectal
9	1	0 / 124	Prostate cancer
10	1	0 / 48	Alzheimer disease, susceptibility to
11	1	0 / 7	Schizophrenia, susceptibility to
12	1	0 / 20	Parkinson disease
13	1	0 / 65	Hepatocellular carcinoma
14	1	0 / 3	Down syndrome, risk of
15	1	0 / 127	Melanoma and neural system tumor syndrome

miRNA target

Rank	p−value	#in/all	Geneset
1	0.001	8 / 394	hsa−miR−301b
2	0.004	4 / 125	hsa−miR−508−3p
3	0.006	3 / 71	hsa−miR−1266
4	0.007	3 / 76	hsa−miR−205
5	0.009	5 / 249	hsa−miR−524−5p
6	0.010	7 / 463	hsa−miR−301a
7	0.010	5 / 256	hsa−miR−520a−3p
8	0.012	6 / 366	hsa−miR−519b−3p
9	0.013	4 / 176	hsa−miR−520f
10	0.013	6 / 379	hsa−miR−454
11	0.015	6 / 389	hsa−miR−519a
12	0.015	3 / 101	hsa−miR−603
13	0.017	6 / 400	hsa−miR−519c−3p
14	0.017	3 / 106	hsa−miR−22
15	0.020	2 / 42	hsa−miR−640

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.06	1 / 13	BENTINK_e2f3.1
2	1.00	0 / 14	GUSTAFSON_PI3K_UP
3	1.00	0 / 15	GUSTAFSON_PI3K_DN
4	1.00	0 / 13	BENTINK_e2f3.2
5	1.00	0 / 13	BENTINK_myc.1
6	1.00	0 / 12	BENTINK_ras.1
7	1.00	0 / 11	BENTINK_ras.4
8	1.00	0 / 14	BENTINK_ras.6
9	1.00	0 / 13	BENTINK_src.10
10	1.00	0 / 12	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Reference Signatures

Rank	p−value	#in/all	Geneset
1	0.002	15 / 1268	PROTEINATLAS_colon
2	0.006	5 / 221	Chaussabel_3,8_Enzymes
3	0.014	11 / 1003	PROTEINATLAS_appendix
4	0.016	3 / 102	Chaussabel_1,2_Platelets
5	0.017	12 / 1173	PROTEINATLAS_rectum
6	0.018	12 / 1176	PROTEINATLAS_duodenum
7	0.028	11 / 1118	PROTEINATLAS_placenta
8	0.032	11 / 1138	PROTEINATLAS_small intestine
9	0.035	4 / 240	Chaussabel_3,3_Inflammation II
10	0.036	4 / 242	Chaussabel_3,2_Inflammation I
11	0.042	3 / 150	Chaussabel_2,6_Myeloid lineage
12	0.053	11 / 1239	PROTEINATLAS_testis
13	0.055	1 / 11	WIRTH_Tonsil
14	0.055	10 / 1097	PROTEINATLAS_kidney
15	0.060	1 / 12	WIRTH_Globus pallidus

Telomeres

Rank	p−value	#in/all	Geneset
1	1	0 / 13	Alternative lengthening of telomeres
2	1	0 / 27	Nabetani_alt len telomeres_genes_ko
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	2e−05	47 / 5188	ICGC_Ebfsc137065_targets
2	2e−04	56 / 7247	ICGC_Runx3_targets
3	5e−04	44 / 5410	ICGC_Foxm1_targets
4	6e−04	32 / 3507	ICGC_Rad21_targets
5	7e−04	49 / 6322	ICGC_Tcf3_targets
6	8e−04	37 / 4345	ICGC_Zeb1_targets
7	8e−04	50 / 6552	ICGC_Pol2_targets
8	1e−03	48 / 6267	ICGC_Yy1_targets
9	1e−03	43 / 5442	ICGC_Pmlsc71910_targets
10	1e−03	51 / 6868	ICGC_Elf1_targets
11	3e−03	41 / 5312	ICGC_Tcf12_targets
12	3e−03	48 / 6578	ICGC_Pou2_targets
13	3e−03	41 / 5383	ICGC_Sp1_targets
14	4e−03	44 / 5961	ICGC_Pol24_targets
15	4e−03	44 / 5984	ICGC_Mta3_targets

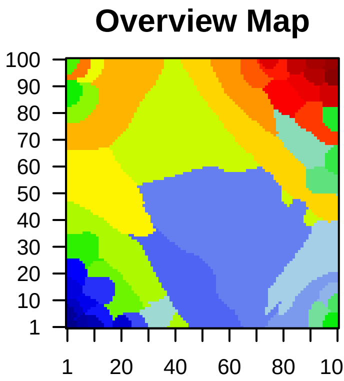
K−Means Cluster

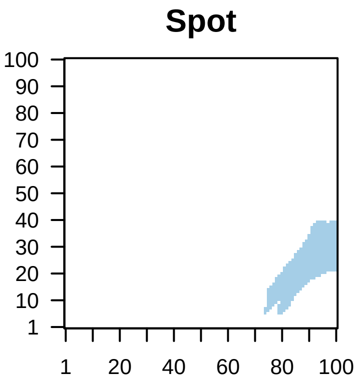
Spot Summary: F

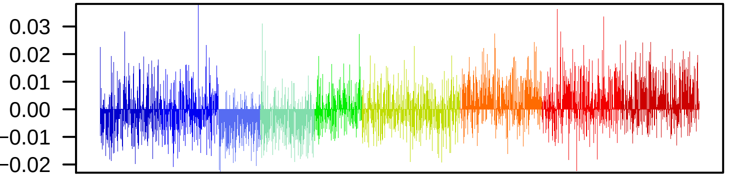
metagenes = 435
genes = 807

<r> metagenes = 0.74
<r> genes = 0.02
beta: r2= 0.23 / log p= −Inf

samples with spot = 0 (0 %)


Overview Map


Spot

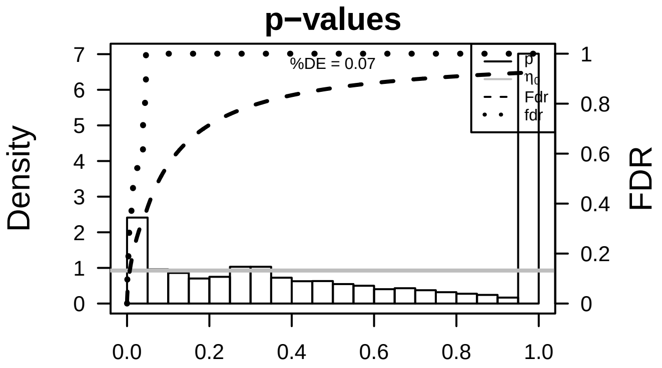


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_213497	0.55	−0.33	0.11	RAB38	RAB38, member RAS oncogene family [Source:HGNC Symb
2	ILMN_325922	0.49	−0.26	0.09		
3	ILMN_215915	0.44	−0.25	0.1	TP53TG3F	TP53 target 3 family member F [Source:HGNC Symbol;Acc:H
4	ILMN_174425	0.42	−0.24	0.09	TP53TG3F	
5	ILMN_165962	0.4	−0.22	0.07		
6	ILMN_238147	0.38	−0.29	0.09	ATL1	atlastin GTPase 1 [Source:HGNC Symbol;Acc:HGNC:11231]
7	ILMN_173454	0.38	−0.21	0.22	WTAP	Wilms tumor 1 associated protein [Source:HGNC Symbol;Acc
8	ILMN_219344	0.37	−0.22	0.09	TRIM16L	tripartite motif containing 16−like [Source:HGNC Symbol;Acc:
9	ILMN_323961	0.37	−0.19	0.12		
10	ILMN_218621	0.36	−0.23	0.15	GOLIM4	golgi integral membrane protein 4 [Source:HGNC Symbol;Acc
11	ILMN_180069	0.36	−0.27	0.1	LDB2	LIM domain binding 2 [Source:HGNC Symbol;Acc:HGNC:653
12	ILMN_239669	0.36	−0.23	0.16	AKAP9	A−kinase anchoring protein 9 [Source:HGNC Symbol;Acc:HG
13	ILMN_169410	0.35	−0.22	0.12	PRIM2	primase (DNA) subunit 2 [Source:HGNC Symbol;Acc:HGNC:
14	ILMN_221800	0.33	−0.22	0.06	LIPC	lipase C, hepatic type [Source:HGNC Symbol;Acc:HGNC:661
15	ILMN_174292	0.33	−0.19	0.12	HESX1	HESX homeobox 1 [Source:HGNC Symbol;Acc:HGNC:4877]
16	ILMN_165482	0.32	−0.2	0.12		ribosomal protein L23a pseudogene 82 [Source:HGNC Symb
17	ILMN_175027	0.32	−0.27	0.08		
18	ILMN_186005	0.32	−0.2	0.11		
19	ILMN_181428	0.32	−0.23	0.1		
20	ILMN_168585	0.31	−0.24	0.21	UBN2	ubinuclein 2 [Source:HGNC Symbol;Acc:HGNC:21931]

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	2e−17	336 / 8990	Chror	15_Quies_Fibroblasts
2	3e−15	393 / 11455	Chror	2_TssA_Fibroblasts
3	8e−14	292 / 7854	Chror	5_Tx_Fibroblasts
4	2e−13	378 / 11130	Chror	15_Quies_Melanocytes
5	6e−13	314 / 8771	Chror	5_Tx_Melanocytes
6	3e−11	338 / 9917	Brain	Overlap_fetal_midbrain_ReprPCWk
7	2e−10	325 / 9555	Colon	TssA_Colon
8	2e−10	299 / 8613	Chror	7_Enh_Fibroblasts
9	3e−10	362 / 10999	Colon	TssWk_Colon
10	3e−10	395 / 12298	Chror	2_TssA_Melanocytes
11	6e−10	265 / 7448	Lympl	HOPP_Strong_enhancer
12	2e−09	249 / 6959	Lympl	HOPP_Weak_enhancer
13	2e−09	327 / 9815	Brain	Overlap_fetal_midbrain_ReprPC
14	3e−09	296 / 8678	Colon	Quies3_Colon
15	3e−09	219 / 5936	Brain	Overlap_fetal_midbrain_HetRpts
16	3e−09	53 / 841	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_UP
17	5e−09	236 / 6559	Lympl	HOPP_Weak_txn
18	6e−09	50 / 783	GSEA	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
19	8e−09	406 / 12983	Chror	2_TssA_Neuronal_Progenitor
20	8e−09	278 / 8098	Lympl	HOPP_Weak_promoter
21	4e−08	337 / 10430	Brain	Overlap_fetal_midbrain_Quies
22	5e−08	87 / 1846	Chror	14_ZNF_Melanocytes
23	6e−08	251 / 7275	Lympl	HOPP_Txn_elongation
24	7e−08	277 / 8226	Lympl	HOPP_Active_promoter
25	8e−08	286 / 8568	Colon	TxWk_Colon
26	2e−07	313 / 9635	Chror	3_TssF_Fibroblasts
27	2e−07	129 / 3194	TF	ICGC_Irf4_targets
28	2e−07	21 / 211	Lifesty	Homuth_BMI−associated−genes_DN
29	2e−07	240 / 6970	Chror	5_Tx_Neuronal_Progenitor
30	2e−07	393 / 12741	Chror	7_Enh_Melanocytes
31	3e−07	175 / 4735	TF	ICGC_Pu1_targets
32	3e−07	20 / 200	GSEA	REACTOME_SIGNALLING_BY_NGF
33	4e−07	42 / 692	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP
34	4e−07	289 / 8818	MF	protein binding
35	5e−07	195 / 5466	TF	ICGC_Nficsc81335_targets
36	8e−07	131 / 3348	TF	ICGC_BatfPcr1_targets
37	8e−07	381 / 12393	Chror	15_Quies_Neuronal_Progenitor
38	2e−06	43 / 757	GSEA	KOINUMA_TARGETS_OF_SMAD2_OR_SMAD3
39	2e−06	43 / 763	GSEA	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP
40	2e−06	291 / 9054	Colon	Tx_Colon


p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.3	4 / 111	HORVATH_aging_genes meth DOWN
2	0.5	4 / 142	HORVATH_aging_genes meth UP
3	0.8	1 / 58	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	1e−05	9 / 56	negative regulation of transforming growth factor beta receptor signaling pathw
2	2e−04	19 / 280	response to drug
3	3e−04	6 / 36	cellular response to UV
4	5e−04	6 / 39	positive regulation of neuron apoptotic process
5	6e−04	6 / 40	extrinsic apoptotic signaling pathway
6	6e−04	6 / 40	response to UV
7	6e−04	5 / 27	cellular response to organic substance
8	6e−04	5 / 27	positive regulation of apoptotic signaling pathway
9	7e−04	8 / 74	cellular response to organic cyclic compound
10	8e−04	5 / 29	extrinsic apoptotic signaling pathway in absence of ligand
11	9e−04	6 / 44	activation of MAPKK activity
12	1e−03	9 / 97	phosphatidylinositol−mediated signaling
13	1e−03	6 / 45	intrinsic apoptotic signaling pathway in response to DNA damage
14	1e−03	6 / 47	protein autoubiquitination
15	1e−03	8 / 83	transforming growth factor beta receptor signaling pathway

Brain

Rank	p−value	#in/all	Geneset
1	3e−11	338 / 9917	Overlap_fetal_midbrain_ReprPCWk
2	2e−09	327 / 9815	Overlap_fetal_midbrain_ReprPC
3	3e−09	219 / 5936	Overlap_fetal_midbrain_HetRpts
4	4e−08	337 / 10430	Overlap_fetal_midbrain_Quies
5	4e−04	288 / 9504	Overlap_fetal_midbrain_K9K27me3
6	6e−03	19 / 386	Fetal_ZNF
7	7e−03	29 / 681	Overlap_fetal_midbrain_EnhP
8	1e−02	32 / 796	Overlap_fetal_midbrain_ZNF
9	1e−02	48 / 1329	Overlap_fetal_midbrain_Enh
10	2e−02	43 / 1171	Fetal_EnhP
11	2e−02	51 / 1436	Fetal_K9K27me3
12	2e−02	42 / 1162	Fetal_Enh
13	4e−02	39 / 1115	Overlap_fetal_midbrain_EnhG
14	5e−02	33 / 937	Fetal_EnhG
15	8e−02	40 / 1213	Fetal_TssP

Cancer

Rank	p−value	#in/all	Geneset
1	2e−05	13 / 125	PanCan_CC+Apop_geneset_nanostring
2	2e−04	11 / 117	PanCan_Driver_Gene_geneset_nanostring
3	6e−04	0 / 15	LIU_PROSTATE_CANCER_DN
4	3e−03	26 / 554	Lembcke_Colonic Inflammation
5	1e−02	11 / 193	PanCan_PI3K_geneset_nanostring
6	1e−02	3 / 20	PanCan_ChromMod_geneset_nanostring
7	3e−02	4 / 46	PanCan_TGF−B_geneset_nanostring
8	1e−01	12 / 301	SPANG_BCL6−index2
9	1e−01	19 / 527	Lembcke_Normal vs Adenoma
10	1e−01	6 / 136	PanCan_RAS_geneset_nanostring
11	2e−01	4 / 82	PanCan_JAK−ST_geneset_nanostring
12	2e−01	6 / 150	PanCan_MAPK_geneset_nanostring
13	2e−01	4 / 91	PanCan_TXmisReg_geneset_nanostring
14	2e−01	2 / 36	PanCan_HK_geneset_nanostring
15	3e−01	1 / 13	WANG_ER_DN

CC

Rank	p−value	#in/all	Geneset
1	3e−06	85 / 1979	membrane
2	2e−04	9 / 80	nucleosome
3	3e−04	24 / 422	protein complex
4	6e−04	159 / 4822	cytoplasm
5	1e−03	90 / 2535	nucleoplasm
6	2e−03	16 / 273	neuron projection
7	3e−03	9 / 115	nuclear chromosome, telomeric region
8	5e−03	152 / 4828	nucleus
9	6e−03	3 / 15	beta−catenin destruction complex
10	7e−03	8 / 106	Z disc
11	9e−03	4 / 32	dendritic shaft
12	1e−02	5 / 50	endocytic vesicle
13	1e−02	4 / 34	nuclear nucleosome
14	1e−02	97 / 2979	cytosol
15	1e−02	6 / 74	cell body

Chr

Rank	p−value	#in/all	Geneset
1	0.03	51 / 1492	Chr 2
2	0.04	42 / 1217	Chr 3
3	0.05	40 / 1170	Chr 7
4	0.10	30 / 902	Chr 4
5	0.12	31 / 954	Chr 9
6	0.20	26 / 836	Chr 8
7	0.24	17 / 536	Chr 22
8	0.34	9 / 289	Chr 21
9	0.42	29 / 1060	Chr 5
10	0.52	26 / 994	Chr X
11	0.54	20 / 769	Chr 15
12	0.71	34 / 1411	Chr 11
13	0.75	56 / 2323	Chr 1
14	0.77	28 / 1211	Chr 6
15	0.80	20 / 904	Chr 10

Chromatin states

Rank	p−value	#in/all	Geneset
1	2e−17	336 / 8990	15_Quies_Fibroblasts
2	3e−15	393 / 11455	2_TssA_Fibroblasts
3	8e−14	292 / 7854	5_Tx_Fibroblasts
4	2e−13	378 / 11130	15_Quies_Melanocytes
5	6e−13	314 / 8771	5_Tx_Melanocytes
6	2e−10	299 / 8613	7_Enh_Fibroblasts
7	3e−10	395 / 12298	2_TssA_Melanocytes
8	8e−09	406 / 12983	2_TssA_Neuronal_Progenitor
9	5e−08	87 / 1846	14_ZNF_Melanocytes
10	2e−07	313 / 9635	3_TssF_Fibroblasts
11	2e−07	240 / 6970	5_Tx_Neuronal_Progenitor
12	2e−07	393 / 12741	7_Enh_Melanocytes
13	8e−07	381 / 12393	15_Quies_Neuronal_Progenitor
14	2e−05	359 / 11836	3_TssF_Melanocytes
15	2e−05	167 / 4795	6_EnhG_Fibroblasts

Colon Cancer

Rank	p−value	#in/all	Geneset
1	2e−10	325 / 9555	TssA_Colon
2	3e−10	362 / 10999	TssWk_Colon
3	3e−09	296 / 8678	Quies3_Colon
4	8e−08	286 / 8568	TxWk_Colon
5	2e−06	291 / 9054	Tx_Colon
6	2e−05	65 / 1470	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
7	4e−05	296 / 9530	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP_
8	2e−04	154 / 4526	Quies1_Colon
9	4e−04	60 / 1468	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
10	6e−04	229 / 7354	TssF_Colon
11	9e−04	173 / 5373	EnhWk1_Colon
12	2e−03	55 / 1404	LaPointe_mucosa−position_kmeans_D_transverse colon_UP_
13	2e−03	44 / 1069	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
14	3e−03	132 / 4034	TssD1_Colon
15	3e−03	74 / 2073	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t

Glio

Rank	p−value	#in/all	Geneset
1	7e−04	19 / 316	WILLSCHER_GBM_Verhaak−PNwt & CL_up
2	3e−03	35 / 820	Sturm_GBM_Meth_overexpression_E_G34_UP
3	8e−03	5 / 48	Vishal_subnetwork signature of survival in GBM
4	2e−02	9 / 150	Hopp_Sturm_GBM_Epi3_E_G34_UP
5	4e−02	58 / 1777	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
6	5e−02	6 / 101	Hopp_Sturm_GBM_Epi3_D1_IDH_UP_adult_fetus_DN
7	6e−02	4 / 56	Christensen_hypomethylated_in_primary_glioblastoma
8	6e−02	2 / 16	neurons_glio
9	7e−02	64 / 2043	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
10	9e−02	4 / 65	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
11	9e−02	11 / 267	WILLSCHER_GBM_Verhaak−CL & MES_up
12	1e−01	4 / 69	WILLSCHER_GBM_Verhaak−PNwt & MES_up
13	1e−01	3 / 44	WILLSCHER_GBM_Verhaak−PNwt_up
14	1e−01	7 / 157	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
15	1e−01	1 / 6	laffaire_hypometh_LGG_vs_control

GSEA C2

Rank	p−value	#in/all	Geneset
1	3e−09	53 / 841	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_UP
2	6e−09	50 / 783	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
3	3e−07	20 / 200	REACTOME_SIGNALLING_BY_NGF
4	4e−07	42 / 692	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP
5	2e−06	43 / 757	KOINUMA_TARGETS_OF_SMAD2_OR_SMAD3
6	2e−06	43 / 763	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP
7	4e−06	44 / 813	WAKABAYASHI_ADIPOGENESIS_PPARG_RXRA_BOUND_8D
8	6e−06	29 / 442	DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN
9	9e−06	20 / 249	OSWALD_HEMATOPOIETIC_STEM_CELL_IN_COLLAGEN_GEL_DN
10	1e−05	6 / 21	BIOCARTA_CASPASE_PATHWAY
11	1e−05	68 / 1535	BLALOCK_ALZHEIMERS_DISEASE_UP
12	1e−05	13 / 118	REACTOME_SIGNALING_BY_FGFR_IN_DISEASE
13	1e−05	5 / 13	BIOCARTA_PS1_PATHWAY
14	5e−05	8 / 51	PID_TGFBR_PATHWAY
15	6e−05	8 / 52	BIOCARTA_HIVNEF_PATHWAY

HM

Rank	p−value	#in/all	Geneset
1	2e−04	14 / 176	HALLMARK_ADIPOGENESIS
2	6e−04	12 / 151	HALLMARK_APOPTOSIS
3	1e−03	13 / 187	HALLMARK_COMPLEMENT
4	6e−03	9 / 127	HALLMARK_COAGULATION
5	9e−03	11 / 183	HALLMARK_APICAL_JUNCTION
6	1e−02	5 / 50	HALLMARK_TGF_BETA_SIGNALING
7	1e−02	11 / 186	HALLMARK_IL2_STAT5_SIGNALING
8	2e−02	4 / 40	HALLMARK_WNT_BETA_CATENIN_SIGNALING
9	3e−02	5 / 69	HALLMARK_CHOLESTEROL_HOMEOSTASIS
10	4e−02	9 / 172	HALLMARK_INTERFERON_GAMMA_RESPONSE
11	7e−02	7 / 137	HALLMARK_UV_RESPONSE_UP
12	1e−01	5 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING
13	1e−01	8 / 185	HALLMARK_MTORC1_SIGNALING
14	1e−01	6 / 132	HALLMARK_UV_RESPONSE_DN
15	2e−01	4 / 85	HALLMARK_INTERFERON_ALPHA_RESPONSE

Lifestyle

Rank	p−value	#in/all	Geneset
1	2e−07	21 / 211	Homuth_BMI−associated−genes_DN
2	4e−01	1 / 17	DUMEAUX_High bmi enriched genes
3	6e−01	1 / 31	DUMEAUX_Fasting enriched genes
4	7e−01	3 / 147	Homuth_BMI−associated−genes_UP
5	9e−01	1 / 94	DUMEAUX_Smoking enriched genes
6	1e+00	0 / 10	DUMEAUX_Smoking literature genes up
7	1e+00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
8	1e+00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
9	1e+00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
10	1e+00	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
11	1e+00	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
12	1e+00	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
13	1e+00	0 / 10	DUMEAUX_Women normal BMI literature genes up
14	1e+00	0 / 18	Huan_blood−pressure_SBP−signature
15	1e+00	0 / 16	Huan_blood−pressure_DBP−signature

Lymphoma

Rank	p−value	#in/all	Geneset
1	6e−10	265 / 7448	HOPP_Strong_enhancer
2	2e−09	249 / 6959	HOPP_Weak_enhancer
3	5e−09	236 / 6559	HOPP_Weak_txn
4	8e−09	278 / 8098	HOPP_Weak_promoter
5	6e−08	251 / 7275	HOPP_Txn_elongation
6	7e−08	277 / 8226	HOPP_Active_promoter
7	5e−05	181 / 5356	HOPP_Txn_transition
8	2e−04	55 / 1270	SPANG_BCR UP
9	2e−04	100 / 2701	HOPP_Repetitive
10	2e−04	51 / 1169	SPANG_BCR DN
11	3e−04	18 / 272	SPANG_IL21 DN
12	5e−04	20 / 331	SPANG_CD40 6hrs UP
13	1e−03	5 / 31	Care_Extended T−cell
14	1e−03	25 / 493	WIRTH_lymphoma937_spot J
15	3e−03	23 / 472	Hopp_June14_MMML937 tumors+controls_group.overexpression_J_GC−B−c

Melanoma

Rank	p−value	#in/all	Geneset
1	0.3	2 / 43	Hugo_melanoma−BRAFmut−MET_UP
2	0.5	1 / 27	Hugo_melanoma−all−LEF1_UP
3	0.8	1 / 54	Hugo_melanoma−all−MET_DN
4	1.0	0 / 30	Hugo_melanoma−all−MET_UP
5	1.0	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
6	1.0	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

MF

Rank	p−value	#in/all	Geneset
1	4e−07	289 / 8818	protein binding
2	9e−05	25 / 413	protein heterodimerization activity
3	1e−04	7 / 42	SMAD binding
4	1e−03	5 / 30	insulin receptor binding
5	1e−03	53 / 1329	ATP binding
6	2e−03	6 / 49	cysteine−type endopeptidase activity
7	2e−03	3 / 10	transmembrane receptor protein tyrosine kinase adaptor activity
8	2e−03	5 / 36	protein complex scaffold
9	2e−03	3 / 11	anion transmembrane−transporting ATPase activity
10	2e−03	3 / 11	insulin receptor substrate binding
11	2e−03	3 / 11	I−SMAD binding
12	3e−03	4 / 23	cadherin binding
13	4e−03	7 / 77	PDZ domain binding
14	5e−03	18 / 351	GTP binding
15	7e−03	5 / 47	scaffold protein binding

miRNA Disease

Rank	p−value	#in/all	Geneset
1	0.3	1 / 13	Psoriasis, susceptibility to
2	0.3	1 / 14	Autism, susceptibility to
3	0.5	1 / 27	Duchenne muscular dystrophy
4	0.5	1 / 28	Miyoshi myopathy
5	0.7	1 / 40	Medulloblastoma
6	0.7	1 / 40	Muscular dystrophy
7	0.7	1 / 48	Alzheimer disease, susceptibility to
8	0.8	1 / 56	Myopathy, nemaline, 3
9	0.8	1 / 57	Cardiomyopathy, dilated
10	0.8	2 / 113	Ovarian cancer
11	0.8	2 / 120	Hematological
12	0.8	2 / 123	Pancreatic cancer
13	0.8	2 / 124	Prostate cancer
14	0.8	2 / 127	Squamous cell carcinoma, head and neck
15	0.9	1 / 73	Stroke, susceptibility to

miRNA target

Rank	p−value	#in/all	Geneset
1	8e−06	21 / 267	hsa−miR−30a
2	1e−05	23 / 315	hsa−miR−30e
3	1e−05	21 / 274	hsa−miR−30b
4	2e−05	21 / 281	hsa−miR−570
5	2e−05	21 / 283	hsa−miR−30c
6	3e−05	29 / 480	hsa−miR−15b
7	4e−05	28 / 463	hsa−miR−301a
8	6e−05	24 / 379	hsa−miR−454
9	1e−04	19 / 272	hsa−miR−30d
10	1e−04	24 / 394	hsa−miR−301b
11	1e−04	23 / 374	hsa−miR−144
12	2e−04	19 / 283	hsa−miR−320a
13	3e−04	10 / 100	hsa−miR−590−5p
14	3e−04	13 / 160	hsa−miR−298
15	3e−04	25 / 449	hsa−miR−130b

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.3	1 / 11	BENTINK_ras.4
2	0.3	1 / 12	BENTINK_ras.1
3	0.3	1 / 13	BENTINK_e2f3.2
4	1.0	0 / 14	GUSTAFSON_PI3K_UP
5	1.0	0 / 15	GUSTAFSON_PI3K_DN
6	1.0	0 / 13	BENTINK_e2f3.1
7	1.0	0 / 13	BENTINK_myc.1
8	1.0	0 / 14	BENTINK_ras.6
9	1.0	0 / 13	BENTINK_src.10
10	1.0	0 / 12	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Reference Signatures

Rank	p−value	#in/all	Geneset
1	2e−05	38 / 695	PROTEINATLAS_bone marrow
2	4e−05	19 / 254	PROTEINATLAS_smooth muscle
3	2e−04	46 / 1003	PROTEINATLAS_appendix
4	2e−04	36 / 726	PROTEINATLAS_cervix, uterine
5	4e−04	32 / 639	PROTEINATLAS_breast
6	5e−04	29 / 571	PROTEINATLAS_oral mucosa
7	6e−04	46 / 1063	PROTEINATLAS_tonsil
8	7e−04	44 / 1016	PROTEINATLAS_cerebral cortex
9	8e−04	42 / 959	PROTEINATLAS_nasopharynx
10	8e−04	49 / 1173	PROTEINATLAS_rectum
11	8e−04	37 / 816	PROTEINATLAS_endometrium
12	9e−04	30 / 619	PROTEINATLAS_salivary gland
13	1e−03	10 / 119	Chaussabel_2,11_Replication
14	1e−03	35 / 782	PROTEINATLAS_thyroid gland
15	1e−03	51 / 1268	PROTEINATLAS_colon

Telomeres

Rank	p−value	#in/all	Geneset
1	0.03	3 / 27	Nabetani_alt len telomeres_genes_ko
2	0.29	1 / 13	Alternative lengthening of telomeres
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	2e−07	129 / 3194	ICGC_Irf4_targets
2	3e−07	175 / 4735	ICGC_Pu1_targets
3	5e−07	195 / 5466	ICGC_Nficsc81335_targets
4	8e−07	131 / 3348	ICGC_BatfPcr1_targets
5	3e−06	68 / 1466	ICGC_NrsfPcr1_targets
6	4e−06	179 / 5067	ICGC_Taf1_targets
7	4e−06	186 / 5312	ICGC_Tcf12_targets
8	6e−06	221 / 6578	ICGC_Pou2_targets
9	2e−05	237 / 7247	ICGC_Runx3_targets
10	2e−05	186 / 5442	ICGC_Pmlsc71910_targets
11	2e−05	210 / 6322	ICGC_Tcf3_targets
12	5e−05	198 / 5961	ICGC_Pol24_targets
13	6e−05	182 / 5410	ICGC_Foxm1_targets
14	8e−05	88 / 2255	ICGC_SrfV0416101_targets
15	9e−05	184 / 5518	ICGC_Stat5_targets

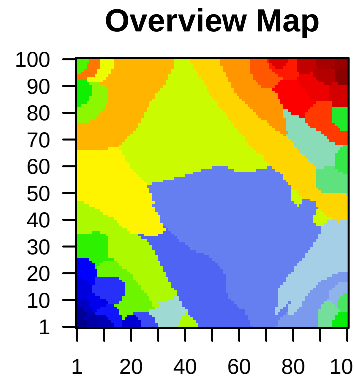
K−Means Cluster

Spot Summary: G

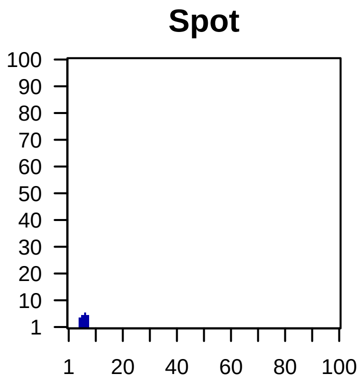
metagenes = 20
genes = 301

<r> metagenes = 0.96
<r> genes = 0.57
beta: r2= 122.17 / log p= −Inf

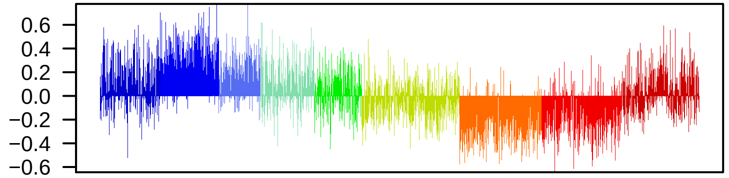
samples with spot = 1017 (30 %)
A * : 157 (45.6 %)
A C * : 279 (85.1 %)
A C F * : 144 (61.3 %)
A F * : 118 (38.3 %)
C F * : 77 (29.1 %)
F * : 83 (15 %)
F J * : 8 (1.7 %)
J * : 19 (4.3 %)
N * : 132 (29.8 %)



Overview Map



Spot

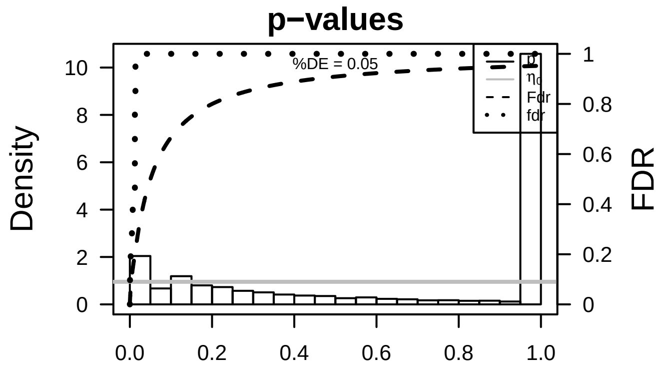


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_173045	2.93	−1.93	0.33	FOLR3	folate receptor 3 [Source:HGNC Symbol;Acc:HGNC:3795]
2	ILMN_169319	2.29	−2.04	0.57	PI3	peptidase inhibitor 3 [Source:HGNC Symbol;Acc:HGNC:8947
3	ILMN_179631	2.16	−1.97	0.81	MMP9	matrix metallopeptidase 9 [Source:HGNC Symbol;Acc:HGNC
4	ILMN_169658	2.03	−1.31	0.6		
5	ILMN_180121	1.96	−2.45	0.51	S100P	S100 calcium binding protein P [Source:HGNC Symbol;Acc:H
6	ILMN_170487	1.95	−1.49	0.8	PGLYRP1	peptidoglycan recognition protein 1 [Source:HGNC Symbol;A
7	ILMN_178573	1.8	−1.22	0.61		
8	ILMN_170160	1.74	−2	0.76	ALPL	alkaline phosphatase, liver/bone/kidney [Source:HGNC Symb
9	ILMN_174891	1.68	−1.3	0.67	S100A12	S100 calcium binding protein A12 [Source:HGNC Symbol;Acc
10	ILMN_176271	1.67	−1.13	0.74	MCEMP1	mast cell expressed membrane protein 1 [Source:HGNC Sym
11	ILMN_169454	1.63	−1.08	0.77	ANXA3	annexin A3 [Source:HGNC Symbol;Acc:HGNC:541]
12	ILMN_170893	1.62	−1.48	0.74	ADM	adrenomedullin [Source:HGNC Symbol;Acc:HGNC:259]
13	ILMN_177525	1.62	−1.53	0.73	PROK2	prokineticin 2 [Source:HGNC Symbol;Acc:HGNC:18455]
14	ILMN_173399	1.53	−1.22	0.51	DHRS9	dehydrogenase/reductase 9 [Source:HGNC Symbol;Acc:HGN
15	ILMN_171681	1.5	−1	0.61	CEACAM1	carcinoembryonic antigen related cell adhesion molecule 1 [S
16	ILMN_177213	1.48	−1.25	0.82	IL1R2	interleukin 1 receptor type 2 [Source:HGNC Symbol;Acc:HGN
17	ILMN_180522	1.47	−1.18	0.89	LRG1	leucine rich alpha−2−glycoprotein 1 [Source:HGNC Symbol;A
18	ILMN_181228	1.46	−0.74	0.67	ARG1	arginase 1 [Source:HGNC Symbol;Acc:HGNC:663]
19	ILMN_318313	1.45	−1.16	0.84		
20	ILMN_330786	1.45	−1.58	0.4	CHI3L1	chitinase 3 like 1 [Source:HGNC Symbol;Acc:HGNC:1932]

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	7e−23	25 / 150	Refer	Chaussabel_2,6_Myeloid lineage
2	1e−22	48 / 810	Colon	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
3	2e−18	82 / 2810	Colon	EnhA_Colon
4	3e−17	179 / 10779	Colon	Enh_Colon
5	6e−17	21 / 164	GSEA	VERHAAK_AML_WITH_NPM1_MUTATED_UP
6	2e−16	79 / 2845	Colon	TxEnhG1_Colon
7	1e−15	23 / 240	Refer	Chaussabel_3,3_Inflammation II
8	3e−14	18 / 150	GSEA	BROWN_MYELOID_CELL_DEVELOPMENT_UP
9	2e−13	16 / 120	GSEA	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_16D_DN
10	3e−13	17 / 147	GSEA	SMIRNOV_CIRCULATING_ENDOTHELIOCYTES_IN_CANCER_UP
11	5e−13	15 / 107	GSEA	LENAOUR_DENDRITIC_CELL_MATURATION_DN
12	2e−12	131 / 7354	Colon	TssF_Colon
13	2e−12	29 / 554	Cance	Lembcke_Colonic Inflammation
14	4e−12	18 / 196	GSEA	MCLACHLAN_DENTAL_CARIES_UP
15	1e−11	20 / 267	Glio	WILLSCHER_GBM_Verhaak−CL & MES_up
16	1e−11	18 / 208	GSEA	THEILGAARD_NEUTROPHIL_AT_SKIN_WOUND_DN
17	1e−11	24 / 409	GSEA	MARTENS_BOUND_BY_PML_RARA_FUSION
18	2e−11	14 / 113	Refer	Chaussabel_1,5_Myeloid lineage
19	2e−11	104 / 5373	Colon	EnhWk1_Colon
20	3e−11	46 / 1470	Colon	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon
21	7e−11	30 / 692	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP
22	1e−10	22 / 382	GSEA	MULLIGHAN_MLL_SIGNATURE_2_UP
23	2e−10	99 / 5188	TF	ICGC_Ebfsc137065_targets
24	3e−10	16 / 192	GSEA	MCLACHLAN_DENTAL_CARIES_DN
25	3e−10	78 / 3662	CC	plasma membrane
26	4e−10	93 / 4795	Chror	6_EnhG_Fibroblasts
27	5e−10	92 / 4735	TF	ICGC_Pu1_targets
28	6e−10	16 / 203	GSEA	VERHAAK_GLIOBLASTOMA_MESENCHYMAL
29	6e−10	20 / 336	BP	inflammatory response
30	8e−10	74 / 3450	Chror	4_TxTrans_Fibroblasts
31	8e−10	15 / 178	BP	response to lipopolysaccharide
32	1e−09	17 / 242	Refer	Chaussabel_3,2_Inflammation I
33	1e−09	16 / 212	GSEA	RUTELLA_RESPONSE_TO_HGF_DN
34	1e−09	15 / 183	GSEA	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_8D_DN
35	2e−09	124 / 7448	Lymp	HOPP_Strong_enhancer
36	2e−09	11 / 87	GSEA	HAHTOLA_SEZARY_SYNDROM_UP
37	2e−09	6 / 13	GSEA	MARTINELLI_IMMATURE_NEUTROPHIL_DN
38	3e−09	18 / 293	BP	immune response
39	4e−09	10 / 71	GSEA	HESS_TARGETS_OF_HOXA9_AND_MEIS1_DN
40	8e−09	70 / 3348	TF	ICGC_BatfPcr1_targets



p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.1	3 / 111	HORVATH_aging_genes meth DOWN
2	0.8	1 / 142	HORVATH_aging_genes meth UP
3	1.0	0 / 58	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Cancer

Rank	p−value	#in/all	Geneset
1	2e−12	29 / 554	Lembcke_Colonic Inflammation
2	4e−04	11 / 301	SPANG_BCL6−index2
3	1e−02	1 / 14	LIU_PROSTATE_CANCER_UP
4	4e−02	5 / 178	SPANG_LPS−index2
5	4e−02	3 / 73	SHAUGHNESSY_MM high risk
6	4e−02	0 / 13	LIU_LIVER_CANCER
7	6e−02	2 / 39	ZHANG_MM up
8	1e−01	9 / 527	Lembcke_Normal vs Adenoma
9	1e−01	1 / 14	LIU_COMMON_CANCER_GENES
10	1e−01	1 / 14	BEN−PORATH_UP
11	1e−01	1 / 14	GENTLES_modul4
12	1e−01	3 / 125	PanCan_CC+Apop_geneset_nanostring
13	1e−01	4 / 193	PanCan_PI3K_geneset_nanostring
14	2e−01	3 / 150	PanCan_MAPK_geneset_nanostring
15	2e−01	1 / 24	PanCan_Notch_geneset_nanostring

Chromatin states

Rank	p−value	#in/all	Geneset
1	4e−10	93 / 4795	6_EnhG_Fibroblasts
2	8e−10	74 / 3450	4_TxTrans_Fibroblasts
3	2e−07	142 / 9635	3_TssF_Fibroblasts
4	1e−06	94 / 5699	6_EnhG_Melanocytes
5	5e−05	55 / 3068	8_EnhP_Fibroblasts
6	8e−05	155 / 11836	3_TssF_Melanocytes
7	9e−05	40 / 2028	4_TxTrans_Melanocytes
8	1e−04	164 / 12741	7_Enh_Melanocytes
9	2e−04	153 / 11847	7_Enh_Neuronal_Progenitor
10	3e−04	66 / 4169	10_ReprPC_Fibroblasts
11	2e−03	62 / 4107	9_ReprPCWk_Fibroblasts
12	4e−03	152 / 12393	15_Quies_Neuronal_Progenitor
13	4e−03	151 / 12298	2_TssA_Melanocytes
14	5e−03	142 / 11455	2_TssA_Fibroblasts
15	6e−03	111 / 8613	7_Enh_Fibroblasts

GSEA C2

Rank	p−value	#in/all	Geneset
1	6e−17	21 / 164	VERHAAK_AML_WITH_NPM1_MUTATED_UP
2	3e−14	18 / 150	BROWN_MYELOID_CELL_DEVELOPMENT_UP
3	2e−13	16 / 120	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_16D_DN
4	3e−13	17 / 147	SMIRNOV_CIRCULATING_ENDOTHELIOCYTES_IN_CANCER_UP
5	5e−13	15 / 107	LENAOUR_DENDRITIC_CELL_MATURATION_DN
6	4e−12	18 / 196	MCLACHLAN_DENTAL_CARIES_UP
7	1e−11	18 / 208	THEILGAARD_NEUTROPHIL_AT_SKIN_WOUND_DN
8	1e−11	24 / 409	MARTENS_BOUND_BY_PML_RARA_FUSION
9	7e−11	30 / 692	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP
10	1e−10	22 / 382	MULLIGHAN_MLL_SIGNATURE_2_UP
11	3e−10	16 / 192	MCLACHLAN_DENTAL_CARIES_DN
12	6e−10	16 / 203	VERHAAK_GLIOBLASTOMA_MESENCHYMAL
13	1e−09	16 / 212	RUTELLA_RESPONSE_TO_HGF_DN
14	1e−09	15 / 183	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_8D_DN
15	2e−09	11 / 87	HAHTOLA_SEZARY_SYNDROM_UP

Lymphoma

Rank	p−value	#in/all	Geneset
1	2e−09	124 / 7448	HOPP_Strong_enhancer
2	6e−07	9 / 92	Hopp_Lymphoma_Epi1_with_zentr_iii_B.cell_GCB_UP
3	1e−06	6 / 33	Subero_T−PLL_hypo_meth
4	2e−05	13 / 300	Hopp_June14_MMML937 tumors+controls_group.overexpression_E_GC−B−
5	3e−05	13 / 306	WIRTH_lymphoma937_spot E
6	4e−05	3 / 7	Care_GCB UP
7	1e−04	14 / 408	TARTE_Mature plasma cell signature
8	1e−04	3 / 10	BENTINK_mBL DOWN
9	2e−04	12 / 318	Hopp_June14_MMML937 tumors+controls_group.overexpression_H_GC−B−
10	2e−04	12 / 331	WIRTH_lymphoma937_spot H
11	5e−04	3 / 15	Subero_B−ALL_hypo_meth
12	6e−04	7 / 133	Hopp_Lymphoma_Epi1_no_zentr_5_B.cell_GCB_UP
13	7e−04	7 / 137	Hopp_June14_MMML937 tumors+controls_group.overexpression_G_tonsil_
14	7e−04	7 / 138	WIRTH_lymphoma937_spot G
15	1e−03	3 / 19	DAVE_BL Inter

miRNA Disease

Rank	p−value	#in/all	Geneset
1	1	0 / 7	Thyroid carcinoma, papillary
2	1	0 / 123	Pancreatic cancer
3	1	0 / 68	Glioblastoma multiforme, somatic
4	1	0 / 63	Gastrointestinal
5	1	0 / 3	Pituitary adenoma
6	1	0 / 116	Cancer
7	1	0 / 95	Colorectal cancer
8	1	0 / 2	Adenomas, multiple colorectal
9	1	0 / 124	Prostate cancer
10	1	0 / 48	Alzheimer disease, susceptibility to
11	1	0 / 7	Schizophrenia, susceptibility to
12	1	0 / 20	Parkinson disease
13	1	0 / 65	Hepatocellular carcinoma
14	1	0 / 3	Down syndrome, risk of
15	1	0 / 127	Melanoma and neural system tumor syndrome

Reference Signatures

Rank	p−value	#in/all	Geneset
1	7e−23	25 / 150	Chaussabel_2,6_Myeloid lineage
2	1e−15	23 / 240	Chaussabel_3,3_Inflammation II
3	2e−11	14 / 113	Chaussabel_1,5_Myeloid lineage
4	1e−09	17 / 242	Chaussabel_3,2_Inflammation I
5	2e−07	7 / 39	Chaussabel_2,2_Neutrophils
6	6e−06	7 / 66	VAQUERIZAS_Whole blood_TF
7	2e−04	19 / 695	PROTEINATLAS_bone marrow
8	2e−04	3 / 11	WIRTH_Prim. lymphoid organs
9	1e−03	3 / 21	JONGENEEL_Monocytes
10	2e−03	14 / 535	PROTEINATLAS_spleen
11	1e−02	2 / 16	VAQUERIZAS_Ovary_TF
12	2e−02	2 / 19	VAQUERIZAS_Bone marrow_TF
13	3e−02	3 / 64	VAQUERIZAS_Lung_TF
14	6e−02	12 / 681	PROTEINATLAS_lung
15	7e−02	8 / 412	WIRTH_Immune system

BP

Rank	p−value	#in/all	Geneset
1	6e−10	20 / 336	inflammatory response
2	8e−10	15 / 178	response to lipopolysaccharide
3	3e−09	18 / 293	immune response
4	6e−07	14 / 254	cell surface receptor signaling pathway
5	2e−06	7 / 56	neutrophil chemotaxis
6	8e−05	6 / 68	positive regulation of inflammatory response
7	9e−05	7 / 99	defense response to bacterium
8	9e−05	6 / 69	cellular response to mechanical stimulus
9	1e−04	7 / 104	positive regulation of angiogenesis
10	1e−04	7 / 105	regulation of immune response
11	1e−04	3 / 10	vacuolar acidification
12	2e−04	24 / 1003	signal transduction
13	2e−04	7 / 115	leukocyte migration
14	3e−04	7 / 118	chemotaxis
15	3e−04	5 / 57	defense response

CC

Rank	p−value	#in/all	Geneset
1	3e−10	78 / 3662	plasma membrane
2	3e−08	56 / 2464	extracellular exosome
3	1e−06	33 / 1252	integral component of plasma membrane
4	1e−06	63 / 3291	integral component of membrane
5	2e−04	3 / 12	specific granule
6	6e−04	6 / 96	anchored component of membrane
7	1e−03	6 / 109	late endosome
8	1e−03	11 / 352	focal adhesion
9	1e−03	7 / 156	cytoplasmic vesicle
10	2e−03	23 / 1101	extracellular space
11	2e−03	9 / 256	apical plasma membrane
12	2e−03	7 / 162	basolateral plasma membrane
13	2e−03	48 / 2979	cytosol
14	2e−03	4 / 51	phagocytic vesicle membrane
15	3e−03	4 / 56	autophagosome

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−22	48 / 810	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
2	2e−18	82 / 2810	EnhA_Colon
3	3e−17	179 / 10779	Enh_Colon
4	2e−16	79 / 2845	TxEnhG1_Colon
5	2e−12	131 / 7354	TssF_Colon
6	2e−11	104 / 5373	EnhWk1_Colon
7	3e−11	46 / 1470	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
8	1e−06	17 / 398	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN
9	1e−06	99 / 6138	TssD2_Colon
10	2e−06	14 / 278	Kosinski_top−crypt−long−list
11	4e−06	131 / 9054	Tx_Colon
12	4e−06	24 / 789	TxEnhG2_Colon
13	7e−06	5 / 26	Ang_CRC−CIMPH−vs−L_hypo
14	2e−05	14 / 338	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
15	3e−05	5 / 35	Ang_CRC_Hypomethylated

HM

Rank	p−value	#in/all	Geneset
1	6e−06	11 / 191	HALLMARK_INFLAMMATORY_RESPONSE
2	2e−04	9 / 185	HALLMARK_TNFA_SIGNALING_VIA_NFKB
3	2e−04	6 / 82	HALLMARK_IL6_JAK_STAT3_SIGNALING
4	8e−03	6 / 162	HALLMARK_ALLOGRAFT_REJECTION
5	1e−02	6 / 176	HALLMARK_KRAS_SIGNALING_UP
6	2e−02	5 / 151	HALLMARK_APOPTOSIS
7	4e−02	3 / 69	HALLMARK_CHOLESTEROL_HOMEOSTASIS
8	4e−02	5 / 175	HALLMARK_XENOBIOTIC_METABOLISM
9	5e−02	5 / 183	HALLMARK_GLYCOLYSIS
10	5e−02	5 / 186	HALLMARK_ESTROGEN_RESPONSE_LATE
11	5e−02	5 / 186	HALLMARK_MYOGENESIS
12	6e−02	3 / 85	HALLMARK_INTERFERON_ALPHA_RESPONSE
13	7e−02	2 / 40	HALLMARK_WNT_BETA_CATENIN_SIGNALING
14	7e−02	2 / 41	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
15	8e−02	3 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING

Melanoma

Rank	p−value	#in/all	Geneset
1	0.08	2 / 43	Hugo_melanoma−BRAFmut−MET_UP
2	0.11	2 / 54	Hugo_melanoma−all−MET_DN
3	1.00	0 / 30	Hugo_melanoma−all−MET_UP
4	1.00	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
5	1.00	0 / 27	Hugo_melanoma−all−LEF1_UP
6	1.00	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

miRNA target

Rank	p−value	#in/all	Geneset
1	0.01	3 / 47	hsa−miR−370
2	0.02	4 / 100	hsa−miR−516b
3	0.03	3 / 60	hsa−miR−492
4	0.03	3 / 60	hsa−miR−514
5	0.03	4 / 106	hsa−miR−146a
6	0.03	2 / 25	hsa−miR−100
7	0.03	2 / 26	hsa−miR−99a
8	0.04	3 / 74	hsa−miR−1290
9	0.04	4 / 125	hsa−miR−383
10	0.04	2 / 32	hsa−miR−1229
11	0.04	2 / 32	hsa−miR−589
12	0.04	2 / 32	hsa−miR−631
13	0.05	6 / 243	hsa−miR−26b
14	0.05	2 / 35	hsa−miR−769−5p
15	0.06	5 / 194	hsa−miR−568

Telomeres

Rank	p−value	#in/all	Geneset
1	1	0 / 13	Alternative lengthening of telomeres
2	1	0 / 27	Nabetani_alt len telomeres_genes_ko
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Brain

Rank	p−value	#in/all	Geneset
1	8e−06	59 / 3164	Mid_Frontal_Lobe_ZNF
2	3e−05	51 / 2700	Fetal_TxTrans
3	3e−05	43 / 2127	Mid_Frontal_Lobe_K9K27me3
4	7e−05	68 / 4112	Mid_Frontal_Lobe_ReprPC
5	2e−04	47 / 2630	Fetal_TssF
6	2e−04	27 / 1213	Fetal_TssP
7	3e−04	35 / 1784	Mid_Frontal_Lobe_ReprPCWk
8	1e−03	45 / 2709	Mid_Frontal_Lobe_HetRpts
9	2e−03	134 / 10430	Overlap_fetal_midbrain_Quies
10	2e−03	34 / 1893	Overlap_fetal_midbrain_TssF
11	3e−03	11 / 383	Mid_Frontal_Lobe_Tx
12	4e−03	27 / 1476	Overlap_fetal_midbrain_TxTrans
13	8e−03	46 / 3046	Fetal_TssA
14	4e−02	14 / 796	Overlap_fetal_midbrain_ZNF
15	2e−01	23 / 1728	Fetal_ReprPCWk

Chr

Rank	p−value	#in/all	Geneset
1	4e−05	33 / 1467	Chr 19
2	5e−02	16 / 959	Chr 16
3	7e−02	32 / 2323	Chr 1
4	1e−01	19 / 1318	Chr 17
5	2e−01	9 / 619	Chr 20
6	3e−01	15 / 1211	Chr 6
7	3e−01	7 / 536	Chr 22
8	4e−01	14 / 1170	Chr 7
9	6e−01	11 / 1060	Chr 5
10	6e−01	3 / 289	Chr 21
11	6e−01	14 / 1411	Chr 11
12	7e−01	3 / 342	Chr 18
13	7e−01	7 / 768	Chr 14
14	8e−01	6 / 769	Chr 15
15	8e−01	7 / 904	Chr 10

Glio

Rank	p−value	#in/all	Geneset
1	1e−11	20 / 267	WILLSCHER_GBM_Verhaak−CL & MES_up
2	2e−06	7 / 56	Christensen_hypomethylated_in_primary_glioblastoma
3	8e−06	7 / 68	Christensen_hypomethylated_in_secondary_glioblastoma
4	3e−05	8 / 113	GIEZELT_GBM_WT_up_VS_mut
5	3e−03	47 / 2988	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
6	4e−03	4 / 61	Sturm_GBM_Meth_overexpression_D_G34_UP
7	5e−03	26 / 1417	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
8	7e−03	3 / 37	Christensen_hypomethylated_in_ependymoma
9	1e−02	2 / 16	Donson−chemokine/cytokine−receptors−associated with LTS in HGA
10	1e−02	3 / 47	Donson−innate immunity−associated with LTS in HGA
11	2e−02	2 / 19	KIM deleted & downregulated in LTS
12	2e−02	16 / 839	Hopp_Sturm_GBM_Epi3_no_zentr_1_G34_DN
13	2e−02	5 / 150	Hopp_Sturm_GBM_Epi3_E_G34_UP
14	3e−02	5 / 158	Hopp_Sturm_GBM_Epi3_D_adult_fetus_IDH_UP
15	3e−02	5 / 166	Sturm_GBM_Meth_overexpression_B_adult_UP

Lifestyle

Rank	p−value	#in/all	Geneset
1	6e−08	14 / 211	Homuth_BMI−associated−genes_DN
2	5e−02	1 / 5	DUMEAUX_Estrogen related in smokers literature genes up
3	5e−02	1 / 5	Huan_blood−pressure_HTN−signature
4	1e−01	1 / 10	DUMEAUX_Smoking literature genes up
5	2e−01	1 / 16	Huan_blood−pressure_DBP−signature
6	6e−01	1 / 94	DUMEAUX_Smoking enriched genes
7	1e+00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
8	1e+00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
9	1e+00	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
10	1e+00	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
11	1e+00	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
12	1e+00	0 / 10	DUMEAUX_Women normal BMI literature genes up
13	1e+00	0 / 17	DUMEAUX_High bmi enriched genes
14	1e+00	0 / 31	DUMEAUX_Fasting enriched genes
15	1e+00	0 / 147	Homuth_BMI−associated−genes_UP

MF

Rank	p−value	#in/all	Geneset
1	1e−05	126 / 8818	protein binding
2	2e−05	20 / 648	calcium ion binding
3	1e−04	3 / 10	glucose binding
4	2e−04	9 / 188	receptor activity
5	4e−03	4 / 60	metallopeptidase activity
6	5e−03	2 / 10	dipeptidyl−peptidase activity
7	5e−03	2 / 10	RAGE receptor binding
8	6e−03	3 / 34	phosphatidylinositol−3,4,5−trisphosphate binding
9	6e−03	2 / 11	dipeptidase activity
10	6e−03	2 / 11	metalloexopeptidase activity
11	7e−03	2 / 12	interleukin−1 receptor binding
12	9e−03	4 / 78	phospholipid binding
13	1e−02	20 / 1065	zinc ion binding
14	1e−02	2 / 15	cysteine−type endopeptidase activator activity involved in apoptotic process
15	1e−02	4 / 81	protease binding

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.1	1 / 13	BENTINK_e2f3.1
2	0.1	1 / 14	GUSTAFSON_PI3K_UP
3	1.0	0 / 15	GUSTAFSON_PI3K_DN
4	1.0	0 / 13	BENTINK_e2f3.2
5	1.0	0 / 13	BENTINK_myc.1
6	1.0	0 / 12	BENTINK_ras.1
7	1.0	0 / 11	BENTINK_ras.4
8	1.0	0 / 14	BENTINK_ras.6
9	1.0	0 / 13	BENTINK_src.10
10	1.0	0 / 12	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	2e−10	99 / 5188	ICGC_Ebfsc137065_targets
2	5e−10	92 / 4735	ICGC_Pu1_targets
3	8e−09	70 / 3348	ICGC_BatfPcr1_targets
4	3e−08	118 / 7247	ICGC_Runx3_targets
5	1e−07	101 / 5984	ICGC_Mta3_targets
6	3e−07	93 / 5466	ICGC_Nficsc81335_targets
7	6e−07	85 / 4881	ICGC_Atf2_targets
8	6e−07	53 / 2497	ICGC_Bcl11_targets
9	1e−06	92 / 5518	ICGC_Stat5_targets
10	1e−06	91 / 5442	ICGC_Pmlsc71910_targets
11	6e−06	45 / 2133	ICGC_Mef2_targets
12	6e−06	102 / 6578	ICGC_Pou2_targets
13	6e−06	88 / 5410	ICGC_Foxm1_targets
14	8e−06	105 / 6868	ICGC_Elf1_targets
15	9e−06	87 / 5383	ICGC_Sp1_targets

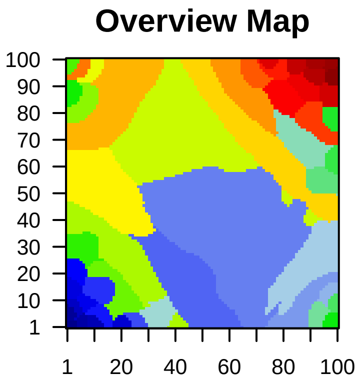
K−Means Cluster

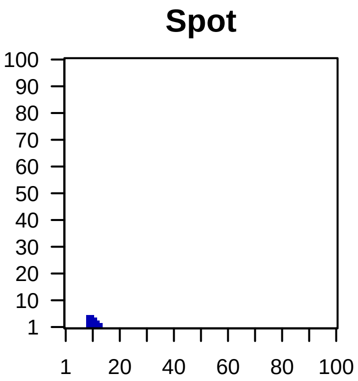
Spot Summary: H

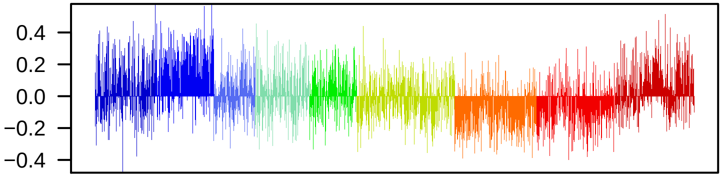
metagenes = 24
genes = 451

<r> metagenes = 0.98
<r> genes = 0.47
beta: r2= 69.09 / log p= −Inf

samples with spot = 753 (22.2 %)
A * : 106 (30.8 %)
A C * : 191 (58.2 %)
A C F * : 52 (22.1 %)
A F * : 72 (23.4 %)
C F * : 61 (23 %)
F * : 77 (13.9 %)
F J * : 17 (3.7 %)
J * : 33 (7.4 %)
N * : 144 (32.5 %)





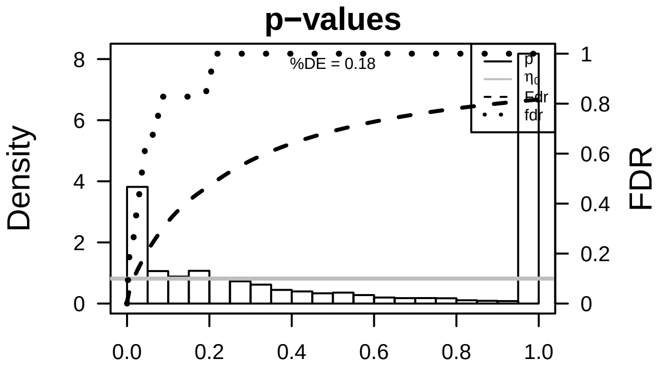


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_240322	1.64	−1.03	0.22	CLEC12A	C−type lectin domain family 12 member A [Source:HGNC Sy
2	ILMN_172176	1.57	−1.48	0.46	IL18RAP	interleukin 18 receptor accessory protein [Source:HGNC Syn
3	ILMN_172111	1.53	−2.22	0.21		
4	ILMN_166163	1.49	−2.04	0.35		
5	ILMN_170498	1.41	−1.25	0.34	CYP27A1	cytochrome P450 family 27 subfamily A member 1 [Source:H
6	ILMN_228332	1.29	−1.13	0.59	WLS	wntless Wnt ligand secretion mediator [Source:HGNC Symbo
7	ILMN_323787	1.28	−1.25	0.38		
8	ILMN_172863	1.28	−1.95	0.72		
9	ILMN_178630	1.28	−1.24	0.38		
10	ILMN_179068	1.26	−1.35	0.73	CRISPLD2	cysteine rich secretory protein LCCL domain containing 2 [So
11	ILMN_218606	1.25	−1	0.71	PFKFB3	6−phosphofructo−2−kinase/fructose−2,6−biphosphatase 3 [S
12	ILMN_174172	1.24	−1.15	0.85	QPCT	glutaminyl−peptide cyclotransferase [Source:HGNC Symbol;
13	ILMN_165387	1.24	−1.57	0.85	NAMPT	nicotinamide phosphoribosyltransferase [Source:HGNC Sym
14	ILMN_239256	1.21	−1.34	0.76	FPR2	formyl peptide receptor 2 [Source:HGNC Symbol;Acc:HGNC:
15	ILMN_169730	1.18	−1.08	0.61		
16	ILMN_209211	1.17	−1.15	0.79	FPR1	formyl peptide receptor 1 [Source:HGNC Symbol;Acc:HGNC:
17	ILMN_175707	1.16	−1.22	0.79	GNG10	G protein subunit gamma 10 [Source:HGNC Symbol;Acc:HG
18	ILMN_239329	1.16	−0.79	0.79	GK	glycerol kinase [Source:HGNC Symbol;Acc:HGNC:4289]
19	ILMN_174087	1.14	−1.35	0.79	FPR2	formyl peptide receptor 2 [Source:HGNC Symbol;Acc:HGNC:
20	ILMN_167126	1.13	−0.79	0.58	WLS	wntless Wnt ligand secretion mediator [Source:HGNC Symbo

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	2e−44	44 / 150	Refer	Chaussabel_2,6_Myeloid lineage
2	2e−33	43 / 240	Refer	Chaussabel_3,3_Inflammation II
3	8e−33	65 / 692	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP
4	8e−27	264 / 10999	Colon	TssWk_Colon
5	7e−24	60 / 841	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_UP
6	8e−21	34 / 282	GSEA	RUTELLA_RESPONSE_TO_CSF2RB_AND_IL4_DN
7	1e−20	30 / 211	Lifesty	Homuth_BMI−associated−genes_DN
8	3e−20	45 / 554	Canc	Lembcke_Colonic Inflammation
9	3e−20	54 / 810	Colon	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
10	7e−20	31 / 242	Refer	Chaussabel_3,2_Inflammation I
11	2e−19	28 / 196	GSEA	MCLACHLAN_DENTAL_CARIES_UP
12	1e−18	271 / 12741	Chror	7_Enh_Melanocytes
13	2e−18	225 / 9555	Colon	TssA_Colon
14	6e−18	24 / 150	GSEA	BROWN_MYELOID_CELL_DEVELOPMENT_UP
15	7e−18	59 / 1081	GSEA	CHEN_METABOLIC_SYNDROM_NETWORK
16	2e−17	246 / 11130	Chror	15_Quies_Melanocytes
17	4e−17	207 / 8613	Chror	7_Enh_Fibroblasts
18	1e−16	26 / 205	GSEA	ZWANG_CLASS_3_TRANSIENTLY_INDUCED_BY_EGF
19	1e−16	187 / 7448	Lympl	HOPP_Strong_enhancer
20	2e−16	26 / 212	GSEA	RUTELLA_RESPONSE_TO_HGF_DN
21	3e−16	212 / 9054	Colon	Tx_Colon
22	6e−16	23 / 164	GSEA	VERHAAK_AML_WITH_NPM1_MUTATED_UP
23	7e−16	25 / 202	GSEA	JAATINEN_HEMATOPOIETIC_STEM_CELL_DN
24	1e−15	58 / 1169	Lympl	SPANG_BCR DN
25	4e−15	203 / 8678	Colon	Quies3_Colon
26	1e−14	31 / 366	GSEA	RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_UP
27	2e−14	23 / 192	GSEA	MCLACHLAN_DENTAL_CARIES_DN
28	2e−14	203 / 8818	MF	protein binding
29	3e−14	199 / 8568	Colon	TxWk_Colon
30	3e−14	44 / 763	GSEA	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP
31	3e−14	112 / 3662	CC	plasma membrane
32	9e−14	22 / 185	HM	HALLMARK_TNFA_SIGNALING_VIA_NFKB
33	1e−13	23 / 208	GSEA	THEILGAARD_NEUTROPHIL_AT_SKIN_WOUND_DN
34	1e−13	24 / 230	GSEA	BOYLAN_MULTIPLE_MYELOMA_C_D_DN
35	1e−13	231 / 10779	Colon	Enh_Colon
36	2e−13	200 / 8771	Chror	5_Tx_Melanocytes
37	2e−13	96 / 2979	CC	cytosol
38	2e−13	203 / 8990	Chror	15_Quies_Fibroblasts
39	3e−13	28 / 335	BP	innate immune response
40	3e−13	28 / 336	BP	inflammatory response



Aging

Rank	p−value	#in/all	Geneset
1	0.007	6 / 111	HORVATH_aging_genes meth DOWN
2	0.057	3 / 58	TESCHENDORFF_age_hypermethylated
3	0.065	5 / 142	HORVATH_aging_genes meth UP
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	3e−13	28 / 335	innate immune response
2	3e−13	28 / 336	inflammatory response
3	5e−09	6 / 11	regulation of cytokine secretion
4	2e−08	27 / 511	apoptotic process
5	5e−08	10 / 66	Fc−gamma receptor signaling pathway involved in phagocytosis
6	6e−08	24 / 434	protein phosphorylation
7	3e−07	11 / 99	defense response to bacterium
8	6e−07	14 / 178	response to lipopolysaccharide
9	6e−07	18 / 293	immune response
10	1e−06	10 / 92	stimulatory C−type lectin receptor signaling pathway
11	2e−06	36 / 1003	signal transduction
12	6e−06	9 / 86	transmembrane receptor protein tyrosine kinase signaling pathway
13	7e−06	6 / 32	MyD88−dependent toll−like receptor signaling pathway
14	2e−05	6 / 39	peptidyl−tyrosine autophosphorylation
15	3e−05	7 / 58	regulation of inflammatory response

Brain

Rank	p−value	#in/all	Geneset
1	1e−11	212 / 9917	Overlap_fetal_midbrain_ReprPCWk
2	6e−07	203 / 10430	Overlap_fetal_midbrain_Quies
3	1e−06	188 / 9504	Overlap_fetal_midbrain_K9K27me3
4	1e−06	41 / 1213	Fetal_TssP
5	3e−06	191 / 9815	Overlap_fetal_midbrain_ReprPC
6	1e−05	126 / 5936	Overlap_fetal_midbrain_HetRpts
7	6e−04	70 / 3164	Mid_Frontal_Lobe_ZNF
8	7e−04	60 / 2630	Fetal_TssF
9	9e−04	61 / 2700	Fetal_TxTrans
10	9e−04	67 / 3046	Fetal_TssA
11	2e−03	60 / 2709	Mid_Frontal_Lobe_HetRpts
12	6e−03	81 / 4112	Mid_Frontal_Lobe_ReprPC
13	6e−03	29 / 1171	Fetal_EnhP
14	7e−03	22 / 818	Mid_Frontal_Lobe_Het
15	1e−02	21 / 796	Overlap_fetal_midbrain_ZNF

Cancer

Rank	p−value	#in/all	Geneset
1	3e−20	45 / 554	Lembcke_Colonic Inflammation
2	2e−10	23 / 301	SPANG_BCL6−index2
3	3e−06	13 / 178	SPANG_LPS−index2
4	8e−03	0 / 15	LIU_PROSTATE_CANCER_DN
5	2e−02	2 / 13	GENTLES_modul12
6	2e−02	4 / 73	SHAUGHNESSY_MM high risk
7	3e−02	6 / 150	PanCan_MAPK_geneset_nanostring
8	6e−02	5 / 136	PanCan_RAS_geneset_nanostring
9	7e−02	6 / 193	PanCan_PI3K_geneset_nanostring
10	8e−02	0 / 13	LIU_LIVER_CANCER
11	1e−01	2 / 39	ZHANG_MM up
12	2e−01	1 / 13	GENTLES_modul18
13	2e−01	1 / 14	BEN−PORATH_UP
14	2e−01	1 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
15	2e−01	1 / 16	GENTLES_modul11

CC

Rank	p−value	#in/all	Geneset
1	3e−14	112 / 3662	plasma membrane
2	2e−13	96 / 2979	cytosol
3	1e−07	70 / 2464	extracellular exosome
4	3e−06	24 / 539	Golgi membrane
5	3e−06	41 / 1252	integral component of plasma membrane
6	3e−06	109 / 4822	cytoplasm
7	2e−05	54 / 1979	membrane
8	3e−05	17 / 352	focal adhesion
9	1e−04	6 / 51	phagocytic vesicle membrane
10	1e−04	26 / 777	Golgi apparatus
11	2e−04	6 / 56	autophagosome
12	3e−04	4 / 21	autophagosome membrane
13	3e−04	6 / 59	endoplasmic reticulum−Golgi intermediate compartment membrane
14	3e−04	6 / 61	extrinsic component of cytoplasmic side of plasma membrane
15	1e−03	10 / 202	early endosome

Chr

Rank	p−value	#in/all	Geneset
1	0.03	21 / 904	Chr 10
2	0.07	25 / 1211	Chr 6
3	0.11	23 / 1160	Chr 12
4	0.13	42 / 2323	Chr 1
5	0.23	12 / 619	Chr 20
6	0.27	6 / 289	Chr 21
7	0.30	25 / 1467	Chr 19
8	0.39	14 / 836	Chr 8
9	0.54	15 / 994	Chr X
10	0.59	14 / 959	Chr 16
11	0.61	13 / 902	Chr 4
12	0.61	11 / 768	Chr 14
13	0.62	11 / 769	Chr 15
14	0.69	13 / 954	Chr 9
15	0.70	7 / 536	Chr 22

Chromatin states

Rank	p−value	#in/all	Geneset
1	1e−18	271 / 12741	7_Enh_Melanocytes
2	2e−17	246 / 11130	15_Quies_Melanocytes
3	4e−17	207 / 8613	7_Enh_Fibroblasts
4	2e−13	200 / 8771	5_Tx_Melanocytes
5	2e−13	203 / 8990	15_Quies_Fibroblasts
6	4e−12	250 / 12393	15_Quies_Neuronal_Progenitor
7	5e−12	209 / 9635	3_TssF_Fibroblasts
8	1e−11	235 / 11455	2_TssA_Fibroblasts
9	1e−11	247 / 12298	2_TssA_Melanocytes
10	2e−11	240 / 11847	7_Enh_Neuronal_Progenitor
11	4e−11	239 / 11836	3_TssF_Melanocytes
12	9e−10	251 / 12983	2_TssA_Neuronal_Progenitor
13	3e−08	132 / 5699	6_EnhG_Melanocytes
14	5e−08	167 / 7854	5_Tx_Fibroblasts
15	1e−06	130 / 5956	3_TssF_Neuronal_Progenitor

Colon Cancer

Rank	p−value	#in/all	Geneset
1	8e−27	264 / 10999	TssWk_Colon
2	3e−20	54 / 810	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
3	2e−18	225 / 9555	TssA_Colon
4	3e−16	212 / 9054	Tx_Colon
5	4e−15	203 / 8678	Quies3_Colon
6	3e−14	199 / 8568	TxWk_Colon
7	1e−13	231 / 10779	Enh_Colon
8	3e−12	139 / 5373	EnhWk1_Colon
9	2e−11	53 / 1281	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv
10	2e−10	85 / 2810	EnhA_Colon
11	1e−09	165 / 7354	TssF_Colon
12	2e−09	106 / 4018	EnhWk2_Colon
13	2e−09	21 / 278	Kosinski_top−crypt−long−list
14	3e−09	143 / 6138	TssD2_Colon
15	5e−09	43 / 1069	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN

Glio

Rank	p−value	#in/all	Geneset
1	4e−13	25 / 267	WILLSCHER_GBM_Verhaak−CL & MES_up
2	2e−07	11 / 94	Weller_LGG_A_vs_O_UP
3	2e−07	11 / 96	Weller_LGG_1p19qDel−vs−intact_DOWN
4	3e−06	3 / 3	WILLSCHER_GBM_STSwt_proteomics−L_UP
5	7e−05	6 / 47	Donson−innate immunity−associated with LTS in HGA
6	8e−05	10 / 147	Christensen_hypermethylated_in_grade2_oligodendroglioma
7	1e−03	8 / 134	Christensen_hypermethylated_in_grade3_oligoastrocytoma
8	2e−03	7 / 115	Christensen_hypermethylated_in_grade3_astrocytoma
9	2e−03	7 / 117	Christensen_hypermethylated_in_grade2_oligoastrocytoma
10	2e−03	6 / 90	Christensen_hypermethylated_in_secondary_glioblastoma
11	3e−03	35 / 1417	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
12	3e−03	12 / 315	Up
13	8e−03	7 / 150	Hopp_Sturm_GBM_Epi3_E_G34_UP
14	1e−02	4 / 57	OL vs. MOG− OL
15	1e−02	3 / 33	Shaw_responders_down_in_oligo_glioma

GSEA C2

Rank	p−value	#in/all	Geneset
1	8e−33	65 / 692	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP
2	7e−24	60 / 841	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_UP
3	8e−21	34 / 282	RUTELLA_RESPONSE_TO_CSF2RB_AND_IL4_DN
4	2e−19	28 / 196	MCLACHLAN_DENTAL_CARIES_UP
5	6e−18	24 / 150	BROWN_MYELOID_CELL_DEVELOPMENT_UP
6	7e−18	59 / 1081	CHEN_METABOLIC_SYNDROM_NETWORK
7	1e−16	26 / 205	ZWANG_CLASS_3_TRANSIENTLY_INDUCED_BY_EGF
8	2e−16	26 / 212	RUTELLA_RESPONSE_TO_HGF_DN
9	6e−16	23 / 164	VERHAAK_AML_WITH_NPM1_MUTATED_UP
10	7e−16	25 / 202	JAATINEN_HEMATOPOIETIC_STEM_CELL_DN
11	1e−14	31 / 366	RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_UP
12	2e−14	23 / 192	MCLACHLAN_DENTAL_CARIES_DN
13	3e−14	44 / 763	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP
14	1e−13	23 / 208	THEILGAARD_NEUTROPHIL_AT_SKIN_WOUND_DN
15	1e−13	24 / 230	BOYLAN_MULTIPLE_MYELOMA_C_D_DN

HM

Rank	p−value	#in/all	Geneset
1	9e−14	22 / 185	HALLMARK_TNFA_SIGNALING_VIA_NFKB
2	1e−12	21 / 187	HALLMARK_COMPLEMENT
3	4e−08	16 / 191	HALLMARK_INFLAMMATORY_RESPONSE
4	4e−06	9 / 82	HALLMARK_IL6_JAK_STAT3_SIGNALING
5	2e−05	11 / 151	HALLMARK_APOPTOSIS
6	3e−05	12 / 186	HALLMARK_IL2_STAT5_SIGNALING
7	4e−04	10 / 176	HALLMARK_KRAS_SIGNALING_UP
8	5e−04	10 / 185	HALLMARK_P53_PATHWAY
9	1e−03	9 / 175	HALLMARK_XENOBIOTIC_METABOLISM
10	5e−03	8 / 172	HALLMARK_INTERFERON_GAMMA_RESPONSE
11	5e−03	7 / 137	HALLMARK_UV_RESPONSE_UP
12	8e−03	8 / 189	HALLMARK_HYPOXIA
13	1e−02	7 / 162	HALLMARK_ALLOGRAFT_REJECTION
14	2e−02	5 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING
15	2e−02	4 / 69	HALLMARK_CHOLESTEROL_HOMEOSTASIS

Lifestyle

Rank	p−value	#in/all	Geneset
1	1e−20	30 / 211	Homuth_BMI−associated−genes_DN
2	1e−04	4 / 18	Huan_blood−pressure_SBP−signature
3	6e−03	2 / 8	DUMEAUX_Monocytes in smokers literature genes up
4	7e−02	1 / 5	DUMEAUX_Estrogen related in smokers literature genes up
5	1e−01	1 / 10	DUMEAUX_Women normal BMI literature genes up
6	2e−01	1 / 16	Huan_blood−pressure_DBP−signature
7	2e−01	1 / 17	DUMEAUX_High bmi enriched genes
8	8e−01	1 / 94	DUMEAUX_Smoking enriched genes
9	9e−01	1 / 147	Homuth_BMI−associated−genes_UP
10	1e+00	0 / 10	DUMEAUX_Smoking literature genes up
11	1e+00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
12	1e+00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
13	1e+00	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
14	1e+00	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
15	1e+00	0 / 31	DUMEAUX_Fasting enriched genes

Lymphoma

Rank	p−value	#in/all	Geneset
1	1e−16	187 / 7448	HOPP_Strong_enhancer
2	1e−15	58 / 1169	SPANG_BCR DN
3	6e−12	25 / 300	Hopp_June14_MMML937 tumors+controls_group.overexpression_E_GC−B−
4	9e−12	25 / 306	WIRTH_lymphoma937_spot E
5	2e−10	182 / 8226	HOPP_Active_promoter
6	3e−10	179 / 8098	HOPP_Weak_promoter
7	7e−07	121 / 5356	HOPP_Txn_transition
8	1e−06	152 / 7275	HOPP_Txn_elongation
9	2e−05	15 / 272	SPANG_IL21 DN
10	5e−05	16 / 331	WIRTH_lymphoma937_spot H
11	5e−05	133 / 6559	HOPP_Weak_txn
12	6e−05	18 / 408	TARTE_Mature plasma cell signature
13	1e−04	138 / 6959	HOPP_Weak_enhancer
14	1e−04	15 / 318	Hopp_June14_MMML937 tumors+controls_group.overexpression_H_GC−B−
15	2e−04	7 / 77	Aukema_BCL2 DN_BCL6 UP

Melanoma

Rank	p−value	#in/all	Geneset
1	0.3	1 / 27	Hugo_melanoma−all−LEF1_UP
2	0.6	1 / 54	Hugo_melanoma−all−MET_DN
3	1.0	0 / 30	Hugo_melanoma−all−MET_UP
4	1.0	0 / 43	Hugo_melanoma−BRAFmut−MET_UP
5	1.0	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
6	1.0	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

MF

Rank	p−value	#in/all	Geneset
1	2e−14	203 / 8818	protein binding
2	6e−10	18 / 188	receptor activity
3	2e−07	16 / 217	protein kinase activity
4	2e−05	16 / 311	enzyme binding
5	6e−05	6 / 45	non−membrane spanning protein tyrosine kinase activity
6	3e−04	15 / 350	protein kinase binding
7	3e−04	14 / 315	protein serine/threonine kinase activity
8	4e−04	3 / 10	RAGE receptor binding
9	5e−04	10 / 182	signal transducer activity
10	5e−04	8 / 120	protein tyrosine kinase activity
11	6e−04	16 / 413	protein heterodimerization activity
12	7e−04	3 / 12	phosphotyrosine binding
13	1e−03	35 / 1329	ATP binding
14	3e−03	3 / 19	1−acylglycerol−3−phosphate O−acyltransferase activity
15	3e−03	3 / 19	G−protein alpha−subunit binding

miRNA Disease

Rank	p−value	#in/all	Geneset
1	1	0 / 7	Thyroid carcinoma, papillary
2	1	0 / 123	Pancreatic cancer
3	1	0 / 68	Glioblastoma multiforme, somatic
4	1	0 / 63	Gastrointestinal
5	1	0 / 3	Pituitary adenoma
6	1	0 / 116	Cancer
7	1	0 / 95	Colorectal cancer
8	1	0 / 2	Adenomas, multiple colorectal
9	1	0 / 124	Prostate cancer
10	1	0 / 48	Alzheimer disease, susceptibility to
11	1	0 / 7	Schizophrenia, susceptibility to
12	1	0 / 20	Parkinson disease
13	1	0 / 65	Hepatocellular carcinoma
14	1	0 / 3	Down syndrome, risk of
15	1	0 / 127	Melanoma and neural system tumor syndrome

miRNA target

Rank	p−value	#in/all	Geneset
1	1e−07	25 / 491	hsa−miR−107
2	2e−07	25 / 493	hsa−miR−103
3	1e−06	6 / 24	hsa−miR−632
4	5e−06	18 / 342	hsa−let−7e
5	1e−05	21 / 467	hsa−miR−195
6	1e−05	22 / 516	hsa−miR−15a
7	2e−05	21 / 489	hsa−miR−16
8	2e−05	19 / 419	hsa−miR−497
9	7e−05	18 / 416	hsa−miR−372
10	9e−05	6 / 49	hsa−miR−556−3p
11	9e−05	18 / 425	hsa−let−7b
12	1e−04	11 / 180	hsa−miR−1283
13	1e−04	9 / 122	hsa−miR−212
14	1e−04	15 / 318	hsa−miR−98
15	1e−04	14 / 283	hsa−miR−320a

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.01	2 / 11	BENTINK_ras.4
2	0.17	1 / 12	BENTINK_ras.1
3	0.18	1 / 13	BENTINK_src.10
4	0.19	1 / 14	BENTINK_ras.6
5	1.00	0 / 14	GUSTAFSON_PI3K_UP
6	1.00	0 / 15	GUSTAFSON_PI3K_DN
7	1.00	0 / 13	BENTINK_e2f3.1
8	1.00	0 / 13	BENTINK_e2f3.2
9	1.00	0 / 13	BENTINK_myc.1
10	1.00	0 / 12	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Reference Signatures

Rank	p−value	#in/all	Geneset
1	2e−44	44 / 150	Chaussabel_2,6_Myeloid lineage
2	2e−33	43 / 240	Chaussabel_3,3_Inflammation II
3	7e−20	31 / 242	Chaussabel_3,2_Inflammation I
4	2e−09	14 / 113	Chaussabel_1,5_Myeloid lineage
5	9e−08	31 / 695	PROTEINATLAS_bone marrow
6	2e−05	22 / 535	PROTEINATLAS_spleen
7	4e−03	20 / 681	PROTEINATLAS_lung
8	4e−03	14 / 412	WIRTH_Immune system
9	9e−03	5 / 84	Chaussabel_2,10_Immune related cell surface molecules
10	1e−02	26 / 1063	PROTEINATLAS_tonsil
11	1e−02	2 / 12	Chaussabel_3,5_Hemoglobin genes
12	1e−02	19 / 724	PROTEINATLAS_lymph node
13	2e−02	4 / 64	VAQUERIZAS_Lung_TF
14	2e−02	29 / 1268	PROTEINATLAS_colon
15	3e−02	2 / 17	JONGENEEL_Lung

Telomeres

Rank	p−value	#in/all	Geneset
1	1	0 / 13	Alternative lengthening of telomeres
2	1	0 / 27	Nabetani_alt len telomeres_genes_ko
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	9e−10	120 / 4735	ICGC_Pu1_targets
2	4e−09	92 / 3348	ICGC_BatfPcr1_targets
3	2e−08	73 / 2497	ICGC_Bcl11_targets
4	2e−07	155 / 7247	ICGC_Runx3_targets
5	2e−07	120 / 5188	ICGC_Ebfsc137065_targets
6	2e−06	121 / 5466	ICGC_Nficsc81335_targets
7	3e−06	80 / 3194	ICGC_Irf4_targets
8	6e−06	120 / 5518	ICGC_Stat5_targets
9	6e−06	49 / 1669	ICGC_P300_targets
10	6e−06	118 / 5410	ICGC_Foxm1_targets
11	7e−06	112 / 5067	ICGC_Taf1_targets
12	8e−06	137 / 6578	ICGC_Pou2_targets
13	9e−06	127 / 5984	ICGC_Mta3_targets
14	1e−05	131 / 6267	ICGC_Yy1_targets
15	2e−05	57 / 2133	ICGC_Mef2_targets

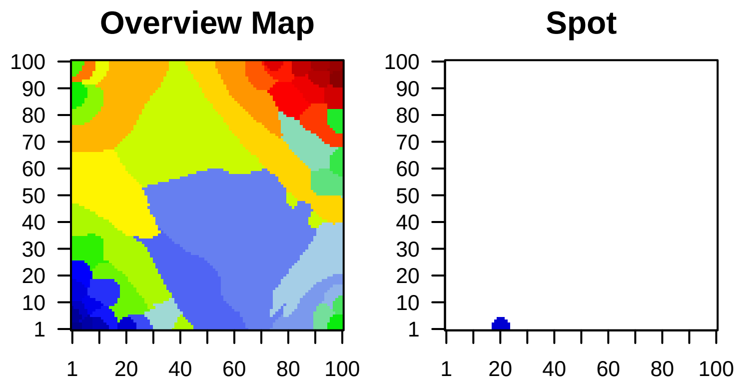
K−Means Cluster

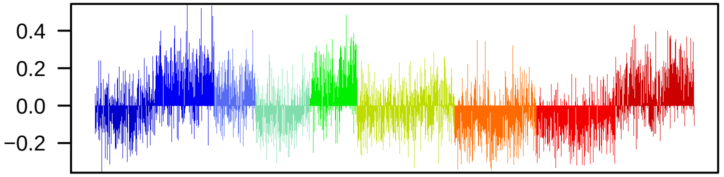
Spot Summary: I

metagenes = 29
genes = 232

<r> metagenes = 0.95
<r> genes = 0.39
beta: r2= 30.62 / log p= −Inf

samples with spot = 698 (20.6 %)
A * : 37 (10.8 %)
A C * : 169 (51.5 %)
A C F * : 65 (27.7 %)
A F * : 21 (6.8 %)
C F * : 123 (46.4 %)
F * : 64 (11.5 %)
F J * : 26 (5.6 %)
J * : 14 (3.1 %)
N * : 179 (40.4 %)



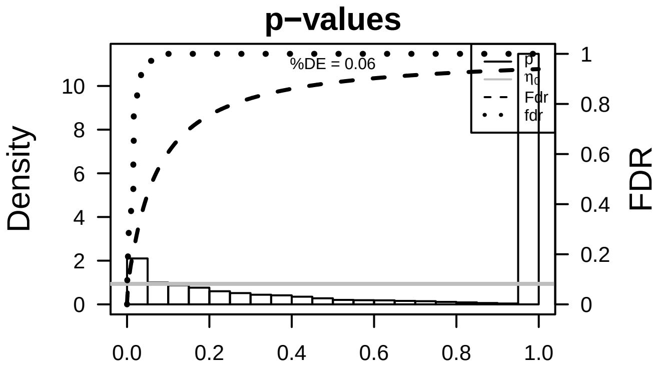


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_180823	1.58	−0.7	0.53	RBPMS2	RNA binding protein with multiple splicing 2 [Source:HGNC S
2	ILMN_172188	1.57	−1.12	0.84	ITGA2B	integrin subunit alpha 2b [Source:HGNC Symbol;Acc:HGNC:
3	ILMN_174329	1.57	−1.44	0.91	GP9	glycoprotein IX platelet [Source:HGNC Symbol;Acc:HGNC:44
4	ILMN_176728	1.52	−1.63	0.87		
5	ILMN_166279	1.43	−1.26	0.58	CA2	carbonic anhydrase 2 [Source:HGNC Symbol;Acc:HGNC:137
6	ILMN_209000	1.4	−0.86	0.72	AQP10	aquaporin 10 [Source:HGNC Symbol;Acc:HGNC:16029]
7	ILMN_175764	1.37	−1.19	0.41	UBE2H	ubiquitin conjugating enzyme E2 H [Source:HGNC Symbol;A
8	ILMN_174510	1.36	−0.87	0.76	CLEC1B	C−type lectin domain family 1 member B [Source:HGNC Sym
9	ILMN_175275	1.32	−0.85	0.71	VWF	von Willebrand factor [Source:HGNC Symbol;Acc:HGNC:127
10	ILMN_171028	1.31	−1.36	0.84	TUBB1	tubulin beta 1 class VI [Source:HGNC Symbol;Acc:HGNC:16
11	ILMN_219943	1.31	−1.09	0.59	CA2	carbonic anhydrase 2 [Source:HGNC Symbol;Acc:HGNC:137
12	ILMN_178241	1.3	−1.32	0.89	GNG11	G protein subunit gamma 11 [Source:HGNC Symbol;Acc:HG
13	ILMN_178962	1.29	−1.46	0.87	GP1BB	glycoprotein Ib platelet beta subunit [Source:HGNC Symbol;A
14	ILMN_174552	1.28	−0.65	0.52	PF4V1	platelet factor 4 variant 1 [Source:HGNC Symbol;Acc:HGNC:
15	ILMN_241353	1.26	−0.84	0.45	HEMGN	hemogen [Source:HGNC Symbol;Acc:HGNC:17509]
16	ILMN_235212	1.26	−0.82	0.44	NT5C3A	5'−nucleotidase, cytosolic IIIA [Source:HGNC Symbol;Acc:HG
17	ILMN_173207	1.26	−0.97	0.63	HIST2H2BE	histone cluster 2, H2be [Source:HGNC Symbol;Acc:HGNC:47
18	ILMN_233983	1.25	−1.25	0.88	PTGS1	prostaglandin−endoperoxide synthase 1 [Source:HGNC Sym
19	ILMN_167192	1.22	−0.8	0.85	PROS1	protein S (alpha) [Source:HGNC Symbol;Acc:HGNC:9456]
20	ILMN_222275	1.21	−0.76	0.29		

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−99	65 / 102	Refer	Chaussabel_1,2_Platelets
2	7e−58	35 / 64	GSEA	RAGHAVACHARI_PLATELET_SPECIFIC_GENES
3	3e−46	40 / 188	GSEA	WIERENGA_STAT5A_TARGETS_DN
4	2e−19	29 / 414	GSEA	REACTOME_HEMOSTASIS
5	2e−17	20 / 181	GSEA	REACTOME_PLATELET_ACTIVATION_SIGNALING_AND_AGGREGATIO
6	7e−16	18 / 162	GSEA	JISON_SICKLE_CELL_DISEASE_UP
7	7e−15	23 / 352	CC	focal adhesion
8	1e−14	13 / 71	GSEA	REACTOME_RESPONSE_TO_ELEVATED_PLATELET_CYTOSOLIC_CA
9	9e−14	12 / 64	GSEA	ROSS_AML_OF_FAB_M7_TYPE
10	3e−13	13 / 90	BP	platelet degranulation
11	5e−13	10 / 40	GSEA	GNATENKO_PLATELET_SIGNATURE
12	4e−12	36 / 1216	Colon	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP
13	3e−11	20 / 387	GSEA	SWEET_LUNG_CANCER_KRAS_DN
14	5e−11	51 / 2464	CC	extracellular exosome
15	7e−11	21 / 451	GSEA	PILON_KLF1_TARGETS_UP
16	8e−11	14 / 171	BP	blood coagulation
17	5e−10	8 / 38	BP	platelet aggregation
18	9e−10	125 / 10779	Colon	Enh_Colon
19	3e−09	7 / 30	GSEA	REACTOME_FORMATION_OF_FIBRIN_CLOT_CLOTTING_CASCADE
20	4e−09	12 / 157	GSEA	BERTUCCI_MEDULLARY_VS_DUCTAL_BREAST_CANCER_DN
21	5e−09	64 / 4018	Colon	EnhWk2_Colon
22	5e−09	20 / 520	GSEA	CHICAS_RB1_TARGETS_CONFLUENT
23	6e−09	114 / 9635	Chror	3_TssF_Fibroblasts
24	8e−09	6 / 20	GSEA	REACTOME_SMOOTH_MUSCLE_CONTRACTION
25	9e−09	7 / 35	GSEA	REACTOME_PLATELET_AGGREGATION_PLUG_FORMATION
26	1e−08	22 / 652	GSEA	WONG_ADULT_TISSUE_STEM_MODULE
27	1e−08	10 / 106	BP	platelet activation
28	2e−08	7 / 38	GSEA	CHUNG_BLISTER_CYTOTOXICITY_DN
29	2e−08	16 / 351	GSEA	LINDGREN_BLADDER_CANCER_CLUSTER_2B
30	5e−08	14 / 279	GSEA	ACEVEDO_FGFR1_TARGETS_IN_PROSTATE_CANCER_MODEL_DN
31	6e−08	14 / 284	GSEA	TORCHIA_TARGETS_OF_EWSR1_FLI1_FUSION_DN
32	6e−08	50 / 2939	Lympl	HOPP_Poised_promoter
33	6e−08	69 / 4795	Chror	6_EnhG_Fibroblasts
34	1e−07	12 / 211	GSEA	SENESE_HDAC1_AND_HDAC2_TARGETS_DN
35	1e−07	134 / 12741	Chror	7_Enh_Melanocytes
36	1e−07	102 / 8613	Chror	7_Enh_Fibroblasts
37	2e−07	5 / 17	GSEA	HAHTOLA_MYCOSIS_FUNGOIDES_UP
38	2e−07	65 / 4526	Colon	Quies1_Colon
39	2e−07	13 / 268	GSEA	WANG_SMARCE1_TARGETS_UP
40	2e−07	19 / 593	GSEA	CASORELLI_ACUTE_PROMYELOCYTIC_LEUKEMIA_DN



Aging

Rank	p−value	#in/all	Geneset
1	0.06	3 / 111	HORVATH_aging_genes meth DOWN
2	0.31	2 / 142	HORVATH_aging_genes meth UP
3	1.00	0 / 58	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	3e−13	13 / 90	platelet degranulation
2	8e−11	14 / 171	blood coagulation
3	5e−10	8 / 38	platelet aggregation
4	1e−08	10 / 106	platelet activation
5	2e−06	14 / 387	cell adhesion
6	4e−06	5 / 31	microtubule−based process
7	1e−05	4 / 18	blood coagulation, intrinsic pathway
8	1e−04	4 / 31	lamellipodium assembly
9	2e−04	6 / 102	muscle contraction
10	3e−04	5 / 76	integrin−mediated signaling pathway
11	3e−04	5 / 77	movement of cell or subcellular component
12	5e−04	5 / 84	cell−matrix adhesion
13	6e−04	7 / 182	extracellular matrix organization
14	7e−04	3 / 23	negative regulation of G1/S transition of mitotic cell cycle
15	8e−04	5 / 93	nucleosome assembly

Brain

Rank	p−value	#in/all	Geneset
1	9e−05	44 / 3164	Mid_Frontal_Lobe_ZNF
2	2e−04	42 / 3046	Fetal_TssA
3	3e−04	105 / 10430	Overlap_fetal_midbrain_Quies
4	1e−03	36 / 2700	Fetal_TxTrans
5	2e−03	97 / 9917	Overlap_fetal_midbrain_ReprPCWk
6	3e−03	19 / 1213	Fetal_TssP
7	4e−03	15 / 869	Mid_Frontal_Lobe_EnhG
8	4e−03	47 / 4112	Mid_Frontal_Lobe_ReprPC
9	8e−03	32 / 2630	Fetal_TssF
10	1e−02	20 / 1476	Overlap_fetal_midbrain_TxTrans
11	2e−02	16 / 1119	Overlap_fetal_midbrain_TssA
12	2e−02	88 / 9504	Overlap_fetal_midbrain_K9K27me3
13	3e−02	14 / 1012	Mid_Frontal_Lobe_Enh
14	3e−02	30 / 2709	Mid_Frontal_Lobe_HetRpts
15	4e−02	17 / 1360	Mid_Frontal_Lobe_TssP

Cancer

Rank	p−value	#in/all	Geneset
1	2e−06	0 / 15	LIU_PROSTATE_CANCER_DN
2	5e−03	2 / 14	GENTLES_modul13
3	3e−02	3 / 91	PanCan_TXmisReg_geneset_nanostring
4	1e−01	1 / 13	LIU_LIVER_CANCER
5	1e−01	1 / 13	WANG_ER_DN
6	1e−01	1 / 13	GENTLES_modul18
7	1e−01	1 / 14	LIU_PROSTATE_CANCER_UP
8	1e−01	1 / 14	GENTLES_modul4
9	1e−01	1 / 16	GENTLES_modul16
10	1e−01	7 / 554	Lembcke_Colonic Inflammation
11	2e−01	1 / 24	PanCan_Notch_geneset_nanostring
12	3e−01	2 / 125	PanCan_CC+Apop_geneset_nanostring
13	3e−01	1 / 39	ZHANG_MM up
14	3e−01	1 / 46	PanCan_TGF−B_geneset_nanostring
15	4e−01	0 / 14	LIU_COMMON_CANCER_GENES

CC

Rank	p−value	#in/all	Geneset
1	7e−15	23 / 352	focal adhesion
2	5e−11	51 / 2464	extracellular exosome
3	4e−07	14 / 330	cytoskeleton
4	2e−06	54 / 3662	plasma membrane
5	2e−06	4 / 12	platelet alpha granule membrane
6	2e−06	6 / 49	platelet alpha granule lumen
7	3e−05	5 / 47	stress fiber
8	8e−05	60 / 4822	cytoplasm
9	1e−04	4 / 34	nuclear nucleosome
10	2e−04	3 / 14	platelet alpha granule
11	2e−04	7 / 149	lamellipodium
12	7e−04	12 / 512	cell surface
13	1e−03	19 / 1101	extracellular space
14	2e−03	20 / 1249	extracellular region
15	2e−03	6 / 170	cell−cell junction

Chr

Rank	p−value	#in/all	Geneset
1	0.01	10 / 536	Chr 22
2	0.13	16 / 1492	Chr 2
3	0.21	7 / 619	Chr 20
4	0.22	10 / 954	Chr 9
5	0.25	12 / 1217	Chr 3
6	0.30	11 / 1160	Chr 12
7	0.35	11 / 1211	Chr 6
8	0.41	8 / 902	Chr 4
9	0.41	8 / 904	Chr 10
10	0.46	11 / 1318	Chr 17
11	0.48	8 / 959	Chr 16
12	0.52	8 / 994	Chr X
13	0.56	6 / 769	Chr 15
14	0.65	3 / 422	Chr 13
15	0.67	10 / 1411	Chr 11

Chromatin states

Rank	p−value	#in/all	Geneset
1	6e−09	114 / 9635	3_TssF_Fibroblasts
2	6e−08	69 / 4795	6_EnhG_Fibroblasts
3	1e−07	134 / 12741	7_Enh_Melanocytes
4	1e−07	102 / 8613	7_Enh_Fibroblasts
5	4e−07	126 / 11847	7_Enh_Neuronal_Progenitor
6	8e−07	125 / 11836	3_TssF_Melanocytes
7	9e−06	126 / 12393	15_Quies_Neuronal_Progenitor
8	8e−05	47 / 3450	4_TxTrans_Fibroblasts
9	8e−05	127 / 12983	2_TssA_Neuronal_Progenitor
10	2e−04	48 / 3691	9_ReprPCWk_Neuronal_Progenitor
11	5e−04	67 / 5956	3_TssF_Neuronal_Progenitor
12	2e−03	107 / 11130	15_Quies_Melanocytes
13	2e−03	116 / 12298	2_TssA_Melanocytes
14	3e−03	89 / 8990	15_Quies_Fibroblasts
15	4e−03	108 / 11455	2_TssA_Fibroblasts

Colon Cancer

Rank	p−value	#in/all	Geneset
1	4e−12	36 / 1216	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_
2	9e−10	125 / 10779	Enh_Colon
3	5e−09	64 / 4018	EnhWk2_Colon
4	2e−07	65 / 4526	Quies1_Colon
5	2e−05	43 / 2894	TssP_Colon
6	3e−05	14 / 489	K9acLow_Colon
7	4e−05	66 / 5373	EnhWk1_Colon
8	7e−05	40 / 2740	ReprPCWk_Colon
9	2e−04	43 / 3173	ReprPC_Colon
10	3e−04	110 / 10999	TssWk_Colon
11	3e−04	20 / 1069	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
12	4e−04	12 / 479	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_
13	5e−04	6 / 129	Marisa_CRC−cluster−b
14	2e−03	8 / 278	Kosinski_top−crypt−long−list
15	2e−03	36 / 2810	EnhA_Colon

Glio

Rank	p−value	#in/all	Geneset
1	4e−05	8 / 158	Hopp_Sturm_GBM_Epi3_D_adult_fetus_IDH_UP
2	7e−04	6 / 134	Christensen_hypermethylated_in_grade3_oligoastrocytoma
3	2e−03	6 / 157	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
4	2e−03	5 / 117	Christensen_hypermethylated_in_grade2_oligoastrocytoma
5	4e−03	2 / 12	Phillips MES up vs Prolif & PN
6	6e−03	5 / 147	Christensen_hypermethylated_in_grade2_oligodendroglioma
7	7e−03	4 / 98	WILLSCHER_GBM_proteomics_wtOnly_SpotB
8	1e−02	3 / 57	OL vs. MOG− OL
9	1e−02	4 / 115	Christensen_hypermethylated_in_grade3_astrocytoma
10	3e−02	2 / 32	WILLSCHER_GBM_proteomics_wtOnly_SpotC
11	3e−02	2 / 34	Shaw_down_in_1p19q
12	3e−02	3 / 90	Christensen_hypermethylated_in_secondary_glioblastoma
13	4e−02	3 / 94	Weller_LGG_A_vs_O_UP
14	6e−02	2 / 52	OL vs. OPC
15	6e−02	2 / 53	mature astrocytes

GSEA C2

Rank	p−value	#in/all	Geneset
1	7e−58	35 / 64	RAGHAVACHARI_PLATELET_SPECIFIC_GENES
2	3e−46	40 / 188	WIERENGA_STAT5A_TARGETS_DN
3	2e−19	29 / 414	REACTOME_HEMOSTASIS
4	2e−17	20 / 181	REACTOME_PLATELET_ACTIVATION_SIGNALING_AND_AGGREGATION
5	7e−16	18 / 162	JISON_SICKLE_CELL_DISEASE_UP
6	1e−14	13 / 71	REACTOME_RESPONSE_TO_ELEVATED_PLATELET_CYTOSOLIC_CA2_
7	9e−14	12 / 64	ROSS_AML_OF_FAB_M7_TYPE
8	5e−13	10 / 40	GNATENKO_PLATELET_SIGNATURE
9	3e−11	20 / 387	SWEET_LUNG_CANCER_KRAS_DN
10	7e−11	21 / 451	PILON_KLF1_TARGETS_UP
11	3e−09	7 / 30	REACTOME_FORMATION_OF_FIBRIN_CLOT_CLOTTING_CASCADE
12	4e−09	12 / 157	BERTUCCI_MEDULLARY_VS_DUCTAL_BREAST_CANCER_DN
13	5e−09	20 / 520	CHICAS_RB1_TARGETS_CONFLUENT
14	8e−09	6 / 20	REACTOME_SMOOTH_MUSCLE_CONTRACTION
15	9e−09	7 / 35	REACTOME_PLATELET_AGGREGATION_PLUG_FORMATION

HM

Rank	p−value	#in/all	Geneset
1	3e−06	10 / 191	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
2	8e−06	7 / 91	HALLMARK_ANDROGEN_RESPONSE
3	1e−04	8 / 183	HALLMARK_APICAL_JUNCTION
4	5e−04	6 / 127	HALLMARK_COAGULATION
5	7e−04	7 / 185	HALLMARK_HEME_METABOLISM
6	4e−03	6 / 186	HALLMARK_MYOGENESIS
7	4e−03	5 / 132	HALLMARK_UV_RESPONSE_DN
8	5e−03	5 / 138	HALLMARK_FATTY_ACID_METABOLISM
9	1e−02	5 / 176	HALLMARK_ADIPOGENESIS
10	1e−02	5 / 176	HALLMARK_KRAS_SIGNALING_UP
11	2e−02	5 / 185	HALLMARK_MTORC1_SIGNALING
12	3e−02	2 / 33	HALLMARK_ANGIOGENESIS
13	3e−02	4 / 151	HALLMARK_APOPTOSIS
14	4e−02	2 / 41	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
15	5e−02	4 / 175	HALLMARK_XENOBIOTIC_METABOLISM

Lifestyle

Rank	p−value	#in/all	Geneset
1	2e−05	8 / 147	Homuth_BMI−associated−genes_UP
2	5e−02	1 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
3	8e−01	1 / 211	Homuth_BMI−associated−genes_DN
4	1e+00	0 / 94	DUMEAUX_Smoking enriched genes
5	1e+00	0 / 10	DUMEAUX_Smoking literature genes up
6	1e+00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
7	1e+00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
8	1e+00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
9	1e+00	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
10	1e+00	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
11	1e+00	0 / 10	DUMEAUX_Women normal BMI literature genes up
12	1e+00	0 / 17	DUMEAUX_High bmi enriched genes
13	1e+00	0 / 31	DUMEAUX_Fasting enriched genes
14	1e+00	0 / 18	Huan_blood−pressure_SBP−signature
15	1e+00	0 / 16	Huan_blood−pressure_DBP−signature

Lymphoma

Rank	p−value	#in/all	Geneset
1	6e−08	50 / 2939	HOPP_Poised_promoter
2	2e−05	10 / 244	LENZ_Stromal signature 1
3	4e−05	66 / 5384	HOPP_Repressed
4	1e−04	7 / 139	Hopp_June14_MMML937 tumors+controls_group.overexpression_F_FL_tons
5	1e−04	7 / 141	WIRTH_lymphoma937_spot F
6	2e−03	35 / 2701	HOPP_Repetitive
7	3e−03	8 / 300	Hopp_June14_MMML937 tumors+controls_group.overexpression_E_GC−B−
8	3e−03	8 / 306	WIRTH_lymphoma937_spot E
9	8e−03	46 / 4167	HOPP_Heterochrom
10	9e−03	6 / 226	Hopp_Lymphoma_Epi1_no_zentr_6_MCL_DN
11	1e−02	3 / 57	Hopp_Lymphoma_Epi1_no_zentr_1_B.cell_DN
12	1e−02	4 / 115	ROSOLOWSKI_green total
13	2e−02	4 / 134	Subero_DLBCL_hyper_meth
14	2e−02	6 / 283	TARTE_Plasmablast signature
15	3e−02	3 / 87	Hopp_Lymphoma_Epi1_with_zentr_v_B.cell_DN

Melanoma

Rank	p−value	#in/all	Geneset
1	0.2	1 / 30	Hugo_melanoma−all−MET_UP
2	0.3	1 / 54	Hugo_melanoma−all−MET_DN
3	1.0	0 / 43	Hugo_melanoma−BRAFmut−MET_UP
4	1.0	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
5	1.0	0 / 27	Hugo_melanoma−all−LEF1_UP
6	1.0	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

MF

Rank	p−value	#in/all	Geneset
1	5e−07	102 / 8818	protein binding
2	1e−06	11 / 213	GTPase activity
3	1e−05	7 / 98	integrin binding
4	2e−05	12 / 351	GTP binding
5	2e−05	13 / 413	protein heterodimerization activity
6	8e−04	5 / 91	structural constituent of cytoskeleton
7	1e−03	8 / 265	cadherin binding involved in cell−cell adhesion
8	1e−03	8 / 268	actin binding
9	2e−03	13 / 648	calcium ion binding
10	4e−03	3 / 39	androgen receptor binding
11	5e−03	12 / 646	protein homodimerization activity
12	5e−03	2 / 14	5'−nucleotidase activity
13	8e−03	2 / 17	myosin V binding
14	1e−02	3 / 57	collagen binding
15	1e−02	2 / 21	G−protein beta/gamma−subunit complex binding

miRNA Disease

Rank	p−value	#in/all	Geneset
1	1	0 / 7	Thyroid carcinoma, papillary
2	1	0 / 123	Pancreatic cancer
3	1	0 / 68	Glioblastoma multiforme, somatic
4	1	0 / 63	Gastrointestinal
5	1	0 / 3	Pituitary adenoma
6	1	0 / 116	Cancer
7	1	0 / 95	Colorectal cancer
8	1	0 / 2	Adenomas, multiple colorectal
9	1	0 / 124	Prostate cancer
10	1	0 / 48	Alzheimer disease, susceptibility to
11	1	0 / 7	Schizophrenia, susceptibility to
12	1	0 / 20	Parkinson disease
13	1	0 / 65	Hepatocellular carcinoma
14	1	0 / 3	Down syndrome, risk of
15	1	0 / 127	Melanoma and neural system tumor syndrome

miRNA target

Rank	p−value	#in/all	Geneset
1	0.001	3 / 25	hsa−miR−941
2	0.002	4 / 67	hsa−miR−299−5p
3	0.002	5 / 113	hsa−miR−498
4	0.004	8 / 317	hsa−miR−18a
5	0.004	8 / 317	hsa−miR−559
6	0.005	4 / 85	hsa−miR−1265
7	0.009	2 / 18	hsa−miR−564
8	0.009	3 / 54	hsa−miR−629
9	0.012	4 / 114	hsa−miR−875−3p
10	0.015	4 / 120	hsa−miR−1248
11	0.015	2 / 24	hsa−miR−609
12	0.017	5 / 190	hsa−miR−128
13	0.018	2 / 26	hsa−miR−675
14	0.020	2 / 28	hsa−miR−519e*
15	0.020	3 / 74	hsa−miR−509−5p

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.1	1 / 13	BENTINK_e2f3.1
2	0.1	1 / 14	GUSTAFSON_PI3K_UP
3	1.0	0 / 15	GUSTAFSON_PI3K_DN
4	1.0	0 / 13	BENTINK_e2f3.2
5	1.0	0 / 13	BENTINK_myc.1
6	1.0	0 / 12	BENTINK_ras.1
7	1.0	0 / 11	BENTINK_ras.4
8	1.0	0 / 14	BENTINK_ras.6
9	1.0	0 / 13	BENTINK_src.10
10	1.0	0 / 12	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Reference Signatures

Rank	p−value	#in/all	Geneset
1	1e−99	65 / 102	Chaussabel_1,2_Platelets
2	2e−06	4 / 13	WIRTH_Sec. lymphoid organs
3	3e−05	13 / 416	PROTEINATLAS_ovary
4	2e−04	12 / 429	PROTEINATLAS_soft tissue
5	3e−04	14 / 598	PROTEINATLAS_prostate
6	3e−04	12 / 465	PROTEINATLAS_liver
7	4e−04	14 / 623	PROTEINATLAS_seminal vesicle
8	8e−04	12 / 514	PROTEINATLAS_vagina
9	1e−03	14 / 681	PROTEINATLAS_lung
10	1e−03	18 / 1016	PROTEINATLAS_cerebral cortex
11	2e−03	14 / 726	PROTEINATLAS_cervix, uterine
12	2e−03	13 / 647	PROTEINATLAS_lateral ventricle
13	3e−03	14 / 759	PROTEINATLAS_epididymis
14	3e−03	15 / 850	PROTEINATLAS_skin
15	4e−03	12 / 619	PROTEINATLAS_salivary gland

Telomeres

Rank	p−value	#in/all	Geneset
1	0.2	1 / 27	Nabetani_alt len telomeres_genes_ko
2	1.0	0 / 13	Alternative lengthening of telomeres
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	0.005	52 / 4735	ICGC_Pu1_targets
2	0.009	33 / 2759	ICGC_Bcl3_targets
3	0.013	54 / 5188	ICGC_Ebfsc137065_targets
4	0.016	1 / 2	MYC_ECM cell adhesion DOWN
5	0.020	29 / 2497	ICGC_Bcl11_targets
6	0.038	20 / 1669	ICGC_P300_targets
7	0.039	1 / 5	MYC_TFs
8	0.044	35 / 3348	ICGC_BatfPcr1_targets
9	0.058	20 / 1753	HEBENSTREIT_low expression TF
10	0.068	1 / 9	MYC_Targets DOWN
11	0.111	22 / 2133	ICGC_Mef2_targets
12	0.132	1 / 18	MYC_Metabolism UP
13	0.196	57 / 6552	ICGC_Pol2_targets
14	0.199	15 / 1501	ICGC_Usf1_targets
15	0.223	62 / 7247	ICGC_Runx3_targets

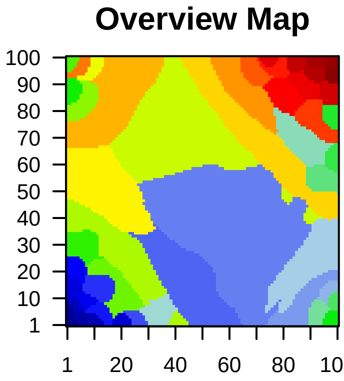
K−Means Cluster

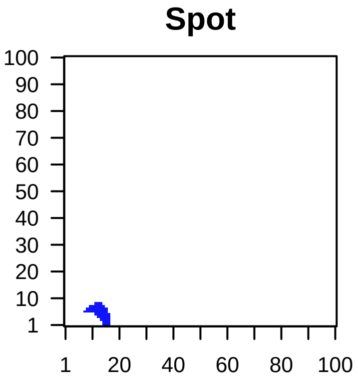
Spot Summary: J

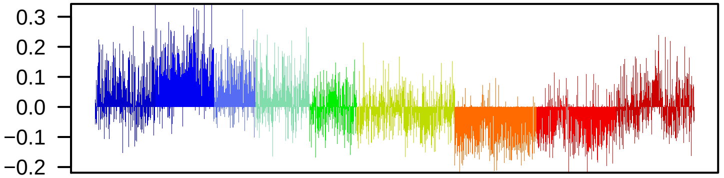
metagenes = 47
genes = 466

<r> metagenes = 0.93
<r> genes = 0.32
beta: r2= 26.93 / log p= −Inf

samples with spot = 364 (10.7 %)
- A * : 63 (18.3 %)
- A C * : 146 (44.5 %)
- A C F * : 58 (24.7 %)
- A F * : 45 (14.6 %)
- C F * : 9 (3.4 %)
- F * : 10 (1.8 %)
- J * : 1 (0.2 %)
- N * : 32 (7.2 %)


Overview Map


Spot

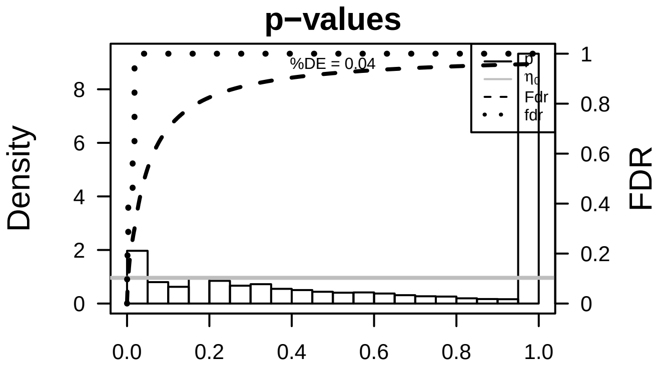


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_177719	1.54	−1.37	0.22	CFD	complement factor D [Source:HGNC Symbol;Acc:HGNC:277
2	ILMN_235994	1.29	−1.26	0.26	CES1	carboxylesterase 1 [Source:HGNC Symbol;Acc:HGNC:1863]
3	ILMN_176332	1.17	−1.24	0.23	CCR3	C−C motif chemokine receptor 3 [Source:HGNC Symbol;Acc:
4	ILMN_178379	1.07	−0.63	0.28	BTNL3	butyrophilin like 3 [Source:HGNC Symbol;Acc:HGNC:1143]
5	ILMN_235856	1.03	−0.56	0.4	TIAM2	T−cell lymphoma invasion and metastasis 2 [Source:HGNC S
6	ILMN_233613	1.01	−0.87	0.43	SULT1A2	sulfotransferase family 1A member 2 [Source:HGNC Symbol;
7	ILMN_171149	0.99	−0.72	0.75		
8	ILMN_178138	0.99	−0.47	0.27	PGM5	phosphoglucomutase 5 [Source:HGNC Symbol;Acc:HGNC:8
9	ILMN_170959	0.96	−0.44	0.27	PGM5	phosphoglucomutase 5 [Source:HGNC Symbol;Acc:HGNC:8
10	ILMN_166002	0.92	−0.57	0.24	FCGR2B	Fc fragment of IgG receptor IIb [Source:HGNC Symbol;Acc:H
11	ILMN_240507	0.92	−0.59	0.3		
12	ILMN_169365	0.92	−0.77	0.78	FES	FES proto−oncogene, tyrosine kinase [Source:HGNC Symbo
13	ILMN_165690	0.91	−0.82	0.53		
14	ILMN_165812	0.88	−0.7	0.74		
15	ILMN_176901	0.88	−0.82	0.42	ASGR1	asialoglycoprotein receptor 1 [Source:HGNC Symbol;Acc:HG
16	ILMN_219359	0.87	−0.65	0.62	UNC93B1	unc−93 homolog B1 (C. elegans) [Source:HGNC Symbol;Acc
17	ILMN_234965	0.86	−0.92	0.57	TSPO	translocator protein [Source:HGNC Symbol;Acc:HGNC:1158]
18	ILMN_171830	0.86	−0.41	0.45	NECTIN2	nectin cell adhesion molecule 2 [Source:HGNC Symbol;Acc:H
19	ILMN_168973	0.86	−0.48	0.4	IL1RN	interleukin 1 receptor antagonist [Source:HGNC Symbol;Acc:
20	ILMN_176725	0.85	−0.69	0.63	RRP12	ribosomal RNA processing 12 homolog [Source:HGNC Symb

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	3e−36	266 / 9054	Colon	Tx_Colon
2	2e−32	230 / 7354	Colon	TssF_Colon
3	1e−31	266 / 9555	Colon	TssA_Colon
4	8e−30	130 / 2845	Colon	TxEnhG1_Colon
5	1e−29	246 / 8568	Colon	TxWk_Colon
6	2e−27	277 / 10779	Colon	Enh_Colon
7	1e−25	167 / 4795	Chror	6_EnhG_Fibroblasts
8	1e−25	194 / 6138	Colon	TssD2_Colon
9	2e−25	218 / 7448	Lympl	HOPP_Strong_enhancer
10	1e−22	179 / 5699	Chror	6_EnhG_Melanocytes
11	7e−22	115 / 2810	Colon	EnhA_Colon
12	2e−21	129 / 3450	Chror	4_TxTrans_Fibroblasts
13	1e−20	168 / 5373	Colon	EnhWk1_Colon
14	2e−19	226 / 8678	Colon	Quies3_Colon
15	5e−19	241 / 9635	Chror	3_TssF_Fibroblasts
16	7e−19	275 / 11836	Chror	3_TssF_Melanocytes
17	2e−18	225 / 8771	Chror	5_Tx_Melanocytes
18	2e−18	252 / 10430	Brain	Overlap_fetal_midbrain_Quies
19	7e−18	28 / 208	GSEA	THEILGAARD_NEUTROPHIL_AT_SKIN_WOUND_DN
20	1e−17	279 / 12298	Chror	2_TssA_Melanocytes
21	1e−16	170 / 5956	Chror	3_TssF_Neuronal_Progenitor
22	3e−16	277 / 12393	Chror	15_Quies_Neuronal_Progenitor
23	3e−15	27 / 240	Refer	Chaussabel_3,3_Inflammation II
24	3e−15	253 / 10999	Colon	TssWk_Colon
25	6e−15	200 / 7854	Chror	5_Tx_Fibroblasts
26	3e−14	19 / 113	Refer	Chaussabel_1,5_Myeloid lineage
27	3e−14	32 / 382	GSEA	MULLIGHAN_MLL_SIGNATURE_2_UP
28	1e−13	65 / 1470	Colon	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon
29	3e−13	185 / 7275	Lympl	HOPP_Txn_elongation
30	8e−13	148 / 5356	Lympl	HOPP_Txn_transition
31	3e−12	275 / 12983	Chror	2_TssA_Neuronal_Progenitor
32	3e−12	271 / 12741	Chror	7_Enh_Melanocytes
33	5e−12	208 / 8818	MF	protein binding
34	8e−12	175 / 6970	Chror	5_Tx_Neuronal_Progenitor
35	9e−12	75 / 2028	Chror	4_TxTrans_Melanocytes
36	2e−11	27 / 346	GSEA	MULLIGHAN_MLL_SIGNATURE_1_UP
37	2e−11	249 / 11455	Chror	2_TssA_Fibroblasts
38	3e−11	217 / 9504	Brain	Overlap_fetal_midbrain_K9K27me3
39	4e−11	18 / 150	Refer	Chaussabel_2,6_Myeloid lineage
40	8e−11	130 / 4735	TF	ICGC_Pu1_targets


p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.3	3 / 111	HORVATH_aging_genes meth DOWN
2	0.9	1 / 142	HORVATH_aging_genes meth UP
3	1.0	0 / 58	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	9e−05	15 / 292	positive regulation of apoptotic process
2	2e−04	16 / 342	intracellular signal transduction
3	2e−04	7 / 75	regulation of Rho protein signal transduction
4	4e−04	15 / 335	protein transport
5	4e−04	15 / 336	inflammatory response
6	8e−04	3 / 12	acrosome assembly
7	8e−04	3 / 12	negative regulation of innate immune response
8	9e−04	4 / 27	positive regulation of phagocytosis
9	1e−03	30 / 1003	signal transduction
10	2e−03	4 / 32	positive regulation of substrate adhesion−dependent cell spreading
11	2e−03	15 / 387	cell adhesion
12	2e−03	3 / 17	cellular response to extracellular stimulus
13	2e−03	5 / 58	endosomal transport
14	3e−03	3 / 18	viral budding via host ESCRT complex
15	3e−03	4 / 37	negative regulation of I−kappaB kinase/NF−kappaB signaling

Brain

Rank	p−value	#in/all	Geneset
1	2e−18	252 / 10430	Overlap_fetal_midbrain_Quies
2	3e−11	217 / 9504	Overlap_fetal_midbrain_K9K27me3
3	8e−11	98 / 3164	Mid_Frontal_Lobe_ZNF
4	1e−09	85 / 2709	Mid_Frontal_Lobe_HetRpts
5	1e−09	218 / 9917	Overlap_fetal_midbrain_ReprPCWk
6	3e−07	140 / 5936	Overlap_fetal_midbrain_HetRpts
7	3e−05	98 / 4112	Mid_Frontal_Lobe_ReprPC
8	7e−05	29 / 818	Mid_Frontal_Lobe_Het
9	1e−04	195 / 9815	Overlap_fetal_midbrain_ReprPC
10	2e−02	47 / 2127	Mid_Frontal_Lobe_K9K27me3
11	2e−02	21 / 796	Overlap_fetal_midbrain_ZNF
12	2e−02	25 / 1012	Mid_Frontal_Lobe_Enh
13	3e−02	55 / 2630	Fetal_TssF
14	3e−02	17 / 630	Mid_Frontal_Lobe_EnhP
15	7e−02	36 / 1728	Fetal_ReprPCWk

Cancer

Rank	p−value	#in/all	Geneset
1	4e−07	27 / 554	Lembcke_Colonic Inflammation
2	4e−04	14 / 301	SPANG_BCL6−index2
3	7e−04	10 / 178	SPANG_LPS−index2
4	1e−02	5 / 82	PanCan_JAK−ST_geneset_nanostring
5	2e−02	3 / 36	PanCan_HK_geneset_nanostring
6	5e−02	14 / 527	Lembcke_Normal vs Adenoma
7	2e−01	1 / 13	GENTLES_modul18
8	2e−01	1 / 14	LIU_PROSTATE_CANCER_UP
9	2e−01	1 / 14	GENTLES_modul10
10	2e−01	1 / 15	LIU_PROSTATE_CANCER_DN
11	2e−01	1 / 15	WANG_ER_UP
12	2e−01	4 / 150	PanCan_MAPK_geneset_nanostring
13	2e−01	1 / 16	BEN−PORATH_DN
14	3e−01	1 / 24	PanCan_Notch_geneset_nanostring
15	4e−01	4 / 193	PanCan_PI3K_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	9e−09	125 / 4822	cytoplasm
2	7e−06	58 / 1979	membrane
3	2e−04	12 / 208	actin cytoskeleton
4	2e−04	63 / 2464	extracellular exosome
5	4e−04	8 / 107	spindle
6	5e−04	105 / 4828	nucleus
7	6e−04	62 / 2535	nucleoplasm
8	9e−04	20 / 561	intracellular membrane−bounded organelle
9	1e−03	14 / 330	cytoskeleton
10	2e−03	14 / 352	focal adhesion
11	3e−03	80 / 3662	plasma membrane
12	3e−03	67 / 2979	cytosol
13	4e−03	3 / 20	protein phosphatase type 2A complex
14	5e−03	10 / 234	lysosomal membrane
15	5e−03	4 / 43	intercellular bridge

Chr

Rank	p−value	#in/all	Geneset
1	0.002	39 / 1467	Chr 19
2	0.003	35 / 1318	Chr 17
3	0.007	26 / 959	Chr 16
4	0.029	15 / 536	Chr 22
5	0.046	16 / 619	Chr 20
6	0.090	25 / 1160	Chr 12
7	0.413	21 / 1217	Chr 3
8	0.474	13 / 768	Chr 14
9	0.496	20 / 1211	Chr 6
10	0.528	19 / 1170	Chr 7
11	0.635	36 / 2323	Chr 1
12	0.649	16 / 1060	Chr 5
13	0.707	13 / 904	Chr 10
14	0.775	13 / 954	Chr 9
15	0.838	20 / 1492	Chr 2

Chromatin states

Rank	p−value	#in/all	Geneset
1	1e−25	167 / 4795	6_EnhG_Fibroblasts
2	1e−22	179 / 5699	6_EnhG_Melanocytes
3	2e−21	129 / 3450	4_TxTrans_Fibroblasts
4	5e−19	241 / 9635	3_TssF_Fibroblasts
5	7e−19	275 / 11836	3_TssF_Melanocytes
6	2e−18	225 / 8771	5_Tx_Melanocytes
7	1e−17	279 / 12298	2_TssA_Melanocytes
8	1e−16	170 / 5956	3_TssF_Neuronal_Progenitor
9	3e−16	277 / 12393	15_Quies_Neuronal_Progenitor
10	6e−15	200 / 7854	5_Tx_Fibroblasts
11	3e−12	275 / 12983	2_TssA_Neuronal_Progenitor
12	3e−12	271 / 12741	7_Enh_Melanocytes
13	8e−12	175 / 6970	5_Tx_Neuronal_Progenitor
14	9e−12	75 / 2028	4_TxTrans_Melanocytes
15	2e−11	249 / 11455	2_TssA_Fibroblasts

Colon Cancer

Rank	p−value	#in/all	Geneset
1	3e−36	266 / 9054	Tx_Colon
2	2e−32	230 / 7354	TssF_Colon
3	1e−31	266 / 9555	TssA_Colon
4	8e−30	130 / 2845	TxEnhG1_Colon
5	1e−29	246 / 8568	TxWk_Colon
6	2e−27	277 / 10779	Enh_Colon
7	1e−25	194 / 6138	TssD2_Colon
8	7e−22	115 / 2810	EnhA_Colon
9	1e−20	168 / 5373	EnhWk1_Colon
10	2e−19	226 / 8678	Quies3_Colon
11	3e−15	253 / 10999	TssWk_Colon
12	1e−13	65 / 1470	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
13	2e−08	49 / 1281	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv
14	5e−07	34 / 810	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
15	2e−05	30 / 789	TxEnhG2_Colon

Glio

Rank	p−value	#in/all	Geneset
1	2e−08	20 / 267	WILLSCHER_GBM_Verhaak−CL & MES_up
2	3e−04	10 / 158	Hopp_Sturm_GBM_Epi3_D_adult_fetus_IDH_UP
3	2e−03	13 / 315	Up
4	4e−03	6 / 94	Weller_LGG_A_vs_O_UP
5	7e−03	4 / 47	Donson−innate immunity−associated with LTS in HGA
6	1e−02	4 / 52	Sturm_GBM_Meth_overexpression_F_IDH_UP
7	1e−02	6 / 115	Christensen_hypermethylated_in_grade3_astrocytoma
8	1e−02	5 / 86	laffaire_hypermeth_LGG_vs_control
9	1e−02	5 / 87	Sturm_GBM_Meth_overexpression_I_RTK I 'PDGFRA'_UP
10	2e−02	7 / 166	Sturm_GBM_Meth_overexpression_B_adult_UP
11	2e−02	6 / 134	Christensen_hypermethylated_in_grade3_oligoastrocytoma
12	2e−02	33 / 1417	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
13	2e−02	2 / 15	VERHAAK_NL subtype
14	2e−02	4 / 68	Christensen_hypermethylated_in_grade2_astrocytoma
15	3e−02	21 / 820	Sturm_GBM_Meth_overexpression_E_G34_UP

GSEA C2

Rank	p−value	#in/all	Geneset
1	7e−18	28 / 208	THEILGAARD_NEUTROPHIL_AT_SKIN_WOUND_DN
2	3e−14	32 / 382	MULLIGHAN_MLL_SIGNATURE_2_UP
3	2e−11	27 / 346	MULLIGHAN_MLL_SIGNATURE_1_UP
4	4e−09	26 / 409	MARTENS_BOUND_BY_PML_RARA_FUSION
5	1e−08	34 / 692	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP
6	2e−08	55 / 1535	BLALOCK_ALZHEIMERS_DISEASE_UP
7	6e−08	24 / 406	RODWELL_AGING_KIDNEY_UP
8	2e−07	42 / 1081	CHEN_METABOLIC_SYNDROM_NETWORK
9	2e−07	16 / 203	VERHAAK_GLIOBLASTOMA_MESENCHYMAL
10	3e−07	15 / 182	MARKEY_RB1_ACUTE_LOF_UP
11	8e−07	34 / 831	LOPEZ_MBD_TARGETS
12	1e−06	21 / 376	REN_ALVEOLAR_RHABDOMYOSARCOMA_DN
13	1e−06	13 / 150	BROWN_MYELOID_CELL_DEVELOPMENT_UP
14	1e−06	9 / 68	ROSS_AML_WITH_MLL_FUSIONS
15	4e−06	21 / 410	MILI_PSEUDOPODIA_CHEMOTAXIS_DN

HM

Rank	p−value	#in/all	Geneset
1	5e−05	6 / 41	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
2	2e−03	9 / 177	HALLMARK_MITOTIC_SPINDLE
3	4e−03	9 / 189	HALLMARK_HYPOXIA
4	1e−02	8 / 185	HALLMARK_P53_PATHWAY
5	1e−02	8 / 186	HALLMARK_MYOGENESIS
6	1e−02	7 / 151	HALLMARK_APOPTOSIS
7	2e−02	7 / 162	HALLMARK_ALLOGRAFT_REJECTION
8	2e−02	5 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING
9	2e−02	7 / 172	HALLMARK_INTERFERON_GAMMA_RESPONSE
10	3e−02	7 / 183	HALLMARK_GLYCOLYSIS
11	3e−02	7 / 185	HALLMARK_TNFA_SIGNALING_VIA_NFKB
12	6e−02	4 / 91	HALLMARK_PEROXISOME
13	6e−02	5 / 130	HALLMARK_DNA_REPAIR
14	9e−02	6 / 191	HALLMARK_INFLAMMATORY_RESPONSE
15	1e−01	3 / 82	HALLMARK_IL6_JAK_STAT3_SIGNALING

Lifestyle

Rank	p−value	#in/all	Geneset
1	1e−08	18 / 211	Homuth_BMI−associated−genes_DN
2	9e−02	1 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
3	1e−01	1 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
4	2e−01	1 / 16	Huan_blood−pressure_DBP−signature
5	3e−01	1 / 18	Huan_blood−pressure_SBP−signature
6	5e−01	2 / 94	DUMEAUX_Smoking enriched genes
7	9e−01	1 / 147	Homuth_BMI−associated−genes_UP
8	1e+00	0 / 10	DUMEAUX_Smoking literature genes up
9	1e+00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
10	1e+00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
11	1e+00	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
12	1e+00	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
13	1e+00	0 / 10	DUMEAUX_Women normal BMI literature genes up
14	1e+00	0 / 17	DUMEAUX_High bmi enriched genes
15	1e+00	0 / 31	DUMEAUX_Fasting enriched genes

Lymphnoma

Rank	p−value	#in/all	Geneset
1	2e−25	218 / 7448	HOPP_Strong_enhancer
2	3e−13	185 / 7275	HOPP_Txn_elongation
3	8e−13	148 / 5356	HOPP_Txn_transition
4	3e−09	23 / 318	Hopp_June14_MMML937 tumors+controls_group.overexpression_H_GC−B−
5	3e−08	22 / 331	WIRTH_lymphoma937_spot H
6	3e−06	41 / 1169	SPANG_BCR DN
7	5e−06	175 / 8226	HOPP_Active_promoter
8	1e−03	17 / 455	SPANG_CD40 6hrs DN
9	2e−03	159 / 8098	HOPP_Weak_promoter
10	2e−03	12 / 272	SPANG_IL21 DN
11	8e−03	11 / 290	SPANG_IL21 UP
12	9e−03	2 / 9	Shaknovich_ABC_hypo_meth
13	1e−02	127 / 6559	HOPP_Weak_txn
14	1e−02	9 / 226	Hopp_Lymphoma_Epi1_no_zentr_6_MCL_DN
15	1e−02	4 / 57	Monti_Host_response_cluster

Melanoma

Rank	p−value	#in/all	Geneset
1	1	0 / 30	Hugo_melanoma−all−MET_UP
2	1	0 / 54	Hugo_melanoma−all−MET_DN
3	1	0 / 43	Hugo_melanoma−BRAFmut−MET_UP
4	1	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
5	1	0 / 27	Hugo_melanoma−all−LEF1_UP
6	1	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

MF

Rank	p−value	#in/all	Geneset
1	5e−12	208 / 8818	protein binding
2	4e−04	4 / 22	calmodulin−dependent protein kinase activity
3	1e−03	6 / 71	Rho guanyl−nucleotide exchange factor activity
4	1e−03	3 / 14	retinoid X receptor binding
5	2e−03	10 / 204	protein domain specific binding
6	2e−03	9 / 174	calmodulin binding
7	3e−03	5 / 60	glycoprotein binding
8	3e−03	4 / 38	RNA polymerase II transcription factor activity, ligand−activated sequence−sp
9	5e−03	12 / 314	RNA polymerase II core promoter proximal region sequence−specific DNA bi
10	7e−03	6 / 103	guanyl−nucleotide exchange factor activity
11	9e−03	4 / 50	steroid hormone receptor activity
12	9e−03	19 / 646	protein homodimerization activity
13	1e−02	8 / 182	signal transducer activity
14	1e−02	4 / 52	calcium−dependent protein binding
15	1e−02	4 / 52	RNA polymerase II core promoter sequence−specific DNA binding

miRNA Disease

Rank	p−value	#in/all	Geneset
1	1	0 / 7	Thyroid carcinoma, papillary
2	1	0 / 123	Pancreatic cancer
3	1	0 / 68	Glioblastoma multiforme, somatic
4	1	0 / 63	Gastrointestinal
5	1	0 / 3	Pituitary adenoma
6	1	0 / 116	Cancer
7	1	0 / 95	Colorectal cancer
8	1	0 / 2	Adenomas, multiple colorectal
9	1	0 / 124	Prostate cancer
10	1	0 / 48	Alzheimer disease, susceptibility to
11	1	0 / 7	Schizophrenia, susceptibility to
12	1	0 / 20	Parkinson disease
13	1	0 / 65	Hepatocellular carcinoma
14	1	0 / 3	Down syndrome, risk of
15	1	0 / 127	Melanoma and neural system tumor syndrome

miRNA target

Rank	p−value	#in/all	Geneset
1	9e−04	11 / 217	hsa−miR−185
2	4e−03	6 / 95	hsa−miR−125a−5p
3	5e−03	3 / 21	hsa−miR−1282
4	6e−03	6 / 100	hsa−miR−376a
5	6e−03	14 / 400	hsa−miR−519c−3p
6	7e−03	5 / 75	hsa−miR−375
7	9e−03	4 / 50	hsa−miR−1224−3p
8	1e−02	7 / 146	hsa−miR−138
9	1e−02	4 / 52	hsa−miR−362−3p
10	1e−02	2 / 10	hsa−miR−1306
11	1e−02	16 / 520	hsa−miR−106a
12	1e−02	7 / 150	hsa−miR−338−3p
13	1e−02	5 / 85	hsa−miR−149
14	2e−02	16 / 540	hsa−miR−17
15	2e−02	3 / 34	hsa−miR−1231

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.2	1 / 11	BENTINK_ras.4
2	0.2	1 / 12	BENTINK_ras.1
3	0.2	1 / 13	BENTINK_e2f3.1
4	0.2	1 / 14	GUSTAFSON_PI3K_UP
5	0.2	1 / 14	BENTINK_ras.6
6	1.0	0 / 15	GUSTAFSON_PI3K_DN
7	1.0	0 / 13	BENTINK_e2f3.2
8	1.0	0 / 13	BENTINK_myc.1
9	1.0	0 / 13	BENTINK_src.10
10	1.0	0 / 12	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Reference Signatures

Rank	p−value	#in/all	Geneset
1	3e−15	27 / 240	Chaussabel_3,3_Inflammation II
2	3e−14	19 / 113	Chaussabel_1,5_Myeloid lineage
3	4e−11	18 / 150	Chaussabel_2,6_Myeloid lineage
4	4e−05	14 / 242	Chaussabel_3,2_Inflammation I
5	9e−05	7 / 66	VAQUERIZAS_Whole blood_TF
6	4e−04	17 / 412	WIRTH_Immune system
7	7e−04	4 / 25	VAQUERIZAS_Adrenal cortex_TF
8	2e−03	3 / 17	VAQUERIZAS_Heart_TF
9	3e−03	2 / 5	VAQUERIZAS_Appendix_TF
10	4e−03	5 / 64	VAQUERIZAS_Lung_TF
11	2e−02	5 / 96	Chaussabel_3,1_Interferon−inducible
12	2e−02	23 / 912	PROTEINATLAS_urinary bladder
13	3e−02	27 / 1118	PROTEINATLAS_placenta
14	3e−02	2 / 16	VAQUERIZAS_Ovary_TF
15	3e−02	29 / 1239	PROTEINATLAS_testis

Telomeres

Rank	p−value	#in/all	Geneset
1	1	0 / 13	Alternative lengthening of telomeres
2	1	0 / 27	Nabetani_alt len telomeres_genes_ko
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	8e−11	130 / 4735	ICGC_Pu1_targets
2	3e−10	123 / 4468	ICGC_Egr1_targets
3	9e−10	133 / 5067	ICGC_Taf1_targets
4	3e−09	140 / 5518	ICGC_Stat5_targets
5	1e−08	136 / 5442	ICGC_Pmlsc71910_targets
6	2e−08	136 / 5466	ICGC_Nficsc81335_targets
7	3e−08	161 / 6868	ICGC_Elf1_targets
8	5e−08	144 / 5984	ICGC_Mta3_targets
9	7e−08	123 / 4881	ICGC_Atf2_targets
10	7e−08	113 / 4362	ICGC_Creb1_targets
11	8e−08	123 / 4890	ICGC_Bclaf101388_targets
12	1e−07	165 / 7247	ICGC_Runx3_targets
13	3e−07	91 / 3348	ICGC_BatfPcr1_targets
14	3e−07	130 / 5383	ICGC_Sp1_targets
15	3e−07	146 / 6267	ICGC_Yy1_targets

K−Means Cluster

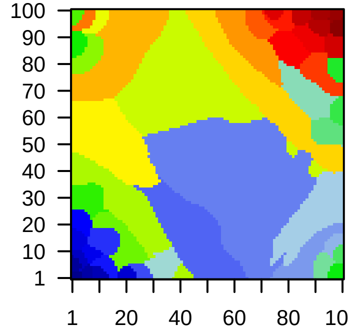
Spot Summary: K

metagenes = 195
genes = 740

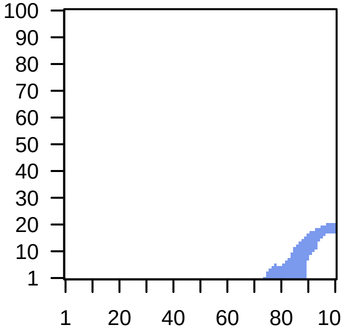
<r> metagenes = 0.79
<r> genes = 0.08
beta: r2= 2.35 / log p= −Inf

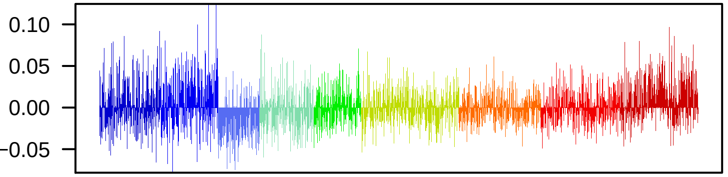
samples with spot = 2 (0.1 %)
A C * : 2 (0.6 %)

Overview Map



Spot





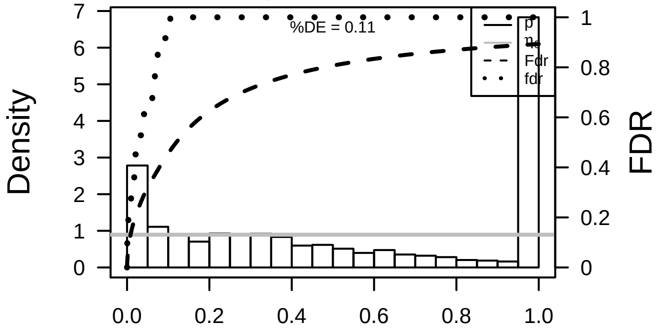
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_323522	2.12	−2.5	0.14		
2	ILMN_222964	1.73	−0.53	0.09		
3	ILMN_206041	1.52	−1.23	0	CD24	CD24 molecule [Source:HGNC Symbol;Acc:HGNC:1645]
4	ILMN_219647	1.51	−0.63	0.07	XRN2	5'−3' exoribonuclease 2 [Source:HGNC Symbol;Acc:HGNC:1
5	ILMN_215078	1.19	−0.41	0.08	HLA−C	major histocompatibility complex, class I, C [Source:HGNC Sy
6	ILMN_166716	1.11	−0.46	0.07		
7	ILMN_178123	0.92	−0.43	0.15		
8	ILMN_167604	0.78	−0.4	0.04	ALOX15	arachidonate 15−lipoxygenase [Source:HGNC Symbol;Acc:H
9	ILMN_172303	0.75	−0.29	0.19	OLR1	oxidized low density lipoprotein receptor 1 [Source:HGNC Sy
10	ILMN_176655	0.69	−0.49	0.18	CPA3	carboxypeptidase A3 [Source:HGNC Symbol;Acc:HGNC:229
11	ILMN_217329	0.68	−0.33	0.11	THNSL2	threonine synthase like 2 [Source:HGNC Symbol;Acc:HGNC:
12	ILMN_223469	0.68	−0.26	0.15	BEX1	brain expressed X−linked 1 [Source:HGNC Symbol;Acc:HGN
13	ILMN_236859	0.66	−0.56	0.14	SMG7	SMG7, nonsense mediated mRNA decay factor [Source:HGN
14	ILMN_167133	0.63	−0.32	0.05	SLC2A5	solute carrier family 2 member 5 [Source:HGNC Symbol;Acc:
15	ILMN_324763	0.61	−0.26	0.25		
16	ILMN_180183	0.6	−0.47	0.39	ARHGAP24	Rho GTPase activating protein 24 [Source:HGNC Symbol;Ac
17	ILMN_181229	0.59	−0.25	0.11	CYP26B1	cytochrome P450 family 26 subfamily B member 1 [Source:H
18	ILMN_231307	0.59	−0.46	0.44	NLRP1	NLR family pyrin domain containing 1 [Source:HGNC Symbol
19	ILMN_172851	0.57	−0.33	0.16	CHURC1−FNTB	CHURC1−FNTB readthrough [Source:HGNC Symbol;Acc:HG
20	ILMN_175364	0.56	−0.37	0.1	TRIM51	tripartite motif−containing 51 [Source:HGNC Symbol;Acc:HG

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	5e−22	391 / 10999	Colon	TssWk_Colon
2	2e−21	330 / 8678	Colon	Quies3_Colon
3	8e−19	325 / 8771	Chror	5_Tx_Melanocytes
4	1e−18	332 / 9054	Colon	Tx_Colon
5	5e−18	317 / 8568	Colon	TxWk_Colon
6	1e−17	420 / 12741	Chror	7_Enh_Melanocytes
7	3e−17	388 / 11455	Chror	2_TssA_Fibroblasts
8	4e−17	342 / 9635	Chror	3_TssF_Fibroblasts
9	8e−17	283 / 7448	Lympl	HOPP_Strong_enhancer
10	8e−17	294 / 7854	Chror	5_Tx_Fibroblasts
11	4e−16	312 / 8613	Chror	7_Enh_Fibroblasts
12	1e−15	403 / 12298	Chror	2_TssA_Melanocytes
13	2e−15	357 / 10430	Brain	Overlap_fetal_midbrain_Quies
14	3e−15	391 / 11836	Chror	3_TssF_Melanocytes
15	7e−15	294 / 8098	Lympl	HOPP_Weak_promoter
16	8e−15	339 / 9815	Brain	Overlap_fetal_midbrain_ReprPC
17	8e−15	372 / 11130	Chror	15_Quies_Melanocytes
18	2e−14	316 / 8990	Chror	15_Quies_Fibroblasts
19	3e−14	415 / 12983	Chror	2_TssA_Neuronal_Progenitor
20	7e−14	329 / 9555	Colon	TssA_Colon
21	8e−14	338 / 9917	Brain	Overlap_fetal_midbrain_ReprPCWk
22	7e−13	396 / 12393	Chror	15_Quies_Neuronal_Progenitor
23	7e−13	227 / 5936	Brain	Overlap_fetal_midbrain_HetRpts
24	8e−13	290 / 8226	Lympl	HOPP_Active_promoter
25	2e−12	263 / 7275	Lympl	HOPP_Txn_elongation
26	2e−12	243 / 6559	Lympl	HOPP_Weak_txn
27	3e−12	76 / 1281	Colon	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_trar
28	1e−11	301 / 8818	MF	protein binding
29	5e−11	349 / 10779	Colon	Enh_Colon
30	1e−10	202 / 5356	Lympl	HOPP_Txn_transition
31	2e−10	247 / 6970	Chror	5_Tx_Neuronal_Progenitor
32	2e−10	90 / 1797	GSEA	PILON_KLF1_TARGETS_DN
33	6e−10	312 / 9504	Brain	Overlap_fetal_midbrain_K9K27me3
34	6e−10	209 / 5699	Chror	6_EnhG_Melanocytes
35	8e−10	50 / 763	GSEA	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP
36	2e−09	198 / 5373	Colon	EnhWk1_Colon
37	3e−09	368 / 11847	Chror	7_Enh_Neuronal_Progenitor
38	3e−09	241 / 6959	Lympl	HOPP_Weak_enhancer
39	4e−09	40 / 559	GSEA	NAKAMURA_TUMOR_ZONE_PERIPHERAL_VS_CENTRAL_DN
40	6e−09	179 / 4795	Chror	6_EnhG_Fibroblasts

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.9	1 / 111	HORVATH_aging_genes meth DOWN
2	1.0	1 / 142	HORVATH_aging_genes meth UP
3	1.0	0 / 58	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	9e−05	7 / 43	sphingolipid biosynthetic process
2	1e−04	21 / 336	inflammatory response
3	3e−04	40 / 889	positive regulation of transcription from RNA polymerase II promoter
4	4e−04	20 / 335	innate immune response
5	4e−04	28 / 550	positive regulation of transcription, DNA−templated
6	5e−04	5 / 27	glycolytic process
7	6e−04	8 / 75	regulation of phosphatidylinositol 3−kinase signaling
8	8e−04	9 / 97	phosphatidylinositol−mediated signaling
9	1e−03	13 / 187	regulation of cell proliferation
10	1e−03	8 / 81	phosphatidylinositol phosphorylation
11	1e−03	17 / 293	positive regulation of gene expression
12	1e−03	13 / 195	regulation of apoptotic process
13	2e−03	10 / 128	actin cytoskeleton organization
14	2e−03	5 / 34	extrinsic apoptotic signaling pathway via death domain receptors
15	2e−03	4 / 21	embryonic placenta development

Brain

Rank	p−value	#in/all	Geneset
1	2e−15	357 / 10430	Overlap_fetal_midbrain_Quies
2	8e−15	339 / 9815	Overlap_fetal_midbrain_ReprPC
3	8e−14	338 / 9917	Overlap_fetal_midbrain_ReprPCWk
4	7e−13	227 / 5936	Overlap_fetal_midbrain_HetRpts
5	6e−10	312 / 9504	Overlap_fetal_midbrain_K9K27me3
6	6e−06	118 / 3164	Mid_Frontal_Lobe_ZNF
7	2e−03	92 / 2700	Fetal_TxTrans
8	2e−03	34 / 796	Overlap_fetal_midbrain_ZNF
9	3e−03	45 / 1162	Fetal_Enh
10	4e−03	46 / 1213	Fetal_TssP
11	4e−03	17 / 328	Fetal_Het
12	6e−03	44 / 1171	Fetal_EnhP
13	9e−03	51 / 1436	Fetal_K9K27me3
14	1e−02	85 / 2630	Fetal_TssF
15	1e−02	35 / 937	Fetal_EnhG

Cancer

Rank	p−value	#in/all	Geneset
1	7e−04	18 / 301	SPANG_BCL6−index2
2	9e−04	27 / 554	Lembcke_Colonic Inflammation
3	1e−03	3 / 14	LIU_PROSTATE_CANCER_UP
4	6e−03	5 / 46	PanCan_TGF−B_geneset_nanostring
5	1e−02	8 / 117	PanCan_Driver_Gene_geneset_nanostring
6	4e−02	9 / 178	SPANG_LPS−index2
7	5e−02	2 / 14	GENTLES_modul13
8	6e−02	2 / 16	GENTLES_modul14
9	6e−02	3 / 36	PanCan_HK_geneset_nanostring
10	9e−02	0 / 15	LIU_PROSTATE_CANCER_DN
11	1e−01	6 / 125	PanCan_CC+Apop_geneset_nanostring
12	1e−01	0 / 12	LIU_BREAST_CANCER
13	1e−01	8 / 193	PanCan_PI3K_geneset_nanostring
14	1e−01	6 / 136	PanCan_RAS_geneset_nanostring
15	2e−01	0 / 14	LIU_COMMON_CANCER_GENES

CC

Rank	p−value	#in/all	Geneset
1	9e−09	179 / 4822	cytoplasm
2	3e−05	162 / 4828	nucleus
3	8e−05	107 / 2979	cytosol
4	4e−04	4 / 15	NuA4 histone acetyltransferase complex
5	8e−04	89 / 2535	nucleoplasm
6	2e−03	3 / 10	protein phosphatase type 1 complex
7	3e−03	3 / 12	specific granule
8	3e−03	43 / 1101	extracellular space
9	5e−03	32 / 775	endoplasmic reticulum
10	5e−03	82 / 2464	extracellular exosome
11	5e−03	12 / 202	early endosome
12	5e−03	24 / 539	Golgi membrane
13	6e−03	25 / 571	perinuclear region of cytoplasm
14	6e−03	32 / 788	endoplasmic reticulum membrane
15	6e−03	11 / 179	nuclear speck

Chr

Rank	p−value	#in/all	Geneset
1	0.01	44 / 1211	Chr 6
2	0.02	33 / 904	Chr 10
3	0.05	71 / 2323	Chr 1
4	0.10	38 / 1217	Chr 3
5	0.25	11 / 342	Chr 18
6	0.34	25 / 902	Chr 4
7	0.35	29 / 1060	Chr 5
8	0.54	21 / 836	Chr 8
9	0.56	29 / 1170	Chr 7
10	0.56	37 / 1492	Chr 2
11	0.57	19 / 769	Chr 15
12	0.62	23 / 954	Chr 9
13	0.68	31 / 1318	Chr 17
14	0.70	33 / 1411	Chr 11
15	0.74	9 / 422	Chr 13

Chromatin states

Rank	p−value	#in/all	Geneset
1	8e−19	325 / 8771	5_Tx_Melanocytes
2	1e−17	420 / 12741	7_Enh_Melanocytes
3	3e−17	388 / 11455	2_TssA_Fibroblasts
4	4e−17	342 / 9635	3_TssF_Fibroblasts
5	8e−17	294 / 7854	5_Tx_Fibroblasts
6	4e−16	312 / 8613	7_Enh_Fibroblasts
7	1e−15	403 / 12298	2_TssA_Melanocytes
8	3e−15	391 / 11836	3_TssF_Melanocytes
9	8e−15	372 / 11130	15_Quies_Melanocytes
10	2e−14	316 / 8990	15_Quies_Fibroblasts
11	3e−14	415 / 12983	2_TssA_Neuronal_Progenitor
12	7e−13	396 / 12393	15_Quies_Neuronal_Progenitor
13	2e−10	247 / 6970	5_Tx_Neuronal_Progenitor
14	6e−10	209 / 5699	6_EnhG_Melanocytes
15	3e−09	368 / 11847	7_Enh_Neuronal_Progenitor

Colon Cancer

Rank	p−value	#in/all	Geneset
1	5e−22	391 / 10999	TssWk_Colon
2	2e−21	330 / 8678	Quies3_Colon
3	1e−18	332 / 9054	Tx_Colon
4	5e−18	317 / 8568	TxWk_Colon
5	7e−14	329 / 9555	TssA_Colon
6	3e−12	76 / 1281	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv
7	5e−11	349 / 10779	Enh_Colon
8	2e−09	198 / 5373	EnhWk1_Colon
9	1e−07	71 / 1470	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
10	5e−07	55 / 1069	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
11	1e−06	147 / 4034	TssD1_Colon
12	4e−05	153 / 4526	Quies1_Colon
13	8e−05	137 / 4018	EnhWk2_Colon
14	2e−04	226 / 7354	TssF_Colon
15	3e−04	61 / 1547	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a

Glio

Rank	p−value	#in/all	Geneset
1	4e−06	76 / 1777	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
2	6e−06	13 / 113	GIEZELT_GBM_WT_up_VS_mut
3	3e−05	81 / 2043	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
4	2e−04	10 / 96	Weller_LGG_1p19qDel−vs−intact_DOWN
5	2e−04	18 / 267	WILLSCHER_GBM_Verhaak−CL & MES_up
6	2e−04	13 / 158	Hopp_Sturm_GBM_Epi3_D_adult_fetus_IDH_UP
7	3e−03	53 / 1417	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
8	3e−03	17 / 316	WILLSCHER_GBM_Verhaak−PNwt & CL_up
9	7e−03	5 / 48	Vishal_subnetwork signature of survival in GBM
10	1e−02	7 / 94	Weller_LGG_A_vs_O_UP
11	2e−02	31 / 820	Sturm_GBM_Meth_overexpression_E_G34_UP
12	3e−02	6 / 92	Weller_LGG_A_vs_O_DOWN
13	5e−02	2 / 15	Donson−chemokines/cytokines−associated with LTS in HGA
14	5e−02	29 / 839	Hopp_Sturm_GBM_Epi3_no_zentr_1_G34_DN
15	8e−02	4 / 65	cultured astroglia vs. in vivo astrocytes

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−10	90 / 1797	PILON_KLF1_TARGETS_DN
2	8e−10	50 / 763	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP
3	4e−09	40 / 559	NAKAMURA_TUMOR_ZONE_PERIPHERAL_VS_CENTRAL_DN
4	9e−09	54 / 924	MARSON_BOUND_BY_FOXP3_STIMULATED
5	4e−08	36 / 515	FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_UP
6	8e−08	21 / 208	ZHANG_RESPONSE_TO_IKK_INHIBITOR_AND_TNF_UP
7	3e−07	45 / 783	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
8	7e−07	27 / 366	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_UP
9	7e−07	45 / 812	GEORGES_TARGETS_OF_MIR192_AND_MIR215
10	1e−06	43 / 770	CUI_TCF21_TARGETS_2_DN
11	1e−06	17 / 166	WANG_CLIM2_TARGETS_DN
12	1e−06	19 / 205	ZWANG_CLASS_3_TRANSIENTLY_INDUCED_BY_EGF
13	2e−06	26 / 358	CHYLA_CBFA2T3_TARGETS_UP
14	2e−06	25 / 343	BASAKI_YBX1_TARGETS_DN
15	3e−06	39 / 692	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP

HM

Rank	p−value	#in/all	Geneset
1	7e−05	15 / 185	HALLMARK_TNFA_SIGNALING_VIA_NFKB
2	6e−04	13 / 177	HALLMARK_MITOTIC_SPINDLE
3	8e−03	7 / 91	HALLMARK_ANDROGEN_RESPONSE
4	9e−03	11 / 191	HALLMARK_INFLAMMATORY_RESPONSE
5	1e−02	10 / 176	HALLMARK_KRAS_SIGNALING_UP
6	2e−02	8 / 127	HALLMARK_COAGULATION
7	2e−02	10 / 187	HALLMARK_COMPLEMENT
8	2e−02	10 / 189	HALLMARK_HYPOXIA
9	2e−02	6 / 87	HALLMARK_PROTEIN_SECRETION
10	5e−02	9 / 185	HALLMARK_HEME_METABOLISM
11	5e−02	3 / 33	HALLMARK_ANGIOGENESIS
12	8e−02	3 / 40	HALLMARK_WNT_BETA_CATENIN_SIGNALING
13	9e−02	7 / 151	HALLMARK_APOPTOSIS
14	1e−01	8 / 186	HALLMARK_IL2_STAT5_SIGNALING
15	1e−01	6 / 132	HALLMARK_UV_RESPONSE_DN

Lifestyle

Rank	p−value	#in/all	Geneset
1	7e−06	18 / 211	Homuth_BMI−associated−genes_DN
2	8e−03	3 / 17	DUMEAUX_High bmi enriched genes
3	2e−01	1 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
4	2e−01	2 / 31	DUMEAUX_Fasting enriched genes
5	3e−01	5 / 147	Homuth_BMI−associated−genes_UP
6	3e−01	1 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
7	9e−01	1 / 94	DUMEAUX_Smoking enriched genes
8	1e+00	0 / 10	DUMEAUX_Smoking literature genes up
9	1e+00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
10	1e+00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
11	1e+00	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
12	1e+00	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
13	1e+00	0 / 10	DUMEAUX_Women normal BMI literature genes up
14	1e+00	0 / 18	Huan_blood−pressure_SBP−signature
15	1e+00	0 / 16	Huan_blood−pressure_DBP−signature

Lymphoma

Rank	p−value	#in/all	Geneset
1	8e−17	283 / 7448	HOPP_Strong_enhancer
2	7e−15	294 / 8098	HOPP_Weak_promoter
3	8e−13	290 / 8226	HOPP_Active_promoter
4	2e−12	263 / 7275	HOPP_Txn_elongation
5	2e−12	243 / 6559	HOPP_Weak_txn
6	1e−10	202 / 5356	HOPP_Txn_transition
7	3e−09	241 / 6959	HOPP_Weak_enhancer
8	3e−05	53 / 1169	SPANG_BCR DN
9	3e−05	101 / 2701	HOPP_Repetitive
10	1e−03	18 / 318	Hopp_June14_MMML937 tumors+controls_group.overexpression_H_GC−B−
11	3e−03	97 / 2939	HOPP_Poised_promoter
12	5e−03	16 / 306	WIRTH_lymphoma937_spot E
13	7e−03	15 / 290	SPANG_IL21 UP
14	9e−03	15 / 300	Hopp_June14_MMML937 tumors+controls_group.overexpression_E_GC−B−
15	1e−02	16 / 331	WIRTH_lymphoma937_spot H

Melanoma

Rank	p−value	#in/all	Geneset
1	0.03	3 / 27	Hugo_melanoma−all−LEF1_UP
2	0.09	3 / 43	Hugo_melanoma−BRAFmut−MET_UP
3	0.18	1 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
4	0.21	1 / 9	Hugo_melanoma−BRAFmut−MET_DN
5	0.53	1 / 30	Hugo_melanoma−all−MET_UP
6	0.75	1 / 54	Hugo_melanoma−all−MET_DN
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

MF

Rank	p−value	#in/all	Geneset
1	1e−11	301 / 8818	protein binding
2	1e−05	24 / 350	protein kinase binding
3	2e−04	4 / 12	G−protein coupled purinergic nucleotide receptor activity
4	2e−04	19 / 301	ubiquitin−protein transferase activity
5	7e−04	15 / 227	transcription coactivator activity
6	7e−04	7 / 59	phosphatidylinositol−4,5−bisphosphate 3−kinase activity
7	8e−04	6 / 44	methylated histone binding
8	8e−04	15 / 232	ligase activity
9	9e−04	44 / 1065	zinc ion binding
10	1e−03	8 / 81	protease binding
11	1e−03	6 / 49	protein serine/threonine phosphatase activity
12	1e−03	56 / 1475	DNA binding
13	2e−03	4 / 22	histone demethylase activity
14	3e−03	12 / 188	receptor activity
15	4e−03	7 / 80	serine−type endopeptidase inhibitor activity

miRNA Disease

Rank	p−value	#in/all	Geneset
1	0.9	1 / 113	Ovarian cancer
2	1.0	0 / 7	Thyroid carcinoma, papillary
3	1.0	0 / 123	Pancreatic cancer
4	1.0	0 / 68	Glioblastoma multiforme, somatic
5	1.0	0 / 63	Gastrointestinal
6	1.0	0 / 3	Pituitary adenoma
7	1.0	0 / 116	Cancer
8	1.0	0 / 95	Colorectal cancer
9	1.0	0 / 2	Adenomas, multiple colorectal
10	1.0	0 / 124	Prostate cancer
11	1.0	0 / 48	Alzheimer disease, susceptibility to
12	1.0	0 / 7	Schizophrenia, susceptibility to
13	1.0	0 / 20	Parkinson disease
14	1.0	0 / 65	Hepatocellular carcinoma
15	1.0	0 / 3	Down syndrome, risk of

miRNA target

Rank	p−value	#in/all	Geneset
1	1e−06	17 / 166	hsa−miR−323b−5p
2	1e−05	19 / 243	hsa−miR−26b
3	2e−05	16 / 184	hsa−miR−196b
4	3e−05	27 / 449	hsa−miR−130b
5	3e−05	22 / 328	hsa−miR−367
6	4e−05	26 / 433	hsa−miR−19b
7	5e−05	27 / 463	hsa−miR−301a
8	5e−05	26 / 438	hsa−miR−19a
9	6e−05	30 / 546	hsa−miR−93
10	7e−05	32 / 602	hsa−miR−20a
11	7e−05	19 / 272	hsa−miR−92a
12	9e−05	15 / 188	hsa−miR−382
13	9e−05	16 / 210	hsa−miR−29b
14	1e−04	21 / 328	hsa−miR−32
15	1e−04	25 / 429	hsa−miR−548n

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.3	1 / 13	BENTINK_e2f3.1
2	0.3	1 / 13	BENTINK_myc.1
3	0.3	1 / 13	BENTINK_src.10
4	0.3	1 / 14	GUSTAFSON_PI3K_UP
5	0.3	1 / 15	GUSTAFSON_PI3K_DN
6	1.0	0 / 13	BENTINK_e2f3.2
7	1.0	0 / 12	BENTINK_ras.1
8	1.0	0 / 11	BENTINK_ras.4
9	1.0	0 / 14	BENTINK_ras.6
10	1.0	0 / 12	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Reference Signatures

Rank	p−value	#in/all	Geneset
1	1e−08	24 / 242	Chaussabel_3,2_Inflammation I
2	4e−07	9 / 39	Chaussabel_2,2_Neutrophils
3	1e−06	16 / 150	Chaussabel_2,6_Myeloid lineage
4	4e−05	18 / 240	Chaussabel_3,3_Inflammation II
5	5e−05	10 / 84	Chaussabel_2,10_Immune related cell surface molecules
6	1e−03	45 / 1118	PROTEINATLAS_placenta
7	2e−03	31 / 695	PROTEINATLAS_bone marrow
8	2e−03	38 / 912	PROTEINATLAS_urinary bladder
9	2e−03	46 / 1167	PROTEINATLAS_gallbladder
10	3e−03	24 / 514	PROTEINATLAS_vagina
11	3e−03	44 / 1138	PROTEINATLAS_small intestine
12	4e−03	20 / 412	WIRTH_Immune system
13	5e−03	32 / 782	PROTEINATLAS_thyroid gland
14	5e−03	14 / 254	PROTEINATLAS_smooth muscle
15	5e−03	10 / 153	Chaussabel_2,9_Cytosceleton

Telomeres

Rank	p−value	#in/all	Geneset
1	0.3	1 / 13	Alternative lengthening of telomeres
2	0.5	1 / 27	Nabetani_alt len telomeres_genes_ko
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	0.003	62 / 1723	HEBENSTREIT_high expression TF
2	0.004	146 / 4735	ICGC_Pu1_targets
3	0.005	149 / 4881	ICGC_Atf2_targets
4	0.005	154 / 5067	ICGC_Taf1_targets
5	0.006	137 / 4468	ICGC_Egr1_targets
6	0.007	106 / 3348	ICGC_BatfPcr1_targets
7	0.009	162 / 5442	ICGC_Pmlsc71910_targets
8	0.013	161 / 5466	ICGC_Nficsc81335_targets
9	0.015	145 / 4890	ICGC_Bclaf101388_targets
10	0.017	173 / 5961	ICGC_Pol24_targets
11	0.019	173 / 5984	ICGC_Mta3_targets
12	0.020	2 / 9	MYC_Targets DOWN
13	0.026	154 / 5312	ICGC_Tcf12_targets
14	0.027	179 / 6267	ICGC_Yy1_targets
15	0.038	121 / 4131	ICGC_Nfatc1_targets

K−Means Cluster

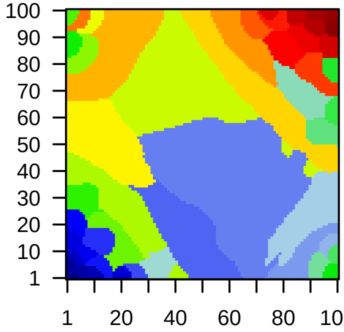
Spot Summary: L

metagenes = 56
genes = 535

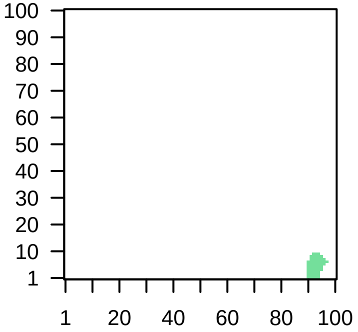
<r> metagenes = 0.9
<r> genes = 0.24
beta: r2= 13.58 / log p= −Inf

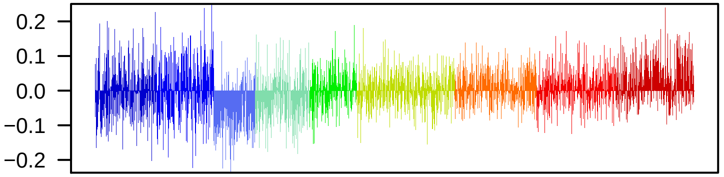
samples with spot = 124 (3.7 %)
A * : 18 (5.2 %)
A C * : 32 (9.8 %)
A C F * : 1 (0.4 %)
A F * : 10 (3.2 %)
C F * : 5 (1.9 %)
F * : 5 (0.9 %)
F J * : 5 (1.1 %)
J * : 10 (2.2 %)
N * : 38 (8.6 %)

Overview Map



Spot





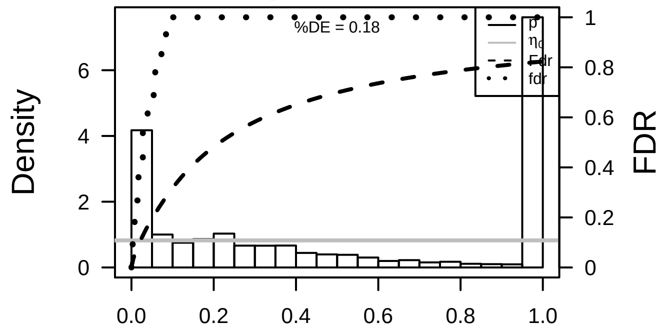
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_173900	1.38	−0.54	0.13	TACSTD2	tumor−associated calcium signal transducer 2 [Source:HGNC
2	ILMN_177844	1.16	−0.92	0.27	FKBP5	FK506 binding protein 5 [Source:HGNC Symbol;Acc:HGNC:3
3	ILMN_168219	1.04	−0.63	0.24	NFXL1	nuclear transcription factor, X−box binding like 1 [Source:HGN
4	ILMN_183046	1.01	−0.99	0.15	XYLT1	xylosyltransferase 1 [Source:HGNC Symbol;Acc:HGNC:1551
5	ILMN_222392	1	−0.47	0.25		
6	ILMN_165170	0.99	−0.84	0.22	CAT	catalase [Source:HGNC Symbol;Acc:HGNC:1516]
7	ILMN_323845	0.98	−0.9	0.18	FAM21C	family with sequence similarity 21 member C [Source:HGNC
8	ILMN_215173	0.93	−0.93	0.31	CAT	catalase [Source:HGNC Symbol;Acc:HGNC:1516]
9	ILMN_220911	0.85	−0.37	0.29	MAK	male germ cell associated kinase [Source:HGNC Symbol;Acc
10	ILMN_165426	0.84	−0.57	0.39	HMGB2	high mobility group box 2 [Source:HGNC Symbol;Acc:HGNC:
11	ILMN_168870	0.83	−1.13	0.47	PJA2	praja ring finger ubiquitin ligase 2 [Source:HGNC Symbol;Acc
12	ILMN_237640	0.81	−0.96	0.37	TSC22D3	TSC22 domain family member 3 [Source:HGNC Symbol;Acc:
13	ILMN_232799	0.8	−0.85	0.24	AZIN1	antizyme inhibitor 1 [Source:HGNC Symbol;Acc:HGNC:1643
14	ILMN_178245	0.79	−0.67	0.56	OSBPL8	oxysterol binding protein like 8 [Source:HGNC Symbol;Acc:H
15	ILMN_237978	0.77	−0.64	0.58	HIF1A	hypoxia inducible factor 1 alpha subunit [Source:HGNC Symb
16	ILMN_168940	0.74	−0.62	0.42	CLK1	CDC like kinase 1 [Source:HGNC Symbol;Acc:HGNC:2068]
17	ILMN_167002	0.71	−0.54	0.32	LPIN2	lipin 2 [Source:HGNC Symbol;Acc:HGNC:14450]
18	ILMN_166927	0.7	−0.86	0.43	PPT1	palmitoyl−protein thioesterase 1 [Source:HGNC Symbol;Acc:
19	ILMN_236871	0.7	−0.48	0.21	UBE2V1	ubiquitin conjugating enzyme E2 V1 [Source:HGNC Symbol;
20	ILMN_324260	0.69	−0.59	0.48		general transcription factor IIH subunit 2B (pseudogene) [Sou

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−84	331 / 7275	Lympl	HOPP_Txn_elongation
2	4e−74	383 / 10999	Colon	TssWk_Colon
3	1e−73	289 / 5936	Brain	Overlap_fetal_midbrain_HetRpts
4	2e−70	341 / 8678	Colon	Quies3_Colon
5	4e−69	359 / 9815	Brain	Overlap_fetal_midbrain_ReprPC
6	2e−68	330 / 8226	Lympl	HOPP_Active_promoter
7	2e−67	335 / 8568	Colon	TxWk_Colon
8	1e−63	334 / 8771	Chror	5_Tx_Melanocytes
9	1e−63	339 / 9054	Colon	Tx_Colon
10	3e−62	336 / 8990	Chror	15_Quies_Fibroblasts
11	2e−61	345 / 9555	Colon	TssA_Colon
12	1e−60	350 / 9917	Brain	Overlap_fetal_midbrain_ReprPCWk
13	1e−59	311 / 7854	Chror	5_Tx_Fibroblasts
14	2e−59	373 / 11455	Chror	2_TssA_Fibroblasts
15	4e−55	380 / 12298	Chror	2_TssA_Melanocytes
16	6e−52	245 / 5356	Lympl	HOPP_Txn_transition
17	1e−50	384 / 12983	Chror	2_TssA_Neuronal_Progenitor
18	1e−49	355 / 11130	Chror	15_Quies_Melanocytes
19	5e−49	277 / 6970	Chror	5_Tx_Neuronal_Progenitor
20	4e−47	284 / 7448	Lympl	HOPP_Strong_enhancer
21	5e−44	335 / 10430	Brain	Overlap_fetal_midbrain_Quies
22	1e−41	288 / 8098	Lympl	HOPP_Weak_promoter
23	1e−41	298 / 8613	Chror	7_Enh_Fibroblasts
24	2e−41	86 / 783	GSEA	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
25	5e−39	359 / 12393	Chror	15_Quies_Neuronal_Progenitor
26	8e−39	364 / 12741	Chror	7_Enh_Melanocytes
27	5e−37	121 / 1797	GSEA	PILON_KLF1_TARGETS_DN
28	4e−34	342 / 11836	Chror	3_TssF_Melanocytes
29	2e−32	298 / 9504	Brain	Overlap_fetal_midbrain_K9K27me3
30	1e−28	231 / 6559	Lympl	HOPP_Weak_txn
31	2e−28	277 / 8818	MF	protein binding
32	1e−25	66 / 763	GSEA	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP
33	7e−25	204 / 5699	Chror	6_EnhG_Melanocytes
34	1e−24	65 / 770	GSEA	CUI_TCF21_TARGETS_2_DN
35	1e−24	231 / 6959	Lympl	HOPP_Weak_enhancer
36	3e−24	168 / 4237	Chror	14_ZNF_Neuronal_Progenitor
37	8e−24	49 / 442	GSEA	DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN
38	5e−21	43 / 388	GSEA	SHEN_SMARCA2_TARGETS_UP
39	1e−20	174 / 4822	CC	cytoplasm
40	9e−20	55 / 692	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.2	4 / 111	HORVATH_aging_genes meth DOWN
2	1.0	0 / 142	HORVATH_aging_genes meth UP
3	1.0	0 / 58	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Cancer

Rank	p−value	#in/all	Geneset
1	6e−08	22 / 301	SPANG_BCL6−index2
2	2e−05	11 / 125	PanCan_CC+Apop_geneset_nanostring
3	3e−05	13 / 178	SPANG_LPS−index2
4	4e−04	9 / 117	PanCan_Driver_Gene_geneset_nanostring
5	6e−03	3 / 20	PanCan_ChromMod_geneset_nanostring
6	7e−03	8 / 150	PanCan_MAPK_geneset_nanostring
7	1e−02	3 / 24	PanCan_Notch_geneset_nanostring
8	1e−02	7 / 136	PanCan_RAS_geneset_nanostring
9	2e−02	18 / 554	Lembcke_Colonic Inflammation
10	2e−02	5 / 82	PanCan_JAK−ST_geneset_nanostring
11	2e−02	2 / 13	GENTLES_modul12
12	3e−02	2 / 14	GENTLES_modul4
13	3e−02	8 / 193	PanCan_PI3K_geneset_nanostring
14	4e−02	2 / 16	GENTLES_modul14
15	8e−02	1 / 14	LIU_PROSTATE_CANCER_UP

Chromatin states

Rank	p−value	#in/all	Geneset
1	1e−63	334 / 8771	5_Tx_Melanocytes
2	3e−62	336 / 8990	15_Quies_Fibroblasts
3	1e−59	311 / 7854	5_Tx_Fibroblasts
4	2e−59	373 / 11455	2_TssA_Fibroblasts
5	4e−55	380 / 12298	2_TssA_Melanocytes
6	1e−50	384 / 12983	2_TssA_Neuronal_Progenitor
7	1e−49	355 / 11130	15_Quies_Melanocytes
8	5e−49	277 / 6970	5_Tx_Neuronal_Progenitor
9	1e−41	298 / 8613	7_Enh_Fibroblasts
10	5e−39	359 / 12393	15_Quies_Neuronal_Progenitor
11	8e−39	364 / 12741	7_Enh_Melanocytes
12	4e−34	342 / 11836	3_TssF_Melanocytes
13	7e−25	204 / 5699	6_EnhG_Melanocytes
14	3e−24	168 / 4237	14_ZNF_Neuronal_Progenitor
15	3e−17	266 / 9635	3_TssF_Fibroblasts

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−41	86 / 783	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
2	5e−37	121 / 1797	PILON_KLF1_TARGETS_DN
3	1e−25	66 / 763	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP
4	1e−24	65 / 770	CUI_TCF21_TARGETS_2_DN
5	8e−24	49 / 442	DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN
6	5e−21	43 / 388	SHEN_SMARCA2_TARGETS_UP
7	9e−20	55 / 692	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP
8	1e−19	52 / 622	SCHLOSSER_SERUM_RESPONSE_DN
9	3e−19	60 / 841	ACEVEDO_LIVER_CANCER_UP
10	5e−18	73 / 1265	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
11	1e−16	33 / 291	DAZARD_RESPONSE_TO_UV_NHEK_DN
12	5e−16	55 / 841	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_UP
13	9e−15	40 / 498	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR_UP
14	1e−14	77 / 1601	GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_DN
15	4e−13	39 / 532	SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_DN

Lymphoma

Rank	p−value	#in/all	Geneset
1	1e−84	331 / 7275	HOPP_Txn_elongation
2	2e−68	330 / 8226	HOPP_Active_promoter
3	6e−52	245 / 5356	HOPP_Txn_transition
4	4e−47	284 / 7448	HOPP_Strong_enhancer
5	1e−41	288 / 8098	HOPP_Weak_promoter
6	1e−28	231 / 6559	HOPP_Weak_txn
7	1e−24	231 / 6959	HOPP_Weak_enhancer
8	1e−13	105 / 2701	HOPP_Repetitive
9	8e−10	54 / 1169	SPANG_BCR DN
10	2e−05	17 / 272	SPANG_IL21 DN
11	3e−05	23 / 472	Hopp_June14_MMML937 tumors+controls_group.overexpression_J_GC−B−
12	6e−05	23 / 493	WIRTH_lymphoma937_spot J
13	6e−05	44 / 1270	SPANG_BCR UP
14	1e−04	17 / 318	Hopp_June14_MMML937 tumors+controls_group.overexpression_H_GC−B−
15	2e−04	17 / 331	WIRTH_lymphoma937_spot H

miRNA Disease

Rank	p−value	#in/all	Geneset
1	1	0 / 7	Thyroid carcinoma, papillary
2	1	0 / 123	Pancreatic cancer
3	1	0 / 68	Glioblastoma multiforme, somatic
4	1	0 / 63	Gastrointestinal
5	1	0 / 3	Pituitary adenoma
6	1	0 / 116	Cancer
7	1	0 / 95	Colorectal cancer
8	1	0 / 2	Adenomas, multiple colorectal
9	1	0 / 124	Prostate cancer
10	1	0 / 48	Alzheimer disease, susceptibility to
11	1	0 / 7	Schizophrenia, susceptibility to
12	1	0 / 20	Parkinson disease
13	1	0 / 65	Hepatocellular carcinoma
14	1	0 / 3	Down syndrome, risk of
15	1	0 / 127	Melanoma and neural system tumor syndrome

Reference Signatures

Rank	p−value	#in/all	Geneset
1	2e−15	32 / 302	Chaussabel_3,4_Protein phosphatases
2	3e−15	37 / 412	WIRTH_Immune system
3	8e−11	19 / 153	Chaussabel_2,9_Cytosceleton
4	2e−10	23 / 242	Chaussabel_3,2_Inflammation I
5	3e−07	48 / 1173	PROTEINATLAS_rectum
6	4e−07	13 / 119	Chaussabel_2,11_Replication
7	5e−07	46 / 1118	PROTEINATLAS_placenta
8	5e−07	43 / 1016	PROTEINATLAS_cerebral cortex
9	7e−07	44 / 1063	PROTEINATLAS_tonsil
10	1e−06	18 / 248	Chaussabel_3,6_Mitochondrial ribosomal proteins
11	1e−06	49 / 1268	PROTEINATLAS_colon
12	2e−06	33 / 724	PROTEINATLAS_lymph node
13	3e−06	17 / 242	Chaussabel_3,9_Kinases
14	4e−06	38 / 912	PROTEINATLAS_urinary bladder
15	5e−06	39 / 960	PROTEINATLAS_cerebellum

BP

Rank	p−value	#in/all	Geneset
1	6e−08	6 / 13	striated muscle cell differentiation
2	7e−07	25 / 434	protein phosphorylation
3	4e−06	9 / 66	vascular endothelial growth factor receptor signaling pathway
4	6e−06	40 / 1003	signal transduction
5	7e−06	13 / 155	positive regulation of I−kappaB kinase/NF−kappaB signaling
6	8e−06	5 / 16	positive regulation of receptor−mediated endocytosis
7	9e−06	8 / 56	I−kappaB kinase/NF−kappaB signaling
8	3e−05	11 / 127	regulation of cell shape
9	3e−05	35 / 889	positive regulation of transcription from RNA polymerase II promoter
10	4e−05	24 / 511	apoptotic process
11	4e−05	17 / 293	positive regulation of gene expression
12	5e−05	23 / 486	negative regulation of transcription, DNA−templated
13	6e−05	12 / 163	protein polyubiquitination
14	8e−05	21 / 435	negative regulation of apoptotic process
15	9e−05	5 / 25	TRIF−dependent toll−like receptor signaling pathway

CC

Rank	p−value	#in/all	Geneset
1	1e−20	174 / 4822	cytoplasm
2	4e−16	163 / 4828	nucleus
3	3e−15	116 / 2979	cytosol
4	8e−14	101 / 2535	nucleoplasm
5	6e−08	71 / 1979	membrane
6	2e−07	37 / 777	Golgi apparatus
7	3e−06	21 / 352	focal adhesion
8	4e−06	27 / 539	Golgi membrane
9	2e−05	17 / 273	neuron projection
10	2e−05	26 / 561	intracellular membrane−bounded organelle
11	3e−05	14 / 202	early endosome
12	3e−05	7 / 49	transcriptional repressor complex
13	4e−05	73 / 2464	extracellular exosome
14	2e−04	30 / 788	endoplasmic reticulum membrane
15	8e−04	5 / 40	cytoplasmic side of plasma membrane

Colon Cancer

Rank	p−value	#in/all	Geneset
1	4e−74	383 / 10999	TssWk_Colon
2	2e−70	341 / 8678	Quies3_Colon
3	2e−67	335 / 8568	TxWk_Colon
4	1e−63	339 / 9054	Tx_Colon
5	2e−61	345 / 9555	TssA_Colon
6	4e−19	84 / 1547	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
7	2e−16	145 / 4034	TssD1_Colon
8	2e−15	62 / 1069	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
9	1e−14	73 / 1470	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
10	4e−14	72 / 1468	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
11	4e−14	278 / 10779	Enh_Colon
12	5e−12	163 / 5373	EnhWk1_Colon
13	4e−10	58 / 1281	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv
14	6e−10	61 / 1404	LaPointe_mucosa−position_kmeans_D_transverse colon_UP_
15	4e−08	74 / 2073	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t

HM

Rank	p−value	#in/all	Geneset
1	5e−05	13 / 187	HALLMARK_COMPLEMENT
2	5e−04	11 / 177	HALLMARK_MITOTIC_SPINDLE
3	9e−04	5 / 41	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
4	1e−03	7 / 87	HALLMARK_PROTEIN_SECRETION
5	2e−03	7 / 91	HALLMARK_ANDROGEN_RESPONSE
6	3e−03	10 / 185	HALLMARK_HEME_METABOLISM
7	3e−03	10 / 189	HALLMARK_HYPOXIA
8	6e−03	9 / 176	HALLMARK_ADIPOGENESIS
9	8e−03	8 / 151	HALLMARK_APOPTOSIS
10	1e−02	7 / 132	HALLMARK_UV_RESPONSE_DN
11	2e−02	8 / 179	HALLMARK_G2M_CHECKPOINT
12	2e−02	6 / 116	HALLMARK_SPERMATOGENESIS
13	2e−02	8 / 183	HALLMARK_APICAL_JUNCTION
14	2e−02	8 / 185	HALLMARK_TNFA_SIGNALING_VIA_NFKB
15	3e−02	3 / 34	HALLMARK_HEDGEHOG_SIGNALING

Melanoma

Rank	p−value	#in/all	Geneset
1	0.008	4 / 43	Hugo_melanoma−BRAFmut−MET_UP
2	0.140	1 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
3	0.432	1 / 30	Hugo_melanoma−all−MET_UP
4	1.000	0 / 54	Hugo_melanoma−all−MET_DN
5	1.000	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
6	1.000	0 / 27	Hugo_melanoma−all−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

miRNA target

Rank	p−value	#in/all	Geneset
1	3e−19	43 / 433	hsa−miR−19b
2	2e−17	41 / 438	hsa−miR−19a
3	1e−16	41 / 463	hsa−miR−301a
4	2e−15	39 / 449	hsa−miR−130b
5	7e−15	35 / 379	hsa−miR−454
6	4e−14	30 / 291	hsa−miR−186
7	4e−14	41 / 546	hsa−miR−93
8	2e−13	27 / 250	hsa−miR−548l
9	3e−13	36 / 455	hsa−miR−130a
10	6e−13	34 / 416	hsa−miR−372
11	7e−13	33 / 394	hsa−miR−301b
12	1e−12	34 / 429	hsa−miR−548n
13	2e−12	29 / 315	hsa−miR−30e
14	2e−12	27 / 272	hsa−miR−30d
15	5e−12	31 / 374	hsa−miR−144

Telomeres

Rank	p−value	#in/all	Geneset
1	0.4	1 / 27	Nabetani_alt len telomeres_genes_ko
2	1.0	0 / 13	Alternative lengthening of telomeres
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Brain

Rank	p−value	#in/all	Geneset
1	1e−73	289 / 5936	Overlap_fetal_midbrain_HetRpts
2	4e−69	359 / 9815	Overlap_fetal_midbrain_ReprPC
3	1e−60	350 / 9917	Overlap_fetal_midbrain_ReprPCWk
4	5e−44	335 / 10430	Overlap_fetal_midbrain_Quies
5	2e−32	298 / 9504	Overlap_fetal_midbrain_K9K27me3
6	4e−06	45 / 1171	Fetal_EnhP
7	7e−06	34 / 796	Overlap_fetal_midbrain_ZNF
8	4e−05	29 / 681	Overlap_fetal_midbrain_EnhP
9	7e−05	41 / 1162	Fetal_Enh
10	1e−04	87 / 3164	Mid_Frontal_Lobe_ZNF
11	1e−04	47 / 1436	Fetal_K9K27me3
12	9e−03	13 / 328	Fetal_Het
13	1e−02	37 / 1329	Overlap_fetal_midbrain_Enh
14	1e−02	28 / 937	Fetal_EnhG
15	5e−02	7 / 180	Overlap_fetal_midbrain_Het

Chr

Rank	p−value	#in/all	Geneset
1	0.005	42 / 1492	Chr 2
2	0.012	13 / 342	Chr 18
3	0.019	26 / 902	Chr 4
4	0.047	31 / 1211	Chr 6
5	0.067	22 / 836	Chr 8
6	0.131	19 / 769	Chr 15
7	0.200	27 / 1217	Chr 3
8	0.255	25 / 1160	Chr 12
9	0.268	17 / 768	Chr 14
10	0.297	47 / 2323	Chr 1
11	0.421	18 / 904	Chr 10
12	0.427	23 / 1170	Chr 7
13	0.577	24 / 1318	Chr 17
14	0.628	5 / 289	Chr 21
15	0.674	7 / 422	Chr 13

Glio

Rank	p−value	#in/all	Geneset
1	8e−15	32 / 316	WILLSCHER_GBM_Verhaak−PNwt & CL_up
2	7e−12	76 / 1777	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
3	2e−11	82 / 2043	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
4	1e−09	25 / 315	Up
5	5e−06	35 / 820	Sturm_GBM_Meth_overexpression_E_G34_UP
6	2e−03	13 / 267	WILLSCHER_GBM_Verhaak−CL & MES_up
7	3e−03	9 / 157	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
8	7e−03	5 / 65	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
9	9e−03	5 / 69	WILLSCHER_GBM_Verhaak−PNwt & MES_up
10	1e−02	2 / 9	Sturm_GBM_Meth_overexpression_G_IDH_UP
11	2e−02	5 / 84	GIEZELT_GBM_WT_down_VS_mut
12	2e−02	3 / 32	Donson−Misc immune function−associated with LTS in HGA
13	2e−02	3 / 33	Shaw_responders_down_in_oligo_glioma
14	2e−02	2 / 13	WILLSCHER_GBM_Verhaak−PNmut_up (M)
15	3e−02	7 / 158	Hopp_Sturm_GBM_Epi3_D_adult_fetus_IDH_UP

Lifestyle

Rank	p−value	#in/all	Geneset
1	5e−10	21 / 211	Homuth_BMI−associated−genes_DN
2	4e−02	2 / 16	Huan_blood−pressure_DBP−signature
3	9e−02	1 / 5	Huan_blood−pressure_HTN−signature
4	1e−01	2 / 31	DUMEAUX_Fasting enriched genes
5	2e−01	1 / 10	DUMEAUX_Women normal BMI literature genes up
6	2e−01	1 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
7	3e−01	1 / 17	DUMEAUX_High bmi enriched genes
8	3e−01	1 / 18	Huan_blood−pressure_SBP−signature
9	5e−01	3 / 147	Homuth_BMI−associated−genes_UP
10	1e+00	0 / 94	DUMEAUX_Smoking enriched genes
11	1e+00	0 / 10	DUMEAUX_Smoking literature genes up
12	1e+00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
13	1e+00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
14	1e+00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
15	1e+00	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up

MF

Rank	p−value	#in/all	Geneset
1	2e−28	277 / 8818	protein binding
2	1e−07	22 / 315	protein serine/threonine kinase activity
3	2e−07	18 / 217	protein kinase activity
4	4e−06	49 / 1329	ATP binding
5	2e−05	18 / 301	ubiquitin−protein transferase activity
6	2e−05	13 / 173	ubiquitin protein ligase activity
7	4e−05	7 / 51	GDP binding
8	5e−05	14 / 213	GTPase activity
9	1e−04	6 / 42	manganese ion binding
10	2e−04	12 / 185	magnesium ion binding
11	2e−04	15 / 274	transcription factor binding
12	3e−04	6 / 49	cysteine−type endopeptidase activity
13	3e−04	6 / 49	protein serine/threonine phosphatase activity
14	5e−04	4 / 20	phosphatidylinositol−4−phosphate binding
15	5e−04	7 / 74	thiol−dependent ubiquitin−specific protease activity

Pathw Act

Rank	p−value	#in/all	Geneset
1	3e−06	5 / 13	BENTINK_src.10
2	2e−01	1 / 11	BENTINK_ras.4
3	2e−01	1 / 12	BENTINK_ras.1
4	2e−01	1 / 12	BENTINK_src.2
5	2e−01	1 / 13	BENTINK_e2f3.1
6	2e−01	1 / 14	BENTINK_ras.6
7	1e+00	0 / 14	GUSTAFSON_PI3K_UP
8	1e+00	0 / 15	GUSTAFSON_PI3K_DN
9	1e+00	0 / 13	BENTINK_e2f3.2
10	1e+00	0 / 13	BENTINK_myc.1
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	9e−17	170 / 5067	ICGC_Taf1_targets
2	3e−15	162 / 4890	ICGC_Bclaf101388_targets
3	3e−13	169 / 5466	ICGC_Nficsc81335_targets
4	6e−13	155 / 4881	ICGC_Atf2_targets
5	1e−12	168 / 5518	ICGC_Stat5_targets
6	4e−12	165 / 5442	ICGC_Pmlsc71910_targets
7	3e−11	138 / 4362	ICGC_Creb1_targets
8	5e−11	173 / 5984	ICGC_Mta3_targets
9	6e−11	132 / 4131	ICGC_Nfatc1_targets
10	9e−11	145 / 4735	ICGC_Pu1_targets
11	1e−10	178 / 6267	ICGC_Yy1_targets
12	1e−10	109 / 3194	ICGC_Irf4_targets
13	3e−10	170 / 5961	ICGC_Pol24_targets
14	3e−10	158 / 5410	ICGC_Foxm1_targets
15	4e−10	111 / 3348	ICGC_BatfPcr1_targets

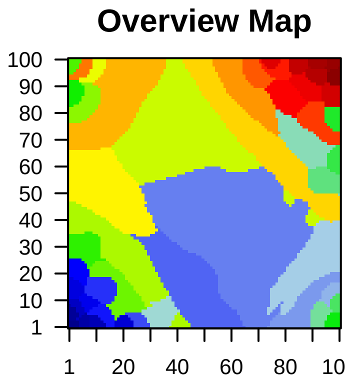
K−Means Cluster

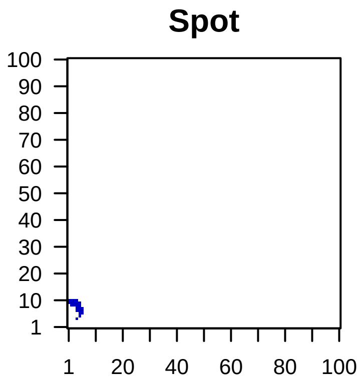
Spot Summary: M

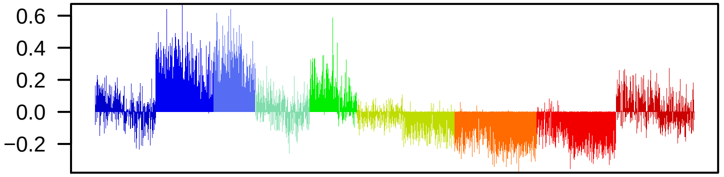
metagenes = 23
genes = 216

<r> metagenes = 0.95
<r> genes = 0.5
beta: r2= 79.26 / log p= −Inf

samples with spot = 762 (22.5 %)
A * : 47 (13.7 %)
A C * : 281 (85.7 %)
A C F * : 217 (92.3 %)
A F * : 32 (10.4 %)
C F * : 119 (44.9 %)
N * : 66 (14.9 %)





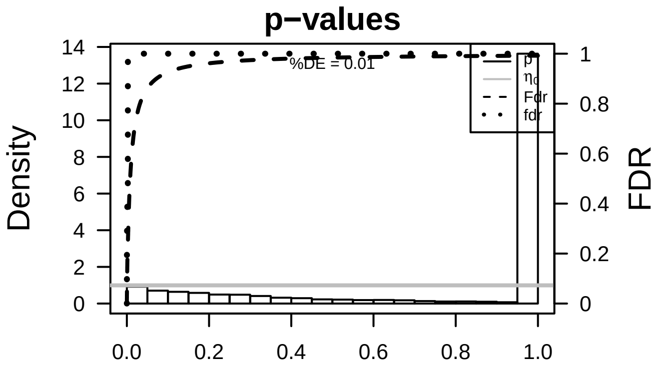


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_178314	4.32	−2.71	0.36		
2	ILMN_175553	3.25	−1.79	0.42	EIF1AY	eukaryotic translation initiation factor 1A, Y−linked [Source:H
3	ILMN_323841	2.6	−1.51	0.33	RPS4Y1	ribosomal protein S4, Y−linked 1 [Source:HGNC Symbol;Acc:
4	ILMN_219133	1.92	−1.09	0.35	RPS4Y2	ribosomal protein S4, Y−linked 2 [Source:HGNC Symbol;Acc:
5	ILMN_168042	1.9	−0.91	0.41	CTSG	cathepsin G [Source:HGNC Symbol;Acc:HGNC:2532]
6	ILMN_176673	1.6	−0.7	0.44	BPI	bactericidal/permeability−increasing protein [Source:HGNC S
7	ILMN_168569	1.57	−0.79	0.36	KDM5D	lysine demethylase 5D [Source:HGNC Symbol;Acc:HGNC:11
8	ILMN_171252	1.48	−0.61	0.38	CEACAM6	carcinoembryonic antigen related cell adhesion molecule 6 [S
9	ILMN_167792	1.42	−0.57	0.41	LTF	lactotransferrin [Source:HGNC Symbol;Acc:HGNC:6720]
10	ILMN_222897	1.42	−0.77	0.41	EIF1AY	eukaryotic translation initiation factor 1A, Y−linked [Source:H
11	ILMN_176846	1.32	−0.8	0.43		
12	ILMN_170518	1.29	−0.54	0.4	MPO	myeloperoxidase [Source:HGNC Symbol;Acc:HGNC:7218]
13	ILMN_323665	1.27	−0.59	0.67		RNA, U1 small nuclear 28, pseudogene [Source:HGNC Sym
14	ILMN_180482	1.26	−1.11	0.49		
15	ILMN_211312	1.26	−0.66	0.29	RNASE3	ribonuclease A family member 3 [Source:HGNC Symbol;Acc:
16	ILMN_316556	1.22	−0.96	0.62		
17	ILMN_316617	1.21	−0.91	0.5		
18	ILMN_316521	1.18	−1.31	0.52		
19	ILMN_316609	1.18	−1	0.56		
20	ILMN_316497	1.17	−0.81	0.59		

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	8e−10	82 / 7354	Colon	TssF_Colon
2	3e−09	107 / 11455	Chror	2_TssA_Fibroblasts
3	2e−08	93 / 9504	Brain	Overlap_fetal_midbrain_K9K27me3
4	3e−08	10 / 147	Lifesty	Homuth_BMI−associated−genes_UP
5	1e−07	5 / 20	GSEA	LIAN_NEUTROPHIL_GRANULE_CONSTITUENTS
6	2e−07	41 / 2845	Colon	TxEnhG1_Colon
7	3e−07	111 / 12983	Chror	2_TssA_Neuronal_Progenitor
8	4e−07	6 / 45	GSEA	DUNNE_TARGETS_OF_AML1_MTG8_FUSION_UP
9	5e−07	5 / 26	GSEA	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
10	6e−07	63 / 5699	Chror	6_EnhG_Melanocytes
11	7e−07	66 / 6138	Colon	TssD2_Colon
12	8e−07	106 / 12298	Chror	2_TssA_Melanocytes
13	1e−06	5 / 29	Refer	JONGENEEL_Bone Marrow
14	2e−06	44 / 3450	Chror	4_TxTrans_Fibroblasts
15	2e−06	88 / 9555	Colon	TssA_Colon
16	2e−06	21 / 1043	GSEA	GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_UP
17	3e−06	9 / 185	HM	HALLMARK_HEME_METABOLISM
18	4e−06	54 / 4795	Chror	6_EnhG_Fibroblasts
19	8e−06	3 / 7	GSEA	MARTINELLI_IMMATURE_NEUTROPHIL_UP
20	9e−06	27 / 1728	Brain	Fetal_ReprPCWk
21	1e−05	3 / 8	GSEA	RUNNE_GENDER_EFFECT_UP
22	2e−05	6 / 86	BP	Wnt signaling pathway, planar cell polarity pathway
23	3e−05	99 / 11836	Chror	3_TssF_Melanocytes
24	3e−05	85 / 9635	Chror	3_TssF_Fibroblasts
25	4e−05	92 / 10779	Colon	Enh_Colon
26	4e−05	3 / 11	CC	endolysosome membrane
27	5e−05	3 / 12	CC	AP−2 adaptor complex
28	5e−05	3 / 12	GSEA	REACTOME_RETROGRADE_NEUROTROPHIN_SIGNALLING
29	5e−05	13 / 558	GSEA	GRAESSMANN_RESPONSE_TO_MC_AND_DOXORUBICIN_UP
30	6e−05	28 / 2028	Chror	4_TxTrans_Melanocytes
31	6e−05	59 / 5956	Chror	3_TssF_Neuronal_Progenitor
32	7e−05	89 / 10430	Brain	Overlap_fetal_midbrain_Quies
33	7e−05	80 / 9054	Colon	Tx_Colon
34	8e−05	3 / 14	GSEA	REACTOME_TRAFFICKING_OF_GLUR2_CONTAINING_AMPA_RECEPT
35	1e−04	4 / 39	Refer	Chaussabel_2,2_Neutrophils
36	1e−04	5 / 74	GSEA	REACTOME_MHC_CLASS_II_ANTIGEN_PRESENTATION
37	1e−04	37 / 3164	Brain	Mid_Frontal_Lobe_ZNF
38	1e−04	84 / 9815	Brain	Overlap_fetal_midbrain_ReprPC
39	2e−04	3 / 17	GSEA	REACTOME_NEF_MEDIATES_DOWN_MODULATION_OF_CELL_SURFA
40	2e−04	20 / 1281	Colon	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_tran



Aging

Rank	p−value	#in/all	Geneset
1	0.5	1 / 111	HORVATH_aging_genes meth DOWN
2	1.0	0 / 142	HORVATH_aging_genes meth UP
3	1.0	0 / 58	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Cancer

Rank	p−value	#in/all	Geneset
1	0.004	2 / 16	GENTLES_modul14
2	0.061	0 / 15	LIU_PROSTATE_CANCER_DN
3	0.073	1 / 12	LIU_BREAST_CANCER
4	0.332	0 / 14	LIU_COMMON_CANCER_GENES
5	0.381	1 / 76	PanCan_Wnt_geneset_nanostring
6	0.423	4 / 527	Lembcke_Normal vs Adenoma
7	0.437	1 / 91	PanCan_TXmisReg_geneset_nanostring
8	0.461	4 / 554	Lembcke_Colonic Inflammation
9	0.546	1 / 125	PanCan_CC+Apop_geneset_nanostring
10	0.566	2 / 301	SPANG_BCL6−index2
11	0.613	1 / 150	PanCan_MAPK_geneset_nanostring
12	0.676	1 / 178	SPANG_LPS−index2
13	0.705	1 / 193	PanCan_PI3K_geneset_nanostring
14	1.000	0 / 13	RHODES_CANCER_META_SIGNATURE
15	1.000	0 / 14	RHODES_UNDIFFERENTIATED_CANCER

Chromatin states

Rank	p−value	#in/all	Geneset
1	3e−09	107 / 11455	2_TssA_Fibroblasts
2	3e−07	111 / 12983	2_TssA_Neuronal_Progenitor
3	6e−07	63 / 5699	6_EnhG_Melanocytes
4	8e−07	106 / 12298	2_TssA_Melanocytes
5	2e−06	44 / 3450	4_TxTrans_Fibroblasts
6	4e−06	54 / 4795	6_EnhG_Fibroblasts
7	3e−05	99 / 11836	3_TssF_Melanocytes
8	3e−05	85 / 9635	3_TssF_Fibroblasts
9	6e−05	28 / 2028	4_TxTrans_Melanocytes
10	6e−05	59 / 5956	3_TssF_Neuronal_Progenitor
11	2e−04	96 / 11847	7_Enh_Neuronal_Progenitor
12	2e−03	67 / 7854	5_Tx_Fibroblasts
13	2e−03	73 / 8771	5_Tx_Melanocytes
14	3e−03	60 / 6970	5_Tx_Neuronal_Progenitor
15	5e−03	96 / 12741	7_Enh_Melanocytes

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−07	5 / 20	LIAN_NEUTROPHIL_GRANULE_CONSTITUENTS
2	4e−07	6 / 45	DUNNE_TARGETS_OF_AML1_MTG8_FUSION_UP
3	5e−07	5 / 26	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
4	2e−06	21 / 1043	GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_UP
5	8e−06	3 / 7	MARTINELLI_IMMATURE_NEUTROPHIL_UP
6	1e−05	3 / 8	RUNNE_GENDER_EFFECT_UP
7	5e−05	3 / 12	REACTOME_RETROGRADE_NEUROTROPHIN_SIGNALLING
8	5e−05	13 / 558	GRAESSMANN_RESPONSE_TO_MC_AND_DOXORUBICIN_UP
9	8e−05	3 / 14	REACTOME_TRAFFICKING_OF_GLUR2_CONTAINING_AMPA_RECEPTOR
10	1e−04	5 / 74	REACTOME_MHC_CLASS_II_ANTIGEN_PRESENTATION
11	2e−04	3 / 17	REACTOME_NEF_MEDIATES_DOWN_MODULATION_OF_CELL_SURFAC
12	3e−04	4 / 52	HENDRICKS_SMARCA4_TARGETS_UP
13	4e−04	7 / 210	CHYLA_CBFA2T3_TARGETS_DN
14	4e−04	3 / 23	REACTOME_EGFR_DOWNREGULATION
15	4e−04	5 / 100	REACTOME_HOST_INTERACTIONS_OF_HIV_FACTORS

Lymphoma

Rank	p−value	#in/all	Geneset
1	3e−04	3 / 21	ROSOLOWSKI_red UP
2	1e−02	65 / 8226	HOPP_Active_promoter
3	2e−02	6 / 318	Hopp_June14_MMML937 tumors+controls_group.overexpression_H_GC−B−
4	2e−02	3 / 88	ROSOLOWSKI_red total
5	2e−02	6 / 331	WIRTH_lymphoma937_spot H
6	2e−02	3 / 92	Hopp_June14_MMML937 tumors+controls_group.overexpression_A_mBL_ce
7	2e−02	7 / 450	Hopp_June14_MMML937 tumors+controls_group.overexpression_I_MM_GC
8	3e−02	7 / 464	WIRTH_lymphoma937_spot I
9	3e−02	44 / 5356	HOPP_Txn_transition
10	3e−02	58 / 7448	HOPP_Strong_enhancer
11	3e−02	62 / 8098	HOPP_Weak_promoter
12	4e−02	2 / 52	Hopp_Lymphoma_Epi1_with_zentr_iv_B.cell_MM_UP
13	5e−02	2 / 57	Monti_Host_response_cluster
14	8e−02	1 / 13	Subero_B−CLL_hypo_meth
15	1e−01	53 / 7275	HOPP_Txn_elongation

miRNA Disease

Rank	p−value	#in/all	Geneset
1	1	0 / 7	Thyroid carcinoma, papillary
2	1	0 / 123	Pancreatic cancer
3	1	0 / 68	Glioblastoma multiforme, somatic
4	1	0 / 63	Gastrointestinal
5	1	0 / 3	Pituitary adenoma
6	1	0 / 116	Cancer
7	1	0 / 95	Colorectal cancer
8	1	0 / 2	Adenomas, multiple colorectal
9	1	0 / 124	Prostate cancer
10	1	0 / 48	Alzheimer disease, susceptibility to
11	1	0 / 7	Schizophrenia, susceptibility to
12	1	0 / 20	Parkinson disease
13	1	0 / 65	Hepatocellular carcinoma
14	1	0 / 3	Down syndrome, risk of
15	1	0 / 127	Melanoma and neural system tumor syndrome

Reference Signatures

Rank	p−value	#in/all	Geneset
1	1e−06	5 / 29	JONGENEEL_Bone Marrow
2	1e−04	4 / 39	Chaussabel_2,2_Neutrophils
3	2e−04	3 / 19	VAQUERIZAS_Bone marrow_TF
4	2e−03	2 / 11	WIRTH_Prim. lymphoid organs
5	3e−03	2 / 13	WIRTH_Bone marrow
6	3e−03	2 / 14	WIRTH_B−cells
7	4e−03	2 / 15	VAQUERIZAS_Fetal liver_TF
8	5e−03	4 / 111	Chaussabel_2,3_Erythrocytes
9	2e−02	3 / 84	Chaussabel_2,1_Cytotoxic cells
10	2e−02	2 / 32	VAQUERIZAS_Liver_TF
11	3e−02	7 / 478	WIRTH_Nervous System
12	6e−02	2 / 66	VAQUERIZAS_Whole blood_TF
13	7e−02	4 / 242	Chaussabel_3,2_Inflammation I
14	7e−02	3 / 150	Chaussabel_2,6_Myeloid lineage
15	8e−02	1 / 13	JONGENEEL_Uterus

BP

Rank	p−value	#in/all	Geneset
1	2e−05	6 / 86	Wnt signaling pathway, planar cell polarity pathway
2	2e−04	3 / 19	clathrin−mediated endocytosis
3	4e−04	3 / 23	immune system process
4	6e−04	3 / 27	regulation of defense response to virus by virus
5	1e−03	4 / 70	hemopoiesis
6	1e−03	3 / 35	negative regulation of epidermal growth factor receptor signaling pathway
7	2e−03	2 / 10	developmental process
8	2e−03	2 / 10	ventricular cardiac muscle cell development
9	2e−03	4 / 81	antigen processing and presentation of exogenous peptide antigen via MHC c
10	2e−03	3 / 40	erythrocyte differentiation
11	2e−03	2 / 12	embryonic camera−type eye morphogenesis
12	2e−03	2 / 12	lateral ventricle development
13	4e−03	2 / 15	negative regulation of growth of symbiont in host
14	4e−03	2 / 15	negative regulation of Rho protein signal transduction
15	4e−03	2 / 16	innate immune response in mucosa

CC

Rank	p−value	#in/all	Geneset
1	4e−05	3 / 11	endolysosome membrane
2	5e−05	3 / 12	AP−2 adaptor complex
3	1e−03	29 / 2535	nucleoplasm
4	1e−03	4 / 75	secretory granule
5	2e−03	46 / 4828	nucleus
6	2e−03	3 / 37	clathrin−coated endocytic vesicle membrane
7	2e−03	4 / 87	PML body
8	2e−03	2 / 12	specific granule
9	3e−03	2 / 14	neuron projection terminus
10	7e−03	2 / 20	protein phosphatase type 2A complex
11	7e−03	3 / 62	endocytic vesicle membrane
12	9e−03	2 / 23	U12−type spliceosomal complex
13	1e−02	2 / 24	MLL1 complex
14	1e−02	2 / 28	cytosolic small ribosomal subunit
15	2e−02	3 / 86	cell projection

Colon Cancer

Rank	p−value	#in/all	Geneset
1	8e−10	82 / 7354	TssF_Colon
2	2e−07	41 / 2845	TxEnhG1_Colon
3	7e−07	66 / 6138	TssD2_Colon
4	2e−06	88 / 9555	TssA_Colon
5	4e−05	92 / 10779	Enh_Colon
6	7e−05	80 / 9054	Tx_Colon
7	2e−04	20 / 1281	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv
8	6e−04	13 / 713	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
9	1e−03	72 / 8568	TxWk_Colon
10	1e−03	50 / 5373	EnhWk1_Colon
11	3e−03	24 / 2073	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
12	9e−03	28 / 2810	EnhA_Colon
13	1e−02	17 / 1470	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
14	1e−02	11 / 789	TxEnhG2_Colon
15	4e−02	15 / 1468	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo

HM

Rank	p−value	#in/all	Geneset
1	3e−06	9 / 185	HALLMARK_HEME_METABOLISM
2	4e−03	3 / 50	HALLMARK_TGF_BETA_SIGNALING
3	2e−02	4 / 151	HALLMARK_APOPTOSIS
4	5e−02	3 / 130	HALLMARK_DNA_REPAIR
5	1e−01	3 / 176	HALLMARK_ADIPOGENESIS
6	1e−01	2 / 87	HALLMARK_PROTEIN_SECRETION
7	1e−01	3 / 185	HALLMARK_TNFA_SIGNALING_VIA_NFKB
8	1e−01	3 / 185	HALLMARK_P53_PATHWAY
9	1e−01	2 / 91	HALLMARK_PEROXISOME
10	1e−01	3 / 187	HALLMARK_COMPLEMENT
11	1e−01	2 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING
12	1e−01	2 / 103	HALLMARK_BILE_ACID_METABOLISM
13	2e−01	1 / 29	HALLMARK_NOTCH_SIGNALING
14	2e−01	2 / 127	HALLMARK_COAGULATION
15	2e−01	2 / 137	HALLMARK_UV_RESPONSE_UP

Melanoma

Rank	p−value	#in/all	Geneset
1	0.3	1 / 54	Hugo_melanoma−all−MET_DN
2	1.0	0 / 30	Hugo_melanoma−all−MET_UP
3	1.0	0 / 43	Hugo_melanoma−BRAFmut−MET_UP
4	1.0	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
5	1.0	0 / 27	Hugo_melanoma−all−LEF1_UP
6	1.0	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

miRNA target

Rank	p−value	#in/all	Geneset
1	0.001	4 / 71	hsa−miR−331−3p
2	0.002	2 / 12	hsa−miR−639
3	0.003	4 / 95	hsa−miR−125a−5p
4	0.003	4 / 96	hsa−miR−125b
5	0.004	3 / 52	hsa−miR−571
6	0.005	5 / 176	hsa−miR−520f
7	0.008	2 / 22	hsa−miR−663
8	0.014	3 / 79	hsa−miR−942
9	0.014	2 / 29	hsa−miR−1225−3p
10	0.016	2 / 31	hsa−miR−1237
11	0.018	5 / 240	hsa−miR−122
12	0.019	4 / 160	hsa−miR−298
13	0.020	3 / 92	hsa−miR−888
14	0.021	3 / 93	hsa−miR−1303
15	0.022	4 / 168	hsa−miR−320b

Telomeres

Rank	p−value	#in/all	Geneset
1	1	0 / 13	Alternative lengthening of telomeres
2	1	0 / 27	Nabetani_alt len telomeres_genes_ko
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Brain

Rank	p−value	#in/all	Geneset
1	2e−08	93 / 9504	Overlap_fetal_midbrain_K9K27me3
2	9e−06	27 / 1728	Fetal_ReprPCWk
3	7e−05	89 / 10430	Overlap_fetal_midbrain_Quies
4	1e−04	37 / 3164	Mid_Frontal_Lobe_ZNF
5	1e−04	84 / 9815	Overlap_fetal_midbrain_ReprPC
6	7e−04	14 / 818	Mid_Frontal_Lobe_Het
7	5e−03	12 / 796	Overlap_fetal_midbrain_ZNF
8	5e−03	13 / 906	Fetal_HetRpts
9	1e−02	27 / 2709	Mid_Frontal_Lobe_HetRpts
10	2e−01	43 / 5936	Overlap_fetal_midbrain_HetRpts
11	2e−01	10 / 1171	Fetal_EnhP
12	3e−01	29 / 4112	Mid_Frontal_Lobe_ReprPC
13	3e−01	3 / 304	Mid_Frontal_Lobe_TssA
14	3e−01	3 / 328	Fetal_Het
15	4e−01	8 / 1115	Overlap_fetal_midbrain_EnhG

Chr

Rank	p−value	#in/all	Geneset
1	0.002	4 / 87	Chr Y
2	0.018	12 / 959	Chr 16
3	0.022	16 / 1467	Chr 19
4	0.195	6 / 619	Chr 20
5	0.207	11 / 1318	Chr 17
6	0.274	11 / 1411	Chr 11
7	0.342	7 / 904	Chr 10
8	0.353	6 / 768	Chr 14
9	0.434	7 / 994	Chr X
10	0.497	3 / 422	Chr 13
11	0.533	5 / 769	Chr 15
12	0.544	2 / 289	Chr 21
13	0.558	6 / 954	Chr 9
14	0.658	3 / 536	Chr 22
15	0.711	13 / 2323	Chr 1

Glio

Rank	p−value	#in/all	Geneset
1	0.002	2 / 11	WILLSCHER_ GBM_LTSwt_proteomics−G_UP
2	0.004	2 / 15	VERHAAK_MES subtype
3	0.031	20 / 2043	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
4	0.031	2 / 44	WILLSCHER_GBM_Verhaak−PNwt_up
5	0.035	3 / 113	GIEZELT_GBM_WT_up_VS_mut
6	0.083	2 / 76	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
7	0.085	1 / 14	Christensen_hypermethylated_in_ependymoma
8	0.093	16 / 1777	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
9	0.102	1 / 17	Christensen_hypomethylated_in_grade2_astrocytoma
10	0.102	1 / 17	Christensen_hypomethylated_in_grade2_oligoastrocytoma
11	0.102	1 / 17	Christensen_hypomethylated_in_grade2_oligodendroglioma
12	0.107	1 / 18	Christensen_hypomethylated_in_grade3_oligoastrocytoma
13	0.146	8 / 820	Sturm_GBM_Meth_overexpression_E_G34_UP
14	0.167	1 / 29	Christensen_hypomethylated_in_grade3_astrocytoma
15	0.183	1 / 32	Donson−Misc immune function−associated with LTS in HGA

Lifestyle

Rank	p−value	#in/all	Geneset
1	3e−08	10 / 147	Homuth_BMI−associated−genes_UP
2	6e−02	1 / 10	Marjolein_ageing−genes_UP
3	7e−01	1 / 211	Homuth_BMI−associated−genes_DN
4	1e+00	0 / 94	DUMEAUX_Smoking enriched genes
5	1e+00	0 / 10	DUMEAUX_Smoking literature genes up
6	1e+00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
7	1e+00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
8	1e+00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
9	1e+00	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
10	1e+00	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
11	1e+00	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
12	1e+00	0 / 10	DUMEAUX_Women normal BMI literature genes up
13	1e+00	0 / 17	DUMEAUX_High bmi enriched genes
14	1e+00	0 / 31	DUMEAUX_Fasting enriched genes
15	1e+00	0 / 18	Huan_blood−pressure_SBP−signature

MF

Rank	p−value	#in/all	Geneset
1	8e−04	3 / 29	rRNA binding
2	1e−03	3 / 32	RNA polymerase II transcription coactivator activity
3	2e−03	2 / 12	ubiquitin−specific protease binding
4	3e−03	4 / 91	peptidase activity
5	3e−03	72 / 8818	protein binding
6	4e−03	5 / 163	serine−type endopeptidase activity
7	6e−03	2 / 18	DNA helicase activity
8	6e−03	2 / 18	peroxidase activity
9	8e−03	2 / 21	protein phosphatase type 2A regulator activity
10	8e−03	4 / 124	transporter activity
11	8e−03	2 / 22	histone demethylase activity
12	8e−03	2 / 22	polyubiquitin binding
13	9e−03	6 / 283	nucleotide binding
14	2e−02	2 / 30	cysteine−type peptidase activity
15	2e−02	2 / 30	WW domain binding

Pathw Act

Rank	p−value	#in/all	Geneset
1	1	0 / 14	GUSTAFSON_PI3K_UP
2	1	0 / 15	GUSTAFSON_PI3K_DN
3	1	0 / 13	BENTINK_e2f3.1
4	1	0 / 13	BENTINK_e2f3.2
5	1	0 / 13	BENTINK_myc.1
6	1	0 / 12	BENTINK_ras.1
7	1	0 / 11	BENTINK_ras.4
8	1	0 / 14	BENTINK_ras.6
9	1	0 / 13	BENTINK_src.10
10	1	0 / 12	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	0.001	57 / 6267	ICGC_Yy1_targets
2	0.002	12 / 733	ICGC_Atf3_targets
3	0.003	42 / 4468	ICGC_Egr1_targets
4	0.005	52 / 5984	ICGC_Mta3_targets
5	0.005	58 / 6868	ICGC_Elf1_targets
6	0.006	48 / 5466	ICGC_Nficsc81335_targets
7	0.009	47 / 5410	ICGC_Foxm1_targets
8	0.011	59 / 7247	ICGC_Runx3_targets
9	0.011	39 / 4362	ICGC_Creb1_targets
10	0.012	47 / 5518	ICGC_Stat5_targets
11	0.019	43 / 5067	ICGC_Taf1_targets
12	0.020	53 / 6552	ICGC_Pol2_targets
13	0.020	45 / 5383	ICGC_Sp1_targets
14	0.020	16 / 1452	ICGC_Six5_targets
15	0.024	45 / 5442	ICGC_Pmlsc71910_targets

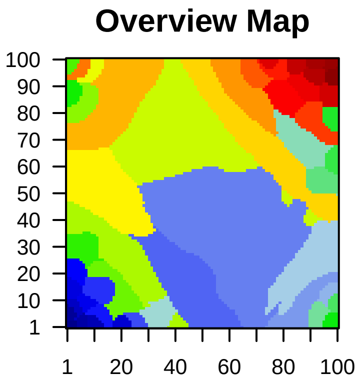
K−Means Cluster

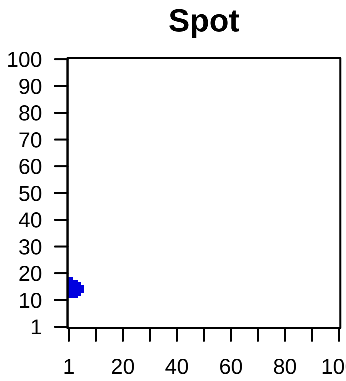
Spot Summary: N

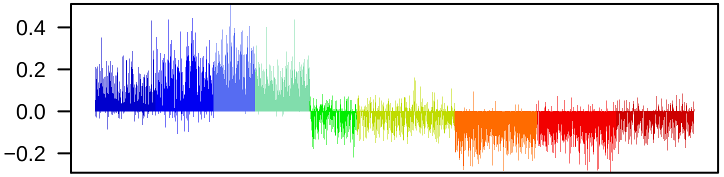
metagenes = 38
genes = 370

<r> metagenes = 0.96
<r> genes = 0.43
beta: r2= 35.17 / log p= −Inf

samples with spot = 564 (16.6 %)
A * : 104 (30.2 %)
A C * : 157 (47.9 %)
A C F * : 167 (71.1 %)
A F * : 133 (43.2 %)
F * : 3 (0.5 %)


Overview Map


Spot

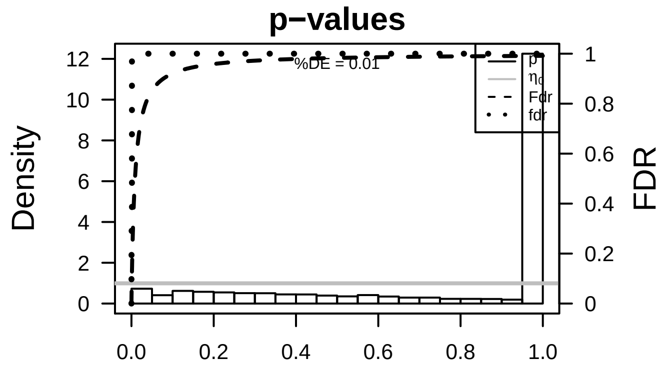


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_165487	1.7	−1.92	0.3	CLC	Charcot−Leyden crystal galectin [Source:HGNC Symbol;Acc:
2	ILMN_323060	1.23	−1.06	0.42	NBPF20	neuroblastoma breakpoint family member 20 [Source:HGNC
3	ILMN_318768	1.23	−0.6	0.32	ACCS	1−aminocyclopropane−1−carboxylate synthase homolog (ina
4	ILMN_165218	1.19	−0.78	0.46	IL4R	interleukin 4 receptor [Source:HGNC Symbol;Acc:HGNC:601
5	ILMN_211549	1.17	−1.21	0.35		
6	ILMN_323676	1.16	−1.22	0.36		
7	ILMN_320036	1.15	−0.81	0.47	NBPF26	neuroblastoma breakpoint family member 9 [Source:HGNC S
8	ILMN_181138	1.1	−0.53	0.5	TFF3	trefoil factor 3 [Source:HGNC Symbol;Acc:HGNC:11757]
9	ILMN_179232	1.09	−0.83	0.36	HDC	histidine decarboxylase [Source:HGNC Symbol;Acc:HGNC:4
10	ILMN_316587	1.07	−0.85	0.55		
11	ILMN_316495	1.06	−0.82	0.66		
12	ILMN_316566	1.04	−0.72	0.65		
13	ILMN_226204	1	−0.66	0.66	PARP10	poly(ADP−ribose) polymerase family member 10 [Source:HG
14	ILMN_316543	1	−0.6	0.69		
15	ILMN_169737	1	−1.03	0.31		
16	ILMN_167266	1	−0.79	0.41	SP110	
17	ILMN_177904	0.98	−0.53	0.48	CACNG6	calcium voltage−gated channel auxiliary subunit gamma 6 [S
18	ILMN_316536	0.97	−0.69	0.62		
19	ILMN_316537	0.97	−0.56	0.69		
20	ILMN_316651	0.97	−0.87	0.53		

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	3e−17	98 / 3450	Chror	4_TxTrans_Fibroblasts
2	1e−16	132 / 5699	Chror	6_EnhG_Melanocytes
3	1e−15	175 / 9054	Colon	Tx_Colon
4	2e−15	84 / 2845	Colon	TxEnhG1_Colon
5	5e−15	115 / 4795	Chror	6_EnhG_Fibroblasts
6	2e−14	150 / 7354	Colon	TssF_Colon
7	1e−13	203 / 11836	Chror	3_TssF_Melanocytes
8	4e−12	160 / 8568	Colon	TxWk_Colon
9	6e−12	62 / 2028	Chror	4_TxTrans_Melanocytes
10	7e−11	159 / 8771	Chror	5_Tx_Melanocytes
11	7e−11	201 / 12298	Chror	2_TssA_Melanocytes
12	9e−11	79 / 3164	Brain	Mid_Frontal_Lobe_ZNF
13	2e−10	123 / 6138	Colon	TssD2_Colon
14	3e−10	168 / 9635	Chror	3_TssF_Fibroblasts
15	3e−10	167 / 9555	Colon	TssA_Colon
16	5e−10	137 / 7275	Lympl	HOPP_Txn_elongation
17	7e−09	141 / 7854	Chror	5_Tx_Fibroblasts
18	8e−09	107 / 5356	Lympl	HOPP_Txn_transition
19	3e−08	160 / 9504	Brain	Overlap_fetal_midbrain_K9K27me3
20	4e−08	127 / 6970	Chror	5_Tx_Neuronal_Progenitor
21	4e−08	183 / 11455	Chror	2_TssA_Fibroblasts
22	4e−08	175 / 10779	Colon	Enh_Colon
23	6e−08	66 / 2810	Colon	EnhA_Colon
24	8e−08	22 / 472	Lympl	Hopp_June14_MMML937 tumors+controls_group.overexpression_J_GC−E
25	9e−08	112 / 5956	Chror	3_TssF_Neuronal_Progenitor
26	2e−07	198 / 12983	Chror	2_TssA_Neuronal_Progenitor
27	5e−07	194 / 12741	Chror	7_Enh_Melanocytes
28	7e−07	21 / 493	Lympl	WIRTH_lymphoma937_spot J
29	7e−07	83 / 4131	TF	ICGC_Nfatc1_targets
30	9e−07	86 / 4362	TF	ICGC_Creb1_targets
31	1e−06	102 / 5518	TF	ICGC_Stat5_targets
32	1e−06	40 / 1470	Colon	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon
33	2e−06	95 / 5067	TF	ICGC_Taf1_targets
34	2e−06	60 / 2709	Brain	Mid_Frontal_Lobe_HetRpts
35	4e−06	98 / 5373	Colon	EnhWk1_Colon
36	4e−06	89 / 4735	TF	ICGC_Pu1_targets
37	5e−06	85 / 4468	TF	ICGC_Egr1_targets
38	7e−06	38 / 1467	Chr	Chr 19
39	8e−06	97 / 5383	TF	ICGC_Sp1_targets
40	8e−06	162 / 10430	Brain	Overlap_fetal_midbrain_Quies


p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.4	2 / 111	HORVATH_aging_genes meth DOWN
2	0.8	1 / 142	HORVATH_aging_genes meth UP
3	1.0	0 / 58	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	9e−04	5 / 62	negative regulation of NF−kappaB transcription factor activity
2	1e−03	3 / 18	regulation of centrosome duplication
3	2e−03	4 / 46	positive regulation of endothelial cell migration
4	3e−03	4 / 50	response to ionizing radiation
5	3e−03	6 / 119	peptidyl−serine phosphorylation
6	5e−03	3 / 29	telomere maintenance
7	5e−03	5 / 93	ion transport
8	6e−03	2 / 10	developmental process
9	7e−03	4 / 62	nucleic acid phosphodiester bond hydrolysis
10	7e−03	10 / 330	protein ubiquitination
11	8e−03	5 / 101	vesicle−mediated transport
12	9e−03	3 / 35	response to reactive oxygen species
13	9e−03	2 / 12	positive regulation of insulin receptor signaling pathway
14	9e−03	2 / 12	regulation of protein catabolic process
15	1e−02	3 / 39	cell death

Brain

Rank	p−value	#in/all	Geneset
1	9e−11	79 / 3164	Mid_Frontal_Lobe_ZNF
2	3e−08	160 / 9504	Overlap_fetal_midbrain_K9K27me3
3	2e−06	60 / 2709	Mid_Frontal_Lobe_HetRpts
4	8e−06	162 / 10430	Overlap_fetal_midbrain_Quies
5	2e−05	25 / 818	Mid_Frontal_Lobe_Het
6	1e−04	149 / 9815	Overlap_fetal_midbrain_ReprPC
7	2e−03	20 / 796	Overlap_fetal_midbrain_ZNF
8	2e−03	93 / 5936	Overlap_fetal_midbrain_HetRpts
9	6e−03	33 / 1728	Fetal_ReprPCWk
10	4e−02	35 / 2127	Mid_Frontal_Lobe_K9K27me3
11	5e−02	61 / 4112	Mid_Frontal_Lobe_ReprPC
12	6e−02	133 / 9917	Overlap_fetal_midbrain_ReprPCWk
13	1e−01	7 / 328	Fetal_Het
14	1e−01	12 / 681	Overlap_fetal_midbrain_EnhP
15	1e−01	27 / 1784	Mid_Frontal_Lobe_ReprPCWk

Cancer

Rank	p−value	#in/all	Geneset
1	0.02	1 / 13	RHODES_CANCER_META_SIGNATURE
2	0.03	0 / 14	RHODES_UNDIFFERENTIATED_CANCER
3	0.04	1 / 14	LIU_COMMON_CANCER_GENES
4	0.10	1 / 9	GENTLES_modul5
5	0.16	1 / 14	GENTLES_modul1
6	0.17	1 / 15	WANG_ER_UP
7	0.22	2 / 73	SHAUGHNESSY_MM high risk
8	0.41	2 / 117	PanCan_Driver_Gene_geneset_nanostring
9	0.43	1 / 46	PanCan_DNARepair_geneset_nanostring
10	0.45	0 / 12	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
11	0.45	2 / 125	PanCan_CC+Apop_geneset_nanostring
12	0.48	1 / 54	KUIPER_MM poor survival
13	0.49	4 / 301	SPANG_BCL6−index2
14	0.63	1 / 82	PanCan_JAK−ST_geneset_nanostring
15	0.65	0 / 14	LIU_PROSTATE_CANCER_UP

CC

Rank	p−value	#in/all	Geneset
1	0.001	48 / 2535	nucleoplasm
2	0.009	36 / 1979	membrane
3	0.009	2 / 12	clathrin adaptor complex
4	0.009	2 / 12	specific granule
5	0.012	7 / 202	early endosome
6	0.012	2 / 14	Cul4−RING E3 ubiquitin ligase complex
7	0.012	3 / 40	SCF ubiquitin ligase complex
8	0.019	73 / 4828	nucleus
9	0.020	2 / 18	exocyst
10	0.024	2 / 20	integral component of mitochondrial outer membrane
11	0.032	47 / 2979	cytosol
12	0.034	2 / 24	ciliary base
13	0.036	71 / 4822	cytoplasm
14	0.045	12 / 571	perinuclear region of cytoplasm
15	0.051	4 / 115	nuclear chromosome, telomeric region

Chr

Rank	p−value	#in/all	Geneset
1	7e−06	38 / 1467	Chr 19
2	3e−03	22 / 959	Chr 16
3	1e−01	10 / 536	Chr 22
4	1e−01	23 / 1492	Chr 2
5	2e−01	12 / 768	Chr 14
6	2e−01	17 / 1170	Chr 7
7	4e−01	11 / 836	Chr 8
8	4e−01	10 / 769	Chr 15
9	5e−01	4 / 289	Chr 21
10	5e−01	12 / 954	Chr 9
11	6e−01	16 / 1411	Chr 11
12	8e−01	4 / 422	Chr 13
13	8e−01	9 / 902	Chr 4
14	8e−01	9 / 904	Chr 10
15	8e−01	12 / 1217	Chr 3

Chromatin states

Rank	p−value	#in/all	Geneset
1	3e−17	98 / 3450	4_TxTrans_Fibroblasts
2	1e−16	132 / 5699	6_EnhG_Melanocytes
3	5e−15	115 / 4795	6_EnhG_Fibroblasts
4	1e−13	203 / 11836	3_TssF_Melanocytes
5	6e−12	62 / 2028	4_TxTrans_Melanocytes
6	7e−11	159 / 8771	5_Tx_Melanocytes
7	7e−11	201 / 12298	2_TssA_Melanocytes
8	3e−10	168 / 9635	3_TssF_Fibroblasts
9	7e−09	141 / 7854	5_Tx_Fibroblasts
10	4e−08	127 / 6970	5_Tx_Neuronal_Progenitor
11	4e−08	183 / 11455	2_TssA_Fibroblasts
12	9e−08	112 / 5956	3_TssF_Neuronal_Progenitor
13	2e−07	198 / 12983	2_TssA_Neuronal_Progenitor
14	5e−07	194 / 12741	7_Enh_Melanocytes
15	1e−05	178 / 11847	7_Enh_Neuronal_Progenitor

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−15	175 / 9054	Tx_Colon
2	2e−15	84 / 2845	TxEnhG1_Colon
3	2e−14	150 / 7354	TssF_Colon
4	4e−12	160 / 8568	TxWk_Colon
5	2e−10	123 / 6138	TssD2_Colon
6	3e−10	167 / 9555	TssA_Colon
7	4e−08	175 / 10779	Enh_Colon
8	6e−08	66 / 2810	EnhA_Colon
9	1e−06	40 / 1470	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
10	4e−06	98 / 5373	EnhWk1_Colon
11	2e−04	34 / 1468	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
12	5e−04	132 / 8678	Quies3_Colon
13	1e−03	158 / 10999	TssWk_Colon
14	2e−03	20 / 789	TxEnhG2_Colon
15	4e−03	18 / 740	LaPointe_mucosa−position_kmeans_C_cecum colon_ascending colon_trans

Glio

Rank	p−value	#in/all	Geneset
1	0.009	3 / 35	Colman_survival_associated
2	0.010	4 / 69	WILLSCHER_GBM_Verhaak−PNwt & MES_up
3	0.016	2 / 16	Donson−chemokine/cytokine−receptors−associated with LTS in HGA
4	0.016	3 / 44	WILLSCHER_GBM_Verhaak−PNwt_up
5	0.024	4 / 90	GIEZELT_GBM_STSwt_down_VS_LTSwt
6	0.034	34 / 2043	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
7	0.088	3 / 87	Sturm_GBM_Meth_overexpression_I_RTK I 'PDGFRA'_UP
8	0.088	28 / 1777	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
9	0.103	1 / 9	Shaw_up_in_1p19qdel
10	0.103	1 / 9	Colman_survival_robust
11	0.123	3 / 101	Hopp_Sturm_GBM_Epi3_D1_IDH_UP_adult_fetus_DN
12	0.135	1 / 12	Phillips PN up vs MES & Prolif
13	0.139	6 / 290	Hopp_Sturm_GBM_Epi3_C_IDH_UP
14	0.156	3 / 113	GIEZELT_GBM_WT_up_VS_mut
15	0.166	1 / 15	VERHAAK_PN subtype

GSEA C2

Rank	p−value	#in/all	Geneset
1	9e−06	14 / 281	GINESTIER_BREAST_CANCER_ZNF217_AMPLIFIED_DN
2	3e−05	18 / 484	ACEVEDO_LIVER_CANCER_DN
3	6e−05	4 / 18	SPIRA_SMOKERS_LUNG_CANCER_DN
4	1e−04	36 / 1541	DODD_NASOPHARYNGEAL_CARCINOMA_UP
5	1e−04	14 / 361	ODONNELL_TFRC_TARGETS_UP
6	3e−04	4 / 27	BARRIER_CANCER_RELAPSE_NORMAL_SAMPLE_DN
7	3e−04	4 / 27	NAKAJIMA_EOSINOPHIL
8	4e−04	3 / 12	CHIN_BREAST_CANCER_COPY_NUMBER_DN
9	6e−04	3 / 14	PID_DNA_PK_PATHWAY
10	8e−04	12 / 333	OSMAN_BLADDER_CANCER_DN
11	9e−04	10 / 247	ACEVEDO_LIVER_TUMOR_VS_NORMAL_ADJACENT_TISSUE_DN
12	9e−04	33 / 1535	BLALOCK_ALZHEIMERS_DISEASE_UP
13	1e−03	8 / 168	LEE_DIFFERENTIATING_T_LYMPHOCYTE
14	1e−03	19 / 708	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_DN
15	1e−03	3 / 17	GENTLES_LEUKEMIC_STEM_CELL_DN

HM

Rank	p−value	#in/all	Geneset
1	0.06	5 / 173	HALLMARK_E2F_TARGETS
2	0.08	3 / 85	HALLMARK_INTERFERON_ALPHA_RESPONSE
3	0.09	2 / 41	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
4	0.12	2 / 50	HALLMARK_TGF_BETA_SIGNALING
5	0.14	2 / 54	HALLMARK_MYC_TARGETS_V2
6	0.19	4 / 185	HALLMARK_HEME_METABOLISM
7	0.19	4 / 186	HALLMARK_ESTROGEN_RESPONSE_LATE
8	0.27	3 / 151	HALLMARK_APOPTOSIS
9	0.34	3 / 172	HALLMARK_INTERFERON_GAMMA_RESPONSE
10	0.35	2 / 103	HALLMARK_BILE_ACID_METABOLISM
11	0.36	3 / 176	HALLMARK_ADIPOGENESIS
12	0.36	3 / 176	HALLMARK_KRAS_SIGNALING_UP
13	0.37	3 / 179	HALLMARK_G2M_CHECKPOINT
14	0.38	3 / 183	HALLMARK_APICAL_JUNCTION
15	0.39	3 / 185	HALLMARK_P53_PATHWAY

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.1	3 / 94	DUMEAUX_Smoking enriched genes
2	0.2	1 / 16	Huan_blood−pressure_DBP−signature
3	0.3	4 / 211	Homuth_BMI−associated−genes_DN
4	0.3	1 / 32	Marjolein_ageing−genes_DN
5	0.5	2 / 147	Homuth_BMI−associated−genes_UP
6	1.0	0 / 10	DUMEAUX_Smoking literature genes up
7	1.0	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
8	1.0	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
9	1.0	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
10	1.0	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
11	1.0	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
12	1.0	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
13	1.0	0 / 10	DUMEAUX_Women normal BMI literature genes up
14	1.0	0 / 17	DUMEAUX_High bmi enriched genes
15	1.0	0 / 31	DUMEAUX_Fasting enriched genes

Lymphoma

Rank	p−value	#in/all	Geneset
1	5e−10	137 / 7275	HOPP_Txn_elongation
2	8e−09	107 / 5356	HOPP_Txn_transition
3	8e−08	22 / 472	Hopp_June14_MMML937 tumors+controls_group.overexpression_J_GC−B−
4	7e−07	21 / 493	WIRTH_lymphoma937_spot J
5	1e−05	124 / 7448	HOPP_Strong_enhancer
6	2e−05	133 / 8226	HOPP_Active_promoter
7	7e−04	12 / 331	WIRTH_lymphoma937_spot H
8	5e−03	119 / 8098	HOPP_Weak_promoter
9	2e−02	9 / 318	Hopp_June14_MMML937 tumors+controls_group.overexpression_H_GC−B−
10	2e−02	9 / 331	SPANG_CD40 6hrs UP
11	2e−02	8 / 283	TARTE_Plasmablast signature
12	3e−02	23 / 1270	SPANG_BCR UP
13	4e−02	93 / 6559	HOPP_Weak_txn
14	6e−02	1 / 5	WRIGHT_custom ABC−DLBCL UP
15	1e−01	9 / 455	SPANG_CD40 6hrs DN

Melanoma

Rank	p−value	#in/all	Geneset
1	0.4	1 / 43	Hugo_melanoma−BRAFmut−MET_UP
2	1.0	0 / 30	Hugo_melanoma−all−MET_UP
3	1.0	0 / 54	Hugo_melanoma−all−MET_DN
4	1.0	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
5	1.0	0 / 27	Hugo_melanoma−all−LEF1_UP
6	1.0	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

MF

Rank	p−value	#in/all	Geneset
1	0.001	11 / 301	ubiquitin−protein transferase activity
2	0.002	11 / 315	protein serine/threonine kinase activity
3	0.002	130 / 8818	protein binding
4	0.005	33 / 1717	metal ion binding
5	0.006	5 / 94	double−stranded DNA binding
6	0.010	2 / 13	SUMO transferase activity
7	0.011	26 / 1329	ATP binding
8	0.014	2 / 15	potassium ion leak channel activity
9	0.014	2 / 15	protein kinase C activity
10	0.016	8 / 268	actin binding
11	0.020	2 / 18	telomeric DNA binding
12	0.022	2 / 19	cyclin binding
13	0.022	2 / 19	lysophospholipase activity
14	0.026	2 / 21	14−3−3 protein binding
15	0.027	3 / 54	flavin adenine dinucleotide binding

miRNA Disease

Rank	p−value	#in/all	Geneset
1	1	0 / 7	Thyroid carcinoma, papillary
2	1	0 / 123	Pancreatic cancer
3	1	0 / 68	Glioblastoma multiforme, somatic
4	1	0 / 63	Gastrointestinal
5	1	0 / 3	Pituitary adenoma
6	1	0 / 116	Cancer
7	1	0 / 95	Colorectal cancer
8	1	0 / 2	Adenomas, multiple colorectal
9	1	0 / 124	Prostate cancer
10	1	0 / 48	Alzheimer disease, susceptibility to
11	1	0 / 7	Schizophrenia, susceptibility to
12	1	0 / 20	Parkinson disease
13	1	0 / 65	Hepatocellular carcinoma
14	1	0 / 3	Down syndrome, risk of
15	1	0 / 127	Melanoma and neural system tumor syndrome

miRNA target

Rank	p−value	#in/all	Geneset
1	0.001	5 / 66	hsa−miR−550
2	0.009	2 / 12	hsa−miR−652
3	0.017	3 / 45	hsa−miR−524−3p
4	0.018	3 / 46	hsa−miR−874
5	0.034	2 / 24	hsa−miR−24−1*
6	0.037	3 / 61	hsa−miR−296−3p
7	0.046	4 / 111	hsa−miR−211
8	0.047	2 / 29	hsa−miR−1293
9	0.050	2 / 30	hsa−miR−626
10	0.056	3 / 72	hsa−miR−708
11	0.066	4 / 126	hsa−miR−223
12	0.068	4 / 127	hsa−miR−204
13	0.073	2 / 37	hsa−miR−518e
14	0.073	2 / 37	hsa−miR−588
15	0.075	5 / 186	hsa−miR−520d−5p

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.2	1 / 14	BENTINK_ras.6
2	1.0	0 / 14	GUSTAFSON_PI3K_UP
3	1.0	0 / 15	GUSTAFSON_PI3K_DN
4	1.0	0 / 13	BENTINK_e2f3.1
5	1.0	0 / 13	BENTINK_e2f3.2
6	1.0	0 / 13	BENTINK_myc.1
7	1.0	0 / 12	BENTINK_ras.1
8	1.0	0 / 11	BENTINK_ras.4
9	1.0	0 / 13	BENTINK_src.10
10	1.0	0 / 12	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Reference Signatures

Rank	p−value	#in/all	Geneset
1	4e−04	4 / 29	Chaussabel_2,7_Unknown function
2	9e−03	20 / 929	PROTEINATLAS_bronchus
3	1e−02	21 / 1003	PROTEINATLAS_appendix
4	2e−02	16 / 759	PROTEINATLAS_epididymis
5	2e−02	10 / 398	PROTEINATLAS_skeletal muscle
6	3e−02	10 / 412	WIRTH_Immune system
7	3e−02	4 / 96	Chaussabel_3,1_Interferon−inducible
8	3e−02	22 / 1194	PROTEINATLAS_stomach
9	3e−02	7 / 254	PROTEINATLAS_smooth muscle
10	5e−02	6 / 221	Chaussabel_3,8_Enzymes
11	6e−02	14 / 726	PROTEINATLAS_cervix, uterine
12	6e−02	11 / 535	PROTEINATLAS_spleen
13	8e−02	20 / 1173	PROTEINATLAS_rectum
14	9e−02	12 / 639	PROTEINATLAS_breast
15	9e−02	18 / 1063	PROTEINATLAS_tonsil

Telomeres

Rank	p−value	#in/all	Geneset
1	0.04	2 / 27	Nabetani_alt len telomeres_genes_ko
2	1.00	0 / 13	Alternative lengthening of telomeres
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	7e−07	83 / 4131	ICGC_Nfatc1_targets
2	9e−07	86 / 4362	ICGC_Creb1_targets
3	1e−06	102 / 5518	ICGC_Stat5_targets
4	2e−06	95 / 5067	ICGC_Taf1_targets
5	4e−06	89 / 4735	ICGC_Pu1_targets
6	5e−06	85 / 4468	ICGC_Egr1_targets
7	8e−06	97 / 5383	ICGC_Sp1_targets
8	1e−05	82 / 4345	ICGC_Zeb1_targets
9	1e−05	97 / 5442	ICGC_Pmlsc71910_targets
10	1e−05	89 / 4881	ICGC_Atf2_targets
11	2e−05	89 / 4890	ICGC_Bclaf101388_targets
12	2e−05	96 / 5410	ICGC_Foxm1_targets
13	3e−05	103 / 5984	ICGC_Mta3_targets
14	4e−05	114 / 6868	ICGC_Elf1_targets
15	5e−05	95 / 5466	ICGC_Nficsc81335_targets

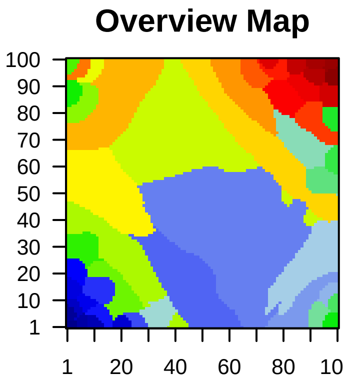
K−Means Cluster

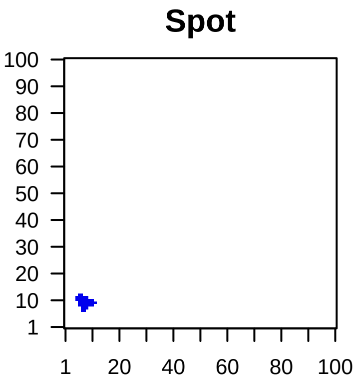
Spot Summary: O

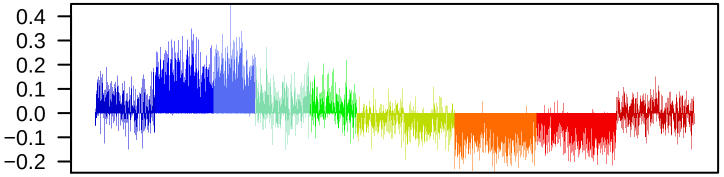
\# metagenes = 32
\# genes = 222

<r> metagenes = 0.95
<r> genes = 0.41
beta: r2= 34.67 / log p= −Inf

\# samples with spot = 461 (13.6 %)
A * : 35 (10.2 %)
A C * : 219 (66.8 %)
A C F * : 149 (63.4 %)
A F * : 34 (11 %)
C F * : 22 (8.3 %)
N * : 2 (0.5 %)


Overview Map


Spot

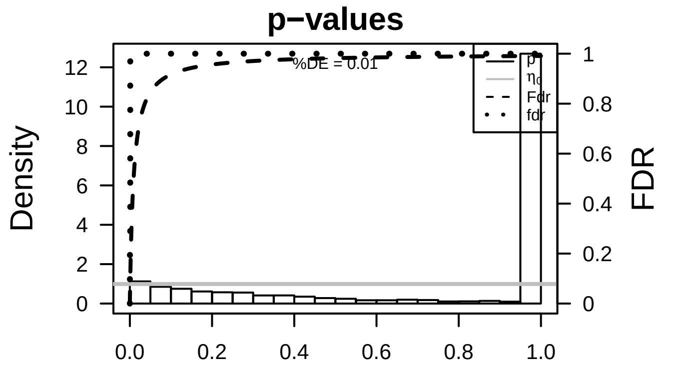


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_173081	1.11	−0.88	0.39	GPR162	G protein−coupled receptor 162 [Source:HGNC Symbol;Acc:
2	ILMN_214070	1.06	−0.62	0.47	CRIPAK	cysteine rich PAK1 inhibitor [Source:HGNC Symbol;Acc:HGN
3	ILMN_173470	1.03	−1.41	0.4	CHST13	carbohydrate sulfotransferase 13 [Source:HGNC Symbol;Acc
4	ILMN_176689	1.03	−0.47	0.48	ZDHHC19	zinc finger DHHC−type containing 19 [Source:HGNC Symbol
5	ILMN_171156	0.98	−0.83	0.5	TIMP1	TIMP metallopeptidase inhibitor 1 [Source:HGNC Symbol;Ac
6	ILMN_176345	0.91	−0.57	0.32		
7	ILMN_180797	0.85	−0.63	0.75	MICAL1	microtubule associated monooxygenase, calponin and LIM d
8	ILMN_212345	0.84	−0.57	0.44		
9	ILMN_237263	0.82	−0.61	0.64	TRAPPC5	trafficking protein particle complex 5 [Source:HGNC Symbol;
10	ILMN_167519	0.82	−0.41	0.42	RETN	resistin [Source:HGNC Symbol;Acc:HGNC:20389]
11	ILMN_169093	0.81	−0.54	0.58	TYMP	thymidine phosphorylase [Source:HGNC Symbol;Acc:HGNC:
12	ILMN_170331	0.81	−0.63	0.72	INAFM1	InaF motif containing 1 [Source:HGNC Symbol;Acc:HGNC:27
13	ILMN_215751	0.79	−0.71	0.58		
14	ILMN_170332	0.78	−0.64	0.75	PSTPIP1	proline−serine−threonine phosphatase interacting protein 1 [
15	ILMN_178473	0.77	−0.98	0.68	S1PR4	sphingosine−1−phosphate receptor 4 [Source:HGNC Symbol
16	ILMN_178828	0.77	−0.86	0.56	COTL1	coactosin like F−actin binding protein 1 [Source:HGNC Symb
17	ILMN_171075	0.75	−1.07	0.5	NAPRT	nicotinate phosphoribosyltransferase [Source:HGNC Symbol;
18	ILMN_165138	0.75	−0.64	0.54	MFN2	mitofusin 2 [Source:HGNC Symbol;Acc:HGNC:16877]
19	ILMN_204751	0.75	−0.69	0.58	COX19	COX19, cytochrome c oxidase assembly factor [Source:HGN
20	ILMN_178060	0.75	−0.59	0.36	ADGRE1	adhesion G protein−coupled receptor E1 [Source:HGNC Sym

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	6e−27	84 / 3450	Chror	4_TxTrans_Fibroblasts
2	1e−20	112 / 7354	Colon	TssF_Colon
3	4e−19	66 / 2845	Colon	TxEnhG1_Colon
4	1e−18	65 / 2810	Colon	EnhA_Colon
5	1e−18	86 / 4795	Chror	6_EnhG_Fibroblasts
6	7e−18	54 / 2028	Chror	4_TxTrans_Melanocytes
7	3e−17	123 / 9555	Colon	TssA_Colon
8	1e−16	137 / 11836	Chror	3_TssF_Melanocytes
9	4e−16	139 / 12298	Chror	2_TssA_Melanocytes
10	7e−15	88 / 5699	Chror	6_EnhG_Melanocytes
11	3e−14	114 / 9054	Colon	Tx_Colon
12	2e−13	89 / 6138	Colon	TssD2_Colon
13	1e−12	114 / 9504	Brain	Overlap_fetal_midbrain_K9K27me3
14	2e−12	137 / 12983	Chror	2_TssA_Neuronal_Progenitor
15	3e−11	112 / 9635	Chror	3_TssF_Fibroblasts
16	1e−10	103 / 8568	Colon	TxWk_Colon
17	1e−10	119 / 10779	Colon	Enh_Colon
18	2e−10	55 / 3164	Brain	Mid_Frontal_Lobe_ZNF
19	2e−10	123 / 11455	Chror	2_TssA_Fibroblasts
20	5e−10	115 / 10430	Brain	Overlap_fetal_midbrain_Quies
21	6e−10	75 / 5373	Colon	EnhWk1_Colon
22	9e−10	92 / 7448	Lympl	HOPP_Strong_enhancer
23	1e−09	102 / 8771	Chror	5_Tx_Melanocytes
24	3e−08	76 / 5956	Chror	3_TssF_Neuronal_Progenitor
25	3e−07	21 / 789	Colon	TxEnhG2_Colon
26	3e−07	96 / 8818	MF	protein binding
27	4e−07	63 / 4822	CC	cytoplasm
28	5e−07	88 / 7854	Chror	5_Tx_Fibroblasts
29	7e−07	111 / 10999	Colon	TssWk_Colon
30	7e−07	6 / 44	Glio	WILLSCHER_GBM_Verhaak−PNwt_up
31	1e−06	12 / 284	GSEA	HELLER_HDAC_TARGETS_UP
32	2e−06	66 / 5356	Lympl	HOPP_Txn_transition
33	2e−06	14 / 409	GSEA	MARTENS_BOUND_BY_PML_RARA_FUSION
34	2e−06	39 / 2464	CC	extracellular exosome
35	2e−06	25 / 1206	Chror	6_EnhG_Neuronal_Progenitor
36	3e−06	4 / 15	GSEA	LIU_IL13_MEMORY_MODEL_UP
37	5e−06	118 / 12393	Chror	15_Quies_Neuronal_Progenitor
38	7e−06	27 / 1470	Colon	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon
39	8e−06	19 / 818	Brain	Mid_Frontal_Lobe_Het
40	8e−06	13 / 405	GSEA	HELLER_HDAC_TARGETS_SILENCED_BY_METHYLATION_UP


p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.3	2 / 142	HORVATH_aging_genes meth UP
2	1.0	0 / 111	HORVATH_aging_genes meth DOWN
3	1.0	0 / 58	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	5e−05	7 / 133	endocytosis
2	2e−03	4 / 70	macroautophagy
3	2e−03	2 / 10	protein localization to pre−autophagosomal structure
4	2e−03	3 / 37	positive regulation of nitric oxide biosynthetic process
5	3e−03	2 / 11	cellular response to follicle−stimulating hormone stimulus
6	3e−03	2 / 11	G−protein coupled receptor internalization
7	3e−03	2 / 11	response to growth hormone
8	3e−03	2 / 11	synaptic vesicle transport
9	3e−03	2 / 12	barbed−end actin filament capping
10	3e−03	2 / 12	stress fiber assembly
11	4e−03	4 / 89	positive regulation of neuron projection development
12	4e−03	5 / 145	peptidyl−tyrosine phosphorylation
13	5e−03	3 / 47	response to stress
14	5e−03	2 / 15	positive regulation of lamellipodium assembly
15	7e−03	5 / 164	protein autophosphorylation

Brain

Rank	p−value	#in/all	Geneset
1	1e−12	114 / 9504	Overlap_fetal_midbrain_K9K27me3
2	2e−10	55 / 3164	Mid_Frontal_Lobe_ZNF
3	5e−10	115 / 10430	Overlap_fetal_midbrain_Quies
4	8e−06	19 / 818	Mid_Frontal_Lobe_Het
5	2e−05	18 / 796	Overlap_fetal_midbrain_ZNF
6	1e−04	37 / 2709	Mid_Frontal_Lobe_HetRpts
7	1e−04	95 / 9815	Overlap_fetal_midbrain_ReprPC
8	6e−04	47 / 4112	Mid_Frontal_Lobe_ReprPC
9	2e−02	85 / 9917	Overlap_fetal_midbrain_ReprPCWk
10	3e−02	12 / 906	Fetal_HetRpts
11	3e−02	54 / 5936	Overlap_fetal_midbrain_HetRpts
12	1e−01	17 / 1728	Fetal_ReprPCWk
13	1e−01	3 / 180	Overlap_fetal_midbrain_Het
14	2e−01	7 / 630	Mid_Frontal_Lobe_EnhP
15	2e−01	23 / 2630	Fetal_TssF

Cancer

Rank	p−value	#in/all	Geneset
1	0.04	4 / 178	SPANG_LPS−index2
2	0.04	1 / 6	ZHANG_MGUS up
3	0.06	1 / 9	GENTLES_modul5
4	0.10	1 / 14	LIU_PROSTATE_CANCER_UP
5	0.10	2 / 73	SHAUGHNESSY_MM high risk
6	0.26	2 / 136	PanCan_RAS_geneset_nanostring
7	0.30	2 / 150	PanCan_MAPK_geneset_nanostring
8	0.32	1 / 54	KUIPER_MM poor survival
9	0.33	5 / 527	Lembcke_Normal vs Adenoma
10	0.37	3 / 301	SPANG_BCL6−index2
11	0.41	2 / 193	PanCan_PI3K_geneset_nanostring
12	0.45	1 / 82	PanCan_JAK−ST_geneset_nanostring
13	0.48	1 / 91	PanCan_TXmisReg_geneset_nanostring
14	0.57	1 / 117	PanCan_Driver_Gene_geneset_nanostring
15	0.77	3 / 554	Lembcke_Colonic Inflammation

CC

Rank	p−value	#in/all	Geneset
1	4e−07	63 / 4822	cytoplasm
2	2e−06	39 / 2464	extracellular exosome
3	1e−05	8 / 149	lamellipodium
4	3e−04	38 / 2979	cytosol
5	4e−04	3 / 21	podosome
6	7e−04	9 / 330	cytoskeleton
7	1e−03	12 / 571	perinuclear region of cytoplasm
8	1e−03	5 / 109	growth cone
9	2e−03	51 / 4828	nucleus
10	3e−03	5 / 139	microtubule cytoskeleton
11	4e−03	25 / 1979	membrane
12	4e−03	13 / 777	Golgi apparatus
13	4e−03	2 / 14	microtubule plus−end
14	5e−03	3 / 47	stress fiber
15	6e−03	2 / 16	pseudopodium

Chr

Rank	p−value	#in/all	Geneset
1	6e−05	25 / 1467	Chr 19
2	6e−04	17 / 959	Chr 16
3	9e−02	15 / 1411	Chr 11
4	2e−01	20 / 2323	Chr 1
5	3e−01	7 / 769	Chr 15
6	3e−01	10 / 1170	Chr 7
7	3e−01	5 / 536	Chr 22
8	5e−01	5 / 619	Chr 20
9	5e−01	10 / 1318	Chr 17
10	6e−01	6 / 904	Chr 10
11	8e−01	7 / 1217	Chr 3
12	8e−01	4 / 768	Chr 14
13	8e−01	5 / 954	Chr 9
14	9e−01	5 / 994	Chr X
15	9e−01	4 / 836	Chr 8

Chromatin states

Rank	p−value	#in/all	Geneset
1	6e−27	84 / 3450	4_TxTrans_Fibroblasts
2	1e−18	86 / 4795	6_EnhG_Fibroblasts
3	7e−18	54 / 2028	4_TxTrans_Melanocytes
4	1e−16	137 / 11836	3_TssF_Melanocytes
5	4e−16	139 / 12298	2_TssA_Melanocytes
6	7e−15	88 / 5699	6_EnhG_Melanocytes
7	2e−12	137 / 12983	2_TssA_Neuronal_Progenitor
8	3e−11	112 / 9635	3_TssF_Fibroblasts
9	2e−10	123 / 11455	2_TssA_Fibroblasts
10	1e−09	102 / 8771	5_Tx_Melanocytes
11	3e−08	76 / 5956	3_TssF_Neuronal_Progenitor
12	5e−07	88 / 7854	5_Tx_Fibroblasts
13	2e−06	25 / 1206	6_EnhG_Neuronal_Progenitor
14	5e−06	118 / 12393	15_Quies_Neuronal_Progenitor
15	1e−05	77 / 6970	5_Tx_Neuronal_Progenitor

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−20	112 / 7354	TssF_Colon
2	4e−19	66 / 2845	TxEnhG1_Colon
3	1e−18	65 / 2810	EnhA_Colon
4	3e−17	123 / 9555	TssA_Colon
5	3e−14	114 / 9054	Tx_Colon
6	2e−13	89 / 6138	TssD2_Colon
7	1e−10	103 / 8568	TxWk_Colon
8	1e−10	119 / 10779	Enh_Colon
9	6e−10	75 / 5373	EnhWk1_Colon
10	3e−07	21 / 789	TxEnhG2_Colon
11	7e−07	111 / 10999	TssWk_Colon
12	7e−06	27 / 1470	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
13	1e−04	22 / 1281	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv
14	2e−03	82 / 8678	Quies3_Colon
15	2e−03	2 / 10	TCGA−CRC_agressive−disease−markers

Glio

Rank	p−value	#in/all	Geneset
1	7e−07	6 / 44	WILLSCHER_GBM_Verhaak−PNwt_up
2	8e−03	7 / 316	WILLSCHER_GBM_Verhaak−PNwt & CL_up
3	1e−02	24 / 2043	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
4	3e−02	20 / 1777	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
5	6e−02	1 / 9	Shaw_up_in_1p19qdel
6	7e−02	6 / 393	Hopp_Sturm_GBM_Epi3_no_zentr_3_RTK II_UP_adult_fetus_K27_DN
7	7e−02	1 / 10	WILLSCHER_ GBM_LTSwt_proteomics−C_UP
8	7e−02	10 / 820	Sturm_GBM_Meth_overexpression_E_G34_UP
9	8e−02	1 / 12	Phillips MES up vs Prolif & PN
10	8e−02	10 / 839	Hopp_Sturm_GBM_Epi3_no_zentr_1_G34_DN
11	9e−02	1 / 13	WILLSCHER_GBM_Verhaak−PNmut_up (M)
12	1e−01	1 / 15	VERHAAK_PN_Brain
13	1e−01	1 / 17	Christensen_hypomethylated_in_grade2_astrocytoma
14	1e−01	1 / 17	Christensen_hypomethylated_in_grade2_oligoastrocytoma
15	1e−01	1 / 17	Christensen_hypomethylated_in_grade2_oligodendroglioma

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−06	12 / 284	HELLER_HDAC_TARGETS_UP
2	2e−06	14 / 409	MARTENS_BOUND_BY_PML_RARA_FUSION
3	3e−06	4 / 15	LIU_IL13_MEMORY_MODEL_UP
4	8e−06	13 / 405	HELLER_HDAC_TARGETS_SILENCED_BY_METHYLATION_UP
5	2e−05	10 / 258	AGUIRRE_PANCREATIC_CANCER_COPY_NUMBER_UP
6	4e−05	9 / 226	REACTOME_AXON_GUIDANCE
7	5e−05	9 / 229	QI_PLASMACYTOMA_UP
8	5e−05	13 / 484	ACEVEDO_LIVER_CANCER_DN
9	6e−05	8 / 185	SHEDDEN_LUNG_CANCER_GOOD_SURVIVAL_A4
10	7e−05	9 / 240	HELLER_SILENCED_BY_METHYLATION_UP
11	7e−05	20 / 1043	GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_UP
12	7e−05	9 / 242	HUTTMANN_B_CLL_POOR_SURVIVAL_UP
13	9e−05	15 / 656	KIM_ALL_DISORDERS_OLIGODENDROCYTE_NUMBER_CORR_UP
14	9e−05	10 / 309	PHONG_TNF_RESPONSE_NOT_VIA_P38
15	1e−04	7 / 157	KEGG_ENDOCYTOSIS

HM

Rank	p−value	#in/all	Geneset
1	0.001	6 / 167	HALLMARK_OXIDATIVE_PHOSPHORYLATION
2	0.002	6 / 177	HALLMARK_MITOTIC_SPINDLE
3	0.004	4 / 91	HALLMARK_ANDROGEN_RESPONSE
4	0.039	4 / 175	HALLMARK_XENOBIOTIC_METABOLISM
5	0.050	4 / 191	HALLMARK_INFLAMMATORY_RESPONSE
6	0.068	3 / 130	HALLMARK_DNA_REPAIR
7	0.071	3 / 132	HALLMARK_UV_RESPONSE_DN
8	0.077	3 / 137	HALLMARK_UV_RESPONSE_UP
9	0.131	2 / 87	HALLMARK_PROTEIN_SECRETION
10	0.135	3 / 176	HALLMARK_ADIPOGENESIS
11	0.147	3 / 183	HALLMARK_GLYCOLYSIS
12	0.157	3 / 189	HALLMARK_HYPOXIA
13	0.190	1 / 29	HALLMARK_NOTCH_SIGNALING
14	0.213	1 / 33	HALLMARK_ANGIOGENESIS
15	0.234	2 / 127	HALLMARK_COAGULATION

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.004	5 / 147	Homuth_BMI−associated−genes_UP
2	0.197	3 / 211	Homuth_BMI−associated−genes_DN
3	0.495	1 / 94	DUMEAUX_Smoking enriched genes
4	1.000	0 / 10	DUMEAUX_Smoking literature genes up
5	1.000	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
6	1.000	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
7	1.000	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
8	1.000	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
9	1.000	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
10	1.000	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
11	1.000	0 / 10	DUMEAUX_Women normal BMI literature genes up
12	1.000	0 / 17	DUMEAUX_High bmi enriched genes
13	1.000	0 / 31	DUMEAUX_Fasting enriched genes
14	1.000	0 / 18	Huan_blood−pressure_SBP−signature
15	1.000	0 / 16	Huan_blood−pressure_DBP−signature

Lymphoma

Rank	p−value	#in/all	Geneset
1	9e−10	92 / 7448	HOPP_Strong_enhancer
2	2e−06	66 / 5356	HOPP_Txn_transition
3	3e−05	78 / 7275	HOPP_Txn_elongation
4	7e−04	80 / 8226	HOPP_Active_promoter
5	9e−03	7 / 318	Hopp_June14_MMML937 tumors+controls_group.overexpression_H_GC−B−
6	1e−02	7 / 331	WIRTH_lymphoma937_spot H
7	2e−02	8 / 455	SPANG_CD40 6hrs DN
8	4e−02	2 / 43	Monti_OxPhos_cluster
9	8e−02	1 / 12	DAVE_BL_DN
10	9e−02	2 / 70	Hopp_Lymphoma_Epi1_no_zentr_3_B.cell_DN
11	1e−01	2 / 72	Hopp_June14_MMML937 tumors+controls_group.overexpression_IM_mBL_
12	1e−01	1 / 14	Subero_T−ALL_hypo_meth
13	1e−01	67 / 8098	HOPP_Weak_promoter
14	1e−01	2 / 74	WIRTH_lymphoma937_spot IM
15	1e−01	9 / 772	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell line

Melanoma

Rank	p−value	#in/all	Geneset
1	1	0 / 30	Hugo_melanoma−all−MET_UP
2	1	0 / 54	Hugo_melanoma−all−MET_DN
3	1	0 / 43	Hugo_melanoma−BRAFmut−MET_UP
4	1	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
5	1	0 / 27	Hugo_melanoma−all−LEF1_UP
6	1	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

MF

Rank	p−value	#in/all	Geneset
1	3e−07	96 / 8818	protein binding
2	3e−05	10 / 268	actin binding
3	6e−04	4 / 54	flavin adenine dinucleotide binding
4	9e−04	7 / 213	protein complex binding
5	1e−03	3 / 28	ubiquitin conjugating enzyme binding
6	2e−03	5 / 115	actin filament binding
7	2e−03	5 / 127	lipid binding
8	4e−03	2 / 14	mitogen−activated protein kinase kinase binding
9	5e−03	2 / 15	FAD binding
10	5e−03	2 / 15	transcriptional activator activity, RNA polymerase II transcription factor binding
11	8e−03	7 / 315	protein serine/threonine kinase activity
12	1e−02	2 / 22	calmodulin−dependent protein kinase activity
13	1e−02	4 / 120	protein tyrosine kinase activity
14	1e−02	6 / 265	cadherin binding involved in cell−cell adhesion
15	1e−02	7 / 351	GTP binding

miRNA Disease

Rank	p−value	#in/all	Geneset
1	1	0 / 7	Thyroid carcinoma, papillary
2	1	0 / 123	Pancreatic cancer
3	1	0 / 68	Glioblastoma multiforme, somatic
4	1	0 / 63	Gastrointestinal
5	1	0 / 3	Pituitary adenoma
6	1	0 / 116	Cancer
7	1	0 / 95	Colorectal cancer
8	1	0 / 2	Adenomas, multiple colorectal
9	1	0 / 124	Prostate cancer
10	1	0 / 48	Alzheimer disease, susceptibility to
11	1	0 / 7	Schizophrenia, susceptibility to
12	1	0 / 20	Parkinson disease
13	1	0 / 65	Hepatocellular carcinoma
14	1	0 / 3	Down syndrome, risk of
15	1	0 / 127	Melanoma and neural system tumor syndrome

miRNA target

Rank	p−value	#in/all	Geneset
1	8e−05	3 / 12	hsa−miR−652
2	1e−02	5 / 182	hsa−miR−34b
3	1e−02	3 / 66	hsa−miR−637
4	2e−02	2 / 26	hsa−miR−675
5	2e−02	4 / 133	hsa−miR−485−5p
6	2e−02	3 / 84	hsa−miR−486−3p
7	5e−02	3 / 110	hsa−miR−190b
8	5e−02	2 / 52	hsa−miR−940
9	6e−02	3 / 120	hsa−miR−493
10	6e−02	2 / 54	hsa−miR−629
11	7e−02	5 / 299	hsa−miR−548c−3p
12	7e−02	3 / 129	hsa−miR−320d
13	8e−02	2 / 64	hsa−miR−9*
14	9e−02	3 / 143	hsa−miR−320c
15	9e−02	3 / 144	hsa−miR−491−5p

Pathw Act

Rank	p−value	#in/all	Geneset
1	1	0 / 14	GUSTAFSON_PI3K_UP
2	1	0 / 15	GUSTAFSON_PI3K_DN
3	1	0 / 13	BENTINK_e2f3.1
4	1	0 / 13	BENTINK_e2f3.2
5	1	0 / 13	BENTINK_myc.1
6	1	0 / 12	BENTINK_ras.1
7	1	0 / 11	BENTINK_ras.4
8	1	0 / 14	BENTINK_ras.6
9	1	0 / 13	BENTINK_src.10
10	1	0 / 12	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Reference Signatures

Rank	p−value	#in/all	Geneset
1	4e−04	13 / 598	PROTEINATLAS_prostate
2	9e−04	20 / 1268	PROTEINATLAS_colon
3	2e−03	7 / 240	Chaussabel_3,3_Inflammation II
4	2e−03	10 / 465	PROTEINATLAS_liver
5	2e−03	18 / 1176	PROTEINATLAS_duodenum
6	6e−03	17 / 1194	PROTEINATLAS_stomach
7	7e−03	14 / 912	PROTEINATLAS_fallopian tube
8	7e−03	11 / 640	PROTEINATLAS_parathyroid gland
9	9e−03	16 / 1138	PROTEINATLAS_small intestine
10	9e−03	4 / 113	Chaussabel_1,5_Myeloid lineage
11	1e−02	16 / 1167	PROTEINATLAS_gallbladder
12	1e−02	11 / 681	PROTEINATLAS_lung
13	1e−02	16 / 1173	PROTEINATLAS_rectum
14	2e−02	13 / 912	PROTEINATLAS_urinary bladder
15	2e−02	12 / 816	PROTEINATLAS_endometrium

Telomeres

Rank	p−value	#in/all	Geneset
1	1	0 / 13	Alternative lengthening of telomeres
2	1	0 / 27	Nabetani_alt len telomeres_genes_ko
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	4e−05	28 / 1723	HEBENSTREIT_high expression TF
2	5e−05	54 / 4468	ICGC_Egr1_targets
3	8e−04	30 / 2255	ICGC_SrfV0416101_targets
4	1e−03	51 / 4735	ICGC_Pu1_targets
5	2e−03	71 / 7247	ICGC_Runx3_targets
6	2e−03	61 / 5984	ICGC_Mta3_targets
7	3e−03	56 / 5518	ICGC_Stat5_targets
8	3e−03	55 / 5410	ICGC_Foxm1_targets
9	3e−03	39 / 3507	ICGC_Rad21_targets
10	5e−03	32 / 2759	ICGC_Bcl3_targets
11	5e−03	50 / 4890	ICGC_Bclaf101388_targets
12	5e−03	54 / 5383	ICGC_Sp1_targets
13	5e−03	61 / 6267	ICGC_Yy1_targets
14	6e−03	26 / 2133	ICGC_Mef2_targets
15	1e−02	60 / 6322	ICGC_Tcf3_targets

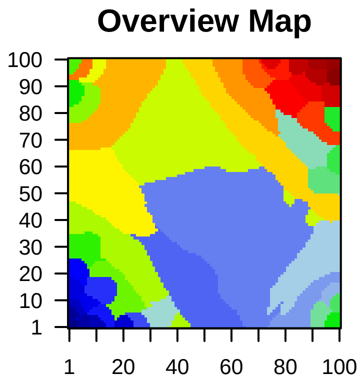
K−Means Cluster

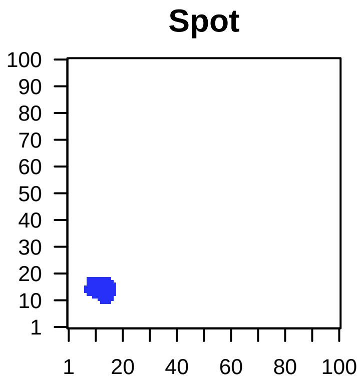
Spot Summary: P

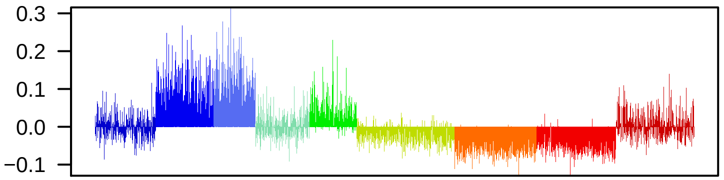
metagenes = 95
genes = 399

<r> metagenes = 0.96
<r> genes = 0.36
beta: r2= 9.53 / log p= −Inf

samples with spot = 166 (4.9 %)
A * : 1 (0.3 %)
A C * : 82 (25 %)
A C F * : 70 (29.8 %)
C F * : 12 (4.5 %)
N * : 1 (0.2 %)


Overview Map


Spot

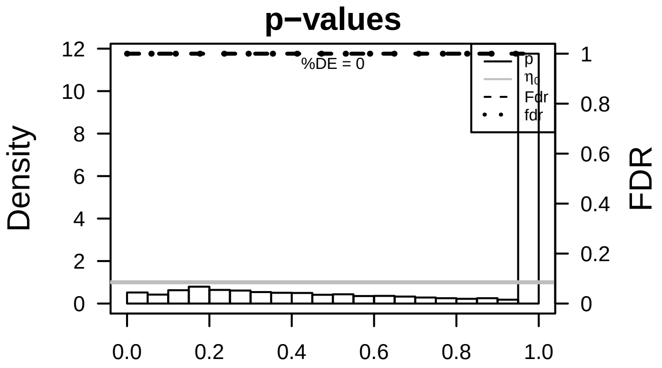


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_172426	0.84	−0.46	0.25	LYPD2	LY6/PLAUR domain containing 2 [Source:HGNC Symbol;Acc:
2	ILMN_174901	0.79	−0.64	0.47	NECAP2	NECAP endocytosis associated 2 [Source:HGNC Symbol;Acc
3	ILMN_169500	0.77	−0.36	0.47	TFIP11	tuftelin interacting protein 11 [Source:HGNC Symbol;Acc:HGI
4	ILMN_172443	0.72	−0.27	0.41	GCAT	glycine C−acetyltransferase [Source:HGNC Symbol;Acc:HGN
5	ILMN_175188	0.71	−0.5	0.37	REC8	REC8 meiotic recombination protein [Source:HGNC Symbol;A
6	ILMN_173086	0.7	−0.31	0.36	AZU1	azurocidin 1 [Source:HGNC Symbol;Acc:HGNC:913]
7	ILMN_326174	0.69	−0.5	0.32		
8	ILMN_177296	0.69	−0.37	0.38	CCL8	C−C motif chemokine ligand 8 [Source:HGNC Symbol;Acc:H
9	ILMN_170963	0.69	−0.35	0.46	CMBL	carboxymethylenebutenolidase homolog [Source:HGNC Sym
10	ILMN_180704	0.65	−0.57	0.46	UBAC1	UBA domain containing 1 [Source:HGNC Symbol;Acc:HGNC
11	ILMN_165128	0.64	−0.32	0.33	MIR936	collagen type XVII alpha 1 chain [Source:HGNC Symbol;Acc:
12	ILMN_225898	0.64	−0.39	0.47	XAGE1B	X antigen family member 1A [Source:HGNC Symbol;Acc:HGI
13	ILMN_134306	0.64	−0.29	0.53		
14	ILMN_134372	0.62	−0.31	0.71		
15	ILMN_175010	0.61	−0.34	0.34		tubulin beta 7 pseudogene [Source:HGNC Symbol;Acc:HGN
16	ILMN_238697	0.61	−0.34	0.67	PKP2	plakophilin 2 [Source:HGNC Symbol;Acc:HGNC:9024]
17	ILMN_166911	0.6	−0.4	0.43	MIR4751	activating transcription factor 5 [Source:HGNC Symbol;Acc:H
18	ILMN_174335	0.58	−0.31	0.74	XPNPEP2	X−prolyl aminopeptidase 2 [Source:HGNC Symbol;Acc:HGN
19	ILMN_230052	0.58	−0.28	0.65		
20	ILMN_324022	0.57	−0.32	0.52		RNA, U1 small nuclear 28, pseudogene [Source:HGNC Symb

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	4e−05	4 / 16	BP	megakaryocyte development
2	4e−04	4 / 29	GSEA	BANDRES_RESPONSE_TO_CARMUSTIN_MGMT_24HR_DN
3	7e−04	53 / 2709	Brain	Mid_Frontal_Lobe_HetRpts
4	7e−04	20 / 713	Colon	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
5	7e−04	8 / 154	GSEA	MIKKELSEN_IPS_LCP_WITH_H3K4ME3
6	8e−04	5 / 58	GSEA	ZHANG_GATA6_TARGETS_DN
7	1e−03	13 / 387	BP	negative regulation of cell proliferation
8	1e−03	3 / 18	BP	platelet formation
9	1e−03	3 / 18	miRN	hsa−miR−564
10	1e−03	6 / 97	GSEA	REACTOME_PPARA_ACTIVATES_GENE_EXPRESSION
11	1e−03	4 / 39	GSEA	KEGG_LYSINE_DEGRADATION
12	2e−03	100 / 6138	Colon	TssD2_Colon
13	2e−03	3 / 19	BP	regulation of vasoconstriction
14	2e−03	3 / 19	GSEA	KYNG_ENVIRONMENTAL_STRESS_RESPONSE_DN
15	2e−03	65 / 3639	Chror	1_TssP_Fibroblasts
16	2e−03	12 / 364	GSEA	MOREAUX_MULTIPLE_MYELOMA_BY_TACI_UP
17	3e−03	8 / 190	GSEA	CHANDRAN_METASTASIS_UP
18	3e−03	11 / 328	Colon	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
19	3e−03	52 / 2845	Colon	TxEnhG1_Colon
20	3e−03	3 / 24	BP	neuromuscular synaptic transmission
21	3e−03	3 / 24	miRN	hsa−miR−1228
22	3e−03	3 / 24	GSEA	REACTOME_RORA_ACTIVATES_CIRCADIAN_EXPRESSION
23	4e−03	3 / 26	GSEA	HOLLEMAN_VINCRISTINE_RESISTANCE_ALL_UP
24	5e−03	6 / 124	GSEA	MIKKELSEN_ES_LCP_WITH_H3K4ME3
25	5e−03	39 / 2028	Chror	4_TxTrans_Melanocytes
26	5e−03	7 / 166	miRN	hsa−miR−7
27	5e−03	91 / 5699	Chror	6_EnhG_Melanocytes
28	6e−03	19 / 794	GSEA	NUYTTEN_NIPP1_TARGETS_DN
29	6e−03	181 / 12741	Chror	7_Enh_Melanocytes
30	6e−03	4 / 59	BP	regulation of protein stability
31	7e−03	2 / 10	BP	regulation of androgen receptor signaling pathway
32	7e−03	2 / 10	GSEA	REACTOME_HIGHLY_CALCIUM_PERMEABLE_POSTSYNAPTIC_NICOT
33	7e−03	142 / 9635	Chror	3_TssF_Fibroblasts
34	7e−03	19 / 808	GSEA	BRUINS_UVC_RESPONSE_VIA_TP53_GROUP_A
35	7e−03	3 / 31	MF	protein tyrosine/serine/threonine phosphatase activity
36	7e−03	3 / 31	GSEA	BIOCARTA_CARM_ER_PATHWAY
37	7e−03	4 / 60	BP	hematopoietic progenitor cell differentiation
38	7e−03	4 / 60	GSEA	CHANG_IMMORTALIZED_BY_HPV31_DN
39	7e−03	10 / 316	GSEA	ACEVEDO_NORMAL_TISSUE_ADJACENT_TO_LIVER_TUMOR_DN
40	7e−03	12 / 419	Glio	Down_a


p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.1	4 / 142	HORVATH_aging_genes meth UP
2	0.5	1 / 58	TESCHENDORFF_age_hypermethylated
3	0.8	1 / 111	HORVATH_aging_genes meth DOWN
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	4e−05	4 / 16	megakaryocyte development
2	1e−03	13 / 387	negative regulation of cell proliferation
3	1e−03	3 / 18	platelet formation
4	2e−03	3 / 19	regulation of vasoconstriction
5	3e−03	3 / 24	neuromuscular synaptic transmission
6	6e−03	4 / 59	regulation of protein stability
7	7e−03	2 / 10	regulation of androgen receptor signaling pathway
8	7e−03	4 / 60	hematopoietic progenitor cell differentiation
9	8e−03	2 / 11	behavioral response to pain
10	9e−03	7 / 185	cell cycle
11	9e−03	5 / 102	single organismal cell−cell adhesion
12	1e−02	3 / 40	establishment of protein localization to plasma membrane
13	1e−02	2 / 15	mRNA transcription from RNA polymerase II promoter
14	1e−02	2 / 15	positive regulation of lamellipodium assembly
15	2e−02	3 / 43	phosphatidylinositol−3−phosphate biosynthetic process

Brain

Rank	p−value	#in/all	Geneset
1	7e−04	53 / 2709	Mid_Frontal_Lobe_HetRpts
2	1e−02	46 / 2654	Fetal_Quies
3	2e−02	53 / 3164	Mid_Frontal_Lobe_ZNF
4	3e−02	17 / 818	Mid_Frontal_Lobe_Het
5	3e−02	64 / 4112	Mid_Frontal_Lobe_ReprPC
6	4e−02	30 / 1728	Fetal_ReprPCWk
7	5e−02	145 / 10430	Overlap_fetal_midbrain_Quies
8	8e−02	47 / 3046	Fetal_TssA
9	1e−01	30 / 1893	Overlap_fetal_midbrain_TssF
10	1e−01	33 / 2127	Mid_Frontal_Lobe_K9K27me3
11	1e−01	19 / 1162	Fetal_Enh
12	2e−01	128 / 9504	Overlap_fetal_midbrain_K9K27me3
13	2e−01	27 / 1784	Mid_Frontal_Lobe_ReprPCWk
14	2e−01	22 / 1476	Overlap_fetal_midbrain_TxTrans
15	2e−01	11 / 681	Overlap_fetal_midbrain_EnhP

Cancer

Rank	p−value	#in/all	Geneset
1	0.03	2 / 20	PanCan_ChromMod_geneset_nanostring
2	0.13	10 / 527	Lembcke_Normal vs Adenoma
3	0.16	0 / 14	RHODES_UNDIFFERENTIATED_CANCER
4	0.18	1 / 16	BEN−PORATH_DN
5	0.22	4 / 193	PanCan_PI3K_geneset_nanostring
6	0.26	1 / 24	PanCan_Notch_geneset_nanostring
7	0.29	3 / 150	PanCan_MAPK_geneset_nanostring
8	0.33	0 / 13	LIU_LIVER_CANCER
9	0.43	2 / 117	PanCan_Driver_Gene_geneset_nanostring
10	0.44	1 / 46	PanCan_TGF−B_geneset_nanostring
11	0.47	2 / 125	PanCan_CC+Apop_geneset_nanostring
12	0.48	0 / 13	RHODES_CANCER_META_SIGNATURE
13	0.51	2 / 136	PanCan_RAS_geneset_nanostring
14	0.55	0 / 14	LIU_COMMON_CANCER_GENES
15	0.62	1 / 76	PanCan_Wnt_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	0.007	5 / 96	anchored component of membrane
2	0.017	2 / 16	acetylcholine−gated channel complex
3	0.017	2 / 16	pre−autophagosomal structure membrane
4	0.026	2 / 20	integral component of mitochondrial outer membrane
5	0.026	2 / 20	protein phosphatase type 2A complex
6	0.026	2 / 20	synaptonemal complex
7	0.031	2 / 22	desmosome
8	0.044	52 / 3291	integral component of membrane
9	0.057	7 / 273	neuron projection
10	0.061	2 / 32	mediator complex
11	0.063	5 / 170	cell−cell junction
12	0.068	2 / 34	polysome
13	0.070	3 / 76	extrinsic component of membrane
14	0.075	3 / 78	basement membrane
15	0.086	9 / 423	cell junction

Chr

Rank	p−value	#in/all	Geneset
1	0.02	40 / 2323	Chr 1
2	0.06	21 / 1160	Chr 12
3	0.16	23 / 1467	Chr 19
4	0.17	14 / 836	Chr 8
5	0.18	16 / 994	Chr X
6	0.36	17 / 1217	Chr 3
7	0.36	8 / 536	Chr 22
8	0.37	9 / 619	Chr 20
9	0.42	13 / 954	Chr 9
10	0.49	17 / 1318	Chr 17
11	0.54	12 / 959	Chr 16
12	0.57	13 / 1060	Chr 5
13	0.63	9 / 768	Chr 14
14	0.70	16 / 1411	Chr 11
15	0.75	13 / 1211	Chr 6

Chromatin states

Rank	p−value	#in/all	Geneset
1	0.002	65 / 3639	1_TssP_Fibroblasts
2	0.005	39 / 2028	4_TxTrans_Melanocytes
3	0.005	91 / 5699	6_EnhG_Melanocytes
4	0.006	181 / 12741	7_Enh_Melanocytes
5	0.007	142 / 9635	3_TssF_Fibroblasts
6	0.024	65 / 4107	9_ReprPCWk_Fibroblasts
7	0.026	171 / 12298	2_TssA_Melanocytes
8	0.038	10 / 416	4_TxTrans_Neuronal_Progenitor
9	0.049	158 / 11455	2_TssA_Fibroblasts
10	0.050	22 / 1206	6_EnhG_Neuronal_Progenitor
11	0.056	87 / 5956	3_TssF_Neuronal_Progenitor
12	0.059	162 / 11836	3_TssF_Melanocytes
13	0.077	161 / 11847	7_Enh_Neuronal_Progenitor
14	0.079	41 / 2620	1_TssP_Neuronal_Progenitor
15	0.087	52 / 3450	4_TxTrans_Fibroblasts

Colon Cancer

Rank	p−value	#in/all	Geneset
1	7e−04	20 / 713	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
2	2e−03	100 / 6138	TssD2_Colon
3	3e−03	11 / 328	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
4	3e−03	52 / 2845	TxEnhG1_Colon
5	7e−03	5 / 96	Pentrack_CRC_TCGA_group.over_A_normal_UP
6	1e−02	49 / 2810	EnhA_Colon
7	1e−02	154 / 10779	Enh_Colon
8	2e−02	109 / 7354	TssF_Colon
9	2e−02	15 / 663	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
10	3e−02	21 / 1069	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
11	3e−02	81 / 5373	EnhWk1_Colon
12	4e−02	47 / 2894	TssP_Colon
13	4e−02	128 / 9054	Tx_Colon
14	6e−02	61 / 4034	TssD1_Colon
15	9e−02	131 / 9530	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP_

Glio

Rank	p−value	#in/all	Geneset
1	0.007	12 / 419	Down_a
2	0.008	2 / 11	Mukasa_UP_in_Oligodendroglioma_with_1intact
3	0.024	4 / 87	Sturm_GBM_Meth_overexpression_I_RTK I 'PDGFRA'_UP
4	0.027	3 / 52	OL vs. OPC
5	0.048	2 / 28	KIM prognostic signature LTS vs. STS
6	0.050	4 / 110	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
7	0.057	4 / 115	Christensen_hypermethylated_in_grade3_astrocytoma
8	0.061	1 / 5	Sturm_GBM_Meth_overexpression_K_mesenchymal_UP
9	0.073	1 / 6	laffaire_hypometh_LGG_vs_control
10	0.088	10 / 487	Hopp_Sturm_GBM_Epi3_B_adult_UP_G34_DN
11	0.089	3 / 84	GIEZELT_GBM_STS_up_VS_LTS
12	0.094	3 / 86	laffaire_hypermeth_LGG_vs_control
13	0.096	1 / 8	WILLSCHER_GBM_STSwt_proteomics−N_UP
14	0.104	3 / 90	Christensen_hypermethylated_in_secondary_glioblastoma
15	0.114	4 / 147	Christensen_hypermethylated_in_grade2_oligodendroglioma

GSEA C2

Rank	p−value	#in/all	Geneset
1	4e−04	4 / 29	BANDRES_RESPONSE_TO_CARMUSTIN_MGMT_24HR_DN
2	7e−04	8 / 154	MIKKELSEN_IPS_LCP_WITH_H3K4ME3
3	8e−04	5 / 58	ZHANG_GATA6_TARGETS_DN
4	1e−03	6 / 97	REACTOME_PPARA_ACTIVATES_GENE_EXPRESSION
5	1e−03	4 / 39	KEGG_LYSINE_DEGRADATION
6	2e−03	3 / 19	KYNG_ENVIRONMENTAL_STRESS_RESPONSE_DN
7	2e−03	12 / 364	MOREAUX_MULTIPLE_MYELOMA_BY_TACI_UP
8	3e−03	8 / 190	CHANDRAN_METASTASIS_UP
9	3e−03	3 / 24	REACTOME_RORA_ACTIVATES_CIRCADIAN_EXPRESSION
10	4e−03	3 / 26	HOLLEMAN_VINCRISTINE_RESISTANCE_ALL_UP
11	5e−03	6 / 124	MIKKELSEN_ES_LCP_WITH_H3K4ME3
12	6e−03	19 / 794	NUYTTEN_NIPP1_TARGETS_DN
13	7e−03	2 / 10	REACTOME_HIGHLY_CALCIUM_PERMEABLE_POSTSYNAPTIC_NICOTIN
14	7e−03	19 / 808	BRUINS_UVC_RESPONSE_VIA_TP53_GROUP_A
15	7e−03	3 / 31	BIOCARTA_CARM_ER_PATHWAY

HM

Rank	p−value	#in/all	Geneset
1	0.2	4 / 167	HALLMARK_OXIDATIVE_PHOSPHORYLATION
2	0.2	4 / 183	HALLMARK_APICAL_JUNCTION
3	0.2	4 / 185	HALLMARK_HEME_METABOLISM
4	0.2	4 / 186	HALLMARK_ESTROGEN_RESPONSE_EARLY
5	0.2	2 / 69	HALLMARK_CHOLESTEROL_HOMEOSTASIS
6	0.2	3 / 138	HALLMARK_FATTY_ACID_METABOLISM
7	0.3	2 / 91	HALLMARK_PEROXISOME
8	0.4	2 / 103	HALLMARK_BILE_ACID_METABOLISM
9	0.4	1 / 37	HALLMARK_PANCREAS_BETA_CELLS
10	0.4	3 / 176	HALLMARK_ADIPOGENESIS
11	0.4	3 / 176	HALLMARK_KRAS_SIGNALING_UP
12	0.4	3 / 177	HALLMARK_KRAS_SIGNALING_DN
13	0.4	3 / 179	HALLMARK_G2M_CHECKPOINT
14	0.4	3 / 183	HALLMARK_GLYCOLYSIS
15	0.4	1 / 41	HALLMARK_APICAL_SURFACE

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.1	4 / 147	Homuth_BMI−associated−genes_UP
2	0.1	1 / 10	Marjolein_ageing−genes_UP
3	0.2	1 / 17	DUMEAUX_High bmi enriched genes
4	0.3	4 / 211	Homuth_BMI−associated−genes_DN
5	0.7	1 / 94	DUMEAUX_Smoking enriched genes
6	1.0	0 / 10	DUMEAUX_Smoking literature genes up
7	1.0	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
8	1.0	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
9	1.0	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
10	1.0	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
11	1.0	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
12	1.0	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
13	1.0	0 / 10	DUMEAUX_Women normal BMI literature genes up
14	1.0	0 / 31	DUMEAUX_Fasting enriched genes
15	1.0	0 / 18	Huan_blood−pressure_SBP−signature

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.008	6 / 137	Hopp_June14_MMML937 tumors+controls_group.overexpression_G_tonsil_L
2	0.008	6 / 138	WIRTH_lymphoma937_spot G
3	0.019	3 / 45	Subero_INT_hypo_meth
4	0.033	2 / 23	Hopp_Lymphoma_Epi1_no_zentr_2_B.cell_MCL_DN
5	0.104	77 / 5384	HOPP_Repressed
6	0.113	2 / 46	Subero_DLBCL_hypo_meth
7	0.114	9 / 450	Hopp_June14_MMML937 tumors+controls_group.overexpression_I_MM_GC-
8	0.130	1 / 11	Subero_MM_hypo_meth
9	0.131	9 / 464	WIRTH_lymphoma937_spot I
10	0.138	2 / 52	Hopp_Lymphoma_Epi1_with_zentr_iv_B.cell_MM_UP
11	0.157	43 / 2939	HOPP_Poised_promoter
12	0.216	100 / 7448	HOPP_Strong_enhancer
13	0.261	1 / 24	Subero_mBL_hypo_meth
14	0.283	87 / 6559	HOPP_Weak_txn
15	0.290	108 / 8226	HOPP_Active_promoter

Melanoma

Rank	p−value	#in/all	Geneset
1	0.1	2 / 43	Hugo_melanoma−BRAFmut−MET_UP
2	0.5	1 / 54	Hugo_melanoma−all−MET_DN
3	1.0	0 / 30	Hugo_melanoma−all−MET_UP
4	1.0	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
5	1.0	0 / 27	Hugo_melanoma−all−LEF1_UP
6	1.0	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

MF

Rank	p−value	#in/all	Geneset
1	0.007	3 / 31	protein tyrosine/serine/threonine phosphatase activity
2	0.008	3 / 33	ligand−gated ion channel activity
3	0.009	3 / 34	histone−lysine N−methyltransferase activity
4	0.010	2 / 12	proton−transporting ATP synthase activity, rotational mechanism
5	0.013	2 / 14	poly(U) RNA binding
6	0.015	22 / 1065	zinc ion binding
7	0.019	2 / 17	heparan sulfate proteoglycan binding
8	0.021	3 / 47	chromatin DNA binding
9	0.023	2 / 19	acetylcholine binding
10	0.023	2 / 19	aspartic−type endopeptidase activity
11	0.028	2 / 21	acetylcholine−activated cation−selective channel activity
12	0.028	2 / 21	acetylcholine receptor activity
13	0.028	2 / 21	protein phosphatase type 2A regulator activity
14	0.033	2 / 23	laminin binding
15	0.033	2 / 23	nuclear hormone receptor binding

miRNA Disease

Rank	p−value	#in/all	Geneset
1	1	0 / 7	Thyroid carcinoma, papillary
2	1	0 / 123	Pancreatic cancer
3	1	0 / 68	Glioblastoma multiforme, somatic
4	1	0 / 63	Gastrointestinal
5	1	0 / 3	Pituitary adenoma
6	1	0 / 116	Cancer
7	1	0 / 95	Colorectal cancer
8	1	0 / 2	Adenomas, multiple colorectal
9	1	0 / 124	Prostate cancer
10	1	0 / 48	Alzheimer disease, susceptibility to
11	1	0 / 7	Schizophrenia, susceptibility to
12	1	0 / 20	Parkinson disease
13	1	0 / 65	Hepatocellular carcinoma
14	1	0 / 3	Down syndrome, risk of
15	1	0 / 127	Melanoma and neural system tumor syndrome

miRNA target

Rank	p−value	#in/all	Geneset
1	0.001	3 / 18	hsa−miR−564
2	0.003	3 / 24	hsa−miR−1228
3	0.005	7 / 166	hsa−miR−7
4	0.010	2 / 12	hsa−miR−652
5	0.013	2 / 14	hsa−miR−638
6	0.014	5 / 114	hsa−miR−875−3p
7	0.017	3 / 43	hsa−miR−412
8	0.018	10 / 366	hsa−miR−519b−3p
9	0.018	6 / 166	hsa−miR−452
10	0.020	5 / 124	hsa−miR−515−3p
11	0.020	9 / 321	hsa−miR−302a
12	0.021	5 / 126	hsa−miR−223
13	0.022	3 / 48	hsa−miR−329
14	0.023	4 / 86	hsa−miR−339−5p
15	0.025	9 / 332	hsa−miR−302d

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.1	1 / 12	BENTINK_ras.1
2	0.2	1 / 13	BENTINK_e2f3.2
3	0.2	1 / 14	BENTINK_ras.6
4	1.0	0 / 14	GUSTAFSON_PI3K_UP
5	1.0	0 / 15	GUSTAFSON_PI3K_DN
6	1.0	0 / 13	BENTINK_e2f3.1
7	1.0	0 / 13	BENTINK_myc.1
8	1.0	0 / 11	BENTINK_ras.4
9	1.0	0 / 13	BENTINK_src.10
10	1.0	0 / 12	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Reference Signatures

Rank	p−value	#in/all	Geneset
1	0.01	6 / 148	VAQUERIZAS_General_TF
2	0.01	3 / 41	VAQUERIZAS_Thymus_TF
3	0.03	2 / 20	JONGENEEL_Thymus
4	0.03	5 / 134	WIRTH_Mucosa
5	0.05	2 / 30	VAQUERIZAS_Smooth muscle_TF
6	0.06	2 / 31	VAQUERIZAS_Fetal lung_TF
7	0.07	6 / 231	Chaussabel_2,5_Immune related molecules
8	0.07	1 / 6	WIRTH_Pituitary gland
9	0.07	1 / 6	JONGENEEL_SpinalCord
10	0.09	2 / 39	VAQUERIZAS_Testis_TF
11	0.09	3 / 84	Chaussabel_2,10_Immune related cell surface molecules
12	0.09	18 / 1016	PROTEINATLAS_cerebral cortex
13	0.12	12 / 650	PROTEINATLAS_hippocampus
14	0.12	1 / 10	JONGENEEL_Colon
15	0.13	19 / 1138	PROTEINATLAS_small intestine

Telomeres

Rank	p−value	#in/all	Geneset
1	1	0 / 13	Alternative lengthening of telomeres
2	1	0 / 27	Nabetani_alt len telomeres_genes_ko
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	0.2	27 / 1753	HEBENSTREIT_low expression TF
2	0.2	12 / 747	ICGC_NrsfPcr2_targets
3	0.3	87 / 6616	ICGC_Pax5_targets
4	0.4	20 / 1466	ICGC_NrsfPcr1_targets
5	0.4	77 / 5961	ICGC_Pol24_targets
6	0.4	10 / 721	ICGC_SrfPcr2_targets
7	0.4	10 / 733	ICGC_Atf3_targets
8	0.5	70 / 5518	ICGC_Stat5_targets
9	0.5	83 / 6578	ICGC_Pou2_targets
10	0.5	75 / 5984	ICGC_Mta3_targets
11	0.6	64 / 5188	ICGC_Ebfsc137065_targets
12	0.6	18 / 1501	ICGC_Usf1_targets
13	0.6	20 / 1669	ICGC_P300_targets
14	0.6	77 / 6322	ICGC_Tcf3_targets
15	0.6	66 / 5442	ICGC_Pmlsc71910_targets

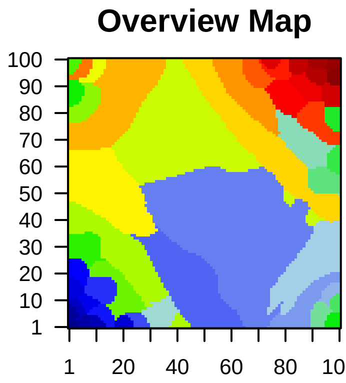
K−Means Cluster

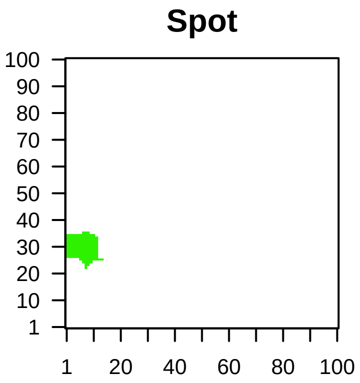
Spot Summary: Q

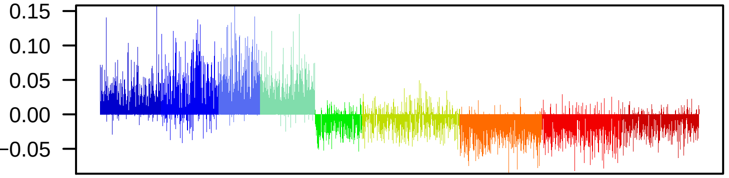
metagenes = 126
genes = 239

<r> metagenes = 0.95
<r> genes = 0.16
beta: r2= 3.03 / log p= −Inf

samples with spot = 20 (0.6 %)
A * : 2 (0.6 %)
A C * : 5 (1.5 %)
A C F * : 10 (4.3 %)
A F * : 3 (1 %)





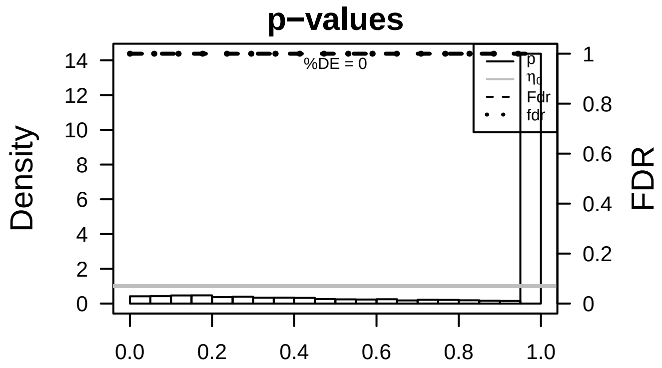


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_165491	0.71	−0.42	0.3		
2	ILMN_238230	0.58	−0.39	0.31		
3	ILMN_174793	0.54	−0.71	0.24	GOLGB1	golgin B1 [Source:HGNC Symbol;Acc:HGNC:4429]
4	ILMN_316678	0.53	−0.31	0.49		
5	ILMN_212355	0.52	−0.38	0.42	MIGA1	mitoguardin 1 [Source:HGNC Symbol;Acc:HGNC:24741]
6	ILMN_167180	0.51	−0.49	0.18	DUSP22	dual specificity phosphatase 22 [Source:HGNC Symbol;Acc:H
7	ILMN_316533	0.49	−0.25	0.49		
8	ILMN_316553	0.48	−0.26	0.49		
9	ILMN_227207	0.47	−0.35	0.45	TROVE2	TROVE domain family member 2 [Source:HGNC Symbol;Acc
10	ILMN_318273	0.47	−0.26	0.59	LOC100129518	superoxide dismutase 2, mitochondrial [Source:HGNC Symbo
11	ILMN_166871	0.46	−0.34	0.46	GABPB2	GA binding protein transcription factor beta subunit 2 [Source
12	ILMN_176920	0.46	−0.28	0.58	KCTD7	potassium channel tetramerization domain containing 7 [Sour
13	ILMN_206131	0.45	−0.27	0.48		
14	ILMN_233037	0.45	−0.47	0.33	TATDN3	TatD DNase domain containing 3 [Source:HGNC Symbol;Acc
15	ILMN_169840	0.45	−0.43	0.3	ERN1	endoplasmic reticulum to nucleus signaling 1 [Source:HGNC
16	ILMN_316575	0.45	−0.26	0.48		
17	ILMN_174562	0.45	−0.48	0.21	KRCC1	lysine rich coiled−coil 1 [Source:HGNC Symbol;Acc:HGNC:2
18	ILMN_165799	0.44	−0.35	0.37	LINC00243	long intergenic non−protein coding RNA 243 [Source:HGNC
19	ILMN_176336	0.44	−0.31	0.43	WHAMM	WAS protein homolog associated with actin, golgi membrane
20	ILMN_177381	0.44	−0.3	0.22	TMLHE	trimethyllysine hydroxylase, epsilon [Source:HGNC Symbol;A

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	2e−05	88 / 7854	Chror	5_Tx_Fibroblasts
2	3e−05	97 / 9054	Colon	Tx_Colon
3	1e−04	69 / 5936	Brain	Overlap_fetal_midbrain_HetRpts
4	1e−04	40 / 2845	Colon	TxEnhG1_Colon
5	2e−04	92 / 8771	Chror	5_Tx_Melanocytes
6	2e−04	90 / 8568	Colon	TxWk_Colon
7	3e−04	33 / 2255	TF	ICGC_SrfV0416101_targets
8	3e−04	53 / 4362	TF	ICGC_Creb1_targets
9	4e−04	97 / 9555	Colon	TssA_Colon
10	6e−04	41 / 3164	Brain	Mid_Frontal_Lobe_ZNF
11	8e−04	95 / 9504	Brain	Overlap_fetal_midbrain_K9K27me3
12	1e−03	74 / 6970	Chror	5_Tx_Neuronal_Progenitor
13	1e−03	63 / 5699	Chror	6_EnhG_Melanocytes
14	1e−03	55 / 4795	Chror	6_EnhG_Fibroblasts
15	1e−03	77 / 7354	Colon	TssF_Colon
16	1e−03	116 / 12298	Chror	2_TssA_Melanocytes
17	1e−03	16 / 877	MF	transcription factor activity, sequence−specific DNA binding
18	2e−03	66 / 6138	Colon	TssD2_Colon
19	2e−03	7 / 221	GSEA	WANG_CLIM2_TARGETS_UP
20	2e−03	4 / 66	BP	cholesterol metabolic process
21	2e−03	4 / 66	GSEA	REACTOME_TRANSCRIPTIONAL_REGULATION_OF_WHITE_ADIPOCY
22	2e−03	20 / 1272	BP	regulation of transcription, DNA−templated
23	2e−03	60 / 5518	TF	ICGC_Stat5_targets
24	2e−03	22 / 1467	Chr	Chr 19
25	2e−03	10 / 438	miRN	hsa−miR−19a
26	2e−03	3 / 34	GSEA	CONRAD_STEM_CELL
27	3e−03	3 / 36	Canc	PanCan_HK_geneset_nanostring
28	3e−03	34 / 2704	TF	ICGC_Pbx3_targets
29	3e−03	58 / 5356	Lympl	HOPP_Txn_transition
30	3e−03	2 / 11	Colon	Juehling−MSI−enriched−in−7
31	3e−03	2 / 11	GSEA	REACTOME_VITAMIN_B5_PANTOTHENATE_METABOLISM
32	4e−03	2 / 12	BP	lipid biosynthetic process
33	4e−03	2 / 12	BP	negative regulation of macrophage derived foam cell differentiation
34	4e−03	55 / 5067	TF	ICGC_Taf1_targets
35	4e−03	92 / 9530	Colon	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP
36	4e−03	2 / 13	BP	positive regulation of cholesterol efflux
37	4e−03	2 / 13	GSEA	REACTOME_HDL_MEDIATED_LIPID_TRANSPORT
38	4e−03	3 / 43	GSEA	PARENT_MTOR_SIGNALING_DN
39	5e−03	53 / 4881	TF	ICGC_Atf2_targets
40	5e−03	2 / 14	BP	high−density lipoprotein particle remodeling



Aging

Rank	p−value	#in/all	Geneset
1	0.6	1 / 111	HORVATH_aging_genes meth DOWN
2	0.7	1 / 142	HORVATH_aging_genes meth UP
3	1.0	0 / 58	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	0.002	4 / 66	cholesterol metabolic process
2	0.002	20 / 1272	regulation of transcription, DNA−templated
3	0.004	2 / 12	lipid biosynthetic process
4	0.004	2 / 12	negative regulation of macrophage derived foam cell differentiation
5	0.004	2 / 13	positive regulation of cholesterol efflux
6	0.005	2 / 14	high−density lipoprotein particle remodeling
7	0.005	2 / 14	mRNA catabolic process
8	0.006	2 / 15	response to lipid
9	0.008	2 / 17	reverse cholesterol transport
10	0.011	2 / 21	cholesterol transport
11	0.012	3 / 62	nucleic acid phosphodiester bond hydrolysis
12	0.017	2 / 26	maturation of SSU−rRNA from tricistronic rRNA transcript (SSU−rRNA, 5.8S r
13	0.021	4 / 134	protein ubiquitination involved in ubiquitin−dependent protein catabolic proces
14	0.024	2 / 31	lamellipodium assembly
15	0.025	2 / 32	photoreceptor cell maintenance

Brain

Rank	p−value	#in/all	Geneset
1	1e−04	69 / 5936	Overlap_fetal_midbrain_HetRpts
2	6e−04	41 / 3164	Mid_Frontal_Lobe_ZNF
3	8e−04	95 / 9504	Overlap_fetal_midbrain_K9K27me3
4	7e−03	93 / 9815	Overlap_fetal_midbrain_ReprPC
5	2e−02	13 / 906	Fetal_HetRpts
6	4e−02	10 / 681	Overlap_fetal_midbrain_EnhP
7	5e−02	20 / 1728	Fetal_ReprPCWk
8	1e−01	5 / 328	Fetal_Het
9	1e−01	11 / 937	Fetal_EnhG
10	1e−01	13 / 1171	Fetal_EnhP
11	1e−01	89 / 10430	Overlap_fetal_midbrain_Quies
12	1e−01	26 / 2654	Fetal_Quies
13	2e−01	84 / 9917	Overlap_fetal_midbrain_ReprPCWk
14	2e−01	3 / 180	Overlap_fetal_midbrain_Het
15	2e−01	12 / 1162	Fetal_Enh

Cancer

Rank	p−value	#in/all	Geneset
1	0.003	3 / 36	PanCan_HK_geneset_nanostring
2	0.006	2 / 15	WANG_ER_UP
3	0.096	1 / 13	WANG_ER_DN
4	0.103	1 / 14	GENTLES_modul1
5	0.103	1 / 14	GENTLES_modul10
6	0.144	1 / 20	PanCan_ChromMod_geneset_nanostring
7	0.488	0 / 14	LIU_PROSTATE_CANCER_UP
8	0.508	1 / 91	PanCan_TXmisReg_geneset_nanostring
9	0.623	0 / 12	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
10	0.623	1 / 125	PanCan_CC+Apop_geneset_nanostring
11	0.669	0 / 15	LIU_PROSTATE_CANCER_DN
12	0.690	1 / 150	PanCan_MAPK_geneset_nanostring
13	0.751	1 / 178	SPANG_LPS−index2
14	0.778	3 / 527	Lembcke_Normal vs Adenoma
15	0.779	1 / 193	PanCan_PI3K_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	0.007	2 / 16	proteasome core complex
2	0.008	2 / 18	NuRD complex
3	0.008	2 / 18	telomerase holoenzyme complex
4	0.025	2 / 32	mediator complex
5	0.034	28 / 2535	nucleoplasm
6	0.059	8 / 539	Golgi membrane
7	0.060	3 / 115	nuclear chromosome, telomeric region
8	0.072	2 / 57	endoplasmic reticulum−Golgi intermediate compartment
9	0.077	2 / 59	endoplasmic reticulum−Golgi intermediate compartment membrane
10	0.079	30 / 2979	cytosol
11	0.082	1 / 11	axonemal dynein complex
12	0.096	1 / 13	Golgi−associated vesicle
13	0.096	1 / 13	intrinsic component of the cytoplasmic side of the plasma membrane
14	0.098	2 / 68	Golgi cisterna membrane
15	0.103	1 / 14	Cul4−RING E3 ubiquitin ligase complex

Chr

Rank	p−value	#in/all	Geneset
1	0.002	22 / 1467	Chr 19
2	0.014	18 / 1318	Chr 17
3	0.075	5 / 289	Chr 21
4	0.143	9 / 768	Chr 14
5	0.147	13 / 1211	Chr 6
6	0.260	21 / 2323	Chr 1
7	0.461	8 / 954	Chr 9
8	0.467	8 / 959	Chr 16
9	0.472	7 / 836	Chr 8
10	0.496	3 / 342	Chr 18
11	0.526	5 / 619	Chr 20
12	0.547	9 / 1160	Chr 12
13	0.706	6 / 904	Chr 10
14	0.726	10 / 1492	Chr 2
15	0.833	5 / 902	Chr 4

Chromatin states

Rank	p−value	#in/all	Geneset
1	2e−05	88 / 7854	5_Tx_Fibroblasts
2	2e−04	92 / 8771	5_Tx_Melanocytes
3	1e−03	74 / 6970	5_Tx_Neuronal_Progenitor
4	1e−03	63 / 5699	6_EnhG_Melanocytes
5	1e−03	55 / 4795	6_EnhG_Fibroblasts
6	1e−03	116 / 12298	2_TssA_Melanocytes
7	5e−03	62 / 5956	3_TssF_Neuronal_Progenitor
8	8e−03	117 / 12983	2_TssA_Neuronal_Progenitor
9	9e−03	108 / 11836	3_TssF_Melanocytes
10	3e−02	88 / 9635	3_TssF_Fibroblasts
11	3e−02	102 / 11455	2_TssA_Fibroblasts
12	3e−02	22 / 1846	14_ZNF_Melanocytes
13	4e−02	36 / 3450	4_TxTrans_Fibroblasts
14	5e−02	42 / 4237	14_ZNF_Neuronal_Progenitor
15	7e−02	22 / 2028	4_TxTrans_Melanocytes

Colon Cancer

Rank	p−value	#in/all	Geneset
1	3e−05	97 / 9054	Tx_Colon
2	1e−04	40 / 2845	TxEnhG1_Colon
3	2e−04	90 / 8568	TxWk_Colon
4	4e−04	97 / 9555	TssA_Colon
5	1e−03	77 / 7354	TssF_Colon
6	2e−03	66 / 6138	TssD2_Colon
7	3e−03	2 / 11	Juehling−MSI−enriched−in−7
8	4e−03	92 / 9530	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP_
9	1e−02	20 / 1468	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
10	1e−02	16 / 1083	ZNF_Colon
11	1e−02	82 / 8678	Quies3_Colon
12	2e−02	100 / 10999	TssWk_Colon
13	3e−02	11 / 740	LaPointe_mucosa−position_kmeans_C_cecum colon_ascending colon_transv
14	4e−02	52 / 5373	EnhWk1_Colon
15	7e−02	94 / 10779	Enh_Colon

Glio

Rank	p−value	#in/all	Geneset
1	0.006	14 / 839	Hopp_Sturm_GBM_Epi3_no_zentr_1_G34_DN
2	0.089	1 / 12	Mukasa_UP_in_Astroglioma
3	0.096	1 / 13	Donson−immune cell intra signaling−associated with LTS in HGA
4	0.096	1 / 13	WILLSCHER_GBM_Verhaak−PNmut_up (M)
5	0.103	1 / 14	Christensen_hypermethylated_in_ependymoma
6	0.112	2 / 74	Weller_LGG_gradeII−vs−III_DOWN
7	0.137	1 / 19	KIM deleted & downregulated in LTS
8	0.152	2 / 89	GIEZELT_GBM_STSwt_up_VS_LTSwt
9	0.160	2 / 92	Weller_LGG_A_vs_O_DOWN
10	0.177	1 / 25	Barbus_GBM_STS_vs._LTS
11	0.185	2 / 101	Hopp_Sturm_GBM_Epi3_D1_IDH_UP_adult_fetus_DN
12	0.196	1 / 28	KIM prognostic signature LTS vs. STS
13	0.218	2 / 113	GIEZELT_GBM_WT_up_VS_mut
14	0.229	4 / 315	Up
15	0.239	5 / 428	Hopp_Sturm_GBM_Epi3_no_zentr_4_IDH_UP_adult_fetus_K27_DN

GSEA C2

Rank	p−value	#in/all	Geneset
1	0.002	7 / 221	WANG_CLIM2_TARGETS_UP
2	0.002	4 / 66	REACTOME_TRANSCRIPTIONAL_REGULATION_OF_WHITE_ADIPOCYTE
3	0.002	3 / 34	CONRAD_STEM_CELL
4	0.003	2 / 11	REACTOME_VITAMIN_B5_PANTOTHENATE_METABOLISM
5	0.004	2 / 13	REACTOME_HDL_MEDIATED_LIPID_TRANSPORT
6	0.004	3 / 43	PARENT_MTOR_SIGNALING_DN
7	0.006	9 / 429	REACTOME_METABOLISM_OF_LIPIDS_AND_LIPOPROTEINS
8	0.007	4 / 97	REACTOME_PPARA_ACTIVATES_GENE_EXPRESSION
9	0.008	2 / 17	RUAN_RESPONSE_TO_TROGLITAZONE_DN
10	0.012	3 / 62	SWEET_KRAS_TARGETS_DN
11	0.012	2 / 22	WANG_METASTASIS_OF_BREAST_CANCER_ESR1_DN
12	0.015	2 / 24	REACTOME_G_BETA_GAMMA_SIGNALLING_THROUGH_PI3KGAMMA
13	0.015	2 / 24	MURATA_VIRULENCE_OF_H_PILORI
14	0.016	2 / 25	REACTOME_LIPOPROTEIN_METABOLISM
15	0.016	4 / 125	ONDER_CDH1_TARGETS_1_UP

HM

Rank	p−value	#in/all	Geneset
1	0.03	3 / 91	HALLMARK_PEROXISOME
2	0.19	2 / 103	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
3	0.27	2 / 130	HALLMARK_DNA_REPAIR
4	0.27	1 / 41	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
5	0.29	2 / 137	HALLMARK_UV_RESPONSE_UP
6	0.39	2 / 172	HALLMARK_INTERFERON_GAMMA_RESPONSE
7	0.39	2 / 175	HALLMARK_XENOBIOTIC_METABOLISM
8	0.42	1 / 69	HALLMARK_CHOLESTEROL_HOMEOSTASIS
9	0.42	2 / 185	HALLMARK_P53_PATHWAY
10	0.42	2 / 186	HALLMARK_MYOGENESIS
11	0.66	1 / 138	HALLMARK_FATTY_ACID_METABOLISM
12	0.69	1 / 151	HALLMARK_APOPTOSIS
13	0.73	1 / 170	HALLMARK_MYC_TARGETS_V1
14	0.75	1 / 176	HALLMARK_ADIPOGENESIS
15	0.75	1 / 177	HALLMARK_KRAS_SIGNALING_DN

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.2	1 / 31	DUMEAUX_Fasting enriched genes
2	0.3	2 / 147	Homuth_BMI−associated−genes_UP
3	0.5	2 / 211	Homuth_BMI−associated−genes_DN
4	1.0	0 / 94	DUMEAUX_Smoking enriched genes
5	1.0	0 / 10	DUMEAUX_Smoking literature genes up
6	1.0	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
7	1.0	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
8	1.0	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
9	1.0	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
10	1.0	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
11	1.0	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
12	1.0	0 / 10	DUMEAUX_Women normal BMI literature genes up
13	1.0	0 / 17	DUMEAUX_High bmi enriched genes
14	1.0	0 / 18	Huan_blood−pressure_SBP−signature
15	1.0	0 / 16	Huan_blood−pressure_DBP−signature

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.003	58 / 5356	HOPP_Txn_transition
2	0.005	73 / 7275	HOPP_Txn_elongation
3	0.009	9 / 450	Hopp_June14_MMML937 tumors+controls_group.overexpression_I_MM_GC-
4	0.009	2 / 19	DAVE_BL Inter
5	0.029	8 / 464	WIRTH_lymphoma937_spot I
6	0.031	70 / 7448	HOPP_Strong_enhancer
7	0.046	1 / 6	CARO_OxPhos_vs_BCR_UP
8	0.065	74 / 8226	HOPP_Active_promoter
9	0.075	7 / 472	Hopp_June14_MMML937 tumors+controls_group.overexpression_J_GC−B−c
10	0.076	5 / 290	SPANG_IL21 UP
11	0.090	7 / 493	WIRTH_lymphoma937_spot J
12	0.096	1 / 13	Subero_B−CLL_hypo_meth
13	0.112	71 / 8098	HOPP_Weak_promoter
14	0.124	1 / 17	YAMANE_AICDA_targets_recruited
15	0.178	4 / 283	TARTE_Plasmablast signature

Melanoma

Rank	p−value	#in/all	Geneset
1	0.06	1 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
2	1.00	0 / 30	Hugo_melanoma−all−MET_UP
3	1.00	0 / 54	Hugo_melanoma−all−MET_DN
4	1.00	0 / 43	Hugo_melanoma−BRAFmut−MET_UP
5	1.00	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
6	1.00	0 / 27	Hugo_melanoma−all−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

MF

Rank	p−value	#in/all	Geneset
1	0.001	16 / 877	transcription factor activity, sequence−specific DNA binding
2	0.008	2 / 18	threonine−type endopeptidase activity
3	0.011	3 / 60	transcriptional repressor activity, RNA polymerase II transcription regulatory r
4	0.012	3 / 62	p53 binding
5	0.014	22 / 1717	metal ion binding
6	0.021	19 / 1475	DNA binding
7	0.024	3 / 79	protein tyrosine phosphatase activity
8	0.024	2 / 31	ADP binding
9	0.029	10 / 646	protein homodimerization activity
10	0.032	2 / 36	histone deacetylase activity
11	0.033	8 / 476	sequence−specific DNA binding
12	0.055	4 / 184	transcription corepressor activity
13	0.075	1 / 10	fucosyltransferase activity
14	0.075	1 / 10	toxic substance binding
15	0.077	2 / 59	damaged DNA binding

miRNA Disease

Rank	p−value	#in/all	Geneset
1	0.02	1 / 2	Immunoglobulin A deficiency
2	0.12	1 / 17	Thyroid carcinoma, follicular
3	0.13	1 / 18	Non−Hodgkin lymphoma, somatic
4	0.16	1 / 22	Pigmented adrenocortical disease, primary isolated
5	0.20	1 / 29	Myelofibrosis, idiopathic
6	0.31	1 / 48	Multiple myeloma
7	0.39	1 / 63	Gastrointestinal
8	0.40	1 / 65	Hepatocellular carcinoma
9	0.52	1 / 95	Colorectal cancer
10	0.55	1 / 102	Leukemia
11	0.59	1 / 113	Ovarian cancer
12	0.60	1 / 116	Cancer
13	0.61	1 / 120	Hematological
14	0.62	1 / 123	Pancreatic cancer
15	0.62	1 / 124	Prostate cancer

miRNA target

Rank	p−value	#in/all	Geneset
1	0.002	10 / 438	hsa−miR−19a
2	0.007	9 / 433	hsa−miR−19b
3	0.010	9 / 463	hsa−miR−301a
4	0.011	3 / 60	hsa−miR−514
5	0.016	4 / 125	hsa−miR−383
6	0.020	2 / 28	hsa−miR−519e*
7	0.022	5 / 206	hsa−miR−148a
8	0.024	3 / 79	hsa−miR−876−5p
9	0.024	8 / 449	hsa−miR−130b
10	0.026	8 / 455	hsa−miR−130a
11	0.029	7 / 379	hsa−miR−454
12	0.030	2 / 35	hsa−miR−517b
13	0.032	7 / 389	hsa−miR−519a
14	0.034	7 / 394	hsa−miR−301b
15	0.039	4 / 164	hsa−miR−495

Pathw Act

Rank	p−value	#in/all	Geneset
1	1	0 / 14	GUSTAFSON_PI3K_UP
2	1	0 / 15	GUSTAFSON_PI3K_DN
3	1	0 / 13	BENTINK_e2f3.1
4	1	0 / 13	BENTINK_e2f3.2
5	1	0 / 13	BENTINK_myc.1
6	1	0 / 12	BENTINK_ras.1
7	1	0 / 11	BENTINK_ras.4
8	1	0 / 14	BENTINK_ras.6
9	1	0 / 13	BENTINK_src.10
10	1	0 / 12	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Reference Signatures

Rank	p−value	#in/all	Geneset
1	0.03	4 / 148	VAQUERIZAS_General_TF
2	0.03	5 / 221	Chaussabel_3,8_Enzymes
3	0.04	2 / 43	VAQUERIZAS_Placenta_TF
4	0.05	11 / 816	PROTEINATLAS_endometrium
5	0.07	11 / 850	PROTEINATLAS_skin
6	0.07	12 / 960	PROTEINATLAS_cerebellum
7	0.07	10 / 759	PROTEINATLAS_epididymis
8	0.10	1 / 13	WIRTH_Thymus
9	0.10	12 / 1016	PROTEINATLAS_cerebral cortex
10	0.10	1 / 14	WIRTH_B−cells
11	0.11	8 / 619	PROTEINATLAS_salivary gland
12	0.12	4 / 242	Chaussabel_3,9_Kinases
13	0.12	1 / 17	VAQUERIZAS_Adrenal gland_TF
14	0.16	1 / 23	JONGENEEL_Heart
15	0.17	1 / 24	JONGENEEL_Prostate

Telomeres

Rank	p−value	#in/all	Geneset
1	1	0 / 13	Alternative lengthening of telomeres
2	1	0 / 27	Nabetani_alt len telomeres_genes_ko
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	3e−04	33 / 2255	ICGC_SrfV0416101_targets
2	3e−04	53 / 4362	ICGC_Creb1_targets
3	2e−03	60 / 5518	ICGC_Stat5_targets
4	3e−03	34 / 2704	ICGC_Pbx3_targets
5	4e−03	55 / 5067	ICGC_Taf1_targets
6	5e−03	53 / 4881	ICGC_Atf2_targets
7	5e−03	48 / 4345	ICGC_Zeb1_targets
8	5e−03	57 / 5383	ICGC_Sp1_targets
9	7e−03	28 / 2215	ICGC_GabpPcr2_targets
10	7e−03	57 / 5442	ICGC_Pmlsc71910_targets
11	7e−03	64 / 6267	ICGC_Yy1_targets
12	1e−02	51 / 4890	ICGC_Bclaf101388_targets
13	1e−02	47 / 4468	ICGC_Egr1_targets
14	1e−02	55 / 5410	ICGC_Foxm1_targets
15	2e−02	54 / 5312	ICGC_Tcf12_targets

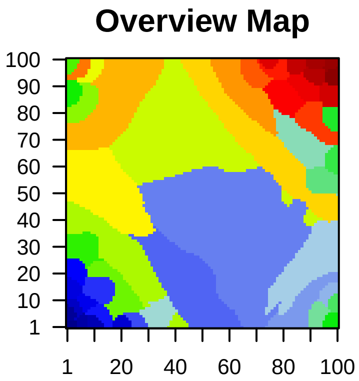
K−Means Cluster

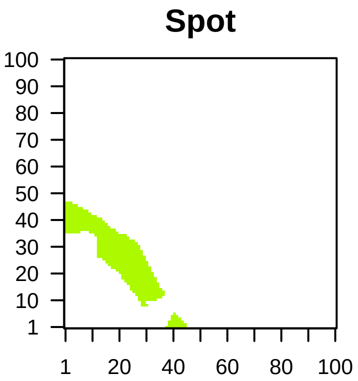
Spot Summary: R

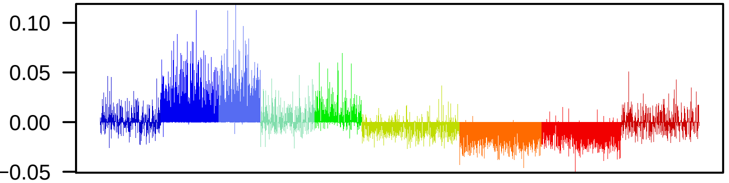
metagenes = 514
genes = 567

<r> metagenes = 0.91
<r> genes = 0.09
beta: r2= 1.25 / log p= −Inf

samples with spot = 3 (0.1 %)
A C * : 1 (0.3 %)
A C F * : 2 (0.9 %)





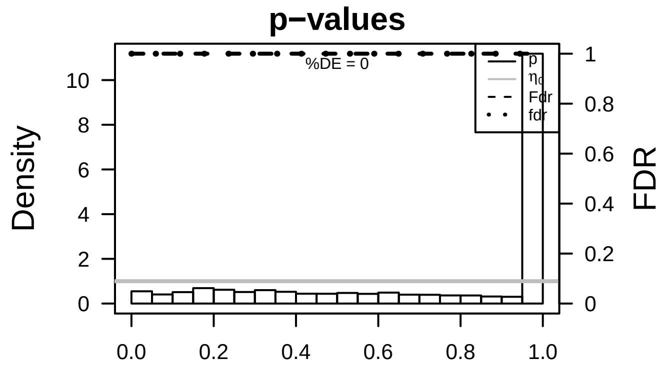


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_181075	1.74	−0.41	0.07	C4BPA	complement component 4 binding protein alpha [Source:HGN
2	ILMN_167170	1.06	−0.96	0.09	ACTA2	actin, alpha 2, smooth muscle, aorta [Source:HGNC Symbol;
3	ILMN_167105	0.95	−1.05	0.1		
4	ILMN_181313	0.73	−0.55	0.06	ANKDD1A	ankyrin repeat and death domain containing 1A [Source:HGN
5	ILMN_181019	0.69	−0.38	0.08	PLA2G4C	phospholipase A2 group IVC [Source:HGNC Symbol;Acc:HG
6	ILMN_221582	0.67	−0.39	0.08		
7	ILMN_178344	0.55	−0.29	0.2	ALOX15	arachidonate 15−lipoxygenase [Source:HGNC Symbol;Acc:H
8	ILMN_232533	0.47	−0.29	0.15	APOL2	apolipoprotein L2 [Source:HGNC Symbol;Acc:HGNC:619]
9	ILMN_211193	0.45	−0.25	0.18	SERINC2	serine incorporator 2 [Source:HGNC Symbol;Acc:HGNC:232
10	ILMN_166846	0.45	−0.22	0.27	PRTN3	proteinase 3 [Source:HGNC Symbol;Acc:HGNC:9495]
11	ILMN_178470	0.44	−0.27	0.24	MIR452	gamma−aminobutyric acid type A receptor epsilon subunit [S
12	ILMN_232781	0.44	−0.26	0.25	IL5RA	interleukin 5 receptor subunit alpha [Source:HGNC Symbol;A
13	ILMN_324031	0.43	−0.23	0.43	SCX	scleraxis bHLH transcription factor [Source:HGNC Symbol;Ac
14	ILMN_173143	0.42	−0.25	0.2	AOC1	amine oxidase, copper containing 1 [Source:HGNC Symbol;A
15	ILMN_324102	0.41	−0.24	0.2	RNY4	RNA, Ro−associated Y4 [Source:HGNC Symbol;Acc:HGNC:
16	ILMN_176126	0.41	−0.3	0.38	MPI	mannose phosphate isomerase [Source:HGNC Symbol;Acc:
17	ILMN_176128	0.41	−0.23	0.22		
18	ILMN_165285	0.41	−0.24	0.18	CHCHD7	coiled−coil−helix−coiled−coil−helix domain containing 7 [Sour
19	ILMN_170878	0.39	−0.33	0.24	MFAP3	microfibrillar associated protein 3 [Source:HGNC Symbol;Acc
20	ILMN_165780	0.39	−0.24	0.26	CFH	complement factor H [Source:HGNC Symbol;Acc:HGNC:488

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	3e−07	83 / 3068	Chror	8_EnhP_Fibroblasts
2	5e−06	86 / 3438	Chror	10_ReprPC_Melanocytes
3	6e−06	55 / 1895	Colon	EnhP_Colon
4	9e−06	101 / 4304	Chror	9_ReprPCWk_Melanocytes
5	6e−05	95 / 4169	Chror	10_ReprPC_Fibroblasts
6	1e−04	21 / 536	GSEA	MIKKELSEN_MEF_HCP_WITH_H3K27ME3
7	2e−04	75 / 3173	Colon	ReprPC_Colon
8	2e−04	65 / 2660	Chror	8_EnhP_Melanocytes
9	3e−04	80 / 3523	Chror	1_TssP_Melanocytes
10	4e−04	3 / 10	BP	hemidesmosome assembly
11	4e−04	3 / 10	GSEA	REACTOME_REGULATION_OF_COMPLEMENT_CASCADE
12	4e−04	3 / 10	GSEA	RADAEVA_RESPONSE_TO_IFNA1_DN
13	7e−04	67 / 2894	Colon	TssP_Colon
14	7e−04	14 / 325	GSEA	MEISSNER_NPC_HCP_WITH_H3K4ME2_AND_H3K27ME3
15	8e−04	4 / 27	BP	membrane depolarization during action potential
16	1e−03	7 / 102	BP	muscle contraction
17	1e−03	6 / 75	GSEA	REACTOME_CELL_JUNCTION_ORGANIZATION
18	1e−03	33 / 1206	Chror	6_EnhG_Neuronal_Progenitor
19	2e−03	87 / 4107	Chror	9_ReprPCWk_Fibroblasts
20	2e−03	17 / 478	Refer	WIRTH_Nervous System
21	2e−03	31 / 1119	Brain	Overlap_fetal_midbrain_TssA
22	2e−03	7 / 109	BP	regulation of ion transmembrane transport
23	2e−03	3 / 16	BP	eye photoreceptor cell development
24	2e−03	44 / 1789	Chror	8_EnhP_Neuronal_Progenitor
25	2e−03	14 / 366	Colon	K9K27me3_Colon
26	2e−03	213 / 11847	Chror	7_Enh_Neuronal_Progenitor
27	3e−03	19 / 589	GSEA	BENPORATH_CYCLING_GENES
28	3e−03	4 / 37	BP	lipoprotein metabolic process
29	3e−03	35 / 1360	Brain	Mid_Frontal_Lobe_TssP
30	3e−03	16 / 465	Brain	Mid_Frontal_Lobe_TxTrans
31	3e−03	3 / 19	BP	positive regulation of protein autophosphorylation
32	3e−03	3 / 19	BP	regulation of complement activation
33	3e−03	6 / 92	GSEA	LABBE_TGFB1_TARGETS_UP
34	3e−03	5 / 64	BP	memory
35	3e−03	4 / 40	MF	voltage−gated calcium channel activity
36	4e−03	2 / 6	miRN	hsa−miR−126
37	4e−03	2 / 6	GSEA	KASLER_HDAC7_TARGETS_2_UP
38	4e−03	3 / 20	GSEA	WANG_LSD1_TARGETS_UP
39	4e−03	58 / 2620	Chror	1_TssP_Neuronal_Progenitor
40	5e−03	60 / 2740	Colon	ReprPCWk_Colon



Aging

Rank	p−value	#in/all	Geneset
1	0.06	3 / 58	TESCHENDORFF_age_hypermethylated
2	0.65	2 / 142	HORVATH_aging_genes meth UP
3	0.83	1 / 111	HORVATH_aging_genes meth DOWN
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	4e−04	3 / 10	hemidesmosome assembly
2	8e−04	4 / 27	membrane depolarization during action potential
3	1e−03	7 / 102	muscle contraction
4	2e−03	7 / 109	regulation of ion transmembrane transport
5	2e−03	3 / 16	eye photoreceptor cell development
6	3e−03	4 / 37	lipoprotein metabolic process
7	3e−03	3 / 19	positive regulation of protein autophosphorylation
8	3e−03	3 / 19	regulation of complement activation
9	3e−03	5 / 64	memory
10	5e−03	3 / 22	positive regulation of cell cycle arrest
11	5e−03	8 / 167	protein homooligomerization
12	6e−03	4 / 47	phagocytosis
13	9e−03	3 / 28	neuronal action potential
14	1e−02	2 / 10	positive regulation of myelination
15	1e−02	2 / 11	gene silencing by miRNA

Brain

Rank	p−value	#in/all	Geneset
1	0.002	31 / 1119	Overlap_fetal_midbrain_TssA
2	0.003	35 / 1360	Mid_Frontal_Lobe_TssP
3	0.003	16 / 465	Mid_Frontal_Lobe_TxTrans
4	0.005	84 / 4112	Mid_Frontal_Lobe_ReprPC
5	0.009	11 / 304	Mid_Frontal_Lobe_TssA
6	0.010	35 / 1476	Overlap_fetal_midbrain_TxTrans
7	0.011	24 / 924	Mid_Frontal_Lobe_TssF
8	0.042	11 / 386	Fetal_ZNF
9	0.095	4 / 110	Overlap_fetal_midbrain_Tx
10	0.096	37 / 1893	Overlap_fetal_midbrain_TssF
11	0.110	23 / 1115	Overlap_fetal_midbrain_EnhG
12	0.143	174 / 10430	Overlap_fetal_midbrain_Quies
13	0.148	48 / 2630	Fetal_TssF
14	0.180	56 / 3164	Mid_Frontal_Lobe_ZNF
15	0.199	12 / 578	Fetal_Tx

Cancer

Rank	p−value	#in/all	Geneset
1	0.02	2 / 15	LIU_PROSTATE_CANCER_DN
2	0.05	4 / 91	PanCan_TXmisReg_geneset_nanostring
3	0.17	4 / 136	PanCan_RAS_geneset_nanostring
4	0.17	1 / 12	LIU_BREAST_CANCER
5	0.19	1 / 13	LIU_LIVER_CANCER
6	0.21	2 / 54	KUIPER_MM poor survival
7	0.21	1 / 15	WANG_ER_UP
8	0.22	1 / 16	BEN−PORATH_DN
9	0.27	1 / 20	PanCan_ChromMod_geneset_nanostring
10	0.42	3 / 150	PanCan_MAPK_geneset_nanostring
11	0.46	1 / 39	ZHANG_MM up
12	0.52	1 / 46	PanCan_DNARepair_geneset_nanostring
13	0.52	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
14	0.55	2 / 117	PanCan_Driver_Gene_geneset_nanostring
15	0.58	3 / 193	PanCan_PI3K_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	0.005	3 / 22	I band
2	0.007	14 / 423	cell junction
3	0.009	3 / 28	voltage−gated calcium channel complex
4	0.010	68 / 3291	integral component of membrane
5	0.014	3 / 32	photoreceptor connecting cilium
6	0.018	4 / 64	collagen trimer
7	0.019	7 / 171	postsynaptic density
8	0.020	2 / 14	contractile fiber
9	0.020	3 / 37	T−tubule
10	0.025	2 / 16	photoreceptor disc membrane
11	0.030	6 / 149	lamellipodium
12	0.042	2 / 21	excitatory synapse
13	0.048	3 / 52	microvillus
14	0.050	4 / 88	keratin filament
15	0.050	3 / 53	photoreceptor outer segment

Chr

Rank	p−value	#in/all	Geneset
1	0.04	9 / 289	Chr 21
2	0.08	20 / 902	Chr 4
3	0.23	15 / 768	Chr 14
4	0.29	26 / 1467	Chr 19
5	0.29	25 / 1411	Chr 11
6	0.32	26 / 1492	Chr 2
7	0.33	10 / 536	Chr 22
8	0.38	20 / 1170	Chr 7
9	0.38	11 / 619	Chr 20
10	0.39	17 / 994	Chr X
11	0.54	15 / 959	Chr 16
12	0.55	36 / 2323	Chr 1
13	0.62	5 / 342	Chr 18
14	0.66	12 / 836	Chr 8
15	0.72	17 / 1217	Chr 3

Chromatin states

Rank	p−value	#in/all	Geneset
1	3e−07	83 / 3068	8_EnhP_Fibroblasts
2	5e−06	86 / 3438	10_ReprPC_Melanocytes
3	9e−06	101 / 4304	9_ReprPCWk_Melanocytes
4	6e−05	95 / 4169	10_ReprPC_Fibroblasts
5	2e−04	65 / 2660	8_EnhP_Melanocytes
6	3e−04	80 / 3523	1_TssP_Melanocytes
7	1e−03	33 / 1206	6_EnhG_Neuronal_Progenitor
8	2e−03	87 / 4107	9_ReprPCWk_Fibroblasts
9	2e−03	44 / 1789	8_EnhP_Neuronal_Progenitor
10	2e−03	213 / 11847	7_Enh_Neuronal_Progenitor
11	4e−03	58 / 2620	1_TssP_Neuronal_Progenitor
12	5e−03	76 / 3639	1_TssP_Fibroblasts
13	7e−03	76 / 3691	9_ReprPCWk_Neuronal_Progenitor
14	2e−02	49 / 2297	10_ReprPC_Neuronal_Progenitor
15	3e−02	48 / 2315	13_HetRpts_Melanocytes

Colon Cancer

Rank	p−value	#in/all	Geneset
1	6e−06	55 / 1895	EnhP_Colon
2	2e−04	75 / 3173	ReprPC_Colon
3	7e−04	67 / 2894	TssP_Colon
4	2e−03	14 / 366	K9K27me3_Colon
5	5e−03	60 / 2740	ReprPCWk_Colon
6	8e−03	14 / 425	Lembcke_TCGA_meth_kmeans_E_CIMP.H_UP_
7	1e−02	191 / 10779	Enh_Colon
8	1e−02	59 / 2810	EnhA_Colon
9	2e−02	6 / 129	Marisa_CRC−cluster−b
10	6e−02	17 / 713	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
11	6e−02	164 / 9530	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP_
12	8e−02	25 / 1186	HetRpts_Colon
13	1e−01	10 / 398	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN
14	1e−01	94 / 5373	EnhWk1_Colon
15	1e−01	17 / 799	LaPointe_mucosa−position_kmeans_B_ascending colon_transverse colon_U

Glio

Rank	p−value	#in/all	Geneset
1	0.01	5 / 84	Weller_LGG_gradeII−vs−III_UP
2	0.04	2 / 19	KIM deleted & downregulated in LTS
3	0.05	3 / 52	OL vs. OPC
4	0.06	2 / 25	Barbus_GBM_STS_vs._LTS
5	0.06	4 / 93	Hopp_Sturm_GBM_Epi3_C2_adult_fetus_DN
6	0.06	3 / 58	in vivo astrocytes vs. cultured astroglia
7	0.07	2 / 28	KIM prognostic signature LTS vs. STS
8	0.08	2 / 29	Christensen_hypomethylated_in_grade3_astrocytoma
9	0.10	5 / 158	Hopp_Sturm_GBM_Epi3_D_adult_fetus_IDH_UP
10	0.10	2 / 35	Colman_survival_associated
11	0.12	3 / 76	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
12	0.12	1 / 8	Shaw_responders_up_in_oligo_glioma
13	0.12	1 / 8	Sturm_GBM_Meth_overexpression_C_G34_UP
14	0.13	1 / 9	oligodendrocytes_glio
15	0.13	1 / 9	Colman_survival_robust

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−04	21 / 536	MIKKELSEN_MEF_HCP_WITH_H3K27ME3
2	4e−04	3 / 10	REACTOME_REGULATION_OF_COMPLEMENT_CASCADE
3	4e−04	3 / 10	RADAEVA_RESPONSE_TO_IFNA1_DN
4	7e−04	14 / 325	MEISSNER_NPC_HCP_WITH_H3K4ME2_AND_H3K27ME3
5	1e−03	6 / 75	REACTOME_CELL_JUNCTION_ORGANIZATION
6	3e−03	19 / 589	BENPORATH_CYCLING_GENES
7	3e−03	6 / 92	LABBE_TGFB1_TARGETS_UP
8	4e−03	2 / 6	KASLER_HDAC7_TARGETS_2_UP
9	4e−03	3 / 20	WANG_LSD1_TARGETS_UP
10	5e−03	14 / 405	MIKKELSEN_MCV6_HCP_WITH_H3K27ME3
11	5e−03	3 / 23	REACTOME_COMPLEMENT_CASCADE
12	5e−03	5 / 72	HADDAD_T_LYMPHOCYTE_AND_NK_PROGENITOR_UP
13	6e−03	3 / 24	PID_INTEGRIN_A9B1_PATHWAY
14	7e−03	3 / 25	REACTOME_LIPOPROTEIN_METABOLISM
15	7e−03	3 / 25	MARCINIAK_ER_STRESS_RESPONSE_VIA_CHOP

HM

Rank	p−value	#in/all	Geneset
1	0.07	6 / 183	HALLMARK_GLYCOLYSIS
2	0.08	6 / 191	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
3	0.09	2 / 33	HALLMARK_ANGIOGENESIS
4	0.10	2 / 34	HALLMARK_HEDGEHOG_SIGNALING
5	0.11	4 / 116	HALLMARK_SPERMATOGENESIS
6	0.17	4 / 137	HALLMARK_UV_RESPONSE_UP
7	0.21	2 / 54	HALLMARK_MYC_TARGETS_V2
8	0.32	3 / 127	HALLMARK_COAGULATION
9	0.33	4 / 185	HALLMARK_P53_PATHWAY
10	0.44	1 / 37	HALLMARK_PANCREAS_BETA_CELLS
11	0.48	1 / 41	HALLMARK_APICAL_SURFACE
12	0.48	2 / 103	HALLMARK_BILE_ACID_METABOLISM
13	0.51	3 / 173	HALLMARK_E2F_TARGETS
14	0.53	3 / 177	HALLMARK_MITOTIC_SPINDLE
15	0.55	1 / 50	HALLMARK_TGF_BETA_SIGNALING

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.2	1 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
2	0.4	1 / 31	DUMEAUX_Fasting enriched genes
3	0.7	2 / 147	Homuth_BMI−associated−genes_UP
4	0.8	1 / 94	DUMEAUX_Smoking enriched genes
5	1.0	1 / 211	Homuth_BMI−associated−genes_DN
6	1.0	0 / 10	DUMEAUX_Smoking literature genes up
7	1.0	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
8	1.0	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
9	1.0	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
10	1.0	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
11	1.0	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
12	1.0	0 / 10	DUMEAUX_Women normal BMI literature genes up
13	1.0	0 / 17	DUMEAUX_High bmi enriched genes
14	1.0	0 / 18	Huan_blood−pressure_SBP−signature
15	1.0	0 / 16	Huan_blood−pressure_DBP−signature

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.007	5 / 77	Aukema_BCL2 DN_BCL6 UP
2	0.013	103 / 5384	HOPP_Repressed
3	0.038	58 / 2939	HOPP_Poised_promoter
4	0.042	2 / 21	ROSOLOWSKI_red UP
5	0.079	4 / 103	Hopp_June14_MMML937 tumors+controls_group.overexpression_MM_MM_
6	0.101	17 / 772	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell line_
7	0.104	3 / 72	Hopp_June14_MMML937 tumors+controls_group.overexpression_IM_mBL_
8	0.110	3 / 74	WIRTH_lymphoma937_spot IM
9	0.130	74 / 4167	HOPP_Heterochrom
10	0.160	3 / 88	ROSOLOWSKI_red total
11	0.164	7 / 286	ZHANG_DLBCL mutated
12	0.193	9 / 408	TARTE_Mature plasma cell signature
13	0.227	3 / 105	WIRTH_lymphoma937_spot MM
14	0.240	15 / 777	WIRTH_lymphoma937_spot D
15	0.286	9 / 455	SPANG_CD40 6hrs DN

Melanoma

Rank	p−value	#in/all	Geneset
1	0.2	2 / 54	Hugo_melanoma−all−MET_DN
2	0.4	1 / 30	Hugo_melanoma−all−MET_UP
3	0.5	1 / 43	Hugo_melanoma−BRAFmut−MET_UP
4	1.0	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
5	1.0	0 / 27	Hugo_melanoma−all−LEF1_UP
6	1.0	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

MF

Rank	p−value	#in/all	Geneset
1	0.003	4 / 40	voltage−gated calcium channel activity
2	0.008	8 / 182	signal transducer activity
3	0.010	2 / 10	high voltage−gated calcium channel activity
4	0.015	2 / 12	neurexin family protein binding
5	0.015	2 / 12	phospholipid transporter activity
6	0.015	8 / 204	protein domain specific binding
7	0.017	3 / 35	kinesin binding
8	0.021	3 / 38	cholesterol binding
9	0.022	2 / 15	platelet−derived growth factor receptor binding
10	0.023	3 / 39	androgen receptor binding
11	0.026	10 / 311	enzyme binding
12	0.028	5 / 108	Ras guanyl−nucleotide exchange factor activity
13	0.029	2 / 17	heparan sulfate proteoglycan binding
14	0.030	3 / 43	phosphatase binding
15	0.034	4 / 78	phospholipid binding

miRNA Disease

Rank	p−value	#in/all	Geneset
1	0.05	1 / 3	Down syndrome, risk of
2	0.48	1 / 41	Melanoma, cutaneous malignant, 2
3	0.53	1 / 48	Gastric cancer
4	0.63	1 / 63	Gastrointestinal
5	0.64	1 / 65	Hepatocellular carcinoma
6	0.65	2 / 142	Lung cancer
7	0.66	1 / 68	Glioblastoma multiforme, somatic
8	0.68	1 / 73	Stroke, susceptibility to
9	0.84	1 / 116	Cancer
10	0.85	1 / 120	Hematological
11	0.86	1 / 123	Pancreatic cancer
12	0.86	1 / 124	Prostate cancer
13	0.87	1 / 127	Squamous cell carcinoma, head and neck
14	0.92	1 / 156	Breast cancer
15	1.00	0 / 7	Thyroid carcinoma, papillary

miRNA target

Rank	p−value	#in/all	Geneset
1	0.004	2 / 6	hsa−miR−126
2	0.007	3 / 25	hsa−miR−943
3	0.015	6 / 126	hsa−miR−223
4	0.029	7 / 188	hsa−miR−548d−3p
5	0.030	3 / 43	hsa−miR−412
6	0.030	4 / 75	hsa−miR−184
7	0.030	4 / 75	hsa−miR−1305
8	0.037	3 / 47	hsa−miR−553
9	0.038	6 / 157	hsa−miR−141
10	0.039	3 / 48	hsa−miR−769−3p
11	0.042	5 / 121	hsa−miR−515−5p
12	0.042	2 / 21	hsa−miR−554
13	0.045	5 / 123	hsa−miR−145
14	0.046	3 / 51	hsa−miR−628−5p
15	0.053	7 / 215	hsa−miR−199a−3p

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.2	1 / 14	BENTINK_ras.6
2	1.0	0 / 14	GUSTAFSON_PI3K_UP
3	1.0	0 / 15	GUSTAFSON_PI3K_DN
4	1.0	0 / 13	BENTINK_e2f3.1
5	1.0	0 / 13	BENTINK_e2f3.2
6	1.0	0 / 13	BENTINK_myc.1
7	1.0	0 / 12	BENTINK_ras.1
8	1.0	0 / 11	BENTINK_ras.4
9	1.0	0 / 13	BENTINK_src.10
10	1.0	0 / 12	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Reference Signatures

Rank	p−value	#in/all	Geneset
1	0.002	17 / 478	WIRTH_Nervous System
2	0.028	3 / 42	VAQUERIZAS_Fetal brain_TF
3	0.041	3 / 49	JONGENEEL_Retina
4	0.079	3 / 64	VAQUERIZAS_Lung_TF
5	0.090	1 / 6	JONGENEEL_SpinalCord
6	0.119	1 / 8	VAQUERIZAS_Tongue_TF
7	0.119	1 / 8	JONGENEEL_Fetal Brain
8	0.135	2 / 41	VAQUERIZAS_Thymus_TF
9	0.146	1 / 10	VAQUERIZAS_Skeletal muscle_TF
10	0.160	1 / 11	WIRTH_Tonsil
11	0.186	1 / 13	WIRTH_Thymus
12	0.186	1 / 13	JONGENEEL_Thyroid
13	0.186	1 / 13	JONGENEEL_Uterus
14	0.198	1 / 14	WIRTH_Thyroid gland
15	0.211	1 / 15	VAQUERIZAS_Fetal liver_TF

Telomeres

Rank	p−value	#in/all	Geneset
1	0.02	2 / 13	Alternative lengthening of telomeres
2	1.00	0 / 27	Nabetani_alt len telomeres_genes_ko
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	0.07	17 / 733	ICGC_Atf3_targets
2	0.12	34 / 1753	HEBENSTREIT_low expression TF
3	0.28	37 / 2133	ICGC_Mef2_targets
4	0.34	13 / 721	ICGC_SrfPcr2_targets
5	0.36	25 / 1466	ICGC_NrsfPcr1_targets
6	0.39	13 / 747	ICGC_NrsfPcr2_targets
7	0.40	41 / 2497	ICGC_Bcl11_targets
8	0.40	11 / 631	ICGC_RxraPcr1_targets
9	0.46	56 / 3507	ICGC_Rad21_targets
10	0.47	44 / 2759	ICGC_Bcl3_targets
11	0.53	50 / 3194	ICGC_Irf4_targets
12	0.57	98 / 6322	ICGC_Tcf3_targets
13	0.58	69 / 4468	ICGC_Egr1_targets
14	0.61	26 / 1723	HEBENSTREIT_high expression TF
15	0.67	50 / 3348	ICGC_BatfPcr1_targets

K−Means Cluster

Spot Summary: S

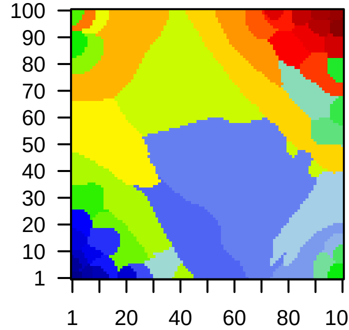
metagenes = 663
genes = 1156

<r> metagenes = 0.83

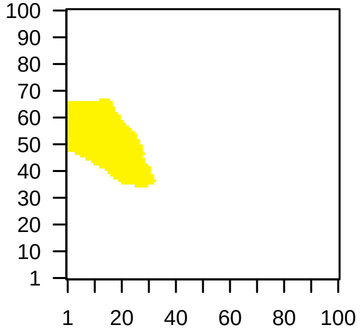
beta: r2= 0.26 / log p= −Inf

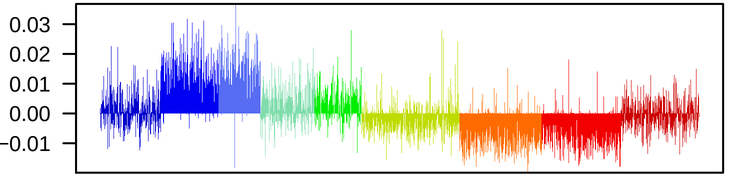
samples with spot = 0 (0 %)

Overview Map



Spot





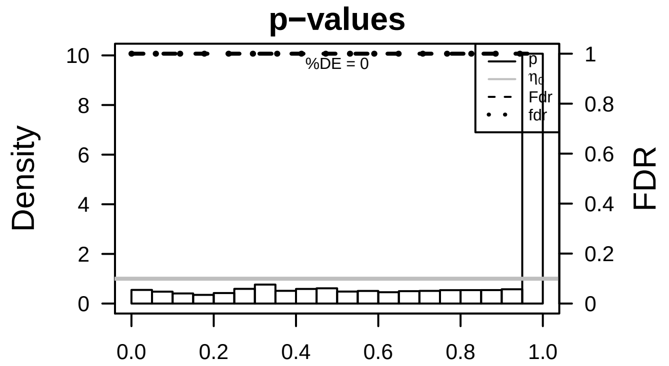
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_169884	0.41	−0.23	0.16	SLC8A2	solute carrier family 8 member A2 [Source:HGNC Symbol;Ac
2	ILMN_166264	0.36	−0.31	0.19		metallothionein 1 pseudogene 3 [Source:HGNC Symbol;Acc:
3	ILMN_320086	0.34	−0.24	0.21	GSE1	Gse1 coiled−coil protein [Source:HGNC Symbol;Acc:HGNC:
4	ILMN_168085	0.34	−0.33	0.14		
5	ILMN_212874	0.34	−0.28	0.2	RDH11	retinol dehydrogenase 11 (all−trans/9−cis/11−cis) [Source:HG
6	ILMN_174325	0.34	−0.24	0.23		
7	ILMN_232857	0.32	−0.21	0.23	CLDN14	claudin 14 [Source:HGNC Symbol;Acc:HGNC:2035]
8	ILMN_324582	0.31	−0.22	0.19		
9	ILMN_187888	0.31	−0.2	0.21		
10	ILMN_324643	0.31	−0.19	0.12		
11	ILMN_177832	0.31	−0.23	0.16	SIMC1	SUMO interacting motifs containing 1 [Source:HGNC Symbol
12	ILMN_168103	0.3	−0.23	0.2		
13	ILMN_324957	0.3	−0.22	0.28	CHRNB4	cholinergic receptor nicotinic beta 4 subunit [Source:HGNC S
14	ILMN_179164	0.3	−0.24	0.12	ZNF468	zinc finger protein 468 [Source:HGNC Symbol;Acc:HGNC:33
15	ILMN_168043	0.29	−0.22	0.07	MAPK8IP1	mitogen−activated protein kinase 8 interacting protein 1 [Sour
16	ILMN_226900	0.29	−0.2	0.16		
17	ILMN_168841	0.29	−0.3	0.16	SNW1	SNW domain containing 1 [Source:HGNC Symbol;Acc:HGNC
18	ILMN_179680	0.29	−0.2	0.12	ABCA8	ATP binding cassette subfamily A member 8 [Source:HGNC
19	ILMN_167015	0.29	−0.18	0.12	FAM83A	family with sequence similarity 83 member A [Source:HGNC
20	ILMN_184265	0.29	−0.17	0.19		

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−14	164 / 3068	Chror	8_EnhP_Fibroblasts
2	8e−13	146 / 2740	Colon	ReprPCWk_Colon
3	1e−12	198 / 4169	Chror	10_ReprPC_Fibroblasts
4	7e−12	193 / 4107	Chror	9_ReprPCWk_Fibroblasts
5	2e−11	158 / 3173	Colon	ReprPC_Colon
6	6e−11	173 / 3639	Chror	1_TssP_Fibroblasts
7	1e−10	232 / 5384	Lympl	HOPP_Repressed
8	4e−10	193 / 4304	Chror	9_ReprPCWk_Melanocytes
9	1e−08	157 / 3438	Chror	10_ReprPC_Melanocytes
10	2e−08	99 / 1895	Colon	EnhP_Colon
11	2e−07	124 / 2660	Chror	8_EnhP_Melanocytes
12	7e−07	152 / 3523	Chror	1_TssP_Melanocytes
13	9e−07	93 / 1893	Brain	Overlap_fetal_midbrain_TssF
14	5e−06	126 / 2894	Colon	TssP_Colon
15	2e−05	110 / 2516	Chror	11_K9K27me3_Melanocytes
16	4e−05	112 / 2620	Chror	1_TssP_Neuronal_Progenitor
17	5e−05	81 / 1753	TF	HEBENSTREIT_low expression TF
18	5e−05	82 / 1789	Chror	8_EnhP_Neuronal_Progenitor
19	7e−05	122 / 2939	Lympl	HOPP_Poised_promoter
20	8e−05	147 / 3691	Chror	9_ReprPCWk_Neuronal_Progenitor
21	1e−04	56 / 1119	Brain	Overlap_fetal_midbrain_TssA
22	1e−04	98 / 2297	Chror	10_ReprPC_Neuronal_Progenitor
23	2e−04	68 / 1476	Brain	Overlap_fetal_midbrain_TxTrans
24	3e−04	122 / 3046	Brain	Fetal_TssA
25	4e−04	61 / 1324	Chror	13_HetRpts_Fibroblasts
26	4e−04	119 / 2988	Glio	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
27	1e−03	11 / 122	GSEA	REACTOME_NEUROTRANSMITTER_RECEPTOR_BINDING_AND_DOW
28	1e−03	4 / 16	MF	cGMP binding
29	1e−03	107 / 2700	Brain	Fetal_TxTrans
30	1e−03	7 / 55	BP	response to stimulus
31	1e−03	4 / 17	Refer	JONGENEEL_Pancreas
32	1e−03	27 / 484	Colon	Quies2_Colon
33	1e−03	22 / 366	Colon	K9K27me3_Colon
34	2e−03	321 / 9530	Colon	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP
35	2e−03	12 / 148	Glio	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up_(MES&CL down)
36	2e−03	7 / 58	BP	protein localization to plasma membrane
37	2e−03	17 / 256	GSEA	KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERACTION
38	2e−03	152 / 4112	Brain	Mid_Frontal_Lobe_ReprPC
39	2e−03	12 / 150	Cance	PanCan_MAPK_geneset_nanostring
40	3e−03	5 / 33	MF	ligand−gated ion channel activity

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.2	3 / 58	TESCHENDORFF_age_hypermethylated
2	0.9	2 / 142	HORVATH_aging_genes meth UP
3	1.0	0 / 111	HORVATH_aging_genes meth DOWN
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Cancer

Rank	p−value	#in/all	Geneset
1	0.002	12 / 150	PanCan_MAPK_geneset_nanostring
2	0.007	10 / 136	PanCan_RAS_geneset_nanostring
3	0.026	1 / 12	LIU_BREAST_CANCER
4	0.063	10 / 193	PanCan_PI3K_geneset_nanostring
5	0.201	2 / 28	PanCan_HH_geneset_nanostring
6	0.215	3 / 54	KUIPER_MM poor survival
7	0.237	1 / 9	GENTLES_modul3
8	0.324	1 / 13	WANG_ER_DN
9	0.334	0 / 15	LIU_PROSTATE_CANCER_DN
10	0.344	1 / 14	GENTLES_modul13
11	0.364	1 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
12	0.364	1 / 15	WANG_ER_UP
13	0.382	1 / 16	GENTLES_modul11
14	0.382	1 / 16	GENTLES_modul14
15	0.382	1 / 16	GENTLES_modul16

Chromatin states

Rank	p−value	#in/all	Geneset
1	1e−14	164 / 3068	8_EnhP_Fibroblasts
2	1e−12	198 / 4169	10_ReprPC_Fibroblasts
3	7e−12	193 / 4107	9_ReprPCWk_Fibroblasts
4	6e−11	173 / 3639	1_TssP_Fibroblasts
5	4e−10	193 / 4304	9_ReprPCWk_Melanocytes
6	1e−08	157 / 3438	10_ReprPC_Melanocytes
7	2e−07	124 / 2660	8_EnhP_Melanocytes
8	7e−07	152 / 3523	1_TssP_Melanocytes
9	2e−05	110 / 2516	11_K9K27me3_Melanocytes
10	4e−05	112 / 2620	1_TssP_Neuronal_Progenitor
11	5e−05	82 / 1789	8_EnhP_Neuronal_Progenitor
12	8e−05	147 / 3691	9_ReprPCWk_Neuronal_Progenitor
13	1e−04	98 / 2297	10_ReprPC_Neuronal_Progenitor
14	4e−04	61 / 1324	13_HetRpts_Fibroblasts
15	9e−03	33 / 717	11_K9K27me3_Fibroblasts

GSEA C2

Rank	p−value	#in/all	Geneset
1	0.001	11 / 122	REACTOME_NEUROTRANSMITTER_RECEPTOR_BINDING_AND_DOWNS
2	0.002	17 / 256	KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERACTION
3	0.004	8 / 85	KEGG_DILATED_CARDIOMYOPATHY
4	0.005	3 / 12	REACTOME_PRESYNAPTIC_NICOTINIC_ACETYLCHOLINE_RECEPTORS
5	0.005	11 / 149	ASTON_MAJOR_DEPRESSIVE_DISORDER_DN
6	0.006	6 / 55	MEISSNER_BRAIN_HCP_WITH_H3K4ME2_AND_H3K27ME3
7	0.006	3 / 13	REACTOME_ACETYLCHOLINE_BINDING_AND_DOWNSTREAM_EVENTS
8	0.006	3 / 13	INAMURA_LUNG_CANCER_SCC_DN
9	0.006	5 / 40	ULE_SPLICING_VIA_NOVA2
10	0.007	16 / 271	SMID_BREAST_CANCER_RELAPSE_IN_BONE_DN
11	0.008	10 / 137	RODRIGUES_NTN1_TARGETS_DN
12	0.008	7 / 77	KEGG_HYPERTROPHIC_CARDIOMYOPATHY_HCM
13	0.009	15 / 252	REACTOME_NEURONAL_SYSTEM
14	0.009	45 / 1050	PEREZ_TP53_TARGETS
15	0.009	3 / 15	MURAKAMI_UV_RESPONSE_1HR_UP

Lymphoma

Rank	p−value	#in/all	Geneset
1	1e−10	232 / 5384	HOPP_Repressed
2	7e−05	122 / 2939	HOPP_Poised_promoter
3	2e−02	9 / 139	Hopp_June14_MMML937 tumors+controls_group.overexpression_F_FL_tons
4	2e−02	9 / 141	WIRTH_lymphoma937_spot F
5	4e−02	2 / 11	Subero_MM_hypo_meth
6	4e−02	95 / 2701	HOPP_Repetitive
7	6e−02	2 / 13	Subero_B−CLL_hypo_meth
8	6e−02	140 / 4167	HOPP_Heterochrom
9	1e−01	5 / 89	Subero_T−ALL_hyper_meth
10	1e−01	3 / 45	Subero_INT_hypo_meth
11	2e−01	10 / 232	WIRTH_lymphoma937_spot B
12	2e−01	4 / 70	Hopp_Lymphoma_Epi1_no_zentr_3_B.cell_DN
13	2e−01	3 / 46	Subero_DLBCL_hypo_meth
14	2e−01	4 / 74	WIRTH_lymphoma937_spot IM
15	2e−01	17 / 450	Hopp_June14_MMML937 tumors+controls_group.overexpression_I_MM_GC-

miRNA Disease

Rank	p−value	#in/all	Geneset
1	0.06	1 / 2	Burkitt lymphoma
2	0.10	2 / 18	Hodgkin lymphoma
3	0.11	1 / 4	Nasopharyngeal carcinoma
4	0.16	3 / 47	Cervical cancer, somatic
5	0.19	2 / 27	Duchenne muscular dystrophy
6	0.20	2 / 28	Immunological
7	0.24	5 / 113	Ovarian cancer
8	0.30	5 / 123	Pancreatic cancer
9	0.32	5 / 127	Melanoma and neural system tumor syndrome
10	0.32	5 / 127	Squamous cell carcinoma, head and neck
11	0.33	2 / 40	Medulloblastoma
12	0.36	4 / 102	Leukemia
13	0.41	5 / 142	Lung cancer
14	0.42	1 / 18	Non−Hodgkin lymphoma, somatic
15	0.45	4 / 116	Cancer

Reference Signatures

Rank	p−value	#in/all	Geneset
1	0.001	4 / 17	JONGENEEL_Pancreas
2	0.003	6 / 48	WIRTH_Pancreas
3	0.005	6 / 53	JONGENEEL_Kidney
4	0.005	25 / 478	WIRTH_Nervous System
5	0.012	2 / 6	WIRTH_Pituitary gland
6	0.034	2 / 10	JONGENEEL_Pituitary Gland
7	0.050	14 / 289	JONGENEEL_Testis
8	0.061	4 / 50	WIRTH_Placenta
9	0.075	5 / 76	WIRTH_Homeostasis
10	0.148	2 / 23	JONGENEEL_Heart
11	0.208	9 / 220	WIRTH_Testis
12	0.212	5 / 107	WIRTH_Liver
13	0.249	9 / 231	Chaussabel_2,5_Immune related molecules
14	0.303	1 / 12	VAQUERIZAS_Kidney_TF
15	0.323	2 / 39	VAQUERIZAS_Testis_TF

BP

Rank	p−value	#in/all	Geneset
1	0.001	7 / 55	response to stimulus
2	0.002	7 / 58	protein localization to plasma membrane
3	0.004	5 / 36	lactation
4	0.004	9 / 106	calcium ion transmembrane transport
5	0.004	4 / 23	positive regulation of protein targeting to membrane
6	0.005	3 / 12	regulation of smooth muscle contraction
7	0.006	4 / 25	membrane depolarization
8	0.007	5 / 41	positive regulation of cell division
9	0.007	3 / 14	regulation of neurotransmitter secretion
10	0.008	6 / 59	protein localization
11	0.009	6 / 60	learning
12	0.009	6 / 60	positive regulation of epithelial cell proliferation
13	0.011	3 / 16	positive regulation of cartilage development
14	0.011	3 / 16	regulation of alpha−amino−3−hydroxy−5−methyl−4−isoxazole propionate sele
15	0.011	7 / 82	positive regulation of MAPK cascade

CC

Rank	p−value	#in/all	Geneset
1	0.003	8 / 83	voltage−gated potassium channel complex
2	0.006	13 / 196	postsynaptic membrane
3	0.006	3 / 13	node of Ranvier
4	0.010	15 / 256	apical plasma membrane
5	0.010	5 / 45	brush border membrane
6	0.013	3 / 17	neuronal cell body membrane
7	0.024	24 / 524	intracellular
8	0.028	49 / 1249	extracellular region
9	0.034	2 / 10	low−density lipoprotein particle
10	0.035	7 / 104	bicellular tight junction
11	0.048	2 / 12	membrane−bounded vesicle
12	0.049	3 / 28	AMPA glutamate receptor complex
13	0.049	3 / 28	voltage−gated calcium channel complex
14	0.054	22 / 512	cell surface
15	0.056	13 / 267	proteinaceous extracellular matrix

Colon Cancer

Rank	p−value	#in/all	Geneset
1	8e−13	146 / 2740	ReprPCWk_Colon
2	2e−11	158 / 3173	ReprPC_Colon
3	2e−08	99 / 1895	EnhP_Colon
4	5e−06	126 / 2894	TssP_Colon
5	1e−03	27 / 484	Quies2_Colon
6	1e−03	22 / 366	K9K27me3_Colon
7	2e−03	321 / 9530	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP_
8	3e−03	30 / 594	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
9	3e−02	2 / 9	Marisa_CRC−C5
10	5e−02	136 / 4018	EnhWk2_Colon
11	5e−02	21 / 479	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_
12	5e−02	18 / 398	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN
13	6e−02	151 / 4526	Quies1_Colon
14	9e−02	6 / 103	Marisa_CRC−cluster−d
15	9e−02	26 / 663	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN

HM

Rank	p−value	#in/all	Geneset
1	0.05	10 / 183	HALLMARK_APICAL_JUNCTION
2	0.11	9 / 189	HALLMARK_HYPOXIA
3	0.12	3 / 41	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
4	0.19	8 / 186	HALLMARK_IL2_STAT5_SIGNALING
5	0.20	6 / 132	HALLMARK_UV_RESPONSE_DN
6	0.27	2 / 34	HALLMARK_HEDGEHOG_SIGNALING
7	0.32	5 / 127	HALLMARK_COAGULATION
8	0.37	4 / 103	HALLMARK_BILE_ACID_METABOLISM
9	0.43	6 / 177	HALLMARK_KRAS_SIGNALING_DN
10	0.48	6 / 186	HALLMARK_MYOGENESIS
11	0.50	6 / 191	HALLMARK_INFLAMMATORY_RESPONSE
12	0.51	3 / 91	HALLMARK_PEROXISOME
13	0.63	1 / 33	HALLMARK_ANGIOGENESIS
14	0.66	4 / 151	HALLMARK_APOPTOSIS
15	0.67	1 / 37	HALLMARK_PANCREAS_BETA_CELLS

Melanoma

Rank	p−value	#in/all	Geneset
1	0.2	3 / 54	Hugo_melanoma−all−MET_DN
2	0.2	1 / 9	Hugo_melanoma−BRAFmut−MET_DN
3	0.7	1 / 43	Hugo_melanoma−BRAFmut−MET_UP
4	1.0	0 / 30	Hugo_melanoma−all−MET_UP
5	1.0	0 / 27	Hugo_melanoma−all−LEF1_UP
6	1.0	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

miRNA target

Rank	p−value	#in/all	Geneset
1	0.08	2 / 16	hsa−miR−551a
2	0.11	3 / 39	hsa−miR−501−3p
3	0.11	3 / 40	hsa−miR−518b
4	0.12	4 / 64	hsa−miR−1826
5	0.17	1 / 6	hsa−miR−126
6	0.22	3 / 54	hsa−miR−513a−5p
7	0.25	2 / 32	hsa−miR−1229
8	0.28	1 / 11	hsa−miR−487b
9	0.28	1 / 11	hsa−miR−369−5p
10	0.32	5 / 126	hsa−miR−223
11	0.33	2 / 40	hsa−miR−502−3p
12	0.34	1 / 14	hsa−miR−551b
13	0.35	4 / 101	hsa−miR−210
14	0.38	2 / 44	hsa−miR−636
15	0.38	3 / 74	hsa−miR−657

Telomeres

Rank	p−value	#in/all	Geneset
1	1	0 / 13	Alternative lengthening of telomeres
2	1	0 / 27	Nabetani_alt len telomeres_genes_ko
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Brain

Rank	p−value	#in/all	Geneset
1	9e−07	93 / 1893	Overlap_fetal_midbrain_TssF
2	1e−04	56 / 1119	Overlap_fetal_midbrain_TssA
3	2e−04	68 / 1476	Overlap_fetal_midbrain_TxTrans
4	3e−04	122 / 3046	Fetal_TssA
5	1e−03	107 / 2700	Fetal_TxTrans
6	2e−03	152 / 4112	Mid_Frontal_Lobe_ReprPC
7	4e−03	58 / 1360	Mid_Frontal_Lobe_TssP
8	4e−03	101 / 2630	Fetal_TssF
9	5e−03	9 / 110	Overlap_fetal_midbrain_Tx
10	8e−03	51 / 1213	Fetal_TssP
11	3e−02	41 / 1012	Mid_Frontal_Lobe_Enh
12	3e−02	36 / 869	Mid_Frontal_Lobe_EnhG
13	4e−02	21 / 465	Mid_Frontal_Lobe_TxTrans
14	4e−02	15 / 304	Mid_Frontal_Lobe_TssA
15	4e−02	25 / 578	Fetal_Tx

Chr

Rank	p−value	#in/all	Geneset
1	0.009	43 / 994	Chr X
2	0.115	35 / 954	Chr 9
3	0.134	51 / 1467	Chr 19
4	0.153	41 / 1170	Chr 7
5	0.182	45 / 1318	Chr 17
6	0.280	28 / 836	Chr 8
7	0.317	12 / 342	Chr 18
8	0.328	18 / 536	Chr 22
9	0.358	29 / 904	Chr 10
10	0.426	24 / 768	Chr 14
11	0.430	28 / 902	Chr 4
12	0.488	9 / 289	Chr 21
13	0.568	18 / 619	Chr 20
14	0.616	67 / 2323	Chr 1
15	0.632	30 / 1060	Chr 5

Glio

Rank	p−value	#in/all	Geneset
1	4e−04	119 / 2988	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
2	2e−03	12 / 148	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up_(MES&CL down)
3	1e−02	12 / 193	Hopp_Sturm_GBM_Epi3_F_RTK II_UP_adult_fetus_K27_DN
4	2e−02	23 / 487	Hopp_Sturm_GBM_Epi3_B_adult_UP_G34_DN
5	2e−02	3 / 20	Mukasa_UP_in_Oligodendroglioma_with_1pLOH
6	2e−02	7 / 95	Weller_LGG_1p19qDel−vs−intact_UP
7	3e−02	5 / 57	OL vs. MOG− OL
8	3e−02	20 / 428	Hopp_Sturm_GBM_Epi3_no_zentr_4_IDH_UP_adult_fetus_K27_DN
9	5e−02	2 / 12	WILLSCHER_GBM_LTSmut_proteomics−B_UP
10	7e−02	4 / 52	Sturm_GBM_Meth_overexpression_F_IDH_UP
11	8e−02	17 / 393	Hopp_Sturm_GBM_Epi3_no_zentr_3_RTK II_UP_adult_fetus_K27_DN
12	8e−02	3 / 35	WIRTH_PN subtype
13	9e−02	6 / 104	WIRTH_Normal Brain
14	9e−02	13 / 290	Hopp_Sturm_GBM_Epi3_C_IDH_UP
15	1e−01	5 / 84	GIEZELT_GBM_WT_down_VS_mut

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.1	5 / 94	DUMEAUX_Smoking enriched genes
2	0.2	1 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
3	0.2	1 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
4	0.6	1 / 31	DUMEAUX_Fasting enriched genes
5	0.6	1 / 32	Marjolein_ageing−genes_DN
6	1.0	1 / 147	Homuth_BMI−associated−genes_UP
7	1.0	0 / 10	DUMEAUX_Smoking literature genes up
8	1.0	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
9	1.0	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
10	1.0	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
11	1.0	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
12	1.0	0 / 10	DUMEAUX_Women normal BMI literature genes up
13	1.0	0 / 17	DUMEAUX_High bmi enriched genes
14	1.0	0 / 211	Homuth_BMI−associated−genes_DN
15	1.0	0 / 18	Huan_blood−pressure_SBP−signature

MF

Rank	p−value	#in/all	Geneset
1	0.001	4 / 16	cGMP binding
2	0.003	5 / 33	ligand−gated ion channel activity
3	0.003	4 / 21	acetylcholine−activated cation−selective channel activity
4	0.003	4 / 21	acetylcholine receptor activity
5	0.006	5 / 40	voltage−gated calcium channel activity
6	0.007	3 / 14	3',5'−cyclic−GMP phosphodiesterase activity
7	0.007	3 / 14	5'−nucleotidase activity
8	0.008	4 / 27	peptide hormone binding
9	0.008	7 / 77	PDZ domain binding
10	0.009	7 / 79	hormone activity
11	0.009	3 / 15	structural constituent of eye lens
12	0.011	10 / 145	growth factor activity
13	0.015	3 / 18	extracellular−glutamate−gated ion channel activity
14	0.018	3 / 19	acetylcholine binding
15	0.019	4 / 35	kinesin binding

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.3	1 / 13	BENTINK_src.10
2	0.3	1 / 14	BENTINK_ras.6
3	1.0	0 / 14	GUSTAFSON_PI3K_UP
4	1.0	0 / 15	GUSTAFSON_PI3K_DN
5	1.0	0 / 13	BENTINK_e2f3.1
6	1.0	0 / 13	BENTINK_e2f3.2
7	1.0	0 / 13	BENTINK_myc.1
8	1.0	0 / 12	BENTINK_ras.1
9	1.0	0 / 11	BENTINK_ras.4
10	1.0	0 / 12	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	5e−05	81 / 1753	HEBENSTREIT_low expression TF
2	6e−02	30 / 747	ICGC_NrsfPcr2_targets
3	2e−01	111 / 3507	ICGC_Rad21_targets
4	3e−01	48 / 1466	ICGC_NrsfPcr1_targets
5	5e−01	50 / 1669	ICGC_P300_targets
6	7e−01	71 / 2497	ICGC_Bcl11_targets
7	7e−01	20 / 733	ICGC_Atf3_targets
8	8e−01	88 / 3194	ICGC_Irf4_targets
9	8e−01	39 / 1501	ICGC_Usf1_targets
10	9e−01	72 / 2704	ICGC_Pbx3_targets
11	9e−01	181 / 6616	ICGC_Pax5_targets
12	9e−01	70 / 2759	ICGC_Bcl3_targets
13	9e−01	13 / 631	ICGC_RxraPcr1_targets
14	9e−01	86 / 3348	ICGC_BatfPcr1_targets
15	9e−01	170 / 6322	ICGC_Tcf3_targets

K−Means Cluster

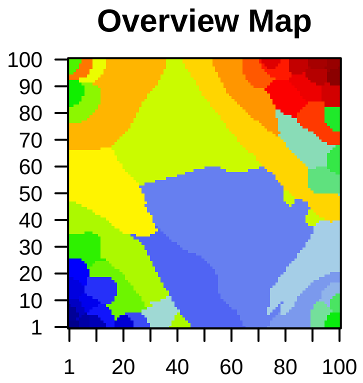
Spot Summary: T

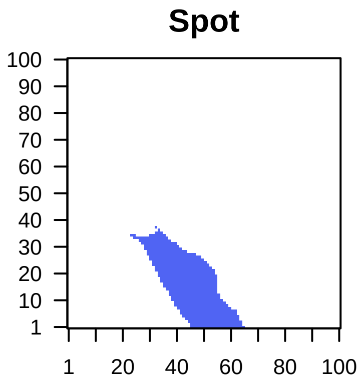
metagenes = 653
genes = 3528

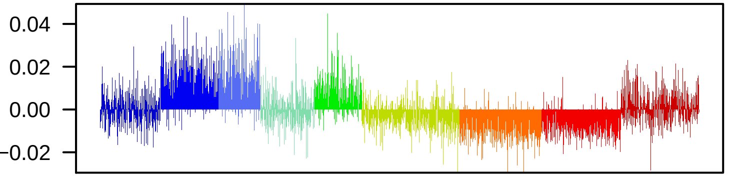
<r> metagenes = 0.79

beta: r2= 0.41 / log p= −Inf

samples with spot = 0 (0 %)





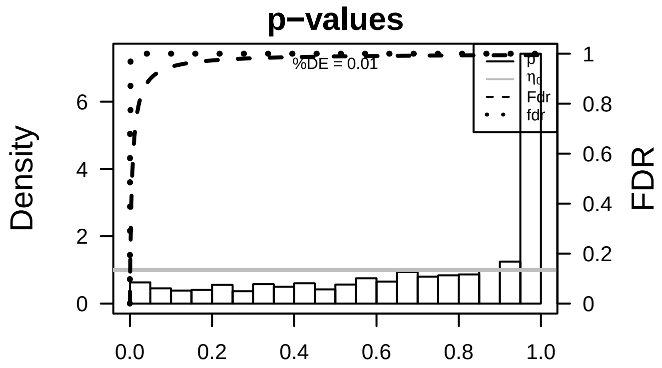


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_212539	1.08	−0.27	0.08	ADGRG7	adhesion G protein−coupled receptor G7 [Source:HGNC Sym
2	ILMN_180807	0.62	−0.27	0.07	ADGRG7	adhesion G protein−coupled receptor G7 [Source:HGNC Sym
3	ILMN_178963	0.59	−0.29	0.21	FMOD	fibromodulin [Source:HGNC Symbol;Acc:HGNC:3774]
4	ILMN_320963	0.56	−0.4	0.09		ribosomal protein L23a pseudogene 49 [Source:HGNC Symb
5	ILMN_321489	0.55	−0.42	0.3		
6	ILMN_175903	0.48	−0.35	0.03	MAP4K5	mitogen−activated protein kinase kinase kinase kinase 5 [Sou
7	ILMN_180882	0.47	−0.2	0.08	NEBL	nebulette [Source:HGNC Symbol;Acc:HGNC:16932]
8	ILMN_184313	0.43	−0.19	0.19		
9	ILMN_169156	0.43	−0.23	0.12		
10	ILMN_241552	0.42	−0.3	0.13		
11	ILMN_165165	0.41	−0.19	0.16	ADAM33	ADAM metallopeptidase domain 33 [Source:HGNC Symbol;A
12	ILMN_175106	0.41	−0.25	0.2	LOC105369277	chromosome 16 open reading frame 54 [Source:HGNC Symb
13	ILMN_165272	0.4	−0.31	0.27	C14orf2	chromosome 14 open reading frame 2 [Source:HGNC Symbo
14	ILMN_183849	0.4	−0.26	0.14		
15	ILMN_166097	0.39	−0.22	0.14	GAD1	glutamate decarboxylase 1 [Source:HGNC Symbol;Acc:HGN
16	ILMN_170810	0.38	−0.25	0.29	EZH2	enhancer of zeste 2 polycomb repressive complex 2 subunit [
17	ILMN_173708	0.38	−0.25	0.23	CAPN5	calpain 5 [Source:HGNC Symbol;Acc:HGNC:1482]
18	ILMN_233658	0.38	−0.2	0.13		
19	ILMN_167317	0.37	−0.3	0.16		
20	ILMN_174941	0.37	−0.39	0.19	PKP4	plakophilin 4 [Source:HGNC Symbol;Acc:HGNC:9026]

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−28	680 / 5384	Lympl	HOPP_Repressed
2	2e−21	542 / 4304	Chror	9_ReprPCWk_Melanocytes
3	4e−18	439 / 3438	Chror	10_ReprPC_Melanocytes
4	3e−17	503 / 4107	Chror	9_ReprPCWk_Fibroblasts
5	3e−17	509 / 4169	Chror	10_ReprPC_Fibroblasts
6	5e−15	345 / 2660	Chror	8_EnhP_Melanocytes
7	5e−13	388 / 3173	Colon	ReprPC_Colon
8	4e−12	373 / 3068	Chror	8_EnhP_Fibroblasts
9	5e−12	355 / 2894	Colon	TssP_Colon
10	8e−12	338 / 2740	Colon	ReprPCWk_Colon
11	2e−11	414 / 3523	Chror	1_TssP_Melanocytes
12	4e−11	312 / 2516	Chror	11_K9K27me3_Melanocytes
13	2e−10	420 / 3639	Chror	1_TssP_Fibroblasts
14	4e−10	349 / 2939	Lympl	HOPP_Poised_promoter
15	1e−09	240 / 1893	Brain	Overlap_fetal_midbrain_TssF
16	3e−09	280 / 2297	Chror	10_ReprPC_Neuronal_Progenitor
17	4e−09	281 / 2315	Chror	13_HetRpts_Melanocytes
18	6e−09	222 / 1753	TF	HEBENSTREIT_low expression TF
19	1e−08	192 / 1476	Brain	Overlap_fetal_midbrain_TxTrans
20	4e−08	410 / 3691	Chror	9_ReprPCWk_Neuronal_Progenitor
21	2e−07	131 / 962	GSEA	BENPORATH_EED_TARGETS
22	2e−07	115 / 819	Brain	Overlap_fetal_midbrain_TssP
23	8e−07	239 / 2031	Chror	12_Het_Melanocytes
24	1e−06	224 / 1895	Colon	EnhP_Colon
25	2e−06	295 / 2620	Chror	1_TssP_Neuronal_Progenitor
26	3e−06	335 / 3046	Brain	Fetal_TssA
27	3e−06	329 / 2988	Glio	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
28	3e−06	132 / 1021	GSEA	BENPORATH_ES_WITH_H3K27ME3
29	6e−06	166 / 1360	Brain	Mid_Frontal_Lobe_TssP
30	9e−06	208 / 1789	Chror	8_EnhP_Neuronal_Progenitor
31	1e−05	139 / 1119	Brain	Overlap_fetal_midbrain_TssA
32	2e−05	143 / 1163	Chror	12_Het_Fibroblasts
33	3e−05	56 / 366	Colon	K9K27me3_Colon
34	3e−05	82 / 598	GSEA	BENPORATH_PRC2_TARGETS
35	3e−05	158 / 1324	Chror	13_HetRpts_Fibroblasts
36	3e−05	75 / 536	GSEA	MIKKELSEN_MEF_HCP_WITH_H3K27ME3
37	4e−05	36 / 204	GSEA	MIKKELSEN_MEF_HCP_WITH_H3_UNMETHYLATED
38	5e−05	14 / 49	BP	negative regulation of Wnt signaling pathway
39	7e−05	115 / 924	Brain	Mid_Frontal_Lobe_TssF
40	1e−04	67 / 484	Colon	Quies2_Colon



Aging

Rank	p−value	#in/all	Geneset
1	0.004	12 / 58	TESCHENDORFF_age_hypermethylated
2	0.593	12 / 142	HORVATH_aging_genes meth UP
3	0.997	3 / 111	HORVATH_aging_genes meth DOWN
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	5e−05	14 / 49	negative regulation of Wnt signaling pathway
2	3e−04	6 / 12	axoneme assembly
3	2e−03	5 / 11	response to peptide
4	2e−03	95 / 803	G−protein coupled receptor signaling pathway
5	2e−03	10 / 39	learning or memory
6	2e−03	9 / 33	regulation of heart contraction
7	2e−03	7 / 22	cochlea morphogenesis
8	2e−03	7 / 22	response to morphine
9	2e−03	17 / 92	anatomical structure morphogenesis
10	3e−03	7 / 23	peripheral nervous system development
11	3e−03	10 / 42	ureteric bud development
12	3e−03	17 / 94	response to estradiol
13	3e−03	6 / 18	startle response
14	5e−03	20 / 122	neuron differentiation
15	5e−03	31 / 217	chemical synaptic transmission

Brain

Rank	p−value	#in/all	Geneset
1	1e−09	240 / 1893	Overlap_fetal_midbrain_TssF
2	1e−08	192 / 1476	Overlap_fetal_midbrain_TxTrans
3	2e−07	115 / 819	Overlap_fetal_midbrain_TssP
4	3e−06	335 / 3046	Fetal_TssA
5	6e−06	166 / 1360	Mid_Frontal_Lobe_TssP
6	1e−05	139 / 1119	Overlap_fetal_midbrain_TssA
7	7e−05	115 / 924	Mid_Frontal_Lobe_TssF
8	5e−04	283 / 2700	Fetal_TxTrans
9	2e−03	42 / 304	Mid_Frontal_Lobe_TssA
10	2e−03	407 / 4112	Mid_Frontal_Lobe_ReprPC
11	4e−03	123 / 1115	Overlap_fetal_midbrain_EnhG
12	5e−03	49 / 383	Mid_Frontal_Lobe_Tx
13	9e−03	141 / 1329	Overlap_fetal_midbrain_Enh
14	9e−03	56 / 465	Mid_Frontal_Lobe_TxTrans
15	1e−02	67 / 578	Fetal_Tx

Cancer

Rank	p−value	#in/all	Geneset
1	8e−04	16 / 76	PanCan_Wnt_geneset_nanostring
2	1e−03	6 / 15	GENTLES_modul17
3	9e−02	5 / 28	PanCan_HH_geneset_nanostring
4	2e−01	1 / 15	LIU_PROSTATE_CANCER_DN
5	3e−01	2 / 13	LIU_LIVER_CANCER
6	3e−01	2 / 14	GENTLES_modul1
7	3e−01	2 / 14	GENTLES_modul13
8	4e−01	5 / 46	PanCan_DNARepair_geneset_nanostring
9	4e−01	13 / 136	PanCan_RAS_geneset_nanostring
10	4e−01	2 / 16	GENTLES_modul14
11	4e−01	14 / 150	PanCan_MAPK_geneset_nanostring
12	5e−01	1 / 14	LIU_PROSTATE_CANCER_UP
13	5e−01	1 / 14	LIU_COMMON_CANCER_GENES
14	5e−01	8 / 91	PanCan_TXmisReg_geneset_nanostring
15	6e−01	7 / 82	PanCan_JAK−ST_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	0.002	19 / 104	bicellular tight junction
2	0.002	13 / 60	motile cilium
3	0.006	35 / 256	apical plasma membrane
4	0.007	14 / 78	Golgi lumen
5	0.007	24 / 162	basolateral plasma membrane
6	0.008	4 / 10	axon initial segment
7	0.022	4 / 13	node of Ranvier
8	0.025	9 / 49	lateral plasma membrane
9	0.028	31 / 248	extracellular matrix
10	0.033	350 / 3662	plasma membrane
11	0.035	17 / 121	receptor complex
12	0.049	8 / 47	adherens junction
13	0.050	3 / 10	sperm midpiece
14	0.052	11 / 73	acrosomal vesicle
15	0.053	13 / 91	perikaryon

Chr

Rank	p−value	#in/all	Geneset
1	0.002	104 / 902	Chr 4
2	0.003	16 / 87	Chr Y
3	0.075	38 / 342	Chr 18
4	0.096	45 / 422	Chr 13
5	0.100	115 / 1170	Chr 7
6	0.114	98 / 994	Chr X
7	0.204	74 / 768	Chr 14
8	0.208	74 / 769	Chr 15
9	0.230	114 / 1217	Chr 3
10	0.255	85 / 904	Chr 10
11	0.389	27 / 289	Chr 21
12	0.496	131 / 1492	Chr 2
13	0.643	52 / 619	Chr 20
14	0.670	70 / 836	Chr 8
15	0.681	111 / 1318	Chr 17

Chromatin states

Rank	p−value	#in/all	Geneset
1	2e−21	542 / 4304	9_ReprPCWk_Melanocytes
2	4e−18	439 / 3438	10_ReprPC_Melanocytes
3	3e−17	503 / 4107	9_ReprPCWk_Fibroblasts
4	3e−17	509 / 4169	10_ReprPC_Fibroblasts
5	5e−15	345 / 2660	8_EnhP_Melanocytes
6	4e−12	373 / 3068	8_EnhP_Fibroblasts
7	2e−11	414 / 3523	1_TssP_Melanocytes
8	4e−11	312 / 2516	11_K9K27me3_Melanocytes
9	2e−10	420 / 3639	1_TssP_Fibroblasts
10	3e−09	280 / 2297	10_ReprPC_Neuronal_Progenitor
11	4e−09	281 / 2315	13_HetRpts_Melanocytes
12	4e−08	410 / 3691	9_ReprPCWk_Neuronal_Progenitor
13	8e−07	239 / 2031	12_Het_Melanocytes
14	2e−06	295 / 2620	1_TssP_Neuronal_Progenitor
15	9e−06	208 / 1789	8_EnhP_Neuronal_Progenitor

Colon Cancer

Rank	p−value	#in/all	Geneset
1	5e−13	388 / 3173	ReprPC_Colon
2	5e−12	355 / 2894	TssP_Colon
3	8e−12	338 / 2740	ReprPCWk_Colon
4	1e−06	224 / 1895	EnhP_Colon
5	3e−05	56 / 366	K9K27me3_Colon
6	1e−04	67 / 484	Quies2_Colon
7	1e−04	86 / 663	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
8	2e−04	78 / 594	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
9	1e−03	448 / 4526	Quies1_Colon
10	2e−03	94 / 799	LaPointe_mucosa−position_kmeans_B_ascending colon_transverse colon_U
11	3e−02	874 / 9530	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP_
12	4e−02	79 / 740	LaPointe_mucosa−position_kmeans_C_cecum colon_ascending colon_transv
13	4e−02	12 / 78	Ang_CRC_Hypermethylated
14	5e−02	3 / 10	KIM_MSI−in−EC
15	6e−02	17 / 129	Marisa_CRC−cluster−b

Glio

Rank	p−value	#in/all	Geneset
1	3e−06	329 / 2988	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
2	4e−04	8 / 22	Shinawi_with_increased_methylation_in_STS
3	5e−04	13 / 53	WILLSCHER_GBM_Verhaak−PNmut_down (G)
4	1e−02	57 / 487	Hopp_Sturm_GBM_Epi3_B_adult_UP_G34_DN
5	2e−02	5 / 19	Sturm_GBM_Meth_overexpression_J_RTK II 'classic'_UP
6	2e−02	6 / 26	Gorovets_LGG_NB_subclass
7	2e−02	90 / 839	Hopp_Sturm_GBM_Epi3_no_zentr_1_G34_DN
8	3e−02	9 / 52	Hopp_Sturm_GBM_Epi3_B1_G34_DN
9	4e−02	10 / 61	Sturm_GBM_Meth_overexpression_D_G34_UP
10	4e−02	90 / 859	Hopp_Sturm_GBM_Epi3_A_adult_fetus_UP_G34_DN
11	5e−02	13 / 89	GIEZELT_GBM_STSwt_up_VS_LTSwt
12	6e−02	12 / 84	Weller_LGG_gradeII−vs−III_UP
13	6e−02	19 / 150	Hopp_Sturm_GBM_Epi3_E_G34_UP
14	7e−02	140 / 1417	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
15	1e−01	13 / 100	GIEZELT_GBM_STS_down_VS_LTS

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−07	131 / 962	BENPORATH_EED_TARGETS
2	3e−06	132 / 1021	BENPORATH_ES_WITH_H3K27ME3
3	3e−05	82 / 598	BENPORATH_PRC2_TARGETS
4	3e−05	75 / 536	MIKKELSEN_MEF_HCP_WITH_H3K27ME3
5	4e−05	36 / 204	MIKKELSEN_MEF_HCP_WITH_H3_UNMETHYLATED
6	1e−04	18 / 79	WONG_ENDMETRIUM_CANCER_DN
7	2e−04	116 / 956	BENPORATH_SUZ12_TARGETS
8	2e−04	47 / 315	MIKKELSEN_NPC_HCP_WITH_H3K27ME3
9	3e−04	9 / 27	LI_WILMS_TUMOR
10	3e−04	17 / 78	SCHLESINGER_METHYLATED_DE_NOVO_IN_CANCER
11	4e−04	14 / 58	MIKKELSEN_ES_HCP_WITH_H3_UNMETHYLATED
12	7e−04	18 / 90	RICKMAN_HEAD_AND_NECK_CANCER_A
13	8e−04	46 / 325	MEISSNER_NPC_HCP_WITH_H3K4ME2_AND_H3K27ME3
14	1e−03	15 / 72	MIKKELSEN_IPS_HCP_WITH_H3_UNMETHYLATED
15	1e−03	14 / 66	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_GREY_DN

HM

Rank	p−value	#in/all	Geneset
1	0.01	18 / 116	HALLMARK_SPERMATOGENESIS
2	0.02	8 / 40	HALLMARK_WNT_BETA_CATENIN_SIGNALING
3	0.09	22 / 186	HALLMARK_ESTROGEN_RESPONSE_EARLY
4	0.11	22 / 191	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
5	0.22	5 / 37	HALLMARK_PANCREAS_BETA_CELLS
6	0.25	4 / 29	HALLMARK_NOTCH_SIGNALING
7	0.29	5 / 41	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
8	0.32	13 / 127	HALLMARK_COAGULATION
9	0.38	17 / 177	HALLMARK_KRAS_SIGNALING_DN
10	0.54	12 / 137	HALLMARK_UV_RESPONSE_UP
11	0.58	3 / 34	HALLMARK_HEDGEHOG_SIGNALING
12	0.64	15 / 183	HALLMARK_APICAL_JUNCTION
13	0.67	15 / 186	HALLMARK_ESTROGEN_RESPONSE_LATE
14	0.71	3 / 41	HALLMARK_APICAL_SURFACE
15	0.73	10 / 132	HALLMARK_UV_RESPONSE_DN

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.3	10 / 94	DUMEAUX_Smoking enriched genes
2	0.4	1 / 5	Huan_blood−pressure_HTN−signature
3	0.4	2 / 17	DUMEAUX_High bmi enriched genes
4	0.5	3 / 32	Marjolein_ageing−genes_DN
5	0.7	11 / 147	Homuth_BMI−associated−genes_UP
6	0.8	1 / 16	Huan_blood−pressure_DBP−signature
7	0.8	1 / 18	Huan_blood−pressure_SBP−signature
8	1.0	7 / 211	Homuth_BMI−associated−genes_DN
9	1.0	0 / 10	DUMEAUX_Smoking literature genes up
10	1.0	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
11	1.0	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
12	1.0	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
13	1.0	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
14	1.0	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
15	1.0	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up

Lymphoma

Rank	p−value	#in/all	Geneset
1	1e−28	680 / 5384	HOPP_Repressed
2	4e−10	349 / 2939	HOPP_Poised_promoter
3	6e−04	419 / 4167	HOPP_Heterochrom
4	5e−02	46 / 408	TARTE_Mature plasma cell signature
5	6e−02	9 / 57	LENZ_Stromal signature 2
6	6e−02	9 / 57	Hopp_Lymphoma_Epi1_no_zentr_1_B.cell_DN
7	8e−02	12 / 87	Hopp_Lymphoma_Epi1_with_zentr_v_B.cell_DN
8	9e−02	12 / 89	Subero_T−ALL_hyper_meth
9	9e−02	17 / 137	Hopp_June14_MMML937 tumors+controls_group.overexpression_G_tonsil_U
10	9e−02	6 / 36	Subero_MM_hyper_meth
11	9e−02	17 / 138	WIRTH_lymphoma937_spot G
12	1e−01	16 / 133	Hopp_Lymphoma_Epi1_no_zentr_5_B.cell_GCB_UP
13	1e−01	16 / 134	Subero_DLBCL_hyper_meth
14	2e−01	9 / 70	Hopp_Lymphoma_Epi1_no_zentr_3_B.cell_DN
15	2e−01	7 / 52	Hopp_Lymphoma_Epi1_with_zentr_iv_B.cell_MM_UP

Melanoma

Rank	p−value	#in/all	Geneset
1	0.3	4 / 30	Hugo_melanoma−all−MET_UP
2	0.3	5 / 43	Hugo_melanoma−BRAFmut−MET_UP
3	0.3	6 / 54	Hugo_melanoma−all−MET_DN
4	0.5	1 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
5	0.9	1 / 27	Hugo_melanoma−all−LEF1_UP
6	1.0	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

MF

Rank	p−value	#in/all	Geneset
1	0.002	6 / 16	alpha−actinin binding
2	0.004	6 / 19	neuropeptide binding
3	0.005	70 / 588	G−protein coupled receptor activity
4	0.006	6 / 20	Wnt−activated receptor activity
5	0.013	44 / 357	olfactory receptor activity
6	0.013	7 / 30	Wnt−protein binding
7	0.016	4 / 12	secondary active sulfate transmembrane transporter activity
8	0.022	11 / 64	calcium channel activity
9	0.029	4 / 14	C2H2 zinc finger domain binding
10	0.029	4 / 14	neurotransmitter:sodium symporter activity
11	0.036	4 / 15	neuropeptide receptor activity
12	0.036	4 / 15	retinoic acid binding
13	0.045	5 / 23	cadherin binding
14	0.045	5 / 23	core promoter proximal region sequence−specific DNA binding
15	0.050	3 / 10	regulatory region DNA binding

miRNA Disease

Rank	p−value	#in/all	Geneset
1	0.01	5 / 17	Bladder cancer
2	0.01	12 / 68	Glioblastoma multiforme, somatic
3	0.02	8 / 40	Muscular dystrophy
4	0.02	10 / 56	Myopathy, nemaline, 3
5	0.03	6 / 27	Duchenne muscular dystrophy
6	0.04	5 / 22	Pigmented adrenocortical disease, primary isolated
7	0.05	16 / 116	Cancer
8	0.05	3 / 10	Dermatitis, atopic
9	0.05	11 / 73	Stroke, susceptibility to
10	0.06	4 / 17	Thyroid carcinoma, follicular
11	0.06	7 / 41	Melanoma, cutaneous malignant, 2
12	0.07	11 / 76	Muscular
13	0.07	15 / 113	Ovarian cancer
14	0.07	16 / 124	Prostate cancer
15	0.09	16 / 127	Melanoma and neural system tumor syndrome

miRNA target

Rank	p−value	#in/all	Geneset
1	0.05	3 / 10	hsa−miR−887
2	0.12	3 / 14	hsa−miR−638
3	0.12	2 / 7	hsa−miR−566
4	0.14	4 / 23	hsa−miR−151−5p
5	0.15	4 / 24	hsa−miR−1228
6	0.19	7 / 54	hsa−miR−518f
7	0.20	6 / 45	hsa−miR−524−3p
8	0.25	2 / 11	hsa−miR−604
9	0.26	6 / 49	hsa−miR−518a−3p
10	0.27	5 / 40	hsa−miR−518b
11	0.29	8 / 72	hsa−miR−518c
12	0.32	2 / 13	hsa−miR−744
13	0.34	5 / 44	hsa−miR−518d−3p
14	0.35	8 / 76	hsa−miR−1827
15	0.35	3 / 24	hsa−miR−1250

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.04	4 / 15	GUSTAFSON_PI3K_DN
2	0.32	2 / 13	BENTINK_e2f3.2
3	0.35	2 / 14	BENTINK_ras.6
4	0.72	1 / 14	GUSTAFSON_PI3K_UP
5	1.00	0 / 13	BENTINK_e2f3.1
6	1.00	0 / 13	BENTINK_myc.1
7	1.00	0 / 12	BENTINK_ras.1
8	1.00	0 / 11	BENTINK_ras.4
9	1.00	0 / 13	BENTINK_src.10
10	1.00	0 / 12	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Reference Signatures

Rank	p−value	#in/all	Geneset
1	0.002	33 / 220	WIRTH_Testis
2	0.004	39 / 289	JONGENEEL_Testis
3	0.031	8 / 43	VAQUERIZAS_Placenta_TF
4	0.055	8 / 48	WIRTH_Pancreas
5	0.060	52 / 478	WIRTH_Nervous System
6	0.061	8 / 49	JONGENEEL_Retina
7	0.069	17 / 132	WIRTH_Muscle
8	0.106	4 / 21	JONGENEEL_Salivary Gland
9	0.110	26 / 231	Chaussabel_2,5_Immune related molecules
10	0.118	3 / 14	WIRTH_Cerebellum
11	0.125	16 / 134	WIRTH_Mucosa
12	0.125	10 / 76	WIRTH_Homeostasis
13	0.136	4 / 23	JONGENEEL_Heart
14	0.144	7 / 50	WIRTH_Placenta
15	0.182	3 / 17	VAQUERIZAS_Heart_TF

Telomeres

Rank	p−value	#in/all	Geneset
1	0.7	2 / 27	Nabetani_alt len telomeres_genes_ko
2	1.0	0 / 13	Alternative lengthening of telomeres
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	6e−09	222 / 1753	HEBENSTREIT_low expression TF
2	5e−01	56 / 631	ICGC_RxraPcr1_targets
3	5e−01	308 / 3507	ICGC_Rad21_targets
4	5e−01	65 / 747	ICGC_NrsfPcr2_targets
5	7e−01	1 / 12	MYC_Protein synthesis degradation UP
6	8e−01	121 / 1466	ICGC_NrsfPcr1_targets
7	8e−01	58 / 721	ICGC_SrfPcr2_targets
8	8e−01	1 / 18	MYC_Metabolism UP
9	1e+00	2 / 55	MYC_Targets UP
10	1e+00	188 / 2497	ICGC_Bcl11_targets
11	1e+00	158 / 2133	ICGC_Mef2_targets
12	1e+00	119 / 1669	ICGC_P300_targets
13	1e+00	207 / 2759	ICGC_Bcl3_targets
14	1e+00	105 / 1501	ICGC_Usf1_targets
15	1e+00	45 / 733	ICGC_Atf3_targets

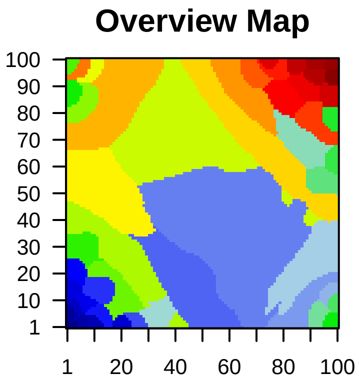
K−Means Cluster

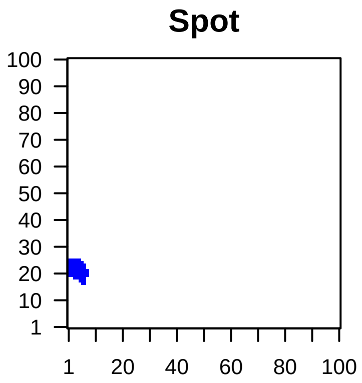
Spot Summary: U

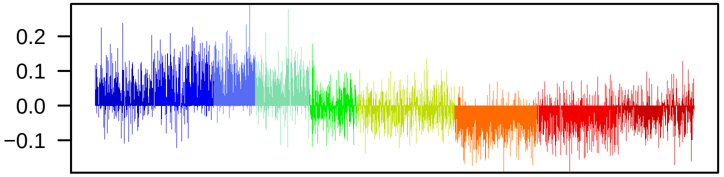
metagenes = 59
genes = 280

<r> metagenes = 0.96
<r> genes = 0.27
beta: r2= 12.17 / log p= −Inf

samples with spot = 205 (6.1 %)
A * : 25 (7.3 %)
A C * : 71 (21.6 %)
A C F * : 65 (27.7 %)
A F * : 39 (12.7 %)
C F * : 3 (1.1 %)
F * : 1 (0.2 %)
N * : 1 (0.2 %)


Overview Map


Spot

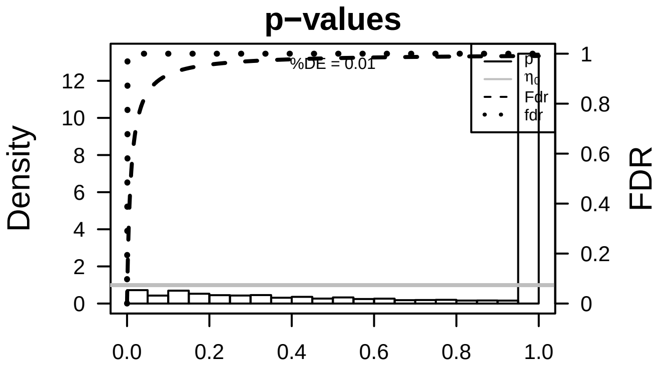


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_165686	0.92	−0.84	0.59	NPIPB5	nuclear pore complex interacting protein family member B5 [S
2	ILMN_330411	0.9	−0.82	0.55		Putative NPIP−like protein LOC729978 [Source:UniProtKB/S
3	ILMN_207005	0.88	−1.05	0.57	LOC613037	Homo sapiens nuclear pore complex interacting protein meml
4	ILMN_233896	0.8	−0.44	0.3	SLC29A1	solute carrier family 29 member 1 (Augustine blood group) [S
5	ILMN_188649	0.8	−0.74	0.35	HNRNPA2B1	heterogeneous nuclear ribonucleoprotein A2/B1 [Source:HGN
6	ILMN_224992	0.76	−0.63	0.6	FYN	FYN proto−oncogene, Src family tyrosine kinase [Source:HGI
7	ILMN_166620	0.74	−0.63	0.66	GSDMB	gasdermin B [Source:HGNC Symbol;Acc:HGNC:23690]
8	ILMN_173761	0.74	−0.53	0.48	VAMP1	vesicle associated membrane protein 1 [Source:HGNC Symb
9	ILMN_179830	0.74	−0.67	0.35		
10	ILMN_181404	0.73	−0.52	0.59	CABIN1	calcineurin binding protein 1 [Source:HGNC Symbol;Acc:HGN
11	ILMN_169762	0.72	−0.6	0.76	PLA2G4B	phospholipase A2 group IVB [Source:HGNC Symbol;Acc:HG
12	ILMN_176875	0.72	−0.63	0.6	PILRA	paired immunoglobin like type 2 receptor alpha [Source:HGN
13	ILMN_324288	0.72	−0.61	0.39		
14	ILMN_180022	0.71	−0.41	0.53		
15	ILMN_178919	0.7	−0.51	0.52	TPM2	tropomyosin 2 (beta) [Source:HGNC Symbol;Acc:HGNC:120
16	ILMN_168512	0.69	−0.37	0.36	COL9A2	collagen type IX alpha 2 chain [Source:HGNC Symbol;Acc:H
17	ILMN_324676	0.69	−0.65	0.43	NPIPB5	nuclear pore complex interacting protein family member B5 [S
18	ILMN_178314	0.69	−0.52	0.35	CDH23	cadherin related 23 [Source:HGNC Symbol;Acc:HGNC:1373
19	ILMN_178380	0.69	−0.5	0.44	PNMA3	paraneoplastic Ma antigen 3 [Source:HGNC Symbol;Acc:HG
20	ILMN_168733	0.68	−0.77	0.46	FLNA	filamin A [Source:HGNC Symbol;Acc:HGNC:3754]

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	3e−31	126 / 4795	Chror	6_EnhG_Fibroblasts
2	1e−30	106 / 3450	Chror	4_TxTrans_Fibroblasts
3	1e−27	132 / 5699	Chror	6_EnhG_Melanocytes
4	3e−24	163 / 9054	Colon	Tx_Colon
5	5e−22	84 / 2845	Colon	TxEnhG1_Colon
6	1e−21	141 / 7354	Colon	TssF_Colon
7	2e−19	150 / 8568	Colon	TxWk_Colon
8	2e−18	24 / 221	Refer	Chaussabel_3,8_Enzymes
9	2e−18	33 / 493	Lympl	WIRTH_lymphoma937_spot J
10	5e−18	32 / 472	Lympl	Hopp_June14_MMML937 tumors+controls_group.overexpression_J_GC−E
11	9e−18	168 / 10779	Colon	Enh_Colon
12	2e−17	81 / 3164	Brain	Mid_Frontal_Lobe_ZNF
13	5e−17	25 / 281	GSEA	GINESTIER_BREAST_CANCER_ZNF217_AMPLIFIED_DN
14	2e−15	152 / 9555	Colon	TssA_Colon
15	8e−15	112 / 5956	Chror	3_TssF_Neuronal_Progenitor
16	9e−15	114 / 6138	Colon	TssD2_Colon
17	1e−14	59 / 2028	Chror	4_TxTrans_Melanocytes
18	2e−14	171 / 11836	Chror	3_TssF_Melanocytes
19	4e−14	70 / 2810	Colon	EnhA_Colon
20	3e−13	139 / 8771	Chror	5_Tx_Melanocytes
21	5e−13	101 / 5356	Lympl	HOPP_Txn_transition
22	1e−12	46 / 1468	Colon	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse c
23	3e−12	121 / 7275	Lympl	HOPP_Txn_elongation
24	4e−12	170 / 12298	Chror	2_TssA_Melanocytes
25	3e−11	174 / 12983	Chror	2_TssA_Neuronal_Progenitor
26	3e−11	143 / 9635	Chror	3_TssF_Fibroblasts
27	4e−11	160 / 11455	Chror	2_TssA_Fibroblasts
28	6e−11	124 / 7854	Chror	5_Tx_Fibroblasts
29	7e−10	138 / 9504	Brain	Overlap_fetal_midbrain_K9K27me3
30	7e−10	147 / 10430	Brain	Overlap_fetal_midbrain_Quies
31	1e−07	105 / 6970	Chror	5_Tx_Neuronal_Progenitor
32	1e−07	110 / 7448	Lympl	HOPP_Strong_enhancer
33	1e−07	87 / 5373	Colon	EnhWk1_Colon
34	2e−07	54 / 2709	Brain	Mid_Frontal_Lobe_HetRpts
35	2e−07	83 / 5067	TF	ICGC_Taf1_targets
36	5e−07	25 / 818	Brain	Mid_Frontal_Lobe_Het
37	7e−07	122 / 8818	MF	protein binding
38	9e−07	24 / 789	Colon	TxEnhG2_Colon
39	1e−06	15 / 331	Lympl	WIRTH_lymphoma937_spot H
40	1e−06	159 / 12741	Chror	7_Enh_Melanocytes


p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.8	1 / 142	HORVATH_aging_genes meth UP
2	1.0	0 / 111	HORVATH_aging_genes meth DOWN
3	1.0	0 / 58	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	5e−05	5 / 42	histone deacetylation
2	3e−04	31 / 1643	transcription, DNA−templated
3	1e−03	3 / 23	spliceosomal complex assembly
4	2e−03	3 / 27	mitotic spindle assembly
5	2e−03	6 / 139	RNA splicing
6	3e−03	5 / 101	vesicle−mediated transport
7	3e−03	7 / 196	mRNA splicing, via spliceosome
8	4e−03	3 / 32	negative regulation of protein catabolic process
9	4e−03	2 / 10	developmental process
10	5e−03	4 / 70	Golgi organization
11	5e−03	11 / 457	regulation of transcription from RNA polymerase II promoter
12	6e−03	9 / 335	protein transport
13	6e−03	2 / 12	protein localization to membrane
14	7e−03	3 / 41	gluconeogenesis
15	8e−03	2 / 14	regulation of I−kappaB kinase/NF−kappaB signaling

Brain

Rank	p−value	#in/all	Geneset
1	2e−17	81 / 3164	Mid_Frontal_Lobe_ZNF
2	7e−10	138 / 9504	Overlap_fetal_midbrain_K9K27me3
3	7e−10	147 / 10430	Overlap_fetal_midbrain_Quies
4	2e−07	54 / 2709	Mid_Frontal_Lobe_HetRpts
5	5e−07	25 / 818	Mid_Frontal_Lobe_Het
6	1e−05	36 / 1728	Fetal_ReprPCWk
7	8e−05	124 / 9815	Overlap_fetal_midbrain_ReprPC
8	1e−04	20 / 796	Overlap_fetal_midbrain_ZNF
9	2e−04	82 / 5936	Overlap_fetal_midbrain_HetRpts
10	2e−03	7 / 180	Overlap_fetal_midbrain_Het
11	2e−02	16 / 906	Fetal_HetRpts
12	7e−02	24 / 1784	Mid_Frontal_Lobe_ReprPCWk
13	7e−02	49 / 4112	Mid_Frontal_Lobe_ReprPC
14	2e−01	9 / 630	Mid_Frontal_Lobe_EnhP
15	3e−01	23 / 2127	Mid_Frontal_Lobe_K9K27me3

Cancer

Rank	p−value	#in/all	Geneset
1	0.1	1 / 14	RHODES_UNDIFFERENTIATED_CANCER
2	0.1	1 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
3	0.4	0 / 13	RHODES_CANCER_META_SIGNATURE
4	0.4	1 / 54	KUIPER_MM poor survival
5	0.4	2 / 150	PanCan_MAPK_geneset_nanostring
6	0.4	0 / 15	LIU_PROSTATE_CANCER_DN
7	0.5	0 / 14	LIU_COMMON_CANCER_GENES
8	0.6	1 / 82	PanCan_JAK−ST_geneset_nanostring
9	0.6	1 / 91	PanCan_TXmisReg_geneset_nanostring
10	0.6	5 / 554	Lembcke_Colonic Inflammation
11	0.7	1 / 117	PanCan_Driver_Gene_geneset_nanostring
12	0.7	1 / 136	PanCan_RAS_geneset_nanostring
13	0.8	4 / 527	Lembcke_Normal vs Adenoma
14	0.9	1 / 301	SPANG_BCL6−index2
15	1.0	0 / 12	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP

CC

Rank	p−value	#in/all	Geneset
1	2e−04	43 / 2535	nucleoplasm
2	9e−04	46 / 2979	cytosol
3	1e−03	67 / 4828	nucleus
4	1e−03	5 / 79	spliceosomal complex
5	5e−03	3 / 36	recycling endosome membrane
6	7e−03	2 / 13	XY body
7	8e−03	3 / 43	cleavage furrow
8	1e−02	12 / 571	perinuclear region of cytoplasm
9	1e−02	4 / 89	centriole
10	1e−02	3 / 50	SNARE complex
11	1e−02	2 / 18	NuRD complex
12	1e−02	2 / 18	postsynapse
13	1e−02	3 / 53	clathrin−coated vesicle
14	2e−02	29 / 1979	membrane
15	2e−02	6 / 221	endosome

Chr

Rank	p−value	#in/all	Geneset
1	0.001	27 / 1467	Chr 19
2	0.003	19 / 959	Chr 16
3	0.057	19 / 1318	Chr 17
4	0.082	10 / 619	Chr 20
5	0.137	16 / 1217	Chr 3
6	0.153	8 / 536	Chr 22
7	0.169	15 / 1170	Chr 7
8	0.190	27 / 2323	Chr 1
9	0.375	11 / 994	Chr X
10	0.400	15 / 1411	Chr 11
11	0.535	3 / 289	Chr 21
12	0.622	7 / 768	Chr 14
13	0.624	7 / 769	Chr 15
14	0.825	7 / 954	Chr 9
15	0.882	8 / 1160	Chr 12

Chromatin states

Rank	p−value	#in/all	Geneset
1	3e−31	126 / 4795	6_EnhG_Fibroblasts
2	1e−30	106 / 3450	4_TxTrans_Fibroblasts
3	1e−27	132 / 5699	6_EnhG_Melanocytes
4	8e−15	112 / 5956	3_TssF_Neuronal_Progenitor
5	1e−14	59 / 2028	4_TxTrans_Melanocytes
6	2e−14	171 / 11836	3_TssF_Melanocytes
7	3e−13	139 / 8771	5_Tx_Melanocytes
8	4e−12	170 / 12298	2_TssA_Melanocytes
9	3e−11	174 / 12983	2_TssA_Neuronal_Progenitor
10	3e−11	143 / 9635	3_TssF_Fibroblasts
11	4e−11	160 / 11455	2_TssA_Fibroblasts
12	6e−11	124 / 7854	5_Tx_Fibroblasts
13	1e−07	105 / 6970	5_Tx_Neuronal_Progenitor
14	1e−06	159 / 12741	7_Enh_Melanocytes
15	2e−05	28 / 1206	6_EnhG_Neuronal_Progenitor

Colon Cancer

Rank	p−value	#in/all	Geneset
1	3e−24	163 / 9054	Tx_Colon
2	5e−22	84 / 2845	TxEnhG1_Colon
3	1e−21	141 / 7354	TssF_Colon
4	2e−19	150 / 8568	TxWk_Colon
5	9e−18	168 / 10779	Enh_Colon
6	2e−15	152 / 9555	TssA_Colon
7	9e−15	114 / 6138	TssD2_Colon
8	4e−14	70 / 2810	EnhA_Colon
9	1e−12	46 / 1468	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
10	1e−07	87 / 5373	EnhWk1_Colon
11	9e−07	24 / 789	TxEnhG2_Colon
12	2e−05	32 / 1470	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
13	2e−04	30 / 1547	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
14	5e−04	109 / 8678	Quies3_Colon
15	5e−04	6 / 103	Marisa_CRC−cluster−d

Glio

Rank	p−value	#in/all	Geneset
1	9e−04	4 / 44	WILLSCHER_GBM_Verhaak−PNwt_up
2	3e−03	17 / 820	Sturm_GBM_Meth_overexpression_E_G34_UP
3	2e−02	9 / 401	Down_b
4	2e−02	4 / 110	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
5	5e−02	2 / 37	WILLSCHER_GBM_proteomics_wtOnly_SpotH
6	7e−02	4 / 157	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
7	7e−02	4 / 158	Hopp_Sturm_GBM_Epi3_D_adult_fetus_IDH_UP
8	8e−02	1 / 8	Sturm_GBM_Meth_overexpression_C_G34_UP
9	8e−02	1 / 9	WILLSCHER_GBM_LTSmut_proteomics−A_UP
10	8e−02	1 / 9	Sturm_GBM_Meth_overexpression_G_IDH_UP
11	9e−02	2 / 50	WILLSCHER_GBM_proteomics_wtOnly_SpotG
12	9e−02	6 / 315	Up
13	1e−01	26 / 2043	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
14	1e−01	1 / 12	Phillips PN up vs MES & Prolif
15	1e−01	2 / 65	WILLSCHER_GBM_proteomics_wtOnly_SpotJ

GSEA C2

Rank	p−value	#in/all	Geneset
1	5e−17	25 / 281	GINESTIER_BREAST_CANCER_ZNF217_AMPLIFIED_DN
2	2e−06	35 / 1535	BLALOCK_ALZHEIMERS_DISEASE_UP
3	5e−06	12 / 242	HUTTMANN_B_CLL_POOR_SURVIVAL_UP
4	5e−06	7 / 69	LAIHO_COLORECTAL_CANCER_SERRATED_DN
5	1e−05	8 / 112	SCHLOSSER_SERUM_RESPONSE_UP
6	4e−05	9 / 168	LEE_DIFFERENTIATING_T_LYMPHOCYTE
7	2e−04	13 / 411	GARY_CD5_TARGETS_UP
8	3e−04	18 / 723	GRADE_COLON_CANCER_UP
9	3e−04	5 / 60	PID_HDAC_CLASSI_PATHWAY
10	3e−04	3 / 14	REACTOME_PROTEOLYTIC_CLEAVAGE_OF_SNARE_COMPLEX_PROTEI
11	3e−04	10 / 268	DACOSTA_UV_RESPONSE_VIA_ERCC3_UP
12	4e−04	11 / 325	DAIRKEE_TERT_TARGETS_UP
13	5e−04	8 / 184	FOSTER_KDM1A_TARGETS_DN
14	5e−04	3 / 16	REACTOME_BOTULINUM_NEUROTOXICITY
15	7e−04	4 / 41	ZHAN_MULTIPLE_MYELOMA_PR_DN

HM

Rank	p−value	#in/all	Geneset
1	0.1	4 / 185	HALLMARK_HEME_METABOLISM
2	0.1	4 / 186	HALLMARK_MYOGENESIS
3	0.1	3 / 127	HALLMARK_COAGULATION
4	0.3	3 / 185	HALLMARK_P53_PATHWAY
5	0.3	3 / 186	HALLMARK_IL2_STAT5_SIGNALING
6	0.3	3 / 189	HALLMARK_HYPOXIA
7	0.4	2 / 130	HALLMARK_DNA_REPAIR
8	0.5	1 / 69	HALLMARK_CHOLESTEROL_HOMEOSTASIS
9	0.5	2 / 176	HALLMARK_ADIPOGENESIS
10	0.5	2 / 177	HALLMARK_MITOTIC_SPINDLE
11	0.5	2 / 183	HALLMARK_GLYCOLYSIS
12	0.5	2 / 187	HALLMARK_COMPLEMENT
13	0.6	2 / 191	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
14	0.6	1 / 87	HALLMARK_PROTEIN_SECRETION
15	0.6	1 / 91	HALLMARK_ANDROGEN_RESPONSE

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.04	2 / 31	DUMEAUX_Fasting enriched genes
2	0.34	3 / 211	Homuth_BMI−associated−genes_DN
3	0.60	1 / 94	DUMEAUX_Smoking enriched genes
4	0.76	1 / 147	Homuth_BMI−associated−genes_UP
5	1.00	0 / 10	DUMEAUX_Smoking literature genes up
6	1.00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
7	1.00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
8	1.00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
9	1.00	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
10	1.00	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
11	1.00	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
12	1.00	0 / 10	DUMEAUX_Women normal BMI literature genes up
13	1.00	0 / 17	DUMEAUX_High bmi enriched genes
14	1.00	0 / 18	Huan_blood−pressure_SBP−signature
15	1.00	0 / 16	Huan_blood−pressure_DBP−signature

Lymphoma

Rank	p−value	#in/all	Geneset
1	2e−18	33 / 493	WIRTH_lymphoma937_spot J
2	5e−18	32 / 472	Hopp_June14_MMML937 tumors+controls_group.overexpression_J_GC−B−
3	5e−13	101 / 5356	HOPP_Txn_transition
4	3e−12	121 / 7275	HOPP_Txn_elongation
5	1e−07	110 / 7448	HOPP_Strong_enhancer
6	1e−06	15 / 331	WIRTH_lymphoma937_spot H
7	3e−06	14 / 318	Hopp_June14_MMML937 tumors+controls_group.overexpression_H_GC−B−
8	5e−05	109 / 8226	HOPP_Active_promoter
9	5e−03	21 / 1169	SPANG_BCR DN
10	2e−02	94 / 8098	HOPP_Weak_promoter
11	7e−02	8 / 450	Hopp_June14_MMML937 tumors+controls_group.overexpression_I_MM_GC
12	8e−02	8 / 464	WIRTH_lymphoma937_spot I
13	1e−01	6 / 331	SPANG_CD40 6hrs UP
14	1e−01	1 / 16	WRIGHT_ABC UP
15	1e−01	5 / 286	ZHANG_DLBCL mutated

Melanoma

Rank	p−value	#in/all	Geneset
1	0.4	1 / 54	Hugo_melanoma−all−MET_DN
2	1.0	0 / 30	Hugo_melanoma−all−MET_UP
3	1.0	0 / 43	Hugo_melanoma−BRAFmut−MET_UP
4	1.0	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
5	1.0	0 / 27	Hugo_melanoma−all−LEF1_UP
6	1.0	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

MF

Rank	p−value	#in/all	Geneset
1	7e−07	122 / 8818	protein binding
2	2e−05	5 / 36	histone deacetylase activity
3	8e−05	5 / 46	ligand−dependent nuclear receptor transcription coactivator activity
4	1e−04	23 / 1013	poly(A) RNA binding
5	4e−04	9 / 227	transcription coactivator activity
6	4e−04	4 / 37	structural constituent of muscle
7	1e−03	3 / 21	calcium−dependent cysteine−type endopeptidase activity
8	2e−03	9 / 283	nucleotide binding
9	3e−03	3 / 30	cysteine−type peptidase activity
10	5e−03	2 / 11	diacylglycerol binding
11	6e−03	3 / 37	SNAP receptor activity
12	8e−03	2 / 14	titin binding
13	1e−02	4 / 92	histone deacetylase binding
14	2e−02	2 / 21	14−3−3 protein binding
15	2e−02	2 / 25	ATP−dependent DNA helicase activity

miRNA Disease

Rank	p−value	#in/all	Geneset
1	1	0 / 7	Thyroid carcinoma, papillary
2	1	0 / 123	Pancreatic cancer
3	1	0 / 68	Glioblastoma multiforme, somatic
4	1	0 / 63	Gastrointestinal
5	1	0 / 3	Pituitary adenoma
6	1	0 / 116	Cancer
7	1	0 / 95	Colorectal cancer
8	1	0 / 2	Adenomas, multiple colorectal
9	1	0 / 124	Prostate cancer
10	1	0 / 48	Alzheimer disease, susceptibility to
11	1	0 / 7	Schizophrenia, susceptibility to
12	1	0 / 20	Parkinson disease
13	1	0 / 65	Hepatocellular carcinoma
14	1	0 / 3	Down syndrome, risk of
15	1	0 / 127	Melanoma and neural system tumor syndrome

miRNA target

Rank	p−value	#in/all	Geneset
1	0.007	3 / 41	hsa−miR−541
2	0.032	3 / 71	hsa−miR−127−5p
3	0.034	2 / 30	hsa−miR−371−3p
4	0.036	2 / 31	hsa−miR−654−5p
5	0.039	3 / 77	hsa−miR−422a
6	0.048	2 / 36	hsa−miR−127−3p
7	0.049	3 / 84	hsa−miR−486−3p
8	0.055	3 / 88	hsa−miR−608
9	0.061	3 / 92	hsa−miR−219−2−3p
10	0.062	3 / 93	hsa−miR−378
11	0.070	4 / 159	hsa−miR−520h
12	0.074	3 / 100	hsa−miR−613
13	0.079	2 / 48	hsa−miR−1291
14	0.079	2 / 48	hsa−miR−346
15	0.084	1 / 9	hsa−miR−615−3p

Pathw Act

Rank	p−value	#in/all	Geneset
1	1	0 / 14	GUSTAFSON_PI3K_UP
2	1	0 / 15	GUSTAFSON_PI3K_DN
3	1	0 / 13	BENTINK_e2f3.1
4	1	0 / 13	BENTINK_e2f3.2
5	1	0 / 13	BENTINK_myc.1
6	1	0 / 12	BENTINK_ras.1
7	1	0 / 11	BENTINK_ras.4
8	1	0 / 14	BENTINK_ras.6
9	1	0 / 13	BENTINK_src.10
10	1	0 / 12	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Reference Signatures

Rank	p−value	#in/all	Geneset
1	2e−18	24 / 221	Chaussabel_3,8_Enzymes
2	2e−04	10 / 254	PROTEINATLAS_smooth muscle
3	1e−03	18 / 816	PROTEINATLAS_endometrium
4	1e−03	20 / 959	PROTEINATLAS_nasopharynx
5	1e−03	22 / 1118	PROTEINATLAS_placenta
6	2e−03	13 / 514	PROTEINATLAS_vagina
7	2e−03	11 / 398	PROTEINATLAS_skeletal muscle
8	2e−03	16 / 724	PROTEINATLAS_lymph node
9	2e−03	16 / 726	PROTEINATLAS_cervix, uterine
10	2e−03	20 / 1016	PROTEINATLAS_cerebral cortex
11	3e−03	14 / 619	PROTEINATLAS_salivary gland
12	3e−03	11 / 429	PROTEINATLAS_soft tissue
13	4e−03	18 / 912	PROTEINATLAS_urinary bladder
14	4e−03	13 / 571	PROTEINATLAS_oral mucosa
15	4e−03	18 / 929	PROTEINATLAS_bronchus

Telomeres

Rank	p−value	#in/all	Geneset
1	0.1	1 / 13	Alternative lengthening of telomeres
2	1.0	0 / 27	Nabetani_alt len telomeres_genes_ko
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	2e−07	83 / 5067	ICGC_Taf1_targets
2	2e−06	69 / 4131	ICGC_Nfatc1_targets
3	2e−06	85 / 5518	ICGC_Stat5_targets
4	5e−06	83 / 5466	ICGC_Nficsc81335_targets
5	7e−06	70 / 4362	ICGC_Creb1_targets
6	2e−05	70 / 4468	ICGC_Egr1_targets
7	2e−05	80 / 5410	ICGC_Foxm1_targets
8	4e−05	79 / 5383	ICGC_Sp1_targets
9	4e−05	92 / 6578	ICGC_Pou2_targets
10	5e−05	73 / 4881	ICGC_Atf2_targets
11	6e−05	34 / 1723	HEBENSTREIT_high expression TF
12	1e−04	93 / 6868	ICGC_Elf1_targets
13	1e−04	65 / 4345	ICGC_Zeb1_targets
14	2e−04	77 / 5442	ICGC_Pmlsc71910_targets
15	3e−04	82 / 5984	ICGC_Mta3_targets

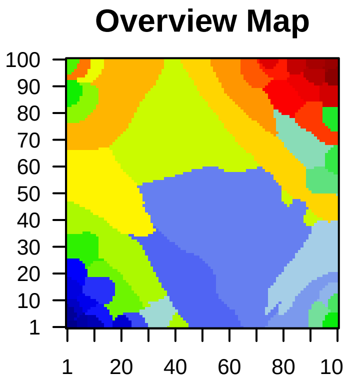
K−Means Cluster

Spot Summary: V

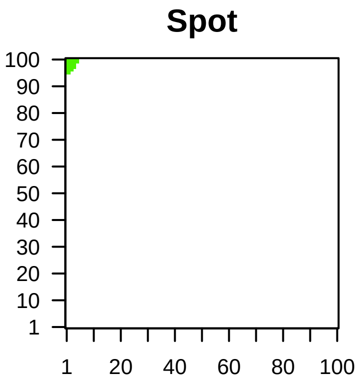
metagenes = 23
genes = 518

<r> metagenes = 0.98
<r> genes = 0.41
beta: r2= 25.72 / log p= −Inf

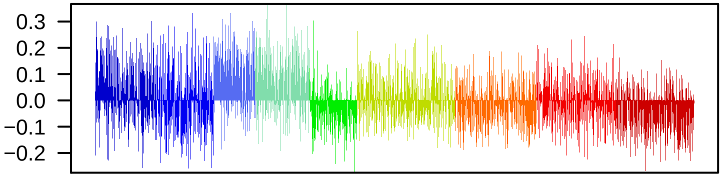
samples with spot = 443 (13.1 %)
A * : 80 (23.3 %)
A C * : 46 (14 %)
A C F * : 101 (43 %)
A F * : 97 (31.5 %)
C F * : 6 (2.3 %)
F * : 52 (9.4 %)
F J * : 19 (4.1 %)
J * : 34 (7.6 %)
N * : 8 (1.8 %)



Overview Map



Spot

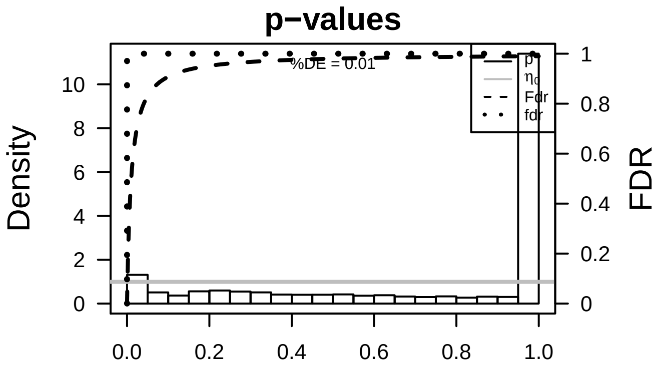


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_220158	1.9	−1.61	0.23		
2	ILMN_239186	1.67	−1.5	0.25	GSTM1	glutathione S−transferase mu 1 [Source:HGNC Symbol;Acc:H
3	ILMN_219323	1.52	−0.67	0.32	MZB1	marginal zone B and B1 cell specific protein [Source:HGNC S
4	ILMN_210941	1.44	−1.31	0.27	NAPSB	napsin B aspartic peptidase, pseudogene [Source:HGNC Syr
5	ILMN_180537	1.13	−0.9	0.25		
6	ILMN_240803	1.03	−0.72	0.7	EEF1D	eukaryotic translation elongation factor 1 delta [Source:HGNC
7	ILMN_168817	0.98	−1.06	0.42	RRP7A	ribosomal RNA processing 7 homolog A [Source:HGNC Syml
8	ILMN_325914	0.92	−0.7	0.43	BST2	bone marrow stromal cell antigen 2 [Source:HGNC Symbol;A
9	ILMN_166258	0.92	−0.62	0.58		
10	ILMN_211204	0.92	−0.7	0.5	CARD9	caspase recruitment domain family member 9 [Source:HGNC
11	ILMN_172348	0.92	−0.72	0.48	BST2	bone marrow stromal cell antigen 2 [Source:HGNC Symbol;A
12	ILMN_178254	0.89	−0.74	0.48	EEF1D	eukaryotic translation elongation factor 1 delta [Source:HGNC
13	ILMN_174921	0.87	−0.57	0.69	SDF2L1	stromal cell derived factor 2 like 1 [Source:HGNC Symbol;Acc
14	ILMN_165692	0.85	−1.08	0.5		
15	ILMN_211225	0.85	−0.61	0.32	TNFRSF4	TNF receptor superfamily member 4 [Source:HGNC Symbol;A
16	ILMN_167423	0.84	−0.91	0.35	HSPB1	heat shock protein family B (small) member 1 [Source:HGNC
17	ILMN_168724	0.83	−0.83	0.26	SPATA20	spermatogenesis associated 20 [Source:HGNC Symbol;Acc:I
18	ILMN_169324	0.83	−0.62	0.61	ZNF296	zinc finger protein 296 [Source:HGNC Symbol;Acc:HGNC:15
19	ILMN_165599	0.81	−0.79	0.36	CDK5RAP2	CDK5 regulatory subunit associated protein 2 [Source:HGNC
20	ILMN_174705	0.81	−0.67	0.79	TRAPPC2L	trafficking protein particle complex 2 like [Source:HGNC Syml

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	2e−91	347 / 7354	Colon	TssF_Colon
2	6e−71	224 / 3450	Chror	4_TxTrans_Fibroblasts
3	8e−70	363 / 9555	Colon	TssA_Colon
4	6e−62	250 / 4795	Chror	6_EnhG_Fibroblasts
5	8e−62	390 / 11836	Chror	3_TssF_Melanocytes
6	3e−59	269 / 5699	Chror	6_EnhG_Melanocytes
7	7e−58	392 / 12298	Chror	2_TssA_Melanocytes
8	6e−51	328 / 9054	Colon	Tx_Colon
9	9e−49	367 / 11455	Chror	2_TssA_Fibroblasts
10	2e−45	328 / 9504	Brain	Overlap_fetal_midbrain_K9K27me3
11	2e−45	386 / 12983	Chror	2_TssA_Neuronal_Progenitor
12	6e−45	257 / 6138	Colon	TssD2_Colon
13	5e−43	347 / 10779	Colon	Enh_Colon
14	3e−42	175 / 3164	Brain	Mid_Frontal_Lobe_ZNF
15	9e−41	163 / 2845	Colon	TxEnhG1_Colon
16	9e−36	129 / 2028	Chror	4_TxTrans_Melanocytes
17	3e−35	292 / 8568	Colon	TxWk_Colon
18	2e−34	311 / 9635	Chror	3_TssF_Fibroblasts
19	6e−34	233 / 5956	Chror	3_TssF_Neuronal_Progenitor
20	2e−26	310 / 10430	Brain	Overlap_fetal_midbrain_Quies
21	3e−24	199 / 5373	Colon	EnhWk1_Colon
22	1e−23	132 / 2810	Colon	EnhA_Colon
23	2e−23	190 / 5067	TF	ICGC_Taf1_targets
24	6e−23	251 / 7854	Chror	5_Tx_Fibroblasts
25	4e−21	89 / 1547	Colon	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP
26	3e−20	108 / 2215	TF	ICGC_GabpPcr2_targets
27	2e−19	261 / 8771	Chror	5_Tx_Melanocytes
28	2e−19	63 / 887	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
29	2e−19	163 / 4345	TF	ICGC_Zeb1_targets
30	2e−19	221 / 6868	TF	ICGC_Elf1_targets
31	1e−18	189 / 5518	TF	ICGC_Stat5_targets
32	2e−18	221 / 6970	Chror	5_Tx_Neuronal_Progenitor
33	4e−18	278 / 9815	Brain	Overlap_fetal_midbrain_ReprPC
34	9e−18	185 / 5442	TF	ICGC_Pmlsc71910_targets
35	3e−17	184 / 5466	TF	ICGC_Nficsc81335_targets
36	4e−17	203 / 6322	TF	ICGC_Tcf3_targets
37	7e−17	208 / 6578	TF	ICGC_Pou2_targets
38	1e−16	151 / 4131	TF	ICGC_Nfatc1_targets
39	2e−16	156 / 4362	TF	ICGC_Creb1_targets
40	2e−16	180 / 5383	TF	ICGC_Sp1_targets



p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.6	2 / 111	HORVATH_aging_genes meth DOWN
2	0.8	2 / 142	HORVATH_aging_genes meth UP
3	1.0	0 / 58	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	7e−07	10 / 69	mitochondrial translational elongation
2	1e−06	10 / 71	mitochondrial translational termination
3	2e−06	7 / 32	mitochondrial electron transport, NADH to ubiquinone
4	3e−05	7 / 46	mitochondrial respiratory chain complex I assembly
5	7e−05	11 / 137	ER to Golgi vesicle−mediated transport
6	5e−04	4 / 20	positive regulation of protein dephosphorylation
7	8e−04	16 / 335	protein transport
8	9e−04	11 / 184	translation
9	9e−04	4 / 23	mitochondrial translation
10	9e−04	7 / 81	antigen processing and presentation of exogenous peptide antigen via MHC c
11	1e−03	3 / 12	spliceosomal tri−snRNP complex assembly
12	1e−03	11 / 196	mRNA splicing, via spliceosome
13	2e−03	6 / 69	methylation
14	2e−03	3 / 14	positive regulation of proteasomal protein catabolic process
15	2e−03	8 / 122	G2/M transition of mitotic cell cycle

Brain

Rank	p−value	#in/all	Geneset
1	2e−45	328 / 9504	Overlap_fetal_midbrain_K9K27me3
2	3e−42	175 / 3164	Mid_Frontal_Lobe_ZNF
3	2e−26	310 / 10430	Overlap_fetal_midbrain_Quies
4	4e−18	278 / 9815	Overlap_fetal_midbrain_ReprPC
5	9e−15	53 / 818	Mid_Frontal_Lobe_Het
6	3e−11	101 / 2709	Mid_Frontal_Lobe_HetRpts
7	5e−11	74 / 1728	Fetal_ReprPCWk
8	6e−06	116 / 4112	Mid_Frontal_Lobe_ReprPC
9	1e−05	154 / 5936	Overlap_fetal_midbrain_HetRpts
10	6e−03	26 / 796	Overlap_fetal_midbrain_ZNF
11	4e−02	25 / 906	Fetal_HetRpts
12	6e−02	62 / 2654	Fetal_Quies
13	1e−01	11 / 386	Fetal_ZNF
14	1e−01	6 / 180	Overlap_fetal_midbrain_Het
15	2e−01	47 / 2127	Mid_Frontal_Lobe_K9K27me3

Cancer

Rank	p−value	#in/all	Geneset
1	2e−04	23 / 527	Lembcke_Normal vs Adenoma
2	2e−02	2 / 13	GENTLES_modul2
3	3e−02	2 / 14	LIU_COMMON_CANCER_GENES
4	3e−02	2 / 14	LIU_PROSTATE_CANCER_UP
5	6e−02	3 / 46	PanCan_DNARepair_geneset_nanostring
6	2e−01	1 / 9	GENTLES_modul3
7	2e−01	1 / 9	GENTLES_modul5
8	2e−01	1 / 14	RHODES_UNDIFFERENTIATED_CANCER
9	2e−01	1 / 14	GENTLES_modul1
10	2e−01	1 / 14	GENTLES_modul10
11	3e−01	1 / 15	LIU_PROSTATE_CANCER_DN
12	3e−01	1 / 15	WANG_ER_UP
13	3e−01	1 / 16	GENTLES_modul7
14	4e−01	1 / 24	PanCan_Notch_geneset_nanostring
15	4e−01	2 / 73	SHAUGHNESSY_MM high risk

CC

Rank	p−value	#in/all	Geneset
1	1e−12	65 / 1304	mitochondrion
2	1e−09	28 / 374	mitochondrial inner membrane
3	4e−08	98 / 2979	cytosol
4	9e−08	86 / 2535	nucleoplasm
5	2e−06	134 / 4822	cytoplasm
6	3e−06	7 / 33	mitochondrial respiratory chain complex I
7	3e−06	19 / 287	mitochondrial matrix
8	3e−05	128 / 4828	nucleus
9	5e−05	63 / 1979	membrane
10	1e−04	13 / 200	nuclear membrane
11	3e−04	71 / 2464	extracellular exosome
12	2e−03	4 / 29	mitochondrial large ribosomal subunit
13	3e−03	7 / 99	recycling endosome
14	3e−03	25 / 721	nucleolus
15	4e−03	20 / 539	Golgi membrane

Chr

Rank	p−value	#in/all	Geneset
1	1e−11	68 / 1467	Chr 19
2	2e−07	43 / 959	Chr 16
3	7e−04	22 / 536	Chr 22
4	5e−03	39 / 1318	Chr 17
5	5e−03	41 / 1411	Chr 11
6	2e−02	20 / 619	Chr 20
7	7e−02	25 / 954	Chr 9
8	5e−01	23 / 1170	Chr 7
9	9e−01	38 / 2323	Chr 1
10	9e−01	18 / 1217	Chr 3
11	9e−01	3 / 289	Chr 21
12	1e+00	10 / 836	Chr 8
13	1e+00	11 / 904	Chr 10
14	1e+00	12 / 994	Chr X
15	1e+00	8 / 769	Chr 15

Chromatin states

Rank	p−value	#in/all	Geneset
1	6e−71	224 / 3450	4_TxTrans_Fibroblasts
2	6e−62	250 / 4795	6_EnhG_Fibroblasts
3	8e−62	390 / 11836	3_TssF_Melanocytes
4	3e−59	269 / 5699	6_EnhG_Melanocytes
5	7e−58	392 / 12298	2_TssA_Melanocytes
6	9e−49	367 / 11455	2_TssA_Fibroblasts
7	2e−45	386 / 12983	2_TssA_Neuronal_Progenitor
8	9e−36	129 / 2028	4_TxTrans_Melanocytes
9	2e−34	311 / 9635	3_TssF_Fibroblasts
10	6e−34	233 / 5956	3_TssF_Neuronal_Progenitor
11	6e−23	251 / 7854	5_Tx_Fibroblasts
12	2e−19	261 / 8771	5_Tx_Melanocytes
13	2e−18	221 / 6970	5_Tx_Neuronal_Progenitor
14	1e−10	293 / 11847	7_Enh_Neuronal_Progenitor
15	3e−10	308 / 12741	7_Enh_Melanocytes

Colon Cancer

Rank	p−value	#in/all	Geneset
1	2e−91	347 / 7354	TssF_Colon
2	8e−70	363 / 9555	TssA_Colon
3	6e−51	328 / 9054	Tx_Colon
4	6e−45	257 / 6138	TssD2_Colon
5	5e−43	347 / 10779	Enh_Colon
6	9e−41	163 / 2845	TxEnhG1_Colon
7	3e−35	292 / 8568	TxWk_Colon
8	3e−24	199 / 5373	EnhWk1_Colon
9	1e−23	132 / 2810	EnhA_Colon
10	4e−21	89 / 1547	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
11	5e−09	78 / 2073	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
12	5e−08	54 / 1281	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv
13	7e−08	39 / 789	TxEnhG2_Colon
14	3e−07	218 / 8678	Quies3_Colon
15	6e−06	257 / 10999	TssWk_Colon

Glio

Rank	p−value	#in/all	Geneset
1	2e−07	13 / 110	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
2	2e−05	7 / 44	WILLSCHER_GBM_Verhaak−PNwt_up
3	5e−05	58 / 1777	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
4	2e−03	58 / 2043	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
5	3e−02	7 / 157	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
6	3e−02	3 / 37	WILLSCHER_GBM_proteomics_wtOnly_SpotH
7	4e−02	4 / 65	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
8	7e−02	22 / 820	Sturm_GBM_Meth_overexpression_E_G34_UP
9	9e−02	3 / 55	Stuehler_Proteins_up_in_STS
10	1e−01	4 / 101	Hopp_Sturm_GBM_Epi3_D1_IDH_UP_adult_fetus_DN
11	1e−01	3 / 69	WILLSCHER_GBM_Verhaak−PNwt & MES_up
12	2e−01	5 / 158	Hopp_Sturm_GBM_Epi3_D_adult_fetus_IDH_UP
13	2e−01	1 / 13	Donson−immune cell intra signaling−associated with LTS in HGA
14	2e−01	2 / 50	WILLSCHER_GBM_proteomics_wtOnly_SpotG
15	3e−01	1 / 15	VERHAAK_NL subtype

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−19	63 / 887	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
2	3e−16	30 / 237	LU_EZH2_TARGETS_UP
3	3e−15	53 / 797	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
4	7e−14	48 / 723	GRADE_COLON_CANCER_UP
5	1e−13	37 / 450	STARK_PREFRONTAL_CORTEX_22Q11_DELETION_DN
6	1e−13	35 / 407	SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_UP
7	2e−13	31 / 325	DAIRKEE_TERT_TARGETS_UP
8	2e−13	20 / 123	KIM_ALL_DISORDERS_DURATION_CORR_DN
9	5e−13	16 / 73	LI_DCP2_BOUND_MRNA
10	3e−12	20 / 141	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_13
11	9e−12	42 / 656	KIM_ALL_DISORDERS_OLIGODENDROCYTE_NUMBER_CORR_UP
12	1e−11	18 / 117	WELCSH_BRCA1_TARGETS_DN
13	4e−10	37 / 593	CASORELLI_ACUTE_PROMYELOCYTIC_LEUKEMIA_DN
14	1e−09	44 / 831	LOPEZ_MBD_TARGETS
15	1e−09	40 / 710	MARTENS_TRETINOIN_RESPONSE_DN

HM

Rank	p−value	#in/all	Geneset
1	3e−08	15 / 130	HALLMARK_DNA_REPAIR
2	4e−04	11 / 167	HALLMARK_OXIDATIVE_PHOSPHORYLATION
3	4e−03	5 / 54	HALLMARK_MYC_TARGETS_V2
4	1e−02	6 / 103	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
5	3e−02	8 / 183	HALLMARK_GLYCOLYSIS
6	4e−02	4 / 69	HALLMARK_CHOLESTEROL_HOMEOSTASIS
7	4e−02	3 / 41	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
8	5e−02	7 / 176	HALLMARK_ADIPOGENESIS
9	5e−02	7 / 177	HALLMARK_MITOTIC_SPINDLE
10	1e−01	6 / 173	HALLMARK_E2F_TARGETS
11	2e−01	5 / 170	HALLMARK_MYC_TARGETS_V1
12	3e−01	4 / 138	HALLMARK_FATTY_ACID_METABOLISM
13	3e−01	5 / 185	HALLMARK_P53_PATHWAY
14	3e−01	3 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING
15	3e−01	3 / 103	HALLMARK_BILE_ACID_METABOLISM

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.008	8 / 147	Homuth_BMI−associated−genes_UP
2	0.074	1 / 4	DUMEAUX_Exercising non smoker literature enriched genes
3	0.176	1 / 10	Marjolein_ageing−genes_UP
4	0.451	1 / 31	DUMEAUX_Fasting enriched genes
5	0.772	3 / 211	Homuth_BMI−associated−genes_DN
6	1.000	0 / 94	DUMEAUX_Smoking enriched genes
7	1.000	0 / 10	DUMEAUX_Smoking literature genes up
8	1.000	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
9	1.000	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
10	1.000	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
11	1.000	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
12	1.000	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
13	1.000	0 / 10	DUMEAUX_Women normal BMI literature genes up
14	1.000	0 / 17	DUMEAUX_High bmi enriched genes
15	1.000	0 / 18	Huan_blood−pressure_SBP−signature

Lymphoma

Rank	p−value	#in/all	Geneset
1	3e−16	179 / 5356	HOPP_Txn_transition
2	3e−13	212 / 7275	HOPP_Txn_elongation
3	2e−12	229 / 8226	HOPP_Active_promoter
4	1e−10	44 / 772	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell line_
5	2e−09	42 / 777	WIRTH_lymphoma937_spot D
6	2e−06	189 / 7448	HOPP_Strong_enhancer
7	9e−06	199 / 8098	HOPP_Weak_promoter
8	2e−04	17 / 318	Hopp_June14_MMML937 tumors+controls_group.overexpression_H_GC−B−
9	2e−04	17 / 331	WIRTH_lymphoma937_spot H
10	6e−03	4 / 39	CARO_OxPhos_in_DLBCL_UP
11	7e−03	3 / 21	ROSOLOWSKI_red UP
12	8e−03	37 / 1270	SPANG_BCR UP
13	2e−02	2 / 13	Subero_B−CLL_hypo_meth
14	3e−02	2 / 15	Subero_B−ALL_hypo_meth
15	3e−02	7 / 158	WIRTH_lymphoma937_spot C

Melanoma

Rank	p−value	#in/all	Geneset
1	1	0 / 30	Hugo_melanoma−all−MET_UP
2	1	0 / 54	Hugo_melanoma−all−MET_DN
3	1	0 / 43	Hugo_melanoma−BRAFmut−MET_UP
4	1	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
5	1	0 / 27	Hugo_melanoma−all−LEF1_UP
6	1	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

MF

Rank	p−value	#in/all	Geneset
1	6e−14	246 / 8818	protein binding
2	3e−09	49 / 1013	poly(A) RNA binding
3	3e−04	5 / 32	NADH dehydrogenase (ubiquinone) activity
4	1e−03	4 / 24	transmembrane transporter activity
5	3e−03	40 / 1329	ATP binding
6	4e−03	3 / 17	S−adenosylmethionine−dependent methyltransferase activity
7	4e−03	8 / 133	ATPase activity
8	5e−03	5 / 58	ubiquitin binding
9	5e−03	9 / 169	structural constituent of ribosome
10	6e−03	3 / 20	DNA−directed RNA polymerase activity
11	1e−02	4 / 44	methylated histone binding
12	1e−02	21 / 627	molecular_function
13	1e−02	5 / 70	chaperone binding
14	1e−02	4 / 46	motor activity
15	1e−02	3 / 26	Ran GTPase binding

miRNA Disease

Rank	p−value	#in/all	Geneset
1	0.3	1 / 18	Non−Hodgkin lymphoma, somatic
2	0.3	1 / 20	Parkinson disease
3	0.4	1 / 28	Immunological
4	0.4	1 / 29	Neuroblastoma
5	0.5	1 / 40	Medulloblastoma
6	0.6	1 / 47	Cervical cancer, somatic
7	0.6	1 / 48	Gastric cancer
8	0.6	1 / 48	Multiple myeloma
9	0.7	1 / 56	Myopathy, nemaline, 3
10	0.7	1 / 63	Gastrointestinal
11	0.7	1 / 65	Hepatocellular carcinoma
12	0.7	1 / 68	Glioblastoma multiforme, somatic
13	0.8	1 / 73	Stroke, susceptibility to
14	0.8	1 / 76	Muscular
15	0.8	1 / 95	Colorectal cancer

miRNA target

Rank	p−value	#in/all	Geneset
1	0.005	3 / 18	hsa−miR−542−5p
2	0.006	4 / 39	hsa−miR−517*
3	0.029	2 / 14	hsa−miR−574−3p
4	0.033	4 / 63	hsa−miR−612
5	0.038	4 / 66	hsa−miR−637
6	0.057	7 / 179	hsa−miR−539
7	0.058	3 / 46	hsa−miR−658
8	0.059	6 / 144	hsa−miR−491−5p
9	0.061	3 / 47	hsa−miR−370
10	0.071	2 / 23	hsa−miR−668
11	0.073	4 / 82	hsa−miR−188−5p
12	0.078	3 / 52	hsa−miR−940
13	0.078	3 / 52	hsa−miR−571
14	0.089	4 / 88	hsa−miR−423−5p
15	0.089	4 / 88	hsa−miR−608

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.02	2 / 12	BENTINK_ras.1
2	0.02	2 / 13	BENTINK_myc.1
3	0.25	1 / 15	GUSTAFSON_PI3K_DN
4	1.00	0 / 14	GUSTAFSON_PI3K_UP
5	1.00	0 / 13	BENTINK_e2f3.1
6	1.00	0 / 13	BENTINK_e2f3.2
7	1.00	0 / 11	BENTINK_ras.4
8	1.00	0 / 14	BENTINK_ras.6
9	1.00	0 / 13	BENTINK_src.10
10	1.00	0 / 12	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Reference Signatures

Rank	p−value	#in/all	Geneset
1	1e−10	25 / 275	Chaussabel_3,7_Spliceosome
2	7e−10	58 / 1268	PROTEINATLAS_colon
3	1e−09	53 / 1118	PROTEINATLAS_placenta
4	2e−09	54 / 1167	PROTEINATLAS_gallbladder
5	2e−09	53 / 1138	PROTEINATLAS_small intestine
6	6e−09	55 / 1239	PROTEINATLAS_testis
7	6e−09	53 / 1173	PROTEINATLAS_rectum
8	1e−08	36 / 640	PROTEINATLAS_parathyroid gland
9	3e−08	52 / 1194	PROTEINATLAS_stomach
10	1e−07	43 / 933	PROTEINATLAS_adrenal gland
11	1e−07	50 / 1176	PROTEINATLAS_duodenum
12	2e−07	38 / 782	PROTEINATLAS_thyroid gland
13	6e−07	45 / 1063	PROTEINATLAS_tonsil
14	6e−07	42 / 959	PROTEINATLAS_nasopharynx
15	2e−06	41 / 963	PROTEINATLAS_pancreas

Telomeres

Rank	p−value	#in/all	Geneset
1	0.2	1 / 13	Alternative lengthening of telomeres
2	0.4	1 / 27	Nabetani_alt len telomeres_genes_ko
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	2e−23	190 / 5067	ICGC_Taf1_targets
2	3e−20	108 / 2215	ICGC_GabpPcr2_targets
3	2e−19	163 / 4345	ICGC_Zeb1_targets
4	2e−19	221 / 6868	ICGC_Elf1_targets
5	1e−18	189 / 5518	ICGC_Stat5_targets
6	9e−18	185 / 5442	ICGC_Pmlsc71910_targets
7	3e−17	184 / 5466	ICGC_Nficsc81335_targets
8	4e−17	203 / 6322	ICGC_Tcf3_targets
9	7e−17	208 / 6578	ICGC_Pou2_targets
10	1e−16	151 / 4131	ICGC_Nfatc1_targets
11	2e−16	156 / 4362	ICGC_Creb1_targets
12	2e−16	180 / 5383	ICGC_Sp1_targets
13	6e−16	177 / 5312	ICGC_Tcf12_targets
14	9e−16	198 / 6267	ICGC_Yy1_targets
15	1e−15	219 / 7247	ICGC_Runx3_targets

K−Means Cluster

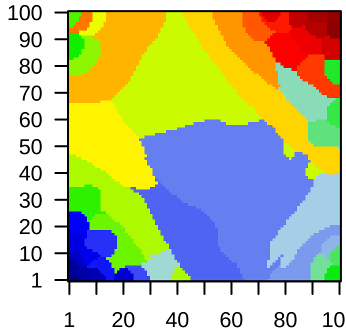
Spot Summary: W

metagenes = 48
genes = 315

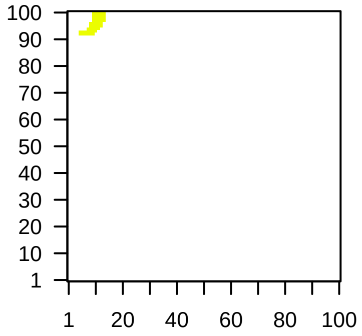
<r> metagenes = 0.86
<r> genes = 0.09
beta: r2= 2.82 / log p= −Inf

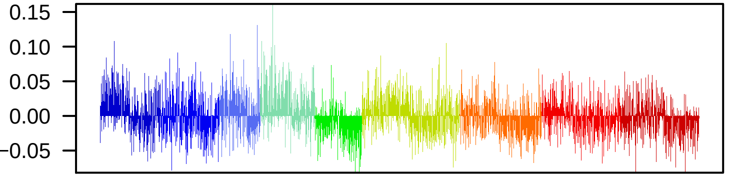
samples with spot = 3 (0.1 %)
ACF* : 2 (0.9 %)
AF* : 1 (0.3 %)

Overview Map



Spot





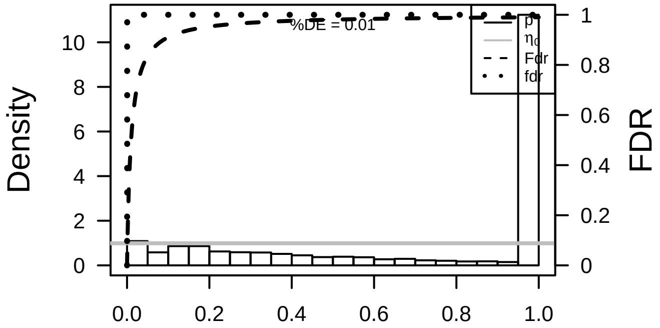
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_167082	0.99	−0.63	0.26	TXLNGY	taxilin gamma pseudogene, Y−linked [Source:HGNC Symbol;
2	ILMN_326745	0.85	−0.41	0.09		glyceraldehyde 3 phosphate dehydrogenase pseudogene 61
3	ILMN_217361	0.77	−0.52	0.13	MT1E	metallothionein 1E [Source:HGNC Symbol;Acc:HGNC:7397]
4	ILMN_177216	0.69	−0.46	0.27	PRKY	protein kinase, Y−linked, pseudogene [Source:HGNC Symbo
5	ILMN_167565	0.61	−0.54	0.3	PPFIBP2	PPFIA binding protein 2 [Source:HGNC Symbol;Acc:HGNC:9
6	ILMN_177482	0.61	−0.38	0.23	RPL34	ribosomal protein L34 [Source:HGNC Symbol;Acc:HGNC:10
7	ILMN_171189	0.6	−0.43	0.23	MYB	MYB proto−oncogene, transcription factor [Source:HGNC Sy
8	ILMN_178463	0.6	−0.7	0.3	KBTBD11	kelch repeat and BTB domain containing 11 [Source:HGNC
9	ILMN_205341	0.59	−0.55	0.21	MIR6886	low density lipoprotein receptor [Source:HGNC Symbol;Acc:
10	ILMN_181327	0.58	−0.58	0.31	DUSP22	dual specificity phosphatase 22 [Source:HGNC Symbol;Acc:
11	ILMN_238815	0.58	−0.47	0.36	CASP3	caspase 3 [Source:HGNC Symbol;Acc:HGNC:1504]
12	ILMN_173071	0.57	−0.38	0.27	ADORA3	adenosine A3 receptor [Source:HGNC Symbol;Acc:HGNC:26
13	ILMN_175160	0.54	−0.42	0.25	FOSB	FosB proto−oncogene, AP−1 transcription factor subunit [Sou
14	ILMN_219370	0.54	−0.29	0.17	HRK	harakiri, BCL2 interacting protein [Source:HGNC Symbol;Acc
15	ILMN_166297	0.54	−0.42	0.13		
16	ILMN_181137	0.52	−0.35	0.17	FAM20B	family with sequence similarity 20 member B [Source:HGNC
17	ILMN_185382	0.52	−0.34	0.16	MGAT3	mannosyl (beta−1,4−)−glycoprotein beta−1,4−N−acetylgluco
18	ILMN_228537	0.51	−0.41	0.3	SORD	sorbitol dehydrogenase [Source:HGNC Symbol;Acc:HGNC:1
19	ILMN_177619	0.51	−0.29	0.24	TMSB4Y	thymosin beta 4, Y−linked [Source:HGNC Symbol;Acc:HGNC
20	ILMN_167940	0.5	−0.31	0.29	TRPM4	transient receptor potential cation channel subfamily M mem

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	4e−32	180 / 7354	Colon	TssF_Colon
2	6e−28	224 / 11836	Chror	3_TssF_Melanocytes
3	2e−27	199 / 9555	Colon	TssA_Colon
4	2e−26	148 / 5699	Chror	6_EnhG_Melanocytes
5	3e−26	226 / 12298	Chror	2_TssA_Melanocytes
6	6e−25	189 / 9054	Colon	Tx_Colon
7	4e−24	150 / 6138	Colon	TssD2_Colon
8	3e−22	191 / 9635	Chror	3_TssF_Fibroblasts
9	3e−22	226 / 12983	Chror	2_TssA_Neuronal_Progenitor
10	4e−22	178 / 8568	Colon	TxWk_Colon
11	5e−22	189 / 9504	Brain	Overlap_fetal_midbrain_K9K27me3
12	6e−22	135 / 5373	Colon	EnhWk1_Colon
13	4e−20	207 / 11455	Chror	2_TssA_Fibroblasts
14	2e−17	86 / 2845	Colon	TxEnhG1_Colon
15	3e−17	190 / 10430	Brain	Overlap_fetal_midbrain_Quies
16	8e−17	193 / 10779	Colon	Enh_Colon
17	1e−15	166 / 8678	Colon	Quies3_Colon
18	1e−15	167 / 8771	Chror	5_Tx_Melanocytes
19	6e−15	112 / 4795	Chror	6_EnhG_Fibroblasts
20	1e−14	128 / 5956	Chror	3_TssF_Neuronal_Progenitor
21	3e−14	85 / 3164	Brain	Mid_Frontal_Lobe_ZNF
22	6e−14	89 / 3450	Chror	4_TxTrans_Fibroblasts
23	1e−13	64 / 2028	Chror	4_TxTrans_Melanocytes
24	3e−12	75 / 2810	Colon	EnhA_Colon
25	4e−12	134 / 6868	TF	ICGC_Elf1_targets
26	7e−12	126 / 6322	TF	ICGC_Tcf3_targets
27	7e−12	146 / 7854	Chror	5_Tx_Fibroblasts
28	4e−11	110 / 5312	TF	ICGC_Tcf12_targets
29	6e−11	96 / 4362	TF	ICGC_Creb1_targets
30	1e−10	111 / 5466	TF	ICGC_Nficsc81335_targets
31	1e−10	131 / 6970	Chror	5_Tx_Neuronal_Progenitor
32	2e−10	147 / 8226	Lympl	HOPP_Active_promoter
33	2e−10	166 / 9815	Brain	Overlap_fetal_midbrain_ReprPC
34	2e−09	131 / 7247	TF	ICGC_Runx3_targets
35	2e−09	108 / 5518	TF	ICGC_Stat5_targets
36	3e−09	99 / 4890	TF	ICGC_Bclaf101388_targets
37	3e−09	131 / 7275	Lympl	HOPP_Txn_elongation
38	3e−09	114 / 5984	TF	ICGC_Mta3_targets
39	4e−09	101 / 5067	TF	ICGC_Taf1_targets
40	5e−09	185 / 11847	Chror	7_Enh_Neuronal_Progenitor

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.4	2 / 111	HORVATH_aging_genes meth DOWN
2	1.0	0 / 142	HORVATH_aging_genes meth UP
3	1.0	0 / 58	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Cancer

Rank	p−value	#in/all	Geneset
1	0.01	2 / 13	GENTLES_modul6
2	0.01	2 / 14	GENTLES_modul10
3	0.08	0 / 14	LIU_PROSTATE_CANCER_UP
4	0.10	1 / 9	GENTLES_modul5
5	0.10	2 / 46	PanCan_DNARepair_geneset_nanostring
6	0.14	1 / 13	LIU_LIVER_CANCER
7	0.15	1 / 14	BEN−PORATH_UP
8	0.16	4 / 178	SPANG_LPS−index2
9	0.16	1 / 15	GENTLES_modul17
10	0.16	9 / 527	Lembcke_Normal vs Adenoma
11	0.17	1 / 16	GENTLES_modul7
12	0.18	3 / 125	PanCan_CC+Apop_geneset_nanostring
13	0.21	1 / 20	PanCan_ChromMod_geneset_nanostring
14	0.34	1 / 36	PanCan_HK_geneset_nanostring
15	0.36	1 / 38	KUIPER_MM good survival

Chromatin states

Rank	p−value	#in/all	Geneset
1	6e−28	224 / 11836	3_TssF_Melanocytes
2	2e−26	148 / 5699	6_EnhG_Melanocytes
3	3e−26	226 / 12298	2_TssA_Melanocytes
4	3e−22	191 / 9635	3_TssF_Fibroblasts
5	3e−22	226 / 12983	2_TssA_Neuronal_Progenitor
6	4e−20	207 / 11455	2_TssA_Fibroblasts
7	1e−15	167 / 8771	5_Tx_Melanocytes
8	6e−15	112 / 4795	6_EnhG_Fibroblasts
9	1e−14	128 / 5956	3_TssF_Neuronal_Progenitor
10	6e−14	89 / 3450	4_TxTrans_Fibroblasts
11	1e−13	64 / 2028	4_TxTrans_Melanocytes
12	7e−12	146 / 7854	5_Tx_Fibroblasts
13	1e−10	131 / 6970	5_Tx_Neuronal_Progenitor
14	5e−09	185 / 11847	7_Enh_Neuronal_Progenitor
15	8e−08	191 / 12741	7_Enh_Melanocytes

GSEA C2

Rank	p−value	#in/all	Geneset
1	5e−08	14 / 187	WONG_MITOCHONDRIA_GENE_MODULE
2	8e−08	12 / 137	KEGG_ALZHEIMERS_DISEASE
3	3e−06	9 / 100	KEGG_OXIDATIVE_PHOSPHORYLATION
4	2e−05	11 / 190	LOCKWOOD_AMPLIFIED_IN_LUNG_CANCER
5	2e−05	7 / 71	MOOTHA_VOXPHOS
6	3e−05	20 / 606	WAKABAYASHI_ADIPOGENESIS_PPARG_BOUND_8D
7	4e−05	6 / 55	ASTIER_INTEGRIN_SIGNALING
8	5e−05	37 / 1601	GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_DN
9	6e−05	4 / 19	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_17
10	8e−05	14 / 355	BERENJENO_TRANSFORMED_BY_RHOA_DN
11	8e−05	3 / 8	RUNNE_GENDER_EFFECT_UP
12	1e−04	15 / 410	MILI_PSEUDOPODIA_CHEMOTAXIS_DN
13	1e−04	6 / 65	REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_SYNTHESIS
14	1e−04	14 / 371	MOOTHA_HUMAN_MITODB_6_2002
15	1e−04	10 / 202	BROWNE_HCMV_INFECTION_1HR_DN

Lymphoma

Rank	p−value	#in/all	Geneset
1	2e−10	147 / 8226	HOPP_Active_promoter
2	3e−09	131 / 7275	HOPP_Txn_elongation
3	9e−09	140 / 8098	HOPP_Weak_promoter
4	3e−08	130 / 7448	HOPP_Strong_enhancer
5	4e−08	102 / 5356	HOPP_Txn_transition
6	9e−05	5 / 39	CARO_OxPhos_in_DLBCL_UP
7	1e−03	14 / 455	SPANG_CD40 6hrs DN
8	2e−03	3 / 21	ROSOLOWSKI_red UP
9	1e−02	94 / 6559	HOPP_Weak_txn
10	1e−02	24 / 1270	SPANG_BCR UP
11	2e−02	4 / 88	ROSOLOWSKI_red total
12	2e−02	11 / 472	Hopp_June14_MMML937 tumors+controls_group.overexpression_J_GC−B−c
13	4e−02	2 / 28	DAVE_Immune response 1
14	4e−02	6 / 220	Hopp_June14_MMML937 tumors+controls_group.overexpression_B_cell line_
15	6e−02	6 / 232	WIRTH_lymphoma937_spot B

miRNA Disease

Rank	p−value	#in/all	Geneset
1	1	0 / 7	Thyroid carcinoma, papillary
2	1	0 / 123	Pancreatic cancer
3	1	0 / 68	Glioblastoma multiforme, somatic
4	1	0 / 63	Gastrointestinal
5	1	0 / 3	Pituitary adenoma
6	1	0 / 116	Cancer
7	1	0 / 95	Colorectal cancer
8	1	0 / 2	Adenomas, multiple colorectal
9	1	0 / 124	Prostate cancer
10	1	0 / 48	Alzheimer disease, susceptibility to
11	1	0 / 7	Schizophrenia, susceptibility to
12	1	0 / 20	Parkinson disease
13	1	0 / 65	Hepatocellular carcinoma
14	1	0 / 3	Down syndrome, risk of
15	1	0 / 127	Melanoma and neural system tumor syndrome

Reference Signatures

Rank	p−value	#in/all	Geneset
1	4e−05	17 / 465	PROTEINATLAS_liver
2	2e−04	25 / 963	PROTEINATLAS_pancreas
3	3e−04	24 / 933	PROTEINATLAS_adrenal gland
4	4e−04	28 / 1194	PROTEINATLAS_stomach
5	9e−04	20 / 782	PROTEINATLAS_thyroid gland
6	9e−04	28 / 1268	PROTEINATLAS_colon
7	1e−03	18 / 681	PROTEINATLAS_lung
8	2e−03	10 / 275	Chaussabel_3,7_Spliceosome
9	2e−03	15 / 535	PROTEINATLAS_spleen
10	3e−03	25 / 1173	PROTEINATLAS_rectum
11	3e−03	21 / 929	PROTEINATLAS_bronchus
12	5e−03	15 / 598	PROTEINATLAS_prostate
13	5e−03	23 / 1097	PROTEINATLAS_kidney
14	5e−03	13 / 490	PROTEINATLAS_heart muscle
15	5e−03	24 / 1167	PROTEINATLAS_gallbladder

BP

Rank	p−value	#in/all	Geneset
1	3e−04	4 / 29	fatty acid beta−oxidation
2	7e−04	5 / 61	apoptotic signaling pathway
3	1e−03	4 / 41	glycosphingolipid metabolic process
4	1e−03	3 / 19	membrane protein ectodomain proteolysis
5	2e−03	3 / 20	signal peptide processing
6	2e−03	10 / 292	positive regulation of apoptotic process
7	3e−03	4 / 52	ER−associated ubiquitin−dependent protein catabolic process
8	4e−03	3 / 27	positive regulation of release of cytochrome c from mitochondria
9	5e−03	3 / 29	ATP metabolic process
10	7e−03	2 / 11	beta−amyloid metabolic process
11	7e−03	2 / 11	MyD88−independent toll−like receptor signaling pathway
12	7e−03	10 / 342	intracellular signal transduction
13	8e−03	2 / 12	anterograde synaptic vesicle transport
14	8e−03	2 / 12	cellular response to epinephrine stimulus
15	8e−03	2 / 12	regulation of dendritic spine morphogenesis

CC

Rank	p−value	#in/all	Geneset
1	5e−07	37 / 1304	mitochondrion
2	1e−03	4 / 42	cell leading edge
3	2e−03	19 / 777	Golgi apparatus
4	2e−03	76 / 4822	cytoplasm
5	3e−03	51 / 2979	cytosol
6	3e−03	8 / 207	lysosome
7	4e−03	5 / 91	perikaryon
8	5e−03	11 / 374	mitochondrial inner membrane
9	8e−03	2 / 12	proteasome regulatory particle
10	9e−03	5 / 109	late endosome
11	1e−02	3 / 38	cis−Golgi network
12	1e−02	3 / 39	chromosome, telomeric region
13	1e−02	2 / 14	BLOC−1 complex
14	1e−02	2 / 15	proteasome accessory complex
15	1e−02	10 / 379	centrosome

Colon Cancer

Rank	p−value	#in/all	Geneset
1	4e−32	180 / 7354	TssF_Colon
2	2e−27	199 / 9555	TssA_Colon
3	6e−25	189 / 9054	Tx_Colon
4	4e−24	150 / 6138	TssD2_Colon
5	4e−22	178 / 8568	TxWk_Colon
6	6e−22	135 / 5373	EnhWk1_Colon
7	2e−17	86 / 2845	TxEnhG1_Colon
8	8e−17	193 / 10779	Enh_Colon
9	1e−15	166 / 8678	Quies3_Colon
10	3e−12	75 / 2810	EnhA_Colon
11	7e−08	42 / 1470	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
12	1e−07	38 / 1281	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv
13	8e−07	168 / 10999	TssWk_Colon
14	1e−03	31 / 1468	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
15	2e−03	5 / 76	Pentrack_CRC_TCGA_corr_N_msi−h_DN

HM

Rank	p−value	#in/all	Geneset
1	2e−04	9 / 167	HALLMARK_OXIDATIVE_PHOSPHORYLATION
2	5e−03	7 / 175	HALLMARK_XENOBIOTIC_METABOLISM
3	5e−03	7 / 176	HALLMARK_ADIPOGENESIS
4	1e−02	3 / 40	HALLMARK_WNT_BETA_CATENIN_SIGNALING
5	2e−02	5 / 137	HALLMARK_UV_RESPONSE_UP
6	2e−02	5 / 138	HALLMARK_FATTY_ACID_METABOLISM
7	4e−02	2 / 29	HALLMARK_NOTCH_SIGNALING
8	5e−02	3 / 69	HALLMARK_CHOLESTEROL_HOMEOSTASIS
9	7e−02	5 / 185	HALLMARK_MTORC1_SIGNALING
10	7e−02	5 / 186	HALLMARK_ESTROGEN_RESPONSE_EARLY
11	7e−02	5 / 186	HALLMARK_ESTROGEN_RESPONSE_LATE
12	7e−02	4 / 132	HALLMARK_UV_RESPONSE_DN
13	1e−01	4 / 151	HALLMARK_APOPTOSIS
14	2e−01	3 / 116	HALLMARK_SPERMATOGENESIS
15	2e−01	4 / 185	HALLMARK_TNFA_SIGNALING_VIA_NFKB

Melanoma

Rank	p−value	#in/all	Geneset
1	0.3	1 / 27	Hugo_melanoma−all−LEF1_UP
2	0.4	1 / 43	Hugo_melanoma−BRAFmut−MET_UP
3	1.0	0 / 30	Hugo_melanoma−all−MET_UP
4	1.0	0 / 54	Hugo_melanoma−all−MET_DN
5	1.0	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
6	1.0	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

miRNA target

Rank	p−value	#in/all	Geneset
1	4e−04	4 / 31	hsa−miR−1237
2	6e−03	4 / 61	hsa−miR−556−5p
3	7e−03	4 / 64	hsa−miR−1275
4	7e−03	6 / 144	hsa−miR−140−5p
5	7e−03	4 / 66	hsa−miR−326
6	8e−03	6 / 150	hsa−miR−338−3p
7	9e−03	3 / 37	hsa−miR−1224−5p
8	1e−02	3 / 39	hsa−miR−601
9	1e−02	4 / 77	hsa−miR−422a
10	1e−02	3 / 43	hsa−miR−412
11	2e−02	5 / 133	hsa−miR−485−5p
12	2e−02	4 / 93	hsa−miR−378
13	3e−02	5 / 146	hsa−miR−138
14	3e−02	2 / 23	hsa−miR−668
15	3e−02	11 / 491	hsa−miR−107

Telomeres

Rank	p−value	#in/all	Geneset
1	0.3	1 / 27	Nabetani_alt len telomeres_genes_ko
2	1.0	0 / 13	Alternative lengthening of telomeres
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Brain

Rank	p−value	#in/all	Geneset
1	5e−22	189 / 9504	Overlap_fetal_midbrain_K9K27me3
2	3e−17	190 / 10430	Overlap_fetal_midbrain_Quies
3	3e−14	85 / 3164	Mid_Frontal_Lobe_ZNF
4	2e−10	166 / 9815	Overlap_fetal_midbrain_ReprPC
5	8e−08	109 / 5936	Overlap_fetal_midbrain_HetRpts
6	2e−06	154 / 9917	Overlap_fetal_midbrain_ReprPCWk
7	1e−04	23 / 818	Mid_Frontal_Lobe_Het
8	3e−04	71 / 4112	Mid_Frontal_Lobe_ReprPC
9	3e−03	47 / 2709	Mid_Frontal_Lobe_HetRpts
10	3e−02	16 / 796	Overlap_fetal_midbrain_ZNF
11	1e−01	26 / 1728	Fetal_ReprPCWk
12	1e−01	3 / 110	Overlap_fetal_midbrain_Tx
13	2e−01	14 / 906	Fetal_HetRpts
14	2e−01	29 / 2127	Mid_Frontal_Lobe_K9K27me3
15	2e−01	21 / 1506	Mid_Frontal_Lobe_Quies

Chr

Rank	p−value	#in/all	Geneset
1	0.002	30 / 1467	Chr 19
2	0.019	4 / 87	Chr Y
3	0.094	16 / 954	Chr 9
4	0.097	16 / 959	Chr 16
5	0.099	10 / 536	Chr 22
6	0.151	21 / 1411	Chr 11
7	0.189	10 / 619	Chr 20
8	0.370	17 / 1318	Chr 17
9	0.379	15 / 1160	Chr 12
10	0.379	29 / 2323	Chr 1
11	0.560	14 / 1217	Chr 3
12	0.644	9 / 836	Chr 8
13	0.658	3 / 289	Chr 21
14	0.729	9 / 902	Chr 4
15	0.875	9 / 1060	Chr 5

Glio

Rank	p−value	#in/all	Geneset
1	0.003	34 / 1777	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
2	0.005	37 / 2043	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
3	0.024	3 / 53	Hopp_Sturm_GBM_Epi3_C1_IDH_UP_fetus_DN
4	0.026	25 / 1417	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
5	0.042	2 / 28	KIM prognostic signature LTS vs. STS
6	0.090	1 / 8	Sturm_GBM_Meth_overexpression_C_G34_UP
7	0.100	1 / 9	WILLSCHER_GBM_LTSmut_proteomics−A_UP
8	0.101	14 / 820	Sturm_GBM_Meth_overexpression_E_G34_UP
9	0.107	3 / 98	WILLSCHER_GBM_proteomics_wtOnly_SpotB
10	0.112	3 / 100	GIEZELT_GBM_STS_down_VS_LTS
11	0.121	1 / 11	KIM amplified & overexpressed in LTS
12	0.123	2 / 52	Sturm_GBM_Meth_overexpression_F_IDH_UP
13	0.125	6 / 290	Hopp_Sturm_GBM_Epi3_C_IDH_UP
14	0.131	1 / 12	WILLSCHER_GBM_LTSmut_proteomics−B_UP
15	0.135	2 / 55	Stuehler_Proteins_up_in_STS

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.002	7 / 147	Homuth_BMI−associated−genes_UP
2	0.448	3 / 211	Homuth_BMI−associated−genes_DN
3	0.669	1 / 94	DUMEAUX_Smoking enriched genes
4	1.000	0 / 10	DUMEAUX_Smoking literature genes up
5	1.000	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
6	1.000	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
7	1.000	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
8	1.000	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
9	1.000	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
10	1.000	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
11	1.000	0 / 10	DUMEAUX_Women normal BMI literature genes up
12	1.000	0 / 17	DUMEAUX_High bmi enriched genes
13	1.000	0 / 31	DUMEAUX_Fasting enriched genes
14	1.000	0 / 18	Huan_blood−pressure_SBP−signature
15	1.000	0 / 16	Huan_blood−pressure_DBP−signature

MF

Rank	p−value	#in/all	Geneset
1	3e−05	136 / 8818	protein binding
2	1e−03	3 / 19	aspartic−type endopeptidase activity
3	2e−03	8 / 185	magnesium ion binding
4	1e−02	9 / 315	protein serine/threonine kinase activity
5	1e−02	2 / 15	cysteine−type endopeptidase activator activity involved in apoptotic process
6	1e−02	2 / 16	hydrogen ion transmembrane transporter activity
7	2e−02	2 / 17	dioxygenase activity
8	2e−02	5 / 133	ATPase activity
9	3e−02	20 / 1065	zinc ion binding
10	3e−02	2 / 24	fatty−acyl−CoA binding
11	3e−02	2 / 24	transmembrane transporter activity
12	3e−02	3 / 60	transcriptional repressor activity, RNA polymerase II transcription regulatory r
13	3e−02	2 / 25	ephrin receptor binding
14	4e−02	5 / 160	carbohydrate binding
15	4e−02	13 / 646	protein homodimerization activity

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.1	1 / 13	BENTINK_e2f3.2
2	0.1	1 / 13	BENTINK_src.10
3	0.2	1 / 14	BENTINK_ras.6
4	0.2	1 / 15	GUSTAFSON_PI3K_DN
5	1.0	0 / 14	GUSTAFSON_PI3K_UP
6	1.0	0 / 13	BENTINK_e2f3.1
7	1.0	0 / 13	BENTINK_myc.1
8	1.0	0 / 12	BENTINK_ras.1
9	1.0	0 / 11	BENTINK_ras.4
10	1.0	0 / 12	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	4e−12	134 / 6868	ICGC_Elf1_targets
2	7e−12	126 / 6322	ICGC_Tcf3_targets
3	4e−11	110 / 5312	ICGC_Tcf12_targets
4	6e−11	96 / 4362	ICGC_Creb1_targets
5	1e−10	111 / 5466	ICGC_Nficsc81335_targets
6	2e−09	131 / 7247	ICGC_Runx3_targets
7	2e−09	108 / 5518	ICGC_Stat5_targets
8	3e−09	99 / 4890	ICGC_Bclaf101388_targets
9	3e−09	114 / 5984	ICGC_Mta3_targets
10	4e−09	101 / 5067	ICGC_Taf1_targets
11	6e−09	117 / 6267	ICGC_Yy1_targets
12	6e−09	98 / 4881	ICGC_Atf2_targets
13	8e−09	105 / 5410	ICGC_Foxm1_targets
14	1e−08	91 / 4468	ICGC_Egr1_targets
15	2e−08	89 / 4345	ICGC_Zeb1_targets

K−Means Cluster

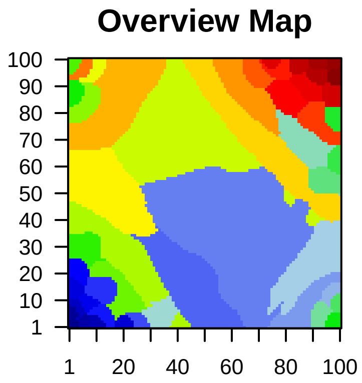
Spot Summary: X

metagenes = 40
genes = 493

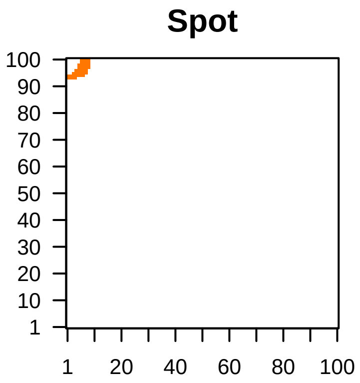
<r> metagenes = 0.89
<r> genes = 0.21
beta: r2= 9.53 / log p= −Inf

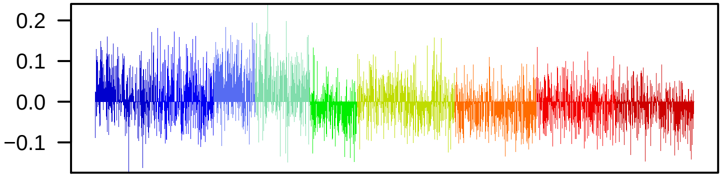
samples with spot = 105 (3.1 %)
A * : 21 (6.1 %)
A C * : 17 (5.2 %)
A C F * : 27 (11.5 %)
A F * : 25 (8.1 %)
C F * : 2 (0.8 %)
F * : 10 (1.8 %)
J * : 3 (0.7 %)

Overview Map



Spot





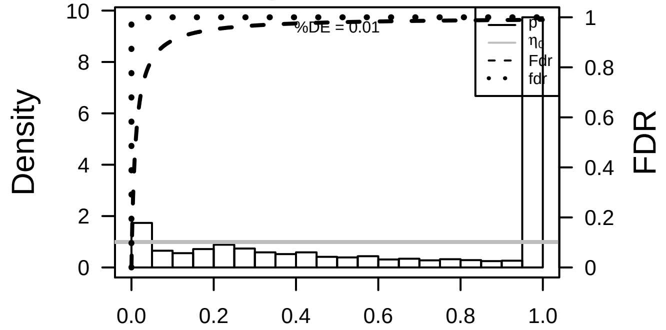
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_168730	1.63	−1.3	0.24	LGALS2	galectin 2 [Source:HGNC Symbol;Acc:HGNC:6562]
2	ILMN_182151	1.46	−1.14	0.23		
3	ILMN_231260	1.31	−1.1	0.21	IRF5	interferon regulatory factor 5 [Source:HGNC Symbol;Acc:HGI
4	ILMN_168610	1.27	−0.47	0.3	CCL23	C−C motif chemokine ligand 23 [Source:HGNC Symbol;Acc:H
5	ILMN_327117	1.14	−0.49	0.19		
6	ILMN_178404	0.93	−0.68	0.41		
7	ILMN_173683	0.93	−0.53	0.31	PRSS33	protease, serine 33 [Source:HGNC Symbol;Acc:HGNC:3040
8	ILMN_169531	0.89	−0.72	0.4	HLA−DMA	major histocompatibility complex, class II, DM alpha [Source:I
9	ILMN_170332	0.87	−0.55	0.3	PTGDR2	prostaglandin D2 receptor 2 [Source:HGNC Symbol;Acc:HGN
10	ILMN_172397	0.86	−0.55	0.38	SLC29A1	solute carrier family 29 member 1 (Augustine blood group) [S
11	ILMN_175692	0.84	−0.72	0.58	ADAM15	ADAM metallopeptidase domain 15 [Source:HGNC Symbol;A
12	ILMN_171962	0.84	−0.59	0.51	SLC27A3	solute carrier family 27 member 3 [Source:HGNC Symbol;Ac
13	ILMN_179452	0.82	−0.8	0.21	EIF5A	eukaryotic translation initiation factor 5A [Source:HGNC Sym
14	ILMN_179191	0.81	−0.92	0.32	SIDT2	SID1 transmembrane family member 2 [Source:HGNC Symb
15	ILMN_134329	0.81	−0.82	0.46	GAPDH	glyceraldehyde−3−phosphate dehydrogenase [Source:HGNC
16	ILMN_239029	0.8	−0.58	0.48	PSMB8	proteasome subunit beta 8 [Source:HGNC Symbol;Acc:HGN
17	ILMN_180225	0.77	−0.73	0.63	GAPDH	glyceraldehyde−3−phosphate dehydrogenase [Source:HGNC
18	ILMN_172397	0.77	−0.81	0.52	LGALS1	galectin 1 [Source:HGNC Symbol;Acc:HGNC:6561]
19	ILMN_166608	0.74	−0.67	0.17	OLIG1	oligodendrocyte transcription factor 1 [Source:HGNC Symbol
20	ILMN_177824	0.73	−0.59	0.34	GFOD1	glucose−fructose oxidoreductase domain containing 1 [Sourc

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−68	311 / 7354	Colon	TssF_Colon
2	3e−62	208 / 3450	Chror	4_TxTrans_Fibroblasts
3	3e−57	337 / 9555	Colon	TssA_Colon
4	3e−52	321 / 9054	Colon	Tx_Colon
5	3e−52	252 / 5699	Chror	6_EnhG_Melanocytes
6	2e−51	175 / 2845	Colon	TxEnhG1_Colon
7	7e−49	225 / 4795	Chror	6_EnhG_Fibroblasts
8	1e−48	362 / 11836	Chror	3_TssF_Melanocytes
9	7e−46	365 / 12298	Chror	2_TssA_Melanocytes
10	6e−42	313 / 9504	Brain	Overlap_fetal_midbrain_K9K27me3
11	1e−40	243 / 6138	Colon	TssD2_Colon
12	5e−39	166 / 3164	Brain	Mid_Frontal_Lobe_ZNF
13	6e−39	131 / 2028	Chror	4_TxTrans_Melanocytes
14	3e−38	329 / 10779	Colon	Enh_Colon
15	2e−34	282 / 8568	Colon	TxWk_Colon
16	6e−34	357 / 12983	Chror	2_TssA_Neuronal_Progenitor
17	1e−30	142 / 2810	Colon	EnhA_Colon
18	1e−29	325 / 11455	Chror	2_TssA_Fibroblasts
19	3e−29	292 / 9635	Chror	3_TssF_Fibroblasts
20	2e−28	216 / 5956	Chror	3_TssF_Neuronal_Progenitor
21	1e−27	201 / 5373	Colon	EnhWk1_Colon
22	1e−20	276 / 9815	Brain	Overlap_fetal_midbrain_ReprPC
23	3e−20	184 / 5356	Lympl	HOPP_Txn_transition
24	1e−18	251 / 8771	Chror	5_Tx_Melanocytes
25	9e−18	280 / 10430	Brain	Overlap_fetal_midbrain_Quies
26	2e−17	55 / 789	Colon	TxEnhG2_Colon
27	3e−17	170 / 5067	TF	ICGC_Taf1_targets
28	2e−16	227 / 7854	Chror	5_Tx_Fibroblasts
29	4e−16	177 / 5518	TF	ICGC_Stat5_targets
30	2e−15	53 / 818	Brain	Mid_Frontal_Lobe_Het
31	4e−14	239 / 8818	MF	protein binding
32	8e−14	169 / 5442	TF	ICGC_Pmlsc71910_targets
33	9e−14	147 / 4468	TF	ICGC_Egr1_targets
34	1e−13	201 / 6970	Chror	5_Tx_Neuronal_Progenitor
35	6e−13	165 / 5383	TF	ICGC_Sp1_targets
36	7e−13	43 / 656	GSEA	KIM_ALL_DISORDERS_OLIGODENDROCYTE_NUMBER_CORR_UP
37	8e−13	291 / 11847	Chror	7_Enh_Neuronal_Progenitor
38	1e−12	136 / 4131	TF	ICGC_Nfatc1_targets
39	1e−12	207 / 7448	Lympl	HOPP_Strong_enhancer
40	2e−12	141 / 4362	TF	ICGC_Creb1_targets

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.3	3 / 111	HORVATH_aging_genes meth DOWN
2	0.5	3 / 142	HORVATH_aging_genes meth UP
3	1.0	0 / 58	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Cancer

Rank	p−value	#in/all	Geneset
1	0.004	4 / 36	PanCan_HK_geneset_nanostring
2	0.025	11 / 301	SPANG_BCL6−index2
3	0.088	0 / 14	RHODES_UNDIFFERENTIATED_CANCER
4	0.171	4 / 117	PanCan_Driver_Gene_geneset_nanostring
5	0.212	0 / 14	LIU_PROSTATE_CANCER_UP
6	0.215	1 / 13	GENTLES_modul2
7	0.215	1 / 13	GENTLES_modul12
8	0.233	5 / 178	SPANG_LPS−index2
9	0.258	1 / 16	GENTLES_modul7
10	0.270	12 / 527	Lembcke_Normal vs Adenoma
11	0.332	0 / 14	LIU_COMMON_CANCER_GENES
12	0.391	2 / 73	SHAUGHNESSY_MM high risk
13	0.573	0 / 15	LIU_PROSTATE_CANCER_DN
14	0.576	1 / 46	PanCan_DNARepair_geneset_nanostring
15	0.584	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN

Chromatin states

Rank	p−value	#in/all	Geneset
1	3e−62	208 / 3450	4_TxTrans_Fibroblasts
2	3e−52	252 / 5699	6_EnhG_Melanocytes
3	7e−49	225 / 4795	6_EnhG_Fibroblasts
4	1e−48	362 / 11836	3_TssF_Melanocytes
5	7e−46	365 / 12298	2_TssA_Melanocytes
6	6e−39	131 / 2028	4_TxTrans_Melanocytes
7	6e−34	357 / 12983	2_TssA_Neuronal_Progenitor
8	1e−29	325 / 11455	2_TssA_Fibroblasts
9	3e−29	292 / 9635	3_TssF_Fibroblasts
10	2e−28	216 / 5956	3_TssF_Neuronal_Progenitor
11	1e−18	251 / 8771	5_Tx_Melanocytes
12	2e−16	227 / 7854	5_Tx_Fibroblasts
13	1e−13	201 / 6970	5_Tx_Neuronal_Progenitor
14	8e−13	291 / 11847	7_Enh_Neuronal_Progenitor
15	4e−09	294 / 12741	7_Enh_Melanocytes

GSEA C2

Rank	p−value	#in/all	Geneset
1	7e−13	43 / 656	KIM_ALL_DISORDERS_OLIGODENDROCYTE_NUMBER_CORR_UP
2	6e−11	38 / 607	MILI_PSEUDOPODIA_HAPTOTAXIS_DN
3	1e−09	16 / 123	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_14
4	8e−09	25 / 346	MULLIGHAN_MLL_SIGNATURE_1_UP
5	3e−08	28 / 451	ENK_UV_RESPONSE_KERATINOCYTE_UP
6	5e−08	26 / 407	SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_UP
7	7e−08	14 / 123	KIM_ALL_DISORDERS_DURATION_CORR_DN
8	8e−08	32 / 594	KIM_BIPOLAR_DISORDER_OLIGODENDROCYTE_DENSITY_CORR_UP
9	8e−08	36 / 723	GRADE_COLON_CANCER_UP
10	9e−08	16 / 167	PURBEY_TARGETS_OF_CTBP1_AND_SATB1_DN
11	1e−07	27 / 450	STARK_PREFRONTAL_CORTEX_22Q11_DELETION_DN
12	1e−07	19 / 237	LU_EZH2_TARGETS_UP
13	7e−07	12 / 107	KEGG_LYSOSOME
14	8e−07	23 / 382	MULLIGHAN_MLL_SIGNATURE_2_UP
15	1e−06	29 / 569	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_DN

Lymphoma

Rank	p−value	#in/all	Geneset
1	3e−20	184 / 5356	HOPP_Txn_transition
2	1e−12	207 / 7448	HOPP_Strong_enhancer
3	4e−12	221 / 8226	HOPP_Active_promoter
4	1e−10	197 / 7275	HOPP_Txn_elongation
5	3e−05	190 / 8098	HOPP_Weak_promoter
6	4e−04	41 / 1270	SPANG_BCR UP
7	1e−03	27 / 777	WIRTH_lymphoma937_spot D
8	2e−03	18 / 455	SPANG_CD40 6hrs DN
9	5e−03	25 / 772	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell line_
10	7e−03	5 / 66	TARTE_Plasma cell signature
11	9e−03	4 / 45	Subero_INT_hypo_meth
12	1e−02	33 / 1169	SPANG_BCR DN
13	2e−02	2 / 13	Subero_B−CLL_hypo_meth
14	3e−02	9 / 232	WIRTH_lymphoma937_spot B
15	4e−02	3 / 39	CARO_OxPhos_in_DLBCL_UP

miRNA Disease

Rank	p−value	#in/all	Geneset
1	1	0 / 7	Thyroid carcinoma, papillary
2	1	0 / 123	Pancreatic cancer
3	1	0 / 68	Glioblastoma multiforme, somatic
4	1	0 / 63	Gastrointestinal
5	1	0 / 3	Pituitary adenoma
6	1	0 / 116	Cancer
7	1	0 / 95	Colorectal cancer
8	1	0 / 2	Adenomas, multiple colorectal
9	1	0 / 124	Prostate cancer
10	1	0 / 48	Alzheimer disease, susceptibility to
11	1	0 / 7	Schizophrenia, susceptibility to
12	1	0 / 20	Parkinson disease
13	1	0 / 65	Hepatocellular carcinoma
14	1	0 / 3	Down syndrome, risk of
15	1	0 / 127	Melanoma and neural system tumor syndrome

Reference Signatures

Rank	p−value	#in/all	Geneset
1	4e−11	41 / 681	PROTEINATLAS_lung
2	3e−09	53 / 1194	PROTEINATLAS_stomach
3	1e−08	48 / 1063	PROTEINATLAS_tonsil
4	2e−08	43 / 912	PROTEINATLAS_fallopian tube
5	9e−08	43 / 960	PROTEINATLAS_cerebellum
6	1e−07	43 / 963	PROTEINATLAS_pancreas
7	9e−07	45 / 1118	PROTEINATLAS_placenta
8	1e−06	39 / 912	PROTEINATLAS_urinary bladder
9	1e−06	46 / 1167	PROTEINATLAS_gallbladder
10	4e−06	38 / 929	PROTEINATLAS_bronchus
11	5e−06	47 / 1268	PROTEINATLAS_colon
12	6e−06	33 / 759	PROTEINATLAS_epididymis
13	2e−05	43 / 1173	PROTEINATLAS_rectum
14	2e−05	28 / 623	PROTEINATLAS_seminal vesicle
15	2e−05	41 / 1097	PROTEINATLAS_kidney

BP

Rank	p−value	#in/all	Geneset
1	5e−06	5 / 15	apoptotic cell clearance
2	4e−05	6 / 35	activation of JUN kinase activity
3	1e−04	8 / 81	antigen processing and presentation of exogenous peptide antigen via MHC c
4	1e−04	4 / 15	fatty acid beta−oxidation using acyl−CoA dehydrogenase
5	2e−04	12 / 185	cell cycle
6	6e−04	10 / 155	positive regulation of I−kappaB kinase/NF−kappaB signaling
7	6e−04	5 / 38	lipid homeostasis
8	7e−04	3 / 10	pentose−phosphate shunt
9	8e−04	4 / 23	mitochondrial translation
10	8e−04	11 / 189	intracellular protein transport
11	9e−04	4 / 24	positive regulation of TOR signaling
12	9e−04	5 / 41	gluconeogenesis
13	9e−04	21 / 530	biological_process
14	1e−03	13 / 255	viral process
15	1e−03	9 / 137	ER to Golgi vesicle−mediated transport

CC

Rank	p−value	#in/all	Geneset
1	6e−09	98 / 2979	cytosol
2	2e−07	134 / 4822	cytoplasm
3	2e−07	81 / 2464	extracellular exosome
4	7e−07	34 / 721	nucleolus
5	1e−06	80 / 2535	nucleoplasm
6	2e−06	130 / 4828	nucleus
7	2e−06	49 / 1304	mitochondrion
8	8e−06	64 / 1979	membrane
9	3e−05	15 / 234	lysosomal membrane
10	3e−05	14 / 207	lysosome
11	2e−04	18 / 374	mitochondrial inner membrane
12	4e−04	9 / 119	vesicle
13	2e−03	4 / 29	mitochondrial large ribosomal subunit
14	3e−03	6 / 78	catalytic step 2 spliceosome
15	4e−03	6 / 81	late endosome membrane

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−68	311 / 7354	TssF_Colon
2	3e−57	337 / 9555	TssA_Colon
3	3e−52	321 / 9054	Tx_Colon
4	2e−51	175 / 2845	TxEnhG1_Colon
5	1e−40	243 / 6138	TssD2_Colon
6	3e−38	329 / 10779	Enh_Colon
7	2e−34	282 / 8568	TxWk_Colon
8	1e−30	142 / 2810	EnhA_Colon
9	1e−27	201 / 5373	EnhWk1_Colon
10	2e−17	55 / 789	TxEnhG2_Colon
11	3e−10	58 / 1281	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv
12	2e−09	220 / 8678	Quies3_Colon
13	3e−09	263 / 10999	TssWk_Colon
14	6e−09	60 / 1470	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
15	9e−08	59 / 1547	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a

HM

Rank	p−value	#in/all	Geneset
1	7e−05	12 / 167	HALLMARK_OXIDATIVE_PHOSPHORYLATION
2	3e−03	7 / 103	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
3	8e−03	9 / 185	HALLMARK_P53_PATHWAY
4	2e−02	4 / 54	HALLMARK_MYC_TARGETS_V2
5	2e−02	8 / 183	HALLMARK_APICAL_JUNCTION
6	2e−02	8 / 186	HALLMARK_IL2_STAT5_SIGNALING
7	3e−02	6 / 130	HALLMARK_DNA_REPAIR
8	3e−02	5 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING
9	5e−02	7 / 176	HALLMARK_ADIPOGENESIS
10	1e−01	5 / 137	HALLMARK_UV_RESPONSE_UP
11	1e−01	6 / 183	HALLMARK_GLYCOLYSIS
12	1e−01	6 / 185	HALLMARK_MTORC1_SIGNALING
13	1e−01	6 / 187	HALLMARK_COMPLEMENT
14	1e−01	6 / 189	HALLMARK_HYPOXIA
15	2e−01	2 / 41	HALLMARK_APICAL_SURFACE

Melanoma

Rank	p−value	#in/all	Geneset
1	0.1	2 / 30	Hugo_melanoma−all−MET_UP
2	0.6	1 / 54	Hugo_melanoma−all−MET_DN
3	1.0	0 / 43	Hugo_melanoma−BRAFmut−MET_UP
4	1.0	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
5	1.0	0 / 27	Hugo_melanoma−all−LEF1_UP
6	1.0	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

miRNA target

Rank	p−value	#in/all	Geneset
1	0.002	4 / 30	hsa−miR−371−3p
2	0.003	5 / 54	hsa−miR−504
3	0.005	6 / 84	hsa−miR−486−3p
4	0.005	6 / 86	hsa−miR−339−5p
5	0.006	5 / 62	hsa−miR−324−3p
6	0.010	5 / 71	hsa−miR−331−3p
7	0.016	3 / 29	hsa−miR−1293
8	0.023	2 / 13	hsa−miR−147b
9	0.024	5 / 88	hsa−miR−608
10	0.026	3 / 35	hsa−miR−197
11	0.029	4 / 63	hsa−miR−455−3p
12	0.034	4 / 66	hsa−miR−637
13	0.034	5 / 97	hsa−miR−125a−3p
14	0.035	3 / 39	hsa−miR−525−3p
15	0.036	8 / 204	hsa−miR−432

Telomeres

Rank	p−value	#in/all	Geneset
1	1	0 / 13	Alternative lengthening of telomeres
2	1	0 / 27	Nabetani_alt len telomeres_genes_ko
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Brain

Rank	p−value	#in/all	Geneset
1	6e−42	313 / 9504	Overlap_fetal_midbrain_K9K27me3
2	5e−39	166 / 3164	Mid_Frontal_Lobe_ZNF
3	1e−20	276 / 9815	Overlap_fetal_midbrain_ReprPC
4	9e−18	280 / 10430	Overlap_fetal_midbrain_Quies
5	2e−15	53 / 818	Mid_Frontal_Lobe_Het
6	8e−11	97 / 2709	Mid_Frontal_Lobe_HetRpts
7	6e−09	67 / 1728	Fetal_ReprPCWk
8	2e−06	153 / 5936	Overlap_fetal_midbrain_HetRpts
9	2e−06	35 / 796	Overlap_fetal_midbrain_ZNF
10	1e−02	94 / 4112	Mid_Frontal_Lobe_ReprPC
11	2e−02	8 / 180	Overlap_fetal_midbrain_Het
12	4e−02	61 / 2654	Fetal_Quies
13	7e−02	199 / 9917	Overlap_fetal_midbrain_ReprPCWk
14	1e−01	11 / 386	Fetal_ZNF
15	1e−01	40 / 1784	Mid_Frontal_Lobe_ReprPCWk

Chr

Rank	p−value	#in/all	Geneset
1	4e−06	39 / 959	Chr 16
2	6e−06	48 / 1318	Chr 17
3	4e−05	49 / 1467	Chr 19
4	5e−03	40 / 1411	Chr 11
5	1e−01	16 / 619	Chr 20
6	4e−01	11 / 536	Chr 22
7	4e−01	6 / 289	Chr 21
8	5e−01	18 / 954	Chr 9
9	5e−01	43 / 2323	Chr 1
10	7e−01	13 / 768	Chr 14
11	8e−01	19 / 1211	Chr 6
12	8e−01	1 / 87	Chr Y
13	9e−01	17 / 1160	Chr 12
14	9e−01	17 / 1170	Chr 7
15	9e−01	21 / 1492	Chr 2

Glio

Rank	p−value	#in/all	Geneset
1	6e−07	37 / 820	Sturm_GBM_Meth_overexpression_E_G34_UP
2	1e−04	6 / 44	WILLSCHER_GBM_Verhaak−PNwt_up
3	4e−04	53 / 1777	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
4	1e−03	57 / 2043	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
5	2e−03	5 / 50	WILLSCHER_GBM_proteomics_wtOnly_SpotG
6	3e−03	9 / 157	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
7	6e−03	6 / 87	Sturm_GBM_Meth_overexpression_I_RTK I 'PDGFRA'_UP
8	2e−02	4 / 52	Sturm_GBM_Meth_overexpression_F_IDH_UP
9	2e−02	6 / 110	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
10	2e−02	4 / 55	Stuehler_Proteins_up_in_STS
11	2e−02	3 / 32	Donson−Misc immune function−associated with LTS in HGA
12	2e−02	14 / 419	Down_a
13	3e−02	2 / 15	WILLSCHER_GBM_STSwt_proteomics−O_UP
14	4e−02	5 / 98	WILLSCHER_GBM_proteomics_wtOnly_SpotB
15	6e−02	5 / 113	GIEZELT_GBM_WT_up_VS_mut

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.06	6 / 147	Homuth_BMI−associated−genes_UP
2	0.11	2 / 31	DUMEAUX_Fasting enriched genes
3	0.14	1 / 8	DUMEAUX_Monocytes in smokers literature genes up
4	0.35	5 / 211	Homuth_BMI−associated−genes_DN
5	0.83	1 / 94	DUMEAUX_Smoking enriched genes
6	1.00	0 / 10	DUMEAUX_Smoking literature genes up
7	1.00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
8	1.00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
9	1.00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
10	1.00	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
11	1.00	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
12	1.00	0 / 10	DUMEAUX_Women normal BMI literature genes up
13	1.00	0 / 17	DUMEAUX_High bmi enriched genes
14	1.00	0 / 18	Huan_blood−pressure_SBP−signature
15	1.00	0 / 16	Huan_blood−pressure_DBP−signature

MF

Rank	p−value	#in/all	Geneset
1	4e−14	239 / 8818	protein binding
2	1e−07	44 / 1013	poly(A) RNA binding
3	9e−04	7 / 83	oxidoreductase activity
4	2e−03	3 / 13	oxidoreductase activity, acting on the CH−CH group of donors, with a flavin as
5	2e−03	12 / 243	GTPase activator activity
6	4e−03	9 / 169	structural constituent of ribosome
7	5e−03	6 / 84	hydrolase activity
8	5e−03	7 / 112	Rab GTPase binding
9	6e−03	8 / 145	nucleic acid binding
10	6e−03	3 / 20	DNA−directed RNA polymerase activity
11	6e−03	3 / 20	L−ascorbic acid binding
12	7e−03	3 / 22	polyubiquitin binding
13	7e−03	3 / 22	protein kinase activator activity
14	7e−03	3 / 22	transferase activity
15	8e−03	3 / 23	proton−transporting ATPase activity, rotational mechanism

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.2	1 / 11	BENTINK_ras.4
2	1.0	0 / 14	GUSTAFSON_PI3K_UP
3	1.0	0 / 15	GUSTAFSON_PI3K_DN
4	1.0	0 / 13	BENTINK_e2f3.1
5	1.0	0 / 13	BENTINK_e2f3.2
6	1.0	0 / 13	BENTINK_myc.1
7	1.0	0 / 12	BENTINK_ras.1
8	1.0	0 / 14	BENTINK_ras.6
9	1.0	0 / 13	BENTINK_src.10
10	1.0	0 / 12	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	3e−17	170 / 5067	ICGC_Taf1_targets
2	4e−16	177 / 5518	ICGC_Stat5_targets
3	8e−14	169 / 5442	ICGC_Pmlsc71910_targets
4	9e−14	147 / 4468	ICGC_Egr1_targets
5	6e−13	165 / 5383	ICGC_Sp1_targets
6	1e−12	136 / 4131	ICGC_Nfatc1_targets
7	2e−12	141 / 4362	ICGC_Creb1_targets
8	8e−12	160 / 5312	ICGC_Tcf12_targets
9	1e−11	163 / 5466	ICGC_Nficsc81335_targets
10	1e−11	180 / 6267	ICGC_Yy1_targets
11	2e−11	173 / 5984	ICGC_Mta3_targets
12	2e−11	87 / 2255	ICGC_SrfV0416101_targets
13	3e−11	191 / 6868	ICGC_Elf1_targets
14	4e−11	179 / 6322	ICGC_Tcf3_targets
15	5e−11	85 / 2215	ICGC_GabpPcr2_targets

K−Means Cluster

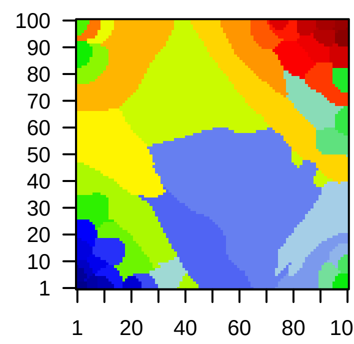
Spot Summary: Y

metagenes = 84
genes = 581

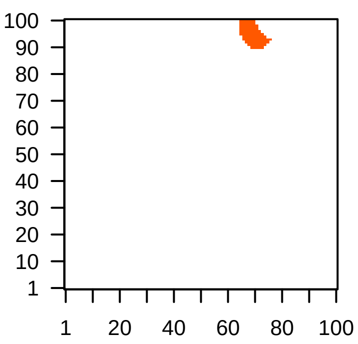
<r> metagenes = 0.91
<r> genes = 0.18
beta: r2= 4.6 / log p= −Inf

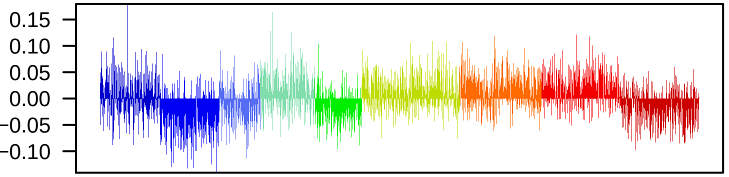
samples with spot = 8 (0.2 %)
A * : 2 (0.6 %)
A F * : 3 (1 %)
F J * : 1 (0.2 %)
J * : 2 (0.4 %)

Overview Map



Spot





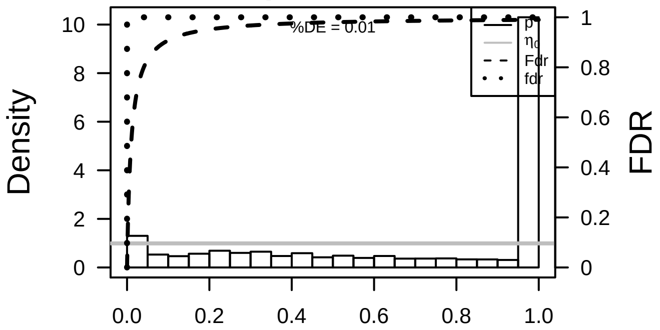
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_324366	0.8	−0.75	0.27	LOC613037	Homo sapiens nuclear pore complex interacting protein meml
2	ILMN_175378	0.76	−0.58	0.4	ZNF266	zinc finger protein 266 [Source:HGNC Symbol;Acc:HGNC:13
3	ILMN_180914	0.75	−0.33	0.1	FAM118A	family with sequence similarity 118 member A [Source:HGNC
4	ILMN_234304	0.75	−0.36	0.3	ABCB9	ATP binding cassette subfamily B member 9 [Source:HGNC
5	ILMN_172598	0.69	−0.36	0.26	EIF3CL	eukaryotic translation initiation factor 3 subunit C−like [Source
6	ILMN_166733	0.66	−0.74	0.16		
7	ILMN_323697	0.64	−0.41	0.23	LINC00667	long intergenic non−protein coding RNA 667 [Source:HGNC
8	ILMN_173005	0.63	−0.55	0.11		
9	ILMN_185990	0.61	−0.37	0.38	TRAPPC2L	trafficking protein particle complex 2 like [Source:HGNC Syml
10	ILMN_206932	0.6	−0.4	0.24		
11	ILMN_167183	0.6	−0.54	0.38	TAF1C	TATA−box binding protein associated factor, RNA polymerase
12	ILMN_323822	0.6	−0.43	0.21		
13	ILMN_323532	0.6	−0.39	0.28		Small nucleolar RNA SNORA71 [Source:RFAM;Acc:RF0005
14	ILMN_323798	0.55	−0.4	0.51	CARNS1	carnosine synthase 1 [Source:HGNC Symbol;Acc:HGNC:292
15	ILMN_237886	0.55	−0.52	0.37	SRSF5	serine and arginine rich splicing factor 5 [Source:HGNC Symt
16	ILMN_206156	0.55	−0.4	0.32	PLCH2	phospholipase C eta 2 [Source:HGNC Symbol;Acc:HGNC:29
17	ILMN_178023	0.54	−0.38	0.62	PMM1	phosphomannomutase 1 [Source:HGNC Symbol;Acc:HGNC:
18	ILMN_166479	0.54	−0.43	0.31	GRHPR	glyoxylate and hydroxypyruvate reductase [Source:HGNC Sy
19	ILMN_165736	0.54	−0.53	0.36	CBX7	chromobox 7 [Source:HGNC Symbol;Acc:HGNC:1557]
20	ILMN_173208	0.53	−0.54	0.3	MRI1	methylthioribose−1−phosphate isomerase 1 [Source:HGNC

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−64	384 / 9555	Colon	TssA_Colon
2	4e−64	373 / 9054	Colon	Tx_Colon
3	2e−63	362 / 8568	Colon	TxWk_Colon
4	4e−59	426 / 12298	Chror	2_TssA_Melanocytes
5	2e−56	324 / 7354	Colon	TssF_Colon
6	1e−53	367 / 9504	Brain	Overlap_fetal_midbrain_K9K27me3
7	5e−53	410 / 11836	Chror	3_TssF_Melanocytes
8	8e−53	403 / 11455	Chror	2_TssA_Fibroblasts
9	2e−51	427 / 12983	Chror	2_TssA_Neuronal_Progenitor
10	5e−47	243 / 4795	Chror	6_EnhG_Fibroblasts
11	7e−46	357 / 9635	Chror	3_TssF_Fibroblasts
12	7e−45	337 / 8771	Chror	5_Tx_Melanocytes
13	2e−43	314 / 7854	Chror	5_Tx_Fibroblasts
14	1e−41	258 / 5699	Chror	6_EnhG_Melanocytes
15	5e−40	287 / 6970	Chror	5_Tx_Neuronal_Progenitor
16	3e−38	291 / 7275	Lympl	HOPP_Txn_elongation
17	1e−37	346 / 9815	Brain	Overlap_fetal_midbrain_ReprPC
18	1e−36	260 / 6138	Colon	TssD2_Colon
19	3e−36	356 / 10430	Brain	Overlap_fetal_midbrain_Quies
20	3e−32	246 / 5936	Brain	Overlap_fetal_midbrain_HetRpts
21	5e−32	177 / 3450	Chror	4_TxTrans_Fibroblasts
22	7e−32	300 / 8226	Lympl	HOPP_Active_promoter
23	1e−30	228 / 5373	Colon	EnhWk1_Colon
24	6e−30	306 / 8678	Colon	Quies3_Colon
25	8e−30	350 / 10779	Colon	Enh_Colon
26	8e−28	237 / 5956	Chror	3_TssF_Neuronal_Progenitor
27	3e−27	376 / 12393	Chror	15_Quies_Neuronal_Progenitor
28	9e−26	156 / 3164	Brain	Mid_Frontal_Lobe_ZNF
29	2e−25	216 / 5356	Lympl	HOPP_Txn_transition
30	5e−23	203 / 5067	TF	ICGC_Taf1_targets
31	9e−22	138 / 2845	Colon	TxEnhG1_Colon
32	8e−21	179 / 4362	TF	ICGC_Creb1_targets
33	9e−20	365 / 12741	Chror	7_Enh_Melanocytes
34	2e−18	344 / 11847	Chror	7_Enh_Neuronal_Progenitor
35	4e−18	222 / 6322	TF	ICGC_Tcf3_targets
36	4e−18	202 / 5518	TF	ICGC_Stat5_targets
37	2e−17	324 / 10999	Colon	TssWk_Colon
38	5e−17	172 / 4468	TF	ICGC_Egr1_targets
39	7e−17	102 / 2028	Chror	4_TxTrans_Melanocytes
40	9e−17	231 / 6868	TF	ICGC_Elf1_targets

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.9	1 / 111	HORVATH_aging_genes meth DOWN
2	1.0	1 / 142	HORVATH_aging_genes meth UP
3	1.0	0 / 58	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	7e−07	65 / 1643	transcription, DNA−templated
2	2e−03	43 / 1272	regulation of transcription, DNA−templated
3	3e−03	3 / 14	apoptotic DNA fragmentation
4	3e−03	3 / 14	cellular response to nitric oxide
5	3e−03	11 / 196	mRNA splicing, via spliceosome
6	4e−03	3 / 15	protein localization to organelle
7	4e−03	4 / 31	nucleobase−containing compound metabolic process
8	4e−03	6 / 73	liver development
9	5e−03	3 / 17	acyl−CoA metabolic process
10	5e−03	3 / 17	brain morphogenesis
11	5e−03	15 / 335	protein transport
12	6e−03	3 / 18	histone methylation
13	7e−03	7 / 104	tumor necrosis factor−mediated signaling pathway
14	7e−03	3 / 19	RNA catabolic process
15	8e−03	5 / 59	protein localization

Brain

Rank	p−value	#in/all	Geneset
1	1e−53	367 / 9504	Overlap_fetal_midbrain_K9K27me3
2	1e−37	346 / 9815	Overlap_fetal_midbrain_ReprPC
3	3e−36	356 / 10430	Overlap_fetal_midbrain_Quies
4	3e−32	246 / 5936	Overlap_fetal_midbrain_HetRpts
5	9e−26	156 / 3164	Mid_Frontal_Lobe_ZNF
6	6e−11	280 / 9917	Overlap_fetal_midbrain_ReprPCWk
7	4e−09	74 / 1728	Fetal_ReprPCWk
8	4e−07	40 / 796	Overlap_fetal_midbrain_ZNF
9	2e−06	39 / 818	Mid_Frontal_Lobe_Het
10	4e−06	91 / 2709	Mid_Frontal_Lobe_HetRpts
11	1e−02	24 / 681	Overlap_fetal_midbrain_EnhP
12	2e−02	29 / 906	Fetal_HetRpts
13	4e−02	28 / 937	Fetal_EnhG
14	9e−02	11 / 328	Fetal_Het
15	1e−01	31 / 1171	Fetal_EnhP

Cancer

Rank	p−value	#in/all	Geneset
1	7e−07	8 / 36	PanCan_HK_geneset_nanostring
2	2e−02	19 / 527	Lembcke_Normal vs Adenoma
3	4e−02	1 / 2	GENTLES_modul8
4	7e−02	3 / 46	PanCan_DNARepair_geneset_nanostring
5	1e−01	3 / 54	KUIPER_MM poor survival
6	2e−01	1 / 14	LIU_COMMON_CANCER_GENES
7	2e−01	1 / 13	WANG_ER_DN
8	3e−01	1 / 14	GENTLES_modul10
9	3e−01	4 / 125	PanCan_CC+Apop_geneset_nanostring
10	3e−01	1 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
11	3e−01	1 / 15	WANG_ER_UP
12	3e−01	1 / 16	GENTLES_modul11
13	3e−01	0 / 13	RHODES_CANCER_META_SIGNATURE
14	3e−01	1 / 20	PanCan_ChromMod_geneset_nanostring
15	4e−01	1 / 24	PanCan_Notch_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	2e−09	62 / 1304	mitochondrion
2	2e−08	154 / 4828	nucleus
3	7e−08	93 / 2535	nucleoplasm
4	4e−06	98 / 2979	cytosol
5	2e−04	31 / 721	nucleolus
6	4e−04	19 / 374	mitochondrial inner membrane
7	4e−03	17 / 392	cellular_component
8	6e−03	6 / 79	spliceosomal complex
9	9e−03	6 / 85	integral component of endoplasmic reticulum membrane
10	1e−02	9 / 173	nuclear chromatin
11	1e−02	3 / 23	vesicle membrane
12	1e−02	3 / 24	mitochondrial ribosome
13	1e−02	9 / 179	nuclear speck
14	2e−02	2 / 10	CD40 receptor complex
15	2e−02	2 / 10	Gemini of coiled bodies

Chr

Rank	p−value	#in/all	Geneset
1	1e−06	44 / 959	Chr 16
2	8e−05	26 / 536	Chr 22
3	5e−03	46 / 1467	Chr 19
4	5e−02	39 / 1411	Chr 11
5	1e−01	26 / 954	Chr 9
6	2e−01	31 / 1217	Chr 3
7	4e−01	14 / 619	Chr 20
8	5e−01	17 / 768	Chr 14
9	6e−01	6 / 289	Chr 21
10	6e−01	48 / 2323	Chr 1
11	7e−01	29 / 1492	Chr 2
12	7e−01	17 / 904	Chr 10
13	7e−01	25 / 1318	Chr 17
14	7e−01	22 / 1170	Chr 7
15	8e−01	1 / 87	Chr Y

Chromatin states

Rank	p−value	#in/all	Geneset
1	4e−59	426 / 12298	2_TssA_Melanocytes
2	5e−53	410 / 11836	3_TssF_Melanocytes
3	8e−53	403 / 11455	2_TssA_Fibroblasts
4	2e−51	427 / 12983	2_TssA_Neuronal_Progenitor
5	5e−47	243 / 4795	6_EnhG_Fibroblasts
6	7e−46	357 / 9635	3_TssF_Fibroblasts
7	7e−45	337 / 8771	5_Tx_Melanocytes
8	2e−43	314 / 7854	5_Tx_Fibroblasts
9	1e−41	258 / 5699	6_EnhG_Melanocytes
10	5e−40	287 / 6970	5_Tx_Neuronal_Progenitor
11	5e−32	177 / 3450	4_TxTrans_Fibroblasts
12	8e−28	237 / 5956	3_TssF_Neuronal_Progenitor
13	3e−27	376 / 12393	15_Quies_Neuronal_Progenitor
14	9e−20	365 / 12741	7_Enh_Melanocytes
15	2e−18	344 / 11847	7_Enh_Neuronal_Progenitor

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−64	384 / 9555	TssA_Colon
2	4e−64	373 / 9054	Tx_Colon
3	2e−63	362 / 8568	TxWk_Colon
4	2e−56	324 / 7354	TssF_Colon
5	1e−36	260 / 6138	TssD2_Colon
6	1e−30	228 / 5373	EnhWk1_Colon
7	6e−30	306 / 8678	Quies3_Colon
8	8e−30	350 / 10779	Enh_Colon
9	9e−22	138 / 2845	TxEnhG1_Colon
10	2e−17	324 / 10999	TssWk_Colon
11	5e−13	116 / 2810	EnhA_Colon
12	5e−11	71 / 1468	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
13	2e−10	88 / 2073	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
14	1e−07	47 / 965	Pentrack_CRC_TCGA_corr_R_normal_DN
15	3e−06	47 / 1083	ZNF_Colon

Glio

Rank	p−value	#in/all	Geneset
1	1e−07	79 / 2043	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
2	1e−07	71 / 1777	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
3	6e−06	38 / 820	Sturm_GBM_Meth_overexpression_E_G34_UP
4	7e−03	14 / 315	Up
5	2e−02	5 / 69	WILLSCHER_GBM_Verhaak−PNwt & MES_up
6	4e−02	3 / 37	WILLSCHER_GBM_proteomics_wtOnly_SpotH
7	6e−02	5 / 98	WILLSCHER_GBM_proteomics_wtOnly_SpotB
8	6e−02	1 / 3	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up (L)
9	6e−02	14 / 419	Down_a
10	8e−02	5 / 110	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
11	1e−01	4 / 87	Sturm_GBM_Meth_overexpression_I_RTK I 'PDGFRA'_UP
12	1e−01	4 / 93	Hopp_Sturm_GBM_Epi3_C2_adult_fetus_DN
13	2e−01	1 / 8	Sturm_GBM_Meth_overexpression_C_G34_UP
14	2e−01	1 / 11	Mukasa_UP_in_Oligodendroglioma_with_1intact
15	2e−01	1 / 12	WILLSCHER_GBM_LTSmut_proteomics−B_UP

GSEA C2

Rank	p−value	#in/all	Geneset
1	3e−11	52 / 887	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
2	2e−10	47 / 797	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
3	3e−10	26 / 281	GINESTIER_BREAST_CANCER_ZNF217_AMPLIFIED_DN
4	4e−09	34 / 509	PARENT_MTOR_SIGNALING_UP
5	1e−08	31 / 459	IVANOVA_HEMATOPOIESIS_EARLY_PROGENITOR
6	4e−07	45 / 952	DANG_BOUND_BY_MYC
7	8e−07	20 / 262	MANALO_HYPOXIA_DN
8	1e−05	15 / 188	SANSOM_APC_TARGETS_REQUIRE_MYC
9	1e−05	29 / 569	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_DN
10	2e−05	15 / 192	SANSOM_APC_TARGETS
11	2e−05	32 / 666	BENPORATH_MYC_MAX_TARGETS
12	6e−05	10 / 101	NIKOLSKY_BREAST_CANCER_16P13_AMPLICON
13	7e−05	12 / 147	NIKOLSKY_BREAST_CANCER_11Q12_Q14_AMPLICON
14	7e−05	20 / 354	MONNIER_POSTRADIATION_TUMOR_ESCAPE_UP
15	1e−04	17 / 279	LIU_SOX4_TARGETS_DN

HM

Rank	p−value	#in/all	Geneset
1	1e−04	7 / 54	HALLMARK_MYC_TARGETS_V2
2	2e−03	9 / 130	HALLMARK_DNA_REPAIR
3	4e−03	10 / 173	HALLMARK_E2F_TARGETS
4	9e−03	8 / 138	HALLMARK_FATTY_ACID_METABOLISM
5	3e−02	8 / 177	HALLMARK_MITOTIC_SPINDLE
6	4e−02	8 / 185	HALLMARK_MTORC1_SIGNALING
7	6e−02	4 / 69	HALLMARK_CHOLESTEROL_HOMEOSTASIS
8	8e−02	7 / 175	HALLMARK_XENOBIOTIC_METABOLISM
9	1e−01	2 / 29	HALLMARK_NOTCH_SIGNALING
10	2e−01	6 / 186	HALLMARK_IL2_STAT5_SIGNALING
11	3e−01	3 / 91	HALLMARK_ANDROGEN_RESPONSE
12	3e−01	3 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING
13	4e−01	5 / 186	HALLMARK_ESTROGEN_RESPONSE_LATE
14	4e−01	3 / 103	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
15	5e−01	4 / 176	HALLMARK_ADIPOGENESIS

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.03	3 / 31	DUMEAUX_Fasting enriched genes
2	0.05	2 / 17	DUMEAUX_High bmi enriched genes
3	0.19	1 / 10	DUMEAUX_Smoking literature genes up
4	0.32	3 / 94	DUMEAUX_Smoking enriched genes
5	0.49	1 / 32	Marjolein_ageing−genes_DN
6	0.82	2 / 147	Homuth_BMI−associated−genes_UP
7	0.94	2 / 211	Homuth_BMI−associated−genes_DN
8	1.00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
9	1.00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
10	1.00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
11	1.00	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
12	1.00	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
13	1.00	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
14	1.00	0 / 10	DUMEAUX_Women normal BMI literature genes up
15	1.00	0 / 18	Huan_blood−pressure_SBP−signature

Lymphoma

Rank	p−value	#in/all	Geneset
1	3e−38	291 / 7275	HOPP_Txn_elongation
2	7e−32	300 / 8226	HOPP_Active_promoter
3	2e−25	216 / 5356	HOPP_Txn_transition
4	6e−15	254 / 8098	HOPP_Weak_promoter
5	2e−12	231 / 7448	HOPP_Strong_enhancer
6	8e−12	49 / 772	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell line_
7	3e−11	48 / 777	WIRTH_lymphoma937_spot D
8	3e−07	30 / 493	WIRTH_lymphoma937_spot J
9	3e−07	29 / 472	Hopp_June14_MMML937 tumors+controls_group.overexpression_J_GC−B−c
10	8e−07	54 / 1270	SPANG_BCR UP
11	2e−05	16 / 220	Hopp_June14_MMML937 tumors+controls_group.overexpression_B_cell line_
12	4e−05	16 / 232	WIRTH_lymphoma937_spot B
13	2e−04	174 / 6559	HOPP_Weak_txn
14	4e−03	2 / 5	MASCQUE_mBL UP
15	5e−03	15 / 331	WIRTH_lymphoma937_spot H

Melanoma

Rank	p−value	#in/all	Geneset
1	1	0 / 30	Hugo_melanoma−all−MET_UP
2	1	0 / 54	Hugo_melanoma−all−MET_DN
3	1	0 / 43	Hugo_melanoma−BRAFmut−MET_UP
4	1	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
5	1	0 / 27	Hugo_melanoma−all−LEF1_UP
6	1	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

MF

Rank	p−value	#in/all	Geneset
1	5e−06	234 / 8818	protein binding
2	8e−06	45 / 1065	zinc ion binding
3	1e−05	43 / 1013	poly(A) RNA binding
4	1e−05	63 / 1717	metal ion binding
5	1e−03	13 / 232	ligase activity
6	2e−03	4 / 25	protein−cysteine S−palmitoyltransferase activity
7	2e−03	3 / 12	phosphatidic acid binding
8	2e−03	3 / 12	pseudouridine synthase activity
9	2e−03	3 / 13	thioesterase binding
10	2e−03	5 / 45	tRNA binding
11	3e−03	4 / 28	tumor necrosis factor receptor binding
12	4e−03	43 / 1329	ATP binding
13	4e−03	7 / 94	double−stranded DNA binding
14	5e−03	46 / 1475	DNA binding
15	6e−03	5 / 56	ATP−dependent RNA helicase activity

miRNA Disease

Rank	p−value	#in/all	Geneset
1	1	0 / 7	Thyroid carcinoma, papillary
2	1	0 / 123	Pancreatic cancer
3	1	0 / 68	Glioblastoma multiforme, somatic
4	1	0 / 63	Gastrointestinal
5	1	0 / 3	Pituitary adenoma
6	1	0 / 116	Cancer
7	1	0 / 95	Colorectal cancer
8	1	0 / 2	Adenomas, multiple colorectal
9	1	0 / 124	Prostate cancer
10	1	0 / 48	Alzheimer disease, susceptibility to
11	1	0 / 7	Schizophrenia, susceptibility to
12	1	0 / 20	Parkinson disease
13	1	0 / 65	Hepatocellular carcinoma
14	1	0 / 3	Down syndrome, risk of
15	1	0 / 127	Melanoma and neural system tumor syndrome

miRNA target

Rank	p−value	#in/all	Geneset
1	0.001	15 / 288	hsa−miR−34a
2	0.002	6 / 61	hsa−miR−671−5p
3	0.003	9 / 138	hsa−miR−132
4	0.004	8 / 122	hsa−miR−212
5	0.004	7 / 97	hsa−miR−1301
6	0.004	7 / 97	hsa−miR−526a
7	0.005	8 / 124	hsa−miR−515−3p
8	0.007	4 / 37	hsa−miR−518e
9	0.009	4 / 39	hsa−miR−484
10	0.011	5 / 63	hsa−miR−518c*
11	0.015	4 / 45	hsa−miR−766
12	0.016	4 / 46	hsa−miR−575
13	0.017	3 / 26	hsa−miR−663b
14	0.021	4 / 50	hsa−miR−1201
15	0.022	4 / 51	hsa−miR−519b−5p

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.2	1 / 12	BENTINK_src.2
2	0.2	1 / 13	BENTINK_src.10
3	1.0	0 / 14	GUSTAFSON_PI3K_UP
4	1.0	0 / 15	GUSTAFSON_PI3K_DN
5	1.0	0 / 13	BENTINK_e2f3.1
6	1.0	0 / 13	BENTINK_e2f3.2
7	1.0	0 / 13	BENTINK_myc.1
8	1.0	0 / 12	BENTINK_ras.1
9	1.0	0 / 11	BENTINK_ras.4
10	1.0	0 / 14	BENTINK_ras.6
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Reference Signatures

Rank	p−value	#in/all	Geneset
1	3e−07	19 / 221	Chaussabel_3,8_Enzymes
2	1e−04	22 / 429	PROTEINATLAS_soft tissue
3	3e−04	16 / 275	Chaussabel_3,7_Spliceosome
4	5e−04	30 / 740	PROTEINATLAS_esophagus
5	6e−04	41 / 1138	PROTEINATLAS_small intestine
6	1e−03	41 / 1167	PROTEINATLAS_gallbladder
7	1e−03	24 / 571	PROTEINATLAS_oral mucosa
8	1e−03	34 / 929	PROTEINATLAS_bronchus
9	2e−03	38 / 1097	PROTEINATLAS_kidney
10	2e−03	25 / 639	PROTEINATLAS_breast
11	3e−03	35 / 1003	PROTEINATLAS_appendix
12	3e−03	42 / 1268	PROTEINATLAS_colon
13	3e−03	4 / 29	Chaussabel_2,7_Unknown function
14	4e−03	39 / 1173	PROTEINATLAS_rectum
15	4e−03	39 / 1176	PROTEINATLAS_duodenum

Telomeres

Rank	p−value	#in/all	Geneset
1	0.02	3 / 27	Nabetani_alt len telomeres_genes_ko
2	1.00	0 / 13	Alternative lengthening of telomeres
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	5e−23	203 / 5067	ICGC_Taf1_targets
2	8e−21	179 / 4362	ICGC_Creb1_targets
3	4e−18	222 / 6322	ICGC_Tcf3_targets
4	4e−18	202 / 5518	ICGC_Stat5_targets
5	5e−17	172 / 4468	ICGC_Egr1_targets
6	9e−17	231 / 6868	ICGC_Elf1_targets
7	1e−16	224 / 6578	ICGC_Pou2_targets
8	2e−16	196 / 5466	ICGC_Nficsc81335_targets
9	2e−16	181 / 4881	ICGC_Atf2_targets
10	6e−15	191 / 5442	ICGC_Pmlsc71910_targets
11	2e−14	233 / 7247	ICGC_Runx3_targets
12	2e−14	156 / 4131	ICGC_Nfatc1_targets
13	2e−14	102 / 2215	ICGC_GabpPcr2_targets
14	7e−14	174 / 4890	ICGC_Bclaf101388_targets
15	7e−14	160 / 4345	ICGC_Zeb1_targets

K−Means Cluster

Spot Summary: Z

\# metagenes = 51
\# genes = 539

<r> metagenes = 0.9
<r> genes = 0.3
beta: r2= 13.38 / log p= −Inf

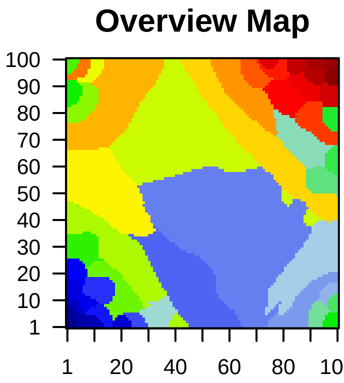
\# samples with spot = 130 (3.8 %)
A * : 13 (3.8 %)
A C F * : 2 (0.9 %)
A F * : 16 (5.2 %)
C F * : 1 (0.4 %)
F * : 24 (4.3 %)
F J * : 40 (8.6 %)
J * : 34 (7.6 %)

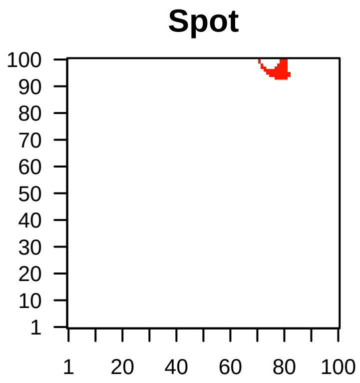
Spot Genelist

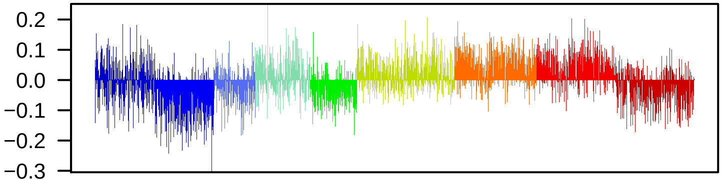
Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_166126	1.62	−1.38	0.13		
2	ILMN_175907	1.03	−0.54	0.36	TNFRSF13B	TNF receptor superfamily member 13B [Source:HGNC Symb
3	ILMN_323603	1.02	−0.68	0.41		
4	ILMN_182230	0.88	−0.73	0.16		
5	ILMN_171876	0.82	−0.83	0.46	MT1F	metallothionein 1F [Source:HGNC Symbol;Acc:HGNC:7398]
6	ILMN_172810	0.8	−0.61	0.35	GNG7	G protein subunit gamma 7 [Source:HGNC Symbol;Acc:HGN
7	ILMN_169443	0.8	−0.62	0.38	CRIP2	cysteine rich protein 2 [Source:HGNC Symbol;Acc:HGNC:23
8	ILMN_173618	0.77	−0.54	0.38	GSTM3	glutathione S−transferase mu 3 [Source:HGNC Symbol;Acc:H
9	ILMN_176348	0.76	−0.52	0.45	CTLA4	cytotoxic T−lymphocyte associated protein 4 [Source:HGNC
10	ILMN_179985	0.75	−0.61	0.24	NOMO3	NODAL modulator 3 [Source:HGNC Symbol;Acc:HGNC:2524
11	ILMN_323043	0.75	−0.69	0.34	VOPP1	vesicular, overexpressed in cancer, prosurvival protein 1 [Sou
12	ILMN_174837	0.71	−0.68	0.13	GOLGA8CP	golgin A8 family member C, pseudogene [Source:HGNC Sym
13	ILMN_179235	0.71	−0.31	0.26	DPYSL4	dihydropyrimidinase like 4 [Source:HGNC Symbol;Acc:HGNC
14	ILMN_171999	0.71	−0.48	0.48	MIR600	MIR600 host gene [Source:HGNC Symbol;Acc:HGNC:23642
15	ILMN_181415	0.7	−0.5	0.6		
16	ILMN_329216	0.7	−0.46	0.55		
17	ILMN_173623	0.69	−0.52	0.4	CHTOP	chromatin target of PRMT1 [Source:HGNC Symbol;Acc:HGN
18	ILMN_173820	0.69	−0.54	0.3	CISH	cytokine inducible SH2 containing protein [Source:HGNC Sym
19	ILMN_181624	0.69	−0.78	0.38		
20	ILMN_224901	0.68	−0.5	0.31	MIR3621	microRNA 3621 [Source:HGNC Symbol;Acc:HGNC:38930]

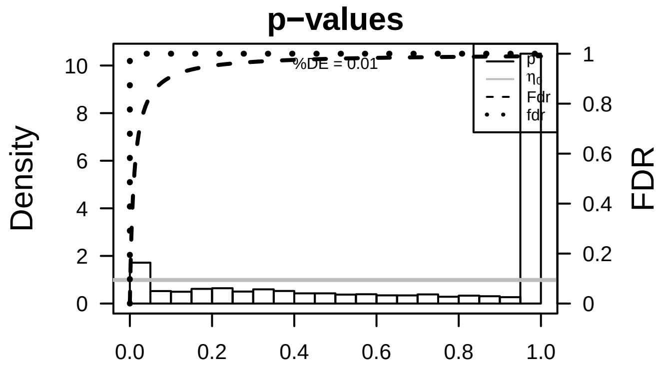
Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	8e−50	348 / 9555	Colon	TssA_Colon
2	7e−48	335 / 9054	Colon	Tx_Colon
3	7e−45	339 / 9504	Brain	Overlap_fetal_midbrain_K9K27me3
4	1e−44	389 / 12298	Chror	2_TssA_Melanocytes
5	4e−41	369 / 11455	Chror	2_TssA_Fibroblasts
6	1e−40	394 / 12983	Chror	2_TssA_Neuronal_Progenitor
7	2e−35	303 / 8568	Colon	TxWk_Colon
8	9e−34	325 / 9815	Brain	Overlap_fetal_midbrain_ReprPC
9	3e−33	362 / 11836	Chror	3_TssF_Melanocytes
10	4e−33	272 / 7354	Colon	TssF_Colon
11	2e−27	258 / 7275	Lympl	HOPP_Txn_elongation
12	3e−27	162 / 3450	Chror	4_TxTrans_Fibroblasts
13	2e−26	219 / 5699	Chror	6_EnhG_Melanocytes
14	4e−26	276 / 8226	Lympl	HOPP_Active_promoter
15	1e−25	209 / 5356	Lympl	HOPP_Txn_transition
16	3e−25	246 / 6970	Chror	5_Tx_Neuronal_Progenitor
17	2e−21	310 / 10430	Brain	Overlap_fetal_midbrain_Quies
18	2e−21	276 / 8771	Chror	5_Tx_Melanocytes
19	6e−20	81 / 1304	CC	mitochondrion
20	7e−20	290 / 9635	Chror	3_TssF_Fibroblasts
21	6e−19	250 / 7854	Chror	5_Tx_Fibroblasts
22	2e−18	309 / 10779	Colon	Enh_Colon
23	2e−18	266 / 8678	Colon	Quies3_Colon
24	8e−18	176 / 4795	Chror	6_EnhG_Fibroblasts
25	1e−17	133 / 3164	Brain	Mid_Frontal_Lobe_ZNF
26	3e−17	310 / 10999	Colon	TssWk_Colon
27	4e−17	61 / 887	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
28	4e−17	123 / 2845	Colon	TxEnhG1_Colon
29	6e−17	201 / 5936	Brain	Overlap_fetal_midbrain_HetRpts
30	1e−16	83 / 1547	Colon	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP
31	5e−16	57 / 831	Colon	Pentrack_CRC_TCGA_group.over_C_normal_DN
32	5e−16	203 / 6138	Colon	TssD2_Colon
33	2e−14	58 / 933	Refer	PROTEINATLAS_adrenal gland
34	4e−14	35 / 374	CC	mitochondrial inner membrane
35	5e−14	47 / 656	GSEA	KIM_ALL_DISORDERS_OLIGODENDROCYTE_NUMBER_CORR_UP
36	1e−13	192 / 5956	Chror	3_TssF_Neuronal_Progenitor
37	3e−13	57 / 965	Colon	Pentrack_CRC_TCGA_corr_R_normal_DN
38	4e−13	55 / 912	Refer	PROTEINATLAS_fallopian tube
39	4e−13	64 / 1176	Refer	PROTEINATLAS_duodenum
40	6e−13	16 / 71	BP	mitochondrial translational termination









Aging

Rank	p−value	#in/all	Geneset
1	0.2	5 / 142	HORVATH_aging_genes meth UP
2	0.4	3 / 111	HORVATH_aging_genes meth DOWN
3	0.7	1 / 58	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Cancer

Rank	p−value	#in/all	Geneset
1	0.003	6 / 73	SHAUGHNESSY_MM high risk
2	0.011	19 / 527	Lembcke_Normal vs Adenoma
3	0.013	2 / 9	GENTLES_modul5
4	0.031	2 / 14	GENTLES_modul4
5	0.040	2 / 16	GENTLES_modul7
6	0.040	1 / 12	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
7	0.065	3 / 46	PanCan_DNARepair_geneset_nanostring
8	0.135	1 / 13	LIU_LIVER_CANCER
9	0.162	2 / 36	PanCan_HK_geneset_nanostring
10	0.177	2 / 38	KUIPER_MM good survival
11	0.184	2 / 39	ZHANG_MM up
12	0.232	1 / 13	RHODES_CANCER_META_SIGNATURE
13	0.232	1 / 13	GENTLES_modul2
14	0.243	1 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
15	0.247	1 / 14	BEN−PORATH_UP

Chromatin states

Rank	p−value	#in/all	Geneset
1	1e−44	389 / 12298	2_TssA_Melanocytes
2	4e−41	369 / 11455	2_TssA_Fibroblasts
3	1e−40	394 / 12983	2_TssA_Neuronal_Progenitor
4	3e−33	362 / 11836	3_TssF_Melanocytes
5	3e−27	162 / 3450	4_TxTrans_Fibroblasts
6	2e−26	219 / 5699	6_EnhG_Melanocytes
7	3e−25	246 / 6970	5_Tx_Neuronal_Progenitor
8	2e−21	276 / 8771	5_Tx_Melanocytes
9	7e−20	290 / 9635	3_TssF_Fibroblasts
10	6e−19	250 / 7854	5_Tx_Fibroblasts
11	8e−18	176 / 4795	6_EnhG_Fibroblasts
12	1e−13	192 / 5956	3_TssF_Neuronal_Progenitor
13	1e−12	89 / 2028	4_TxTrans_Melanocytes
14	5e−11	317 / 12393	15_Quies_Neuronal_Progenitor
15	2e−08	314 / 12741	7_Enh_Melanocytes

GSEA C2

Rank	p−value	#in/all	Geneset
1	4e−17	61 / 887	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
2	5e−14	47 / 656	KIM_ALL_DISORDERS_OLIGODENDROCYTE_NUMBER_CORR_UP
3	7e−13	40 / 529	CAIRO_HEPATOBLASTOMA_CLASSES_UP
4	9e−13	71 / 1417	PUJANA_BRCA1_PCC_NETWORK
5	1e−11	48 / 797	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
6	1e−11	24 / 217	PENG_RAPAMYCIN_RESPONSE_DN
7	2e−10	33 / 450	STARK_PREFRONTAL_CORTEX_22Q11_DELETION_DN
8	6e−10	42 / 716	WEI_MYCN_TARGETS_WITH_E_BOX
9	6e−10	34 / 499	TIEN_INTESTINE_PROBIOTICS_24HR_UP
10	1e−09	20 / 187	WONG_MITOCHONDRIA_GENE_MODULE
11	3e−09	39 / 669	PUJANA_CHEK2_PCC_NETWORK
12	3e−09	32 / 478	STEIN_ESRRA_TARGETS
13	5e−09	36 / 594	KIM_BIPOLAR_DISORDER_OLIGODENDROCYTE_DENSITY_CORR_UP
14	5e−09	40 / 710	MARTENS_TRETINOIN_RESPONSE_DN
15	6e−09	28 / 388	MOOTHA_MITOCHONDRIA

Lymphoma

Rank	p−value	#in/all	Geneset
1	2e−27	258 / 7275	HOPP_Txn_elongation
2	4e−26	276 / 8226	HOPP_Active_promoter
3	1e−25	209 / 5356	HOPP_Txn_transition
4	4e−12	48 / 772	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell line_
5	2e−11	232 / 8098	HOPP_Weak_promoter
6	6e−11	46 / 777	WIRTH_lymphoma937_spot D
7	7e−06	194 / 7448	HOPP_Strong_enhancer
8	1e−04	6 / 39	CARO_OxPhos_in_DLBCL_UP
9	2e−04	8 / 77	Aukema_BCL2 DN_BCL6 UP
10	4e−04	4 / 18	Aukema_BCL2 UP_BCL6 DN
11	9e−04	13 / 232	WIRTH_lymphoma937_spot B
12	1e−03	42 / 1270	SPANG_BCR UP
13	2e−03	12 / 220	Hopp_June14_MMML937 tumors+controls_group.overexpression_B_cell line_
14	5e−03	13 / 283	TARTE_Plasmablast signature
15	7e−03	5 / 60	SPANG_BAFF 9hrs DN

miRNA Disease

Rank	p−value	#in/all	Geneset
1	1	0 / 7	Thyroid carcinoma, papillary
2	1	0 / 123	Pancreatic cancer
3	1	0 / 68	Glioblastoma multiforme, somatic
4	1	0 / 63	Gastrointestinal
5	1	0 / 3	Pituitary adenoma
6	1	0 / 116	Cancer
7	1	0 / 95	Colorectal cancer
8	1	0 / 2	Adenomas, multiple colorectal
9	1	0 / 124	Prostate cancer
10	1	0 / 48	Alzheimer disease, susceptibility to
11	1	0 / 7	Schizophrenia, susceptibility to
12	1	0 / 20	Parkinson disease
13	1	0 / 65	Hepatocellular carcinoma
14	1	0 / 3	Down syndrome, risk of
15	1	0 / 127	Melanoma and neural system tumor syndrome

Reference Signatures

Rank	p−value	#in/all	Geneset
1	2e−14	58 / 933	PROTEINATLAS_adrenal gland
2	4e−13	55 / 912	PROTEINATLAS_fallopian tube
3	4e−13	64 / 1176	PROTEINATLAS_duodenum
4	8e−13	63 / 1167	PROTEINATLAS_gallbladder
5	3e−12	62 / 1173	PROTEINATLAS_rectum
6	2e−11	61 / 1194	PROTEINATLAS_stomach
7	5e−11	57 / 1097	PROTEINATLAS_kidney
8	7e−11	58 / 1138	PROTEINATLAS_small intestine
9	3e−10	51 / 960	PROTEINATLAS_cerebellum
10	4e−10	25 / 275	Chaussabel_3,7_Spliceosome
11	9e−10	39 / 640	PROTEINATLAS_parathyroid gland
12	1e−09	43 / 759	PROTEINATLAS_epididymis
13	1e−09	48 / 912	PROTEINATLAS_urinary bladder
14	1e−09	38 / 623	PROTEINATLAS_seminal vesicle
15	2e−09	58 / 1239	PROTEINATLAS_testis

BP

Rank	p−value	#in/all	Geneset
1	6e−13	16 / 71	mitochondrial translational termination
2	6e−12	15 / 69	mitochondrial translational elongation
3	8e−10	19 / 163	rRNA processing
4	2e−07	17 / 184	translation
5	4e−06	18 / 255	viral process
6	5e−06	10 / 81	viral transcription
7	3e−05	7 / 46	mitochondrial respiratory chain complex I assembly
8	4e−05	6 / 32	mitochondrial electron transport, NADH to ubiquinone
9	6e−05	9 / 86	mRNA export from nucleus
10	6e−05	9 / 87	nuclear−transcribed mRNA catabolic process, nonsense−mediated decay
11	1e−04	5 / 25	tRNA processing
12	1e−04	9 / 96	translational initiation
13	2e−04	13 / 196	mRNA splicing, via spliceosome
14	3e−04	12 / 181	proteasome−mediated ubiquitin−dependent protein catabolic process
15	3e−04	7 / 65	SRP−dependent cotranslational protein targeting to membrane

CC

Rank	p−value	#in/all	Geneset
1	6e−20	81 / 1304	mitochondrion
2	4e−14	35 / 374	mitochondrial inner membrane
3	5e−11	99 / 2535	nucleoplasm
4	2e−10	155 / 4828	nucleus
5	3e−09	9 / 29	mitochondrial large ribosomal subunit
6	4e−07	21 / 287	mitochondrial matrix
7	2e−05	134 / 4822	cytoplasm
8	4e−05	6 / 33	mitochondrial respiratory chain complex I
9	2e−04	30 / 721	nucleolus
10	2e−04	4 / 16	Ada2/Gcn5/Ada3 transcription activator complex
11	2e−04	4 / 16	proteasome core complex
12	3e−04	6 / 45	cytosolic large ribosomal subunit
13	3e−04	86 / 2979	cytosol
14	5e−04	6 / 51	proteasome complex
15	6e−04	4 / 20	mitochondrial small ribosomal subunit

Colon Cancer

Rank	p−value	#in/all	Geneset
1	8e−50	348 / 9555	TssA_Colon
2	7e−48	335 / 9054	Tx_Colon
3	2e−35	303 / 8568	TxWk_Colon
4	4e−33	272 / 7354	TssF_Colon
5	2e−18	309 / 10779	Enh_Colon
6	2e−18	266 / 8678	Quies3_Colon
7	3e−17	310 / 10999	TssWk_Colon
8	4e−17	123 / 2845	TxEnhG1_Colon
9	1e−16	83 / 1547	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
10	5e−16	57 / 831	Pentrack_CRC_TCGA_group.over_C_normal_DN
11	5e−16	203 / 6138	TssD2_Colon
12	3e−13	57 / 965	Pentrack_CRC_TCGA_corr_R_normal_DN
13	5e−10	166 / 5373	EnhWk1_Colon
14	2e−05	87 / 2810	EnhA_Colon
15	3e−05	34 / 789	TxEnhG2_Colon

HM

Rank	p−value	#in/all	Geneset
1	2e−10	20 / 167	HALLMARK_OXIDATIVE_PHOSPHORYLATION
2	7e−06	11 / 103	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
3	1e−05	8 / 54	HALLMARK_MYC_TARGETS_V2
4	1e−03	11 / 183	HALLMARK_GLYCOLYSIS
5	1e−03	9 / 130	HALLMARK_DNA_REPAIR
6	3e−03	10 / 176	HALLMARK_ADIPOGENESIS
7	2e−02	7 / 138	HALLMARK_FATTY_ACID_METABOLISM
8	2e−02	8 / 170	HALLMARK_MYC_TARGETS_V1
9	3e−02	8 / 185	HALLMARK_MTORC1_SIGNALING
10	4e−02	8 / 189	HALLMARK_HYPOXIA
11	6e−02	7 / 173	HALLMARK_E2F_TARGETS
12	1e−01	5 / 137	HALLMARK_UV_RESPONSE_UP
13	2e−01	6 / 186	HALLMARK_ESTROGEN_RESPONSE_EARLY
14	3e−01	3 / 91	HALLMARK_PEROXISOME
15	3e−01	5 / 179	HALLMARK_G2M_CHECKPOINT

Melanoma

Rank	p−value	#in/all	Geneset
1	0.6	1 / 43	Hugo_melanoma−BRAFmut−MET_UP
2	1.0	0 / 30	Hugo_melanoma−all−MET_UP
3	1.0	0 / 54	Hugo_melanoma−all−MET_DN
4	1.0	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
5	1.0	0 / 27	Hugo_melanoma−all−LEF1_UP
6	1.0	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

miRNA target

Rank	p−value	#in/all	Geneset
1	2e−04	11 / 144	hsa−miR−140−5p
2	3e−04	8 / 85	hsa−miR−510
3	1e−03	6 / 58	hsa−miR−379
4	3e−03	6 / 71	hsa−miR−1266
5	4e−03	4 / 33	hsa−miR−1296
6	9e−03	9 / 175	hsa−miR−29c
7	1e−02	14 / 342	hsa−let−7e
8	1e−02	7 / 119	hsa−miR−509−3p
9	1e−02	4 / 46	hsa−miR−575
10	2e−02	9 / 191	hsa−miR−222
11	2e−02	13 / 328	hsa−miR−32
12	2e−02	4 / 52	hsa−miR−940
13	2e−02	5 / 78	hsa−miR−30a*
14	2e−02	8 / 169	hsa−miR−29a
15	2e−02	13 / 343	hsa−let−7a

Telomeres

Rank	p−value	#in/all	Geneset
1	0.4	1 / 27	Nabetani_alt len telomeres_genes_ko
2	1.0	0 / 13	Alternative lengthening of telomeres
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Brain

Rank	p−value	#in/all	Geneset
1	7e−45	339 / 9504	Overlap_fetal_midbrain_K9K27me3
2	9e−34	325 / 9815	Overlap_fetal_midbrain_ReprPC
3	2e−21	310 / 10430	Overlap_fetal_midbrain_Quies
4	1e−17	133 / 3164	Mid_Frontal_Lobe_ZNF
5	6e−17	201 / 5936	Overlap_fetal_midbrain_HetRpts
6	1e−09	44 / 796	Overlap_fetal_midbrain_ZNF
7	4e−06	37 / 818	Mid_Frontal_Lobe_Het
8	1e−05	244 / 9917	Overlap_fetal_midbrain_ReprPCWk
9	2e−05	14 / 180	Overlap_fetal_midbrain_Het
10	8e−04	33 / 906	Fetal_HetRpts
11	8e−04	54 / 1728	Fetal_ReprPCWk
12	2e−02	14 / 386	Fetal_ZNF
13	3e−02	68 / 2709	Mid_Frontal_Lobe_HetRpts
14	7e−02	11 / 328	Fetal_Het
15	9e−02	18 / 630	Mid_Frontal_Lobe_EnhP

Chr

Rank	p−value	#in/all	Geneset
1	0.02	18 / 536	Chr 22
2	0.06	38 / 1467	Chr 19
3	0.08	26 / 959	Chr 16
4	0.12	17 / 619	Chr 20
5	0.13	29 / 1160	Chr 12
6	0.14	20 / 769	Chr 15
7	0.15	34 / 1411	Chr 11
8	0.30	24 / 1060	Chr 5
9	0.36	21 / 954	Chr 9
10	0.48	27 / 1318	Chr 17
11	0.55	24 / 1211	Chr 6
12	0.61	8 / 422	Chr 13
13	0.62	19 / 994	Chr X
14	0.65	22 / 1170	Chr 7
15	0.72	22 / 1217	Chr 3

Glio

Rank	p−value	#in/all	Geneset
1	7e−05	4 / 12	WILLSCHER_GBM_LTSmut_proteomics−B_UP
2	1e−04	7 / 55	Stuehler_Proteins_up_in_STS
3	1e−03	2 / 3	WILLSCHER_GBM_LTSmut_proteomics−E_UP
4	5e−03	9 / 157	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
5	2e−02	4 / 50	WILLSCHER_GBM_proteomics_wtOnly_SpotG
6	4e−02	24 / 820	Sturm_GBM_Meth_overexpression_E_G34_UP
7	4e−02	52 / 2043	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
8	5e−02	5 / 98	WILLSCHER_GBM_proteomics_wtOnly_SpotB
9	5e−02	11 / 315	Up
10	6e−02	11 / 316	WILLSCHER_GBM_Verhaak−PNwt & CL_up
11	6e−02	45 / 1777	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
12	8e−02	1 / 4	WILLSCHER_GBM_Verhaak−CL_up (E)
13	1e−01	12 / 401	Down_b
14	2e−01	1 / 9	oligodendrocytes_glio
15	2e−01	3 / 76	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.004	4 / 32	Marjolein_ageing−genes_DN
2	0.016	2 / 10	DUMEAUX_Smoking literature genes up
3	0.027	9 / 211	Homuth_BMI−associated−genes_DN
4	0.174	5 / 147	Homuth_BMI−associated−genes_UP
5	0.467	1 / 31	DUMEAUX_Fasting enriched genes
6	0.852	1 / 94	DUMEAUX_Smoking enriched genes
7	1.000	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
8	1.000	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
9	1.000	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
10	1.000	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
11	1.000	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
12	1.000	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
13	1.000	0 / 10	DUMEAUX_Women normal BMI literature genes up
14	1.000	0 / 17	DUMEAUX_High bmi enriched genes
15	1.000	0 / 18	Huan_blood−pressure_SBP−signature

MF

Rank	p−value	#in/all	Geneset
1	7e−13	58 / 1013	poly(A) RNA binding
2	2e−10	20 / 169	structural constituent of ribosome
3	2e−10	243 / 8818	protein binding
4	3e−06	7 / 32	NADH dehydrogenase (ubiquinone) activity
5	7e−05	4 / 12	exonuclease activity
6	4e−04	4 / 18	threonine−type endopeptidase activity
7	6e−04	4 / 20	DNA−directed RNA polymerase activity
8	9e−04	7 / 77	electron carrier activity
9	1e−03	11 / 185	magnesium ion binding
10	3e−03	4 / 29	rRNA binding
11	3e−03	5 / 48	methyltransferase activity
12	3e−03	17 / 399	RNA binding
13	3e−03	6 / 72	single−stranded DNA binding
14	4e−03	3 / 17	S−adenosylmethionine−dependent methyltransferase activity
15	5e−03	3 / 18	DNA helicase activity

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.03	2 / 14	GUSTAFSON_PI3K_UP
2	0.22	1 / 12	BENTINK_ras.1
3	0.22	1 / 12	BENTINK_src.2
4	0.23	1 / 13	BENTINK_myc.1
5	0.23	1 / 13	BENTINK_src.10
6	1.00	0 / 15	GUSTAFSON_PI3K_DN
7	1.00	0 / 13	BENTINK_e2f3.1
8	1.00	0 / 13	BENTINK_e2f3.2
9	1.00	0 / 11	BENTINK_ras.4
10	1.00	0 / 14	BENTINK_ras.6
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	9e−13	65 / 1231	KIM_MYC targets
2	8e−12	165 / 5067	ICGC_Taf1_targets
3	1e−09	166 / 5442	ICGC_Pmlsc71910_targets
4	4e−09	139 / 4362	ICGC_Creb1_targets
5	5e−09	64 / 1478	ICGC_Myc_targets
6	8e−09	84 / 2215	ICGC_GabpPcr2_targets
7	4e−08	135 / 4345	ICGC_Zeb1_targets
8	4e−08	162 / 5518	ICGC_Stat5_targets
9	8e−08	60 / 1452	ICGC_Six5_targets
10	1e−07	159 / 5466	ICGC_Nficsc81335_targets
11	2e−07	156 / 5383	ICGC_Sp1_targets
12	5e−07	59 / 1498	ICGC_Ets1_targets
13	6e−07	187 / 6868	ICGC_Elf1_targets
14	8e−07	167 / 5984	ICGC_Mta3_targets
15	1e−06	124 / 4131	ICGC_Nfatc1_targets

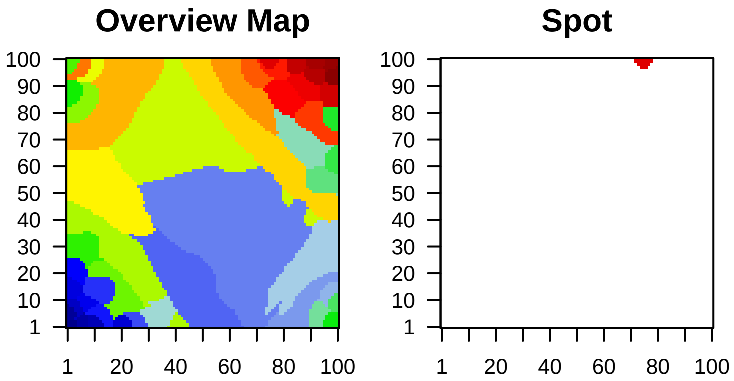
K−Means Cluster

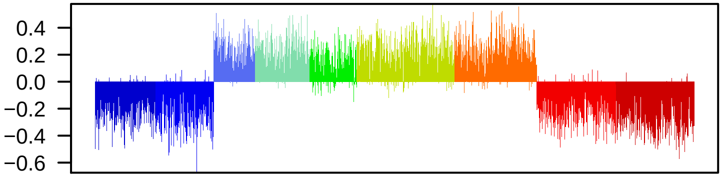
Spot Summary: A1

metagenes = 22
genes = 90

<r> metagenes = 0.96
<r> genes = 0.34
beta: r2= 25.95 / log p= −Inf

samples with spot = 1241 (36.6 %)
A C F * : 157 (66.8 %)
A F * : 213 (69.2 %)
C F * : 135 (50.9 %)
F * : 389 (70.1 %)
F J * : 347 (74.9 %)



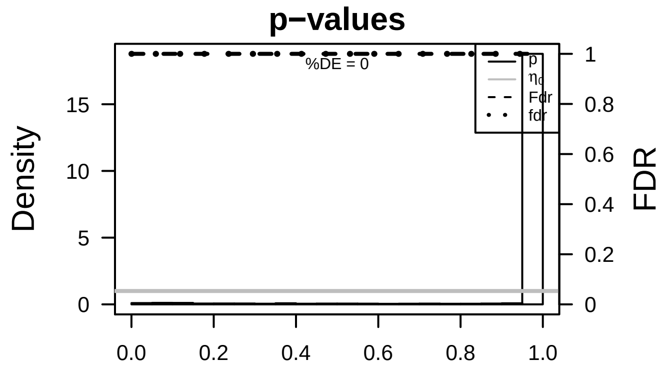


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_175063	2.47	−2.69	0.91		
2	ILMN_218086	2.33	−2.64	0.9		ribosomal protein S26 pseudogene 11 [Source:HGNC Symbo
3	ILMN_172664	2.23	−2.64	0.89		ribosomal protein S26 pseudogene 15 [Source:HGNC Symbo
4	ILMN_324883	2.2	−2.25	0.91		ribosomal protein S26 pseudogene 15 [Source:HGNC Symbo
5	ILMN_231070	2.2	−2.41	0.91		
6	ILMN_320919	2.15	−2.18	0.9	LOC101929876	ribosomal protein S26 [Source:HGNC Symbol;Acc:HGNC:10
7	ILMN_167852	2.13	−2.24	0.9		
8	ILMN_220902	2.12	−2.29	0.9	LOC101929876	ribosomal protein S26 [Source:HGNC Symbol;Acc:HGNC:10
9	ILMN_169558	2.09	−2.34	0.9	LOC101929876	ribosomal protein S26 [Source:HGNC Symbol;Acc:HGNC:10
10	ILMN_329699	2.07	−2.21	0.92		
11	ILMN_329001	2.01	−1.81	0.9		ribosomal protein S26 pseudogene 2 [Source:HGNC Symbol
12	ILMN_167769	2.01	−2.28	0.93		ribosomal protein S26 pseudogene 35 [Source:HGNC Symbo
13	ILMN_328515	1.94	−2.25	0.93	LOC101929876	ribosomal protein S26 [Source:HGNC Symbol;Acc:HGNC:10
14	ILMN_324228	1.92	−2.21	0.92	LOC101929876	ribosomal protein S26 [Source:HGNC Symbol;Acc:HGNC:10
15	ILMN_325449	1.92	−1.96	0.9		ribosomal protein S26 pseudogene 55 [Source:HGNC Symbo
16	ILMN_329995	1.62	−2.05	0.88	LOC101929876	ribosomal protein S26 [Source:HGNC Symbol;Acc:HGNC:10
17	ILMN_169581	1.47	−0.98	0.14	KRT72	keratin 72 [Source:HGNC Symbol;Acc:HGNC:28932]
18	ILMN_173799	1.42	−0.99	0.89		ribosomal protein S26 pseudogene 54 [Source:HGNC Symbo
19	ILMN_329151	1.39	−1.4	0.92		ribosomal protein S26 pseudogene 54 [Source:HGNC Symbo
20	ILMN_165795	1.29	−0.97	0.91		

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	5e−10	9 / 132	Refer	Chaussabel_1,7_MHC Ribosomal proteins
2	9e−05	11 / 831	Colon	Pentrack_CRC_TCGA_group.over_C_normal_DN
3	3e−04	11 / 965	Colon	Pentrack_CRC_TCGA_corr_R_normal_DN
4	7e−04	2 / 12	CC	small ribosomal subunit
5	9e−04	3 / 56	GSEA	REACTOME_PEPTIDE_CHAIN_ELONGATION
6	9e−04	3 / 58	GSEA	KEGG_RIBOSOME
7	1e−03	3 / 65	BP	SRP−dependent cotranslational protein targeting to membrane
8	2e−03	3 / 68	GSEA	REACTOME_INFLUENZA_VIRAL_RNA_TRANSCRIPTION_AND_REPLIC
9	2e−03	3 / 69	GSEA	REACTOME_3_UTR_MEDIATED_TRANSLATIONAL_REGULATION
10	2e−03	3 / 74	GSEA	REACTOME_SRP_DEPENDENT_COTRANSLATIONAL_PROTEIN_TARG
11	2e−03	3 / 74	GSEA	REACTOME_NONSENSE_MEDIATED_DECAY_ENHANCED_BY_THE_E
12	2e−03	3 / 81	BP	viral transcription
13	3e−03	3 / 87	BP	nuclear−transcribed mRNA catabolic process, nonsense−mediated decay
14	4e−03	2 / 28	CC	cytosolic small ribosomal subunit
15	4e−03	2 / 28	GSEA	REACTOME_FORMATION_OF_THE_TERNARY_COMPLEX_AND_SUBS
16	4e−03	3 / 96	BP	translational initiation
17	4e−03	3 / 99	GSEA	REACTOME_INFLUENZA_LIFE_CYCLE
18	5e−03	3 / 101	GSEA	REACTOME_TRANSLATION
19	6e−03	3 / 110	GSEA	PECE_MAMMARY_STEM_CELL_UP
20	6e−03	2 / 35	GSEA	REACTOME_ACTIVATION_OF_THE_MRNA_UPON_BINDING_OF_THE_
21	9e−03	2 / 42	GSEA	NATSUME_RESPONSE_TO_INTERFERON_BETA_DN
22	1e−02	3 / 155	GSEA	REACTOME_METABOLISM_OF_MRNA
23	1e−02	2 / 56	GSEA	GAZDA_DIAMOND_BLACKFAN_ANEMIA_PROGENITOR_DN
24	2e−02	2 / 58	GSEA	BILANGES_RAPAMYCIN_SENSITIVE_VIA_TSC1_AND_TSC2
25	2e−02	3 / 163	BP	rRNA processing
26	2e−02	3 / 169	MF	structural constituent of ribosome
27	2e−02	1 / 6	GSEA	MCBRYAN_TERMINAL_END_BUD_DN
28	2e−02	1 / 6	GSEA	MIKKELSEN_ES_LCP_WITH_H3K4ME3_AND_H3K27ME3
29	2e−02	1 / 7	GSEA	FARDIN_HYPOXIA_9
30	2e−02	3 / 184	BP	translation
31	3e−02	3 / 196	GSEA	REACTOME_METABOLISM_OF_RNA
32	3e−02	1 / 9	GSEA	MIKKELSEN_IPS_LCP_WITH_H3K27ME3
33	3e−02	1 / 10	BP	fructose metabolic process
34	3e−02	1 / 10	MF	inositol−1,4,5−trisphosphate 3−kinase activity
35	3e−02	1 / 10	GSEA	XU_HGF_TARGETS_REPRESSED_BY_AKT1_UP
36	3e−02	2 / 88	Colon	Pentrack_CRC_TCGA_corr_S_normal_DN
37	4e−02	1 / 11	BP	glycoprotein metabolic process
38	4e−02	1 / 11	BP	intra−S DNA damage checkpoint
39	4e−02	1 / 11	GSEA	GOERING_BLOOD_HDL_CHOLESTEROL_QTL_CIS
40	4e−02	1 / 12	BP	synaptic vesicle fusion to presynaptic active zone membrane



Aging

Rank	p−value	#in/all	Geneset
1	1	0 / 111	HORVATH_aging_genes meth DOWN
2	1	0 / 142	HORVATH_aging_genes meth UP
3	1	0 / 58	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	0.001	3 / 65	SRP−dependent cotranslational protein targeting to membrane
2	0.002	3 / 81	viral transcription
3	0.003	3 / 87	nuclear−transcribed mRNA catabolic process, nonsense−mediated decay
4	0.004	3 / 96	translational initiation
5	0.017	3 / 163	rRNA processing
6	0.023	3 / 184	translation
7	0.033	1 / 10	fructose metabolic process
8	0.036	1 / 11	glycoprotein metabolic process
9	0.036	1 / 11	intra−S DNA damage checkpoint
10	0.039	1 / 12	synaptic vesicle fusion to presynaptic active zone membrane
11	0.042	1 / 13	proteoglycan biosynthetic process
12	0.045	1 / 14	glutamine metabolic process
13	0.045	1 / 14	ribosomal small subunit biogenesis
14	0.049	1 / 15	translational elongation
15	0.055	1 / 17	sulfur compound metabolic process

Brain

Rank	p−value	#in/all	Geneset
1	0.5	3 / 818	Mid_Frontal_Lobe_Het
2	0.7	1 / 328	Fetal_Het
3	0.7	1 / 383	Mid_Frontal_Lobe_Tx
4	0.7	1 / 386	Fetal_ZNF
5	0.9	2 / 1012	Mid_Frontal_Lobe_Enh
6	0.9	1 / 578	Fetal_Tx
7	0.9	6 / 2630	Fetal_TssF
8	0.9	4 / 2127	Mid_Frontal_Lobe_K9K27me3
9	0.9	1 / 796	Overlap_fetal_midbrain_ZNF
10	0.9	3 / 1728	Fetal_ReprPCWk
11	0.9	1 / 869	Mid_Frontal_Lobe_EnhG
12	0.9	5 / 2654	Fetal_Quies
13	1.0	1 / 906	Fetal_HetRpts
14	1.0	4 / 2700	Fetal_TxTrans
15	1.0	4 / 2709	Mid_Frontal_Lobe_HetRpts

Cancer

Rank	p−value	#in/all	Geneset
1	0.04	1 / 13	WANG_ER_DN
2	0.05	1 / 16	GENTLES_modul7
3	0.12	1 / 38	KUIPER_MM good survival
4	0.22	1 / 73	SHAUGHNESSY_MM high risk
5	0.45	1 / 178	SPANG_LPS−index2
6	0.83	1 / 527	Lembcke_Normal vs Adenoma
7	1.00	0 / 13	RHODES_CANCER_META_SIGNATURE
8	1.00	0 / 14	RHODES_UNDIFFERENTIATED_CANCER
9	1.00	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
10	1.00	0 / 12	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
11	1.00	0 / 12	LIU_BREAST_CANCER
12	1.00	0 / 14	LIU_COMMON_CANCER_GENES
13	1.00	0 / 13	LIU_LIVER_CANCER
14	1.00	0 / 15	LIU_PROSTATE_CANCER_DN
15	1.00	0 / 14	LIU_PROSTATE_CANCER_UP

CC

Rank	p−value	#in/all	Geneset
1	7e−04	2 / 12	small ribosomal subunit
2	4e−03	2 / 28	cytosolic small ribosomal subunit
3	8e−02	1 / 25	preribosome, large subunit precursor
4	1e−01	1 / 45	cytosolic large ribosomal subunit
5	1e−01	1 / 46	intermediate filament cytoskeleton
6	2e−01	1 / 50	SNARE complex
7	2e−01	1 / 68	Golgi cisterna membrane
8	2e−01	1 / 83	synaptic vesicle
9	3e−01	1 / 88	keratin filament
10	3e−01	1 / 107	spindle
11	4e−01	1 / 133	microtubule organizing center
12	4e−01	1 / 134	myelin sheath
13	4e−01	1 / 173	nuclear chromatin
14	6e−01	2 / 561	intracellular membrane−bounded organelle
15	6e−01	1 / 295	cell−cell adherens junction

Chr

Rank	p−value	#in/all	Geneset
1	0.06	9 / 1492	Chr 2
2	0.09	7 / 1160	Chr 12
3	0.11	5 / 769	Chr 15
4	0.14	11 / 2323	Chr 1
5	0.16	3 / 422	Chr 13
6	0.19	6 / 1170	Chr 7
7	0.27	6 / 1318	Chr 17
8	0.53	3 / 836	Chr 8
9	0.57	4 / 1211	Chr 6
10	0.58	3 / 902	Chr 4
11	0.62	3 / 959	Chr 16
12	0.68	1 / 342	Chr 18
13	0.78	3 / 1217	Chr 3
14	0.81	2 / 904	Chr 10
15	0.83	2 / 954	Chr 9

Chromatin states

Rank	p−value	#in/all	Geneset
1	0.4	5 / 1206	6_EnhG_Neuronal_Progenitor
2	0.4	2 / 416	4_TxTrans_Neuronal_Progenitor
3	0.9	1 / 717	11_K9K27me3_Fibroblasts
4	0.9	4 / 2028	4_TxTrans_Melanocytes
5	1.0	6 / 3450	4_TxTrans_Fibroblasts
6	1.0	4 / 3068	8_EnhP_Fibroblasts
7	1.0	3 / 2660	8_EnhP_Melanocytes
8	1.0	3 / 2682	12_Het_Neuronal_Progenitor
9	1.0	4 / 3272	13_HetRpts_Neuronal_Progenitor
10	1.0	2 / 2315	13_HetRpts_Melanocytes
11	1.0	5 / 4107	9_ReprPCWk_Fibroblasts
12	1.0	1 / 2031	12_Het_Melanocytes
13	1.0	3 / 3438	10_ReprPC_Melanocytes
14	1.0	3 / 3523	1_TssP_Melanocytes
15	1.0	8 / 5956	3_TssF_Neuronal_Progenitor

Colon Cancer

Rank	p−value	#in/all	Geneset
1	9e−05	11 / 831	Pentrack_CRC_TCGA_group.over_C_normal_DN
2	3e−04	11 / 965	Pentrack_CRC_TCGA_corr_R_normal_DN
3	3e−02	2 / 88	Pentrack_CRC_TCGA_corr_S_normal_DN
4	5e−01	1 / 217	Lembcke_TCGA_meth_kmeans_B_Cluster4_DN
5	6e−01	1 / 278	Kosinski_top−crypt−long−list
6	7e−01	1 / 366	K9K27me3_Colon
7	7e−01	2 / 789	TxEnhG2_Colon
8	8e−01	3 / 1168	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_
9	9e−01	1 / 599	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
10	9e−01	3 / 1468	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
11	9e−01	2 / 1069	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
12	9e−01	4 / 1895	EnhP_Colon
13	9e−01	1 / 713	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
14	9e−01	4 / 2073	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
15	9e−01	1 / 799	LaPointe_mucosa−position_kmeans_B_ascending colon_transverse colon_U

Glio

Rank	p−value	#in/all	Geneset
1	0.05	1 / 14	astrocytes_glio
2	0.19	1 / 65	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
3	0.25	1 / 87	Sturm_GBM_Meth_overexpression_I_RTK I 'PDGFRA'_UP
4	0.28	1 / 100	GIEZELT_GBM_STS_down_VS_LTS
5	0.65	1 / 315	Up
6	0.74	1 / 401	Down_b
7	0.76	2 / 820	Sturm_GBM_Meth_overexpression_E_G34_UP
8	0.80	1 / 487	Hopp_Sturm_GBM_Epi3_B_adult_UP_G34_DN
9	0.99	1 / 1417	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
10	1.00	2 / 2988	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
11	1.00	0 / 15	VERHAAK_CL subtype
12	1.00	0 / 15	VERHAAK_MES subtype
13	1.00	0 / 15	VERHAAK_NL subtype
14	1.00	0 / 15	VERHAAK_PN subtype
15	1.00	0 / 35	WIRTH_PN subtype

GSEA C2

Rank	p−value	#in/all	Geneset
1	9e−04	3 / 56	REACTOME_PEPTIDE_CHAIN_ELONGATION
2	9e−04	3 / 58	KEGG_RIBOSOME
3	2e−03	3 / 68	REACTOME_INFLUENZA_VIRAL_RNA_TRANSCRIPTION_AND_REPLICAT
4	2e−03	3 / 69	REACTOME_3_UTR_MEDIATED_TRANSLATIONAL_REGULATION
5	2e−03	3 / 74	REACTOME_SRP_DEPENDENT_COTRANSLATIONAL_PROTEIN_TARGET
6	2e−03	3 / 74	REACTOME_NONSENSE_MEDIATED_DECAY_ENHANCED_BY_THE_EXC
7	4e−03	2 / 28	REACTOME_FORMATION_OF_THE_TERNARY_COMPLEX_AND_SUBSEC
8	4e−03	3 / 99	REACTOME_INFLUENZA_LIFE_CYCLE
9	5e−03	3 / 101	REACTOME_TRANSLATION
10	6e−03	3 / 110	PECE_MAMMARY_STEM_CELL_UP
11	6e−03	2 / 35	REACTOME_ACTIVATION_OF_THE_MRNA_UPON_BINDING_OF_THE_CA
12	9e−03	2 / 42	NATSUME_RESPONSE_TO_INTERFERON_BETA_DN
13	1e−02	3 / 155	REACTOME_METABOLISM_OF_MRNA
14	1e−02	2 / 56	GAZDA_DIAMOND_BLACKFAN_ANEMIA_PROGENITOR_DN
15	2e−02	2 / 58	BILANGES_RAPAMYCIN_SENSITIVE_VIA_TSC1_AND_TSC2

HM

Rank	p−value	#in/all	Geneset
1	0.2	1 / 69	HALLMARK_CHOLESTEROL_HOMEOSTASIS
2	0.4	1 / 173	HALLMARK_E2F_TARGETS
3	0.5	1 / 185	HALLMARK_MTORC1_SIGNALING
4	0.5	1 / 185	HALLMARK_P53_PATHWAY
5	0.5	1 / 189	HALLMARK_HYPOXIA
6	1.0	0 / 185	HALLMARK_TNFA_SIGNALING_VIA_NFKB
7	1.0	0 / 177	HALLMARK_MITOTIC_SPINDLE
8	1.0	0 / 40	HALLMARK_WNT_BETA_CATENIN_SIGNALING
9	1.0	0 / 50	HALLMARK_TGF_BETA_SIGNALING
10	1.0	0 / 82	HALLMARK_IL6_JAK_STAT3_SIGNALING
11	1.0	0 / 130	HALLMARK_DNA_REPAIR
12	1.0	0 / 179	HALLMARK_G2M_CHECKPOINT
13	1.0	0 / 151	HALLMARK_APOPTOSIS
14	1.0	0 / 29	HALLMARK_NOTCH_SIGNALING
15	1.0	0 / 176	HALLMARK_ADIPOGENESIS

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.1	1 / 32	Marjolein_ageing−genes_DN
2	0.3	1 / 94	DUMEAUX_Smoking enriched genes
3	1.0	0 / 10	DUMEAUX_Smoking literature genes up
4	1.0	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
5	1.0	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
6	1.0	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
7	1.0	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
8	1.0	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
9	1.0	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
10	1.0	0 / 10	DUMEAUX_Women normal BMI literature genes up
11	1.0	0 / 17	DUMEAUX_High bmi enriched genes
12	1.0	0 / 31	DUMEAUX_Fasting enriched genes
13	1.0	0 / 147	Homuth_BMI−associated−genes_UP
14	1.0	0 / 211	Homuth_BMI−associated−genes_DN
15	1.0	0 / 18	Huan_blood−pressure_SBP−signature

Lymphoma

Rank	p−value	#in/all	Geneset
1	0.08	1 / 25	SPANG_BAFF 9hrs UP
2	0.09	19 / 4167	HOPP_Heterochrom
3	0.09	1 / 28	DAVE_Immune response 1
4	0.10	2 / 158	WIRTH_lymphoma937_spot C
5	0.10	2 / 159	Hopp_June14_MMML937 tumors+controls_group.overexpression_C_cell line_
6	0.30	2 / 331	SPANG_CD40 6hrs UP
7	0.37	1 / 139	Hopp_June14_MMML937 tumors+controls_group.overexpression_F_FL_tons
8	0.37	1 / 141	WIRTH_lymphoma937_spot F
9	0.52	1 / 220	Hopp_June14_MMML937 tumors+controls_group.overexpression_B_cell line_
10	0.54	1 / 232	WIRTH_lymphoma937_spot B
11	0.60	1 / 272	SPANG_IL21 DN
12	0.73	2 / 772	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell line_
13	0.73	2 / 777	WIRTH_lymphoma937_spot D
14	0.75	1 / 408	TARTE_Mature plasma cell signature
15	0.78	1 / 450	Hopp_June14_MMML937 tumors+controls_group.overexpression_I_MM_GC−

Melanoma

Rank	p−value	#in/all	Geneset
1	1	0 / 30	Hugo_melanoma−all−MET_UP
2	1	0 / 54	Hugo_melanoma−all−MET_DN
3	1	0 / 43	Hugo_melanoma−BRAFmut−MET_UP
4	1	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
5	1	0 / 27	Hugo_melanoma−all−LEF1_UP
6	1	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

MF

Rank	p−value	#in/all	Geneset
1	0.02	3 / 169	structural constituent of ribosome
2	0.03	1 / 10	inositol−1,4,5−trisphosphate 3−kinase activity
3	0.07	1 / 22	protein kinase activator activity
4	0.07	1 / 22	tumor necrosis factor−activated receptor activity
5	0.09	1 / 28	NAD binding
6	0.12	1 / 37	SNAP receptor activity
7	0.14	1 / 45	cytoskeletal protein binding
8	0.14	1 / 45	tRNA binding
9	0.16	1 / 52	SNARE binding
10	0.23	1 / 77	electron carrier activity
11	0.28	1 / 99	mRNA binding
12	0.47	1 / 188	receptor activity
13	0.49	1 / 202	structural molecule activity
14	0.49	1 / 204	protein domain specific binding
15	0.59	1 / 265	cadherin binding involved in cell−cell adhesion

miRNA Disease

Rank	p−value	#in/all	Geneset
1	0.06	1 / 20	Parkinson disease
2	0.07	1 / 22	Pigmented adrenocortical disease, primary isolated
3	0.09	1 / 27	Duchenne muscular dystrophy
4	0.09	1 / 28	Miyoshi myopathy
5	0.09	1 / 29	Myelofibrosis, idiopathic
6	0.12	1 / 40	Muscular dystrophy
7	0.14	1 / 47	Cervical cancer, somatic
8	0.15	1 / 48	Multiple myeloma
9	0.17	1 / 56	Myopathy, nemaline, 3
10	0.17	1 / 57	Cardiomyopathy, dilated
11	0.19	1 / 65	Hepatocellular carcinoma
12	0.20	1 / 68	Glioblastoma multiforme, somatic
13	0.22	1 / 73	Stroke, susceptibility to
14	0.22	1 / 76	Muscular
15	0.27	1 / 95	Colorectal cancer

miRNA target

Rank	p−value	#in/all	Geneset
1	0.2	1 / 85	hsa−miR−510
2	0.3	1 / 87	hsa−miR−299−3p
3	0.3	1 / 98	hsa−miR−653
4	0.3	1 / 100	hsa−miR−613
5	0.4	1 / 135	hsa−miR−576−3p
6	0.4	1 / 148	hsa−miR−409−3p
7	0.4	1 / 152	hsa−miR−583
8	0.5	1 / 180	hsa−miR−1
9	0.5	1 / 196	hsa−miR−206
10	0.6	1 / 274	hsa−miR−1244
11	0.6	1 / 287	hsa−miR−548j
12	0.6	1 / 289	hsa−miR−202
13	0.6	1 / 303	hsa−miR−548i
14	0.7	1 / 317	hsa−miR−559
15	1.0	0 / 419	hsa−miR−497

Pathw Act

Rank	p−value	#in/all	Geneset
1	1	0 / 14	GUSTAFSON_PI3K_UP
2	1	0 / 15	GUSTAFSON_PI3K_DN
3	1	0 / 13	BENTINK_e2f3.1
4	1	0 / 13	BENTINK_e2f3.2
5	1	0 / 13	BENTINK_myc.1
6	1	0 / 12	BENTINK_ras.1
7	1	0 / 11	BENTINK_ras.4
8	1	0 / 14	BENTINK_ras.6
9	1	0 / 13	BENTINK_src.10
10	1	0 / 12	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Reference Signatures

Rank	p−value	#in/all	Geneset
1	5e−10	9 / 132	Chaussabel_1,7_MHC Ribosomal proteins
2	6e−02	2 / 119	Chaussabel_2,4_Ribosomal proteins
3	5e−01	2 / 478	WIRTH_Nervous System
4	6e−01	1 / 289	JONGENEEL_Testis
5	8e−01	1 / 416	PROTEINATLAS_ovary
6	8e−01	1 / 465	PROTEINATLAS_liver
7	8e−01	1 / 514	PROTEINATLAS_vagina
8	9e−01	1 / 598	PROTEINATLAS_prostate
9	9e−01	1 / 619	PROTEINATLAS_salivary gland
10	9e−01	1 / 623	PROTEINATLAS_seminal vesicle
11	9e−01	1 / 639	PROTEINATLAS_breast
12	9e−01	1 / 647	PROTEINATLAS_lateral ventricle
13	9e−01	1 / 650	PROTEINATLAS_hippocampus
14	9e−01	1 / 724	PROTEINATLAS_lymph node
15	9e−01	1 / 726	PROTEINATLAS_cervix, uterine

Telomeres

Rank	p−value	#in/all	Geneset
1	1	0 / 13	Alternative lengthening of telomeres
2	1	0 / 27	Nabetani_alt len telomeres_genes_ko
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	0.4	5 / 1231	KIM_MYC targets
2	0.7	2 / 721	ICGC_SrfPcr2_targets
3	0.7	2 / 733	ICGC_Atf3_targets
4	0.9	16 / 5961	ICGC_Pol24_targets
5	0.9	1 / 631	ICGC_RxraPcr1_targets
6	0.9	1 / 747	ICGC_NrsfPcr2_targets
7	0.9	3 / 1669	ICGC_P300_targets
8	0.9	5 / 2497	ICGC_Bcl11_targets
9	0.9	4 / 2255	ICGC_SrfV0416101_targets
10	1.0	2 / 1452	ICGC_Six5_targets
11	1.0	4 / 2704	ICGC_Pbx3_targets
12	1.0	14 / 6552	ICGC_Pol2_targets
13	1.0	14 / 6578	ICGC_Pou2_targets
14	1.0	1 / 1466	ICGC_NrsfPcr2_targets
15	1.0	1 / 1478	ICGC_Myc_targets

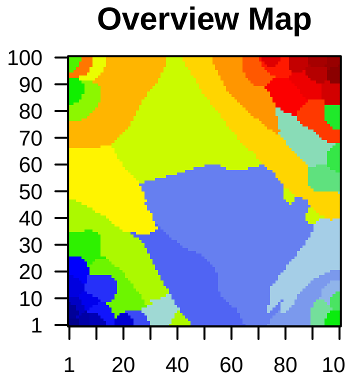
K−Means Cluster

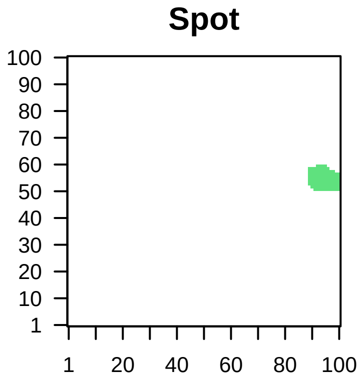
Spot Summary: B1

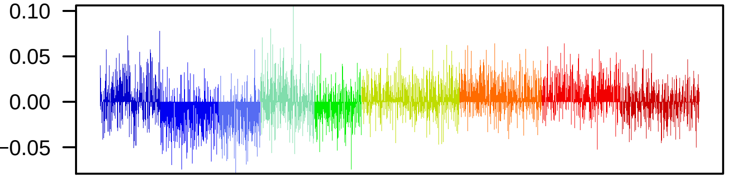
metagenes = 103
genes = 754

<r> metagenes = 0.71
<r> genes = 0.07
beta: r2= 1.54 / log p= −Inf

samples with spot = 0 (0 %)





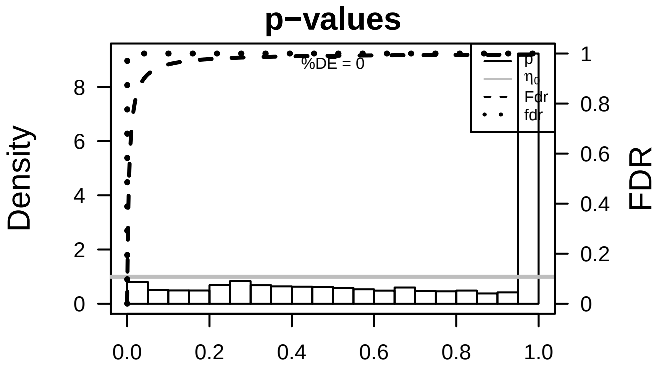


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_215969	2.92	−1.39	0.16		
2	ILMN_216575	2.67	−3.76	0.19		
3	ILMN_179153	2.13	−0.79	0.19		
4	ILMN_324215	1.9	−0.58	0.19		
5	ILMN_166607	1.73	−2.16	0.22		
6	ILMN_210557	1.53	−0.75	0.09	CCL3L3	C−C motif chemokine ligand 3 like 3 [Source:HGNC Symbol;
7	ILMN_324371	1.44	−1.23	0.23		
8	ILMN_165667	0.98	−0.73	0.11	HLA−G	major histocompatibility complex, class I, G [Source:HGNC S
9	ILMN_170713	0.97	−0.63	0.05	C17orf97	chromosome 17 open reading frame 97 [Source:HGNC Symb
10	ILMN_173324	0.91	−0.52	0.33		
11	ILMN_176286	0.88	−0.93	0.27	HLA−F	major histocompatibility complex, class I, F [Source:HGNC Sy
12	ILMN_178823	0.84	−0.38	0.15		
13	ILMN_169180	0.83	−0.57	0.13		
14	ILMN_167888	0.83	−0.55	0.19	LOC105379645	killer cell immunoglobulin like receptor, two Ig domains and lo
15	ILMN_179357	0.82	−0.39	0.23	ANKRD20A11P	ankyrin repeat domain 20 family member A11, pseudogene [S
16	ILMN_208259	0.79	−0.51	0.24	KIR3DL3	killer cell immunoglobulin like receptor, three Ig domains and
17	ILMN_323602	0.75	−0.59	0.4		
18	ILMN_176855	0.74	−0.44	0.38	PATL2	PAT1 homolog 2 [Source:HGNC Symbol;Acc:HGNC:33630]
19	ILMN_172162	0.74	−0.6	0.48	NKTR	natural killer cell triggering receptor [Source:HGNC Symbol;A
20	ILMN_320473	0.68	−0.54	0.32	STAG3L5P	stromal antigen 3−like 5 pseudogene [Source:HGNC Symbol;

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	2e−20	237 / 5699	Chror	6_EnhG_Melanocytes
2	2e−20	296 / 7854	Chror	5_Tx_Fibroblasts
3	2e−20	404 / 12298	Chror	2_TssA_Melanocytes
4	7e−20	281 / 7354	Colon	TssF_Colon
5	3e−19	316 / 8771	Chror	5_Tx_Melanocytes
6	3e−18	163 / 3450	Chror	4_TxTrans_Fibroblasts
7	3e−18	320 / 9054	Colon	Tx_Colon
8	4e−18	204 / 4795	Chror	6_EnhG_Fibroblasts
9	4e−17	151 / 3164	Brain	Mid_Frontal_Lobe_ZNF
10	8e−17	374 / 11455	Chror	2_TssA_Fibroblasts
11	2e−16	408 / 12983	Chror	2_TssA_Neuronal_Progenitor
12	2e−16	327 / 9555	Colon	TssA_Colon
13	3e−16	48 / 493	Lympl	WIRTH_lymphoma937_spot J
14	8e−16	300 / 8568	Colon	TxWk_Colon
15	1e−15	266 / 7275	Lympl	HOPP_Txn_elongation
16	1e−15	379 / 11836	Chror	3_TssF_Melanocytes
17	3e−15	325 / 9635	Chror	3_TssF_Fibroblasts
18	3e−15	31 / 221	Refer	Chaussabel_3,8_Enzymes
19	4e−14	230 / 6138	Colon	TssD2_Colon
20	2e−13	283 / 8226	Lympl	HOPP_Active_promoter
21	5e−13	42 / 472	Lympl	Hopp_June14_MMML937 tumors+controls_group.overexpression_J_GC−E
22	9e−13	313 / 9504	Brain	Overlap_fetal_midbrain_K9K27me3
23	5e−12	217 / 5936	Brain	Overlap_fetal_midbrain_HetRpts
24	8e−12	80 / 1468	Colon	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse c
25	2e−11	272 / 8098	Lympl	HOPP_Weak_promoter
26	3e−11	124 / 2845	Colon	TxEnhG1_Colon
27	1e−10	196 / 5356	Lympl	HOPP_Txn_transition
28	2e−10	283 / 8678	Colon	Quies3_Colon
29	4e−10	250 / 7448	Lympl	HOPP_Strong_enhancer
30	7e−10	379 / 12741	Chror	7_Enh_Melanocytes
31	9e−10	236 / 6970	Chror	5_Tx_Neuronal_Progenitor
32	5e−09	116 / 2810	Colon	EnhA_Colon
33	9e−09	304 / 9815	Brain	Overlap_fetal_midbrain_ReprPC
34	1e−08	327 / 10779	Colon	Enh_Colon
35	2e−08	318 / 10430	Brain	Overlap_fetal_midbrain_Quies
36	2e−08	187 / 5373	Colon	EnhWk1_Colon
37	9e−08	200 / 5956	Chror	3_TssF_Neuronal_Progenitor
38	2e−07	86 / 2028	Chror	4_TxTrans_Melanocytes
39	5e−06	352 / 12393	Chror	15_Quies_Neuronal_Progenitor
40	1e−05	205 / 6559	Lympl	HOPP_Weak_txn



Aging

Rank	p−value	#in/all	Geneset
1	0.5	4 / 142	HORVATH_aging_genes meth UP
2	0.9	1 / 111	HORVATH_aging_genes meth DOWN
3	1.0	0 / 58	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	5e−04	4 / 16	mRNA splice site selection
2	8e−04	6 / 46	mitochondrial respiratory chain complex I assembly
3	8e−04	6 / 46	regulation of translation
4	1e−03	6 / 50	response to ionizing radiation
5	2e−03	3 / 11	lysosomal transport
6	3e−03	6 / 60	interferon−gamma−mediated signaling pathway
7	3e−03	3 / 13	positive regulation of protein ubiquitination involved in ubiquitin−dependent pr
8	4e−03	3 / 14	high−density lipoprotein particle remodeling
9	4e−03	3 / 14	negative regulation of oxidative stress−induced intrinsic apoptotic signaling pa
10	5e−03	4 / 29	neuromuscular junction development
11	5e−03	3 / 15	fatty acid beta−oxidation using acyl−CoA dehydrogenase
12	6e−03	4 / 30	membrane fusion
13	7e−03	3 / 17	positive regulation of dendrite morphogenesis
14	9e−03	3 / 18	positive regulation of protein localization to nucleus
15	1e−02	4 / 37	activation of protein kinase activity

Brain

Rank	p−value	#in/all	Geneset
1	4e−17	151 / 3164	Mid_Frontal_Lobe_ZNF
2	9e−13	313 / 9504	Overlap_fetal_midbrain_K9K27me3
3	5e−12	217 / 5936	Overlap_fetal_midbrain_HetRpts
4	9e−09	304 / 9815	Overlap_fetal_midbrain_ReprPC
5	2e−08	318 / 10430	Overlap_fetal_midbrain_Quies
6	2e−05	40 / 818	Mid_Frontal_Lobe_Het
7	8e−05	285 / 9917	Overlap_fetal_midbrain_ReprPCWk
8	5e−04	92 / 2709	Mid_Frontal_Lobe_HetRpts
9	9e−04	46 / 1171	Fetal_EnhP
10	1e−02	120 / 4112	Mid_Frontal_Lobe_ReprPC
11	2e−02	56 / 1728	Fetal_ReprPCWk
12	8e−02	29 / 906	Fetal_HetRpts
13	9e−02	14 / 386	Fetal_ZNF
14	1e−01	29 / 937	Fetal_EnhG
15	1e−01	25 / 796	Overlap_fetal_midbrain_ZNF

Cancer

Rank	p−value	#in/all	Geneset
1	0.01	4 / 36	PanCan_HK_geneset_nanostring
2	0.06	2 / 16	GENTLES_modul16
3	0.11	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
4	0.16	5 / 117	PanCan_Driver_Gene_geneset_nanostring
5	0.26	1 / 12	LIU_BREAST_CANCER
6	0.27	1 / 13	GENTLES_modul18
7	0.29	1 / 14	LIU_COMMON_CANCER_GENES
8	0.30	5 / 150	PanCan_MAPK_geneset_nanostring
9	0.31	1 / 15	GENTLES_modul17
10	0.43	5 / 178	SPANG_LPS−index2
11	0.45	8 / 301	SPANG_BCL6−index2
12	0.50	1 / 28	PanCan_HH_geneset_nanostring
13	0.50	5 / 193	PanCan_PI3K_geneset_nanostring
14	0.51	0 / 15	LIU_PROSTATE_CANCER_DN
15	0.55	2 / 76	PanCan_Wnt_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	0.008	8 / 117	cell cortex
2	0.011	45 / 1304	mitochondrion
3	0.012	10 / 179	nuclear speck
4	0.014	3 / 21	integral component of lumenal side of endoplasmic reticulum membrane
5	0.023	2 / 10	CD40 receptor complex
6	0.023	2 / 10	nuclear pore outer ring
7	0.023	2 / 10	nucleotide−activated protein kinase complex
8	0.023	16 / 379	centrosome
9	0.028	2 / 11	mRNA cleavage and polyadenylation specificity factor complex
10	0.028	11 / 234	lysosomal membrane
11	0.030	3 / 28	AMPA glutamate receptor complex
12	0.033	2 / 12	membrane−bounded vesicle
13	0.033	2 / 12	paranode region of axon
14	0.035	3 / 30	cytoplasmic stress granule
15	0.044	2 / 14	basal lamina

Chr

Rank	p−value	#in/all	Geneset
1	0.02	47 / 1411	Chr 11
2	0.03	70 / 2323	Chr 1
3	0.16	35 / 1211	Chr 6
4	0.18	28 / 959	Chr 16
5	0.23	27 / 954	Chr 9
6	0.24	22 / 769	Chr 15
7	0.31	35 / 1318	Chr 17
8	0.32	15 / 536	Chr 22
9	0.33	17 / 619	Chr 20
10	0.41	31 / 1217	Chr 3
11	0.55	7 / 289	Chr 21
12	0.62	23 / 994	Chr X
13	0.63	2 / 87	Chr Y
14	0.67	34 / 1492	Chr 2
15	0.70	33 / 1467	Chr 19

Chromatin states

Rank	p−value	#in/all	Geneset
1	2e−20	237 / 5699	6_EnhG_Melanocytes
2	2e−20	296 / 7854	5_Tx_Fibroblasts
3	2e−20	404 / 12298	2_TssA_Melanocytes
4	3e−19	316 / 8771	5_Tx_Melanocytes
5	3e−18	163 / 3450	4_TxTrans_Fibroblasts
6	4e−18	204 / 4795	6_EnhG_Fibroblasts
7	8e−17	374 / 11455	2_TssA_Fibroblasts
8	2e−16	408 / 12983	2_TssA_Neuronal_Progenitor
9	1e−15	379 / 11836	3_TssF_Melanocytes
10	3e−15	325 / 9635	3_TssF_Fibroblasts
11	7e−10	379 / 12741	7_Enh_Melanocytes
12	9e−10	236 / 6970	5_Tx_Neuronal_Progenitor
13	9e−08	200 / 5956	3_TssF_Neuronal_Progenitor
14	2e−07	86 / 2028	4_TxTrans_Melanocytes
15	5e−06	352 / 12393	15_Quies_Neuronal_Progenitor

Colon Cancer

Rank	p−value	#in/all	Geneset
1	7e−20	281 / 7354	TssF_Colon
2	3e−18	320 / 9054	Tx_Colon
3	2e−16	327 / 9555	TssA_Colon
4	8e−16	300 / 8568	TxWk_Colon
5	4e−14	230 / 6138	TssD2_Colon
6	8e−12	80 / 1468	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
7	3e−11	124 / 2845	TxEnhG1_Colon
8	2e−10	283 / 8678	Quies3_Colon
9	5e−09	116 / 2810	EnhA_Colon
10	1e−08	327 / 10779	Enh_Colon
11	2e−08	187 / 5373	EnhWk1_Colon
12	5e−05	60 / 1470	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
13	2e−04	76 / 2073	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
14	7e−03	7 / 91	Pentrack_CRC_TCGA_corr_H_mss_UP_msi−h_DN
15	9e−03	295 / 10999	TssWk_Colon

Glio

Rank	p−value	#in/all	Geneset
1	0.03	3 / 29	Christensen_hypomethylated_in_grade3_astrocytoma
2	0.04	45 / 1417	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
3	0.04	2 / 14	astrocytes_glio
4	0.05	3 / 35	WIRTH_PN subtype
5	0.05	3 / 35	Colman_survival_associated
6	0.06	2 / 17	Christensen_hypomethylated_in_grade2_astrocytoma
7	0.06	2 / 17	Christensen_hypomethylated_in_grade2_oligoastrocytoma
8	0.06	2 / 17	Christensen_hypomethylated_in_grade2_oligodendroglioma
9	0.07	2 / 18	Christensen_hypomethylated_in_grade3_oligoastrocytoma
10	0.07	1 / 3	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up (L)
11	0.08	4 / 68	Christensen_hypomethylated_in_secondary_glioblastoma
12	0.10	5 / 100	GIEZELT_GBM_STS_down_VS_LTS
13	0.10	2 / 22	Shinawi_with_increased_methylation_in_STS
14	0.12	2 / 25	Sturm_GBM_Meth_overexpression_H_K27_UP
15	0.14	1 / 6	laffaire_hypometh_LGG_vs_control

GSEA C2

Rank	p−value	#in/all	Geneset
1	3e−05	13 / 139	GINESTIER_BREAST_CANCER_20Q13_AMPLIFICATION_DN
2	1e−04	20 / 319	WANG_RESPONSE_TO_GSK3_INHIBITOR_SB216763_UP
3	2e−04	9 / 86	PYEON_HPV_POSITIVE_TUMORS_UP
4	3e−04	8 / 69	LAIHO_COLORECTAL_CANCER_SERRATED_DN
5	5e−04	17 / 281	GINESTIER_BREAST_CANCER_ZNF217_AMPLIFIED_DN
6	6e−04	19 / 336	CHARAFE_BREAST_CANCER_LUMINAL_VS_BASAL_UP
7	6e−04	4 / 17	HOLLEMAN_ASPARAGINASE_RESISTANCE_ALL_UP
8	8e−04	7 / 63	PID_MTOR_4PATHWAY
9	1e−03	10 / 127	WHITFIELD_CELL_CYCLE_G1_S
10	1e−03	5 / 33	YOKOE_CANCER_TESTIS_ANTIGENS
11	1e−03	7 / 69	GROSS_HYPOXIA_VIA_HIF1A_UP
12	1e−03	14 / 229	WAMUNYOKOLI_OVARIAN_CANCER_LMP_UP
13	2e−03	12 / 182	PEREZ_TP53_AND_TP63_TARGETS
14	2e−03	8 / 92	REN_ALVEOLAR_RHABDOMYOSARCOMA_UP
15	3e−03	5 / 42	BRACHAT_RESPONSE_TO_CAMPTOTHECIN_DN

HM

Rank	p−value	#in/all	Geneset
1	0.01	10 / 183	HALLMARK_APICAL_JUNCTION
2	0.07	3 / 40	HALLMARK_WNT_BETA_CATENIN_SIGNALING
3	0.08	8 / 186	HALLMARK_ESTROGEN_RESPONSE_LATE
4	0.09	4 / 69	HALLMARK_CHOLESTEROL_HOMEOSTASIS
5	0.18	4 / 91	HALLMARK_ANDROGEN_RESPONSE
6	0.18	7 / 191	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
7	0.20	2 / 34	HALLMARK_HEDGEHOG_SIGNALING
8	0.24	4 / 103	HALLMARK_BILE_ACID_METABOLISM
9	0.28	6 / 183	HALLMARK_GLYCOLYSIS
10	0.29	6 / 185	HALLMARK_TNFA_SIGNALING_VIA_NFKB
11	0.30	6 / 186	HALLMARK_ESTROGEN_RESPONSE_EARLY
12	0.30	6 / 186	HALLMARK_MYOGENESIS
13	0.38	5 / 167	HALLMARK_OXIDATIVE_PHOSPHORYLATION
14	0.39	4 / 130	HALLMARK_DNA_REPAIR
15	0.59	2 / 82	HALLMARK_IL6_JAK_STAT3_SIGNALING

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.01	11 / 211	Homuth_BMI−associated−genes_DN
2	0.04	3 / 31	DUMEAUX_Fasting enriched genes
3	0.09	1 / 4	DUMEAUX_Exercising non smoker literature enriched genes
4	0.22	1 / 10	DUMEAUX_Women normal BMI literature genes up
5	0.69	3 / 147	Homuth_BMI−associated−genes_UP
6	1.00	0 / 94	DUMEAUX_Smoking enriched genes
7	1.00	0 / 10	DUMEAUX_Smoking literature genes up
8	1.00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
9	1.00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
10	1.00	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
11	1.00	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
12	1.00	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
13	1.00	0 / 17	DUMEAUX_High bmi enriched genes
14	1.00	0 / 18	Huan_blood−pressure_SBP−signature
15	1.00	0 / 16	Huan_blood−pressure_DBP−signature

Lymphnoma

Rank	p−value	#in/all	Geneset
1	3e−16	48 / 493	WIRTH_lymphoma937_spot J
2	1e−15	266 / 7275	HOPP_Txn_elongation
3	2e−13	283 / 8226	HOPP_Active_promoter
4	5e−13	42 / 472	Hopp_June14_MMML937 tumors+controls_group.overexpression_J_GC−B−c
5	2e−11	272 / 8098	HOPP_Weak_promoter
6	1e−10	196 / 5356	HOPP_Txn_transition
7	4e−10	250 / 7448	HOPP_Strong_enhancer
8	1e−05	205 / 6559	HOPP_Weak_txn
9	2e−04	25 / 464	WIRTH_lymphoma937_spot I
10	1e−03	18 / 331	WIRTH_lymphoma937_spot H
11	6e−03	2 / 5	DAVE_MHCCII BL DN
12	7e−03	196 / 6959	HOPP_Weak_enhancer
13	7e−03	42 / 1169	SPANG_BCR DN
14	8e−03	4 / 33	Subero_T−PLL_hypo_meth
15	1e−02	15 / 318	Hopp_June14_MMML937 tumors+controls_group.overexpression_H_GC−B−

Melanoma

Rank	p−value	#in/all	Geneset
1	0.7	1 / 54	Hugo_melanoma−all−MET_DN
2	1.0	0 / 30	Hugo_melanoma−all−MET_UP
3	1.0	0 / 43	Hugo_melanoma−BRAFmut−MET_UP
4	1.0	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
5	1.0	0 / 27	Hugo_melanoma−all−LEF1_UP
6	1.0	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

MF

Rank	p−value	#in/all	Geneset
1	0.001	4 / 21	14−3−3 protein binding
2	0.002	16 / 283	nucleotide binding
3	0.002	4 / 24	fatty−acyl−CoA binding
4	0.003	3 / 13	oxidoreductase activity, acting on the CH−CH group of donors, with a flavin as
5	0.005	3 / 15	mitogen−activated protein kinase binding
6	0.007	3 / 17	inorganic anion exchanger activity
7	0.009	3 / 18	protein disulfide isomerase activity
8	0.011	8 / 124	transporter activity
9	0.011	4 / 36	protein complex scaffold
10	0.012	3 / 20	peptide antigen binding
11	0.015	5 / 60	metallopeptidase activity
12	0.018	17 / 399	RNA binding
13	0.022	9 / 169	structural constituent of ribosome
14	0.023	35 / 1013	poly(A) RNA binding
15	0.028	2 / 11	I−SMAD binding

miRNA Disease

Rank	p−value	#in/all	Geneset
1	0.6	1 / 40	Medulloblastoma
2	0.7	1 / 47	Cervical cancer, somatic
3	0.7	1 / 56	Myopathy, nemaline, 3
4	0.8	1 / 57	Cardiomyopathy, dilated
5	0.8	1 / 65	Hepatocellular carcinoma
6	0.8	1 / 73	Stroke, susceptibility to
7	0.8	1 / 76	Muscular
8	0.9	1 / 95	Colorectal cancer
9	0.9	1 / 102	Leukemia
10	0.9	1 / 113	Ovarian cancer
11	0.9	1 / 116	Cancer
12	0.9	1 / 120	Hematological
13	1.0	1 / 123	Pancreatic cancer
14	1.0	1 / 124	Prostate cancer
15	1.0	1 / 127	Melanoma and neural system tumor syndrome

miRNA target

Rank	p−value	#in/all	Geneset
1	7e−05	9 / 74	hsa−miR−1254
2	6e−04	9 / 98	hsa−miR−653
3	2e−03	6 / 54	hsa−miR−504
4	3e−03	6 / 59	hsa−miR−665
5	4e−03	6 / 61	hsa−miR−671−5p
6	4e−03	7 / 84	hsa−miR−486−3p
7	6e−03	2 / 5	hsa−miR−1268
8	6e−03	5 / 48	hsa−miR−769−3p
9	1e−02	7 / 98	hsa−miR−544
10	1e−02	2 / 7	hsa−miR−611
11	1e−02	4 / 38	hsa−miR−647
12	1e−02	7 / 104	hsa−miR−33b
13	2e−02	6 / 84	hsa−miR−767−5p
14	2e−02	3 / 24	hsa−miR−632
15	2e−02	19 / 467	hsa−miR−195

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.04	2 / 14	BENTINK_ras.6
2	0.26	1 / 12	BENTINK_src.2
3	0.27	1 / 13	BENTINK_src.10
4	1.00	0 / 14	GUSTAFSON_PI3K_UP
5	1.00	0 / 15	GUSTAFSON_PI3K_DN
6	1.00	0 / 13	BENTINK_e2f3.1
7	1.00	0 / 13	BENTINK_e2f3.2
8	1.00	0 / 13	BENTINK_myc.1
9	1.00	0 / 12	BENTINK_ras.1
10	1.00	0 / 11	BENTINK_ras.4
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Reference Signatures

Rank	p−value	#in/all	Geneset
1	3e−15	31 / 221	Chaussabel_3,8_Enzymes
2	2e−03	37 / 929	PROTEINATLAS_bronchus
3	1e−02	9 / 148	VAQUERIZAS_General_TF
4	1e−02	35 / 959	PROTEINATLAS_nasopharynx
5	2e−02	6 / 84	Chaussabel_2,1_Cytotoxic cells
6	3e−02	23 / 619	PROTEINATLAS_salivary gland
7	4e−02	3 / 30	VAQUERIZAS_Lymph node_TF
8	4e−02	41 / 1268	PROTEINATLAS_colon
9	4e−02	16 / 412	WIRTH_Immune system
10	5e−02	38 / 1194	PROTEINATLAS_stomach
11	6e−02	37 / 1176	PROTEINATLAS_duodenum
12	9e−02	36 / 1173	PROTEINATLAS_rectum
13	1e−01	19 / 571	PROTEINATLAS_oral mucosa
14	1e−01	9 / 231	Chaussabel_2,5_Immune related molecules
15	1e−01	35 / 1167	PROTEINATLAS_gallbladder

Telomeres

Rank	p−value	#in/all	Geneset
1	0.1	2 / 27	Nabetani_alt len telomeres_genes_ko
2	1.0	0 / 13	Alternative lengthening of telomeres
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	0.005	86 / 2704	ICGC_Pbx3_targets
2	0.008	50 / 1452	ICGC_Six5_targets
3	0.010	156 / 5442	ICGC_Pmlsc71910_targets
4	0.011	43 / 1231	KIM_MYC targets
5	0.014	145 / 5067	ICGC_Taf1_targets
6	0.014	140 / 4881	ICGC_Atf2_targets
7	0.018	154 / 5466	ICGC_Nficsc81335_targets
8	0.024	181 / 6578	ICGC_Pou2_targets
9	0.024	48 / 1478	ICGC_Myc_targets
10	0.025	124 / 4345	ICGC_Zeb1_targets
11	0.027	174 / 6322	ICGC_Tcf3_targets
12	0.033	126 / 4468	ICGC_Egr1_targets
13	0.037	164 / 5984	ICGC_Mta3_targets
14	0.045	116 / 4131	ICGC_Nfatc1_targets
15	0.055	121 / 4362	ICGC_Creb1_targets

K−Means Cluster

Spot Summary: C1

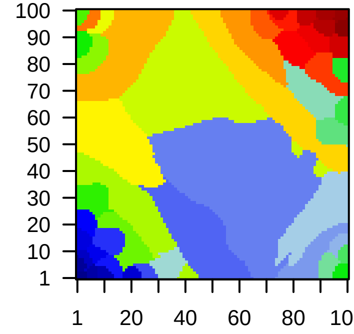
metagenes = 2131
genes = 11778

<r> metagenes = 0.36

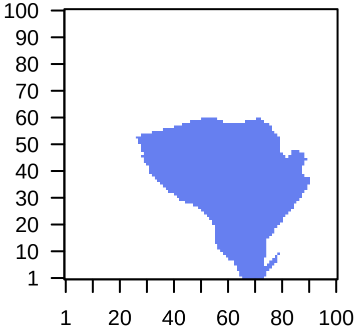
beta: r2= 0.09 / log p= −Inf

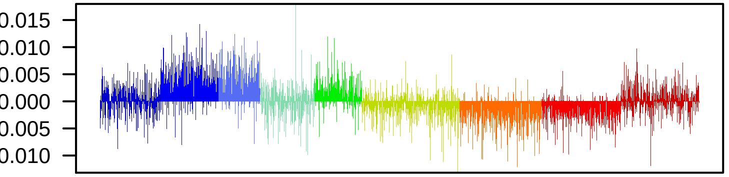
samples with spot = 0 (0 %)

Overview Map



Spot

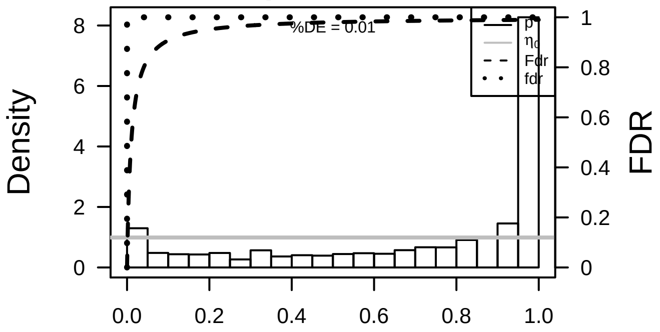




Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	2e−63	1701 / 4304	Chror	9_ReprPCWk_Melanocytes
2	5e−59	2031 / 5384	Lympl	HOPP_Repressed
3	7e−53	1375 / 3438	Chror	10_ReprPC_Melanocytes
4	3e−44	1253 / 3173	Colon	ReprPC_Colon
5	2e−40	1093 / 2740	Colon	ReprPCWk_Colon
6	2e−39	1014 / 2516	Chror	11_K9K27me3_Melanocytes
7	2e−37	1054 / 2660	Chror	8_EnhP_Melanocytes
8	6e−37	1543 / 4169	Chror	10_ReprPC_Fibroblasts
9	2e−36	1128 / 2894	Colon	TssP_Colon
10	1e−33	732 / 1753	TF	HEBENSTREIT_low expression TF
11	3e−32	1499 / 4107	Chror	9_ReprPCWk_Fibroblasts
12	1e−30	769 / 1893	Brain	Overlap_fetal_midbrain_TssF
13	3e−29	1125 / 2988	Glio	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
14	3e−27	1287 / 3523	Chror	1_TssP_Melanocytes
15	3e−27	560 / 1324	Chror	13_HetRpts_Fibroblasts
16	4e−25	496 / 1163	Chror	12_Het_Fibroblasts
17	2e−22	1296 / 3639	Chror	1_TssP_Fibroblasts
18	5e−22	592 / 1476	Brain	Overlap_fetal_midbrain_TxTrans
19	2e−21	376 / 859	Glio	Hopp_Sturm_GBM_Epi3_A_adult_fetus_UP_G34_DN
20	4e−20	428 / 1021	GSEA	BENPORATH_ES_WITH_H3K27ME3
21	1e−19	93 / 142	miRN	Lung cancer
22	2e−19	99 / 156	miRN	Breast cancer
23	3e−18	1049 / 2939	Lympl	HOPP_Poised_promoter
24	4e−18	1089 / 3068	Chror	8_EnhP_Fibroblasts
25	9e−18	711 / 1895	Colon	EnhP_Colon
26	1e−17	452 / 1119	Brain	Overlap_fetal_midbrain_TssA
27	5e−17	751 / 2031	Chror	12_Het_Melanocytes
28	6e−17	82 / 127	miRN	Melanoma and neural system tumor syndrome
29	6e−17	82 / 127	miRN	Squamous cell carcinoma, head and neck
30	1e−16	75 / 113	miRN	Ovarian cancer
31	1e−16	840 / 2315	Chror	13_HetRpts_Melanocytes
32	2e−16	528 / 1360	Brain	Mid_Frontal_Lobe_TssP
33	4e−16	79 / 123	miRN	Pancreatic cancer
34	7e−16	306 / 717	Chror	11_K9K27me3_Fibroblasts
35	1e−15	65 / 95	miRN	Colorectal cancer
36	2e−15	827 / 2297	Chror	10_ReprPC_Neuronal_Progenitor
37	3e−15	339 / 819	Brain	Overlap_fetal_midbrain_TssP
38	4e−15	76 / 120	miRN	Hematological
39	5e−15	74 / 116	miRN	Cancer
40	1e−14	386 / 962	GSEA	BENPORATH_EED_TARGETS

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.01	25 / 58	TESCHENDORFF_age_hypermethylated
2	0.20	46 / 142	HORVATH_aging_genes meth UP
3	0.99	22 / 111	HORVATH_aging_genes meth DOWN
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Cancer

Rank	p−value	#in/all	Geneset
1	0.02	9 / 16	BEN−PORATH_DN
2	0.07	3 / 15	LIU_PROSTATE_CANCER_DN
3	0.08	12 / 28	PanCan_HH_geneset_nanostring
4	0.16	45 / 136	PanCan_RAS_geneset_nanostring
5	0.16	31 / 91	PanCan_TXmisReg_geneset_nanostring
6	0.17	49 / 150	PanCan_MAPK_geneset_nanostring
7	0.22	61 / 193	PanCan_PI3K_geneset_nanostring
8	0.24	6 / 15	GENTLES_modul17
9	0.25	25 / 76	PanCan_Wnt_geneset_nanostring
10	0.31	5 / 13	WANG_ER_DN
11	0.45	3 / 13	LIU_LIVER_CANCER
12	0.51	3 / 9	GENTLES_modul3
13	0.59	13 / 46	PanCan_TGF−B_geneset_nanostring
14	0.61	4 / 14	LIU_COMMON_CANCER_GENES
15	0.61	4 / 14	BEN−PORATH_UP

Chromatin states

Rank	p−value	#in/all	Geneset
1	2e−63	1701 / 4304	9_ReprPCWk_Melanocytes
2	7e−53	1375 / 3438	10_ReprPC_Melanocytes
3	2e−39	1014 / 2516	11_K9K27me3_Melanocytes
4	2e−37	1054 / 2660	8_EnhP_Melanocytes
5	6e−37	1543 / 4169	10_ReprPC_Fibroblasts
6	3e−32	1499 / 4107	9_ReprPCWk_Fibroblasts
7	3e−27	1287 / 3523	1_TssP_Melanocytes
8	3e−27	560 / 1324	13_HetRpts_Fibroblasts
9	4e−25	496 / 1163	12_Het_Fibroblasts
10	2e−22	1296 / 3639	1_TssP_Fibroblasts
11	4e−18	1089 / 3068	8_EnhP_Fibroblasts
12	5e−17	751 / 2031	12_Het_Melanocytes
13	1e−16	840 / 2315	13_HetRpts_Melanocytes
14	7e−16	306 / 717	11_K9K27me3_Fibroblasts
15	2e−15	827 / 2297	10_ReprPC_Neuronal_Progenitor

GSEA C2

Rank	p−value	#in/all	Geneset
1	4e−20	428 / 1021	BENPORATH_ES_WITH_H3K27ME3
2	1e−14	386 / 962	BENPORATH_EED_TARGETS
3	3e−14	382 / 956	BENPORATH_SUZ12_TARGETS
4	4e−13	254 / 598	BENPORATH_PRC2_TARGETS
5	4e−13	232 / 536	MIKKELSEN_MEF_HCP_WITH_H3K27ME3
6	1e−12	162 / 347	KEGG_OLFACTORY_TRANSDUCTION
7	9e−11	134 / 287	REACTOME_OLFACTORY_SIGNALING_PATHWAY
8	2e−09	345 / 916	NABA_MATRISOME
9	4e−09	516 / 1448	ZWANG_TRANSIENTLY_UP_BY_2ND_EGF_PULSE_ONLY
10	3e−07	108 / 246	MEISSNER_BRAIN_HCP_WITH_H3K27ME3
11	4e−07	83 / 179	KONDO_PROSTATE_CANCER_WITH_H3K27ME3
12	5e−07	268 / 720	REACTOME_GPCR_DOWNSTREAM_SIGNALING
13	6e−07	89 / 196	MIKKELSEN_NPC_HCP_WITH_H3K4ME3_AND_H3K27ME3
14	2e−06	298 / 822	REACTOME_SIGNALING_BY_GPCR
15	2e−06	90 / 204	MIKKELSEN_MEF_HCP_WITH_H3_UNMETHYLATED

Lymphoma

Rank	p−value	#in/all	Geneset
1	5e−59	2031 / 5384	HOPP_Repressed
2	3e−18	1049 / 2939	HOPP_Poised_promoter
3	7e−10	1363 / 4167	HOPP_Heterochrom
4	7e−06	38 / 70	LEE_Developmental_regulators
5	3e−05	100 / 244	LENZ_Stromal signature 1
6	2e−04	60 / 138	WIRTH_lymphoma937_spot G
7	5e−04	58 / 137	Hopp_June14_MMML937 tumors+controls_group.overexpression_G_tonsil_
8	8e−04	32 / 67	Hopp_Lymphoma_Epi1_with_zentr_i_B.cell_DN
9	9e−04	56 / 134	Subero_DLBCL_hyper_meth
10	5e−03	26 / 57	Hopp_Lymphoma_Epi1_no_zentr_1_B.cell_DN
11	1e−02	25 / 57	LENZ_Stromal signature 2
12	2e−02	45 / 118	Subero_INT_hyper_meth
13	2e−02	12 / 24	Subero_mBL_hypo_meth
14	3e−02	49 / 133	Hopp_Lymphoma_Epi1_no_zentr_5_B.cell_GCB_UP
15	4e−02	34 / 89	Subero_T−ALL_hyper_meth

miRNA Disease

Rank	p−value	#in/all	Geneset
1	1e−19	93 / 142	Lung cancer
2	2e−19	99 / 156	Breast cancer
3	6e−17	82 / 127	Melanoma and neural system tumor syndrome
4	6e−17	82 / 127	Squamous cell carcinoma, head and neck
5	1e−16	75 / 113	Ovarian cancer
6	4e−16	79 / 123	Pancreatic cancer
7	1e−15	65 / 95	Colorectal cancer
8	4e−15	76 / 120	Hematological
9	5e−15	74 / 116	Cancer
10	1e−14	77 / 124	Prostate cancer
11	6e−14	66 / 102	Leukemia
12	5e−11	36 / 48	Gastric cancer
13	1e−10	43 / 63	Gastrointestinal
14	5e−10	48 / 76	Muscular
15	2e−09	34 / 48	Alzheimer disease, susceptibility to

Reference Signatures

Rank	p−value	#in/all	Geneset
1	3e−14	144 / 289	JONGENEEL_Testis
2	2e−13	212 / 478	WIRTH_Nervous System
3	4e−10	107 / 220	WIRTH_Testis
4	6e−06	98 / 231	Chaussabel_2,5_Immune related molecules
5	7e−06	62 / 132	WIRTH_Muscle
6	2e−05	29 / 50	WIRTH_Placenta
7	3e−04	48 / 107	WIRTH_Liver
8	3e−04	26 / 49	JONGENEEL_Retina
9	5e−04	36 / 76	WIRTH_Homeostasis
10	1e−03	18 / 32	JONGENEEL_Placenta
11	3e−03	54 / 134	WIRTH_Mucosa
12	8e−03	24 / 53	JONGENEEL_Kidney
13	1e−02	8 / 13	JONGENEEL_Thyroid
14	2e−02	8 / 14	WIRTH_Hippocampus
15	2e−02	8 / 14	WIRTH_Thalamus

BP

Rank	p−value	#in/all	Geneset
1	1e−14	171 / 357	detection of chemical stimulus involved in sensory perception of smell
2	4e−09	76 / 147	homophilic cell adhesion via plasma membrane adhesion molecules
3	1e−08	304 / 803	G−protein coupled receptor signaling pathway
4	2e−07	98 / 217	chemical synaptic transmission
5	1e−05	53 / 110	potassium ion transmembrane transport
6	4e−05	131 / 337	spermatogenesis
7	1e−04	77 / 185	visual perception
8	2e−04	12 / 16	negative regulation of chondrocyte differentiation
9	2e−04	30 / 58	synapse assembly
10	4e−04	53 / 122	sensory perception of sound
11	4e−04	13 / 19	cardiac muscle tissue development
12	4e−04	9 / 11	heart contraction
13	5e−04	11 / 15	regulation of potassium ion transmembrane transport
14	5e−04	37 / 79	regulation of membrane potential
15	5e−04	16 / 26	phototransduction

CC

Rank	p−value	#in/all	Geneset
1	4e−14	480 / 1249	extracellular region
2	1e−07	49 / 88	keratin filament
3	1e−04	49 / 106	Z disc
4	1e−04	81 / 196	postsynaptic membrane
5	1e−04	105 / 267	proteinaceous extracellular matrix
6	1e−04	40 / 83	voltage−gated potassium channel complex
7	4e−04	12 / 17	GABA−A receptor complex
8	1e−03	23 / 45	ciliary membrane
9	2e−03	12 / 19	costamere
10	2e−03	19 / 36	myofibril
11	2e−03	22 / 44	sarcomere
12	4e−03	1123 / 3662	plasma membrane
13	4e−03	147 / 423	cell junction
14	6e−03	355 / 1101	extracellular space
15	6e−03	81 / 220	synapse

Colon Cancer

Rank	p−value	#in/all	Geneset
1	3e−44	1253 / 3173	ReprPC_Colon
2	2e−40	1093 / 2740	ReprPCWk_Colon
3	2e−36	1128 / 2894	TssP_Colon
4	9e−18	711 / 1895	EnhP_Colon
5	1e−13	279 / 663	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
6	9e−11	205 / 484	Quies2_Colon
7	1e−09	159 / 366	K9K27me3_Colon
8	1e−07	156 / 377	Lembcke_TCGA_meth_kmeans_H_CIMP.L_UP_CIMP.H_DN
9	9e−07	225 / 594	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
10	2e−05	162 / 425	Lembcke_TCGA_meth_kmeans_E_CIMP.H_UP_
11	3e−05	119 / 299	Lembcke_TCGA_meth_kmeans_A_Cluster4_DN
12	6e−04	209 / 599	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
13	1e−03	2849 / 9530	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP_
14	3e−03	166 / 479	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_
15	6e−03	51 / 129	Marisa_CRC−cluster−b

HM

Rank	p−value	#in/all	Geneset
1	8e−04	74 / 186	HALLMARK_MYOGENESIS
2	1e−02	65 / 177	HALLMARK_KRAS_SIGNALING_DN
3	2e−01	14 / 37	HALLMARK_PANCREAS_BETA_CELLS
4	2e−01	13 / 34	HALLMARK_HEDGEHOG_SIGNALING
5	2e−01	61 / 191	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
6	2e−01	38 / 116	HALLMARK_SPERMATOGENESIS
7	3e−01	41 / 132	HALLMARK_UV_RESPONSE_DN
8	3e−01	56 / 183	HALLMARK_APICAL_JUNCTION
9	3e−01	11 / 33	HALLMARK_ANGIOGENESIS
10	5e−01	9 / 29	HALLMARK_NOTCH_SIGNALING
11	6e−01	52 / 186	HALLMARK_ESTROGEN_RESPONSE_EARLY
12	7e−01	26 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING
13	8e−01	27 / 103	HALLMARK_BILE_ACID_METABOLISM
14	8e−01	12 / 50	HALLMARK_TGF_BETA_SIGNALING
15	8e−01	32 / 127	HALLMARK_COAGULATION

Melanoma

Rank	p−value	#in/all	Geneset
1	0.01	24 / 54	Hugo_melanoma−all−MET_DN
2	0.06	13 / 30	Hugo_melanoma−all−MET_UP
3	0.51	3 / 9	Hugo_melanoma−BRAFmut−MET_DN
4	0.54	8 / 27	Hugo_melanoma−all−LEF1_UP
5	0.73	11 / 43	Hugo_melanoma−BRAFmut−MET_UP
6	1.00	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

miRNA target

Rank	p−value	#in/all	Geneset
1	0.2	3 / 6	hsa−miR−886−5p
2	0.3	4 / 10	hsa−miR−933
3	0.5	11 / 36	hsa−miR−644
4	0.5	4 / 13	hsa−miR−1249
5	0.5	4 / 13	hsa−miR−744
6	0.5	4 / 13	hsa−miR−147b
7	0.6	2 / 6	hsa−miR−126
8	0.6	6 / 21	hsa−miR−1282
9	0.6	7 / 25	hsa−miR−941
10	0.6	6 / 22	hsa−miR−663
11	0.7	8 / 31	hsa−miR−1237
12	0.8	5 / 21	hsa−miR−323−5p
13	0.8	5 / 21	hsa−miR−554
14	0.8	6 / 25	hsa−miR−100
15	0.8	6 / 25	hsa−miR−220b

Telomeres

Rank	p−value	#in/all	Geneset
1	0.3	5 / 13	Alternative lengthening of telomeres
2	0.5	8 / 27	Nabetani_alt len telomeres_genes_ko
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Brain

Rank	p−value	#in/all	Geneset
1	1e−30	769 / 1893	Overlap_fetal_midbrain_TssF
2	5e−22	592 / 1476	Overlap_fetal_midbrain_TxTrans
3	1e−17	452 / 1119	Overlap_fetal_midbrain_TssA
4	2e−16	528 / 1360	Mid_Frontal_Lobe_TssP
5	3e−15	339 / 819	Overlap_fetal_midbrain_TssP
6	4e−08	899 / 2700	Fetal_TxTrans
7	5e−08	1004 / 3046	Fetal_TssA
8	6e−08	322 / 869	Mid_Frontal_Lobe_EnhG
9	1e−07	338 / 924	Mid_Frontal_Lobe_TssF
10	4e−07	396 / 1115	Overlap_fetal_midbrain_EnhG
11	1e−06	154 / 383	Mid_Frontal_Lobe_Tx
12	6e−06	178 / 465	Mid_Frontal_Lobe_TxTrans
13	8e−06	354 / 1012	Mid_Frontal_Lobe_Enh
14	1e−05	53 / 110	Overlap_fetal_midbrain_Tx
15	3e−05	211 / 578	Fetal_Tx

Chr

Rank	p−value	#in/all	Geneset
1	1e−05	347 / 994	Chr X
2	2e−04	41 / 87	Chr Y
3	1e−02	271 / 836	Chr 8
4	3e−02	366 / 1170	Chr 7
5	5e−02	242 / 769	Chr 15
6	1e−01	277 / 904	Chr 10
7	1e−01	322 / 1060	Chr 5
8	1e−01	132 / 422	Chr 13
9	2e−01	423 / 1411	Chr 11
10	2e−01	107 / 342	Chr 18
11	2e−01	189 / 619	Chr 20
12	3e−01	87 / 289	Chr 21
13	4e−01	278 / 954	Chr 9
14	6e−01	220 / 768	Chr 14
15	6e−01	256 / 902	Chr 4

Glio

Rank	p−value	#in/all	Geneset
1	3e−29	1125 / 2988	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
2	2e−21	376 / 859	Hopp_Sturm_GBM_Epi3_A_adult_fetus_UP_G34_DN
3	2e−09	201 / 487	Hopp_Sturm_GBM_Epi3_B_adult_UP_G34_DN
4	3e−05	66 / 148	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up_(MES&CL down)
5	7e−05	31 / 58	in vivo astrocytes vs. cultured astroglia
6	2e−04	44 / 95	Weller_LGG_1p19qDel−vs−intact_UP
7	3e−04	287 / 839	Hopp_Sturm_GBM_Epi3_no_zentr_1_G34_DN
8	5e−04	16 / 26	Gorovets_LGG_NB_subclass
9	6e−04	27 / 53	WILLSCHER_GBM_Verhaak−PNmut_down (G)
10	9e−04	67 / 166	Sturm_GBM_Meth_overexpression_B_adult_UP
11	1e−03	28 / 58	OPC
12	2e−03	75 / 193	Hopp_Sturm_GBM_Epi3_F_RTK II_UP_adult_fetus_K27_DN
13	4e−03	43 / 104	WIRTH_Normal Brain
14	5e−03	39 / 93	Hopp_Sturm_GBM_Epi3_C2_adult_fetus_DN
15	2e−02	141 / 419	Down_a

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.2	3 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
2	0.3	30 / 94	DUMEAUX_Smoking enriched genes
3	0.3	3 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
4	0.9	6 / 31	DUMEAUX_Fasting enriched genes
5	1.0	1 / 10	DUMEAUX_Smoking literature genes up
6	1.0	1 / 10	DUMEAUX_Women normal BMI literature genes up
7	1.0	1 / 10	Marjolein_ageing−genes_UP
8	1.0	2 / 17	DUMEAUX_High bmi enriched genes
9	1.0	4 / 32	Marjolein_ageing−genes_DN
10	1.0	1 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
11	1.0	20 / 147	Homuth_BMI−associated−genes_UP
12	1.0	21 / 211	Homuth_BMI−associated−genes_DN
13	1.0	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
14	1.0	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
15	1.0	0 / 8	DUMEAUX_Monocytes in smokers literature genes up

MF

Rank	p−value	#in/all	Geneset
1	1e−14	171 / 357	olfactory receptor activity
2	2e−12	248 / 588	G−protein coupled receptor activity
3	5e−09	49 / 82	odorant binding
4	6e−06	67 / 145	growth factor activity
5	8e−05	231 / 648	calcium ion binding
6	8e−04	169 / 476	sequence−specific DNA binding
7	1e−03	12 / 18	GABA−A receptor activity
8	2e−03	13 / 21	fibroblast growth factor receptor binding
9	2e−03	83 / 218	transcriptional activator activity, RNA polymerase II core promoter proximal re
10	3e−03	19 / 37	structural constituent of muscle
11	4e−03	23 / 48	voltage−gated potassium channel activity
12	5e−03	10 / 16	cGMP binding
13	8e−03	11 / 19	sodium−independent organic anion transmembrane transporter activity
14	9e−03	26 / 59	extracellular matrix structural constituent
15	1e−02	33 / 80	serine−type endopeptidase inhibitor activity

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.003	10 / 15	GUSTAFSON_PI3K_DN
2	0.771	3 / 13	BENTINK_e2f3.1
3	0.925	2 / 13	BENTINK_e2f3.2
4	0.943	2 / 14	GUSTAFSON_PI3K_UP
5	0.976	1 / 11	BENTINK_ras.4
6	0.983	1 / 12	BENTINK_ras.1
7	0.983	1 / 12	BENTINK_src.2
8	1.000	0 / 13	BENTINK_myc.1
9	1.000	0 / 14	BENTINK_ras.6
10	1.000	0 / 13	BENTINK_src.10
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	1e−33	732 / 1753	HEBENSTREIT_low expression TF
2	8e−02	2 / 2	MYC_ECM cell adhesion DOWN
3	3e−01	2 / 4	MYC_Apoptosis UP
4	5e−01	217 / 747	ICGC_NrsfPcr2_targets
5	5e−01	1 / 2	MYC_Cell cycle DOWN
6	5e−01	1 / 2	MYC_Signal transduction UP
7	5e−01	3 / 9	MYC_Targets DOWN
8	7e−01	2 / 8	MYC_DNA repair UP
9	8e−01	3 / 14	NOWICK_TF
10	8e−01	1 / 5	MYC_TFs
11	8e−01	1 / 5	MYC_TF and cofactors
12	9e−01	2 / 12	MYC_Protein synthesis degradation UP
13	9e−01	1 / 7	MYC_Cell cycle UP
14	9e−01	1 / 8	MYC_RNA processing binding UP
15	1e+00	2 / 18	MYC_Metabolism UP

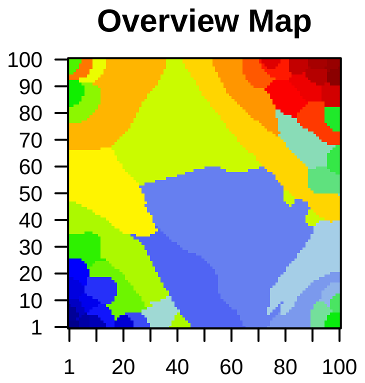
K−Means Cluster

Spot Summary: D1

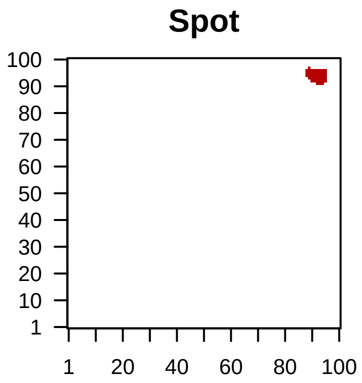
metagenes = 41
genes = 487

<r> metagenes = 0.96
<r> genes = 0.44
beta: r2= 33.14 / log p= −Inf

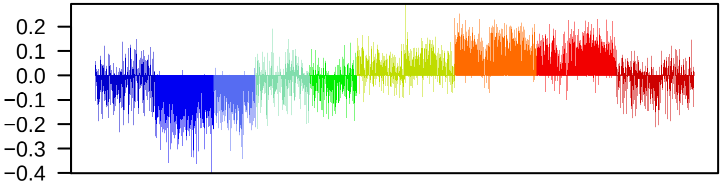
samples with spot = 450 (13.3 %)
A * : 7 (2 %)
A F * : 2 (0.6 %)
C F * : 2 (0.8 %)
F * : 43 (7.7 %)
F J * : 213 (46 %)
J * : 181 (40.5 %)
N * : 2 (0.5 %)



Overview Map



Spot

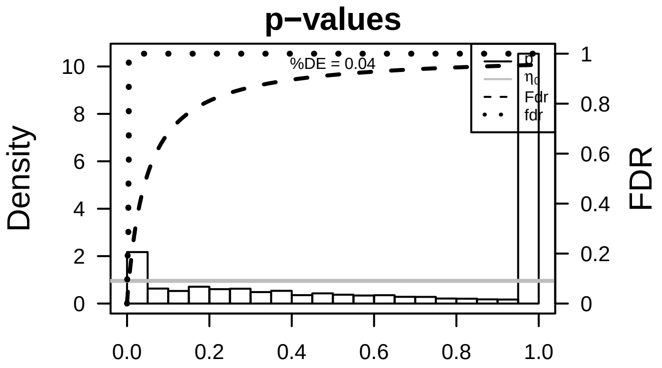


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_174314	1.89	−2.07	0.14	ERAP2	endoplasmic reticulum aminopeptidase 2 [Source:HGNC Syn
2	ILMN_168842	1.05	−1.38	0.28	FCER1A	Fc fragment of IgE receptor Ia [Source:HGNC Symbol;Acc:H
3	ILMN_210354	0.99	−0.9	0.38	GOLGA8B	golgin A8 family member B [Source:HGNC Symbol;Acc:HGN
4	ILMN_170168	0.98	−0.74	0.65		
5	ILMN_223353	0.89	−0.49	0.34	SLC39A8	solute carrier family 39 member 8 [Source:HGNC Symbol;Ac
6	ILMN_180590	0.88	−0.56	0.38		
7	ILMN_189872	0.88	−0.57	0.56	SLC9A7	solute carrier family 9 member A7 [Source:HGNC Symbol;Ac
8	ILMN_175995	0.87	−0.7	0.47	MIR1244−1	prothymosin, alpha [Source:HGNC Symbol;Acc:HGNC:9623]
9	ILMN_172704	0.84	−0.56	0.57	RASGRP3	RAS guanyl releasing protein 3 [Source:HGNC Symbol;Acc:H
10	ILMN_177523	0.83	−0.6	0.58	AFF3	AF4/FMR2 family member 3 [Source:HGNC Symbol;Acc:HGN
11	ILMN_171012	0.82	−0.61	0.38		
12	ILMN_175424	0.79	−0.69	0.39		
13	ILMN_168279	0.77	−0.65	0.76	STAMBPL1	STAM binding protein like 1 [Source:HGNC Symbol;Acc:HGN
14	ILMN_169342	0.77	−0.67	0.54		
15	ILMN_171861	0.76	−0.57	0.63	ARHGAP17	Rho GTPase activating protein 17 [Source:HGNC Symbol;Ac
16	ILMN_179865	0.76	−0.64	0.66	MCM6	minichromosome maintenance complex component 6 [Source
17	ILMN_323188	0.76	−0.65	0.5		
18	ILMN_169763	0.74	−0.79	0.46	OGT	O−linked N−acetylglucosamine (GlcNAc) transferase [Source
19	ILMN_173419	0.73	−0.66	0.68	RNGTT	RNA guanylyltransferase and 5'−phosphatase [Source:HGNC
20	ILMN_169417	0.72	−0.62	0.73	PCNA	proliferating cell nuclear antigen [Source:HGNC Symbol;Acc:I

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	9e−52	327 / 9815	Brain	Overlap_fetal_midbrain_ReprPC
2	3e−48	275 / 7275	Lympl	HOPP_Txn_elongation
3	2e−42	224 / 5356	Lympl	HOPP_Txn_transition
4	3e−42	308 / 9555	Colon	TssA_Colon
5	4e−41	282 / 8226	Lympl	HOPP_Active_promoter
6	2e−39	348 / 12298	Chror	2_TssA_Melanocytes
7	8e−39	334 / 11455	Chror	2_TssA_Fibroblasts
8	2e−34	223 / 5936	Brain	Overlap_fetal_midbrain_HetRpts
9	1e−33	275 / 8568	Colon	TxWk_Colon
10	2e−33	292 / 9504	Brain	Overlap_fetal_midbrain_K9K27me3
11	1e−32	282 / 9054	Colon	Tx_Colon
12	4e−32	276 / 8771	Chror	5_Tx_Melanocytes
13	6e−32	346 / 12983	Chror	2_TssA_Neuronal_Progenitor
14	9e−32	240 / 6970	Chror	5_Tx_Neuronal_Progenitor
15	6e−31	313 / 10999	Colon	TssWk_Colon
16	5e−29	94 / 1417	GSEA	PUJANA_BRCA1_PCC_NETWORK
17	1e−26	263 / 8678	Colon	Quies3_Colon
18	1e−25	245 / 7854	Chror	5_Tx_Fibroblasts
19	3e−25	249 / 8098	Lympl	HOPP_Weak_promoter
20	5e−25	60 / 669	GSEA	PUJANA_CHEK2_PCC_NETWORK
21	2e−24	71 / 965	Colon	Pentrack_CRC_TCGA_corr_R_normal_DN
22	1e−23	312 / 11836	Chror	3_TssF_Melanocytes
23	3e−22	63 / 831	Colon	Pentrack_CRC_TCGA_group.over_C_normal_DN
24	3e−22	77 / 1222	GSEA	DODD_NASOPHARYNGEAL_CARCINOMA_DN
25	4e−20	174 / 5067	TF	ICGC_Taf1_targets
26	2e−19	58 / 811	GSEA	LEE_BMP2_TARGETS_DN
27	1e−18	276 / 10430	Brain	Overlap_fetal_midbrain_Quies
28	2e−17	264 / 9917	Brain	Overlap_fetal_midbrain_ReprPCWk
29	5e−17	69 / 1241	GSEA	PUJANA_ATM_PCC_NETWORK
30	8e−17	78 / 1547	Colon	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP
31	1e−16	61 / 1013	MF	poly(A) RNA binding
32	2e−16	53 / 800	GSEA	JOHNSTONE_PARVB_TARGETS_3_DN
33	3e−16	56 / 887	GSEA	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
34	1e−15	103 / 2535	CC	nucleoplasm
35	1e−15	302 / 12393	Chror	15_Quies_Neuronal_Progenitor
36	1e−15	171 / 5466	TF	ICGC_Nficsc81335_targets
37	1e−14	168 / 5442	TF	ICGC_Pmlsc71910_targets
38	2e−14	169 / 5518	TF	ICGC_Stat5_targets
39	3e−14	71 / 1478	TF	ICGC_Myc_targets
40	3e−14	80 / 1797	GSEA	PILON_KLF1_TARGETS_DN



p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.3	3 / 111	HORVATH_aging_genes meth DOWN
2	0.5	3 / 142	HORVATH_aging_genes meth UP
3	1.0	0 / 58	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	4e−07	10 / 69	mitochondrial translational elongation
2	6e−07	10 / 71	mitochondrial translational termination
3	2e−06	14 / 163	rRNA processing
4	1e−05	7 / 44	RNA export from nucleus
5	2e−05	5 / 19	error−free translesion synthesis
6	2e−05	5 / 19	error−prone translesion synthesis
7	2e−05	5 / 19	nucleotide−excision repair, DNA gap filling
8	6e−05	13 / 196	mRNA splicing, via spliceosome
9	1e−04	51 / 1643	transcription, DNA−templated
10	1e−04	4 / 15	ribosomal large subunit assembly
11	1e−04	7 / 62	transcription−coupled nucleotide−excision repair
12	2e−04	8 / 86	mRNA export from nucleus
13	2e−04	5 / 30	nucleotide−excision repair, DNA incision, 5'−to lesion
14	2e−04	5 / 30	transcription from RNA polymerase III promoter
15	2e−04	5 / 31	DNA damage response, detection of DNA damage

Brain

Rank	p−value	#in/all	Geneset
1	9e−52	327 / 9815	Overlap_fetal_midbrain_ReprPC
2	2e−34	223 / 5936	Overlap_fetal_midbrain_HetRpts
3	2e−33	292 / 9504	Overlap_fetal_midbrain_K9K27me3
4	1e−18	276 / 10430	Overlap_fetal_midbrain_Quies
5	2e−17	264 / 9917	Overlap_fetal_midbrain_ReprPCWk
6	1e−04	30 / 796	Overlap_fetal_midbrain_ZNF
7	8e−03	33 / 1171	Fetal_EnhP
8	1e−02	14 / 386	Fetal_ZNF
9	1e−02	26 / 906	Fetal_HetRpts
10	2e−02	12 / 328	Fetal_Het
11	2e−02	20 / 681	Overlap_fetal_midbrain_EnhP
12	4e−02	70 / 3164	Mid_Frontal_Lobe_ZNF
13	1e−01	6 / 180	Overlap_fetal_midbrain_Het
14	1e−01	56 / 2654	Fetal_Quies
15	2e−01	21 / 937	Fetal_EnhG

Cancer

Rank	p−value	#in/all	Geneset
1	3e−04	0 / 13	RHODES_CANCER_META_SIGNATURE
2	6e−04	5 / 39	ZHANG_MM up
3	3e−03	3 / 16	GENTLES_modul11
4	9e−03	4 / 46	PanCan_DNARepair_geneset_nanostring
5	2e−02	17 / 527	Lembcke_Normal vs Adenoma
6	2e−02	0 / 14	RHODES_UNDIFFERENTIATED_CANCER
7	2e−02	2 / 13	GENTLES_modul6
8	3e−02	2 / 14	LIU_COMMON_CANCER_GENES
9	3e−02	2 / 14	GENTLES_modul1
10	3e−02	2 / 15	WOLFER_overlap genes
11	3e−02	2 / 16	GENTLES_modul16
12	7e−02	1 / 14	LIU_PROSTATE_CANCER_UP
13	1e−01	3 / 73	SHAUGHNESSY_MM high risk
14	1e−01	2 / 38	KUIPER_MM good survival
15	2e−01	1 / 9	GENTLES_modul3

CC

Rank	p−value	#in/all	Geneset
1	1e−15	103 / 2535	nucleoplasm
2	2e−11	145 / 4828	nucleus
3	1e−09	56 / 1304	mitochondrion
4	4e−09	38 / 721	nucleolus
5	4e−07	23 / 374	mitochondrial inner membrane
6	1e−05	9 / 78	catalytic step 2 spliceosome
7	4e−05	11 / 138	mitochondrial outer membrane
8	5e−05	4 / 12	small ribosomal subunit
9	1e−04	80 / 2979	cytosol
10	4e−04	116 / 4822	cytoplasm
11	4e−04	4 / 20	mitochondrial small ribosomal subunit
12	8e−04	14 / 287	mitochondrial matrix
13	8e−04	4 / 24	mitochondrial ribosome
14	1e−03	4 / 25	preribosome, large subunit precursor
15	1e−03	11 / 200	nuclear membrane

Chr

Rank	p−value	#in/all	Geneset
1	0.004	16 / 422	Chr 13
2	0.020	38 / 1492	Chr 2
3	0.059	25 / 994	Chr X
4	0.060	23 / 902	Chr 4
5	0.095	22 / 904	Chr 10
6	0.202	25 / 1160	Chr 12
7	0.276	8 / 342	Chr 18
8	0.342	24 / 1211	Chr 6
9	0.523	22 / 1217	Chr 3
10	0.540	19 / 1060	Chr 5
11	0.542	15 / 836	Chr 8
12	0.560	11 / 619	Chr 20
13	0.591	23 / 1318	Chr 17
14	0.597	5 / 289	Chr 21
15	0.626	20 / 1170	Chr 7

Chromatin states

Rank	p−value	#in/all	Geneset
1	2e−39	348 / 12298	2_TssA_Melanocytes
2	8e−39	334 / 11455	2_TssA_Fibroblasts
3	4e−32	276 / 8771	5_Tx_Melanocytes
4	6e−32	346 / 12983	2_TssA_Neuronal_Progenitor
5	9e−32	240 / 6970	5_Tx_Neuronal_Progenitor
6	1e−25	245 / 7854	5_Tx_Fibroblasts
7	1e−23	312 / 11836	3_TssF_Melanocytes
8	1e−15	302 / 12393	15_Quies_Neuronal_Progenitor
9	9e−13	233 / 8990	15_Quies_Fibroblasts
10	2e−10	292 / 12741	7_Enh_Melanocytes
11	2e−10	264 / 11130	15_Quies_Melanocytes
12	3e−07	205 / 8613	7_Enh_Fibroblasts
13	6e−07	147 / 5699	6_EnhG_Melanocytes
14	2e−06	220 / 9635	3_TssF_Fibroblasts
15	1e−04	107 / 4237	14_ZNF_Neuronal_Progenitor

Colon Cancer

Rank	p−value	#in/all	Geneset
1	3e−42	308 / 9555	TssA_Colon
2	1e−33	275 / 8568	TxWk_Colon
3	1e−32	282 / 9054	Tx_Colon
4	6e−31	313 / 10999	TssWk_Colon
5	1e−26	263 / 8678	Quies3_Colon
6	2e−24	71 / 965	Pentrack_CRC_TCGA_corr_R_normal_DN
7	3e−22	63 / 831	Pentrack_CRC_TCGA_group.over_C_normal_DN
8	8e−17	78 / 1547	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
9	8e−11	195 / 7354	TssF_Colon
10	1e−07	49 / 1216	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_
11	5e−07	54 / 1468	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
12	1e−06	111 / 4034	TssD1_Colon
13	3e−04	59 / 2073	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
14	1e−03	34 / 1083	ZNF_Colon
15	2e−03	224 / 10779	Enh_Colon

Glio

Rank	p−value	#in/all	Geneset
1	2e−11	73 / 1777	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
2	6e−11	79 / 2043	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
3	8e−03	25 / 820	Sturm_GBM_Meth_overexpression_E_G34_UP
4	1e−02	12 / 316	WILLSCHER_GBM_Verhaak−PNwt & CL_up
5	6e−02	12 / 401	Down_b
6	7e−02	4 / 84	GIEZELT_GBM_WT_down_VS_mut
7	7e−02	2 / 25	Sturm_GBM_Meth_overexpression_H_K27_UP
8	1e−01	3 / 65	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
9	1e−01	9 / 315	Up
10	1e−01	2 / 37	WILLSCHER_GBM_proteomics_wtOnly_SpotH
11	2e−01	1 / 9	WILLSCHER_GBM_LTSmut_proteomics−A_UP
12	2e−01	5 / 158	Hopp_Sturm_GBM_Epi3_D_adult_fetus_IDH_UP
13	2e−01	3 / 76	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
14	2e−01	1 / 15	VERHAAK_CL subtype
15	2e−01	2 / 52	Hopp_Sturm_GBM_Epi3_B1_G34_DN

GSEA C2

Rank	p−value	#in/all	Geneset
1	5e−29	94 / 1417	PUJANA_BRCA1_PCC_NETWORK
2	5e−25	60 / 669	PUJANA_CHEK2_PCC_NETWORK
3	3e−22	77 / 1222	DODD_NASOPHARYNGEAL_CARCINOMA_DN
4	2e−19	58 / 811	LEE_BMP2_TARGETS_DN
5	5e−17	69 / 1241	PUJANA_ATM_PCC_NETWORK
6	2e−16	53 / 800	JOHNSTONE_PARVB_TARGETS_3_DN
7	3e−16	56 / 887	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
8	3e−14	80 / 1797	PILON_KLF1_TARGETS_DN
9	6e−13	59 / 1161	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
10	1e−12	32 / 393	ZHANG_BREAST_CANCER_PROGENITORS_UP
11	2e−12	48 / 841	ACEVEDO_LIVER_CANCER_UP
12	2e−12	37 / 529	CAIRO_HEPATOBLASTOMA_CLASSES_UP
13	4e−12	44 / 737	ACEVEDO_LIVER_TUMOR_VS_NORMAL_ADJACENT_TISSUE_UP
14	5e−12	43 / 716	WEI_MYCN_TARGETS_WITH_E_BOX
15	6e−12	60 / 1265	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP

HM

Rank	p−value	#in/all	Geneset
1	2e−09	18 / 170	HALLMARK_MYC_TARGETS_V1
2	2e−05	13 / 173	HALLMARK_E2F_TARGETS
3	4e−04	6 / 54	HALLMARK_MYC_TARGETS_V2
4	2e−03	10 / 179	HALLMARK_G2M_CHECKPOINT
5	3e−03	9 / 167	HALLMARK_OXIDATIVE_PHOSPHORYLATION
6	3e−02	6 / 130	HALLMARK_DNA_REPAIR
7	4e−02	5 / 103	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
8	4e−02	7 / 176	HALLMARK_ADIPOGENESIS
9	5e−02	7 / 185	HALLMARK_MTORC1_SIGNALING
10	2e−01	4 / 116	HALLMARK_SPERMATOGENESIS
11	2e−01	4 / 137	HALLMARK_UV_RESPONSE_UP
12	2e−01	5 / 183	HALLMARK_GLYCOLYSIS
13	2e−01	4 / 138	HALLMARK_FATTY_ACID_METABOLISM
14	2e−01	5 / 186	HALLMARK_IL2_STAT5_SIGNALING
15	4e−01	2 / 69	HALLMARK_CHOLESTEROL_HOMEOSTASIS

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.002	4 / 32	Marjolein_ageing−genes_DN
2	0.037	2 / 17	DUMEAUX_High bmi enriched genes
3	0.107	2 / 31	DUMEAUX_Fasting enriched genes
4	0.238	1 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
5	0.240	3 / 94	DUMEAUX_Smoking enriched genes
6	0.252	1 / 16	Huan_blood−pressure_DBP−signature
7	0.273	4 / 147	Homuth_BMI−associated−genes_UP
8	0.979	1 / 211	Homuth_BMI−associated−genes_DN
9	1.000	0 / 10	DUMEAUX_Smoking literature genes up
10	1.000	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
11	1.000	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
12	1.000	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
13	1.000	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
14	1.000	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
15	1.000	0 / 10	DUMEAUX_Women normal BMI literature genes up

Lymphoma

Rank	p−value	#in/all	Geneset
1	3e−48	275 / 7275	HOPP_Txn_elongation
2	2e−42	224 / 5356	HOPP_Txn_transition
3	4e−41	282 / 8226	HOPP_Active_promoter
4	3e−25	249 / 8098	HOPP_Weak_promoter
5	5e−12	45 / 772	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell line_
6	6e−12	45 / 777	WIRTH_lymphoma937_spot D
7	1e−10	196 / 7448	HOPP_Strong_enhancer
8	1e−08	53 / 1270	SPANG_BCR UP
9	7e−08	176 / 6959	HOPP_Weak_enhancer
10	2e−07	47 / 1169	SPANG_BCR DN
11	7e−07	164 / 6559	HOPP_Weak_txn
12	6e−06	13 / 158	WIRTH_lymphoma937_spot C
13	6e−06	13 / 159	Hopp_June14_MMML937 tumors+controls_group.overexpression_C_cell line_
14	8e−06	10 / 94	Sha_BL UP
15	2e−04	15 / 283	TARTE_Plasmablast signature

Melanoma

Rank	p−value	#in/all	Geneset
1	0.2	1 / 9	Hugo_melanoma−BRAFmut−MET_DN
2	0.5	1 / 43	Hugo_melanoma−BRAFmut−MET_UP
3	1.0	0 / 30	Hugo_melanoma−all−MET_UP
4	1.0	0 / 54	Hugo_melanoma−all−MET_DN
5	1.0	0 / 27	Hugo_melanoma−all−LEF1_UP
6	1.0	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

MF

Rank	p−value	#in/all	Geneset
1	1e−16	61 / 1013	poly(A) RNA binding
2	6e−08	212 / 8818	protein binding
3	4e−06	18 / 283	nucleotide binding
4	1e−05	21 / 399	RNA binding
5	3e−04	11 / 169	structural constituent of ribosome
6	2e−03	4 / 30	WW domain binding
7	2e−03	42 / 1475	DNA binding
8	3e−03	3 / 17	structural constituent of nuclear pore
9	5e−03	3 / 19	nucleocytoplasmic transporter activity
10	9e−03	5 / 70	chaperone binding
11	1e−02	4 / 48	enzyme activator activity
12	1e−02	3 / 26	Ran GTPase binding
13	1e−02	5 / 76	kinase binding
14	1e−02	2 / 10	adenyl−nucleotide exchange factor activity
15	1e−02	2 / 10	poly(A) binding

miRNA Disease

Rank	p−value	#in/all	Geneset
1	1	0 / 7	Thyroid carcinoma, papillary
2	1	0 / 123	Pancreatic cancer
3	1	0 / 68	Glioblastoma multiforme, somatic
4	1	0 / 63	Gastrointestinal
5	1	0 / 3	Pituitary adenoma
6	1	0 / 116	Cancer
7	1	0 / 95	Colorectal cancer
8	1	0 / 2	Adenomas, multiple colorectal
9	1	0 / 124	Prostate cancer
10	1	0 / 48	Alzheimer disease, susceptibility to
11	1	0 / 7	Schizophrenia, susceptibility to
12	1	0 / 20	Parkinson disease
13	1	0 / 65	Hepatocellular carcinoma
14	1	0 / 3	Down syndrome, risk of
15	1	0 / 127	Melanoma and neural system tumor syndrome

miRNA target

Rank	p−value	#in/all	Geneset
1	6e−05	10 / 119	hsa−miR−105
2	9e−05	12 / 176	hsa−miR−199b−3p
3	1e−04	10 / 130	hsa−miR−194
4	2e−04	11 / 166	hsa−miR−452
5	2e−04	15 / 288	hsa−miR−34a
6	3e−04	12 / 199	hsa−miR−545
7	3e−04	8 / 93	hsa−miR−378
8	3e−04	14 / 263	hsa−miR−449a
9	4e−04	7 / 75	hsa−miR−1305
10	5e−04	11 / 184	hsa−miR−129−5p
11	6e−04	14 / 281	hsa−miR−570
12	6e−04	11 / 188	hsa−miR−548d−3p
13	6e−04	20 / 491	hsa−miR−107
14	7e−04	20 / 493	hsa−miR−103
15	7e−04	11 / 190	hsa−miR−330−3p

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.001	3 / 13	BENTINK_myc.1
2	0.019	2 / 12	BENTINK_src.2
3	0.029	2 / 15	GUSTAFSON_PI3K_DN
4	0.196	1 / 12	BENTINK_ras.1
5	0.210	1 / 13	BENTINK_e2f3.1
6	0.225	1 / 14	BENTINK_ras.6
7	1.000	0 / 14	GUSTAFSON_PI3K_UP
8	1.000	0 / 13	BENTINK_e2f3.2
9	1.000	0 / 11	BENTINK_ras.4
10	1.000	0 / 13	BENTINK_src.10
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Reference Signatures

Rank	p−value	#in/all	Geneset
1	7e−11	48 / 933	PROTEINATLAS_adrenal gland
2	1e−10	41 / 726	PROTEINATLAS_cervix, uterine
3	2e−09	39 / 740	PROTEINATLAS_esophagus
4	4e−09	42 / 850	PROTEINATLAS_skin
5	6e−09	22 / 275	Chaussabel_3,7_Spliceosome
6	6e−09	35 / 640	PROTEINATLAS_parathyroid gland
7	2e−08	34 / 639	PROTEINATLAS_breast
8	3e−08	38 / 782	PROTEINATLAS_thyroid gland
9	5e−08	44 / 1003	PROTEINATLAS_appendix
10	7e−08	49 / 1194	PROTEINATLAS_stomach
11	9e−08	48 / 1167	PROTEINATLAS_gallbladder
12	1e−07	48 / 1173	PROTEINATLAS_rectum
13	1e−07	32 / 619	PROTEINATLAS_salivary gland
14	2e−07	21 / 302	Chaussabel_3,4_Protein phosphatases
15	2e−07	46 / 1118	PROTEINATLAS_placenta

Telomeres

Rank	p−value	#in/all	Geneset
1	0.08	2 / 27	Nabetani_alt len telomeres_genes_ko
2	1.00	0 / 13	Alternative lengthening of telomeres
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	4e−20	174 / 5067	ICGC_Taf1_targets
2	1e−15	171 / 5466	ICGC_Nficsc81335_targets
3	1e−14	168 / 5442	ICGC_Pmlsc71910_targets
4	2e−14	169 / 5518	ICGC_Stat5_targets
5	3e−14	71 / 1478	ICGC_Myc_targets
6	2e−13	164 / 5410	ICGC_Foxm1_targets
7	4e−13	140 / 4362	ICGC_Creb1_targets
8	5e−13	151 / 4881	ICGC_Atf2_targets
9	6e−13	61 / 1231	KIM_MYC targets
10	9e−13	186 / 6578	ICGC_Pou2_targets
11	1e−12	150 / 4890	ICGC_Bclaf101388_targets
12	1e−12	159 / 5312	ICGC_Tcf12_targets
13	2e−12	173 / 5984	ICGC_Mta3_targets
14	4e−11	156 / 5383	ICGC_Sp1_targets
15	5e−11	174 / 6267	ICGC_Yy1_targets

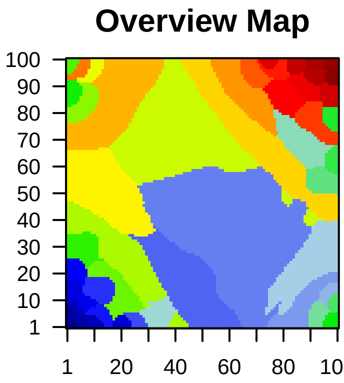
K−Means Cluster

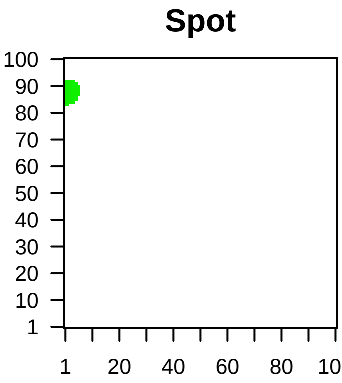
Spot Summary: E1

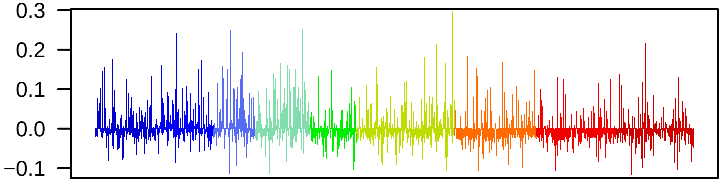
metagenes = 49
genes = 751

<r> metagenes = 0.94
<r> genes = 0.21
beta: r2= 5.03 / log p= −Inf

samples with spot = 90 (2.7 %)
- A * : 10 (2.9 %)
- A C * : 10 (3 %)
- A C F * : 16 (6.8 %)
- A F * : 16 (5.2 %)
- C F * : 3 (1.1 %)
- F * : 13 (2.3 %)
- F J * : 10 (2.2 %)
- J * : 6 (1.3 %)
- N * : 6 (1.4 %)





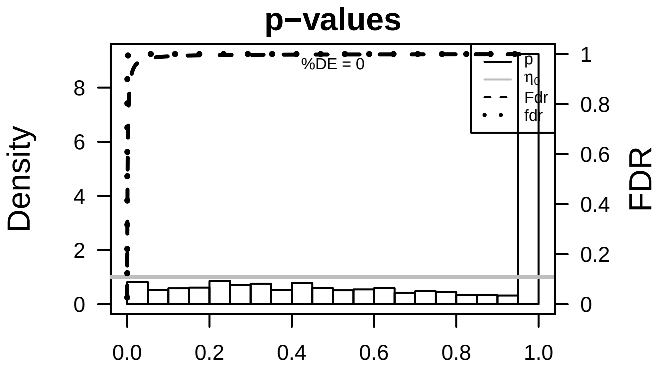


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_166406	0.86	−0.57	0.45	ERGIC1	endoplasmic reticulum−golgi intermediate compartment 1 [Sc
2	ILMN_324781	0.75	−0.41	0.31		RAS p21 protein activator 4CD, pseudogene [Source:HGNC
3	ILMN_168507	0.72	−0.49	0.28	TELO2	telomere maintenance 2 [Source:HGNC Symbol;Acc:HGNC:
4	ILMN_326869	0.72	−0.54	0.26		
5	ILMN_330822	0.69	−0.43	0.34	MIR1282	microRNA 1282 [Source:HGNC Symbol;Acc:HGNC:35360]
6	ILMN_324665	0.68	−0.42	0.33		
7	ILMN_186927	0.68	−0.4	0.31		
8	ILMN_165761	0.65	−0.35	0.7	WTAP	Wilms tumor 1 associated protein [Source:HGNC Symbol;Acc
9	ILMN_170981	0.63	−0.45	0.29	SLC35A5	solute carrier family 35 member A5 [Source:HGNC Symbol;A
10	ILMN_134394	0.62	−0.4	0.32		
11	ILMN_180048	0.61	−0.38	0.36	CT47B1	cancer/testis antigen family 47, member B1 [Source:HGNC S
12	ILMN_224967	0.57	−0.36	0.65	LSR	lipolysis stimulated lipoprotein receptor [Source:HGNC Symb
13	ILMN_328824	0.57	−0.43	0.53		
14	ILMN_183964	0.56	−0.31	0.63	LINC00323	long intergenic non−protein coding RNA 323 [Source:HGNC
15	ILMN_176111	0.56	−0.35	0.65	PORCN	porcupine homolog (Drosophila) [Source:HGNC Symbol;Acc:
16	ILMN_178092	0.56	−0.32	0.68	SLC43A1	solute carrier family 43 member 1 [Source:HGNC Symbol;Acc
17	ILMN_190200	0.55	−0.35	0.43		
18	ILMN_165712	0.55	−0.34	0.39	PTPRU	protein tyrosine phosphatase, receptor type U [Source:HGNC
19	ILMN_324766	0.55	−0.36	0.69		
20	ILMN_323756	0.54	−0.32	0.45	PP14571	uncharacterized LOC100130449 [Source:EntrezGene;Acc:10

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	3e−06	115 / 3639	Chror	1_TssP_Fibroblasts
2	5e−06	276 / 10779	Colon	Enh_Colon
3	5e−05	69 / 2028	Chror	4_TxTrans_Melanocytes
4	1e−04	4 / 13	GSEA	WORSCHECH_TUMOR_EVASION_AND_TOLEROGENICITY_DN
5	1e−04	119 / 4112	Brain	Mid_Frontal_Lobe_ReprPC
6	1e−04	96 / 3164	Brain	Mid_Frontal_Lobe_ZNF
7	1e−04	87 / 2810	Colon	EnhA_Colon
8	2e−04	93 / 3068	Chror	8_EnhP_Fibroblasts
9	2e−04	84 / 2709	Brain	Mid_Frontal_Lobe_HetRpts
10	2e−04	7 / 59	GSEA	DACOSTA_UV_RESPONSE_VIA_ERCC3_TTD_UP
11	4e−04	190 / 7354	Colon	TssF_Colon
12	7e−04	6 / 51	GSEA	LAU_APOPTOSIS_CDKN2A_UP
13	8e−04	8 / 93	CC	ubiquitin ligase complex
14	8e−04	30 / 759	Refer	PROTEINATLAS_epididymis
15	1e−03	9 / 120	MF	protein tyrosine kinase activity
16	1e−03	4 / 22	BP	positive regulation of epidermal growth factor receptor signaling pathway
17	1e−03	78 / 2620	Chror	1_TssP_Neuronal_Progenitor
18	1e−03	160 / 6138	Colon	TssD2_Colon
19	1e−03	12 / 202	GSEA	BROWNE_HCMV_INFECTION_1HR_DN
20	1e−03	3 / 11	BP	cytoplasmic sequestering of transcription factor
21	1e−03	5 / 40	MF	mRNA 3'−UTR binding
22	1e−03	34 / 933	Refer	PROTEINATLAS_adrenal gland
23	2e−03	59 / 1895	Colon	EnhP_Colon
24	2e−03	69 / 2297	Chror	10_ReprPC_Neuronal_Progenitor
25	2e−03	14 / 268	GSEA	DACOSTA_UV_RESPONSE_VIA_ERCC3_UP
26	2e−03	3 / 12	miRN	hsa−miR−652
27	2e−03	40 / 1167	Refer	PROTEINATLAS_gallbladder
28	2e−03	19 / 425	GSEA	ZHOU_INFLAMMATORY_RESPONSE_LIVE_UP
29	2e−03	4 / 26	BP	chromatin modification
30	2e−03	4 / 26	GSEA	PETROVA_PROX1_TARGETS_UP
31	2e−03	83 / 2894	Colon	TssP_Colon
32	2e−03	3 / 13	Telom	Alternative lengthening of telomeres
33	2e−03	3 / 13	GSEA	NIKOLSKY_BREAST_CANCER_12Q24_AMPLICON
34	2e−03	4 / 27	GSEA	PID_AURORA_A_PATHWAY
35	2e−03	4 / 27	GSEA	TIAN_TNF_SIGNALING_VIA_NFKB
36	3e−03	2 / 4	GSEA	COURTOIS_SENESCENCE_TRIGGERS
37	3e−03	2 / 4	GSEA	FIGUEROA_AML_METHYLATION_CLUSTER_7_DN
38	3e−03	7 / 88	GSEA	SMID_BREAST_CANCER_RELAPSE_IN_BONE_UP
39	3e−03	5 / 46	BP	vesicle fusion
40	3e−03	9 / 139	GSEA	GINESTIER_BREAST_CANCER_20Q13_AMPLIFICATION_DN



Aging

Rank	p−value	#in/all	Geneset
1	0.2	5 / 142	HORVATH_aging_genes meth UP
2	0.3	2 / 58	TESCHENDORFF_age_hypermethylated
3	0.4	3 / 111	HORVATH_aging_genes meth DOWN
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	0.001	4 / 22	positive regulation of epidermal growth factor receptor signaling pathway
2	0.001	3 / 11	cytoplasmic sequestering of transcription factor
3	0.002	4 / 26	chromatin modification
4	0.003	5 / 46	vesicle fusion
5	0.003	3 / 14	positive regulation of glycogen biosynthetic process
6	0.004	9 / 145	peptidyl−tyrosine phosphorylation
7	0.005	5 / 52	positive regulation of protein catabolic process
8	0.006	3 / 18	B cell homeostasis
9	0.006	3 / 18	response to iron ion
10	0.007	5 / 57	defense response
11	0.007	3 / 19	myoblast fusion
12	0.007	3 / 19	negative regulation of phosphorylation
13	0.007	4 / 37	positive regulation of nitric oxide biosynthetic process
14	0.008	3 / 20	cartilage condensation
15	0.008	3 / 20	G2 DNA damage checkpoint

Brain

Rank	p−value	#in/all	Geneset
1	1e−04	119 / 4112	Mid_Frontal_Lobe_ReprPC
2	1e−04	96 / 3164	Mid_Frontal_Lobe_ZNF
3	2e−04	84 / 2709	Mid_Frontal_Lobe_HetRpts
4	3e−03	44 / 1360	Mid_Frontal_Lobe_TssP
5	4e−03	57 / 1893	Overlap_fetal_midbrain_TssF
6	5e−03	229 / 9504	Overlap_fetal_midbrain_K9K27me3
7	8e−03	45 / 1476	Overlap_fetal_midbrain_TxTrans
8	9e−03	28 / 818	Mid_Frontal_Lobe_Het
9	2e−02	34 / 1119	Overlap_fetal_midbrain_TssA
10	3e−02	49 / 1784	Mid_Frontal_Lobe_ReprPCWk
11	4e−02	25 / 819	Overlap_fetal_midbrain_TssP
12	7e−02	68 / 2700	Fetal_TxTrans
13	8e−02	40 / 1506	Mid_Frontal_Lobe_Quies
14	1e−01	73 / 3046	Fetal_TssA
15	1e−01	232 / 10430	Overlap_fetal_midbrain_Quies

Cancer

Rank	p−value	#in/all	Geneset
1	0.005	9 / 150	PanCan_MAPK_geneset_nanostring
2	0.032	18 / 527	Lembcke_Normal vs Adenoma
3	0.049	6 / 125	PanCan_CC+Apop_geneset_nanostring
4	0.073	3 / 46	PanCan_DNARepair_geneset_nanostring
5	0.077	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
6	0.095	4 / 82	PanCan_JAK−ST_geneset_nanostring
7	0.115	7 / 193	PanCan_PI3K_geneset_nanostring
8	0.120	1 / 6	ZHANG_MGUS up
9	0.146	1 / 13	LIU_LIVER_CANCER
10	0.161	5 / 136	PanCan_RAS_geneset_nanostring
11	0.188	9 / 301	SPANG_BCL6−index2
12	0.234	4 / 117	PanCan_Driver_Gene_geneset_nanostring
13	0.242	1 / 13	GENTLES_modul2
14	0.289	1 / 16	GENTLES_modul11
15	0.301	3 / 91	PanCan_TXmisReg_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	8e−04	8 / 93	ubiquitin ligase complex
2	5e−03	28 / 788	endoplasmic reticulum membrane
3	6e−03	21 / 539	Golgi membrane
4	1e−02	4 / 40	SCF ubiquitin ligase complex
5	1e−02	4 / 45	extracellular vesicle
6	2e−02	3 / 27	intrinsic component of plasma membrane
7	2e−02	3 / 27	presynaptic active zone
8	2e−02	4 / 49	axon terminus
9	3e−02	2 / 12	STAGA complex
10	3e−02	6 / 109	growth cone
11	3e−02	4 / 55	synaptic vesicle membrane
12	4e−02	4 / 59	presynaptic membrane
13	4e−02	3 / 36	condensed nuclear chromosome
14	4e−02	24 / 775	endoplasmic reticulum
15	5e−02	9 / 221	endosome

Chr

Rank	p−value	#in/all	Geneset
1	0.01	44 / 1467	Chr 19
2	0.11	27 / 994	Chr X
3	0.11	31 / 1170	Chr 7
4	0.13	34 / 1318	Chr 17
5	0.14	21 / 768	Chr 14
6	0.16	56 / 2323	Chr 1
7	0.28	3 / 87	Chr Y
8	0.40	26 / 1160	Chr 12
9	0.41	27 / 1211	Chr 6
10	0.45	20 / 904	Chr 10
11	0.46	21 / 959	Chr 16
12	0.57	6 / 289	Chr 21
13	0.66	24 / 1217	Chr 3
14	0.70	29 / 1492	Chr 2
15	0.75	14 / 769	Chr 15

Chromatin states

Rank	p−value	#in/all	Geneset
1	3e−06	115 / 3639	1_TssP_Fibroblasts
2	5e−05	69 / 2028	4_TxTrans_Melanocytes
3	2e−04	93 / 3068	8_EnhP_Fibroblasts
4	1e−03	78 / 2620	1_TssP_Neuronal_Progenitor
5	2e−03	69 / 2297	10_ReprPC_Neuronal_Progenitor
6	3e−03	280 / 11836	3_TssF_Melanocytes
7	3e−03	280 / 11847	7_Enh_Neuronal_Progenitor
8	4e−03	126 / 4795	6_EnhG_Fibroblasts
9	4e−03	152 / 5956	3_TssF_Neuronal_Progenitor
10	5e−03	54 / 1789	8_EnhP_Neuronal_Progenitor
11	9e−03	94 / 3523	1_TssP_Melanocytes
12	1e−02	92 / 3450	4_TxTrans_Fibroblasts
13	1e−02	143 / 5699	6_EnhG_Melanocytes
14	2e−02	106 / 4169	10_ReprPC_Fibroblasts
15	2e−02	225 / 9635	3_TssF_Fibroblasts

Colon Cancer

Rank	p−value	#in/all	Geneset
1	5e−06	276 / 10779	Enh_Colon
2	1e−04	87 / 2810	EnhA_Colon
3	4e−04	190 / 7354	TssF_Colon
4	1e−03	160 / 6138	TssD2_Colon
5	2e−03	59 / 1895	EnhP_Colon
6	2e−03	83 / 2894	TssP_Colon
7	3e−03	29 / 789	TxEnhG2_Colon
8	6e−03	87 / 3173	ReprPC_Colon
9	6e−03	79 / 2845	TxEnhG1_Colon
10	8e−03	76 / 2740	ReprPCWk_Colon
11	3e−02	132 / 5373	EnhWk1_Colon
12	3e−02	17 / 479	Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_
13	4e−02	41 / 1470	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
14	6e−02	40 / 1468	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
15	6e−02	1 / 3	Juehling_HNPCC−mutated−in−6−to−8

Glio

Rank	p−value	#in/all	Geneset
1	0.01	5 / 68	Christensen_hypomethylated_in_secondary_glioblastoma
2	0.02	12 / 290	Hopp_Sturm_GBM_Epi3_C_IDH_UP
3	0.02	7 / 134	Christensen_hypermethylated_in_grade3_oligoastrocytoma
4	0.04	5 / 86	laffaire_hypermeth_LGG_vs_control
5	0.06	2 / 19	KIM deleted & downregulated in LTS
6	0.08	5 / 110	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
7	0.09	6 / 147	Christensen_hypermethylated_in_grade2_oligodendroglioma
8	0.10	3 / 52	OL vs. OPC
9	0.10	1 / 5	Phillips Prolif up vs PN & MES
10	0.10	5 / 117	Christensen_hypermethylated_in_grade2_oligoastrocytoma
11	0.11	3 / 56	Christensen_hypomethylated_in_primary_glioblastoma
12	0.12	1 / 6	laffaire_hypometh_LGG_vs_control
13	0.18	12 / 419	Down_a
14	0.18	2 / 37	Christensen_hypomethylated_in_ependymoma
15	0.20	5 / 148	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up_(MES&CL down)

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−04	4 / 13	WORSCHECH_TUMOR_EVASION_AND_TOLEROGENICITY_DN
2	2e−04	7 / 59	DACOSTA_UV_RESPONSE_VIA_ERCC3_TTD_UP
3	7e−04	6 / 51	LAU_APOPTOSIS_CDKN2A_UP
4	1e−03	12 / 202	BROWNE_HCMV_INFECTION_1HR_DN
5	2e−03	14 / 268	DACOSTA_UV_RESPONSE_VIA_ERCC3_UP
6	2e−03	19 / 425	ZHOU_INFLAMMATORY_RESPONSE_LIVE_UP
7	2e−03	4 / 26	PETROVA_PROX1_TARGETS_UP
8	2e−03	3 / 13	NIKOLSKY_BREAST_CANCER_12Q24_AMPLICON
9	2e−03	4 / 27	PID_AURORA_A_PATHWAY
10	2e−03	4 / 27	TIAN_TNF_SIGNALING_VIA_NFKB
11	3e−03	2 / 4	COURTOIS_SENESCENCE_TRIGGERS
12	3e−03	2 / 4	FIGUEROA_AML_METHYLATION_CLUSTER_7_DN
13	3e−03	7 / 88	SMID_BREAST_CANCER_RELAPSE_IN_BONE_UP
14	3e−03	9 / 139	GINESTIER_BREAST_CANCER_20Q13_AMPLIFICATION_DN
15	3e−03	7 / 90	ROVERSI_GLIOMA_COPY_NUMBER_UP

HM

Rank	p−value	#in/all	Geneset
1	0.006	10 / 186	HALLMARK_ESTROGEN_RESPONSE_LATE
2	0.011	4 / 41	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
3	0.013	9 / 177	HALLMARK_KRAS_SIGNALING_DN
4	0.026	7 / 137	HALLMARK_UV_RESPONSE_UP
5	0.030	5 / 82	HALLMARK_IL6_JAK_STAT3_SIGNALING
6	0.098	7 / 185	HALLMARK_TNFA_SIGNALING_VIA_NFKB
7	0.129	6 / 162	HALLMARK_ALLOGRAFT_REJECTION
8	0.178	6 / 179	HALLMARK_G2M_CHECKPOINT
9	0.215	5 / 151	HALLMARK_APOPTOSIS
10	0.336	3 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING
11	0.343	5 / 183	HALLMARK_APICAL_JUNCTION
12	0.352	5 / 185	HALLMARK_P53_PATHWAY
13	0.444	3 / 116	HALLMARK_SPERMATOGENESIS
14	0.497	4 / 173	HALLMARK_E2F_TARGETS
15	0.505	1 / 33	HALLMARK_ANGIOGENESIS

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.1	4 / 94	DUMEAUX_Smoking enriched genes
2	0.4	4 / 147	Homuth_BMI−associated−genes_UP
3	0.9	2 / 211	Homuth_BMI−associated−genes_DN
4	1.0	0 / 10	DUMEAUX_Smoking literature genes up
5	1.0	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
6	1.0	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
7	1.0	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
8	1.0	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
9	1.0	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
10	1.0	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
11	1.0	0 / 10	DUMEAUX_Women normal BMI literature genes up
12	1.0	0 / 17	DUMEAUX_High bmi enriched genes
13	1.0	0 / 31	DUMEAUX_Fasting enriched genes
14	1.0	0 / 18	Huan_blood−pressure_SBP−signature
15	1.0	0 / 16	Huan_blood−pressure_DBP−signature

Lymphnoma

Rank	p−value	#in/all	Geneset
1	0.009	8 / 137	Hopp_June14_MMML937 tumors+controls_group.overexpression_G_tonsil_U
2	0.009	8 / 138	WIRTH_lymphoma937_spot G
3	0.017	17 / 455	SPANG_CD40 6hrs DN
4	0.028	132 / 5384	HOPP_Repressed
5	0.074	4 / 75	SPANG_LPS 6hrs DN
6	0.084	2 / 23	Hopp_Lymphoma_Epi1_no_zentr_2_B.cell_MCL_DN
7	0.095	8 / 220	Hopp_June14_MMML937 tumors+controls_group.overexpression_B_cell line_
8	0.101	1 / 5	WRIGHT_custom ABC−DLBCL UP
9	0.112	4 / 87	Hopp_Lymphoma_Epi1_with_zentr_v_B.cell_DN
10	0.114	66 / 2701	HOPP_Repetitive
11	0.119	8 / 232	WIRTH_lymphoma937_spot B
12	0.133	3 / 60	SPANG_BAFF 9hrs DN
13	0.137	4 / 94	Sha_BL_UP
14	0.139	2 / 31	Care_Extended T−cell
15	0.142	21 / 772	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell line_

Melanoma

Rank	p−value	#in/all	Geneset
1	0.01	2 / 9	Hugo_melanoma−BRAFmut−MET_DN
2	0.11	3 / 54	Hugo_melanoma−all−MET_DN
3	0.44	1 / 27	Hugo_melanoma−all−LEF1_UP
4	0.60	1 / 43	Hugo_melanoma−BRAFmut−MET_UP
5	1.00	0 / 30	Hugo_melanoma−all−MET_UP
6	1.00	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

MF

Rank	p−value	#in/all	Geneset
1	0.001	9 / 120	protein tyrosine kinase activity
2	0.001	5 / 40	mRNA 3'−UTR binding
3	0.005	5 / 52	SNARE binding
4	0.006	3 / 18	peroxidase activity
5	0.009	3 / 21	protein phosphatase type 2A regulator activity
6	0.010	4 / 40	1−phosphatidylinositol−3−kinase activity
7	0.011	34 / 1065	zinc ion binding
8	0.015	3 / 25	protein phosphatase 2A binding
9	0.015	10 / 213	protein complex binding
10	0.021	3 / 28	transmembrane receptor protein tyrosine kinase activity
11	0.022	2 / 11	NAD−dependent histone deacetylase activity (H3−K14 specific)
12	0.022	2 / 11	ubiquitin−ubiquitin ligase activity
13	0.025	2 / 12	insulin−like growth factor I binding
14	0.025	2 / 12	tau−protein kinase activity
15	0.027	207 / 8818	protein binding

miRNA Disease

Rank	p−value	#in/all	Geneset
1	0.1	1 / 7	Thyroid carcinoma, papillary
2	0.3	1 / 18	Hodgkin lymphoma
3	0.4	1 / 28	Immunological
4	0.5	1 / 30	Systemic lupus erythematosus (SLE)
5	0.6	1 / 40	Medulloblastoma
6	0.6	1 / 41	Melanoma, cutaneous malignant, 2
7	0.6	1 / 47	Cervical cancer, somatic
8	0.6	1 / 48	Alzheimer disease, susceptibility to
9	0.6	1 / 48	Gastric cancer
10	0.6	1 / 48	Multiple myeloma
11	0.7	2 / 113	Ovarian cancer
12	0.7	1 / 56	Myopathy, nemaline, 3
13	0.7	1 / 63	Gastrointestinal
14	0.8	1 / 65	Hepatocellular carcinoma
15	0.8	1 / 68	Glioblastoma multiforme, somatic

miRNA target

Rank	p−value	#in/all	Geneset
1	0.002	3 / 12	hsa−miR−652
2	0.007	7 / 105	hsa−miR−376b
3	0.009	4 / 39	hsa−miR−635
4	0.011	6 / 88	hsa−miR−608
5	0.018	4 / 48	hsa−miR−329
6	0.019	9 / 188	hsa−miR−548d−3p
7	0.019	3 / 27	hsa−miR−1292
8	0.019	6 / 100	hsa−miR−376a
9	0.020	9 / 190	hsa−miR−330−3p
10	0.025	4 / 53	hsa−miR−431
11	0.028	10 / 235	hsa−miR−26a
12	0.029	3 / 32	hsa−miR−1229
13	0.031	5 / 83	hsa−miR−630
14	0.034	4 / 58	hsa−miR−187
15	0.045	6 / 122	hsa−miR−519e

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.2	1 / 13	BENTINK_e2f3.1
2	0.3	1 / 15	GUSTAFSON_PI3K_DN
3	1.0	0 / 14	GUSTAFSON_PI3K_UP
4	1.0	0 / 13	BENTINK_e2f3.2
5	1.0	0 / 13	BENTINK_myc.1
6	1.0	0 / 12	BENTINK_ras.1
7	1.0	0 / 11	BENTINK_ras.4
8	1.0	0 / 14	BENTINK_ras.6
9	1.0	0 / 13	BENTINK_src.10
10	1.0	0 / 12	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Reference Signatures

Rank	p−value	#in/all	Geneset
1	8e−04	30 / 759	PROTEINATLAS_epididymis
2	1e−03	34 / 933	PROTEINATLAS_adrenal gland
3	2e−03	40 / 1167	PROTEINATLAS_gallbladder
4	4e−03	39 / 1173	PROTEINATLAS_rectum
5	4e−03	32 / 912	PROTEINATLAS_fallopian tube
6	4e−03	32 / 912	PROTEINATLAS_urinary bladder
7	5e−03	37 / 1118	PROTEINATLAS_placenta
8	8e−03	33 / 1003	PROTEINATLAS_appendix
9	1e−02	35 / 1097	PROTEINATLAS_kidney
10	1e−02	39 / 1268	PROTEINATLAS_colon
11	1e−02	31 / 963	PROTEINATLAS_pancreas
12	1e−02	22 / 623	PROTEINATLAS_seminal vesicle
13	1e−02	28 / 850	PROTEINATLAS_skin
14	2e−02	21 / 598	PROTEINATLAS_prostate
15	2e−02	36 / 1176	PROTEINATLAS_duodenum

Telomeres

Rank	p−value	#in/all	Geneset
1	0.002	3 / 13	Alternative lengthening of telomeres
2	0.110	2 / 27	Nabetani_alt len telomeres_genes_ko
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	0.04	23 / 733	ICGC_Atf3_targets
2	0.05	55 / 2087	ICGC_Cebpbsc150_targets
3	0.06	87 / 3507	ICGC_Rad21_targets
4	0.07	79 / 3194	ICGC_Irf4_targets
5	0.07	44 / 1669	ICGC_P300_targets
6	0.10	68 / 2759	ICGC_Bcl3_targets
7	0.10	1 / 5	MYC_TFs
8	0.11	44 / 1723	HEBENSTREIT_high expression TF
9	0.12	66 / 2704	ICGC_Pbx3_targets
10	0.14	37 / 1452	ICGC_Six5_targets
11	0.14	55 / 2255	ICGC_SrfV0416101_targets
12	0.14	143 / 6267	ICGC_Yy1_targets
13	0.15	149 / 6552	ICGC_Pol2_targets
14	0.16	96 / 4131	ICGC_Nfatc1_targets
15	0.17	1 / 9	MYC_Targets DOWN

K−Means Cluster

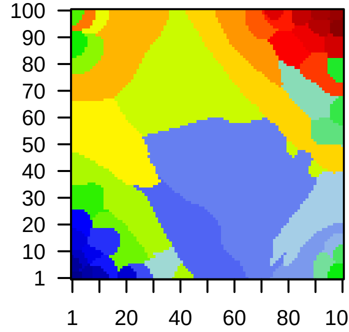
Spot Summary: F1

metagenes = 108
genes = 980

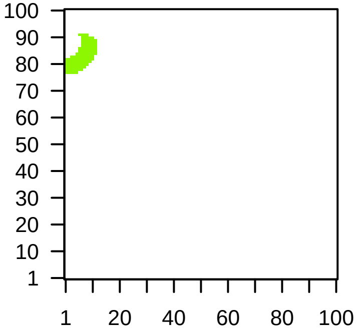
<r> metagenes = 0.93
<r> genes = 0.08
beta: r2= 1.35 / log p= −Inf

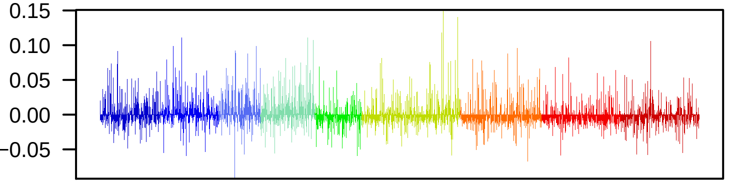
samples with spot = 3 (0.1 %)
F * : 3 (0.5 %)

Overview Map



Spot





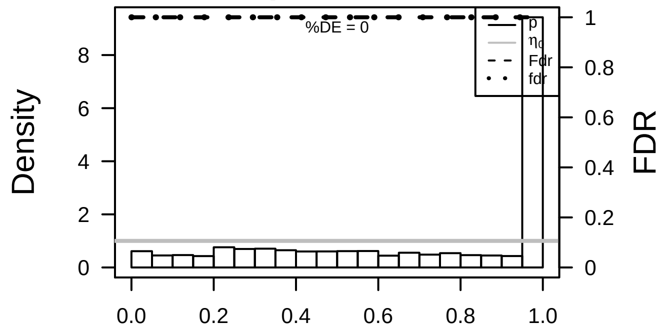
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_170872	0.55	−0.44	0.14		
2	ILMN_187004	0.48	−0.29	0.22		
3	ILMN_168782	0.41	−0.3	0.26	SEPHS2	selenophosphate synthetase 2 [Source:HGNC Symbol;Acc:H
4	ILMN_181224	0.4	−0.26	0.26		chromosome 15 open reading frame 54 [Source:HGNC Symb
5	ILMN_172299	0.39	−0.26	0.31		
6	ILMN_174772	0.38	−0.23	0.34	MLC1	megalencephalic leukoencephalopathy with subcortical cysts
7	ILMN_176769	0.37	−0.35	0.27		
8	ILMN_236774	0.37	−0.32	0.31	TUBG1	tubulin gamma 1 [Source:HGNC Symbol;Acc:HGNC:12417]
9	ILMN_176430	0.37	−0.26	0.34		
10	ILMN_238307	0.37	−0.27	0.28	SLC39A7	solute carrier family 39 member 7 [Source:HGNC Symbol;Acc
11	ILMN_165880	0.37	−0.27	0.25	HMOX2	heme oxygenase 2 [Source:HGNC Symbol;Acc:HGNC:5014]
12	ILMN_331051	0.36	−0.23	0.3	MIR639	trans−2,3−enoyl−CoA reductase [Source:HGNC Symbol;Acc:
13	ILMN_241430	0.36	−0.2	0.24	FDXR	ferredoxin reductase [Source:HGNC Symbol;Acc:HGNC:3642
14	ILMN_217374	0.36	−0.47	0.23	ASB8	ankyrin repeat and SOCS box containing 8 [Source:HGNC Sy
15	ILMN_231343	0.36	−0.33	0.25	TCP1	t−complex 1 [Source:HGNC Symbol;Acc:HGNC:11655]
16	ILMN_218199	0.36	−0.28	0.27	MTRF1	mitochondrial translational release factor 1 [Source:HGNC Sy
17	ILMN_167024	0.35	−0.22	0.27	KLF3	Kruppel like factor 3 [Source:HGNC Symbol;Acc:HGNC:1651
18	ILMN_165134	0.35	−0.25	0.3		NOC2 like nucleolar associated transcriptional repressor pseu
19	ILMN_172499	0.35	−0.22	0.29	COL4A2	collagen type IV alpha 2 chain [Source:HGNC Symbol;Acc:H
20	ILMN_178585	0.35	−0.31	0.26	ISY1	ISY1 splicing factor homolog [Source:HGNC Symbol;Acc:HG

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	3e−09	91 / 1895	Colon	EnhP_Colon
2	4e−09	132 / 3173	Colon	ReprPC_Colon
3	5e−09	123 / 2894	Colon	TssP_Colon
4	6e−09	146 / 3639	Chror	1_TssP_Fibroblasts
5	6e−09	162 / 4169	Chror	10_ReprPC_Fibroblasts
6	1e−08	114 / 2660	Chror	8_EnhP_Melanocytes
7	5e−08	136 / 3438	Chror	10_ReprPC_Melanocytes
8	1e−07	86 / 1893	Brain	Overlap_fetal_midbrain_TssF
9	2e−07	160 / 4304	Chror	9_ReprPCWk_Melanocytes
10	4e−07	104 / 2516	Chror	11_K9K27me3_Melanocytes
11	4e−07	121 / 3068	Chror	8_EnhP_Fibroblasts
12	1e−06	109 / 2740	Colon	ReprPCWk_Colon
13	4e−06	184 / 5384	Lympl	HOPP_Repressed
14	1e−05	145 / 4107	Chror	9_ReprPCWk_Fibroblasts
15	3e−05	291 / 9530	Colon	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP
16	5e−05	108 / 2939	Lympl	HOPP_Poised_promoter
17	8e−05	141 / 4112	Brain	Mid_Frontal_Lobe_ReprPC
18	1e−04	20 / 304	Brain	Mid_Frontal_Lobe_TssA
19	1e−04	123 / 3523	Chror	1_TssP_Melanocytes
20	1e−04	61 / 1476	Brain	Overlap_fetal_midbrain_TxTrans
21	2e−04	57 / 1360	Brain	Mid_Frontal_Lobe_TssP
22	2e−04	10 / 99	BP	axonogenesis
23	2e−04	17 / 249	CC	axon
24	3e−04	14 / 188	GSEA	SANSOM_APC_TARGETS_REQUIRE_MYC
25	4e−04	35 / 746	GSEA	MARTENS_TRETINOIN_RESPONSE_UP
26	6e−04	47 / 1119	Brain	Overlap_fetal_midbrain_TssA
27	6e−04	9 / 93	BP	ion transport
28	7e−04	6 / 43	GSEA	MCCLUNG_DELTA_FOSB_TARGETS_2WK
29	8e−04	33 / 717	Chror	11_K9K27me3_Fibroblasts
30	1e−03	82 / 2297	Chror	10_ReprPC_Neuronal_Progenitor
31	1e−03	36 / 819	Brain	Overlap_fetal_midbrain_TssP
32	1e−03	10 / 122	BP	neuron differentiation
33	1e−03	4 / 20	MF	anion:anion antiporter activity
34	2e−03	17 / 297	BP	nervous system development
35	2e−03	3 / 10	MF	sodium−dependent phosphate transmembrane transporter activity
36	2e−03	3 / 10	BP	sulfate transmembrane transport
37	2e−03	90 / 2620	Chror	1_TssP_Neuronal_Progenitor
38	2e−03	8 / 90	GSEA	RICKMAN_HEAD_AND_NECK_CANCER_A
39	2e−03	102 / 3046	Brain	Fetal_TssA
40	2e−03	3 / 11	MF	oxalate transmembrane transporter activity

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.2	3 / 58	TESCHENDORFF_age_hypermethylated
2	0.9	2 / 142	HORVATH_aging_genes meth UP
3	0.9	1 / 111	HORVATH_aging_genes meth DOWN
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Cancer

Rank	p−value	#in/all	Geneset
1	0.02	2 / 12	LIU_BREAST_CANCER
2	0.03	1 / 15	LIU_PROSTATE_CANCER_DN
3	0.05	2 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
4	0.20	4 / 91	PanCan_TXmisReg_geneset_nanostring
5	0.21	1 / 9	GENTLES_modul3
6	0.27	1 / 12	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
7	0.28	1 / 13	GENTLES_modul2
8	0.28	1 / 13	GENTLES_modul6
9	0.28	1 / 13	GENTLES_modul12
10	0.30	1 / 14	LIU_COMMON_CANCER_GENES
11	0.30	1 / 14	BEN−PORATH_UP
12	0.30	1 / 14	GENTLES_modul4
13	0.32	1 / 15	GENTLES_modul17
14	0.37	0 / 14	LIU_PROSTATE_CANCER_UP
15	0.40	1 / 20	PanCan_ChromMod_geneset_nanostring

Chromatin states

Rank	p−value	#in/all	Geneset
1	6e−09	146 / 3639	1_TssP_Fibroblasts
2	6e−09	162 / 4169	10_ReprPC_Fibroblasts
3	1e−08	114 / 2660	8_EnhP_Melanocytes
4	5e−08	136 / 3438	10_ReprPC_Melanocytes
5	2e−07	160 / 4304	9_ReprPCWk_Melanocytes
6	4e−07	104 / 2516	11_K9K27me3_Melanocytes
7	4e−07	121 / 3068	8_EnhP_Fibroblasts
8	1e−05	145 / 4107	9_ReprPCWk_Fibroblasts
9	1e−04	123 / 3523	1_TssP_Melanocytes
10	8e−04	33 / 717	11_K9K27me3_Fibroblasts
11	1e−03	82 / 2297	10_ReprPC_Neuronal_Progenitor
12	2e−03	90 / 2620	1_TssP_Neuronal_Progenitor
13	6e−03	117 / 3691	9_ReprPCWk_Neuronal_Progenitor
14	1e−02	61 / 1789	8_EnhP_Neuronal_Progenitor
15	1e−01	93 / 3272	13_HetRpts_Neuronal_Progenitor

GSEA C2

Rank	p−value	#in/all	Geneset
1	3e−04	14 / 188	SANSOM_APC_TARGETS_REQUIRE_MYC
2	4e−04	35 / 746	MARTENS_TRETINOIN_RESPONSE_UP
3	7e−04	6 / 43	MCCLUNG_DELTA_FOSB_TARGETS_2WK
4	2e−03	8 / 90	RICKMAN_HEAD_AND_NECK_CANCER_A
5	2e−03	3 / 11	REACTOME_SEROTONIN_RECEPTORS
6	2e−03	4 / 23	REACTOME_A_TETRASACCHARIDE_LINKER_SEQUENCE_IS_REQUIRE
7	3e−03	25 / 536	MIKKELSEN_MEF_HCP_WITH_H3K27ME3
8	3e−03	8 / 95	SCHLOSSER_SERUM_RESPONSE_AUGMENTED_BY_MYC
9	3e−03	5 / 39	RICKMAN_HEAD_AND_NECK_CANCER_B
10	3e−03	3 / 12	BOYERINAS_ONCOFETAL_TARGETS_OF_LET7A1
11	4e−03	9 / 121	KEGG_AXON_GUIDANCE
12	4e−03	7 / 79	REACTOME_TRANSPORT_OF_INORGANIC_CATIONS_ANIONS_AND_AM
13	4e−03	7 / 79	CAMPS_COLON_CANCER_COPY_NUMBER_UP
14	4e−03	4 / 26	LI_WILMS_TUMOR_VS_FETAL_KIDNEY_2_UP
15	4e−03	5 / 42	VANHARANTA_UTERINE_FIBROID_UP

Lymphoma

Rank	p−value	#in/all	Geneset
1	4e−06	184 / 5384	HOPP_Repressed
2	5e−05	108 / 2939	HOPP_Poised_promoter
3	3e−02	13 / 286	ZHANG_DLBCL mutated
4	6e−02	7 / 137	Hopp_June14_MMML937 tumors+controls_group.overexpression_G_tonsil_U
5	6e−02	7 / 138	WIRTH_lymphoma937_spot G
6	1e−01	3 / 52	Hopp_Lymphoma_Epi1_with_zentr_iv_B.cell_MM_UP
7	2e−01	3 / 57	Monti_Host_response_cluster
8	2e−01	1 / 8	MASCQUE_ABC UP
9	2e−01	1 / 8	YAMANE_AICDA_targets_nonrecruited
10	2e−01	11 / 331	SPANG_CD40 6hrs UP
11	2e−01	2 / 36	Subero_MM_hyper_meth
12	2e−01	113 / 4167	HOPP_Heterochrom
13	2e−01	3 / 67	Hopp_Lymphoma_Epi1_with_zentr_i_B.cell_DN
14	2e−01	1 / 11	Subero_MM_hypo_meth
15	3e−01	3 / 70	Hopp_Lymphoma_Epi1_no_zentr_3_B.cell_DN

miRNA Disease

Rank	p−value	#in/all	Geneset
1	0.05	1 / 2	Adenomas, multiple colorectal
2	0.14	1 / 6	Thrombocytopenic purpurea, autoimmune
3	0.21	1 / 9	Systemic lupus erythematosus, susceptibility
4	0.32	1 / 15	Supravalvar aortic stenosis
5	0.35	1 / 17	Thyroid carcinoma, follicular
6	0.42	2 / 56	Myopathy, nemaline, 3
7	0.45	1 / 23	Esophageal cancer
8	0.52	2 / 68	Glioblastoma multiforme, somatic
9	0.53	1 / 29	Myelofibrosis, idiopathic
10	0.54	1 / 30	Systemic lupus erythematosus (SLE)
11	0.56	2 / 73	Stroke, susceptibility to
12	0.65	1 / 41	Melanoma, cutaneous malignant, 2
13	0.70	1 / 47	Cervical cancer, somatic
14	0.71	1 / 48	Multiple myeloma
15	0.77	1 / 57	Cardiomyopathy, dilated

Reference Signatures

Rank	p−value	#in/all	Geneset
1	0.003	4 / 25	VAQUERIZAS_Adrenal cortex_TF
2	0.013	6 / 76	WIRTH_Homeostasis
3	0.020	7 / 107	WIRTH_Liver
4	0.021	20 / 478	WIRTH_Nervous System
5	0.055	2 / 15	VAQUERIZAS_Fetal liver_TF
6	0.056	7 / 134	WIRTH_Mucosa
7	0.076	3 / 39	VAQUERIZAS_Testis_TF
8	0.083	2 / 19	JONGENEEL_Small Intestine
9	0.099	2 / 21	JONGENEEL_Salivary Gland
10	0.123	3 / 48	WIRTH_Pancreas
11	0.165	1 / 7	JONGENEEL_Bladder
12	0.186	2 / 31	VAQUERIZAS_Fetal lung_TF
13	0.195	2 / 32	VAQUERIZAS_Liver_TF
14	0.195	2 / 32	JONGENEEL_Placenta
15	0.203	10 / 289	JONGENEEL_Testis

BP

Rank	p−value	#in/all	Geneset
1	2e−04	10 / 99	axonogenesis
2	6e−04	9 / 93	ion transport
3	1e−03	10 / 122	neuron differentiation
4	2e−03	17 / 297	nervous system development
5	2e−03	3 / 10	sulfate transmembrane transport
6	2e−03	3 / 11	oxalate transport
7	3e−03	6 / 56	negative regulation of transforming growth factor beta receptor signaling pathw
8	3e−03	3 / 12	biosynthetic process
9	4e−03	3 / 13	serotonin receptor signaling pathway
10	4e−03	7 / 79	regulation of membrane potential
11	4e−03	4 / 26	glycosaminoglycan metabolic process
12	4e−03	10 / 147	homophilic cell adhesion via plasma membrane adhesion molecules
13	7e−03	4 / 30	regulation of intracellular pH
14	7e−03	3 / 16	androgen metabolic process
15	9e−03	3 / 17	smooth muscle contraction

CC

Rank	p−value	#in/all	Geneset
1	2e−04	17 / 249	axon
2	4e−03	7 / 78	Golgi lumen
3	5e−03	3 / 14	axolemma
4	7e−03	3 / 16	apicolateral plasma membrane
5	9e−03	3 / 17	pericentriolar material
6	2e−02	5 / 59	presynaptic membrane
7	2e−02	5 / 61	extrinsic component of cytoplasmic side of plasma membrane
8	3e−02	43 / 1252	integral component of plasma membrane
9	4e−02	6 / 96	anchored component of membrane
10	4e−02	3 / 30	RNA polymerase II transcription factor complex
11	4e−02	5 / 74	lysosomal lumen
12	8e−02	2 / 18	spindle midzone
13	8e−02	5 / 90	chromatin
14	8e−02	5 / 91	perikaryon
15	8e−02	6 / 119	vesicle

Colon Cancer

Rank	p−value	#in/all	Geneset
1	3e−09	91 / 1895	EnhP_Colon
2	4e−09	132 / 3173	ReprPC_Colon
3	5e−09	123 / 2894	TssP_Colon
4	1e−06	109 / 2740	ReprPCWk_Colon
5	3e−05	291 / 9530	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP_
6	2e−02	2 / 9	Marisa_CRC−C4
7	4e−02	40 / 1168	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_
8	4e−02	4 / 52	Marisa_CRC−cluster−e
9	5e−02	15 / 366	K9K27me3_Colon
10	5e−02	22 / 594	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
11	8e−02	2 / 18	Vilar_non−hypermutated−in−CRC
12	9e−02	39 / 1224	LaPointe_mucosa−position_kmeans_A_ascending colon_UP_
13	9e−02	2 / 20	Budinska_B_Lower crypt−like_UP
14	1e−01	128 / 4526	Quies1_Colon
15	1e−01	14 / 377	Lembcke_TCGA_meth_kmeans_H_CIMP.L_UP_CIMP.H_DN

HM

Rank	p−value	#in/all	Geneset
1	0.1	8 / 187	HALLMARK_COMPLEMENT
2	0.1	8 / 189	HALLMARK_HYPOXIA
3	0.2	7 / 173	HALLMARK_E2F_TARGETS
4	0.2	7 / 183	HALLMARK_APICAL_JUNCTION
5	0.2	7 / 186	HALLMARK_MYOGENESIS
6	0.2	5 / 127	HALLMARK_COAGULATION
7	0.2	4 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING
8	0.2	2 / 37	HALLMARK_PANCREAS_BETA_CELLS
9	0.3	2 / 41	HALLMARK_APICAL_SURFACE
10	0.3	2 / 41	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
11	0.3	6 / 176	HALLMARK_KRAS_SIGNALING_UP
12	0.4	2 / 50	HALLMARK_TGF_BETA_SIGNALING
13	0.4	5 / 162	HALLMARK_ALLOGRAFT_REJECTION
14	0.4	3 / 91	HALLMARK_ANDROGEN_RESPONSE
15	0.5	5 / 177	HALLMARK_KRAS_SIGNALING_DN

Melanoma

Rank	p−value	#in/all	Geneset
1	0.5	1 / 30	Hugo_melanoma−all−MET_UP
2	0.8	1 / 54	Hugo_melanoma−all−MET_DN
3	1.0	0 / 43	Hugo_melanoma−BRAFmut−MET_UP
4	1.0	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
5	1.0	0 / 27	Hugo_melanoma−all−LEF1_UP
6	1.0	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

miRNA target

Rank	p−value	#in/all	Geneset
1	0.007	5 / 47	hsa−miR−208b
2	0.008	4 / 32	hsa−miR−1229
3	0.009	4 / 33	hsa−miR−1296
4	0.011	16 / 331	hsa−let−7g
5	0.012	5 / 54	hsa−miR−518f
6	0.015	16 / 343	hsa−let−7a
7	0.017	15 / 318	hsa−miR−98
8	0.019	17 / 382	hsa−let−7c
9	0.020	16 / 355	hsa−let−7i
10	0.023	5 / 64	hsa−miR−1275
11	0.024	11 / 217	hsa−miR−185
12	0.025	4 / 44	hsa−miR−660
13	0.027	4 / 45	hsa−miR−766
14	0.028	5 / 67	hsa−miR−299−5p
15	0.031	10 / 198	hsa−miR−221

Telomeres

Rank	p−value	#in/all	Geneset
1	1	0 / 13	Alternative lengthening of telomeres
2	1	0 / 27	Nabetani_alt len telomeres_genes_ko
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Brain

Rank	p−value	#in/all	Geneset
1	1e−07	86 / 1893	Overlap_fetal_midbrain_TssF
2	8e−05	141 / 4112	Mid_Frontal_Lobe_ReprPC
3	1e−04	20 / 304	Mid_Frontal_Lobe_TssA
4	1e−04	61 / 1476	Overlap_fetal_midbrain_TxTrans
5	2e−04	57 / 1360	Mid_Frontal_Lobe_TssP
6	6e−04	47 / 1119	Overlap_fetal_midbrain_TssA
7	1e−03	36 / 819	Overlap_fetal_midbrain_TssP
8	2e−03	102 / 3046	Fetal_TssA
9	2e−03	75 / 2127	Mid_Frontal_Lobe_K9K27me3
10	1e−02	87 / 2700	Fetal_TxTrans
11	2e−02	20 / 465	Mid_Frontal_Lobe_TxTrans
12	2e−02	85 / 2709	Mid_Frontal_Lobe_HetRpts
13	5e−02	13 / 307	Fetal_ReprPC
14	1e−01	28 / 869	Mid_Frontal_Lobe_EnhG
15	1e−01	29 / 924	Mid_Frontal_Lobe_TssF

Chr

Rank	p−value	#in/all	Geneset
1	0.02	51 / 1492	Chr 2
2	0.03	13 / 289	Chr 21
3	0.04	17 / 422	Chr 13
4	0.07	32 / 959	Chr 16
5	0.09	19 / 536	Chr 22
6	0.18	35 / 1170	Chr 7
7	0.29	37 / 1318	Chr 17
8	0.37	29 / 1060	Chr 5
9	0.37	10 / 342	Chr 18
10	0.38	38 / 1411	Chr 11
11	0.47	25 / 954	Chr 9
12	0.49	20 / 769	Chr 15
13	0.68	35 / 1467	Chr 19
14	0.73	28 / 1211	Chr 6
15	0.77	20 / 902	Chr 4

Glio

Rank	p−value	#in/all	Geneset
1	0.01	18 / 393	Hopp_Sturm_GBM_Epi3_no_zentr_3_RTK II_UP_adult_fetus_K27_DN
2	0.02	2 / 8	Shaw_responders_up_in_oligo_glioma
3	0.03	9 / 166	Sturm_GBM_Meth_overexpression_B_adult_UP
4	0.03	92 / 2988	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
5	0.04	2 / 12	Phillips MES up vs Prolif & PN
6	0.04	4 / 52	Sturm_GBM_Meth_overexpression_F_IDH_UP
7	0.05	2 / 14	astrocytes_glio
8	0.05	6 / 104	WIRTH_Normal Brain
9	0.06	9 / 193	Hopp_Sturm_GBM_Epi3_F_RTK II_UP_adult_fetus_K27_DN
10	0.07	4 / 61	Sturm_GBM_Meth_overexpression_D_G34_UP
11	0.07	1 / 3	WILLSCHER_ GBM_LTSwt_proteomics−M_UP
12	0.10	6 / 126	Hopp_Sturm_GBM_Epi3_A1_Mesenchymal_UP
13	0.15	3 / 53	Hopp_Sturm_GBM_Epi3_C1_IDH_UP_fetus_DN
14	0.17	1 / 7	Donson−cytotoxic effectors−associated with LTS in HGA
15	0.19	1 / 8	Donson−migration tethering and rolling−associated with LTS in HGA

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.2	2 / 31	DUMEAUX_Fasting enriched genes
2	0.2	4 / 94	DUMEAUX_Smoking enriched genes
3	0.3	1 / 16	Huan_blood−pressure_DBP−signature
4	0.4	1 / 18	Huan_blood−pressure_SBP−signature
5	0.9	3 / 211	Homuth_BMI−associated−genes_DN
6	1.0	1 / 147	Homuth_BMI−associated−genes_UP
7	1.0	0 / 10	DUMEAUX_Smoking literature genes up
8	1.0	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
9	1.0	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
10	1.0	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
11	1.0	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
12	1.0	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
13	1.0	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
14	1.0	0 / 10	DUMEAUX_Women normal BMI literature genes up
15	1.0	0 / 17	DUMEAUX_High bmi enriched genes

MF

Rank	p−value	#in/all	Geneset
1	0.001	4 / 20	anion:anion antiporter activity
2	0.002	3 / 10	sodium−dependent phosphate transmembrane transporter activity
3	0.002	3 / 11	oxalate transmembrane transporter activity
4	0.002	3 / 11	sulfate transmembrane transporter activity
5	0.003	3 / 12	hormone binding
6	0.003	3 / 12	secondary active sulfate transmembrane transporter activity
7	0.005	3 / 14	G−protein coupled serotonin receptor activity
8	0.006	5 / 45	non−membrane spanning protein tyrosine kinase activity
9	0.006	3 / 15	bicarbonate transmembrane transporter activity
10	0.012	9 / 145	growth factor activity
11	0.015	3 / 21	insulin−like growth factor binding
12	0.023	4 / 43	tubulin binding
13	0.033	9 / 173	ubiquitin protein ligase activity
14	0.036	4 / 49	G−protein coupled receptor binding
15	0.037	3 / 29	repressing transcription factor binding

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.3	1 / 15	GUSTAFSON_PI3K_DN
2	1.0	0 / 14	GUSTAFSON_PI3K_UP
3	1.0	0 / 13	BENTINK_e2f3.1
4	1.0	0 / 13	BENTINK_e2f3.2
5	1.0	0 / 13	BENTINK_myc.1
6	1.0	0 / 12	BENTINK_ras.1
7	1.0	0 / 11	BENTINK_ras.4
8	1.0	0 / 14	BENTINK_ras.6
9	1.0	0 / 13	BENTINK_src.10
10	1.0	0 / 12	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	0.05	1 / 2	MYC_ECM cell adhesion DOWN
2	0.06	55 / 1753	HEBENSTREIT_low expression TF
3	0.12	1 / 5	MYC_TFs
4	0.20	23 / 747	ICGC_NrsfPcr2_targets
5	0.21	1 / 9	MYC_Targets DOWN
6	0.27	1 / 12	MYC_Protein synthesis degradation UP
7	0.37	1 / 18	MYC_Metabolism UP
8	0.40	40 / 1501	ICGC_Usf1_targets
9	0.44	91 / 3507	ICGC_Rad21_targets
10	0.47	19 / 721	ICGC_SrfPcr2_targets
11	0.54	16 / 631	ICGC_RxraPcr1_targets
12	0.73	115 / 4735	ICGC_Pu1_targets
13	0.76	1 / 55	MYC_Targets UP
14	0.79	58 / 2497	ICGC_Bcl11_targets
15	0.88	37 / 1723	HEBENSTREIT_high expression TF

K−Means Cluster

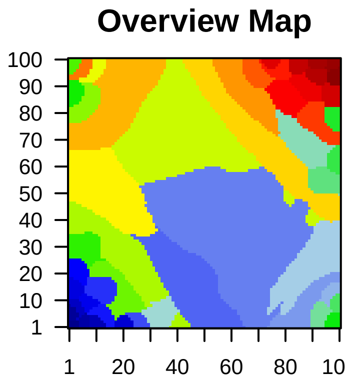
Spot Summary: G1

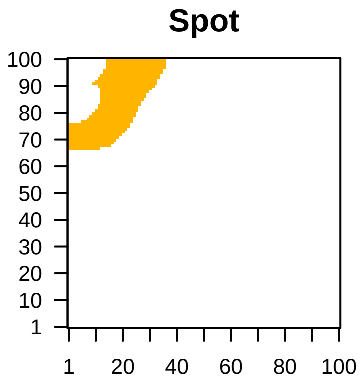
metagenes = 654
genes = 1915

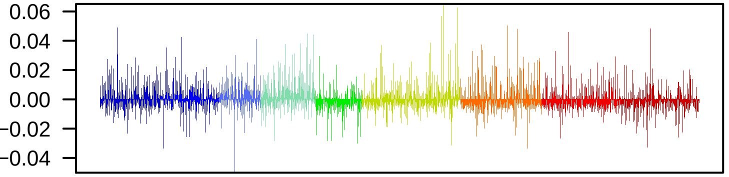
<r> metagenes = 0.82

beta: r2= 0.27 / log p= −Inf

samples with spot = 0 (0 %)





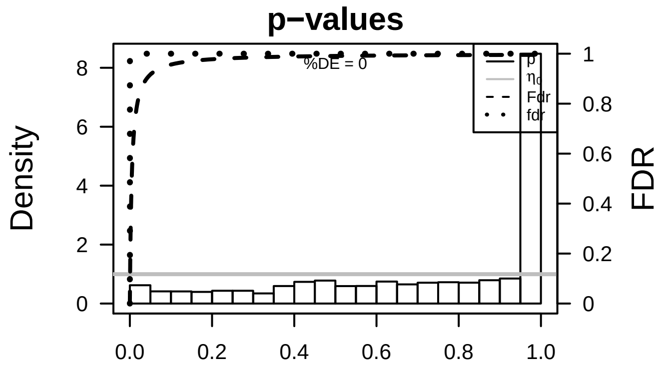


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_178383	0.43	−0.22	0.09		
2	ILMN_219415	0.41	−0.21	0.17	ADAM29	ADAM metallopeptidase domain 29 [Source:HGNC Symbol;A
3	ILMN_330104	0.38	−0.33	0.11	FLVCR1−AS1	FLVCR1 antisense RNA 1 (head to head) [Source:HGNC Syr
4	ILMN_172449	0.37	−0.3	0.23	ABI2	abl interactor 2 [Source:HGNC Symbol;Acc:HGNC:24011]
5	ILMN_178270	0.36	−0.23	0.19		G antigen 2E [Source:HGNC Symbol;Acc:HGNC:31960]
6	ILMN_209924	0.35	−0.27	0.09	MTERF1	mitochondrial transcription termination factor 1 [Source:HGN(
7	ILMN_179077	0.33	−0.22	0.2	PNMA2	paraneoplastic Ma antigen 2 [Source:HGNC Symbol;Acc:HGI
8	ILMN_175755	0.32	−0.21	0.15	PTRF	polymerase I and transcript release factor [Source:HGNC Syr
9	ILMN_240217	0.32	−0.19	0.15		
10	ILMN_330795	0.31	−0.21	0.15	L3MBTL4	l(3)mbt−like 4 (Drosophila) [Source:HGNC Symbol;Acc:HGN(
11	ILMN_176156	0.3	−0.28	0.09	PHF13	PHD finger protein 13 [Source:HGNC Symbol;Acc:HGNC:229
12	ILMN_216182	0.3	−0.19	0.16		
13	ILMN_166622	0.3	−0.21	0.22	IL17RC	interleukin 17 receptor C [Source:HGNC Symbol;Acc:HGNC::
14	ILMN_321955	0.3	−0.21	0.16		
15	ILMN_173925	0.3	−0.33	0.14	STAMBP	STAM binding protein [Source:HGNC Symbol;Acc:HGNC:169
16	ILMN_168205	0.3	−0.26	0.14	SRI	sorcin [Source:HGNC Symbol;Acc:HGNC:11292]
17	ILMN_324575	0.29	−0.23	0.21		
18	ILMN_171803	0.29	−0.2	0.14		
19	ILMN_172596	0.28	−0.21	0.19		
20	ILMN_171506	0.28	−0.21	0.19	ZNF580	zinc finger protein 580 [Source:HGNC Symbol;Acc:HGNC:29

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	5e−23	336 / 4304	Chror	9_ReprPCWk_Melanocytes
2	9e−20	275 / 3438	Chror	10_ReprPC_Melanocytes
3	2e−19	218 / 2516	Chror	11_K9K27me3_Melanocytes
4	3e−19	383 / 5384	Lympl	HOPP_Repressed
5	1e−17	310 / 4169	Chror	10_ReprPC_Fibroblasts
6	3e−17	305 / 4107	Chror	9_ReprPCWk_Fibroblasts
7	7e−15	217 / 2740	Colon	ReprPCWk_Colon
8	8e−15	212 / 2660	Chror	8_EnhP_Melanocytes
9	1e−13	238 / 3173	Colon	ReprPC_Colon
10	3e−13	263 / 3639	Chror	1_TssP_Fibroblasts
11	4e−13	168 / 2031	Chror	12_Het_Melanocytes
12	3e−11	107 / 1163	Chror	12_Het_Fibroblasts
13	6e−11	152 / 1893	Brain	Overlap_fetal_midbrain_TssF
14	9e−11	116 / 1324	Chror	13_HetRpts_Fibroblasts
15	1e−10	75 / 717	Chror	11_K9K27me3_Fibroblasts
16	4e−10	174 / 2315	Chror	13_HetRpts_Melanocytes
17	4e−10	217 / 3068	Chror	8_EnhP_Fibroblasts
18	5e−10	242 / 3523	Chror	1_TssP_Melanocytes
19	4e−09	203 / 2894	Colon	TssP_Colon
20	4e−09	208 / 2988	Glio	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
21	1e−08	135 / 1753	TF	HEBENSTREIT_low expression TF
22	2e−07	238 / 3691	Chror	9_ReprPCWk_Neuronal_Progenitor
23	3e−07	106 / 1360	Brain	Mid_Frontal_Lobe_TssP
24	5e−07	112 / 1476	Brain	Overlap_fetal_midbrain_TxTrans
25	1e−06	277 / 4526	Colon	Quies1_Colon
26	6e−06	38 / 366	Colon	K9K27me3_Colon
27	1e−05	130 / 1895	Colon	EnhP_Colon
28	1e−05	193 / 3046	Brain	Fetal_TssA
29	1e−05	173 / 2682	Chror	12_Het_Neuronal_Progenitor
30	1e−05	114 / 1623	Colon	Het_Colon
31	2e−05	61 / 735	GSEA	ACEVEDO_METHYLATED_IN_LIVER_CANCER_DN
32	3e−05	18 / 126	Glio	Hopp_Sturm_GBM_Epi3_A1_Mesenchymal_UP
33	3e−05	83 / 1115	Brain	Overlap_fetal_midbrain_EnhG
34	3e−05	33 / 325	GSEA	MEISSNER_NPC_HCP_WITH_H3K4ME2_AND_H3K27ME3
35	4e−05	71 / 924	Brain	Mid_Frontal_Lobe_TssF
36	7e−05	39 / 425	Colon	Lembcke_TCGA_meth_kmeans_E_CIMP.H_UP_
37	7e−05	200 / 3272	Chror	13_HetRpts_Neuronal_Progenitor
38	8e−05	182 / 2939	Lympl	HOPP_Poised_promoter
39	1e−04	119 / 1789	Chror	8_EnhP_Neuronal_Progenitor
40	1e−04	83 / 1154	Chror	11_K9K27me3_Neuronal_Progenitor



Aging

Rank	p−value	#in/all	Geneset
1	0.5	3 / 58	TESCHENDORFF_age_hypermethylated
2	0.8	4 / 111	HORVATH_aging_genes meth DOWN
3	1.0	1 / 142	HORVATH_aging_genes meth UP
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Cancer

Rank	p−value	#in/all	Geneset
1	0.04	3 / 16	GENTLES_modul16
2	0.07	8 / 91	PanCan_TXmisReg_geneset_nanostring
3	0.18	10 / 150	PanCan_MAPK_geneset_nanostring
4	0.21	1 / 15	LIU_PROSTATE_CANCER_DN
5	0.25	4 / 54	KUIPER_MM poor survival
6	0.28	1 / 12	LIU_BREAST_CANCER
7	0.29	1 / 14	RHODES_UNDIFFERENTIATED_CANCER
8	0.32	2 / 24	PanCan_Notch_geneset_nanostring
9	0.32	7 / 117	PanCan_Driver_Gene_geneset_nanostring
10	0.35	1 / 9	GENTLES_modul3
11	0.35	1 / 9	GENTLES_modul5
12	0.37	27 / 527	Lembcke_Normal vs Adenoma
13	0.44	1 / 12	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
14	0.47	1 / 13	GENTLES_modul2
15	0.49	1 / 14	LIU_PROSTATE_CANCER_UP

Chromatin states

Rank	p−value	#in/all	Geneset
1	5e−23	336 / 4304	9_ReprPCWk_Melanocytes
2	9e−20	275 / 3438	10_ReprPC_Melanocytes
3	2e−19	218 / 2516	11_K9K27me3_Melanocytes
4	1e−17	310 / 4169	10_ReprPC_Fibroblasts
5	3e−17	305 / 4107	9_ReprPCWk_Fibroblasts
6	8e−15	212 / 2660	8_EnhP_Melanocytes
7	3e−13	263 / 3639	1_TssP_Fibroblasts
8	4e−13	168 / 2031	12_Het_Melanocytes
9	3e−11	107 / 1163	12_Het_Fibroblasts
10	9e−11	116 / 1324	13_HetRpts_Fibroblasts
11	1e−10	75 / 717	11_K9K27me3_Fibroblasts
12	4e−10	174 / 2315	13_HetRpts_Melanocytes
13	4e−10	217 / 3068	8_EnhP_Fibroblasts
14	5e−10	242 / 3523	1_TssP_Melanocytes
15	2e−07	238 / 3691	9_ReprPCWk_Neuronal_Progenitor

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−05	61 / 735	ACEVEDO_METHYLATED_IN_LIVER_CANCER_DN
2	3e−05	33 / 325	MEISSNER_NPC_HCP_WITH_H3K4ME2_AND_H3K27ME3
3	1e−04	7 / 25	SU_PLACENTA
4	2e−04	23 / 210	NABA_ECM_REGULATORS
5	2e−04	5 / 13	REACTOME_CYTOSOLIC_SULFONATION_OF_SMALL_MOLECULES
6	5e−04	4 / 9	FUJIWARA_PARK2_HEPATOCYTE_PROLIFERATION_UP
7	1e−03	5 / 18	NIELSEN_LEIOMYOSARCOMA_CNN1_DN
8	1e−03	13 / 105	CERVERA_SDHB_TARGETS_1_UP
9	2e−03	22 / 234	YAUCH_HEDGEHOG_SIGNALING_PARACRINE_DN
10	2e−03	33 / 405	MIKKELSEN_MCV6_HCP_WITH_H3K27ME3
11	2e−03	5 / 20	REACTOME_KINESINS
12	2e−03	67 / 989	MEISSNER_BRAIN_HCP_WITH_H3K4ME3_AND_H3K27ME3
13	2e−03	27 / 315	MIKKELSEN_NPC_HCP_WITH_H3K27ME3
14	3e−03	32 / 398	SCHAEFFER_PROSTATE_DEVELOPMENT_48HR_DN
15	3e−03	6 / 31	LIEN_BREAST_CARCINOMA_METAPLASTIC

Lymphoma

Rank	p−value	#in/all	Geneset
1	3e−19	383 / 5384	HOPP_Repressed
2	8e−05	182 / 2939	HOPP_Poised_promoter
3	4e−04	241 / 4167	HOPP_Heterochrom
4	8e−04	16 / 137	Hopp_June14_MMML937 tumors+controls_group.overexpression_G_tonsil_
5	2e−03	15 / 138	WIRTH_lymphoma937_spot G
6	5e−03	156 / 2701	HOPP_Repetitive
7	7e−02	17 / 244	LENZ_Stromal signature 1
8	3e−01	2 / 21	Subero_MCL_hyper_meth
9	3e−01	16 / 286	ZHANG_DLBCL mutated
10	3e−01	4 / 57	Hopp_Lymphoma_Epi1_no_zentr_1_B.cell_DN
11	3e−01	8 / 133	Hopp_Lymphoma_Epi1_no_zentr_5_B.cell_GCB_UP
12	4e−01	6 / 105	WIRTH_lymphoma937_spot MM
13	4e−01	1 / 12	Hopp_Lymphoma_Epi1_with_zentr_ii_MCL_mBL_UP
14	5e−01	3 / 52	Hopp_Lymphoma_Epi1_with_zentr_iv_B.cell_MM_UP
15	5e−01	4 / 75	SPANG_LPS 6hrs DN

miRNA Disease

Rank	p−value	#in/all	Geneset
1	0.1	1 / 3	Renal cell carcinoma
2	0.2	3 / 29	Myelofibrosis, idiopathic
3	0.2	1 / 4	Myocardial infarction, susceptibility to
4	0.2	1 / 4	Carcinoid tumors, intestinal
5	0.2	4 / 47	Cervical cancer, somatic
6	0.2	2 / 18	Hodgkin lymphoma
7	0.3	1 / 7	Multiple sclerosis, susceptibility to
8	0.3	3 / 40	Medulloblastoma
9	0.3	1 / 8	Cardiomyopathy, idiopathic dilated
10	0.4	4 / 65	Hepatocellular carcinoma
11	0.4	1 / 10	Dermatitis, atopic
12	0.4	2 / 29	Neuroblastoma
13	0.4	4 / 68	Glioblastoma multiforme, somatic
14	0.4	2 / 30	Systemic lupus erythematosus (SLE)
15	0.5	4 / 73	Stroke, susceptibility to

Reference Signatures

Rank	p−value	#in/all	Geneset
1	2e−04	41 / 478	WIRTH_Nervous System
2	2e−03	15 / 134	WIRTH_Mucosa
3	3e−03	8 / 53	JONGENEEL_Kidney
4	7e−03	20 / 231	Chaussabel_2,5_Immune related molecules
5	1e−02	11 / 107	WIRTH_Liver
6	3e−02	8 / 76	WIRTH_Homeostasis
7	4e−02	3 / 17	VAQUERIZAS_Adrenal gland_TF
8	6e−02	20 / 289	JONGENEEL_Testis
9	6e−02	16 / 220	WIRTH_Testis
10	6e−02	4 / 32	VAQUERIZAS_Liver_TF
11	8e−02	2 / 10	JONGENEEL_Pituitary Gland
12	9e−02	5 / 50	WIRTH_Placenta
13	1e−01	3 / 25	VAQUERIZAS_Adrenal cortex_TF
14	1e−01	4 / 43	VAQUERIZAS_Placenta_TF
15	2e−01	2 / 19	JONGENEEL_Small Intestine

BP

Rank	p−value	#in/all	Geneset
1	1e−04	5 / 12	3'−phosphoadenosine 5'−phosphosulfate metabolic process
2	2e−04	35 / 383	proteolysis
3	2e−04	7 / 27	neurotransmitter transport
4	2e−03	14 / 125	central nervous system development
5	5e−03	5 / 24	complement activation
6	5e−03	6 / 34	steroid metabolic process
7	6e−03	7 / 46	digestion
8	6e−03	4 / 16	regulation of sodium ion transmembrane transporter activity
9	7e−03	28 / 357	detection of chemical stimulus involved in sensory perception of smell
10	8e−03	5 / 27	complement activation, classical pathway
11	1e−02	5 / 29	regulation of heart rate by cardiac conduction
12	1e−02	8 / 66	microtubule−based movement
13	1e−02	3 / 11	behavioral response to pain
14	1e−02	3 / 11	cardiac muscle cell action potential involved in contraction
15	1e−02	3 / 11	lymphangiogenesis

CC

Rank	p−value	#in/all	Geneset
1	0.002	13 / 106	Z disc
2	0.002	4 / 12	interstitial matrix
3	0.005	11 / 93	blood microparticle
4	0.006	6 / 36	myofibril
5	0.009	5 / 28	stereocilium
6	0.009	5 / 28	voltage−gated calcium channel complex
7	0.015	20 / 249	axon
8	0.017	181 / 3291	integral component of membrane
9	0.023	6 / 47	presynapse
10	0.026	3 / 14	myosin filament
11	0.030	20 / 267	proteinaceous extracellular matrix
12	0.039	7 / 67	filopodium
13	0.045	6 / 55	synaptic vesicle membrane
14	0.052	5 / 43	cleavage furrow
15	0.052	6 / 57	terminal bouton

Colon Cancer

Rank	p−value	#in/all	Geneset
1	7e−15	217 / 2740	ReprPCWk_Colon
2	1e−13	238 / 3173	ReprPC_Colon
3	4e−09	203 / 2894	TssP_Colon
4	1e−06	277 / 4526	Quies1_Colon
5	6e−06	38 / 366	K9K27me3_Colon
6	1e−05	130 / 1895	EnhP_Colon
7	1e−05	114 / 1623	Het_Colon
8	7e−05	39 / 425	Lembcke_TCGA_meth_kmeans_E_CIMP.H_UP_
9	1e−04	49 / 594	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
10	2e−04	84 / 1186	HetRpts_Colon
11	4e−03	50 / 713	Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN
12	4e−03	47 / 663	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
13	8e−03	42 / 599	Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
14	8e−03	491 / 9530	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP_
15	1e−02	3 / 11	Juehling_HNPCC−mutated−in−5

HM

Rank	p−value	#in/all	Geneset
1	0.05	11 / 132	HALLMARK_UV_RESPONSE_DN
2	0.17	12 / 186	HALLMARK_ESTROGEN_RESPONSE_LATE
3	0.22	11 / 177	HALLMARK_MITOTIC_SPINDLE
4	0.26	3 / 37	HALLMARK_PANCREAS_BETA_CELLS
5	0.26	8 / 127	HALLMARK_COAGULATION
6	0.30	11 / 191	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
7	0.31	3 / 41	HALLMARK_APICAL_SURFACE
8	0.40	2 / 29	HALLMARK_NOTCH_SIGNALING
9	0.48	2 / 34	HALLMARK_HEDGEHOG_SIGNALING
10	0.52	9 / 186	HALLMARK_ESTROGEN_RESPONSE_EARLY
11	0.53	9 / 187	HALLMARK_COMPLEMENT
12	0.61	8 / 177	HALLMARK_KRAS_SIGNALING_DN
13	0.62	8 / 179	HALLMARK_G2M_CHECKPOINT
14	0.63	4 / 91	HALLMARK_ANDROGEN_RESPONSE
15	0.64	3 / 69	HALLMARK_CHOLESTEROL_HOMEOSTASIS

Melanoma

Rank	p−value	#in/all	Geneset
1	0.1	3 / 27	Hugo_melanoma−all−LEF1_UP
2	0.3	1 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
3	0.4	2 / 30	Hugo_melanoma−all−MET_UP
4	0.6	2 / 43	Hugo_melanoma−BRAFmut−MET_UP
5	0.7	2 / 54	Hugo_melanoma−all−MET_DN
6	1.0	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

miRNA target

Rank	p−value	#in/all	Geneset
1	0.08	5 / 48	hsa−miR−610
2	0.10	6 / 67	hsa−miR−1246
3	0.12	4 / 40	hsa−miR−885−5p
4	0.12	2 / 13	hsa−miR−744
5	0.12	2 / 13	hsa−miR−1234
6	0.18	5 / 63	hsa−miR−455−3p
7	0.19	3 / 32	hsa−miR−1229
8	0.20	4 / 49	hsa−miR−549
9	0.20	3 / 33	hsa−miR−1296
10	0.21	4 / 50	hsa−miR−337−3p
11	0.24	4 / 53	hsa−miR−345
12	0.24	2 / 20	hsa−miR−516a−5p
13	0.25	1 / 6	hsa−miR−937
14	0.26	3 / 37	hsa−miR−1224−5p
15	0.26	4 / 55	hsa−miR−409−5p

Telomeres

Rank	p−value	#in/all	Geneset
1	1	0 / 13	Alternative lengthening of telomeres
2	1	0 / 27	Nabetani_alt len telomeres_genes_ko
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Brain

Rank	p−value	#in/all	Geneset
1	6e−11	152 / 1893	Overlap_fetal_midbrain_TssF
2	3e−07	106 / 1360	Mid_Frontal_Lobe_TssP
3	5e−07	112 / 1476	Overlap_fetal_midbrain_TxTrans
4	1e−05	193 / 3046	Fetal_TssA
5	3e−05	83 / 1115	Overlap_fetal_midbrain_EnhG
6	4e−05	71 / 924	Mid_Frontal_Lobe_TssF
7	1e−04	74 / 1012	Mid_Frontal_Lobe_Enh
8	2e−04	80 / 1119	Overlap_fetal_midbrain_TssA
9	8e−04	38 / 465	Mid_Frontal_Lobe_TxTrans
10	9e−04	235 / 4112	Mid_Frontal_Lobe_ReprPC
11	1e−03	32 / 383	Mid_Frontal_Lobe_Tx
12	2e−03	160 / 2700	Fetal_TxTrans
13	3e−03	85 / 1329	Overlap_fetal_midbrain_Enh
14	4e−03	59 / 869	Mid_Frontal_Lobe_EnhG
15	4e−03	56 / 819	Overlap_fetal_midbrain_TssP

Chr

Rank	p−value	#in/all	Geneset
1	0.02	9 / 87	Chr Y
2	0.09	78 / 1411	Chr 11
3	0.09	82 / 1492	Chr 2
4	0.12	122 / 2323	Chr 1
5	0.14	58 / 1060	Chr 5
6	0.14	71 / 1318	Chr 17
7	0.21	45 / 836	Chr 8
8	0.30	62 / 1217	Chr 3
9	0.36	22 / 422	Chr 13
10	0.36	18 / 342	Chr 18
11	0.41	49 / 994	Chr X
12	0.48	26 / 536	Chr 22
13	0.51	14 / 289	Chr 21
14	0.60	44 / 954	Chr 9
15	0.61	44 / 959	Chr 16

Glio

Rank	p−value	#in/all	Geneset
1	4e−09	208 / 2988	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
2	3e−05	18 / 126	Hopp_Sturm_GBM_Epi3_A1_Mesenchymal_UP
3	2e−03	19 / 193	Hopp_Sturm_GBM_Epi3_F_RTK II_UP_adult_fetus_K27_DN
4	3e−03	59 / 859	Hopp_Sturm_GBM_Epi3_A_adult_fetus_UP_G34_DN
5	1e−02	7 / 53	WILLSCHER_GBM_Verhaak−PNmut_down (G)
6	1e−02	3 / 11	VERHAAK_Brain
7	4e−02	9 / 95	Weller_LGG_1p19qDel−vs−intact_UP
8	5e−02	9 / 101	Hopp_Sturm_GBM_Epi3_D1_IDH_UP_adult_fetus_DN
9	5e−02	2 / 8	Shaw_responders_up_in_oligo_glioma
10	9e−02	11 / 148	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up_(MES&CL down)
11	1e−01	12 / 166	Sturm_GBM_Meth_overexpression_B_adult_UP
12	1e−01	26 / 419	Down_a
13	1e−01	7 / 84	GIEZELT_GBM_STS_up_VS_LTS
14	1e−01	5 / 53	mature astrocytes
15	1e−01	8 / 104	WIRTH_Normal Brain

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.08	8 / 94	DUMEAUX_Smoking enriched genes
2	0.99	4 / 211	Homuth_BMI−associated−genes_DN
3	0.99	2 / 147	Homuth_BMI−associated−genes_UP
4	1.00	0 / 10	DUMEAUX_Smoking literature genes up
5	1.00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
6	1.00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
7	1.00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
8	1.00	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
9	1.00	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
10	1.00	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
11	1.00	0 / 10	DUMEAUX_Women normal BMI literature genes up
12	1.00	0 / 17	DUMEAUX_High bmi enriched genes
13	1.00	0 / 31	DUMEAUX_Fasting enriched genes
14	1.00	0 / 18	Huan_blood−pressure_SBP−signature
15	1.00	0 / 16	Huan_blood−pressure_DBP−signature

MF

Rank	p−value	#in/all	Geneset
1	2e−04	7 / 27	sulfotransferase activity
2	9e−04	9 / 54	serine−type peptidase activity
3	4e−03	5 / 23	endopeptidase inhibitor activity
4	6e−03	6 / 35	beta−tubulin binding
5	7e−03	28 / 357	olfactory receptor activity
6	7e−03	11 / 99	metalloendopeptidase activity
7	9e−03	5 / 28	sodium channel regulator activity
8	1e−02	3 / 10	high voltage−gated calcium channel activity
9	1e−02	3 / 10	vinculin binding
10	1e−02	6 / 40	receptor tyrosine kinase binding
11	1e−02	15 / 163	serine−type endopeptidase activity
12	1e−02	5 / 29	cysteine−type endopeptidase inhibitor activity
13	2e−02	3 / 12	gap junction channel activity
14	2e−02	10 / 98	transcriptional activator activity, RNA polymerase II transcription regulatory re
15	2e−02	12 / 130	protein dimerization activity

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.1	2 / 13	BENTINK_e2f3.2
2	0.1	2 / 13	BENTINK_src.10
3	0.5	1 / 13	BENTINK_e2f3.1
4	1.0	0 / 14	GUSTAFSON_PI3K_UP
5	1.0	0 / 15	GUSTAFSON_PI3K_DN
6	1.0	0 / 13	BENTINK_myc.1
7	1.0	0 / 12	BENTINK_ras.1
8	1.0	0 / 11	BENTINK_ras.4
9	1.0	0 / 14	BENTINK_ras.6
10	1.0	0 / 12	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	1e−08	135 / 1753	HEBENSTREIT_low expression TF
2	4e−02	46 / 747	ICGC_NrsfPcr2_targets
3	2e−01	1 / 5	MYC_TFs
4	4e−01	1 / 12	MYC_Protein synthesis degradation UP
5	5e−01	1 / 14	NOWICK_TF
6	6e−01	164 / 3507	ICGC_Rad21_targets
7	6e−01	67 / 1466	ICGC_NrsfPcr1_targets
8	9e−01	28 / 721	ICGC_SrfPcr2_targets
9	9e−01	1 / 55	MYC_Targets UP
10	9e−01	104 / 2497	ICGC_Bcl11_targets
11	1e+00	25 / 733	ICGC_Atf3_targets
12	1e+00	218 / 5188	ICGC_Ebfsc137065_targets
13	1e+00	107 / 2759	ICGC_Bcl3_targets
14	1e+00	104 / 2704	ICGC_Pbx3_targets
15	1e+00	18 / 631	ICGC_RxraPcr1_targets

K−Means Cluster

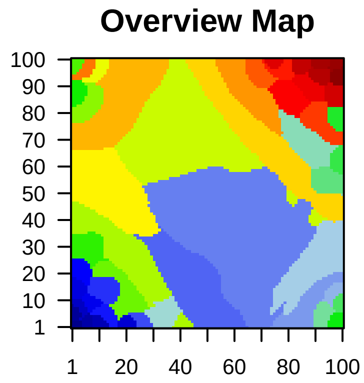
Spot Summary: H1

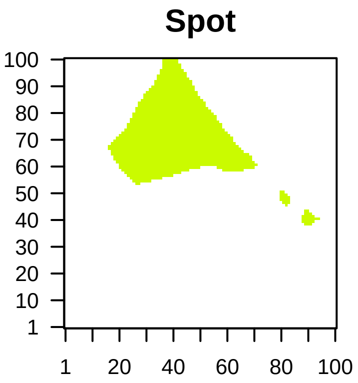
metagenes = 1342
genes = 6388

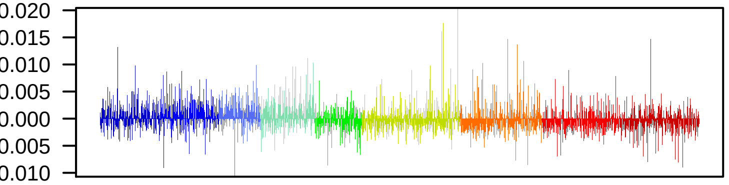
<r> metagenes = 0.26

beta: r2= 0.07 / log p= −Inf

samples with spot = 0 (0 %)

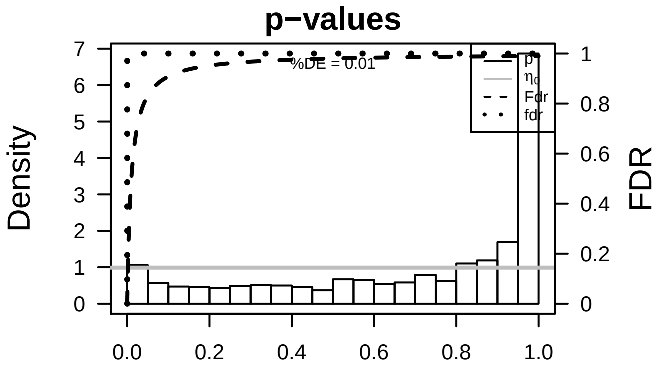






Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	9e−64	1104 / 4304	Chror	9_ReprPCWk_Melanocytes
2	2e−54	901 / 3438	Chror	10_ReprPC_Melanocytes
3	2e−53	1275 / 5384	Lympl	HOPP_Repressed
4	2e−50	698 / 2516	Chror	11_K9K27me3_Melanocytes
5	6e−49	829 / 3173	Colon	ReprPC_Colon
6	4e−42	718 / 2740	Colon	ReprPCWk_Colon
7	6e−40	694 / 2660	Chror	8_EnhP_Melanocytes
8	9e−39	975 / 4107	Chror	9_ReprPCWk_Fibroblasts
9	4e−37	731 / 2894	Colon	TssP_Colon
10	7e−37	979 / 4169	Chror	10_ReprPC_Fibroblasts
11	2e−31	832 / 3523	Chror	1_TssP_Melanocytes
12	8e−31	741 / 3068	Chror	8_EnhP_Fibroblasts
13	6e−27	834 / 3639	Chror	1_TssP_Fibroblasts
14	1e−25	332 / 1163	Chror	12_Het_Fibroblasts
15	2e−25	366 / 1324	Chror	13_HetRpts_Fibroblasts
16	8e−25	454 / 1753	TF	HEBENSTREIT_low expression TF
17	2e−22	474 / 1895	Colon	EnhP_Colon
18	3e−20	464 / 1893	Brain	Overlap_fetal_midbrain_TssF
19	4e−20	677 / 2988	Glio	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
20	5e−19	803 / 3691	Chror	9_ReprPCWk_Neuronal_Progenitor
21	3e−17	155 / 484	Colon	Quies2_Colon
22	5e−17	367 / 1476	Brain	Overlap_fetal_midbrain_TxTrans
23	8e−17	476 / 2031	Chror	12_Het_Melanocytes
24	4e−15	232 / 859	Glio	Hopp_Sturm_GBM_Epi3_A_adult_fetus_UP_G34_DN
25	6e−15	119 / 357	BP	detection of chemical stimulus involved in sensory perception of smell
26	6e−15	119 / 357	MF	olfactory receptor activity
27	1e−14	638 / 2939	Lympl	HOPP_Poised_promoter
28	1e−14	173 / 594	Colon	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
29	4e−14	416 / 1789	Chror	8_EnhP_Neuronal_Progenitor
30	5e−14	158 / 536	GSEA	MIKKELSEN_MEF_HCP_WITH_H3K27ME3
31	8e−14	512 / 2297	Chror	10_ReprPC_Neuronal_Progenitor
32	2e−13	346 / 1448	GSEA	ZWANG_TRANSIENTLY_UP_BY_2ND_EGF_PULSE_ONLY
33	3e−13	167 / 588	MF	G−protein coupled receptor activity
34	5e−13	285 / 1154	Chror	11_K9K27me3_Neuronal_Progenitor
35	6e−13	647 / 3046	Brain	Fetal_TssA
36	7e−13	244 / 956	GSEA	BENPORATH_SUZ12_TARGETS
37	1e−12	914 / 4526	Colon	Quies1_Colon
38	1e−12	566 / 2620	Chror	1_TssP_Neuronal_Progenitor
39	1e−12	211 / 803	BP	G−protein coupled receptor signaling pathway
40	2e−12	255 / 1021	GSEA	BENPORATH_ES_WITH_H3K27ME3



Aging

Rank	p−value	#in/all	Geneset
1	3e−04	21 / 58	TESCHENDORFF_age_hypermethylated
2	1e−01	29 / 142	HORVATH_aging_genes meth UP
3	9e−01	14 / 111	HORVATH_aging_genes meth DOWN
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Cancer

Rank	p−value	#in/all	Geneset
1	0.02	43 / 193	PanCan_PI3K_geneset_nanostring
2	0.04	31 / 136	PanCan_RAS_geneset_nanostring
3	0.07	5 / 14	GENTLES_modul13
4	0.09	5 / 15	WANG_ER_UP
5	0.10	0 / 15	LIU_PROSTATE_CANCER_DN
6	0.23	4 / 15	GENTLES_modul17
7	0.30	22 / 117	PanCan_Driver_Gene_geneset_nanostring
8	0.32	6 / 28	PanCan_HH_geneset_nanostring
9	0.36	27 / 150	PanCan_MAPK_geneset_nanostring
10	0.37	3 / 13	WANG_ER_DN
11	0.42	3 / 14	LIU_COMMON_CANCER_GENES
12	0.45	2 / 13	LIU_LIVER_CANCER
13	0.51	8 / 46	PanCan_TGF−B_geneset_nanostring
14	0.51	3 / 16	BEN−PORATH_DN
15	0.55	9 / 54	KUIPER_MM poor survival

Chromatin states

Rank	p−value	#in/all	Geneset
1	9e−64	1104 / 4304	9_ReprPCWk_Melanocytes
2	2e−54	901 / 3438	10_ReprPC_Melanocytes
3	2e−50	698 / 2516	11_K9K27me3_Melanocytes
4	6e−40	694 / 2660	8_EnhP_Melanocytes
5	9e−39	975 / 4107	9_ReprPCWk_Fibroblasts
6	7e−37	979 / 4169	10_ReprPC_Fibroblasts
7	2e−31	832 / 3523	1_TssP_Melanocytes
8	8e−31	741 / 3068	8_EnhP_Fibroblasts
9	6e−27	834 / 3639	1_TssP_Fibroblasts
10	1e−25	332 / 1163	12_Het_Fibroblasts
11	2e−25	366 / 1324	13_HetRpts_Fibroblasts
12	5e−19	803 / 3691	9_ReprPCWk_Neuronal_Progenitor
13	8e−17	476 / 2031	12_Het_Melanocytes
14	4e−14	416 / 1789	8_EnhP_Neuronal_Progenitor
15	8e−14	512 / 2297	10_ReprPC_Neuronal_Progenitor

GSEA C2

Rank	p−value	#in/all	Geneset
1	5e−14	158 / 536	MIKKELSEN_MEF_HCP_WITH_H3K27ME3
2	2e−13	346 / 1448	ZWANG_TRANSIENTLY_UP_BY_2ND_EGF_PULSE_ONLY
3	7e−13	244 / 956	BENPORATH_SUZ12_TARGETS
4	2e−12	255 / 1021	BENPORATH_ES_WITH_H3K27ME3
5	5e−12	104 / 325	MEISSNER_NPC_HCP_WITH_H3K4ME2_AND_H3K27ME3
6	3e−11	93 / 287	REACTOME_OLFACTORY_SIGNALING_PATHWAY
7	8e−11	106 / 347	KEGG_OLFACTORY_TRANSDUCTION
8	7e−10	223 / 916	NABA_MATRISOME
9	2e−09	95 / 315	MIKKELSEN_NPC_HCP_WITH_H3K27ME3
10	1e−08	153 / 598	BENPORATH_PRC2_TARGETS
11	2e−08	177 / 720	REACTOME_GPCR_DOWNSTREAM_SIGNALING
12	1e−07	74 / 246	MEISSNER_BRAIN_HCP_WITH_H3K27ME3
13	1e−07	194 / 822	REACTOME_SIGNALING_BY_GPCR
14	2e−06	104 / 405	MIKKELSEN_MCV6_HCP_WITH_H3K27ME3
15	4e−06	169 / 735	ACEVEDO_METHYLATED_IN_LIVER_CANCER_DN

Lymphoma

Rank	p−value	#in/all	Geneset
1	2e−53	1275 / 5384	HOPP_Repressed
2	1e−14	638 / 2939	HOPP_Poised_promoter
3	1e−10	834 / 4167	HOPP_Heterochrom
4	2e−05	526 / 2701	HOPP_Repetitive
5	2e−04	24 / 70	LEE_Developmental_regulators
6	7e−04	38 / 137	Hopp_June14_MMML937 tumors+controls_group.overexpression_G_tonsil_U
7	1e−03	17 / 48	Subero_B−ALL_hyper_meth
8	2e−03	37 / 138	WIRTH_lymphoma937_spot G
9	2e−03	36 / 134	Subero_DLBCL_hyper_meth
10	2e−03	26 / 89	Subero_T−ALL_hyper_meth
11	3e−03	32 / 118	Subero_INT_hyper_meth
12	4e−03	21 / 70	Hopp_Lymphoma_Epi1_no_zentr_3_B.cell_DN
13	9e−03	17 / 57	LENZ_Stromal signature 2
14	2e−02	8 / 21	Subero_MCL_hyper_meth
15	2e−02	4 / 7	MASCQUE_GCB UP

miRNA Disease

Rank	p−value	#in/all	Geneset
1	0.09	5 / 15	Supravalvar aortic stenosis
2	0.10	3 / 7	Schizophrenia, susceptibility to
3	0.10	8 / 29	Neuroblastoma
4	0.11	8 / 30	Systemic lupus erythematosus (SLE)
5	0.27	10 / 48	Alzheimer disease, susceptibility to
6	0.28	13 / 65	Hepatocellular carcinoma
7	0.30	1 / 2	Hepatic adenoma
8	0.30	1 / 2	Medulloblastoma, desmoplastic
9	0.33	26 / 142	Lung cancer
10	0.33	2 / 7	Multiple sclerosis, susceptibility to
11	0.34	22 / 120	Hematological
12	0.34	8 / 40	Medulloblastoma
13	0.34	8 / 40	Muscular dystrophy
14	0.35	4 / 18	Hodgkin lymphoma
15	0.35	4 / 18	Non−Hodgkin lymphoma, somatic

Reference Signatures

Rank	p−value	#in/all	Geneset
1	8e−10	132 / 478	WIRTH_Nervous System
2	4e−05	41 / 134	WIRTH_Mucosa
3	5e−05	60 / 220	WIRTH_Testis
4	1e−04	19 / 48	WIRTH_Pancreas
5	2e−04	60 / 231	Chaussabel_2,5_Immune related molecules
6	1e−03	36 / 132	WIRTH_Muscle
7	2e−03	30 / 107	WIRTH_Liver
8	2e−03	23 / 76	WIRTH_Homeostasis
9	2e−02	62 / 289	JONGENEEL_Testis
10	2e−02	15 / 53	JONGENEEL_Kidney
11	3e−02	8 / 24	JONGENEEL_Prostate
12	5e−02	7 / 21	JONGENEEL_Adrenal Gland
13	5e−02	7 / 21	JONGENEEL_Salivary Gland
14	6e−02	3 / 6	WIRTH_Pituitary gland
15	7e−02	5 / 14	WIRTH_Thalamus

BP

Rank	p−value	#in/all	Geneset
1	6e−15	119 / 357	detection of chemical stimulus involved in sensory perception of smell
2	1e−12	211 / 803	G−protein coupled receptor signaling pathway
3	5e−09	35 / 78	detection of chemical stimulus involved in sensory perception
4	2e−06	81 / 297	nervous system development
5	1e−05	42 / 132	sensory perception of smell
6	1e−05	29 / 79	regulation of membrane potential
7	2e−05	36 / 109	regulation of ion transmembrane transport
8	6e−05	59 / 217	chemical synaptic transmission
9	2e−04	8 / 12	oocyte development
10	2e−04	42 / 147	homophilic cell adhesion via plasma membrane adhesion molecules
11	4e−04	43 / 156	axon guidance
12	6e−04	7 / 11	replicative senescence
13	8e−04	32 / 110	potassium ion transmembrane transport
14	1e−03	9 / 18	startle response
15	1e−03	8 / 15	anatomical structure development

CC

Rank	p−value	#in/all	Geneset
1	1e−07	719 / 3662	plasma membrane
2	4e−07	77 / 267	proteinaceous extracellular matrix
3	3e−06	64 / 220	synapse
4	1e−05	30 / 83	voltage−gated potassium channel complex
5	2e−05	263 / 1249	extracellular region
6	3e−05	262 / 1252	integral component of plasma membrane
7	5e−05	24 / 64	collagen trimer
8	8e−05	54 / 196	postsynaptic membrane
9	2e−04	99 / 423	cell junction
10	2e−04	26 / 78	Golgi lumen
11	9e−04	20 / 59	presynaptic membrane
12	1e−03	221 / 1101	extracellular space
13	2e−03	27 / 93	intermediate filament
14	5e−03	14 / 41	cornified envelope
15	1e−02	21 / 76	ruffle membrane

Colon Cancer

Rank	p−value	#in/all	Geneset
1	6e−49	829 / 3173	ReprPC_Colon
2	4e−42	718 / 2740	ReprPCWk_Colon
3	4e−37	731 / 2894	TssP_Colon
4	2e−22	474 / 1895	EnhP_Colon
5	3e−17	155 / 484	Quies2_Colon
6	1e−14	173 / 594	Lembcke_TCGA−expr_kmeans_M_CIMP.H_DN
7	1e−12	914 / 4526	Quies1_Colon
8	3e−12	1778 / 9530	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP_
9	6e−08	114 / 425	Lembcke_TCGA_meth_kmeans_E_CIMP.H_UP_
10	5e−07	343 / 1623	Het_Colon
11	1e−04	147 / 663	Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN
12	3e−04	87 / 366	K9K27me3_Colon
13	3e−04	73 / 299	Lembcke_TCGA_meth_kmeans_A_Cluster4_DN
14	5e−04	24 / 73	Ang_CRC−CIMPH−vs−L_hyper
15	8e−04	238 / 1186	HetRpts_Colon

HM

Rank	p−value	#in/all	Geneset
1	0.007	12 / 34	HALLMARK_HEDGEHOG_SIGNALING
2	0.136	37 / 186	HALLMARK_ESTROGEN_RESPONSE_EARLY
3	0.150	9 / 37	HALLMARK_PANCREAS_BETA_CELLS
4	0.208	23 / 116	HALLMARK_SPERMATOGENESIS
5	0.270	25 / 132	HALLMARK_UV_RESPONSE_DN
6	0.291	35 / 191	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
7	0.331	32 / 177	HALLMARK_KRAS_SIGNALING_DN
8	0.336	34 / 189	HALLMARK_HYPOXIA
9	0.447	32 / 186	HALLMARK_ESTROGEN_RESPONSE_LATE
10	0.449	18 / 103	HALLMARK_BILE_ACID_METABOLISM
11	0.525	31 / 186	HALLMARK_MYOGENESIS
12	0.643	29 / 183	HALLMARK_APICAL_JUNCTION
13	0.748	7 / 50	HALLMARK_TGF_BETA_SIGNALING
14	0.767	13 / 91	HALLMARK_PEROXISOME
15	0.781	27 / 183	HALLMARK_GLYCOLYSIS

Melanoma

Rank	p−value	#in/all	Geneset
1	0.01	16 / 54	Hugo_melanoma−all−MET_DN
2	0.03	4 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
3	0.15	7 / 27	Hugo_melanoma−all−LEF1_UP
4	0.46	2 / 9	Hugo_melanoma−BRAFmut−MET_DN
5	0.57	5 / 30	Hugo_melanoma−all−MET_UP
6	0.74	6 / 43	Hugo_melanoma−BRAFmut−MET_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

miRNA target

Rank	p−value	#in/all	Geneset
1	0.2	3 / 10	hsa−miR−933
2	0.2	3 / 10	hsa−miR−720
3	0.3	2 / 6	hsa−miR−126
4	0.3	2 / 7	hsa−miR−339−3p
5	0.4	3 / 13	hsa−miR−1249
6	0.5	6 / 35	hsa−miR−197
7	0.6	2 / 11	hsa−miR−369−5p
8	0.6	5 / 30	hsa−miR−371−3p
9	0.6	5 / 30	hsa−miR−486−5p
10	0.6	7 / 43	hsa−miR−412
11	0.6	3 / 18	hsa−miR−542−5p
12	0.6	3 / 18	hsa−miR−564
13	0.6	1 / 5	hsa−miR−585
14	0.6	6 / 38	hsa−miR−1277
15	0.6	5 / 32	hsa−miR−342−5p

Telomeres

Rank	p−value	#in/all	Geneset
1	0.7	4 / 27	Nabetani_alt len telomeres_genes_ko
2	0.9	1 / 13	Alternative lengthening of telomeres
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Brain

Rank	p−value	#in/all	Geneset
1	3e−20	464 / 1893	Overlap_fetal_midbrain_TssF
2	5e−17	367 / 1476	Overlap_fetal_midbrain_TxTrans
3	6e−13	647 / 3046	Fetal_TssA
4	5e−12	212 / 819	Overlap_fetal_midbrain_TssP
5	6e−10	263 / 1115	Overlap_fetal_midbrain_EnhG
6	7e−09	299 / 1329	Overlap_fetal_midbrain_Enh
7	1e−08	304 / 1360	Mid_Frontal_Lobe_TssP
8	1e−08	208 / 869	Mid_Frontal_Lobe_EnhG
9	3e−08	255 / 1119	Overlap_fetal_midbrain_TssA
10	5e−06	205 / 924	Mid_Frontal_Lobe_TssF
11	1e−05	113 / 465	Mid_Frontal_Lobe_TxTrans
12	1e−05	515 / 2630	Fetal_TssF
13	4e−05	133 / 578	Fetal_Tx
14	6e−05	521 / 2700	Fetal_TxTrans
15	2e−04	211 / 1012	Mid_Frontal_Lobe_Enh

Chr

Rank	p−value	#in/all	Geneset
1	1e−08	37 / 87	Chr Y
2	9e−03	64 / 289	Chr 21
3	3e−02	188 / 994	Chr X
4	5e−02	119 / 619	Chr 20
5	8e−02	254 / 1411	Chr 11
6	1e−01	65 / 342	Chr 18
7	2e−01	188 / 1060	Chr 5
8	2e−01	138 / 769	Chr 15
9	2e−01	260 / 1492	Chr 2
10	2e−01	96 / 536	Chr 22
11	4e−01	73 / 422	Chr 13
12	4e−01	162 / 954	Chr 9
13	5e−01	386 / 2323	Chr 1
14	6e−01	138 / 836	Chr 8
15	6e−01	148 / 902	Chr 4

Glio

Rank	p−value	#in/all	Geneset
1	4e−20	677 / 2988	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
2	4e−15	232 / 859	Hopp_Sturm_GBM_Epi3_A_adult_fetus_UP_G34_DN
3	5e−07	60 / 193	Hopp_Sturm_GBM_Epi3_F_RTK II_UP_adult_fetus_K27_DN
4	4e−06	47 / 148	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up_(MES&CL down)
5	6e−05	114 / 487	Hopp_Sturm_GBM_Epi3_B_adult_UP_G34_DN
6	1e−04	47 / 166	Sturm_GBM_Meth_overexpression_B_adult_UP
7	1e−04	28 / 84	Weller_LGG_gradeII−vs−III_UP
8	3e−04	97 / 419	Down_a
9	6e−04	31 / 104	WIRTH_Normal Brain
10	1e−03	29 / 100	GIEZELT_GBM_STS_down_VS_LTS
11	3e−03	87 / 393	Hopp_Sturm_GBM_Epi3_no_zentr_3_RTK II_UP_adult_fetus_K27_DN
12	3e−03	170 / 839	Hopp_Sturm_GBM_Epi3_no_zentr_1_G34_DN
13	4e−03	26 / 92	Weller_LGG_A_vs_O_DOWN
14	4e−03	26 / 93	Hopp_Sturm_GBM_Epi3_C2_adult_fetus_DN
15	1e−02	25 / 95	Weller_LGG_1p19qDel−vs−intact_UP

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.4	17 / 94	DUMEAUX_Smoking enriched genes
2	0.7	1 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
3	0.8	1 / 10	DUMEAUX_Women normal BMI literature genes up
4	0.8	1 / 10	Marjolein_ageing−genes_UP
5	0.9	1 / 16	Huan_blood−pressure_DBP−signature
6	1.0	1 / 17	DUMEAUX_High bmi enriched genes
7	1.0	2 / 31	DUMEAUX_Fasting enriched genes
8	1.0	14 / 147	Homuth_BMI−associated−genes_UP
9	1.0	1 / 32	Marjolein_ageing−genes_DN
10	1.0	10 / 211	Homuth_BMI−associated−genes_DN
11	1.0	0 / 10	DUMEAUX_Smoking literature genes up
12	1.0	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
13	1.0	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
14	1.0	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
15	1.0	0 / 8	DUMEAUX_Monocytes in smokers literature genes up

MF

Rank	p−value	#in/all	Geneset
1	6e−15	119 / 357	olfactory receptor activity
2	3e−13	167 / 588	G−protein coupled receptor activity
3	1e−06	154 / 648	calcium ion binding
4	3e−05	14 / 27	peptide hormone binding
5	9e−05	49 / 174	transmembrane signaling receptor activity
6	4e−04	18 / 48	voltage−gated potassium channel activity
7	1e−03	25 / 82	odorant binding
8	2e−03	50 / 202	structural molecule activity
9	4e−03	9 / 21	steroid hydroxylase activity
10	6e−03	16 / 50	chloride channel activity
11	7e−03	36 / 145	growth factor activity
12	8e−03	8 / 19	sodium−independent organic anion transmembrane transporter activity
13	8e−03	6 / 12	hormone binding
14	9e−03	26 / 98	transcriptional activator activity, RNA polymerase II transcription regulatory re
15	1e−02	12 / 36	potassium channel activity

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.09	5 / 15	GUSTAFSON_PI3K_DN
2	0.37	3 / 13	BENTINK_myc.1
3	0.66	2 / 13	BENTINK_e2f3.1
4	0.70	2 / 14	BENTINK_ras.6
5	0.89	1 / 12	BENTINK_ras.1
6	0.91	1 / 13	BENTINK_e2f3.2
7	0.91	1 / 13	BENTINK_src.10
8	1.00	0 / 14	GUSTAFSON_PI3K_UP
9	1.00	0 / 11	BENTINK_ras.4
10	1.00	0 / 12	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	8e−25	454 / 1753	HEBENSTREIT_low expression TF
2	1e−02	148 / 747	ICGC_NrsfPcr2_targets
3	3e−01	1 / 2	MYC_Chromatin_modification UP
4	3e−01	1 / 2	MYC_DNA replication UP
5	3e−01	3 / 12	MYC_Protein synthesis degradation UP
6	3e−01	2 / 7	MYC_Cell cycle UP
7	4e−01	2 / 8	MYC_DNA repair UP
8	4e−01	1 / 3	MYC_Cell growth and proliferation UP
9	5e−01	582 / 3507	ICGC_Rad21_targets
10	6e−01	1 / 5	MYC_TFs
11	7e−01	2 / 14	NOWICK_TF
12	7e−01	8 / 55	MYC_Targets UP
13	8e−01	1 / 8	MYC_RNA processing binding UP
14	8e−01	1 / 9	MYC_Targets DOWN
15	8e−01	265 / 1669	ICGC_P300_targets

K−Means Cluster

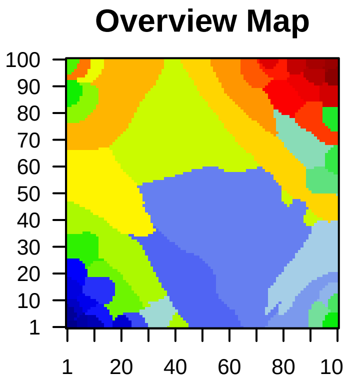
Spot Summary: I1

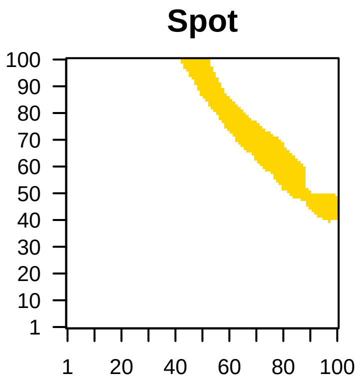
metagenes = 731
genes = 2091

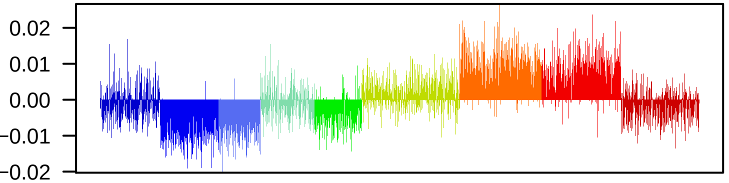
<r> metagenes = 0.63

beta: r2= 0.22 / log p= −Inf

samples with spot = 0 (0 %)





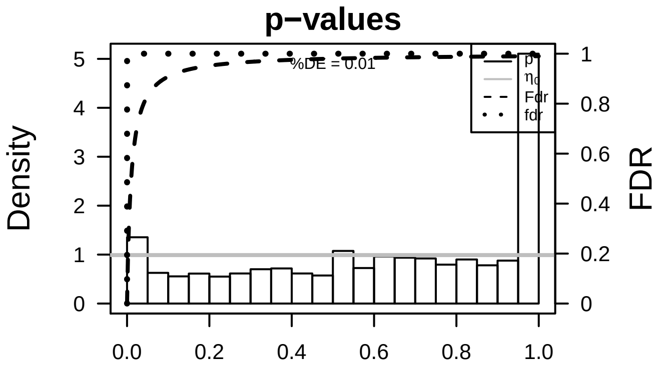


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_167181	0.84	−0.38	0.03	UTS2	urotensin 2 [Source:HGNC Symbol;Acc:HGNC:12636]
2	ILMN_170980	0.53	−0.35	0.05		
3	ILMN_181374	0.52	−0.36	0.08	CORO2A	coronin 2A [Source:HGNC Symbol;Acc:HGNC:2255]
4	ILMN_223418	0.48	−0.23	0.11	CDO1	cysteine dioxygenase type 1 [Source:HGNC Symbol;Acc:HGI
5	ILMN_241333	0.39	−0.25	0.09	SNORD118	small nucleolar RNA, C/D box 118 [Source:HGNC Symbol;Ac
6	ILMN_176744	0.38	−0.21	0.05	RNF150	ring finger protein 150 [Source:HGNC Symbol;Acc:HGNC:23
7	ILMN_186309	0.36	−0.19	0.15		T cell receptor delta variable 3 [Source:HGNC Symbol;Acc:H
8	ILMN_323739	0.36	−0.35	0.1	AAGAB	alpha− and gamma−adaptin binding protein [Source:HGNC S
9	ILMN_175565	0.36	−0.2	0.05	RASIP1	Ras interacting protein 1 [Source:HGNC Symbol;Acc:HGNC:
10	ILMN_176983	0.35	−0.21	0.14		Y RNA [Source:RFAM;Acc:RF00019]
11	ILMN_325121	0.35	−0.29	0.06	PDXDC2P	pyridoxal dependent decarboxylase domain containing 2, pse
12	ILMN_174978	0.35	−0.21	0.07	HIST1H1D	histone cluster 1, H1d [Source:HGNC Symbol;Acc:HGNC:47
13	ILMN_238523	0.35	−0.22	0.17	PBRM1	polybromo 1 [Source:HGNC Symbol;Acc:HGNC:30064]
14	ILMN_180650	0.34	−0.23	0.13	CPNE5	copine 5 [Source:HGNC Symbol;Acc:HGNC:2318]
15	ILMN_327720	0.34	−0.23	0.08		HOXA cluster antisense RNA 2 [Source:HGNC Symbol;Acc:H
16	ILMN_174888	0.33	−0.28	0.1	TOB2	transducer of ERBB2, 2 [Source:HGNC Symbol;Acc:HGNC:1
17	ILMN_165561	0.33	−0.22	0.06	DSP	desmoplakin [Source:HGNC Symbol;Acc:HGNC:3052]
18	ILMN_170664	0.32	−0.22	0.07	COL6A3	collagen type VI alpha 3 chain [Source:HGNC Symbol;Acc:H
19	ILMN_175006	0.32	−0.19	0.12	PPARGC1A	PPARG coactivator 1 alpha [Source:HGNC Symbol;Acc:HGN
20	ILMN_172242	0.32	−0.18	0.06	OR7D2	olfactory receptor family 7 subfamily D member 2 [Source:HG

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	2e−20	1079 / 12983	Chror	2_TssA_Neuronal_Progenitor
2	4e−19	1027 / 12298	Chror	2_TssA_Melanocytes
3	5e−19	969 / 11455	Chror	2_TssA_Fibroblasts
4	7e−16	921 / 10999	Colon	TssWk_Colon
5	5e−15	925 / 11130	Chror	15_Quies_Melanocytes
6	8e−14	767 / 8990	Chror	15_Quies_Fibroblasts
7	2e−13	823 / 9815	Brain	Overlap_fetal_midbrain_ReprPC
8	2e−12	743 / 8771	Chror	5_Tx_Melanocytes
9	3e−12	35 / 132	Glio	WILLSCHER_GBM_Verhaak−CL_up (C)
10	5e−12	956 / 11836	Chror	3_TssF_Melanocytes
11	2e−11	120 / 926	GSEA	NUYTTEN_EZH2_TARGETS_DN
12	5e−11	29 / 103	GSEA	WHITEFORD_PEDIATRIC_CANCER_MARKERS
13	6e−11	32 / 124	GSEA	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
14	1e−10	786 / 9530	Colon	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP
15	1e−10	200 / 1846	Chror	14_ZNF_Melanocytes
16	1e−09	388 / 4237	Chror	14_ZNF_Neuronal_Progenitor
17	1e−09	776 / 9504	Brain	Overlap_fetal_midbrain_K9K27me3
18	2e−09	409 / 4526	Colon	Quies1_Colon
19	2e−09	804 / 9917	Brain	Overlap_fetal_midbrain_ReprPCWk
20	3e−09	999 / 12741	Chror	7_Enh_Melanocytes
21	4e−09	782 / 9635	Chror	3_TssF_Fibroblasts
22	6e−09	653 / 7854	Chror	5_Tx_Fibroblasts
23	7e−09	3 / 12	Cance	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
24	1e−08	970 / 12393	Chror	15_Quies_Neuronal_Progenitor
25	3e−08	82 / 630	Chror	14_ZNF_Fibroblasts
26	3e−08	424 / 4828	CC	nucleus
27	4e−08	151 / 1404	Colon	LaPointe_mucosa−position_kmeans_D_transverse colon_UP_
28	5e−08	40 / 228	GSEA	KOBAYASHI_EGFR_SIGNALING_24HR_DN
29	7e−08	26 / 115	GSEA	ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_24HR
30	7e−08	70 / 518	GSEA	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
31	7e−08	60 / 418	GSEA	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
32	1e−07	703 / 8678	Colon	Quies3_Colon
33	1e−07	661 / 8098	Lympl	HOPP_Weak_promoter
34	1e−07	579 / 6970	Chror	5_Tx_Neuronal_Progenitor
35	1e−07	13 / 33	GSEA	AMUNDSON_GAMMA_RADIATION_RESPONSE
36	1e−07	47 / 300	BP	cell division
37	1e−07	133 / 1222	GSEA	DODD_NASOPHARYNGEAL_CARCINOMA_DN
38	2e−07	52 / 350	GSEA	BENPORATH_ES_1
39	2e−07	358 / 4034	Colon	TssD1_Colon
40	2e−07	29 / 145	GSEA	HOFFMANN_LARGE_TO_SMALL_PRE_BII_LYMPHOCYTE_UP



Aging

Rank	p−value	#in/all	Geneset
1	0.5	10 / 142	HORVATH_aging_genes meth UP
2	0.9	5 / 111	HORVATH_aging_genes meth DOWN
3	0.9	2 / 58	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	1e−07	47 / 300	cell division
2	5e−07	37 / 219	mitotic nuclear division
3	2e−06	163 / 1643	transcription, DNA−templated
4	3e−06	131 / 1272	regulation of transcription, DNA−templated
5	3e−04	5 / 10	response to caffeine
6	3e−04	6 / 15	mitotic spindle assembly checkpoint
7	5e−04	7 / 22	regulation of mitotic nuclear division
8	6e−04	9 / 36	meiotic cell cycle
9	7e−04	20 / 130	DNA replication
10	1e−03	11 / 56	chromosome segregation
11	1e−03	18 / 119	regulation of cell cycle
12	1e−03	15 / 91	sister chromatid cohesion
13	2e−03	6 / 20	regulation of transcription involved in G1/S transition of mitotic cell cycle
14	2e−03	5 / 14	positive regulation of ossification
15	2e−03	11 / 59	DNA recombination

Brain

Rank	p−value	#in/all	Geneset
1	2e−13	823 / 9815	Overlap_fetal_midbrain_ReprPC
2	1e−09	776 / 9504	Overlap_fetal_midbrain_K9K27me3
3	2e−09	804 / 9917	Overlap_fetal_midbrain_ReprPCWk
4	2e−07	84 / 681	Overlap_fetal_midbrain_EnhP
5	8e−05	111 / 1115	Overlap_fetal_midbrain_EnhG
6	9e−05	799 / 10430	Overlap_fetal_midbrain_Quies
7	2e−04	127 / 1329	Overlap_fetal_midbrain_Enh
8	3e−04	91 / 906	Fetal_HetRpts
9	4e−03	223 / 2709	Mid_Frontal_Lobe_HetRpts
10	5e−03	458 / 5936	Overlap_fetal_midbrain_HetRpts
11	6e−03	104 / 1171	Fetal_EnhP
12	1e−02	214 / 2654	Fetal_Quies
13	2e−02	210 / 2630	Fetal_TssF
14	7e−02	54 / 630	Mid_Frontal_Lobe_EnhP
15	8e−02	97 / 1213	Fetal_TssP

Cancer

Rank	p−value	#in/all	Geneset
1	7e−09	3 / 12	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
2	6e−07	68 / 527	Lembcke_Normal vs Adenoma
3	1e−02	5 / 20	PanCan_ChromMod_geneset_nanostring
4	1e−02	8 / 46	PanCan_DNARepair_geneset_nanostring
5	1e−02	4 / 14	RHODES_UNDIFFERENTIATED_CANCER
6	2e−02	4 / 15	WOLFER_overlap genes
7	3e−02	8 / 54	KUIPER_MM poor survival
8	5e−02	3 / 15	LIU_PROSTATE_CANCER_DN
9	1e−01	13 / 125	PanCan_CC+Apop_geneset_nanostring
10	1e−01	3 / 16	GENTLES_modul14
11	1e−01	10 / 91	PanCan_TXmisReg_geneset_nanostring
12	1e−01	2 / 9	GENTLES_modul3
13	1e−01	5 / 39	ZHANG_MM up
14	2e−01	11 / 117	PanCan_Driver_Gene_geneset_nanostring
15	2e−01	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN

CC

Rank	p−value	#in/all	Geneset
1	3e−08	424 / 4828	nucleus
2	3e−05	8 / 20	synaptonemal complex
3	2e−04	17 / 92	chromosome
4	2e−04	12 / 53	chromosome, centromeric region
5	3e−04	14 / 70	kinetochore
6	3e−04	5 / 10	chromocenter
7	5e−04	218 / 2535	nucleoplasm
8	6e−04	44 / 379	centrosome
9	1e−03	12 / 64	axoneme
10	3e−03	8 / 36	condensed nuclear chromosome
11	3e−03	16 / 107	spindle
12	5e−03	6 / 24	ciliary base
13	5e−03	12 / 75	condensed chromosome kinetochore
14	6e−03	13 / 85	ciliary basal body
15	1e−02	13 / 93	ubiquitin ligase complex

Chr

Rank	p−value	#in/all	Geneset
1	0.05	80 / 954	Chr 9
2	0.05	83 / 994	Chr X
3	0.06	95 / 1170	Chr 7
4	0.11	26 / 289	Chr 21
5	0.13	62 / 769	Chr 15
6	0.14	44 / 536	Chr 22
7	0.19	111 / 1467	Chr 19
8	0.24	80 / 1060	Chr 5
9	0.28	27 / 342	Chr 18
10	0.28	58 / 768	Chr 14
11	0.31	67 / 904	Chr 10
12	0.37	95 / 1318	Chr 17
13	0.40	45 / 619	Chr 20
14	0.55	103 / 1492	Chr 2
15	0.56	29 / 422	Chr 13

Chromatin states

Rank	p−value	#in/all	Geneset
1	2e−20	1079 / 12983	2_TssA_Neuronal_Progenitor
2	4e−19	1027 / 12298	2_TssA_Melanocytes
3	5e−19	969 / 11455	2_TssA_Fibroblasts
4	5e−15	925 / 11130	15_Quies_Melanocytes
5	8e−14	767 / 8990	15_Quies_Fibroblasts
6	2e−12	743 / 8771	5_Tx_Melanocytes
7	5e−12	956 / 11836	3_TssF_Melanocytes
8	1e−10	200 / 1846	14_ZNF_Melanocytes
9	1e−09	388 / 4237	14_ZNF_Neuronal_Progenitor
10	3e−09	999 / 12741	7_Enh_Melanocytes
11	4e−09	782 / 9635	3_TssF_Fibroblasts
12	6e−09	653 / 7854	5_Tx_Fibroblasts
13	1e−08	970 / 12393	15_Quies_Neuronal_Progenitor
14	3e−08	82 / 630	14_ZNF_Fibroblasts
15	1e−07	579 / 6970	5_Tx_Neuronal_Progenitor

Colon Cancer

Rank	p−value	#in/all	Geneset
1	7e−16	921 / 10999	TssWk_Colon
2	1e−10	786 / 9530	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP_
3	2e−09	409 / 4526	Quies1_Colon
4	4e−08	151 / 1404	LaPointe_mucosa−position_kmeans_D_transverse colon_UP_
5	1e−07	703 / 8678	Quies3_Colon
6	2e−07	358 / 4034	TssD1_Colon
7	1e−06	163 / 1623	Het_Colon
8	3e−06	753 / 9555	TssA_Colon
9	8e−06	122 / 1186	HetRpts_Colon
10	2e−05	112 / 1083	ZNF_Colon
11	1e−04	335 / 4018	EnhWk2_Colon
12	2e−04	490 / 6138	TssD2_Colon
13	2e−04	96 / 965	Pentrack_CRC_TCGA_corr_R_normal_DN
14	4e−04	573 / 7354	TssF_Colon
15	9e−04	26 / 193	Kosinski_lower−crypt−long−list

Glio

Rank	p−value	#in/all	Geneset
1	3e−12	35 / 132	WILLSCHER_GBM_Verhaak−CL_up (C)
2	7e−05	165 / 1777	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
3	7e−05	186 / 2043	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
4	9e−04	81 / 820	Sturm_GBM_Meth_overexpression_E_G34_UP
5	4e−03	10 / 55	developing astrocytes
6	5e−03	12 / 74	Weller_LGG_gradeII−vs−III_DOWN
7	1e−02	2 / 3	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up (L)
8	4e−02	4 / 19	Sturm_GBM_Meth_overexpression_J_RTK II 'classic'_UP
9	7e−02	7 / 53	mature astrocytes
10	8e−02	3 / 15	VERHAAK_MES subtype
11	8e−02	3 / 15	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up (I)
12	1e−01	111 / 1417	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
13	1e−01	7 / 58	OPC
14	1e−01	26 / 290	Hopp_Sturm_GBM_Epi3_C_IDH_UP
15	1e−01	9 / 86	laffaire_hypermeth_LGG_vs_control

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−11	120 / 926	NUYTTEN_EZH2_TARGETS_DN
2	5e−11	29 / 103	WHITEFORD_PEDIATRIC_CANCER_MARKERS
3	6e−11	32 / 124	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
4	7e−09	3 / 12	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
5	5e−08	40 / 228	KOBAYASHI_EGFR_SIGNALING_24HR_DN
6	7e−08	26 / 115	ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_24HR
7	7e−08	70 / 518	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
8	7e−08	60 / 418	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
9	1e−07	13 / 33	AMUNDSON_GAMMA_RADIATION_RESPONSE
10	1e−07	133 / 1222	DODD_NASOPHARYNGEAL_CARCINOMA_DN
11	2e−07	52 / 350	BENPORATH_ES_1
12	2e−07	29 / 145	HOFFMANN_LARGE_TO_SMALL_PRE_BII_LYMPHOCYTE_UP
13	6e−07	50 / 343	CHEMNITZ_RESPONSE_TO_PROSTAGLANDIN_E2_DN
14	8e−07	16 / 56	MOLENAAR_TARGETS_OF_CCND1_AND_CDK4_DN
15	2e−06	39 / 249	ZHANG_TLX_TARGETS_60HR_DN

HM

Rank	p−value	#in/all	Geneset
1	1e−04	27 / 179	HALLMARK_G2M_CHECKPOINT
2	2e−04	26 / 173	HALLMARK_E2F_TARGETS
3	4e−02	20 / 186	HALLMARK_MYOGENESIS
4	5e−02	15 / 137	HALLMARK_UV_RESPONSE_UP
5	6e−02	6 / 40	HALLMARK_WNT_BETA_CATENIN_SIGNALING
6	2e−01	5 / 41	HALLMARK_APICAL_SURFACE
7	2e−01	16 / 177	HALLMARK_MITOTIC_SPINDLE
8	2e−01	12 / 132	HALLMARK_UV_RESPONSE_DN
9	2e−01	16 / 189	HALLMARK_HYPOXIA
10	3e−01	15 / 177	HALLMARK_KRAS_SIGNALING_DN
11	3e−01	10 / 116	HALLMARK_SPERMATOGENESIS
12	3e−01	9 / 103	HALLMARK_BILE_ACID_METABOLISM
13	4e−01	15 / 191	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
14	4e−01	7 / 91	HALLMARK_ANDROGEN_RESPONSE
15	5e−01	13 / 176	HALLMARK_KRAS_SIGNALING_UP

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.3	1 / 4	DUMEAUX_Exercising non smoker literature enriched genes
2	0.5	1 / 10	DUMEAUX_Women normal BMI literature genes up
3	0.5	1 / 10	Marjolein_ageing−genes_UP
4	0.6	6 / 94	DUMEAUX_Smoking enriched genes
5	0.7	1 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
6	0.7	2 / 32	Marjolein_ageing−genes_DN
7	0.9	1 / 31	DUMEAUX_Fasting enriched genes
8	1.0	5 / 147	Homuth_BMI−associated−genes_UP
9	1.0	7 / 211	Homuth_BMI−associated−genes_DN
10	1.0	0 / 10	DUMEAUX_Smoking literature genes up
11	1.0	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
12	1.0	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
13	1.0	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
14	1.0	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
15	1.0	0 / 17	DUMEAUX_High bmi enriched genes

Lymphoma

Rank	p−value	#in/all	Geneset
1	1e−07	661 / 8098	HOPP_Weak_promoter
2	3e−07	667 / 8226	HOPP_Active_promoter
3	1e−06	90 / 777	WIRTH_lymphoma937_spot D
4	4e−06	536 / 6559	HOPP_Weak_txn
5	6e−06	87 / 772	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell line_
6	1e−05	128 / 1270	SPANG_BCR UP
7	5e−05	257 / 2939	HOPP_Poised_promoter
8	1e−03	227 / 2701	HOPP_Repetitive
9	3e−03	14 / 88	WIRTH_lymphoma937_spot A
10	4e−03	14 / 92	Hopp_June14_MMML937 tumors+controls_group.overexpression_A_mBL_ce
11	5e−03	553 / 7275	HOPP_Txn_elongation
12	6e−03	28 / 244	LENZ_Stromal signature 1
13	1e−02	4 / 13	Subero_B−CLL_hypo_meth
14	1e−02	25 / 220	Hopp_June14_MMML937 tumors+controls_group.overexpression_B_cell line_
15	1e−02	4 / 14	BENTINK_mBL UP

Melanoma

Rank	p−value	#in/all	Geneset
1	0.3	5 / 54	Hugo_melanoma−all−MET_DN
2	0.4	4 / 43	Hugo_melanoma−BRAFmut−MET_UP
3	0.5	1 / 9	Hugo_melanoma−BRAFmut−MET_DN
4	0.9	1 / 27	Hugo_melanoma−all−LEF1_UP
5	0.9	1 / 30	Hugo_melanoma−all−MET_UP
6	1.0	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

MF

Rank	p−value	#in/all	Geneset
1	3e−07	153 / 1475	DNA binding
2	9e−07	171 / 1717	metal ion binding
3	1e−03	6 / 18	proline−rich region binding
4	3e−03	83 / 877	transcription factor activity, sequence−specific DNA binding
5	3e−03	4 / 10	nucleoside kinase activity
6	4e−03	664 / 8818	protein binding
7	5e−03	5 / 17	histone methyltransferase activity (H3−K4 specific)
8	8e−03	7 / 34	histone−lysine N−methyltransferase activity
9	8e−03	10 / 60	microtubule motor activity
10	9e−03	37 / 355	chromatin binding
11	1e−02	22 / 185	microtubule binding
12	1e−02	6 / 28	Hsp90 protein binding
13	1e−02	59 / 627	molecular_function
14	2e−02	4 / 15	cytoskeletal adaptor activity
15	2e−02	17 / 145	nucleic acid binding

miRNA Disease

Rank	p−value	#in/all	Geneset
1	0.1	1 / 2	Burkitt lymphoma
2	0.2	1 / 3	Pituitary adenoma
3	0.3	4 / 40	Medulloblastoma
4	0.4	1 / 6	Thrombocytopenic purpurea, autoimmune
5	0.4	2 / 20	Parkinson disease
6	0.5	1 / 9	Systemic lupus erythematosus, susceptibility
7	0.6	2 / 29	Neuroblastoma
8	0.6	2 / 30	Systemic lupus erythematosus (SLE)
9	0.6	4 / 63	Gastrointestinal
10	0.7	4 / 68	Glioblastoma multiforme, somatic
11	0.7	1 / 18	Hodgkin lymphoma
12	0.7	1 / 18	Non−Hodgkin lymphoma, somatic
13	0.8	3 / 56	Myopathy, nemaline, 3
14	0.8	1 / 22	Pigmented adrenocortical disease, primary isolated
15	0.8	1 / 23	Esophageal cancer

miRNA target

Rank	p−value	#in/all	Geneset
1	0.005	23 / 184	hsa−miR−129−5p
2	0.005	13 / 83	hsa−miR−630
3	0.020	19 / 164	hsa−miR−153
4	0.022	4 / 16	hsa−miR−1298
5	0.030	13 / 105	hsa−miR−376b
6	0.035	24 / 233	hsa−miR−1252
7	0.035	35 / 366	hsa−let−7d
8	0.041	15 / 132	hsa−miR−28−5p
9	0.042	9 / 67	hsa−miR−1246
10	0.047	7 / 48	hsa−miR−769−3p
11	0.051	13 / 113	hsa−miR−376c
12	0.051	13 / 113	hsa−miR−217
13	0.051	6 / 39	hsa−miR−1274a
14	0.054	30 / 317	hsa−miR−559
15	0.057	3 / 13	hsa−miR−147b

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.01	4 / 13	BENTINK_e2f3.2
2	0.20	2 / 12	BENTINK_ras.1
3	0.25	2 / 14	GUSTAFSON_PI3K_UP
4	0.55	1 / 11	BENTINK_ras.4
5	0.58	1 / 12	BENTINK_src.2
6	0.61	1 / 13	BENTINK_myc.1
7	0.61	1 / 13	BENTINK_src.10
8	0.64	1 / 14	BENTINK_ras.6
9	0.66	1 / 15	GUSTAFSON_PI3K_DN
10	1.00	0 / 13	BENTINK_e2f3.1
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Reference Signatures

Rank	p−value	#in/all	Geneset
1	0.003	28 / 231	Chaussabel_2,5_Immune related molecules
2	0.019	8 / 49	VAQUERIZAS_Uterus_TF
3	0.046	4 / 20	JONGENEEL_Thymus
4	0.047	7 / 48	WIRTH_Pancreas
5	0.051	6 / 39	VAQUERIZAS_Testis_TF
6	0.057	3 / 13	JONGENEEL_Uterus
7	0.097	41 / 478	WIRTH_Nervous System
8	0.130	13 / 132	WIRTH_Muscle
9	0.150	24 / 275	Chaussabel_3,7_Spliceosome
10	0.163	11 / 113	Chaussabel_1,4_Replication
11	0.202	2 / 12	Chaussabel_3,5_Hemoglobin genes
12	0.205	21 / 248	Chaussabel_3,6_Mitochondrial ribosomal proteins
13	0.228	2 / 13	JONGENEEL_Thyroid
14	0.251	3 / 25	VAQUERIZAS_Adrenal cortex_TF
15	0.254	2 / 14	WIRTH_B−cells

Telomeres

Rank	p−value	#in/all	Geneset
1	0.6	2 / 27	Nabetani_alt len telomeres_genes_ko
2	0.6	1 / 13	Alternative lengthening of telomeres
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	4e−05	549 / 6868	ICGC_Elf1_targets
2	7e−04	4 / 7	MYC_Cell cycle UP
3	7e−04	361 / 4468	ICGC_Egr1_targets
4	2e−03	408 / 5188	ICGC_Ebfsc137065_targets
5	3e−03	347 / 4362	ICGC_Creb1_targets
6	4e−03	483 / 6267	ICGC_Yy1_targets
7	4e−03	396 / 5067	ICGC_Taf1_targets
8	5e−03	185 / 2215	ICGC_GabpPcr2_targets
9	5e−03	327 / 4131	ICGC_Nfatc1_targets
10	7e−03	483 / 6322	ICGC_Tcf3_targets
11	9e−03	548 / 7247	ICGC_Runx3_targets
12	9e−03	339 / 4345	ICGC_Zeb1_targets
13	1e−02	422 / 5518	ICGC_Stat5_targets
14	1e−02	123 / 1452	ICGC_Six5_targets
15	1e−02	413 / 5410	ICGC_Foxm1_targets

K−Means Cluster

Spot Summary: J1

metagenes = 287
genes = 455

<r> metagenes = 0.89
<r> genes = 0.08
beta: r2= 1.09 / log p= −Inf

samples with spot = 0 (0 %)

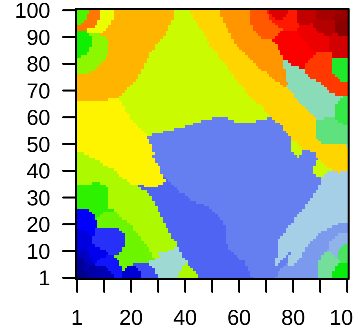
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_235316	1.3	−0.28	0.08	MSLN	mesothelin [Source:HGNC Symbol;Acc:HGNC:7371]
2	ILMN_172517	1.13	−0.61	0.07		
3	ILMN_167966	0.81	−0.26	0.1	SCGB3A1	secretoglobin family 3A member 1 [Source:HGNC Symbol;Ac
4	ILMN_323794	0.64	−0.27	0.19	PXDN	peroxidasin [Source:HGNC Symbol;Acc:HGNC:14966]
5	ILMN_323087	0.57	−0.29	0.12		phosphodiesterase 4D interacting protein pseudogene 1 [Sou
6	ILMN_166667	0.54	−0.37	0.09		
7	ILMN_328377	0.45	−0.26	0.15		
8	ILMN_181357	0.44	−0.47	0.14	IL16	interleukin 16 [Source:HGNC Symbol;Acc:HGNC:5980]
9	ILMN_210102	0.43	−0.49	0.16	ZNF75D	zinc finger protein 75D [Source:HGNC Symbol;Acc:HGNC:13
10	ILMN_232380	0.43	−0.21	0.29	MOCS1	molybdenum cofactor synthesis 1 [Source:HGNC Symbol;Acc
11	ILMN_319283	0.42	−0.44	0.21		ribosomal protein S2 pseudogene 5 [Source:HGNC Symbol;
12	ILMN_176322	0.37	−0.42	0.11	MEF2D	myocyte enhancer factor 2D [Source:HGNC Symbol;Acc:HG
13	ILMN_324169	0.37	−0.35	0.12	MICA	MHC class I polypeptide−related sequence A [Source:HGNC
14	ILMN_170356	0.36	−0.39	0.15	DYNLRB1	dynein light chain roadblock−type 1 [Source:HGNC Symbol;
15	ILMN_170790	0.36	−0.25	0.29	LEF1−AS1	LEF1 antisense RNA 1 [Source:HGNC Symbol;Acc:HGNC:4
16	ILMN_222380	0.36	−0.25	0.31	CEP41	centrosomal protein 41 [Source:HGNC Symbol;Acc:HGNC:1
17	ILMN_173151	0.36	−0.24	0.24	PLD6	phospholipase D family member 6 [Source:HGNC Symbol;Ac
18	ILMN_178751	0.36	−0.29	0.09	CAPN12	calpain 12 [Source:HGNC Symbol;Acc:HGNC:13249]
19	ILMN_167554	0.35	−0.26	0.36		eukaryotic translation elongation factor 1 beta 2 pseudogene
20	ILMN_181117	0.34	−0.42	0.18	GPR132	G protein−coupled receptor 132 [Source:HGNC Symbol;Acc:

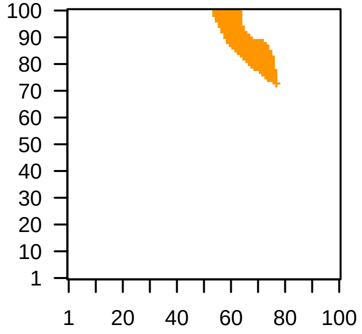
Geneset Overrepresentation

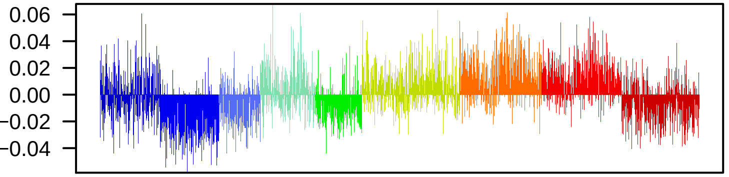
Rank	p−value	#in/all	Geneset	
1	5e−05	10 / 132	Refer	Chaussabel_1,7_MHC Ribosomal proteins
2	2e−04	5 / 35	GSEA	VANDESLUIS_COMMD1_TARGETS_GROUP_3_DN
3	4e−04	3 / 10	GSEA	NIKOLSKY_BREAST_CANCER_17P11_AMPLICON
4	6e−04	3 / 11	GSEA	REACTOME_RESOLUTION_OF_AP_SITES_VIA_THE_SINGLE_NUCLE
5	8e−04	14 / 325	GSEA	DAIRKEE_TERT_TARGETS_UP
6	8e−04	4 / 27	GSEA	KEGG_BASE_EXCISION_REPAIR
7	9e−04	96 / 4468	TF	ICGC_Egr1_targets
8	9e−04	125 / 6138	Colon	TssD2_Colon
9	2e−03	3 / 15	GSEA	REACTOME_BASE_EXCISION_REPAIR
10	2e−03	24 / 777	Lymp	WIRTH_lymphoma937_spot D
11	2e−03	28 / 965	Colon	Pentrack_CRC_TCGA_corr_R_normal_DN
12	3e−03	7 / 119	Refer	Chaussabel_2,4_Ribosomal proteins
13	4e−03	13 / 343	GSEA	CHEMNITZ_RESPONSE_TO_PROSTAGLANDIN_E2_DN
14	5e−03	141 / 7354	Colon	TssF_Colon
15	5e−03	3 / 22	MF	ion channel activity
16	5e−03	6 / 100	Glio	GIEZELT_GBM_STS_down_VS_LTS
17	7e−03	5 / 74	GSEA	REACTOME_NONSENSE_MEDIATED_DECAY_ENHANCED_BY_THE_E
18	8e−03	2 / 9	GSEA	REACTOME_SLBP_DEPENDENT_PROCESSING_OF_REPLICATION_D
19	8e−03	2 / 9	GSEA	YANG_MUC2_TARGETS_DUODENUM_6MO_UP
20	1e−02	2 / 10	CC	cytosolic ribosome
21	1e−02	2 / 10	MF	DNA N−glycosylase activity
22	1e−02	2 / 10	BP	histone mRNA metabolic process
23	1e−02	2 / 10	BP	nuclear export
24	1e−02	2 / 10	GSEA	REACTOME_BASE_FREE_SUGAR_PHOSPHATE_REMOVAL_VIA_THE_
25	1e−02	83 / 4112	Brain	Mid_Frontal_Lobe_ReprPC
26	1e−02	4 / 56	GSEA	REACTOME_PEPTIDE_CHAIN_ELONGATION
27	1e−02	5 / 87	BP	nuclear−transcribed mRNA catabolic process, nonsense−mediated decay
28	1e−02	8 / 195	BP	ion transmembrane transport
29	1e−02	4 / 58	GSEA	HESS_TARGETS_OF_HOXA9_AND_MEIS1_UP
30	1e−02	1 / 13	Canc	LIU_LIVER_CANCER
31	2e−02	2 / 12	BP	protein localization to synapse
32	2e−02	2 / 12	TF	MYC_Protein synthesis degradation UP
33	2e−02	2 / 12	GSEA	HOLLEMAN_VINCRISTINE_RESISTANCE_ALL_DN
34	2e−02	129 / 6868	TF	ICGC_Elf1_targets
35	2e−02	35 / 1501	TF	ICGC_Usf1_targets
36	2e−02	5 / 92	GSEA	KIM_GASTRIC_CANCER_CHEMOSENSITIVITY
37	2e−02	15 / 505	GSEA	WEST_ADRENOCORTICAL_TUMOR_DN
38	2e−02	13 / 416	GSEA	CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_2
39	2e−02	48 / 2215	TF	ICGC_GabpPcr2_targets
40	2e−02	19 / 710	GSEA	MARTENS_TRETINOIN_RESPONSE_DN

Overview Map

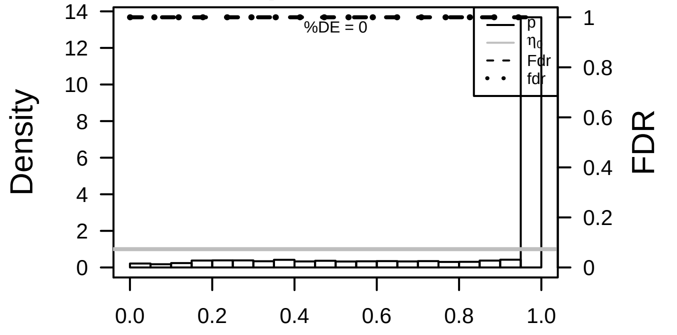


Spot





p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.6	1 / 58	TESCHENDORFF_age_hypermethylated
2	0.7	2 / 142	HORVATH_aging_genes meth UP
3	0.8	1 / 111	HORVATH_aging_genes meth DOWN
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	0.01	2 / 10	histone mRNA metabolic process
2	0.01	2 / 10	nuclear export
3	0.01	5 / 87	nuclear−transcribed mRNA catabolic process, nonsense−mediated decay
4	0.01	8 / 195	ion transmembrane transport
5	0.02	2 / 12	protein localization to synapse
6	0.02	2 / 14	piRNA metabolic process
7	0.02	2 / 14	positive regulation of telomerase RNA localization to Cajal body
8	0.02	2 / 14	protein ADP−ribosylation
9	0.02	3 / 37	CENP−A containing nucleosome assembly
10	0.03	2 / 17	axonal fasciculation
11	0.03	2 / 17	DNA methylation involved in gamete generation
12	0.04	2 / 20	renal system development
13	0.04	3 / 49	generation of precursor metabolites and energy
14	0.04	2 / 21	tissue development
15	0.05	2 / 23	regulation of neuron projection development

Brain

Rank	p−value	#in/all	Geneset
1	0.01	83 / 4112	Mid_Frontal_Lobe_ReprPC
2	0.07	19 / 818	Mid_Frontal_Lobe_Het
3	0.13	15 / 681	Overlap_fetal_midbrain_EnhP
4	0.14	58 / 3164	Mid_Frontal_Lobe_ZNF
5	0.16	33 / 1728	Fetal_ReprPCWk
6	0.19	49 / 2709	Mid_Frontal_Lobe_HetRpts
7	0.21	7 / 304	Mid_Frontal_Lobe_TssA
8	0.26	158 / 9504	Overlap_fetal_midbrain_K9K27me3
9	0.27	100 / 5936	Overlap_fetal_midbrain_HetRpts
10	0.30	12 / 630	Mid_Frontal_Lobe_EnhP
11	0.38	36 / 2127	Mid_Frontal_Lobe_K9K27me3
12	0.41	30 / 1784	Mid_Frontal_Lobe_ReprPCWk
13	0.50	13 / 796	Overlap_fetal_midbrain_ZNF
14	0.51	15 / 924	Mid_Frontal_Lobe_TssF
15	0.52	18 / 1119	Overlap_fetal_midbrain_TssA

Cancer

Rank	p−value	#in/all	Geneset
1	0.01	1 / 13	LIU_LIVER_CANCER
2	0.02	15 / 527	Lembcke_Normal vs Adenoma
3	0.19	1 / 13	RHODES_CANCER_META_SIGNATURE
4	0.19	1 / 13	GENTLES_modul6
5	0.20	1 / 14	GENTLES_modul4
6	0.27	0 / 14	LIU_COMMON_CANCER_GENES
7	0.32	1 / 24	PanCan_Notch_geneset_nanostring
8	0.36	1 / 28	PanCan_HH_geneset_nanostring
9	0.40	0 / 14	LIU_PROSTATE_CANCER_UP
10	0.47	1 / 39	ZHANG_MM up
11	0.52	1 / 46	PanCan_DNARepair_geneset_nanostring
12	0.58	1 / 54	KUIPER_MM poor survival
13	0.59	0 / 12	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
14	0.60	3 / 193	PanCan_PI3K_geneset_nanostring
15	0.64	2 / 136	PanCan_RAS_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	0.01	2 / 10	cytosolic ribosome
2	0.02	4 / 69	primary cilium
3	0.03	2 / 16	replication fork
4	0.04	2 / 21	U4/U6 x U5 tri−snRNP complex
5	0.05	4 / 85	ciliary basal body
6	0.06	2 / 24	ciliary transition zone
7	0.09	2 / 32	photoreceptor connecting cilium
8	0.12	2 / 38	ciliary tip
9	0.14	6 / 220	synapse
10	0.14	26 / 1304	mitochondrion
11	0.15	7 / 273	neuron projection
12	0.15	1 / 10	axon initial segment
13	0.15	1 / 10	low−density lipoprotein particle
14	0.15	1 / 10	methylosome
15	0.15	1 / 10	secretory granule lumen

Chr

Rank	p−value	#in/all	Geneset
1	0.09	13 / 536	Chr 22
2	0.15	26 / 1318	Chr 17
3	0.17	23 / 1160	Chr 12
4	0.18	7 / 289	Chr 21
5	0.24	22 / 1170	Chr 7
6	0.33	19 / 1060	Chr 5
7	0.34	14 / 768	Chr 14
8	0.36	15 / 836	Chr 8
9	0.37	16 / 904	Chr 10
10	0.38	21 / 1217	Chr 3
11	0.39	25 / 1467	Chr 19
12	0.57	12 / 769	Chr 15
13	0.60	36 / 2323	Chr 1
14	0.60	23 / 1492	Chr 2
15	0.76	13 / 954	Chr 9

Chromatin states

Rank	p−value	#in/all	Geneset
1	0.05	16 / 630	14_ZNF_Fibroblasts
2	0.08	65 / 3450	4_TxTrans_Fibroblasts
3	0.10	87 / 4795	6_EnhG_Fibroblasts
4	0.12	101 / 5699	6_EnhG_Melanocytes
5	0.12	57 / 3068	8_EnhP_Fibroblasts
6	0.17	65 / 3639	1_TssP_Fibroblasts
7	0.22	22 / 1154	11_K9K27me3_Neuronal_Progenitor
8	0.25	101 / 5956	3_TssF_Neuronal_Progenitor
9	0.38	143 / 8771	5_Tx_Melanocytes
10	0.40	34 / 2028	4_TxTrans_Melanocytes
11	0.49	67 / 4169	10_ReprPC_Fibroblasts
12	0.49	7 / 416	4_TxTrans_Neuronal_Progenitor
13	0.51	207 / 12983	2_TssA_Neuronal_Progenitor
14	0.54	188 / 11836	3_TssF_Melanocytes
15	0.55	19 / 1206	6_EnhG_Neuronal_Progenitor

Colon Cancer

Rank	p−value	#in/all	Geneset
1	9e−04	125 / 6138	TssD2_Colon
2	2e−03	28 / 965	Pentrack_CRC_TCGA_corr_R_normal_DN
3	5e−03	141 / 7354	TssF_Colon
4	4e−02	20 / 831	Pentrack_CRC_TCGA_group.over_C_normal_DN
5	5e−02	1 / 3	Budinska_E_Mixed_DOWN
6	5e−02	56 / 2845	TxEnhG1_Colon
7	7e−02	24 / 1083	ZNF_Colon
8	1e−01	1 / 7	Budinska_A_Surface crypt−like_UP
9	1e−01	1 / 9	Marisa_CRC−C3
10	1e−01	1 / 9	Marisa_CRC−C5
11	2e−01	3 / 88	Pentrack_CRC_TCGA_corr_S_normal_DN
12	2e−01	3 / 91	Pentrack_CRC_TCGA_corr_H_mss_UP_msi−h_DN
13	2e−01	16 / 789	TxEnhG2_Colon
14	2e−01	3 / 96	Pentrack_CRC_TCGA_group.over_A_normal_UP
15	2e−01	2 / 52	Marisa_CRC−cluster−e

Glio

Rank	p−value	#in/all	Geneset
1	0.005	6 / 100	GIEZELT_GBM_STS_down_VS_LTS
2	0.023	4 / 68	Christensen_hypermethylated_in_grade2_astrocytoma
3	0.045	4 / 84	GIEZELT_GBM_WT_down_VS_mut
4	0.049	4 / 86	laffaire_hypermeth_LGG_vs_control
5	0.056	4 / 90	Christensen_hypermethylated_in_secondary_glioblastoma
6	0.064	2 / 26	Gorovets_LGG_NB_subclass
7	0.092	1 / 6	laffaire_hypometh_LGG_vs_control
8	0.099	4 / 110	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
9	0.112	4 / 115	Christensen_hypermethylated_in_grade3_astrocytoma
10	0.117	4 / 117	Christensen_hypermethylated_in_grade2_oligoastrocytoma
11	0.121	1 / 8	WILLSCHER_GBM_STSwt_proteomics−N_UP
12	0.166	4 / 134	Christensen_hypermethylated_in_grade3_oligoastrocytoma
13	0.169	3 / 89	GIEZELT_GBM_STSwt_up_VS_LTSwt
14	0.175	1 / 12	Phillips PN up vs MES & Prolif
15	0.208	4 / 147	Christensen_hypermethylated_in_grade2_oligodendroglioma

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−04	5 / 35	VANDESLUIS_COMMD1_TARGETS_GROUP_3_DN
2	4e−04	3 / 10	NIKOLSKY_BREAST_CANCER_17P11_AMPLICON
3	6e−04	3 / 11	REACTOME_RESOLUTION_OF_AP_SITES_VIA_THE_SINGLE_NUCLEOT
4	8e−04	14 / 325	DAIRKEE_TERT_TARGETS_UP
5	8e−04	4 / 27	KEGG_BASE_EXCISION_REPAIR
6	2e−03	3 / 15	REACTOME_BASE_EXCISION_REPAIR
7	4e−03	13 / 343	CHEMNITZ_RESPONSE_TO_PROSTAGLANDIN_E2_DN
8	7e−03	5 / 74	REACTOME_NONSENSE_MEDIATED_DECAY_ENHANCED_BY_THE_EXC
9	8e−03	2 / 9	REACTOME_SLBP_DEPENDENT_PROCESSING_OF_REPLICATION_DEP
10	8e−03	2 / 9	YANG_MUC2_TARGETS_DUODENUM_6MO_UP
11	1e−02	2 / 10	REACTOME_BASE_FREE_SUGAR_PHOSPHATE_REMOVAL_VIA_THE_SI
12	1e−02	4 / 56	REACTOME_PEPTIDE_CHAIN_ELONGATION
13	1e−02	4 / 58	HESS_TARGETS_OF_HOXA9_AND_MEIS1_UP
14	1e−02	1 / 13	LIU_LIVER_CANCER
15	2e−02	2 / 12	HOLLEMAN_VINCRISTINE_RESISTANCE_ALL_DN

HM

Rank	p−value	#in/all	Geneset
1	0.2	4 / 138	HALLMARK_FATTY_ACID_METABOLISM
2	0.3	4 / 183	HALLMARK_APICAL_JUNCTION
3	0.3	3 / 130	HALLMARK_DNA_REPAIR
4	0.3	4 / 186	HALLMARK_ESTROGEN_RESPONSE_LATE
5	0.4	1 / 34	HALLMARK_HEDGEHOG_SIGNALING
6	0.5	2 / 103	HALLMARK_BILE_ACID_METABOLISM
7	0.5	3 / 176	HALLMARK_ADIPOGENESIS
8	0.5	3 / 176	HALLMARK_KRAS_SIGNALING_UP
9	0.5	3 / 179	HALLMARK_G2M_CHECKPOINT
10	0.6	2 / 116	HALLMARK_SPERMATOGENESIS
11	0.6	3 / 183	HALLMARK_GLYCOLYSIS
12	0.6	3 / 185	HALLMARK_P53_PATHWAY
13	0.7	1 / 82	HALLMARK_IL6_JAK_STAT3_SIGNALING
14	0.8	2 / 170	HALLMARK_MYC_TARGETS_V1
15	0.8	1 / 91	HALLMARK_ANDROGEN_RESPONSE

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.8	1 / 94	DUMEAUX_Smoking enriched genes
2	0.9	1 / 147	Homuth_BMI−associated−genes_UP
3	1.0	1 / 211	Homuth_BMI−associated−genes_DN
4	1.0	0 / 10	DUMEAUX_Smoking literature genes up
5	1.0	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
6	1.0	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
7	1.0	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
8	1.0	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
9	1.0	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
10	1.0	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
11	1.0	0 / 10	DUMEAUX_Women normal BMI literature genes up
12	1.0	0 / 17	DUMEAUX_High bmi enriched genes
13	1.0	0 / 31	DUMEAUX_Fasting enriched genes
14	1.0	0 / 18	Huan_blood−pressure_SBP−signature
15	1.0	0 / 16	Huan_blood−pressure_DBP−signature

Lymphnoma

Rank	p−value	#in/all	Geneset
1	0.002	24 / 777	WIRTH_lymphoma937_spot D
2	0.020	2 / 14	Subero_T−ALL_hypo_meth
3	0.023	20 / 772	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell line
4	0.069	12 / 464	WIRTH_lymphoma937_spot I
5	0.077	1 / 5	Shaknovich_ABC_hyper_meth
6	0.107	11 / 450	Hopp_June14_MMML937 tumors+controls_group.overexpression_I_MM_GC
7	0.115	26 / 1270	SPANG_BCR UP
8	0.121	1 / 8	MASCQUE_ABC UP
9	0.148	1 / 10	Care_ABC UP
10	0.162	1 / 11	Subero_MM_hypo_meth
11	0.165	3 / 88	WIRTH_lymphoma937_spot A
12	0.175	1 / 12	Hopp_Lymphoma_Epi1_with_zentr_ii_MCL_mBL_UP
13	0.181	3 / 92	Hopp_June14_MMML937 tumors+controls_group.overexpression_A_mBL_ce
14	0.251	1 / 18	Aukema_BCL2 UP_BCL6 DN
15	0.275	1 / 20	DAVE_NFkB BL DN

Melanoma

Rank	p−value	#in/all	Geneset
1	1	0 / 30	Hugo_melanoma−all−MET_UP
2	1	0 / 54	Hugo_melanoma−all−MET_DN
3	1	0 / 43	Hugo_melanoma−BRAFmut−MET_UP
4	1	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
5	1	0 / 27	Hugo_melanoma−all−LEF1_UP
6	1	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

MF

Rank	p−value	#in/all	Geneset
1	0.005	3 / 22	ion channel activity
2	0.010	2 / 10	DNA N−glycosylase activity
3	0.020	2 / 14	telomerase RNA binding
4	0.026	2 / 16	acetylglucosaminyltransferase activity
5	0.026	5 / 105	histone binding
6	0.036	2 / 19	NAD+ ADP−ribosyltransferase activity
7	0.037	4 / 79	hormone activity
8	0.040	2 / 20	peptide antigen binding
9	0.071	3 / 60	microtubule motor activity
10	0.078	15 / 627	molecular_function
11	0.107	2 / 35	4 iron, 4 sulfur cluster binding
12	0.107	2 / 35	beta−tubulin binding
13	0.125	3 / 77	electron carrier activity
14	0.136	4 / 124	transporter activity
15	0.148	1 / 10	glucose binding

miRNA Disease

Rank	p−value	#in/all	Geneset
1	0.06	1 / 4	Carcinoid tumors, intestinal
2	0.54	1 / 48	Alzheimer disease, susceptibility to
3	0.64	1 / 63	Gastrointestinal
4	0.84	1 / 113	Ovarian cancer
5	0.87	1 / 127	Melanoma and neural system tumor syndrome
6	0.92	1 / 156	Breast cancer
7	1.00	0 / 7	Thyroid carcinoma, papillary
8	1.00	0 / 123	Pancreatic cancer
9	1.00	0 / 68	Glioblastoma multiforme, somatic
10	1.00	0 / 3	Pituitary adenoma
11	1.00	0 / 116	Cancer
12	1.00	0 / 95	Colorectal cancer
13	1.00	0 / 2	Adenomas, multiple colorectal
14	1.00	0 / 124	Prostate cancer
15	1.00	0 / 7	Schizophrenia, susceptibility to

miRNA target

Rank	p−value	#in/all	Geneset
1	0.08	4 / 101	hsa−miR−210
2	0.12	3 / 77	hsa−miR−569
3	0.14	2 / 41	hsa−miR−423−3p
4	0.15	2 / 43	hsa−miR−661
5	0.17	2 / 47	hsa−miR−875−5p
6	0.19	1 / 13	hsa−miR−671−3p
7	0.20	1 / 14	hsa−miR−191*
8	0.24	2 / 58	hsa−miR−187
9	0.28	2 / 65	hsa−miR−1285
10	0.29	2 / 67	hsa−miR−1262
11	0.29	2 / 67	hsa−miR−502−5p
12	0.30	3 / 121	hsa−miR−515−5p
13	0.31	1 / 23	hsa−miR−517a
14	0.31	1 / 23	hsa−miR−151−5p
15	0.31	2 / 71	hsa−miR−939

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.2	1 / 11	BENTINK_ras.4
2	1.0	0 / 14	GUSTAFSON_PI3K_UP
3	1.0	0 / 15	GUSTAFSON_PI3K_DN
4	1.0	0 / 13	BENTINK_e2f3.1
5	1.0	0 / 13	BENTINK_e2f3.2
6	1.0	0 / 13	BENTINK_myc.1
7	1.0	0 / 12	BENTINK_ras.1
8	1.0	0 / 14	BENTINK_ras.6
9	1.0	0 / 13	BENTINK_src.10
10	1.0	0 / 12	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Reference Signatures

Rank	p−value	#in/all	Geneset
1	5e−05	10 / 132	Chaussabel_1,7_MHC Ribosomal proteins
2	3e−03	7 / 119	Chaussabel_2,4_Ribosomal proteins
3	9e−02	1 / 6	WIRTH_Pituitary gland
4	2e−01	1 / 12	WIRTH_Globus pallidus
5	2e−01	1 / 14	WIRTH_Telencephalon
6	2e−01	1 / 14	JONGENEEL_Peripheral Blood Lymphocytes
7	2e−01	1 / 16	VAQUERIZAS_Ovary_TF
8	2e−01	1 / 17	VAQUERIZAS_Adrenal gland_TF
9	2e−01	1 / 17	VAQUERIZAS_Heart_TF
10	3e−01	1 / 18	JONGENEEL_Trachea
11	3e−01	1 / 20	JONGENEEL_Thymus
12	3e−01	5 / 221	Chaussabel_3,8_Enzymes
13	3e−01	1 / 23	JONGENEEL_Heart
14	3e−01	1 / 24	VAQUERIZAS_Pituitary_TF
15	3e−01	1 / 25	VAQUERIZAS_Adrenal cortex_TF

Telomeres

Rank	p−value	#in/all	Geneset
1	0.4	1 / 27	Nabetani_alt len telomeres_genes_ko
2	1.0	0 / 13	Alternative lengthening of telomeres
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	9e−04	96 / 4468	ICGC_Egr1_targets
2	2e−02	2 / 12	MYC_Protein synthesis degradation UP
3	2e−02	129 / 6868	ICGC_Elf1_targets
4	2e−02	35 / 1501	ICGC_Usf1_targets
5	2e−02	48 / 2215	ICGC_GabpPcr2_targets
6	3e−02	19 / 733	ICGC_Atf3_targets
7	3e−02	45 / 2133	ICGC_Mef2_targets
8	3e−02	33 / 1478	ICGC_Myc_targets
9	3e−02	47 / 2255	ICGC_SrfV0416101_targets
10	4e−02	33 / 1498	ICGC_Ets1_targets
11	4e−02	102 / 5466	ICGC_Nficsc81335_targets
12	4e−02	83 / 4345	ICGC_Zeb1_targets
13	4e−02	115 / 6267	ICGC_Yy1_targets
14	4e−02	120 / 6578	ICGC_Pou2_targets
15	5e−02	68 / 3507	ICGC_Rad21_targets

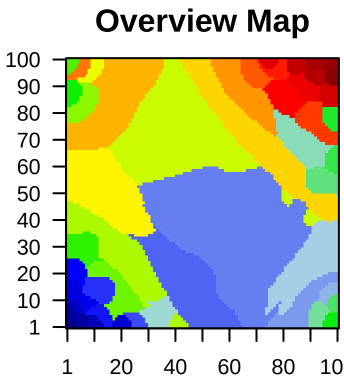
K−Means Cluster

Spot Summary: K1

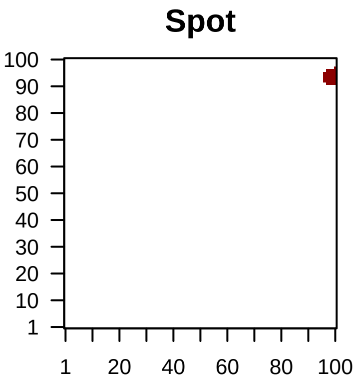
metagenes = 29
genes = 596

<r> metagenes = 0.98
<r> genes = 0.53
beta: r2= 53.43 / log p= −Inf

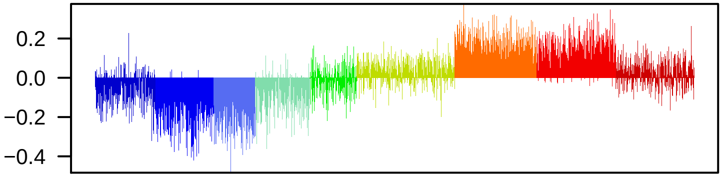
samples with spot = 694 (20.5 %)
- A * : 2 (0.6 %)
- A F * : 2 (0.6 %)
- C F * : 8 (3 %)
- F * : 42 (7.6 %)
- F J * : 347 (74.9 %)
- J * : 254 (56.8 %)
- N * : 39 (8.8 %)



Overview Map



Spot

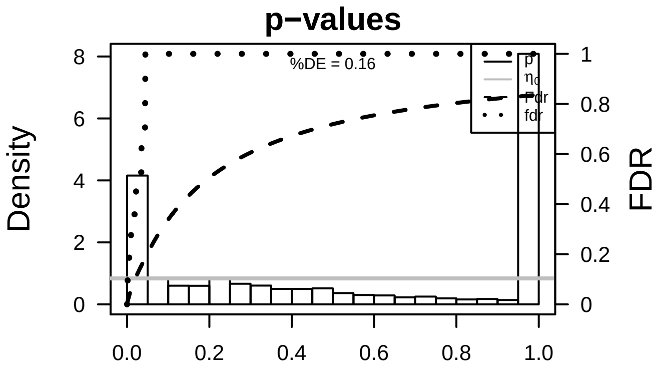


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_181589	1.69	−2.79	0.18		
2	ILMN_175259	1.47	−1.51	0.42		
3	ILMN_238175	1.25	−1.46	0.39	G3BP2	G3BP stress granule assembly factor 2 [Source:HGNC Symb
4	ILMN_171726	1.21	−1.06	0.34		
5	ILMN_170123	1.12	−0.93	0.39	SH2D1B	SH2 domain containing 1B [Source:HGNC Symbol;Acc:HGN
6	ILMN_207328	1.1	−0.98	0.57	MTSS1	metastasis suppressor 1 [Source:HGNC Symbol;Acc:HGNC:
7	ILMN_209334	1.09	−0.92	0.66	PLAC8	placenta specific 8 [Source:HGNC Symbol;Acc:HGNC:19254
8	ILMN_172042	1.05	−0.98	0.41	G3BP2	G3BP stress granule assembly factor 2 [Source:HGNC Symb
9	ILMN_177221	1.05	−1	0.61	HLA−DPA1	major histocompatibility complex, class II, DP alpha 1 [Source
10	ILMN_322868	1.04	−0.87	0.53	HLA−DRB1	major histocompatibility complex, class II, DR beta 1 [Source:
11	ILMN_176641	1.03	−0.96	0.72	AP1S2	adaptor related protein complex 1 sigma 2 subunit [Source:H
12	ILMN_165493	1.03	−1.25	0.75	TMED2	transmembrane p24 trafficking protein 2 [Source:HGNC Sym
13	ILMN_174907	0.99	−0.68	0.44	HLA−DPB1	major histocompatibility complex, class II, DP beta 1 [Source:
14	ILMN_173656	0.96	−1.09	0.51	CD74	CD74 molecule [Source:HGNC Symbol;Acc:HGNC:1697]
15	ILMN_171806	0.96	−0.89	0.59	LIPA	lipase A, lysosomal acid type [Source:HGNC Symbol;Acc:HG
16	ILMN_179338	0.93	−1.32	0.74	JAK1	Janus kinase 1 [Source:HGNC Symbol;Acc:HGNC:6190]
17	ILMN_166401	0.93	−0.82	0.79	ELF1	E74 like ETS transcription factor 1 [Source:HGNC Symbol;Ac
18	ILMN_167740	0.92	−0.9	0.64	RAP2A	RAP2A, member of RAS oncogene family [Source:HGNC Sy
19	ILMN_168965	0.92	−1	0.65	HLA−DRA	major histocompatibility complex, class II, DR alpha [Source:
20	ILMN_165302	0.91	−0.71	0.58	PLAC8	placenta specific 8 [Source:HGNC Symbol;Acc:HGNC:19254

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	1e−99	388 / 7275	Lymp	HOPP_Txn_elongation
2	4e−92	324 / 5356	Lymp	HOPP_Txn_transition
3	8e−87	414 / 9555	Colon	TssA_Colon
4	4e−84	384 / 8226	Lymp	HOPP_Active_promoter
5	5e−84	401 / 9054	Colon	Tx_Colon
6	9e−83	328 / 5936	Brain	Overlap_fetal_midbrain_HetRpts
7	3e−82	389 / 8568	Colon	TxWk_Colon
8	3e−81	392 / 8771	Chror	5_Tx_Melanocytes
9	2e−77	408 / 9815	Brain	Overlap_fetal_midbrain_ReprPC
10	8e−72	378 / 8678	Colon	Quies3_Colon
11	9e−70	428 / 11455	Chror	2_TssA_Fibroblasts
12	1e−69	357 / 7854	Chror	5_Tx_Fibroblasts
13	1e−65	437 / 12298	Chror	2_TssA_Melanocytes
14	6e−64	142 / 1265	GSEA	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
15	4e−63	327 / 6970	Chror	5_Tx_Neuronal_Progenitor
16	1e−62	411 / 10999	Colon	TssWk_Colon
17	9e−62	443 / 12983	Chror	2_TssA_Neuronal_Progenitor
18	1e−61	164 / 1797	GSEA	PILON_KLF1_TARGETS_DN
19	8e−57	147 / 1547	Colon	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP
20	1e−54	360 / 8990	Chror	15_Quies_Fibroblasts
21	8e−49	370 / 9917	Brain	Overlap_fetal_midbrain_ReprPCWk
22	2e−48	361 / 9504	Brain	Overlap_fetal_midbrain_K9K27me3
23	2e−46	327 / 8098	Lymp	HOPP_Weak_promoter
24	3e−43	371 / 10430	Brain	Overlap_fetal_midbrain_Quies
25	4e−41	121 / 1417	GSEA	PUJANA_BRCA1_PCC_NETWORK
26	5e−40	66 / 388	GSEA	SHEN_SMARCA2_TARGETS_UP
27	4e−39	401 / 12393	Chror	15_Quies_Neuronal_Progenitor
28	6e−37	387 / 11836	Chror	3_TssF_Melanocytes
29	5e−36	100 / 1098	GSEA	BLALOCK_ALZHEIMERS_DISEASE_DN
30	2e−35	401 / 12741	Chror	7_Enh_Melanocytes
31	1e−34	86 / 841	GSEA	ACEVEDO_LIVER_CANCER_UP
32	5e−33	366 / 11130	Chror	15_Quies_Melanocytes
33	1e−32	317 / 8818	MF	protein binding
34	3e−32	65 / 498	GSEA	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR_UP
35	7e−31	51 / 302	Refer	Chaussabel_3,4_Protein phosphatases
36	1e−30	89 / 1013	MF	poly(A) RNA binding
37	2e−30	61 / 463	miRN	hsa−miR−301a
38	4e−30	280 / 7448	Lymp	HOPP_Strong_enhancer
39	2e−29	71 / 669	GSEA	PUJANA_CHEK2_PCC_NETWORK
40	2e−28	233 / 5699	Chror	6_EnhG_Melanocytes



p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.7	2 / 111	HORVATH_aging_genes meth DOWN
2	1.0	1 / 142	HORVATH_aging_genes meth UP
3	1.0	0 / 58	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	1e−09	24 / 255	viral process
2	1e−08	17 / 145	mRNA processing
3	3e−08	22 / 254	cell−cell adhesion
4	3e−07	15 / 139	RNA splicing
5	5e−07	14 / 126	T cell receptor signaling pathway
6	3e−06	5 / 12	negative regulation of DNA damage response, signal transduction by p53 clas
7	3e−06	11 / 90	regulation of mRNA stability
8	1e−05	15 / 189	intracellular protein transport
9	2e−05	9 / 71	response to endoplasmic reticulum stress
10	2e−05	15 / 196	mRNA splicing, via spliceosome
11	4e−05	6 / 31	regulation of alternative mRNA splicing, via spliceosome
12	5e−05	5 / 20	negative regulation of mRNA splicing, via spliceosome
13	8e−05	18 / 300	cell division
14	1e−04	9 / 91	sister chromatid cohesion
15	2e−04	11 / 137	ER to Golgi vesicle−mediated transport

Brain

Rank	p−value	#in/all	Geneset
1	9e−83	328 / 5936	Overlap_fetal_midbrain_HetRpts
2	2e−77	408 / 9815	Overlap_fetal_midbrain_ReprPC
3	8e−49	370 / 9917	Overlap_fetal_midbrain_ReprPCWk
4	2e−48	361 / 9504	Overlap_fetal_midbrain_K9K27me3
5	3e−43	371 / 10430	Overlap_fetal_midbrain_Quies
6	1e−09	46 / 796	Overlap_fetal_midbrain_ZNF
7	5e−05	46 / 1171	Fetal_EnhP
8	9e−05	19 / 328	Fetal_Het
9	3e−04	20 / 386	Fetal_ZNF
10	6e−04	42 / 1162	Fetal_Enh
11	1e−03	35 / 937	Fetal_EnhG
12	2e−02	9 / 180	Overlap_fetal_midbrain_Het
13	2e−02	42 / 1436	Fetal_K9K27me3
14	6e−02	80 / 3164	Mid_Frontal_Lobe_ZNF
15	8e−02	26 / 906	Fetal_HetRpts

Cancer

Rank	p−value	#in/all	Geneset
1	1e−05	3 / 13	RHODES_CANCER_META_SIGNATURE
2	2e−03	11 / 178	SPANG_LPS−index2
3	2e−03	3 / 13	GENTLES_modul12
4	4e−03	3 / 16	GENTLES_modul14
5	5e−03	14 / 301	SPANG_BCL6−index2
6	1e−02	7 / 117	PanCan_Driver_Gene_geneset_nanostring
7	4e−02	2 / 15	WOLFER_overlap genes
8	4e−02	2 / 16	GENTLES_modul11
9	4e−02	2 / 16	GENTLES_modul16
10	5e−02	0 / 14	LIU_COMMON_CANCER_GENES
11	7e−02	4 / 73	SHAUGHNESSY_MM high risk
12	2e−01	1 / 9	GENTLES_modul3
13	2e−01	1 / 12	LIU_BREAST_CANCER
14	2e−01	1 / 13	WANG_ER_DN
15	2e−01	1 / 13	GENTLES_modul2

CC

Rank	p−value	#in/all	Geneset
1	3e−22	112 / 1979	membrane
2	7e−22	195 / 4822	cytoplasm
3	2e−17	184 / 4828	nucleus
4	7e−16	116 / 2535	nucleoplasm
5	1e−14	126 / 2979	cytosol
6	3e−11	102 / 2464	extracellular exosome
7	4e−09	42 / 721	nucleolus
8	5e−09	25 / 295	cell−cell adherens junction
9	4e−08	42 / 777	Golgi apparatus
10	2e−06	12 / 101	intracellular ribonucleoprotein complex
11	2e−06	8 / 41	ER to Golgi transport vesicle membrane
12	2e−06	23 / 352	focal adhesion
13	4e−06	6 / 21	integral component of lumenal side of endoplasmic reticulum membrane
14	5e−06	37 / 775	endoplasmic reticulum
15	5e−06	5 / 13	MHC class II protein complex

Chr

Rank	p−value	#in/all	Geneset
1	0.02	37 / 1217	Chr 3
2	0.02	33 / 1060	Chr 5
3	0.04	24 / 768	Chr 14
4	0.06	12 / 342	Chr 18
5	0.07	14 / 422	Chr 13
6	0.09	59 / 2323	Chr 1
7	0.15	24 / 902	Chr 4
8	0.21	29 / 1160	Chr 12
9	0.22	30 / 1211	Chr 6
10	0.30	35 / 1492	Chr 2
11	0.33	20 / 836	Chr 8
12	0.42	7 / 289	Chr 21
13	0.45	22 / 994	Chr X
14	0.46	20 / 904	Chr 10
15	0.57	16 / 769	Chr 15

Chromatin states

Rank	p−value	#in/all	Geneset
1	3e−81	392 / 8771	5_Tx_Melanocytes
2	9e−70	428 / 11455	2_TssA_Fibroblasts
3	1e−69	357 / 7854	5_Tx_Fibroblasts
4	1e−65	437 / 12298	2_TssA_Melanocytes
5	4e−63	327 / 6970	5_Tx_Neuronal_Progenitor
6	9e−62	443 / 12983	2_TssA_Neuronal_Progenitor
7	1e−54	360 / 8990	15_Quies_Fibroblasts
8	4e−39	401 / 12393	15_Quies_Neuronal_Progenitor
9	6e−37	387 / 11836	3_TssF_Melanocytes
10	2e−35	401 / 12741	7_Enh_Melanocytes
11	5e−33	366 / 11130	15_Quies_Melanocytes
12	2e−28	233 / 5699	6_EnhG_Melanocytes
13	9e−24	292 / 8613	7_Enh_Fibroblasts
14	1e−10	275 / 9635	3_TssF_Fibroblasts
15	2e−09	144 / 4237	14_ZNF_Neuronal_Progenitor

Colon Cancer

Rank	p−value	#in/all	Geneset
1	8e−87	414 / 9555	TssA_Colon
2	5e−84	401 / 9054	Tx_Colon
3	3e−82	389 / 8568	TxWk_Colon
4	8e−72	378 / 8678	Quies3_Colon
5	1e−62	411 / 10999	TssWk_Colon
6	8e−57	147 / 1547	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
7	2e−15	101 / 2073	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
8	3e−12	66 / 1216	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_
9	7e−12	60 / 1069	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
10	7e−12	228 / 7354	TssF_Colon
11	2e−11	302 / 10779	Enh_Colon
12	5e−11	144 / 4034	TssD1_Colon
13	2e−08	65 / 1468	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
14	5e−08	58 / 1281	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv
15	1e−07	165 / 5373	EnhWk1_Colon

Glio

Rank	p−value	#in/all	Geneset
1	4e−17	95 / 1777	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
2	6e−16	101 / 2043	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
3	9e−15	34 / 316	WILLSCHER_GBM_Verhaak−PNwt & CL_up
4	3e−13	32 / 315	Up
5	2e−05	37 / 820	Sturm_GBM_Meth_overexpression_E_G34_UP
6	5e−05	10 / 98	WILLSCHER_GBM_proteomics_wtOnly_SpotB
7	7e−05	8 / 65	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
8	1e−04	12 / 157	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
9	6e−03	4 / 35	Colman_survival_associated
10	1e−02	2 / 9	WILLSCHER_GBM_LTSmut_proteomics−A_UP
11	2e−02	4 / 48	Vishal_subnetwork signature of survival in GBM
12	3e−02	4 / 55	Stuehler_Proteins_up_in_STS
13	3e−02	3 / 32	WILLSCHER_GBM_proteomics_wtOnly_SpotC
14	4e−02	2 / 15	WILLSCHER_GBM_STSwt_proteomics−O_UP
15	6e−02	4 / 69	WILLSCHER_GBM_Verhaak−PNwt & MES_up

GSEA C2

Rank	p−value	#in/all	Geneset
1	6e−64	142 / 1265	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
2	1e−61	164 / 1797	PILON_KLF1_TARGETS_DN
3	4e−41	121 / 1417	PUJANA_BRCA1_PCC_NETWORK
4	5e−40	66 / 388	SHEN_SMARCA2_TARGETS_UP
5	5e−36	100 / 1098	BLALOCK_ALZHEIMERS_DISEASE_DN
6	1e−34	86 / 841	ACEVEDO_LIVER_CANCER_UP
7	3e−32	65 / 498	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR_UP
8	2e−29	71 / 669	PUJANA_CHEK2_PCC_NETWORK
9	6e−27	57 / 465	MILI_PSEUDOPODIA_HAPTOTAXIS_UP
10	4e−25	63 / 622	SCHLOSSER_SERUM_RESPONSE_DN
11	7e−25	49 / 368	OSMAN_BLADDER_CANCER_UP
12	1e−22	68 / 800	JOHNSTONE_PARVB_TARGETS_3_DN
13	1e−22	83 / 1161	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
14	2e−22	65 / 737	ACEVEDO_LIVER_TUMOR_VS_NORMAL_ADJACENT_TISSUE_UP
15	5e−22	50 / 445	ENK_UV_RESPONSE_KERATINOCYTE_DN

HM

Rank	p−value	#in/all	Geneset
1	3e−20	31 / 170	HALLMARK_MYC_TARGETS_V1
2	2e−08	19 / 185	HALLMARK_MTORC1_SIGNALING
3	2e−05	10 / 87	HALLMARK_PROTEIN_SECRETION
4	1e−04	13 / 179	HALLMARK_G2M_CHECKPOINT
5	3e−04	12 / 167	HALLMARK_OXIDATIVE_PHOSPHORYLATION
6	3e−03	9 / 138	HALLMARK_FATTY_ACID_METABOLISM
7	1e−02	9 / 173	HALLMARK_E2F_TARGETS
8	1e−02	9 / 176	HALLMARK_ADIPOGENESIS
9	2e−02	9 / 183	HALLMARK_GLYCOLYSIS
10	2e−02	4 / 50	HALLMARK_TGF_BETA_SIGNALING
11	2e−02	6 / 103	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
12	2e−02	7 / 132	HALLMARK_UV_RESPONSE_DN
13	4e−02	3 / 37	HALLMARK_PANCREAS_BETA_CELLS
14	4e−02	5 / 91	HALLMARK_PEROXISOME
15	5e−02	8 / 186	HALLMARK_ESTROGEN_RESPONSE_LATE

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.006	11 / 211	Homuth_BMI−associated−genes_DN
2	0.044	2 / 16	Huan_blood−pressure_DBP−signature
3	0.102	1 / 5	DUMEAUX_Estrogen related in smokers literature genes up
4	0.487	1 / 31	DUMEAUX_Fasting enriched genes
5	0.608	3 / 147	Homuth_BMI−associated−genes_UP
6	1.000	0 / 94	DUMEAUX_Smoking enriched genes
7	1.000	0 / 10	DUMEAUX_Smoking literature genes up
8	1.000	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
9	1.000	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
10	1.000	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
11	1.000	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
12	1.000	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
13	1.000	0 / 10	DUMEAUX_Women normal BMI literature genes up
14	1.000	0 / 17	DUMEAUX_High bmi enriched genes
15	1.000	0 / 18	Huan_blood−pressure_SBP−signature

Lymphoma

Rank	p−value	#in/all	Geneset
1	1e−99	388 / 7275	HOPP_Txn_elongation
2	4e−92	324 / 5356	HOPP_Txn_transition
3	4e−84	384 / 8226	HOPP_Active_promoter
4	2e−46	327 / 8098	HOPP_Weak_promoter
5	4e−30	280 / 7448	HOPP_Strong_enhancer
6	8e−19	231 / 6559	HOPP_Weak_txn
7	2e−16	234 / 6959	HOPP_Weak_enhancer
8	2e−09	58 / 1169	SPANG_BCR DN
9	7e−05	9 / 84	ROSOLOWSKI_green UP
10	2e−04	47 / 1270	SPANG_BCR UP
11	2e−04	10 / 115	ROSOLOWSKI_green total
12	2e−04	84 / 2701	HOPP_Repetitive
13	4e−04	23 / 493	WIRTH_lymphoma937_spot J
14	5e−04	22 / 472	Hopp_June14_MMML937 tumors+controls_group.overexpression_J_GC−B−c
15	2e−03	20 / 455	SPANG_CD40 6hrs DN

Melanoma

Rank	p−value	#in/all	Geneset
1	0.2	2 / 43	Hugo_melanoma−BRAFmut−MET_UP
2	1.0	0 / 30	Hugo_melanoma−all−MET_UP
3	1.0	0 / 54	Hugo_melanoma−all−MET_DN
4	1.0	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
5	1.0	0 / 27	Hugo_melanoma−all−LEF1_UP
6	1.0	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

MF

Rank	p−value	#in/all	Geneset
1	1e−32	317 / 8818	protein binding
2	1e−30	89 / 1013	poly(A) RNA binding
3	6e−10	25 / 265	cadherin binding involved in cell−cell adhesion
4	4e−08	28 / 399	RNA binding
5	5e−05	8 / 63	protein transporter activity
6	7e−05	7 / 48	SH3/SH2 adaptor activity
7	1e−04	17 / 283	nucleotide binding
8	1e−04	27 / 580	identical protein binding
9	2e−04	4 / 14	MHC class II protein complex binding
10	2e−04	6 / 40	mRNA 3'−UTR binding
11	2e−04	6 / 40	receptor tyrosine kinase binding
12	4e−04	5 / 30	insulin receptor binding
13	4e−04	17 / 311	enzyme binding
14	5e−04	4 / 18	TBP−class protein binding
15	6e−04	18 / 351	GTP binding

miRNA Disease

Rank	p−value	#in/all	Geneset
1	1	0 / 7	Thyroid carcinoma, papillary
2	1	0 / 123	Pancreatic cancer
3	1	0 / 68	Glioblastoma multiforme, somatic
4	1	0 / 63	Gastrointestinal
5	1	0 / 3	Pituitary adenoma
6	1	0 / 116	Cancer
7	1	0 / 95	Colorectal cancer
8	1	0 / 2	Adenomas, multiple colorectal
9	1	0 / 124	Prostate cancer
10	1	0 / 48	Alzheimer disease, susceptibility to
11	1	0 / 7	Schizophrenia, susceptibility to
12	1	0 / 20	Parkinson disease
13	1	0 / 65	Hepatocellular carcinoma
14	1	0 / 3	Down syndrome, risk of
15	1	0 / 127	Melanoma and neural system tumor syndrome

miRNA target

Rank	p−value	#in/all	Geneset
1	2e−30	61 / 463	hsa−miR−301a
2	7e−28	56 / 429	hsa−miR−548n
3	8e−24	46 / 338	hsa−miR−548d−5p
4	3e−23	43 / 299	hsa−miR−548c−3p
5	3e−23	52 / 455	hsa−miR−130a
6	7e−23	45 / 338	hsa−miR−548b−5p
7	1e−22	48 / 394	hsa−miR−301b
8	1e−21	41 / 295	hsa−miR−561
9	1e−21	38 / 250	hsa−miR−548l
10	4e−21	42 / 321	hsa−miR−590−3p
11	5e−21	49 / 449	hsa−miR−130b
12	6e−21	33 / 187	hsa−miR−586
13	8e−21	51 / 493	hsa−miR−103
14	2e−20	47 / 425	hsa−let−7b
15	4e−20	50 / 491	hsa−miR−107

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.03	2 / 14	BENTINK_ras.6
2	0.21	1 / 11	BENTINK_ras.4
3	0.23	1 / 12	BENTINK_src.2
4	0.24	1 / 13	BENTINK_e2f3.1
5	0.24	1 / 13	BENTINK_e2f3.2
6	1.00	0 / 14	GUSTAFSON_PI3K_UP
7	1.00	0 / 15	GUSTAFSON_PI3K_DN
8	1.00	0 / 13	BENTINK_myc.1
9	1.00	0 / 12	BENTINK_ras.1
10	1.00	0 / 13	BENTINK_src.10
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Reference Signatures

Rank	p−value	#in/all	Geneset
1	7e−31	51 / 302	Chaussabel_3,4_Protein phosphatases
2	5e−25	41 / 242	Chaussabel_3,9_Kinases
3	3e−23	80 / 1063	PROTEINATLAS_tonsil
4	3e−22	64 / 724	PROTEINATLAS_lymph node
5	2e−21	84 / 1239	PROTEINATLAS_testis
6	3e−19	65 / 850	PROTEINATLAS_skin
7	7e−19	69 / 963	PROTEINATLAS_pancreas
8	2e−18	60 / 759	PROTEINATLAS_epididymis
9	9e−18	67 / 960	PROTEINATLAS_cerebellum
10	1e−17	65 / 912	PROTEINATLAS_urinary bladder
11	2e−17	27 / 153	Chaussabel_2,9_Cytosceleton
12	3e−17	75 / 1194	PROTEINATLAS_stomach
13	3e−17	65 / 933	PROTEINATLAS_adrenal gland
14	4e−17	74 / 1173	PROTEINATLAS_rectum
15	4e−17	64 / 912	PROTEINATLAS_fallopian tube

Telomeres

Rank	p−value	#in/all	Geneset
1	1	0 / 13	Alternative lengthening of telomeres
2	1	0 / 27	Nabetani_alt len telomeres_genes_ko
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	2e−19	98 / 1723	HEBENSTREIT_high expression TF
2	2e−17	190 / 5067	ICGC_Taf1_targets
3	2e−13	188 / 5466	ICGC_Nficsc81335_targets
4	2e−12	157 / 4362	ICGC_Creb1_targets
5	5e−12	169 / 4881	ICGC_Atf2_targets
6	5e−12	169 / 4890	ICGC_Bclaf101388_targets
7	8e−12	184 / 5518	ICGC_Stat5_targets
8	1e−11	74 / 1498	ICGC_Ets1_targets
9	1e−11	181 / 5410	ICGC_Foxm1_targets
10	2e−11	181 / 5442	ICGC_Pmlsc71910_targets
11	1e−10	63 / 1231	KIM_MYC targets
12	4e−10	173 / 5312	ICGC_Tcf12_targets
13	1e−09	90 / 2215	ICGC_GabpPcr2_targets
14	2e−09	172 / 5383	ICGC_Sp1_targets
15	4e−09	192 / 6267	ICGC_Yy1_targets

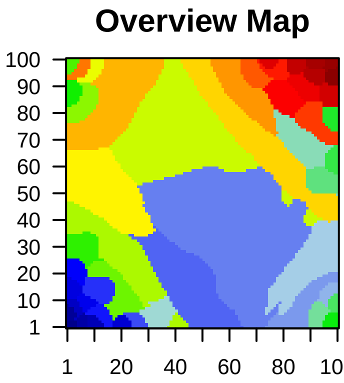
K−Means Cluster

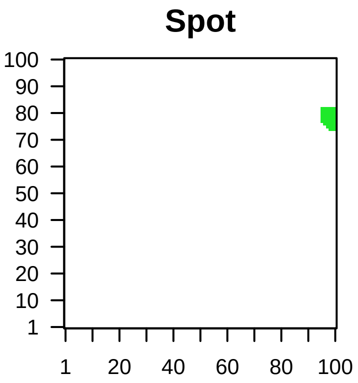
Spot Summary: L1

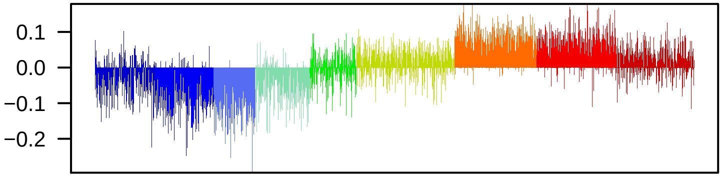
metagenes = 48
genes = 670

<r> metagenes = 0.96
<r> genes = 0.36
beta: r2= 12.43 / log p= −Inf

samples with spot = 85 (2.5 %)
F J * : 52 (11.2 %)
J * : 32 (7.2 %)
N * : 1 (0.2 %)


Overview Map


Spot

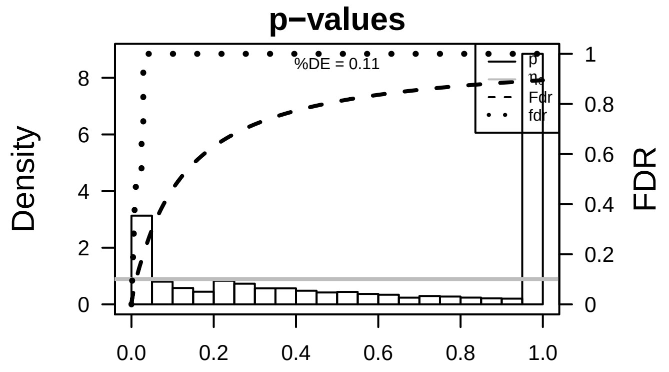


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_176146	0.96	−0.79	0.49	CD74	CD74 molecule [Source:HGNC Symbol;Acc:HGNC:1697]
2	ILMN_166860	0.89	−0.76	0.41		
3	ILMN_178617	0.85	−0.97	0.43	CD37	CD37 molecule [Source:HGNC Symbol;Acc:HGNC:1666]
4	ILMN_165798	0.82	−0.55	0.51	TERF2IP	TERF2 interacting protein [Source:HGNC Symbol;Acc:HGNC
5	ILMN_174216	0.79	−0.89	0.63	TUBA1B	tubulin alpha 1b [Source:HGNC Symbol;Acc:HGNC:18809]
6	ILMN_232088	0.78	−0.79	0.49	CXCR4	C−X−C motif chemokine receptor 4 [Source:HGNC Symbol;A
7	ILMN_178181	0.76	−0.72	0.35	PAPSS1	3'−phosphoadenosine 5'−phosphosulfate synthase 1 [Source
8	ILMN_228556	0.76	−0.7	0.41		
9	ILMN_177801	0.75	−0.6	0.31	PDPR	pyruvate dehydrogenase phosphatase regulatory subunit [So
10	ILMN_235945	0.72	−0.67	0.34	ERGIC3	ERGIC and golgi 3 [Source:HGNC Symbol;Acc:HGNC:15927
11	ILMN_173185	0.71	−0.59	0.55		
12	ILMN_177279	0.7	−0.49	0.58	ARPP19	cAMP regulated phosphoprotein 19 [Source:HGNC Symbol;A
13	ILMN_165611	0.68	−0.67	0.4	MYLIP	myosin regulatory light chain interacting protein [Source:HGN
14	ILMN_324439	0.68	−0.68	0.58		
15	ILMN_169579	0.67	−0.52	0.48	CUL4A	cullin 4A [Source:HGNC Symbol;Acc:HGNC:2554]
16	ILMN_170684	0.66	−0.72	0.59	PGAM4	phosphoglycerate mutase family member 4 [Source:HGNC S
17	ILMN_225118	0.65	−0.74	0.72	ERP29	endoplasmic reticulum protein 29 [Source:HGNC Symbol;Acc
18	ILMN_165588	0.64	−0.59	0.71	ATP2A2	ATPase sarcoplasmic/endoplasmic reticulum Ca2+ transporti
19	ILMN_237416	0.64	−0.6	0.69		
20	ILMN_177602	0.64	−0.65	0.67	EIF4H	eukaryotic translation initiation factor 4H [Source:HGNC Syml

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	2e−87	382 / 7275	Lympl	HOPP_Txn_elongation
2	1e−77	400 / 8568	Colon	TxWk_Colon
3	2e−75	331 / 5936	Brain	Overlap_fetal_midbrain_HetRpts
4	7e−75	407 / 9054	Colon	Tx_Colon
5	1e−72	420 / 9815	Brain	Overlap_fetal_midbrain_ReprPC
6	4e−69	410 / 9555	Colon	TssA_Colon
7	2e−67	303 / 5356	Lympl	HOPP_Txn_transition
8	2e−65	375 / 8226	Lympl	HOPP_Active_promoter
9	2e−64	386 / 8771	Chror	5_Tx_Melanocytes
10	1e−63	383 / 8678	Colon	Quies3_Colon
11	5e−62	339 / 6970	Chror	5_Tx_Neuronal_Progenitor
12	6e−62	361 / 7854	Chror	5_Tx_Fibroblasts
13	6e−61	452 / 12298	Chror	2_TssA_Melanocytes
14	3e−54	427 / 11455	Chror	2_TssA_Fibroblasts
15	1e−48	447 / 12983	Chror	2_TssA_Neuronal_Progenitor
16	8e−45	403 / 10999	Colon	TssWk_Colon
17	2e−41	374 / 9917	Brain	Overlap_fetal_midbrain_ReprPCWk
18	6e−41	364 / 9504	Brain	Overlap_fetal_midbrain_K9K27me3
19	1e−37	346 / 8990	Chror	15_Quies_Fibroblasts
20	7e−37	112 / 1265	GSEA	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
21	6e−33	315 / 8098	Lympl	HOPP_Weak_promoter
22	4e−32	127 / 1797	GSEA	PILON_KLF1_TARGETS_DN
23	2e−31	395 / 11836	Chror	3_TssF_Melanocytes
24	2e−31	406 / 12393	Chror	15_Quies_Neuronal_Progenitor
25	8e−31	364 / 10430	Brain	Overlap_fetal_midbrain_Quies
26	7e−29	56 / 388	GSEA	SHEN_SMARCA2_TARGETS_UP
27	2e−28	407 / 12741	Chror	7_Enh_Melanocytes
28	3e−27	371 / 11130	Chror	15_Quies_Melanocytes
29	4e−27	44 / 242	Refer	Chaussabel_3,9_Kinases
30	9e−27	48 / 302	Refer	Chaussabel_3,4_Protein phosphatases
31	4e−25	141 / 2535	CC	nucleoplasm
32	4e−23	102 / 1547	Colon	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP
33	1e−22	212 / 5067	TF	ICGC_Taf1_targets
34	4e−22	228 / 5699	Chror	6_EnhG_Melanocytes
35	1e−21	305 / 8818	MF	protein binding
36	3e−21	299 / 8613	Chror	7_Enh_Fibroblasts
37	4e−21	67 / 783	GSEA	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
38	7e−20	91 / 1417	GSEA	PUJANA_BRCA1_PCC_NETWORK
39	3e−19	80 / 1161	GSEA	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
40	4e−19	265 / 7448	Lympl	HOPP_Strong_enhancer


p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.5	3 / 111	HORVATH_aging_genes meth DOWN
2	0.8	2 / 142	HORVATH_aging_genes meth UP
3	1.0	0 / 58	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	5e−07	15 / 137	ER to Golgi vesicle−mediated transport
2	4e−06	11 / 86	mRNA export from nucleus
3	8e−06	22 / 335	protein transport
4	1e−05	53 / 1272	regulation of transcription, DNA−templated
5	3e−05	15 / 189	intracellular protein transport
6	4e−05	6 / 29	tRNA export from nucleus
7	5e−05	62 / 1643	transcription, DNA−templated
8	6e−05	11 / 115	regulation of signal transduction by p53 class mediator
9	7e−05	4 / 11	regulation of mRNA splicing, via spliceosome
10	2e−04	6 / 37	DNA duplex unwinding
11	2e−04	18 / 300	cell division
12	2e−04	5 / 25	tricarboxylic acid cycle
13	2e−04	6 / 39	mitotic nuclear envelope disassembly
14	2e−04	16 / 255	viral process
15	2e−04	13 / 181	proteasome−mediated ubiquitin−dependent protein catabolic process

Brain

Rank	p−value	#in/all	Geneset
1	2e−75	331 / 5936	Overlap_fetal_midbrain_HetRpts
2	1e−72	420 / 9815	Overlap_fetal_midbrain_ReprPC
3	2e−41	374 / 9917	Overlap_fetal_midbrain_ReprPCWk
4	6e−41	364 / 9504	Overlap_fetal_midbrain_K9K27me3
5	8e−31	364 / 10430	Overlap_fetal_midbrain_Quies
6	2e−08	58 / 1171	Fetal_EnhP
7	5e−06	108 / 3164	Mid_Frontal_Lobe_ZNF
8	5e−06	39 / 796	Overlap_fetal_midbrain_ZNF
9	6e−05	20 / 328	Fetal_Het
10	8e−05	32 / 681	Overlap_fetal_midbrain_EnhP
11	2e−03	50 / 1436	Fetal_K9K27me3
12	3e−02	15 / 386	Fetal_ZNF
13	3e−02	36 / 1162	Fetal_Enh
14	3e−02	30 / 937	Fetal_EnhG
15	5e−02	8 / 180	Overlap_fetal_midbrain_Het

Cancer

Rank	p−value	#in/all	Geneset
1	0.004	3 / 15	WOLFER_overlap genes
2	0.005	8 / 117	PanCan_Driver_Gene_geneset_nanostring
3	0.006	0 / 13	RHODES_CANCER_META_SIGNATURE
4	0.020	9 / 178	SPANG_LPS−index2
5	0.047	3 / 36	PanCan_HK_geneset_nanostring
6	0.064	6 / 125	PanCan_CC+Apop_geneset_nanostring
7	0.082	4 / 73	SHAUGHNESSY_MM high risk
8	0.085	3 / 46	PanCan_DNARepair_geneset_nanostring
9	0.087	1 / 12	LIU_BREAST_CANCER
10	0.185	1 / 9	GENTLES_modul3
11	0.185	1 / 9	GENTLES_modul5
12	0.245	3 / 76	PanCan_Wnt_geneset_nanostring
13	0.256	1 / 13	GENTLES_modul2
14	0.256	1 / 13	GENTLES_modul6
15	0.256	1 / 13	GENTLES_modul18

CC

Rank	p−value	#in/all	Geneset
1	4e−25	141 / 2535	nucleoplasm
2	5e−15	185 / 4828	nucleus
3	2e−11	92 / 1979	membrane
4	1e−10	170 / 4822	cytoplasm
5	3e−09	44 / 721	nucleolus
6	8e−08	110 / 2979	cytosol
7	7e−06	9 / 60	nuclear pore
8	3e−05	10 / 88	peroxisome
9	6e−05	14 / 179	nuclear speck
10	1e−04	7 / 51	peroxisomal membrane
11	2e−04	34 / 777	Golgi apparatus
12	2e−04	27 / 561	intracellular membrane−bounded organelle
13	2e−04	6 / 39	chromosome, telomeric region
14	2e−04	34 / 788	endoplasmic reticulum membrane
15	3e−04	26 / 539	Golgi membrane

Chr

Rank	p−value	#in/all	Geneset
1	0.001	44 / 1217	Chr 3
2	0.038	33 / 1060	Chr 5
3	0.043	25 / 768	Chr 14
4	0.047	13 / 342	Chr 18
5	0.103	23 / 769	Chr 15
6	0.109	33 / 1170	Chr 7
7	0.159	13 / 422	Chr 13
8	0.185	31 / 1160	Chr 12
9	0.236	38 / 1492	Chr 2
10	0.385	22 / 904	Chr 10
11	0.423	20 / 836	Chr 8
12	0.531	14 / 619	Chr 20
13	0.650	19 / 902	Chr 4
14	0.708	49 / 2323	Chr 1
15	0.741	19 / 954	Chr 9

Chromatin states

Rank	p−value	#in/all	Geneset
1	2e−64	386 / 8771	5_Tx_Melanocytes
2	5e−62	339 / 6970	5_Tx_Neuronal_Progenitor
3	6e−62	361 / 7854	5_Tx_Fibroblasts
4	6e−61	452 / 12298	2_TssA_Melanocytes
5	3e−54	427 / 11455	2_TssA_Fibroblasts
6	1e−48	447 / 12983	2_TssA_Neuronal_Progenitor
7	1e−37	346 / 8990	15_Quies_Fibroblasts
8	2e−31	395 / 11836	3_TssF_Melanocytes
9	2e−31	406 / 12393	15_Quies_Neuronal_Progenitor
10	2e−28	407 / 12741	7_Enh_Melanocytes
11	3e−27	371 / 11130	15_Quies_Melanocytes
12	4e−22	228 / 5699	6_EnhG_Melanocytes
13	3e−21	299 / 8613	7_Enh_Fibroblasts
14	3e−17	175 / 4237	14_ZNF_Neuronal_Progenitor
15	8e−11	339 / 11847	7_Enh_Neuronal_Progenitor

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−77	400 / 8568	TxWk_Colon
2	7e−75	407 / 9054	Tx_Colon
3	4e−69	410 / 9555	TssA_Colon
4	1e−63	383 / 8678	Quies3_Colon
5	8e−45	403 / 10999	TssWk_Colon
6	4e−23	102 / 1547	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
7	1e−15	252 / 7354	TssF_Colon
8	2e−14	82 / 1468	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
9	2e−11	95 / 2073	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_tı
10	4e−09	56 / 1069	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
11	6e−09	69 / 1470	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
12	4e−08	304 / 10779	Enh_Colon
13	2e−07	172 / 5373	EnhWk1_Colon
14	5e−06	51 / 1168	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_
15	1e−05	39 / 831	Pentrack_CRC_TCGA_group.over_C_normal_DN

Glio

Rank	p−value	#in/all	Geneset
1	2e−16	106 / 2043	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
2	2e−16	97 / 1777	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
3	9e−15	35 / 316	WILLSCHER_GBM_Verhaak−PNwt & CL_up
4	2e−10	50 / 820	Sturm_GBM_Meth_overexpression_E_G34_UP
5	2e−04	8 / 69	WILLSCHER_GBM_Verhaak−PNwt & MES_up
6	2e−03	16 / 315	Up
7	2e−02	6 / 98	WILLSCHER_GBM_proteomics_wtOnly_SpotB
8	4e−02	15 / 401	Down_b
9	5e−02	3 / 37	WILLSCHER_GBM_proteomics_wtOnly_SpotH
10	7e−02	7 / 157	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
11	2e−01	3 / 65	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
12	2e−01	1 / 9	Sturm_GBM_Meth_overexpression_G_IDH_UP
13	2e−01	4 / 101	Hopp_Sturm_GBM_Epi3_D1_IDH_UP_adult_fetus_DN
14	2e−01	1 / 12	WILLSCHER_GBM_LTSmut_proteomics−B_UP
15	3e−01	4 / 113	GIEZELT_GBM_WT_up_VS_mut

GSEA C2

Rank	p−value	#in/all	Geneset
1	7e−37	112 / 1265	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
2	4e−32	127 / 1797	PILON_KLF1_TARGETS_DN
3	7e−29	56 / 388	SHEN_SMARCA2_TARGETS_UP
4	4e−21	67 / 783	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
5	7e−20	91 / 1417	PUJANA_BRCA1_PCC_NETWORK
6	3e−19	80 / 1161	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
7	5e−16	50 / 581	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_UP
8	2e−15	52 / 649	RODRIGUES_THYROID_CARCINOMA_ANAPLASTIC_UP
9	5e−15	88 / 1601	GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_DN
10	5e−15	43 / 465	MILI_PSEUDOPODIA_HAPTOTAXIS_UP
11	1e−13	48 / 622	SCHLOSSER_SERUM_RESPONSE_DN
12	2e−13	72 / 1241	PUJANA_ATM_PCC_NETWORK
13	2e−13	71 / 1222	DODD_NASOPHARYNGEAL_CARCINOMA_DN
14	2e−13	37 / 393	ZHANG_BREAST_CANCER_PROGENITORS_UP
15	4e−13	39 / 442	DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN

HM

Rank	p−value	#in/all	Geneset
1	1e−04	10 / 103	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
2	2e−04	13 / 173	HALLMARK_E2F_TARGETS
3	3e−03	11 / 185	HALLMARK_MTORC1_SIGNALING
4	5e−03	10 / 167	HALLMARK_OXIDATIVE_PHOSPHORYLATION
5	1e−02	8 / 138	HALLMARK_FATTY_ACID_METABOLISM
6	1e−02	6 / 87	HALLMARK_PROTEIN_SECRETION
7	2e−02	9 / 179	HALLMARK_G2M_CHECKPOINT
8	3e−02	6 / 103	HALLMARK_BILE_ACID_METABOLISM
9	4e−02	8 / 170	HALLMARK_MYC_TARGETS_V1
10	5e−02	8 / 176	HALLMARK_ADIPOGENESIS
11	5e−02	5 / 91	HALLMARK_ANDROGEN_RESPONSE
12	5e−02	5 / 91	HALLMARK_PEROXISOME
13	7e−02	5 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING
14	7e−02	6 / 130	HALLMARK_DNA_REPAIR
15	8e−02	6 / 132	HALLMARK_UV_RESPONSE_DN

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.02	10 / 211	Homuth_BMI−associated−genes_DN
2	0.15	2 / 31	DUMEAUX_Fasting enriched genes
3	0.24	5 / 147	Homuth_BMI−associated−genes_UP
4	0.52	1 / 32	Marjolein_ageing−genes_DN
5	0.88	1 / 94	DUMEAUX_Smoking enriched genes
6	1.00	0 / 10	DUMEAUX_Smoking literature genes up
7	1.00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
8	1.00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
9	1.00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
10	1.00	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
11	1.00	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
12	1.00	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
13	1.00	0 / 10	DUMEAUX_Women normal BMI literature genes up
14	1.00	0 / 17	DUMEAUX_High bmi enriched genes
15	1.00	0 / 18	Huan_blood−pressure_SBP−signature

Lymphoma

Rank	p−value	#in/all	Geneset
1	2e−87	382 / 7275	HOPP_Txn_elongation
2	2e−67	303 / 5356	HOPP_Txn_transition
3	2e−65	375 / 8226	HOPP_Active_promoter
4	6e−33	315 / 8098	HOPP_Weak_promoter
5	4e−19	265 / 7448	HOPP_Strong_enhancer
6	1e−14	229 / 6559	HOPP_Weak_txn
7	3e−14	238 / 6959	HOPP_Weak_enhancer
8	5e−10	65 / 1270	SPANG_BCR UP
9	9e−09	34 / 493	WIRTH_lymphoma937_spot J
10	1e−08	33 / 472	Hopp_June14_MMML937 tumors+controls_group.overexpression_J_GC−B−c
11	5e−08	43 / 772	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell line_
12	2e−07	42 / 777	WIRTH_lymphoma937_spot D
13	2e−07	55 / 1169	SPANG_BCR DN
14	4e−05	11 / 109	ROSOLOWSKI_blue total
15	3e−04	17 / 283	TARTE_Plasmablast signature

Melanoma

Rank	p−value	#in/all	Geneset
1	0.3	2 / 43	Hugo_melanoma−BRAFmut−MET_UP
2	0.5	1 / 27	Hugo_melanoma−all−LEF1_UP
3	1.0	0 / 30	Hugo_melanoma−all−MET_UP
4	1.0	0 / 54	Hugo_melanoma−all−MET_DN
5	1.0	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
6	1.0	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

MF

Rank	p−value	#in/all	Geneset
1	1e−21	305 / 8818	protein binding
2	9e−12	60 / 1013	poly(A) RNA binding
3	4e−06	12 / 105	histone binding
4	5e−06	21 / 301	ubiquitin−protein transferase activity
5	2e−05	17 / 232	ligase activity
6	3e−05	58 / 1475	DNA binding
7	4e−05	14 / 173	ubiquitin protein ligase activity
8	4e−05	23 / 399	RNA binding
9	1e−04	6 / 34	histone−lysine N−methyltransferase activity
10	2e−04	43 / 1065	zinc ion binding
11	2e−04	5 / 25	ATP−dependent DNA helicase activity
12	2e−04	16 / 256	ubiquitin protein ligase binding
13	4e−04	14 / 215	transcription regulatory region DNA binding
14	5e−04	4 / 17	histone methyltransferase activity (H3−K4 specific)
15	7e−04	16 / 283	nucleotide binding

miRNA Disease

Rank	p−value	#in/all	Geneset
1	1	0 / 7	Thyroid carcinoma, papillary
2	1	0 / 123	Pancreatic cancer
3	1	0 / 68	Glioblastoma multiforme, somatic
4	1	0 / 63	Gastrointestinal
5	1	0 / 3	Pituitary adenoma
6	1	0 / 116	Cancer
7	1	0 / 95	Colorectal cancer
8	1	0 / 2	Adenomas, multiple colorectal
9	1	0 / 124	Prostate cancer
10	1	0 / 48	Alzheimer disease, susceptibility to
11	1	0 / 7	Schizophrenia, susceptibility to
12	1	0 / 20	Parkinson disease
13	1	0 / 65	Hepatocellular carcinoma
14	1	0 / 3	Down syndrome, risk of
15	1	0 / 127	Melanoma and neural system tumor syndrome

miRNA target

Rank	p−value	#in/all	Geneset
1	2e−13	26 / 190	hsa−miR−330−3p
2	2e−11	33 / 366	hsa−miR−519b−3p
3	2e−11	34 / 389	hsa−miR−519a
4	3e−11	19 / 121	hsa−miR−421
5	4e−11	34 / 400	hsa−miR−519c−3p
6	6e−11	35 / 429	hsa−miR−548n
7	3e−10	34 / 433	hsa−miR−19b
8	4e−10	34 / 438	hsa−miR−19a
9	6e−10	37 / 513	hsa−miR−106b
10	1e−09	23 / 221	hsa−miR−181d
11	5e−09	27 / 321	hsa−miR−590−3p
12	7e−09	26 / 303	hsa−miR−548i
13	9e−09	16 / 117	hsa−miR−543
14	9e−09	14 / 87	hsa−miR−496
15	1e−08	19 / 172	hsa−miR−548k

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.03	2 / 12	BENTINK_src.2
2	0.22	1 / 11	BENTINK_ras.4
3	0.26	1 / 13	BENTINK_myc.1
4	0.27	1 / 14	GUSTAFSON_PI3K_UP
5	1.00	0 / 15	GUSTAFSON_PI3K_DN
6	1.00	0 / 13	BENTINK_e2f3.1
7	1.00	0 / 13	BENTINK_e2f3.2
8	1.00	0 / 12	BENTINK_ras.1
9	1.00	0 / 14	BENTINK_ras.6
10	1.00	0 / 13	BENTINK_src.10
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Reference Signatures

Rank	p−value	#in/all	Geneset
1	4e−27	44 / 242	Chaussabel_3,9_Kinases
2	9e−27	48 / 302	Chaussabel_3,4_Protein phosphatases
3	2e−09	18 / 139	Chaussabel_1,8_Metabolism Biosynthesis
4	7e−09	59 / 1173	PROTEINATLAS_rectum
5	7e−09	50 / 912	PROTEINATLAS_urinary bladder
6	8e−09	59 / 1176	PROTEINATLAS_duodenum
7	1e−08	18 / 153	Chaussabel_2,9_Cytosceleton
8	2e−08	43 / 740	PROTEINATLAS_esophagus
9	3e−08	58 / 1194	PROTEINATLAS_stomach
10	3e−08	43 / 759	PROTEINATLAS_epididymis
11	4e−08	49 / 933	PROTEINATLAS_adrenal gland
12	5e−08	22 / 248	Chaussabel_3,6_Mitochondrial ribosomal proteins
13	2e−07	54 / 1138	PROTEINATLAS_small intestine
14	2e−07	40 / 726	PROTEINATLAS_cervix, uterine
15	3e−07	28 / 412	WIRTH_Immune system

Telomeres

Rank	p−value	#in/all	Geneset
1	0.003	3 / 13	Alternative lengthening of telomeres
2	0.022	3 / 27	Nabetani_alt len telomeres_genes_ko
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	1e−22	212 / 5067	ICGC_Taf1_targets
2	7e−16	204 / 5442	ICGC_Pmlsc71910_targets
3	2e−15	173 / 4362	ICGC_Creb1_targets
4	2e−14	185 / 4890	ICGC_Bclaf101388_targets
5	2e−14	107 / 2215	ICGC_GabpPcr2_targets
6	1e−13	106 / 2255	ICGC_SrfV0416101_targets
7	2e−13	195 / 5383	ICGC_Sp1_targets
8	2e−13	167 / 4345	ICGC_Zeb1_targets
9	2e−13	197 / 5466	ICGC_Nficsc81335_targets
10	3e−13	181 / 4881	ICGC_Atf2_targets
11	3e−13	217 / 6267	ICGC_Yy1_targets
12	5e−13	197 / 5518	ICGC_Stat5_targets
13	5e−13	209 / 5984	ICGC_Mta3_targets
14	3e−12	69 / 1231	KIM_MYC targets
15	3e−12	189 / 5312	ICGC_Tcf12_targets

K−Means Cluster

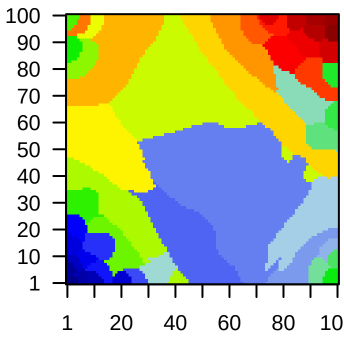
Spot Summary: M1

metagenes = 38
genes = 366

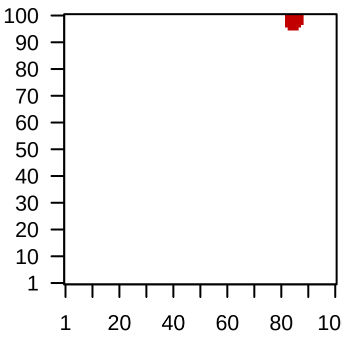
<r> metagenes = 0.95
<r> genes = 0.35
beta: r2= 35.45 / log p= −Inf

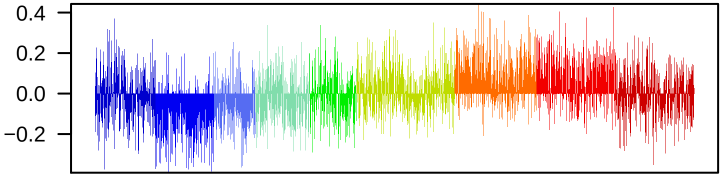
samples with spot = 631 (18.6 %)
A * : 56 (16.3 %)
A C * : 6 (1.8 %)
A C F * : 16 (6.8 %)
A F * : 41 (13.3 %)
C F * : 30 (11.3 %)
F * : 89 (16 %)
F J * : 154 (33.3 %)
J * : 174 (38.9 %)
N * : 65 (14.7 %)

Overview Map



Spot





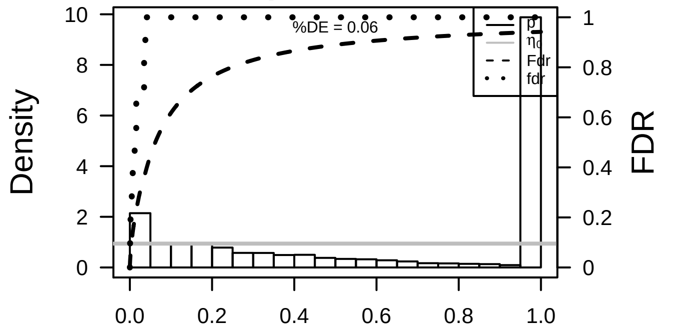
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_171673	3.14	−1.47	0.16	MYOM2	myomesin 2 [Source:HGNC Symbol;Acc:HGNC:7614]
2	ILMN_206606	2.72	−3.26	0.09	HLA−DRB6	major histocompatibility complex, class II, DR beta 6 (pseudo
3	ILMN_178681	2.01	−1.2	0.31	LOC105379645	killer cell immunoglobulin like receptor, two Ig domains and lo
4	ILMN_173123	1.91	−2.04	0.74	GZMH	granzyme H [Source:HGNC Symbol;Acc:HGNC:4710]
5	ILMN_173975	1.64	−1.34	0.49		
6	ILMN_179069	1.63	−1.97	0.73		
7	ILMN_176848	1.63	−1.62	0.69	CD8A	CD8a molecule [Source:HGNC Symbol;Acc:HGNC:1706]
8	ILMN_170877	1.59	−1.49	0.65	GNLY	granulysin [Source:HGNC Symbol;Acc:HGNC:4414]
9	ILMN_166446	1.59	−1.05	0.38		
10	ILMN_166723	1.58	−1.63	0.53	KIR2DL3	killer cell immunoglobulin like receptor, two Ig domains and lo
11	ILMN_235373	1.57	−1.6	0.7	CD8A	CD8a molecule [Source:HGNC Symbol;Acc:HGNC:1706]
12	ILMN_210948	1.56	−1.77	0.71	GZMB	granzyme B [Source:HGNC Symbol;Acc:HGNC:4709]
13	ILMN_176194	1.56	−1.84	0.81	FGFBP2	fibroblast growth factor binding protein 2 [Source:HGNC Sym
14	ILMN_238412	1.53	−1.65	0.84	ADGRG1	adhesion G protein−coupled receptor G1 [Source:HGNC Sym
15	ILMN_167823	1.5	−0.8	0.5	ZNF683	zinc finger protein 683 [Source:HGNC Symbol;Acc:HGNC:28
16	ILMN_235209	1.45	−1.7	0.84	ADGRG1	adhesion G protein−coupled receptor G1 [Source:HGNC Sym
17	ILMN_180749	1.44	−0.9	0.34	LAIR2	leukocyte associated immunoglobulin like receptor 2 [Source:
18	ILMN_232393	1.39	−0.82	0.33	LAIR2	leukocyte associated immunoglobulin like receptor 2 [Source:
19	ILMN_174063	1.37	−1.55	0.83	PRF1	perforin 1 [Source:HGNC Symbol;Acc:HGNC:9360]
20	ILMN_165839	1.36	−1.2	0.7	KLRG1	killer cell lectin like receptor G1 [Source:HGNC Symbol;Acc:H

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−82	54 / 84	Refer	Chaussabel_2,1_Cytotoxic cells
2	9e−30	61 / 810	Colon	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
3	6e−23	34 / 288	GSEA	DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_DN
4	4e−20	15 / 34	GSEA	HAHTOLA_SEZARY_SYNDROM_DN
5	1e−19	10 / 10	Lifesty	Marjolein_ageing−genes_UP
6	4e−17	33 / 412	Refer	WIRTH_Immune system
7	8e−17	19 / 105	BP	regulation of immune response
8	2e−15	23 / 202	GSEA	JAATINEN_HEMATOPOIETIC_STEM_CELL_DN
9	3e−14	8 / 10	GSEA	CHAN_INTERFERON_PRODUCING_DENDRITIC_CELL
10	4e−14	30 / 425	GSEA	MATSUDA_NATURAL_KILLER_DIFFERENTIATION
11	1e−13	200 / 10779	Colon	Enh_Colon
12	2e−13	25 / 306	Lympl	WIRTH_lymphoma937_spot E
13	2e−13	82 / 2810	Colon	EnhA_Colon
14	3e−13	136 / 6138	Colon	TssD2_Colon
15	5e−13	153 / 7354	Colon	TssF_Colon
16	6e−13	171 / 8678	Colon	Quies3_Colon
17	1e−12	24 / 301	GSEA	GOLDRATH_ANTIGEN_RESPONSE
18	1e−12	23 / 277	GSEA	LI_INDUCED_T_TO_NATURAL_KILLER_UP
19	3e−12	122 / 5373	Colon	EnhWk1_Colon
20	7e−12	23 / 300	Lympl	Hopp_June14_MMML937 tumors+controls_group.overexpression_E_GC−E
21	2e−11	169 / 8818	MF	protein binding
22	3e−11	178 / 9555	Colon	TssA_Colon
23	9e−11	11 / 55	GSEA	PID_IL12_2PATHWAY
24	2e−10	8 / 22	GSEA	ONO_AML1_TARGETS_UP
25	3e−10	176 / 9635	Chror	3_TssF_Fibroblasts
26	9e−10	145 / 7448	Lympl	HOPP_Strong_enhancer
27	1e−09	202 / 11836	Chror	3_TssF_Melanocytes
28	2e−09	30 / 656	GSEA	KIM_ALL_DISORDERS_OLIGODENDROCYTE_NUMBER_CORR_UP
29	3e−09	15 / 162	HM	HALLMARK_ALLOGRAFT_REJECTION
30	5e−09	9 / 45	GSEA	REACTOME_IMMUNOREGULATORY_INTERACTIONS_BETWEEN_A_LY
31	7e−09	17 / 230	GSEA	BOYLAN_MULTIPLE_MYELOMA_C_D_DN
32	8e−09	12 / 103	GSEA	BOSCO_TH1_CYTOTOXIC_MODULE
33	1e−08	12 / 106	GSEA	KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY
34	1e−08	163 / 9054	Colon	Tx_Colon
35	1e−08	26 / 554	Cance	Lembcke_Colonic Inflammation
36	1e−08	188 / 10999	Colon	TssWk_Colon
37	2e−08	168 / 9504	Brain	Overlap_fetal_midbrain_K9K27me3
38	3e−08	149 / 8098	Lympl	HOPP_Weak_promoter
39	3e−08	55 / 1979	CC	membrane
40	3e−08	17 / 253	GSEA	WALLACE_PROSTATE_CANCER_RACE_UP

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.01	5 / 111	HORVATH_aging_genes meth DOWN
2	0.11	4 / 142	HORVATH_aging_genes meth UP
3	0.53	1 / 58	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	8e−17	19 / 105	regulation of immune response
2	2e−07	8 / 48	cellular defense response
3	1e−06	15 / 254	cell surface receptor signaling pathway
4	2e−06	5 / 17	cytolysis
5	6e−06	15 / 293	immune response
6	1e−05	7 / 62	positive regulation of phosphatidylinositol 3−kinase signaling
7	4e−05	4 / 16	natural killer cell mediated cytotoxicity
8	7e−05	6 / 55	negative regulation of ERK1 and ERK2 cascade
9	1e−04	7 / 86	transmembrane receptor protein tyrosine kinase signaling pathway
10	1e−04	15 / 387	cell adhesion
11	4e−04	3 / 12	natural killer cell differentiation
12	5e−04	6 / 77	movement of cell or subcellular component
13	5e−04	5 / 51	cellular response to transforming growth factor beta stimulus
14	5e−04	3 / 13	positive regulation of Rho protein signal transduction
15	5e−04	4 / 30	platelet−derived growth factor receptor signaling pathway

Brain

Rank	p−value	#in/all	Geneset
1	2e−08	168 / 9504	Overlap_fetal_midbrain_K9K27me3
2	1e−06	174 / 10430	Overlap_fetal_midbrain_Quies
3	4e−06	69 / 3164	Mid_Frontal_Lobe_ZNF
4	5e−04	155 / 9917	Overlap_fetal_midbrain_ReprPCWk
5	1e−03	151 / 9815	Overlap_fetal_midbrain_ReprPC
6	2e−03	52 / 2700	Fetal_TxTrans
7	4e−03	35 / 1728	Fetal_ReprPCWk
8	8e−03	69 / 4112	Mid_Frontal_Lobe_ReprPC
9	2e−02	35 / 1893	Overlap_fetal_midbrain_TssF
10	3e−02	46 / 2709	Mid_Frontal_Lobe_HetRpts
11	3e−02	23 / 1171	Fetal_EnhP
12	3e−02	17 / 796	Overlap_fetal_midbrain_ZNF
13	3e−02	37 / 2127	Mid_Frontal_Lobe_K9K27me3
14	4e−02	50 / 3046	Fetal_TssA
15	6e−02	9 / 383	Mid_Frontal_Lobe_Tx

Cancer

Rank	p−value	#in/all	Geneset
1	1e−08	26 / 554	Lembcke_Colonic Inflammation
2	6e−03	5 / 91	PanCan_TXmisReg_geneset_nanostring
3	1e−02	1 / 15	LIU_PROSTATE_CANCER_DN
4	1e−02	7 / 193	PanCan_PI3K_geneset_nanostring
5	2e−02	2 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
6	2e−02	9 / 301	SPANG_BCL6−index2
7	3e−02	0 / 12	LIU_BREAST_CANCER
8	6e−02	4 / 117	PanCan_Driver_Gene_geneset_nanostring
9	1e−01	2 / 46	PanCan_DNARepair_geneset_nanostring
10	1e−01	2 / 46	PanCan_TGF−B_geneset_nanostring
11	1e−01	0 / 13	RHODES_CANCER_META_SIGNATURE
12	2e−01	2 / 54	KUIPER_MM poor survival
13	2e−01	1 / 13	GENTLES_modul18
14	2e−01	0 / 14	RHODES_UNDIFFERENTIATED_CANCER
15	2e−01	1 / 14	GENTLES_modul1

CC

Rank	p−value	#in/all	Geneset
1	3e−08	55 / 1979	membrane
2	2e−06	96 / 4822	cytoplasm
3	2e−06	12 / 167	external side of plasma membrane
4	2e−06	78 / 3662	plasma membrane
5	6e−06	57 / 2464	extracellular exosome
6	3e−05	34 / 1252	integral component of plasma membrane
7	4e−05	5 / 30	immunological synapse
8	5e−05	4 / 17	T cell receptor complex
9	1e−04	8 / 119	vesicle
10	3e−04	17 / 512	cell surface
11	9e−04	9 / 194	membrane raft
12	1e−03	61 / 3291	integral component of membrane
13	2e−03	10 / 268	microtubule
14	3e−03	5 / 74	cell body
15	3e−03	16 / 571	perinuclear region of cytoplasm

Chr

Rank	p−value	#in/all	Geneset
1	0.008	43 / 2323	Chr 1
2	0.021	13 / 536	Chr 22
3	0.024	23 / 1160	Chr 12
4	0.126	24 / 1467	Chr 19
5	0.340	14 / 959	Chr 16
6	0.436	19 / 1411	Chr 11
7	0.442	5 / 342	Chr 18
8	0.504	4 / 289	Chr 21
9	0.534	8 / 619	Chr 20
10	0.630	18 / 1492	Chr 2
11	0.634	14 / 1170	Chr 7
12	0.684	14 / 1211	Chr 6
13	0.691	14 / 1217	Chr 3
14	0.717	10 / 902	Chr 4
15	0.720	10 / 904	Chr 10

Chromatin states

Rank	p−value	#in/all	Geneset
1	3e−10	176 / 9635	3_TssF_Fibroblasts
2	1e−09	202 / 11836	3_TssF_Melanocytes
3	1e−07	201 / 12298	2_TssA_Melanocytes
4	7e−07	199 / 12393	15_Quies_Neuronal_Progenitor
5	8e−07	203 / 12741	7_Enh_Melanocytes
6	1e−06	150 / 8613	7_Enh_Fibroblasts
7	1e−06	96 / 4795	6_EnhG_Fibroblasts
8	1e−06	109 / 5699	6_EnhG_Melanocytes
9	2e−06	191 / 11847	7_Enh_Neuronal_Progenitor
10	2e−06	186 / 11455	2_TssA_Fibroblasts
11	7e−06	110 / 5956	3_TssF_Neuronal_Progenitor
12	8e−06	202 / 12983	2_TssA_Neuronal_Progenitor
13	4e−05	121 / 6970	5_Tx_Neuronal_Progenitor
14	1e−04	143 / 8771	5_Tx_Melanocytes
15	3e−04	172 / 11130	15_Quies_Melanocytes

Colon Cancer

Rank	p−value	#in/all	Geneset
1	9e−30	61 / 810	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
2	1e−13	200 / 10779	Enh_Colon
3	2e−13	82 / 2810	EnhA_Colon
4	3e−13	136 / 6138	TssD2_Colon
5	5e−13	153 / 7354	TssF_Colon
6	6e−13	171 / 8678	Quies3_Colon
7	3e−12	122 / 5373	EnhWk1_Colon
8	3e−11	178 / 9555	TssA_Colon
9	1e−08	163 / 9054	Tx_Colon
10	1e−08	188 / 10999	TssWk_Colon
11	2e−07	152 / 8568	TxWk_Colon
12	8e−07	66 / 2845	TxEnhG1_Colon
13	6e−05	16 / 398	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN
14	6e−05	37 / 1468	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
15	6e−05	22 / 676	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN

Glio

Rank	p−value	#in/all	Geneset
1	9e−07	4 / 7	Donson−cytotoxic effectors−associated with LTS in HGA
2	7e−04	4 / 32	Donson−Misc immune function−associated with LTS in HGA
3	1e−03	3 / 16	Donson−chemokine/cytokine−receptors−associated with LTS in HGA
4	2e−03	5 / 68	Christensen_hypermethylated_in_grade2_astrocytoma
5	4e−03	6 / 115	Christensen_hypermethylated_in_grade3_astrocytoma
6	4e−03	6 / 117	Christensen_hypermethylated_in_grade2_oligoastrocytoma
7	7e−03	5 / 94	Weller_LGG_A_vs_O_UP
8	8e−03	6 / 134	Christensen_hypermethylated_in_grade3_oligoastrocytoma
9	8e−03	12 / 419	Down_a
10	1e−02	6 / 147	Christensen_hypermethylated_in_grade2_oligodendroglioma
11	1e−02	4 / 69	WILLSCHER_GBM_Verhaak−PNwt & MES_up
12	1e−02	6 / 150	Hopp_Sturm_GBM_Epi3_E_G34_UP
13	2e−02	51 / 2988	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
14	2e−02	4 / 86	laffaire_hypermeth_LGG_vs_control
15	3e−02	4 / 90	Christensen_hypermethylated_in_secondary_glioblastoma

GSEA C2

Rank	p−value	#in/all	Geneset
1	6e−23	34 / 288	DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_DN
2	4e−20	15 / 34	HAHTOLA_SEZARY_SYNDROM_DN
3	2e−15	23 / 202	JAATINEN_HEMATOPOIETIC_STEM_CELL_DN
4	3e−14	8 / 10	CHAN_INTERFERON_PRODUCING_DENDRITIC_CELL
5	4e−14	30 / 425	MATSUDA_NATURAL_KILLER_DIFFERENTIATION
6	1e−12	24 / 301	GOLDRATH_ANTIGEN_RESPONSE
7	1e−12	23 / 277	LI_INDUCED_T_TO_NATURAL_KILLER_UP
8	9e−11	11 / 55	PID_IL12_2PATHWAY
9	2e−10	8 / 22	ONO_AML1_TARGETS_UP
10	2e−09	30 / 656	KIM_ALL_DISORDERS_OLIGODENDROCYTE_NUMBER_CORR_UP
11	5e−09	9 / 45	REACTOME_IMMUNOREGULATORY_INTERACTIONS_BETWEEN_A_LYM
12	7e−09	17 / 230	BOYLAN_MULTIPLE_MYELOMA_C_D_DN
13	8e−09	12 / 103	BOSCO_TH1_CYTOTOXIC_MODULE
14	1e−08	12 / 106	KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY
15	3e−08	17 / 253	WALLACE_PROSTATE_CANCER_RACE_UP

HM

Rank	p−value	#in/all	Geneset
1	3e−09	15 / 162	HALLMARK_ALLOGRAFT_REJECTION
2	8e−05	10 / 172	HALLMARK_INTERFERON_GAMMA_RESPONSE
3	1e−04	9 / 151	HALLMARK_APOPTOSIS
4	1e−04	10 / 186	HALLMARK_IL2_STAT5_SIGNALING
5	3e−03	8 / 185	HALLMARK_P53_PATHWAY
6	6e−03	5 / 91	HALLMARK_PEROXISOME
7	6e−03	7 / 170	HALLMARK_MYC_TARGETS_V1
8	7e−03	6 / 132	HALLMARK_UV_RESPONSE_DN
9	9e−03	7 / 183	HALLMARK_GLYCOLYSIS
10	1e−02	7 / 185	HALLMARK_MTORC1_SIGNALING
11	3e−02	6 / 176	HALLMARK_KRAS_SIGNALING_UP
12	3e−02	6 / 186	HALLMARK_ESTROGEN_RESPONSE_EARLY
13	3e−02	6 / 186	HALLMARK_ESTROGEN_RESPONSE_LATE
14	3e−02	6 / 189	HALLMARK_HYPOXIA
15	4e−02	6 / 191	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION

Lifestyle

Rank	p−value	#in/all	Geneset
1	1e−19	10 / 10	Marjolein_ageing−genes_UP
2	8e−08	5 / 10	DUMEAUX_Women normal BMI literature genes up
3	2e−06	5 / 18	Huan_blood−pressure_SBP−signature
4	8e−06	3 / 4	DUMEAUX_Exercising non smoker literature enriched genes
5	6e−04	8 / 147	Homuth_BMI−associated−genes_UP
6	2e−02	2 / 16	Huan_blood−pressure_DBP−signature
7	6e−02	1 / 5	Huan_blood−pressure_HTN−signature
8	1e−01	1 / 10	DUMEAUX_Smoking literature genes up
9	2e−01	1 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
10	2e−01	1 / 17	DUMEAUX_High bmi enriched genes
11	5e−01	3 / 211	Homuth_BMI−associated−genes_DN
12	1e+00	0 / 94	DUMEAUX_Smoking enriched genes
13	1e+00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
14	1e+00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
15	1e+00	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up

Lymphoma

Rank	p−value	#in/all	Geneset
1	2e−13	25 / 306	WIRTH_lymphoma937_spot E
2	7e−12	23 / 300	Hopp_June14_MMML937 tumors+controls_group.overexpression_E_GC−B−
3	9e−10	145 / 7448	HOPP_Strong_enhancer
4	3e−08	149 / 8098	HOPP_Weak_promoter
5	1e−07	108 / 5356	HOPP_Txn_transition
6	2e−06	6 / 31	Care_Extended T−cell
7	3e−06	35 / 1169	SPANG_BCR DN
8	8e−05	13 / 283	TARTE_Plasmablast signature
9	3e−04	117 / 6959	HOPP_Weak_enhancer
10	3e−04	111 / 6559	HOPP_Weak_txn
11	5e−04	120 / 7275	HOPP_Txn_elongation
12	5e−04	3 / 13	Care_Polarized immune response
13	8e−04	5 / 57	Monti_Host_response_cluster
14	1e−03	131 / 8226	HOPP_Active_promoter
15	2e−03	6 / 103	Hopp_June14_MMML937 tumors+controls_group.overexpression_MM_MM_

Melanoma

Rank	p−value	#in/all	Geneset
1	0.2	2 / 54	Hugo_melanoma−all−MET_DN
2	0.3	1 / 27	Hugo_melanoma−all−LEF1_UP
3	1.0	0 / 30	Hugo_melanoma−all−MET_UP
4	1.0	0 / 43	Hugo_melanoma−BRAFmut−MET_UP
5	1.0	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
6	1.0	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

MF

Rank	p−value	#in/all	Geneset
1	2e−11	169 / 8818	protein binding
2	2e−05	15 / 324	receptor binding
3	3e−05	4 / 15	MHC class I protein binding
4	8e−05	10 / 174	transmembrane signaling receptor activity
5	2e−04	10 / 188	receptor activity
6	5e−04	4 / 30	coreceptor activity
7	9e−04	5 / 59	cell adhesion molecule binding
8	1e−03	8 / 160	carbohydrate binding
9	1e−03	3 / 17	phosphatidylinositol 3−kinase binding
10	2e−03	3 / 19	chemokine receptor activity
11	3e−03	5 / 77	PDZ domain binding
12	4e−03	6 / 120	protein tyrosine kinase activity
13	6e−03	3 / 30	antigen binding
14	7e−03	6 / 130	protein dimerization activity
15	1e−02	2 / 12	activin binding

miRNA Disease

Rank	p−value	#in/all	Geneset
1	1	0 / 7	Thyroid carcinoma, papillary
2	1	0 / 123	Pancreatic cancer
3	1	0 / 68	Glioblastoma multiforme, somatic
4	1	0 / 63	Gastrointestinal
5	1	0 / 3	Pituitary adenoma
6	1	0 / 116	Cancer
7	1	0 / 95	Colorectal cancer
8	1	0 / 2	Adenomas, multiple colorectal
9	1	0 / 124	Prostate cancer
10	1	0 / 48	Alzheimer disease, susceptibility to
11	1	0 / 7	Schizophrenia, susceptibility to
12	1	0 / 20	Parkinson disease
13	1	0 / 65	Hepatocellular carcinoma
14	1	0 / 3	Down syndrome, risk of
15	1	0 / 127	Melanoma and neural system tumor syndrome

miRNA target

Rank	p−value	#in/all	Geneset
1	0.005	7 / 164	hsa−miR−153
2	0.008	5 / 97	hsa−miR−624
3	0.013	2 / 14	hsa−miR−191*
4	0.013	3 / 39	hsa−miR−593
5	0.020	6 / 166	hsa−miR−323b−5p
6	0.022	3 / 47	hsa−miR−370
7	0.022	5 / 125	hsa−miR−508−3p
8	0.023	14 / 602	hsa−miR−20a
9	0.023	3 / 48	hsa−miR−146b−3p
10	0.023	3 / 48	hsa−miR−1291
11	0.025	12 / 493	hsa−miR−103
12	0.031	7 / 234	hsa−miR−27a
13	0.032	4 / 94	hsa−miR−133a
14	0.033	12 / 513	hsa−miR−106b
15	0.033	3 / 55	hsa−miR−634

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.2	1 / 14	GUSTAFSON_PI3K_UP
2	1.0	0 / 15	GUSTAFSON_PI3K_DN
3	1.0	0 / 13	BENTINK_e2f3.1
4	1.0	0 / 13	BENTINK_e2f3.2
5	1.0	0 / 13	BENTINK_myc.1
6	1.0	0 / 12	BENTINK_ras.1
7	1.0	0 / 11	BENTINK_ras.4
8	1.0	0 / 14	BENTINK_ras.6
9	1.0	0 / 13	BENTINK_src.10
10	1.0	0 / 12	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Reference Signatures

Rank	p−value	#in/all	Geneset
1	1e−82	54 / 84	Chaussabel_2,1_Cytotoxic cells
2	4e−17	33 / 412	WIRTH_Immune system
3	2e−05	24 / 724	PROTEINATLAS_lymph node
4	2e−05	4 / 14	JONGENEEL_Peripheral Blood Lymphocytes
5	2e−04	28 / 1063	PROTEINATLAS_tonsil
6	1e−03	16 / 535	PROTEINATLAS_spleen
7	9e−03	9 / 275	Chaussabel_3,7_Spliceosome
8	2e−02	3 / 41	VAQUERIZAS_Thymus_TF
9	2e−02	21 / 1003	PROTEINATLAS_appendix
10	2e−02	11 / 416	PROTEINATLAS_ovary
11	2e−02	2 / 19	VAQUERIZAS_Bone marrow_TF
12	3e−02	2 / 21	VAQUERIZAS_Tonsil_TF
13	4e−02	21 / 1097	PROTEINATLAS_kidney
14	5e−02	23 / 1239	PROTEINATLAS_testis
15	5e−02	21 / 1118	PROTEINATLAS_placenta

Telomeres

Rank	p−value	#in/all	Geneset
1	0.2	1 / 13	Alternative lengthening of telomeres
2	0.3	1 / 27	Nabetani_alt len telomeres_genes_ko
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	9e−07	74 / 3348	ICGC_BatfPcr1_targets
2	5e−06	93 / 4735	ICGC_Pu1_targets
3	5e−06	116 / 6322	ICGC_Tcf3_targets
4	8e−06	44 / 1723	HEBENSTREIT_high expression TF
5	2e−05	50 / 2133	ICGC_Mef2_targets
6	2e−05	117 / 6578	ICGC_Pou2_targets
7	3e−05	120 / 6868	ICGC_Elf1_targets
8	4e−05	55 / 2497	ICGC_Bcl11_targets
9	1e−04	123 / 7247	ICGC_Runx3_targets
10	2e−04	93 / 5188	ICGC_Ebfsc137065_targets
11	4e−04	38 / 1669	ICGC_P300_targets
12	4e−04	81 / 4468	ICGC_Egr1_targets
13	5e−04	95 / 5466	ICGC_Nficsc81335_targets
14	7e−04	78 / 4345	ICGC_Zeb1_targets
15	8e−04	105 / 6267	ICGC_Yy1_targets

K−Means Cluster

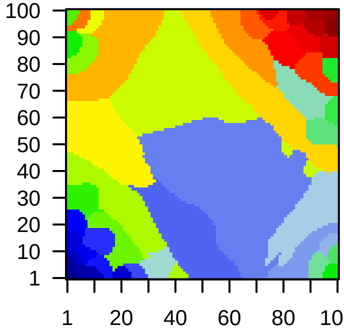
Spot Summary: N1

metagenes = 131
genes = 385

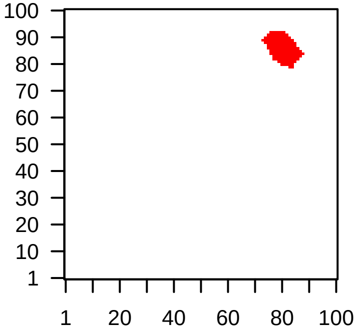
<r> metagenes = 0.95
<r> genes = 0.21
beta: r2= 4.94 / log p= −Inf

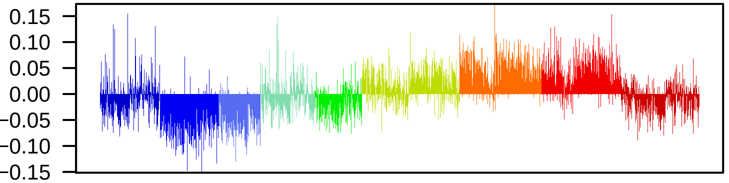
samples with spot = 16 (0.5 %)
A * : 4 (1.2 %)
A F * : 2 (0.6 %)
F * : 1 (0.2 %)
F J * : 4 (0.9 %)
J * : 5 (1.1 %)

Overview Map



Spot





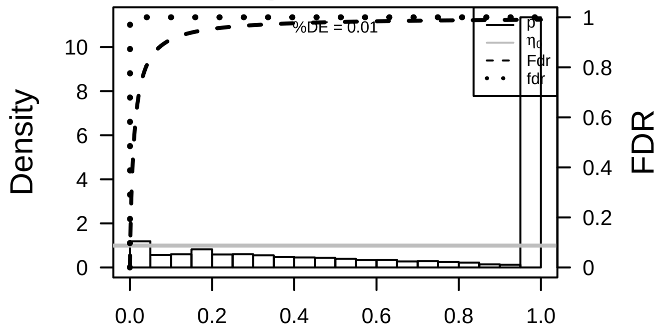
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_175289	1.07	−0.84	0.54	BCL11A	B−cell CLL/lymphoma 11A [Source:HGNC Symbol;Acc:HGN
2	ILMN_178884	1.05	−0.61	0.58	TCL1A	T−cell leukemia/lymphoma 1A [Source:HGNC Symbol;Acc:H
3	ILMN_218496	0.93	−0.8	0.27	ZHX2	zinc fingers and homeoboxes 2 [Source:HGNC Symbol;Acc:H
4	ILMN_166827	0.92	−0.54	0.55	BLK	BLK proto−oncogene, Src family tyrosine kinase [Source:HG
5	ILMN_181419	0.91	−0.63	0.62	TCF4	transcription factor 4 [Source:HGNC Symbol;Acc:HGNC:116
6	ILMN_171001	0.89	−0.65	0.65	CD79B	CD79b molecule [Source:HGNC Symbol;Acc:HGNC:1699]
7	ILMN_181104	0.89	−0.58	0.64	POU2AF1	POU class 2 associating factor 1 [Source:HGNC Symbol;Acc
8	ILMN_165922	0.89	−0.58	0.69	CD79A	CD79a molecule [Source:HGNC Symbol;Acc:HGNC:1698]
9	ILMN_168278	0.87	−0.29	0.44	TEAD2	TEA domain transcription factor 2 [Source:HGNC Symbol;Ac
10	ILMN_177859	0.78	−0.61	0.47	SP140	SP140 nuclear body protein [Source:HGNC Symbol;Acc:HG
11	ILMN_211682	0.78	−0.43	0.2	RGPD1	RANBP2−like and GRIP domain containing 1 [Source:HGNC
12	ILMN_177356	0.76	−0.43	0.5	MIR4758	laminin subunit alpha 5 [Source:HGNC Symbol;Acc:HGNC:6
13	ILMN_172300	0.75	−0.44	0.5		
14	ILMN_171151	0.74	−0.39	0.45	COCH	cochlin [Source:HGNC Symbol;Acc:HGNC:2180]
15	ILMN_229695	0.74	−0.53	0.54	APOBEC3F	apolipoprotein B mRNA editing enzyme catalytic subunit 3F [
16	ILMN_225531	0.72	−0.93	0.15	RPS15A	ribosomal protein S15a [Source:HGNC Symbol;Acc:HGNC:1
17	ILMN_174135	0.71	−0.48	0.54	PRICKLE1	prickle planar cell polarity protein 1 [Source:HGNC Symbol;A
18	ILMN_166406	0.71	−0.46	0.54		
19	ILMN_171443	0.68	−0.55	0.29	MARCKSL1	MARCKS like 1 [Source:HGNC Symbol;Acc:HGNC:7142]
20	ILMN_181516	0.68	−0.61	0.38	HVCN1	hydrogen voltage gated channel 1 [Source:HGNC Symbol;Ac

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	3e−26	21 / 51	Refer	Chaussabel_1,3_B−cells
2	3e−19	245 / 12298	Chror	2_TssA_Melanocytes
3	5e−18	226 / 10999	Colon	TssWk_Colon
4	1e−16	248 / 12983	Chror	2_TssA_Neuronal_Progenitor
5	1e−16	207 / 9815	Brain	Overlap_fetal_midbrain_ReprPC
6	3e−14	223 / 11455	Chror	2_TssA_Fibroblasts
7	2e−12	181 / 8771	Chror	5_Tx_Melanocytes
8	7e−12	105 / 4034	Colon	TssD1_Colon
9	2e−11	50 / 1270	Lympl	SPANG_BCR UP
10	6e−11	193 / 9917	Brain	Overlap_fetal_midbrain_ReprPCWk
11	1e−10	166 / 8098	Lympl	HOPP_Weak_promoter
12	2e−10	149 / 6970	Chror	5_Tx_Neuronal_Progenitor
13	3e−10	186 / 9555	Colon	TssA_Colon
14	3e−10	10 / 44	GSEA	KLEIN_PRIMARY_EFFUSION_LYMPHOMA_DN
15	4e−10	207 / 11130	Chror	15_Quies_Melanocytes
16	5e−10	178 / 9054	Colon	Tx_Colon
17	5e−10	171 / 8568	Colon	TxWk_Colon
18	1e−09	215 / 11836	Chror	3_TssF_Melanocytes
19	1e−09	22 / 331	Lympl	SPANG_CD40 6hrs UP
20	2e−09	159 / 7854	Chror	5_Tx_Fibroblasts
21	2e−09	171 / 8678	Colon	Quies3_Colon
22	2e−09	175 / 8990	Chror	15_Quies_Fibroblasts
23	4e−09	163 / 8226	Lympl	HOPP_Active_promoter
24	5e−09	220 / 12393	Chror	15_Quies_Neuronal_Progenitor
25	2e−08	149 / 7448	Lympl	HOPP_Strong_enhancer
26	2e−08	25 / 493	Lympl	WIRTH_lymphoma937_spot J
27	2e−08	41 / 1156	Colon	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
28	3e−08	140 / 6868	TF	ICGC_Elf1_targets
29	4e−08	125 / 5936	Brain	Overlap_fetal_midbrain_HetRpts
30	4e−08	7 / 26	GSEA	MORI_PLASMA_CELL_DN
31	7e−08	209 / 11847	Chror	7_Enh_Neuronal_Progenitor
32	9e−08	17 / 254	GSEA	HADDAD_B_LYMPHOCYTE_PROGENITOR
33	1e−07	38 / 1083	Colon	ZNF_Colon
34	1e−07	116 / 5466	TF	ICGC_Nficsc81335_targets
35	1e−07	176 / 9504	Brain	Overlap_fetal_midbrain_K9K27me3
36	2e−07	23 / 472	Lympl	Hopp_June14_MMML937 tumors+controls_group.overexpression_J_GC−E
37	2e−07	105 / 4828	CC	nucleus
38	2e−07	49 / 1643	BP	transcription, DNA−templated
39	2e−07	100 / 4526	Colon	Quies1_Colon
40	4e−07	187 / 10430	Brain	Overlap_fetal_midbrain_Quies

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.1	4 / 142	HORVATH_aging_genes meth UP
2	0.5	2 / 111	HORVATH_aging_genes meth DOWN
3	1.0	0 / 58	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	2e−07	49 / 1643	transcription, DNA−templated
2	9e−07	40 / 1272	regulation of transcription, DNA−templated
3	4e−05	5 / 29	B cell receptor signaling pathway
4	6e−04	4 / 29	B cell proliferation
5	9e−04	5 / 55	cilium morphogenesis
6	2e−03	3 / 18	cell recognition
7	2e−03	9 / 208	cellular response to DNA damage stimulus
8	4e−03	8 / 187	DNA repair
9	5e−03	3 / 25	ribosome biogenesis
10	5e−03	3 / 26	B cell activation
11	6e−03	3 / 27	mitotic spindle assembly
12	6e−03	3 / 28	DNA damage checkpoint
13	8e−03	2 / 10	endothelial cell activation
14	8e−03	2 / 10	negative regulation of pathway−restricted SMAD protein phosphorylation
15	8e−03	2 / 10	retina morphogenesis in camera−type eye

Brain

Rank	p−value	#in/all	Geneset
1	1e−16	207 / 9815	Overlap_fetal_midbrain_ReprPC
2	6e−11	193 / 9917	Overlap_fetal_midbrain_ReprPCWk
3	4e−08	125 / 5936	Overlap_fetal_midbrain_HetRpts
4	1e−07	176 / 9504	Overlap_fetal_midbrain_K9K27me3
5	4e−07	187 / 10430	Overlap_fetal_midbrain_Quies
6	1e−03	19 / 630	Mid_Frontal_Lobe_EnhP
7	1e−03	20 / 681	Overlap_fetal_midbrain_EnhP
8	3e−03	54 / 2709	Mid_Frontal_Lobe_HetRpts
9	5e−03	28 / 1213	Fetal_TssP
10	9e−03	32 / 1506	Mid_Frontal_Lobe_Quies
11	3e−02	24 / 1171	Fetal_EnhP
12	4e−02	19 / 906	Fetal_HetRpts
13	5e−02	17 / 796	Overlap_fetal_midbrain_ZNF
14	6e−02	22 / 1115	Overlap_fetal_midbrain_EnhG
15	7e−02	25 / 1329	Overlap_fetal_midbrain_Enh

Cancer

Rank	p−value	#in/all	Geneset
1	3e−05	21 / 554	Lembcke_Colonic Inflammation
2	3e−02	2 / 20	PanCan_ChromMod_geneset_nanostring
3	4e−02	1 / 12	LIU_BREAST_CANCER
4	4e−02	0 / 15	LIU_PROSTATE_CANCER_DN
5	6e−02	0 / 14	LIU_COMMON_CANCER_GENES
6	8e−02	1 / 6	ZHANG_MGUS up
7	1e−01	2 / 39	ZHANG_MM up
8	1e−01	11 / 527	Lembcke_Normal vs Adenoma
9	1e−01	1 / 14	LIU_PROSTATE_CANCER_UP
10	2e−01	1 / 12	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
11	2e−01	1 / 13	LIU_LIVER_CANCER
12	2e−01	1 / 13	GENTLES_modul12
13	2e−01	1 / 14	RHODES_UNDIFFERENTIATED_CANCER
14	3e−01	1 / 24	PanCan_Notch_geneset_nanostring
15	3e−01	1 / 28	PanCan_HH_geneset_nanostring

CC

Rank	p−value	#in/all	Geneset
1	2e−07	105 / 4828	nucleus
2	5e−04	9 / 167	external side of plasma membrane
3	2e−03	52 / 2535	nucleoplasm
4	5e−03	16 / 561	intracellular membrane−bounded organelle
5	5e−03	19 / 721	nucleolus
6	6e−03	5 / 85	ciliary basal body
7	6e−03	12 / 379	centrosome
8	6e−03	8 / 200	nuclear membrane
9	8e−03	9 / 249	axon
10	8e−03	2 / 10	axon initial segment
11	8e−03	2 / 10	MKS complex
12	9e−03	4 / 59	Cul3−RING ubiquitin ligase complex
13	1e−02	19 / 777	Golgi apparatus
14	1e−02	2 / 12	paranode region of axon
15	1e−02	28 / 1304	mitochondrion

Chr

Rank	p−value	#in/all	Geneset
1	0.006	21 / 836	Chr 8
2	0.019	22 / 994	Chr X
3	0.120	11 / 536	Chr 22
4	0.145	12 / 619	Chr 20
5	0.182	20 / 1170	Chr 7
6	0.210	24 / 1467	Chr 19
7	0.326	18 / 1160	Chr 12
8	0.468	13 / 904	Chr 10
9	0.482	11 / 768	Chr 14
10	0.493	17 / 1211	Chr 6
11	0.501	17 / 1217	Chr 3
12	0.504	5 / 342	Chr 18
13	0.635	17 / 1318	Chr 17
14	0.659	12 / 954	Chr 9
15	0.699	1 / 87	Chr Y

Chromatin states

Rank	p−value	#in/all	Geneset
1	3e−19	245 / 12298	2_TssA_Melanocytes
2	1e−16	248 / 12983	2_TssA_Neuronal_Progenitor
3	3e−14	223 / 11455	2_TssA_Fibroblasts
4	2e−12	181 / 8771	5_Tx_Melanocytes
5	2e−10	149 / 6970	5_Tx_Neuronal_Progenitor
6	4e−10	207 / 11130	15_Quies_Melanocytes
7	1e−09	215 / 11836	3_TssF_Melanocytes
8	2e−09	159 / 7854	5_Tx_Fibroblasts
9	2e−09	175 / 8990	15_Quies_Fibroblasts
10	5e−09	220 / 12393	15_Quies_Neuronal_Progenitor
11	7e−08	209 / 11847	7_Enh_Neuronal_Progenitor
12	2e−06	215 / 12741	7_Enh_Melanocytes
13	3e−06	50 / 1846	14_ZNF_Melanocytes
14	1e−05	89 / 4237	14_ZNF_Neuronal_Progenitor
15	2e−05	154 / 8613	7_Enh_Fibroblasts

Colon Cancer

Rank	p−value	#in/all	Geneset
1	5e−18	226 / 10999	TssWk_Colon
2	7e−12	105 / 4034	TssD1_Colon
3	3e−10	186 / 9555	TssA_Colon
4	5e−10	178 / 9054	Tx_Colon
5	5e−10	171 / 8568	TxWk_Colon
6	2e−09	171 / 8678	Quies3_Colon
7	2e−08	41 / 1156	Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN
8	1e−07	38 / 1083	ZNF_Colon
9	2e−07	100 / 4526	Quies1_Colon
10	7e−07	38 / 1168	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_
11	2e−05	27 / 810	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
12	4e−05	34 / 1186	HetRpts_Colon
13	8e−05	133 / 7354	TssF_Colon
14	1e−04	41 / 1623	Het_Colon
15	2e−04	18 / 489	K9acLow_Colon

Glio

Rank	p−value	#in/all	Geneset
1	0.004	38 / 1777	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
2	0.020	2 / 16	Donson−chemokine/cytokine−receptors−associated with LTS in HGA
3	0.022	39 / 2043	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
4	0.049	2 / 26	Gorovets_LGG_NB_subclass
5	0.079	26 / 1417	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
6	0.083	2 / 35	WIRTH_PN subtype
7	0.086	3 / 76	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
8	0.104	1 / 8	Sturm_GBM_Meth_overexpression_C_G34_UP
9	0.150	2 / 50	WILLSCHER_GBM_proteomics_wtOnly_SpotG
10	0.152	1 / 12	Mukasa_UP_in_Astroglioma
11	0.154	2 / 51	Gorovets_LGG_EPL_subclass
12	0.161	3 / 101	Hopp_Sturm_GBM_Epi3_D1_IDH_UP_adult_fetus_DN
13	0.164	2 / 53	Hopp_Sturm_GBM_Epi3_C1_IDH_UP_fetus_DN
14	0.176	1 / 14	Christensen_hypermethylated_in_ependymoma
15	0.186	8 / 401	Down_b

GSEA C2

Rank	p−value	#in/all	Geneset
1	3e−10	10 / 44	KLEIN_PRIMARY_EFFUSION_LYMPHOMA_DN
2	4e−08	7 / 26	MORI_PLASMA_CELL_DN
3	9e−08	17 / 254	HADDAD_B_LYMPHOCYTE_PROGENITOR
4	2e−06	17 / 316	REACTOME_GENERIC_TRANSCRIPTION_PATHWAY
5	1e−05	18 / 402	SMID_BREAST_CANCER_NORMAL_LIKE_UP
6	1e−05	21 / 529	CAIRO_HEPATOBLASTOMA_CLASSES_UP
7	4e−05	4 / 15	SHIN_B_CELL_LYMPHOMA_CLUSTER_9
8	4e−05	6 / 47	MORI_LARGE_PRE_BII_LYMPHOCYTE_DN
9	5e−05	11 / 183	KIM_MYC_AMPLIFICATION_TARGETS_UP
10	5e−05	6 / 48	ZHAN_MULTIPLE_MYELOMA_CD1_VS_CD2_DN
11	9e−05	3 / 7	GUTIERREZ_WALDENSTROEMS_MACROGLOBULINEMIA_1_UP
12	9e−05	14 / 305	RICKMAN_METASTASIS_UP
13	1e−04	22 / 652	WONG_ADULT_TISSUE_STEM_MODULE
14	3e−04	29 / 1050	PEREZ_TP53_TARGETS
15	3e−04	22 / 704	NUYTTEN_NIPP1_TARGETS_UP

HM

Rank	p−value	#in/all	Geneset
1	0.04	6 / 186	HALLMARK_IL2_STAT5_SIGNALING
2	0.07	5 / 162	HALLMARK_ALLOGRAFT_REJECTION
3	0.08	2 / 34	HALLMARK_HEDGEHOG_SIGNALING
4	0.10	4 / 130	HALLMARK_DNA_REPAIR
5	0.24	4 / 183	HALLMARK_APICAL_JUNCTION
6	0.25	4 / 185	HALLMARK_TNFA_SIGNALING_VIA_NFKB
7	0.33	2 / 87	HALLMARK_PROTEIN_SECRETION
8	0.35	2 / 91	HALLMARK_ANDROGEN_RESPONSE
9	0.35	2 / 91	HALLMARK_PEROXISOME
10	0.40	3 / 167	HALLMARK_OXIDATIVE_PHOSPHORYLATION
11	0.41	3 / 170	HALLMARK_MYC_TARGETS_V1
12	0.42	3 / 172	HALLMARK_INTERFERON_GAMMA_RESPONSE
13	0.42	3 / 173	HALLMARK_E2F_TARGETS
14	0.42	1 / 40	HALLMARK_WNT_BETA_CATENIN_SIGNALING
15	0.43	3 / 175	HALLMARK_XENOBIOTIC_METABOLISM

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.009	3 / 32	Marjolein_ageing−genes_DN
2	0.209	1 / 17	DUMEAUX_High bmi enriched genes
3	0.327	3 / 147	Homuth_BMI−associated−genes_UP
4	0.554	3 / 211	Homuth_BMI−associated−genes_DN
5	1.000	0 / 94	DUMEAUX_Smoking enriched genes
6	1.000	0 / 10	DUMEAUX_Smoking literature genes up
7	1.000	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
8	1.000	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
9	1.000	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
10	1.000	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
11	1.000	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
12	1.000	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
13	1.000	0 / 10	DUMEAUX_Women normal BMI literature genes up
14	1.000	0 / 31	DUMEAUX_Fasting enriched genes
15	1.000	0 / 18	Huan_blood−pressure_SBP−signature

Lymphoma

Rank	p−value	#in/all	Geneset
1	2e−11	50 / 1270	SPANG_BCR UP
2	1e−10	166 / 8098	HOPP_Weak_promoter
3	1e−09	22 / 331	SPANG_CD40 6hrs UP
4	4e−09	163 / 8226	HOPP_Active_promoter
5	2e−08	149 / 7448	HOPP_Strong_enhancer
6	2e−08	25 / 493	WIRTH_lymphoma937_spot J
7	2e−07	23 / 472	Hopp_June14_MMML937 tumors+controls_group.overexpression_J_GC−B−c
8	7e−06	10 / 121	SPANG_LPS 6hrs UP
9	6e−05	4 / 16	WRIGHT_ABC UP
10	1e−04	131 / 7275	HOPP_Txn_elongation
11	2e−04	5 / 40	Monti_BCR_cluster
12	1e−03	4 / 35	TARTE_B−cell signature
13	1e−03	11 / 272	SPANG_IL21 DN
14	2e−03	2 / 5	WRIGHT_custom ABC−DLBCL UP
15	2e−03	3 / 20	DAVE_NFkB BL DN

Melanoma

Rank	p−value	#in/all	Geneset
1	0.4	1 / 43	Hugo_melanoma−BRAFmut−MET_UP
2	1.0	0 / 30	Hugo_melanoma−all−MET_UP
3	1.0	0 / 54	Hugo_melanoma−all−MET_DN
4	1.0	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
5	1.0	0 / 27	Hugo_melanoma−all−LEF1_UP
6	1.0	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

MF

Rank	p−value	#in/all	Geneset
1	8e−07	49 / 1717	metal ion binding
2	2e−06	31 / 877	transcription factor activity, sequence−specific DNA binding
3	1e−05	41 / 1475	DNA binding
4	2e−03	146 / 8818	protein binding
5	4e−03	4 / 46	ligand−dependent nuclear receptor transcription coactivator activity
6	6e−03	25 / 1065	zinc ion binding
7	1e−02	2 / 13	enhancer binding
8	1e−02	2 / 13	NAD+ binding
9	1e−02	2 / 13	transmembrane receptor protein tyrosine phosphatase activity
10	2e−02	4 / 71	Rho guanyl−nucleotide exchange factor activity
11	2e−02	4 / 72	single−stranded DNA binding
12	2e−02	3 / 40	protein self−association
13	2e−02	2 / 15	FAD binding
14	2e−02	4 / 79	protein tyrosine phosphatase activity
15	3e−02	2 / 19	NAD+ ADP−ribosyltransferase activity

miRNA Disease

Rank	p−value	#in/all	Geneset
1	0.09	1 / 7	Multiple sclerosis, susceptibility to
2	1.00	0 / 7	Thyroid carcinoma, papillary
3	1.00	0 / 123	Pancreatic cancer
4	1.00	0 / 68	Glioblastoma multiforme, somatic
5	1.00	0 / 63	Gastrointestinal
6	1.00	0 / 3	Pituitary adenoma
7	1.00	0 / 116	Cancer
8	1.00	0 / 95	Colorectal cancer
9	1.00	0 / 2	Adenomas, multiple colorectal
10	1.00	0 / 124	Prostate cancer
11	1.00	0 / 48	Alzheimer disease, susceptibility to
12	1.00	0 / 7	Schizophrenia, susceptibility to
13	1.00	0 / 20	Parkinson disease
14	1.00	0 / 65	Hepatocellular carcinoma
15	1.00	0 / 3	Down syndrome, risk of

miRNA target

Rank	p−value	#in/all	Geneset
1	2e−04	9 / 150	hsa−miR−338−3p
2	1e−03	3 / 16	hsa−miR−891a
3	3e−03	5 / 70	hsa−miR−193b
4	3e−03	8 / 176	hsa−miR−199b−3p
5	4e−03	5 / 77	hsa−miR−569
6	6e−03	5 / 84	hsa−miR−767−5p
7	6e−03	6 / 120	hsa−miR−493
8	7e−03	5 / 87	hsa−miR−299−3p
9	7e−03	5 / 87	hsa−miR−362−5p
10	8e−03	4 / 58	hsa−miR−193a−3p
11	8e−03	14 / 493	hsa−miR−103
12	9e−03	8 / 210	hsa−miR−29b
13	9e−03	7 / 169	hsa−miR−29a
14	9e−03	7 / 169	hsa−miR−369−3p
15	1e−02	7 / 175	hsa−miR−29c

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.01	2 / 13	BENTINK_myc.1
2	1.00	0 / 14	GUSTAFSON_PI3K_UP
3	1.00	0 / 15	GUSTAFSON_PI3K_DN
4	1.00	0 / 13	BENTINK_e2f3.1
5	1.00	0 / 13	BENTINK_e2f3.2
6	1.00	0 / 12	BENTINK_ras.1
7	1.00	0 / 11	BENTINK_ras.4
8	1.00	0 / 14	BENTINK_ras.6
9	1.00	0 / 13	BENTINK_src.10
10	1.00	0 / 12	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Reference Signatures

Rank	p−value	#in/all	Geneset
1	3e−26	21 / 51	Chaussabel_1,3_B−cells
2	2e−02	3 / 42	VAQUERIZAS_Fetal brain_TF
3	2e−02	8 / 248	Chaussabel_3,6_Mitochondrial ribosomal proteins
4	3e−02	2 / 21	VAQUERIZAS_Tonsil_TF
5	4e−02	2 / 22	Chaussabel_1,1_Plasma Cells
6	4e−02	8 / 275	Chaussabel_3,7_Spliceosome
7	4e−02	7 / 231	Chaussabel_2,5_Immune related molecules
8	6e−02	2 / 30	VAQUERIZAS_Lymph node_TF
9	7e−02	12 / 535	PROTEINATLAS_spleen
10	7e−02	4 / 113	Chaussabel_1,4_Replication
11	7e−02	15 / 724	PROTEINATLAS_lymph node
12	8e−02	4 / 119	Chaussabel_2,8_T−cells
13	1e−01	19 / 1003	PROTEINATLAS_appendix
14	1e−01	9 / 412	WIRTH_Immune system
15	1e−01	2 / 44	VAQUERIZAS_Whole brain_TF

Telomeres

Rank	p−value	#in/all	Geneset
1	0.05	2 / 27	Nabetani_alt len telomeres_genes_ko
2	1.00	0 / 13	Alternative lengthening of telomeres
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	3e−08	140 / 6868	ICGC_Elf1_targets
2	1e−07	116 / 5466	ICGC_Nficsc81335_targets
3	1e−06	103 / 4881	ICGC_Atf2_targets
4	1e−06	113 / 5518	ICGC_Stat5_targets
5	2e−06	125 / 6322	ICGC_Tcf3_targets
6	3e−06	138 / 7247	ICGC_Runx3_targets
7	4e−06	93 / 4362	ICGC_Creb1_targets
8	4e−06	104 / 5067	ICGC_Taf1_targets
9	1e−05	125 / 6578	ICGC_Pou2_targets
10	2e−05	120 / 6267	ICGC_Yy1_targets
11	4e−05	97 / 4890	ICGC_Bclaf101388_targets
12	5e−05	88 / 4345	ICGC_Zeb1_targets
13	7e−05	113 / 5984	ICGC_Mta3_targets
14	7e−05	39 / 1478	ICGC_Myc_targets
15	8e−05	122 / 6616	ICGC_Pax5_targets

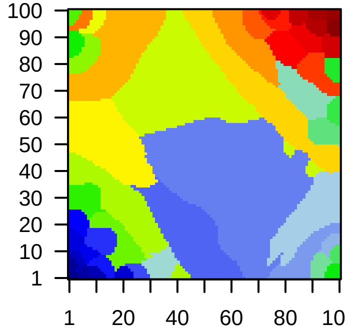
K−Means Cluster

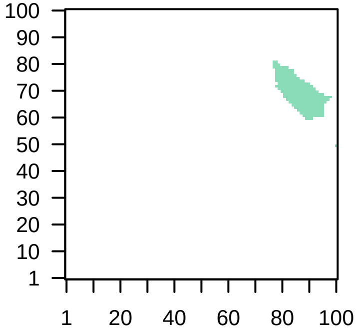
Spot Summary: O1

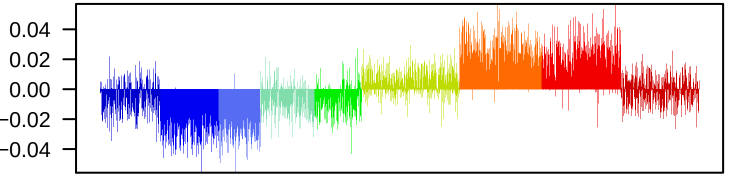
metagenes = 224
genes = 981

<r> metagenes = 0.9
<r> genes = 0.1
beta: r2= 1.18 / log p= −Inf

samples with spot = 0 (0 %)


Overview Map


Spot

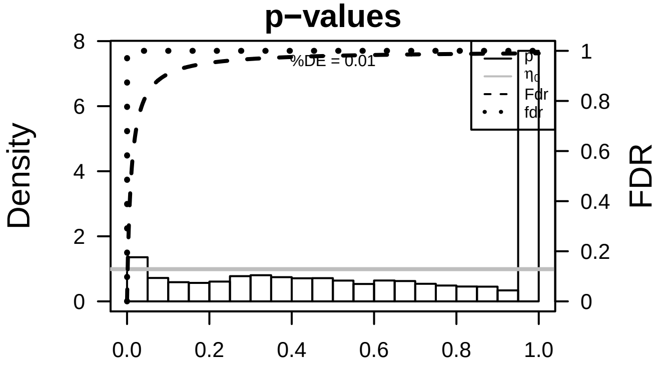


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_173219	0.79	−0.26	0.14	UTS2	urotensin 2 [Source:HGNC Symbol;Acc:HGNC:12636]
2	ILMN_180473	0.6	−0.28	0.23	RAVER2	ribonucleoprotein, PTB binding 2 [Source:HGNC Symbol;Acc
3	ILMN_327815	0.45	−0.27	0.16		
4	ILMN_171356	0.44	−0.3	0.22	LAMP5	lysosomal associated membrane protein family member 5 [Sc
5	ILMN_171757	0.39	−0.21	0.14	PGA5	pepsinogen 5, group I (pepsinogen A) [Source:HGNC Symbo
6	ILMN_204116	0.38	−0.28	0.12	DENND4A	DENN domain containing 4A [Source:HGNC Symbol;Acc:HG
7	ILMN_168225	0.38	−0.28	0.22		
8	ILMN_173857	0.38	−0.2	0.36	FILIP1L	filamin A interacting protein 1 like [Source:HGNC Symbol;Acc
9	ILMN_241331	0.36	−0.29	0.28	C15orf57	chromosome 15 open reading frame 57 [Source:HGNC Symb
10	ILMN_169625	0.35	−0.28	0.26	CYB5D2	cytochrome b5 domain containing 2 [Source:HGNC Symbol;A
11	ILMN_170933	0.34	−0.21	0.38		
12	ILMN_172753	0.34	−0.22	0.09	PGA4	pepsinogen 4, group I (pepsinogen A) [Source:HGNC Symbo
13	ILMN_322681	0.33	−0.19	0.35		
14	ILMN_172478	0.33	−0.27	0.3		
15	ILMN_206350	0.32	−0.3	0.24		
16	ILMN_167964	0.32	−0.36	0.21	FAM120B	family with sequence similarity 120B [Source:HGNC Symbol;A
17	ILMN_324357	0.32	−0.18	0.25		
18	ILMN_182536	0.31	−0.19	0.21		
19	ILMN_232502	0.31	−0.26	0.14	ODF2L	outer dense fiber of sperm tails 2 like [Source:HGNC Symbol;
20	ILMN_180597	0.31	−0.21	0.33	GPR19	G protein−coupled receptor 19 [Source:HGNC Symbol;Acc:H

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	1e−48	544 / 9815	Brain	Overlap_fetal_midbrain_ReprPC
2	6e−46	501 / 8771	Chror	5_Tx_Melanocytes
3	1e−45	508 / 8990	Chror	15_Quies_Fibroblasts
4	3e−45	618 / 12298	Chror	2_TssA_Melanocytes
5	2e−43	635 / 12983	Chror	2_TssA_Neuronal_Progenitor
6	2e−42	459 / 7854	Chror	5_Tx_Fibroblasts
7	4e−40	580 / 11455	Chror	2_TssA_Fibroblasts
8	6e−36	457 / 8226	Lympl	HOPP_Active_promoter
9	8e−34	554 / 11130	Chror	15_Quies_Melanocytes
10	1e−33	512 / 9917	Brain	Overlap_fetal_midbrain_ReprPCWk
11	2e−33	361 / 5936	Brain	Overlap_fetal_midbrain_HetRpts
12	3e−33	548 / 10999	Colon	TssWk_Colon
13	4e−29	391 / 6970	Chror	5_Tx_Neuronal_Progenitor
14	2e−28	485 / 9555	Colon	TssA_Colon
15	2e−27	429 / 8098	Lympl	HOPP_Weak_promoter
16	1e−26	448 / 8678	Colon	Quies3_Colon
17	4e−26	394 / 7275	Lympl	HOPP_Txn_elongation
18	5e−24	436 / 8568	Colon	TxWk_Colon
19	6e−22	562 / 12393	Chror	15_Quies_Neuronal_Progenitor
20	2e−21	257 / 4237	Chror	14_ZNF_Neuronal_Progenitor
21	1e−20	144 / 1846	Chror	14_ZNF_Melanocytes
22	4e−20	441 / 9054	Colon	Tx_Colon
23	3e−19	454 / 9504	Brain	Overlap_fetal_midbrain_K9K27me3
24	8e−19	343 / 6559	Lympl	HOPP_Weak_txn
25	9e−19	533 / 11836	Chror	3_TssF_Melanocytes
26	1e−14	548 / 12741	Chror	7_Enh_Melanocytes
27	6e−14	224 / 4034	Colon	TssD1_Colon
28	8e−13	133 / 2043	Glio	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
29	2e−12	89 / 1161	GSEA	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
30	4e−12	458 / 10430	Brain	Overlap_fetal_midbrain_Quies
31	1e−11	83 / 1083	Colon	ZNF_Colon
32	3e−11	328 / 6959	Lympl	HOPP_Weak_enhancer
33	4e−11	60 / 681	Brain	Overlap_fetal_midbrain_EnhP
34	5e−11	65 / 772	Lympl	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell li
35	6e−11	65 / 777	Lympl	WIRTH_lymphoma937_spot D
36	8e−11	66 / 800	GSEA	JOHNSTONE_PARVB_TARGETS_3_DN
37	2e−10	242 / 4828	CC	nucleus
38	9e−10	104 / 1623	Colon	Het_Colon
39	1e−09	54 / 630	Chror	14_ZNF_Fibroblasts
40	2e−09	63 / 812	GSEA	GEORGES_TARGETS_OF_MIR192_AND_MIR215


p−values

Aging

Rank	p−value	#in/all	Geneset
1	0.04	8 / 111	HORVATH_aging_genes meth DOWN
2	0.12	8 / 142	HORVATH_aging_genes meth UP
3	1.00	0 / 58	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Cancer

Rank	p−value	#in/all	Geneset
1	0.03	27 / 527	Lembcke_Normal vs Adenoma
2	0.04	6 / 73	SHAUGHNESSY_MM high risk
3	0.10	2 / 16	GENTLES_modul16
4	0.16	5 / 82	PanCan_JAK−ST_geneset_nanostring
5	0.22	6 / 117	PanCan_Driver_Gene_geneset_nanostring
6	0.22	0 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
7	0.29	3 / 54	KUIPER_MM poor survival
8	0.35	1 / 12	LIU_BREAST_CANCER
9	0.35	1 / 14	LIU_PROSTATE_CANCER_UP
10	0.36	8 / 193	PanCan_PI3K_geneset_nanostring
11	0.36	2 / 36	PanCan_HK_geneset_nanostring
12	0.37	1 / 13	GENTLES_modul12
13	0.37	0 / 15	LIU_PROSTATE_CANCER_DN
14	0.38	0 / 14	LIU_COMMON_CANCER_GENES
15	0.39	1 / 14	GENTLES_modul4

Chromatin states

Rank	p−value	#in/all	Geneset
1	6e−46	501 / 8771	5_Tx_Melanocytes
2	1e−45	508 / 8990	15_Quies_Fibroblasts
3	3e−45	618 / 12298	2_TssA_Melanocytes
4	2e−43	635 / 12983	2_TssA_Neuronal_Progenitor
5	2e−42	459 / 7854	5_Tx_Fibroblasts
6	4e−40	580 / 11455	2_TssA_Fibroblasts
7	8e−34	554 / 11130	15_Quies_Melanocytes
8	4e−29	391 / 6970	5_Tx_Neuronal_Progenitor
9	6e−22	562 / 12393	15_Quies_Neuronal_Progenitor
10	2e−21	257 / 4237	14_ZNF_Neuronal_Progenitor
11	1e−20	144 / 1846	14_ZNF_Melanocytes
12	9e−19	533 / 11836	3_TssF_Melanocytes
13	1e−14	548 / 12741	7_Enh_Melanocytes
14	1e−09	54 / 630	14_ZNF_Fibroblasts
15	6e−08	372 / 8613	7_Enh_Fibroblasts

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−12	89 / 1161	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
2	8e−11	66 / 800	JOHNSTONE_PARVB_TARGETS_3_DN
3	2e−09	63 / 812	GEORGES_TARGETS_OF_MIR192_AND_MIR215
4	6e−09	34 / 316	REACTOME_GENERIC_TRANSCRIPTION_PATHWAY
5	1e−08	99 / 1601	GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_DN
6	1e−07	46 / 569	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_DN
7	2e−07	78 / 1222	DODD_NASOPHARYNGEAL_CARCINOMA_DN
8	2e−07	58 / 811	LEE_BMP2_TARGETS_DN
9	3e−07	63 / 926	NUYTTEN_EZH2_TARGETS_DN
10	4e−07	35 / 393	ZHANG_BREAST_CANCER_PROGENITORS_UP
11	1e−06	55 / 797	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
12	1e−06	44 / 581	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_UP
13	7e−06	57 / 887	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
14	9e−06	39 / 527	HAMAI_APOPTOSIS_VIA_TRAIL_UP
15	8e−05	45 / 708	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_DN

Lymphoma

Rank	p−value	#in/all	Geneset
1	6e−36	457 / 8226	HOPP_Active_promoter
2	2e−27	429 / 8098	HOPP_Weak_promoter
3	4e−26	394 / 7275	HOPP_Txn_elongation
4	8e−19	343 / 6559	HOPP_Weak_txn
5	3e−11	328 / 6959	HOPP_Weak_enhancer
6	5e−11	65 / 772	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell line_
7	6e−11	65 / 777	WIRTH_lymphoma937_spot D
8	5e−08	77 / 1169	SPANG_BCR DN
9	9e−08	81 / 1270	SPANG_BCR UP
10	7e−06	23 / 232	WIRTH_lymphoma937_spot B
11	9e−06	22 / 220	Hopp_June14_MMML937 tumors+controls_group.overexpression_B_cell line_
12	1e−05	238 / 5356	HOPP_Txn_transition
13	3e−04	305 / 7448	HOPP_Strong_enhancer
14	1e−03	21 / 290	SPANG_IL21 UP
15	1e−02	26 / 464	WIRTH_lymphoma937_spot I

miRNA Disease

Rank	p−value	#in/all	Geneset
1	0.8	1 / 41	Melanoma, cutaneous malignant, 2
2	1.0	0 / 7	Thyroid carcinoma, papillary
3	1.0	0 / 123	Pancreatic cancer
4	1.0	0 / 68	Glioblastoma multiforme, somatic
5	1.0	0 / 63	Gastrointestinal
6	1.0	0 / 3	Pituitary adenoma
7	1.0	0 / 116	Cancer
8	1.0	0 / 95	Colorectal cancer
9	1.0	0 / 2	Adenomas, multiple colorectal
10	1.0	0 / 124	Prostate cancer
11	1.0	0 / 48	Alzheimer disease, susceptibility to
12	1.0	0 / 7	Schizophrenia, susceptibility to
13	1.0	0 / 20	Parkinson disease
14	1.0	0 / 65	Hepatocellular carcinoma
15	1.0	0 / 3	Down syndrome, risk of

Reference Signatures

Rank	p−value	#in/all	Geneset
1	4e−04	23 / 302	Chaussabel_3,4_Protein phosphatases
2	2e−03	11 / 113	Chaussabel_1,4_Replication
3	6e−03	17 / 248	Chaussabel_3,6_Mitochondrial ribosomal proteins
4	2e−02	15 / 231	Chaussabel_2,5_Immune related molecules
5	2e−02	4 / 29	Chaussabel_2,7_Unknown function
6	2e−02	40 / 816	PROTEINATLAS_endometrium
7	2e−02	15 / 242	Chaussabel_3,9_Kinases
8	2e−02	38 / 782	PROTEINATLAS_thyroid gland
9	3e−02	2 / 8	VAQUERIZAS_Tongue_TF
10	3e−02	10 / 148	VAQUERIZAS_General_TF
11	5e−02	13 / 221	Chaussabel_3,8_Enzymes
12	5e−02	9 / 139	Chaussabel_1,8_Metabolism Biosynthesis
13	6e−02	43 / 963	PROTEINATLAS_pancreas
14	7e−02	4 / 44	VAQUERIZAS_Whole brain_TF
15	9e−02	20 / 416	PROTEINATLAS_ovary

BP

Rank	p−value	#in/all	Geneset
1	1e−08	84 / 1272	regulation of transcription, DNA−templated
2	1e−07	98 / 1643	transcription, DNA−templated
3	8e−05	5 / 14	dolichol−linked oligosaccharide biosynthetic process
4	1e−04	6 / 23	tRNA methylation
5	8e−04	4 / 13	intraciliary transport
6	1e−03	4 / 15	folic acid metabolic process
7	3e−03	4 / 18	post−Golgi vesicle−mediated transport
8	5e−03	5 / 32	neuron apoptotic process
9	5e−03	14 / 184	translation
10	5e−03	4 / 21	nuclear−transcribed mRNA poly(A) tail shortening
11	6e−03	3 / 11	G−protein coupled purinergic nucleotide receptor signaling pathway
12	6e−03	3 / 11	sulfur amino acid metabolic process
13	7e−03	3 / 12	melanin biosynthetic process
14	8e−03	4 / 23	positive regulation of interleukin−12 production
15	8e−03	6 / 51	stem cell population maintenance

CC

Rank	p−value	#in/all	Geneset
1	2e−10	242 / 4828	nucleus
2	7e−06	41 / 561	intracellular membrane−bounded organelle
3	3e−04	137 / 2979	cytosol
4	4e−04	119 / 2535	nucleoplasm
5	1e−03	25 / 374	mitochondrial inner membrane
6	2e−03	15 / 179	nuclear speck
7	2e−03	65 / 1304	mitochondrion
8	4e−03	3 / 10	mitotic spindle pole
9	4e−03	3 / 10	npBAF complex
10	5e−03	198 / 4822	cytoplasm
11	8e−03	6 / 51	peroxisomal membrane
12	9e−03	11 / 139	microtubule cytoskeleton
13	1e−02	3 / 14	integral component of peroxisomal membrane
14	1e−02	8 / 88	peroxisome
15	1e−02	3 / 15	U1 snRNP

Colon Cancer

Rank	p−value	#in/all	Geneset
1	3e−33	548 / 10999	TssWk_Colon
2	2e−28	485 / 9555	TssA_Colon
3	1e−26	448 / 8678	Quies3_Colon
4	5e−24	436 / 8568	TxWk_Colon
5	4e−20	441 / 9054	Tx_Colon
6	6e−14	224 / 4034	TssD1_Colon
7	1e−11	83 / 1083	ZNF_Colon
8	9e−10	104 / 1623	Het_Colon
9	2e−07	76 / 1186	HetRpts_Colon
10	5e−06	81 / 1404	LaPointe_mucosa−position_kmeans_D_transverse colon_UP_
11	6e−06	392 / 9530	LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP_
12	6e−06	50 / 740	LaPointe_mucosa−position_kmeans_C_cecum colon_ascending colon_transv
13	1e−05	52 / 799	LaPointe_mucosa−position_kmeans_B_ascending colon_transverse colon_U
14	4e−05	203 / 4526	Quies1_Colon
15	5e−05	307 / 7354	TssF_Colon

HM

Rank	p−value	#in/all	Geneset
1	0.03	11 / 167	HALLMARK_OXIDATIVE_PHOSPHORYLATION
2	0.04	7 / 91	HALLMARK_PEROXISOME
3	0.11	10 / 183	HALLMARK_APICAL_JUNCTION
4	0.11	8 / 138	HALLMARK_FATTY_ACID_METABOLISM
5	0.15	6 / 103	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
6	0.15	9 / 173	HALLMARK_E2F_TARGETS
7	0.17	3 / 41	HALLMARK_APICAL_SURFACE
8	0.17	9 / 179	HALLMARK_G2M_CHECKPOINT
9	0.20	9 / 186	HALLMARK_ESTROGEN_RESPONSE_EARLY
10	0.21	5 / 91	HALLMARK_ANDROGEN_RESPONSE
11	0.24	8 / 170	HALLMARK_MYC_TARGETS_V1
12	0.26	8 / 175	HALLMARK_XENOBIOTIC_METABOLISM
13	0.27	8 / 176	HALLMARK_KRAS_SIGNALING_UP
14	0.29	3 / 54	HALLMARK_MYC_TARGETS_V2
15	0.33	7 / 162	HALLMARK_ALLOGRAFT_REJECTION

Melanoma

Rank	p−value	#in/all	Geneset
1	0.6	2 / 54	Hugo_melanoma−all−MET_DN
2	0.6	1 / 27	Hugo_melanoma−all−LEF1_UP
3	0.7	1 / 30	Hugo_melanoma−all−MET_UP
4	0.8	1 / 43	Hugo_melanoma−BRAFmut−MET_UP
5	1.0	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
6	1.0	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

miRNA target

Rank	p−value	#in/all	Geneset
1	2e−08	25 / 193	hsa−miR−513a−3p
2	5e−05	20 / 210	hsa−miR−29b
3	1e−04	29 / 389	hsa−miR−519a
4	1e−04	14 / 125	hsa−miR−383
5	1e−04	17 / 175	hsa−miR−29c
6	2e−04	39 / 602	hsa−miR−20a
7	2e−04	27 / 366	hsa−miR−519b−3p
8	3e−04	34 / 513	hsa−miR−106b
9	3e−04	16 / 169	hsa−miR−29a
10	4e−04	28 / 400	hsa−miR−519c−3p
11	5e−04	11 / 97	hsa−miR−624
12	7e−04	33 / 520	hsa−miR−106a
13	8e−04	8 / 57	hsa−miR−1260
14	8e−04	13 / 134	hsa−miR−155
15	1e−03	22 / 303	hsa−miR−548i

Telomeres

Rank	p−value	#in/all	Geneset
1	0.07	2 / 13	Alternative lengthening of telomeres
2	0.62	1 / 27	Nabetani_alt len telomeres_genes_ko
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Brain

Rank	p−value	#in/all	Geneset
1	1e−48	544 / 9815	Overlap_fetal_midbrain_ReprPC
2	1e−33	512 / 9917	Overlap_fetal_midbrain_ReprPCWk
3	2e−33	361 / 5936	Overlap_fetal_midbrain_HetRpts
4	3e−19	454 / 9504	Overlap_fetal_midbrain_K9K27me3
5	4e−12	458 / 10430	Overlap_fetal_midbrain_Quies
6	4e−11	60 / 681	Overlap_fetal_midbrain_EnhP
7	7e−06	77 / 1329	Overlap_fetal_midbrain_Enh
8	3e−05	65 / 1115	Overlap_fetal_midbrain_EnhG
9	6e−05	78 / 1436	Fetal_K9K27me3
10	2e−04	64 / 1171	Fetal_EnhP
11	9e−04	61 / 1162	Fetal_Enh
12	1e−03	37 / 630	Mid_Frontal_Lobe_EnhP
13	3e−03	118 / 2654	Fetal_Quies
14	9e−03	23 / 386	Fetal_ZNF
15	1e−02	46 / 937	Fetal_EnhG

Chr

Rank	p−value	#in/all	Geneset
1	0.004	47 / 902	Chr 4
2	0.005	57 / 1160	Chr 12
3	0.029	37 / 769	Chr 15
4	0.176	23 / 536	Chr 22
5	0.209	42 / 1060	Chr 5
6	0.221	36 / 904	Chr 10
7	0.300	17 / 422	Chr 13
8	0.348	29 / 768	Chr 14
9	0.356	37 / 994	Chr X
10	0.401	44 / 1211	Chr 6
11	0.527	12 / 342	Chr 18
12	0.531	29 / 836	Chr 8
13	0.566	40 / 1170	Chr 7
14	0.570	51 / 1492	Chr 2
15	0.635	49 / 1467	Chr 19

Glio

Rank	p−value	#in/all	Geneset
1	8e−13	133 / 2043	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
2	6e−06	54 / 820	Sturm_GBM_Meth_overexpression_E_G34_UP
3	2e−05	95 / 1777	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
4	3e−04	10 / 76	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
5	2e−03	22 / 316	WILLSCHER_GBM_Verhaak−PNwt & CL_up
6	5e−02	2 / 11	KIM amplified & overexpressed in LTS
7	7e−02	2 / 13	WILLSCHER_GBM_Verhaak−PNmut_up (M)
8	8e−02	4 / 47	Donson−innate immunity−associated with LTS in HGA
9	8e−02	4 / 48	Vishal_subnetwork signature of survival in GBM
10	9e−02	8 / 132	WILLSCHER_GBM_Verhaak−CL_up (C)
11	9e−02	2 / 15	VERHAAK_CL subtype
12	1e−01	1 / 4	WILLSCHER_GBM_Verhaak−PNmut_up (N)
13	2e−01	5 / 84	GIEZELT_GBM_WT_down_VS_mut
14	2e−01	5 / 89	GIEZELT_GBM_STSwt_up_VS_LTSwt
15	2e−01	5 / 96	Weller_LGG_1p19qDel−vs−intact_DOWN

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.004	5 / 31	DUMEAUX_Fasting enriched genes
2	0.191	1 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
3	0.228	5 / 94	DUMEAUX_Smoking enriched genes
4	0.452	1 / 17	DUMEAUX_High bmi enriched genes
5	0.756	4 / 147	Homuth_BMI−associated−genes_UP
6	0.979	3 / 211	Homuth_BMI−associated−genes_DN
7	1.000	0 / 10	DUMEAUX_Smoking literature genes up
8	1.000	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
9	1.000	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
10	1.000	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
11	1.000	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
12	1.000	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
13	1.000	0 / 10	DUMEAUX_Women normal BMI literature genes up
14	1.000	0 / 18	Huan_blood−pressure_SBP−signature
15	1.000	0 / 16	Huan_blood−pressure_DBP−signature

MF

Rank	p−value	#in/all	Geneset
1	2e−07	100 / 1717	metal ion binding
2	5e−07	88 / 1475	DNA binding
3	4e−04	353 / 8818	protein binding
4	4e−04	50 / 877	transcription factor activity, sequence−specific DNA binding
5	5e−04	14 / 145	nucleic acid binding
6	6e−03	13 / 169	structural constituent of ribosome
7	7e−03	3 / 12	G−protein coupled purinergic nucleotide receptor activity
8	7e−03	3 / 12	oxidoreductase activity, acting on paired donors, with incorporation or reductio
9	9e−03	3 / 13	Ral GTPase binding
10	1e−02	3 / 15	FAD binding
11	1e−02	3 / 15	magnesium ion transmembrane transporter activity
12	1e−02	7 / 74	thiol−dependent ubiquitin−specific protease activity
13	2e−02	7 / 77	electron carrier activity
14	3e−02	3 / 19	aspartic−type endopeptidase activity
15	3e−02	3 / 19	FK506 binding

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.06	2 / 12	BENTINK_src.2
2	0.08	2 / 14	BENTINK_ras.6
3	0.41	1 / 15	GUSTAFSON_PI3K_DN
4	1.00	0 / 14	GUSTAFSON_PI3K_UP
5	1.00	0 / 13	BENTINK_e2f3.1
6	1.00	0 / 13	BENTINK_e2f3.2
7	1.00	0 / 13	BENTINK_myc.1
8	1.00	0 / 12	BENTINK_ras.1
9	1.00	0 / 11	BENTINK_ras.4
10	1.00	0 / 13	BENTINK_src.10
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	5e−09	245 / 5067	ICGC_Taf1_targets
2	1e−07	253 / 5442	ICGC_Pmlsc71910_targets
3	4e−07	317 / 7247	ICGC_Runx3_targets
4	7e−07	302 / 6868	ICGC_Elf1_targets
5	8e−07	279 / 6267	ICGC_Yy1_targets
6	2e−06	118 / 2215	ICGC_GabpPcr2_targets
7	2e−06	225 / 4890	ICGC_Bclaf101388_targets
8	3e−06	96 / 1723	HEBENSTREIT_high expression TF
9	2e−05	241 / 5466	ICGC_Nficsc81335_targets
10	3e−05	258 / 5984	ICGC_Mta3_targets
11	4e−05	70 / 1231	KIM_MYC targets
12	4e−05	240 / 5518	ICGC_Stat5_targets
13	5e−05	196 / 4362	ICGC_Creb1_targets
14	6e−05	278 / 6578	ICGC_Pou2_targets
15	8e−05	233 / 5383	ICGC_Sp1_targets

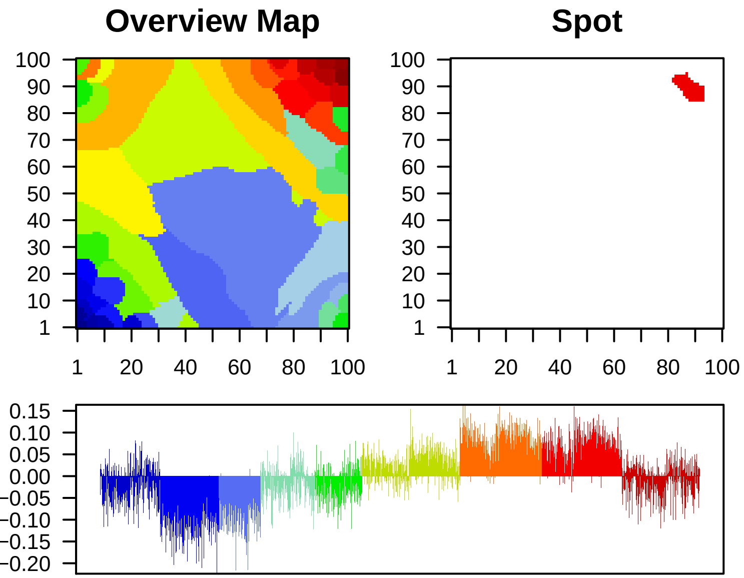
K−Means Cluster

Spot Summary: P1

metagenes = 78
genes = 521

<r> metagenes = 0.94
<r> genes = 0.33
beta: r2= 12.77 / log p= −Inf

samples with spot = 80 (2.4 %)
F * : 2 (0.4 %)
F J * : 49 (10.6 %)
J * : 29 (6.5 %)

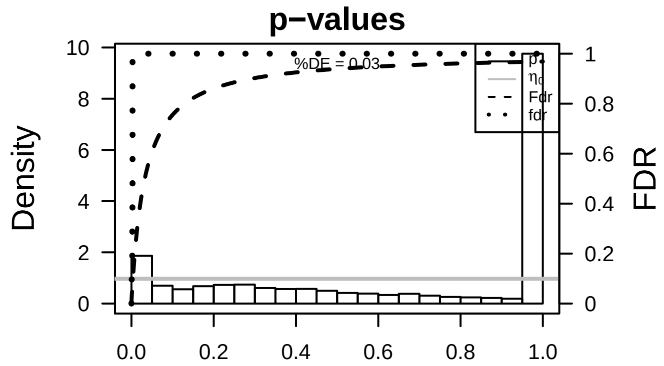


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_176457	1.25	−0.92	0.13		XIST 3' intron conserved motif [Source:RFAM;Acc:RF02266]
2	ILMN_323649	1.04	−0.81	0.19		
3	ILMN_179855	0.74	−0.54	0.37	FAM153A	family with sequence similarity 153 member A [Source:HGNC
4	ILMN_165559	0.73	−0.6	0.34	SERPINE2	serpin family E member 2 [Source:HGNC Symbol;Acc:HGNC
5	ILMN_177500	0.72	−0.55	0.31	NCAPD2	non−SMC condensin I complex subunit D2 [Source:HGNC Sy
6	ILMN_167424	0.71	−0.52	0.3		
7	ILMN_165968	0.71	−0.41	0.31	LGALS3BP	galectin 3 binding protein [Source:HGNC Symbol;Acc:HGNC:
8	ILMN_187512	0.7	−0.54	0.4		
9	ILMN_165140	0.7	−0.43	0.51		
10	ILMN_179894	0.68	−0.5	0.43	ANKRD55	ankyrin repeat domain 55 [Source:HGNC Symbol;Acc:HGNC
11	ILMN_234172	0.68	−0.5	0.4	ANKRD55	ankyrin repeat domain 55 [Source:HGNC Symbol;Acc:HGNC
12	ILMN_182197	0.66	−0.43	0.61		T cell receptor beta variable 29−1 [Source:HGNC Symbol;Acc
13	ILMN_167689	0.65	−0.57	0.33	ADCY3	adenylate cyclase 3 [Source:HGNC Symbol;Acc:HGNC:234]
14	ILMN_181027	0.64	−0.61	0.34	HOXB2	homeobox B2 [Source:HGNC Symbol;Acc:HGNC:5113]
15	ILMN_325141	0.63	−0.52	0.39	RBM43	RNA binding motif protein 43 [Source:HGNC Symbol;Acc:HG
16	ILMN_178429	0.62	−0.67	0.55		
17	ILMN_207859	0.61	−0.36	0.55		
18	ILMN_170808	0.6	−0.49	0.41	LCLAT1	lysocardiolipin acyltransferase 1 [Source:HGNC Symbol;Acc:I
19	ILMN_179789	0.6	−0.53	0.3	N4BP2L2	NEDD4 binding protein 2 like 2 [Source:HGNC Symbol;Acc:H
20	ILMN_166706	0.6	−0.54	0.59	ZC3HAV1	zinc finger CCCH−type containing, antiviral 1 [Source:HGNC

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	2e−47	363 / 11455	Chror	2_TssA_Fibroblasts
2	8e−46	374 / 12298	Chror	2_TssA_Melanocytes
3	2e−45	332 / 9815	Brain	Overlap_fetal_midbrain_ReprPC
4	4e−41	320 / 9555	Colon	TssA_Colon
5	1e−40	304 / 8771	Chror	5_Tx_Melanocytes
6	2e−39	375 / 12983	Chror	2_TssA_Neuronal_Progenitor
7	2e−39	291 / 8226	Lympl	HOPP_Active_promoter
8	5e−38	239 / 5936	Brain	Overlap_fetal_midbrain_HetRpts
9	1e−36	295 / 8678	Colon	Quies3_Colon
10	7e−36	277 / 7854	Chror	5_Tx_Fibroblasts
11	1e−35	291 / 8568	Colon	TxWk_Colon
12	3e−34	298 / 9054	Colon	Tx_Colon
13	2e−29	252 / 7275	Lympl	HOPP_Txn_elongation
14	3e−28	243 / 6970	Chror	5_Tx_Neuronal_Progenitor
15	1e−27	321 / 10999	Colon	TssWk_Colon
16	2e−25	331 / 11836	Chror	3_TssF_Melanocytes
17	3e−25	296 / 9917	Brain	Overlap_fetal_midbrain_ReprPCWk
18	8e−25	287 / 9504	Brain	Overlap_fetal_midbrain_K9K27me3
19	3e−23	336 / 12393	Chror	15_Quies_Neuronal_Progenitor
20	4e−23	255 / 8098	Lympl	HOPP_Weak_promoter
21	4e−21	268 / 8990	Chror	15_Quies_Fibroblasts
22	3e−19	186 / 5356	Lympl	HOPP_Txn_transition
23	5e−19	332 / 12741	Chror	7_Enh_Melanocytes
24	7e−19	303 / 11130	Chror	15_Quies_Melanocytes
25	5e−17	285 / 10430	Brain	Overlap_fetal_midbrain_Quies
26	6e−17	23 / 119	Refer	Chaussabel_2,8_T−cells
27	4e−16	171 / 5067	TF	ICGC_Taf1_targets
28	5e−16	221 / 7354	Colon	TssF_Colon
29	1e−15	54 / 811	GSEA	LEE_BMP2_TARGETS_DN
30	2e−12	47 / 772	Lympl	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell li
31	3e−12	47 / 777	Lympl	WIRTH_lymphoma937_spot D
32	5e−12	61 / 1222	GSEA	DODD_NASOPHARYNGEAL_CARCINOMA_DN
33	1e−11	253 / 9635	Chror	3_TssF_Fibroblasts
34	2e−11	78 / 1846	Chror	14_ZNF_Melanocytes
35	2e−11	58 / 1161	GSEA	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
36	2e−11	153 / 4890	TF	ICGC_Bclaf101388_targets
37	3e−11	61 / 1270	Lympl	SPANG_BCR UP
38	3e−11	96 / 2535	CC	nucleoplasm
39	4e−11	231 / 8613	Chror	7_Enh_Fibroblasts
40	4e−11	137 / 4237	Chror	14_ZNF_Neuronal_Progenitor



Aging

Rank	p−value	#in/all	Geneset
1	0.8	2 / 142	HORVATH_aging_genes meth UP
2	0.9	1 / 111	HORVATH_aging_genes meth DOWN
3	1.0	0 / 58	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	2e−07	62 / 1643	transcription, DNA−templated
2	1e−05	47 / 1272	regulation of transcription, DNA−templated
3	1e−04	9 / 102	protein sumoylation
4	2e−04	7 / 61	snRNA transcription from RNA polymerase II promoter
5	2e−04	16 / 300	cell division
6	3e−04	11 / 163	rRNA processing
7	3e−04	8 / 91	sister chromatid cohesion
8	7e−04	6 / 56	double−strand break repair
9	9e−04	7 / 81	viral transcription
10	1e−03	11 / 187	DNA repair
11	1e−03	3 / 11	DNA strand elongation involved in DNA replication
12	1e−03	5 / 41	beta−catenin−TCF complex assembly
13	1e−03	4 / 26	adipose tissue development
14	2e−03	4 / 27	telomere maintenance via recombination
15	2e−03	3 / 13	mitotic chromosome condensation

Brain

Rank	p−value	#in/all	Geneset
1	2e−45	332 / 9815	Overlap_fetal_midbrain_ReprPC
2	5e−38	239 / 5936	Overlap_fetal_midbrain_HetRpts
3	3e−25	296 / 9917	Overlap_fetal_midbrain_ReprPCWk
4	8e−25	287 / 9504	Overlap_fetal_midbrain_K9K27me3
5	5e−17	285 / 10430	Overlap_fetal_midbrain_Quies
6	4e−07	34 / 681	Overlap_fetal_midbrain_EnhP
7	5e−04	25 / 630	Mid_Frontal_Lobe_EnhP
8	6e−04	85 / 3164	Mid_Frontal_Lobe_ZNF
9	1e−03	44 / 1436	Fetal_K9K27me3
10	1e−02	34 / 1171	Fetal_EnhP
11	4e−02	23 / 818	Mid_Frontal_Lobe_Het
12	6e−02	30 / 1162	Fetal_Enh
13	1e−01	10 / 328	Fetal_Het
14	1e−01	23 / 906	Fetal_HetRpts
15	1e−01	20 / 796	Overlap_fetal_midbrain_ZNF

Cancer

Rank	p−value	#in/all	Geneset
1	5e−04	22 / 527	Lembcke_Normal vs Adenoma
2	2e−02	2 / 13	RHODES_CANCER_META_SIGNATURE
3	3e−02	2 / 14	GENTLES_modul4
4	4e−02	3 / 38	KUIPER_MM good survival
5	4e−02	2 / 16	GENTLES_modul7
6	4e−02	0 / 15	LIU_PROSTATE_CANCER_DN
7	9e−02	1 / 14	RHODES_UNDIFFERENTIATED_CANCER
8	1e−01	0 / 14	LIU_COMMON_CANCER_GENES
9	2e−01	1 / 9	GENTLES_modul3
10	2e−01	3 / 73	SHAUGHNESSY_MM high risk
11	2e−01	1 / 13	GENTLES_modul6
12	2e−01	1 / 14	GENTLES_modul1
13	2e−01	1 / 14	GENTLES_modul10
14	3e−01	1 / 15	WOLFER_overlap genes
15	3e−01	1 / 16	GENTLES_modul16

CC

Rank	p−value	#in/all	Geneset
1	3e−11	96 / 2535	nucleoplasm
2	3e−09	144 / 4828	nucleus
3	1e−08	56 / 1304	mitochondrion
4	2e−08	38 / 721	nucleolus
5	2e−05	7 / 44	Cajal body
6	3e−04	122 / 4822	cytoplasm
7	5e−04	81 / 2979	cytosol
8	6e−04	7 / 75	condensed chromosome kinetochore
9	9e−04	17 / 374	mitochondrial inner membrane
10	1e−03	14 / 287	mitochondrial matrix
11	1e−03	4 / 26	condensed chromosome
12	3e−03	16 / 379	centrosome
13	4e−03	3 / 17	pericentriolar material
14	5e−03	3 / 19	transcription elongation factor complex
15	6e−03	4 / 38	ciliary tip

Chr

Rank	p−value	#in/all	Geneset
1	0.003	44 / 1492	Chr 2
2	0.056	30 / 1160	Chr 12
3	0.148	19 / 768	Chr 14
4	0.152	23 / 959	Chr 16
5	0.183	11 / 422	Chr 13
6	0.206	9 / 342	Chr 18
7	0.217	24 / 1060	Chr 5
8	0.276	20 / 904	Chr 10
9	0.277	21 / 954	Chr 9
10	0.431	20 / 994	Chr X
11	0.544	23 / 1217	Chr 3
12	0.605	14 / 769	Chr 15
13	0.649	16 / 902	Chr 4
14	0.675	26 / 1467	Chr 19
15	0.694	9 / 536	Chr 22

Chromatin states

Rank	p−value	#in/all	Geneset
1	2e−47	363 / 11455	2_TssA_Fibroblasts
2	8e−46	374 / 12298	2_TssA_Melanocytes
3	1e−40	304 / 8771	5_Tx_Melanocytes
4	2e−39	375 / 12983	2_TssA_Neuronal_Progenitor
5	7e−36	277 / 7854	5_Tx_Fibroblasts
6	3e−28	243 / 6970	5_Tx_Neuronal_Progenitor
7	2e−25	331 / 11836	3_TssF_Melanocytes
8	3e−23	336 / 12393	15_Quies_Neuronal_Progenitor
9	4e−21	268 / 8990	15_Quies_Fibroblasts
10	5e−19	332 / 12741	7_Enh_Melanocytes
11	7e−19	303 / 11130	15_Quies_Melanocytes
12	1e−11	253 / 9635	3_TssF_Fibroblasts
13	2e−11	78 / 1846	14_ZNF_Melanocytes
14	4e−11	231 / 8613	7_Enh_Fibroblasts
15	4e−11	137 / 4237	14_ZNF_Neuronal_Progenitor

Colon Cancer

Rank	p−value	#in/all	Geneset
1	4e−41	320 / 9555	TssA_Colon
2	1e−36	295 / 8678	Quies3_Colon
3	1e−35	291 / 8568	TxWk_Colon
4	3e−34	298 / 9054	Tx_Colon
5	1e−27	321 / 10999	TssWk_Colon
6	5e−16	221 / 7354	TssF_Colon
7	5e−11	51 / 965	Pentrack_CRC_TCGA_corr_R_normal_DN
8	3e−10	53 / 1083	ZNF_Colon
9	1e−08	42 / 831	Pentrack_CRC_TCGA_group.over_C_normal_DN
10	3e−08	262 / 10779	Enh_Colon
11	2e−07	149 / 5373	EnhWk1_Colon
12	3e−07	165 / 6138	TssD2_Colon
13	1e−06	55 / 1468	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
14	2e−06	116 / 4034	TssD1_Colon
15	4e−05	65 / 2073	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t

Glio

Rank	p−value	#in/all	Geneset
1	1e−06	63 / 1777	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
2	4e−06	68 / 2043	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
3	2e−05	34 / 820	Sturm_GBM_Meth_overexpression_E_G34_UP
4	2e−03	17 / 401	Down_b
5	1e−02	6 / 98	WILLSCHER_GBM_proteomics_wtOnly_SpotB
6	2e−02	12 / 315	Up
7	3e−02	2 / 15	VERHAAK_NL subtype
8	4e−02	4 / 65	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
9	6e−02	13 / 419	Down_a
10	7e−02	1 / 4	WILLSCHER_GBM_Verhaak−CL_up (E)
11	8e−02	6 / 157	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
12	9e−02	1 / 5	Phillips Prolif up vs PN & MES
13	9e−02	5 / 126	Hopp_Sturm_GBM_Epi3_A1_Mesenchymal_UP
14	1e−01	4 / 100	GIEZELT_GBM_STS_down_VS_LTS
15	1e−01	1 / 8	WILLSCHER_GBM_STSwt_proteomics−N_UP

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−15	54 / 811	LEE_BMP2_TARGETS_DN
2	5e−12	61 / 1222	DODD_NASOPHARYNGEAL_CARCINOMA_DN
3	2e−11	58 / 1161	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
4	8e−10	62 / 1417	PUJANA_BRCA1_PCC_NETWORK
5	9e−10	32 / 478	STEIN_ESRRA_TARGETS
6	9e−10	67 / 1601	GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_DN
7	1e−08	55 / 1265	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
8	2e−08	43 / 887	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
9	6e−08	24 / 345	STEIN_ESRRA_TARGETS_UP
10	8e−08	39 / 797	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
11	2e−07	24 / 373	PUJANA_BRCA2_PCC_NETWORK
12	4e−07	35 / 716	WEI_MYCN_TARGETS_WITH_E_BOX
13	6e−07	24 / 393	ZHANG_BREAST_CANCER_PROGENITORS_UP
14	7e−07	33 / 669	PUJANA_CHEK2_PCC_NETWORK
15	1e−06	8 / 43	REACTOME_METABOLISM_OF_NON_CODING_RNA

HM

Rank	p−value	#in/all	Geneset
1	0.003	8 / 130	HALLMARK_DNA_REPAIR
2	0.004	8 / 132	HALLMARK_UV_RESPONSE_DN
3	0.005	9 / 167	HALLMARK_OXIDATIVE_PHOSPHORYLATION
4	0.010	9 / 186	HALLMARK_IL2_STAT5_SIGNALING
5	0.030	5 / 91	HALLMARK_PEROXISOME
6	0.120	6 / 176	HALLMARK_ADIPOGENESIS
7	0.121	5 / 137	HALLMARK_UV_RESPONSE_UP
8	0.127	6 / 179	HALLMARK_G2M_CHECKPOINT
9	0.134	4 / 103	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
10	0.176	2 / 40	HALLMARK_WNT_BETA_CATENIN_SIGNALING
11	0.224	5 / 170	HALLMARK_MYC_TARGETS_V1
12	0.234	5 / 173	HALLMARK_E2F_TARGETS
13	0.245	5 / 176	HALLMARK_KRAS_SIGNALING_UP
14	0.274	2 / 54	HALLMARK_MYC_TARGETS_V2
15	0.379	2 / 69	HALLMARK_CHOLESTEROL_HOMEOSTASIS

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.003	4 / 32	Marjolein_ageing−genes_DN
2	0.117	2 / 31	DUMEAUX_Fasting enriched genes
3	0.307	4 / 147	Homuth_BMI−associated−genes_UP
4	0.572	4 / 211	Homuth_BMI−associated−genes_DN
5	1.000	0 / 94	DUMEAUX_Smoking enriched genes
6	1.000	0 / 10	DUMEAUX_Smoking literature genes up
7	1.000	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
8	1.000	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
9	1.000	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
10	1.000	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
11	1.000	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
12	1.000	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
13	1.000	0 / 10	DUMEAUX_Women normal BMI literature genes up
14	1.000	0 / 17	DUMEAUX_High bmi enriched genes
15	1.000	0 / 18	Huan_blood−pressure_SBP−signature

Lymphoma

Rank	p−value	#in/all	Geneset
1	2e−39	291 / 8226	HOPP_Active_promoter
2	2e−29	252 / 7275	HOPP_Txn_elongation
3	4e−23	255 / 8098	HOPP_Weak_promoter
4	3e−19	186 / 5356	HOPP_Txn_transition
5	2e−12	47 / 772	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell line_
6	3e−12	47 / 777	WIRTH_lymphoma937_spot D
7	3e−11	61 / 1270	SPANG_BCR UP
8	8e−11	196 / 6959	HOPP_Weak_enhancer
9	3e−08	178 / 6559	HOPP_Weak_txn
10	3e−07	192 / 7448	HOPP_Strong_enhancer
11	4e−07	15 / 158	WIRTH_lymphoma937_spot C
12	4e−07	15 / 159	Hopp_June14_MMML937 tumors+controls_group.overexpression_C_cell line_
13	1e−03	14 / 283	TARTE_Plasmablast signature
14	1e−03	9 / 139	Hopp_June14_MMML937 tumors+controls_group.overexpression_F_FL_tons
15	2e−03	9 / 141	WIRTH_lymphoma937_spot F

Melanoma

Rank	p−value	#in/all	Geneset
1	0.4	1 / 30	Hugo_melanoma−all−MET_UP
2	0.6	1 / 43	Hugo_melanoma−BRAFmut−MET_UP
3	1.0	0 / 54	Hugo_melanoma−all−MET_DN
4	1.0	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
5	1.0	0 / 27	Hugo_melanoma−all−LEF1_UP
6	1.0	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

MF

Rank	p−value	#in/all	Geneset
1	3e−08	224 / 8818	protein binding
2	3e−05	57 / 1717	metal ion binding
3	7e−04	46 / 1475	DNA binding
4	1e−03	5 / 41	core promoter sequence−specific DNA binding
5	2e−03	10 / 169	structural constituent of ribosome
6	2e−03	4 / 29	rRNA binding
7	2e−03	5 / 49	cysteine−type endopeptidase activity
8	4e−03	3 / 17	histone methyltransferase activity (H3−K4 specific)
9	4e−03	16 / 399	RNA binding
10	8e−03	38 / 1329	ATP binding
11	1e−02	4 / 45	tRNA binding
12	1e−02	2 / 10	adenyl−nucleotide exchange factor activity
13	1e−02	2 / 10	nucleoside kinase activity
14	1e−02	2 / 10	proteasome binding
15	1e−02	4 / 50	catalytic activity

miRNA Disease

Rank	p−value	#in/all	Geneset
1	1	0 / 7	Thyroid carcinoma, papillary
2	1	0 / 123	Pancreatic cancer
3	1	0 / 68	Glioblastoma multiforme, somatic
4	1	0 / 63	Gastrointestinal
5	1	0 / 3	Pituitary adenoma
6	1	0 / 116	Cancer
7	1	0 / 95	Colorectal cancer
8	1	0 / 2	Adenomas, multiple colorectal
9	1	0 / 124	Prostate cancer
10	1	0 / 48	Alzheimer disease, susceptibility to
11	1	0 / 7	Schizophrenia, susceptibility to
12	1	0 / 20	Parkinson disease
13	1	0 / 65	Hepatocellular carcinoma
14	1	0 / 3	Down syndrome, risk of
15	1	0 / 127	Melanoma and neural system tumor syndrome

miRNA target

Rank	p−value	#in/all	Geneset
1	3e−06	26 / 489	hsa−miR−16
2	3e−06	13 / 141	hsa−miR−522
3	5e−06	22 / 382	hsa−let−7c
4	7e−06	26 / 516	hsa−miR−15a
5	3e−05	24 / 493	hsa−miR−103
6	4e−05	19 / 343	hsa−let−7a
7	5e−05	23 / 480	hsa−miR−15b
8	7e−05	18 / 331	hsa−let−7g
9	7e−05	21 / 425	hsa−let−7b
10	8e−05	13 / 190	hsa−miR−128
11	8e−05	23 / 491	hsa−miR−107
12	9e−05	10 / 119	hsa−miR−509−3p
13	2e−04	20 / 419	hsa−miR−497
14	2e−04	15 / 272	hsa−miR−101
15	3e−04	17 / 342	hsa−let−7e

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.2	1 / 13	BENTINK_myc.1
2	0.3	1 / 15	GUSTAFSON_PI3K_DN
3	1.0	0 / 14	GUSTAFSON_PI3K_UP
4	1.0	0 / 13	BENTINK_e2f3.1
5	1.0	0 / 13	BENTINK_e2f3.2
6	1.0	0 / 12	BENTINK_ras.1
7	1.0	0 / 11	BENTINK_ras.4
8	1.0	0 / 14	BENTINK_ras.6
9	1.0	0 / 13	BENTINK_src.10
10	1.0	0 / 12	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Reference Signatures

Rank	p−value	#in/all	Geneset
1	6e−17	23 / 119	Chaussabel_2,8_T−cells
2	1e−06	17 / 221	Chaussabel_3,8_Enzymes
3	2e−06	19 / 275	Chaussabel_3,7_Spliceosome
4	1e−05	45 / 1194	PROTEINATLAS_stomach
5	3e−05	41 / 1097	PROTEINATLAS_kidney
6	3e−05	40 / 1063	PROTEINATLAS_tonsil
7	7e−05	42 / 1173	PROTEINATLAS_rectum
8	3e−04	40 / 1167	PROTEINATLAS_gallbladder
9	3e−04	33 / 912	PROTEINATLAS_urinary bladder
10	4e−04	41 / 1239	PROTEINATLAS_testis
11	5e−04	28 / 740	PROTEINATLAS_esophagus
12	8e−04	27 / 724	PROTEINATLAS_lymph node
13	9e−04	24 / 619	PROTEINATLAS_salivary gland
14	1e−03	32 / 929	PROTEINATLAS_bronchus
15	1e−03	34 / 1016	PROTEINATLAS_cerebral cortex

Telomeres

Rank	p−value	#in/all	Geneset
1	1	0 / 13	Alternative lengthening of telomeres
2	1	0 / 27	Nabetani_alt len telomeres_genes_ko
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	4e−16	171 / 5067	ICGC_Taf1_targets
2	2e−11	153 / 4890	ICGC_Bclaf101388_targets
3	5e−11	164 / 5442	ICGC_Pmlsc71910_targets
4	1e−10	181 / 6267	ICGC_Yy1_targets
5	6e−10	191 / 6868	ICGC_Elf1_targets
6	9e−10	159 / 5410	ICGC_Foxm1_targets
7	1e−09	147 / 4881	ICGC_Atf2_targets
8	1e−09	83 / 2215	ICGC_GabpPcr2_targets
9	2e−09	160 / 5518	ICGC_Stat5_targets
10	4e−09	158 / 5466	ICGC_Nficsc81335_targets
11	4e−09	169 / 5984	ICGC_Mta3_targets
12	7e−09	155 / 5383	ICGC_Sp1_targets
13	8e−09	180 / 6552	ICGC_Pol2_targets
14	9e−09	132 / 4362	ICGC_Creb1_targets
15	1e−08	180 / 6578	ICGC_Pou2_targets

K−Means Cluster

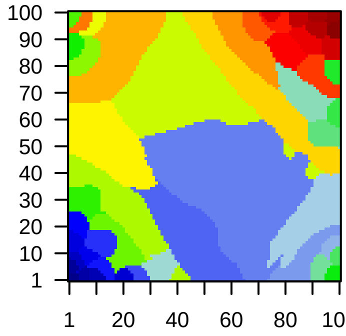
Spot Summary: Q1

metagenes = 26
genes = 507

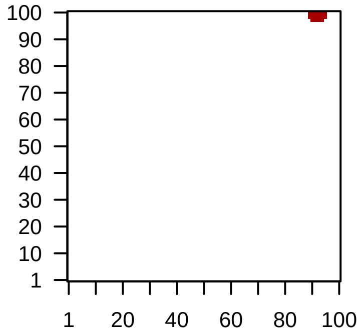
<r> metagenes = 0.97
<r> genes = 0.51
beta: r2= 74.06 / log p= −Inf

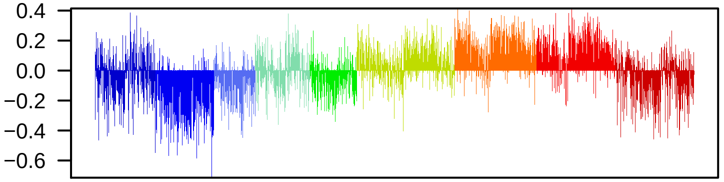
samples with spot = 875 (25.8 %)
- A * : 59 (17.2 %)
- A C * : 2 (0.6 %)
- A C F * : 8 (3.4 %)
- A F * : 61 (19.8 %)
- C F * : 11 (4.2 %)
- F * : 174 (31.4 %)
- F J * : 278 (60 %)
- J * : 240 (53.7 %)
- N * : 42 (9.5 %)

Overview Map



Spot





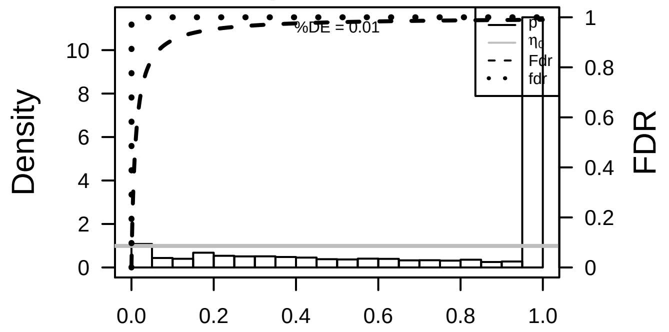
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_239376	2.36	−2.48	0.31	IGLL1	immunoglobulin lambda like polypeptide 1 [Source:HGNC Syı
2	ILMN_177365	1.78	−1.17	0.57	LRRN3	leucine rich repeat neuronal 3 [Source:HGNC Symbol;Acc:H(
3	ILMN_169107	1.77	−1.46	0.52	FCRLA	Fc receptor like A [Source:HGNC Symbol;Acc:HGNC:18504]
4	ILMN_177245	1.73	−2.05	0.39	RPS23	ribosomal protein S23 [Source:HGNC Symbol;Acc:HGNC:10
5	ILMN_168027	1.73	−0.94	0.33		immunoglobulin kappa variable 1−33 [Source:HGNC Symbol;
6	ILMN_240485	1.7	−1.35	0.33	RPL14	ribosomal protein L14 [Source:HGNC Symbol;Acc:HGNC:10
7	ILMN_173487	1.64	−1.96	0.57	CD79A	CD79a molecule [Source:HGNC Symbol;Acc:HGNC:1698]
8	ILMN_178270	1.6	−1.28	0.43		
9	ILMN_165379	1.59	−1.31	0.31		
10	ILMN_233792	1.41	−1.24	0.63	CXCR5	C−X−C motif chemokine receptor 5 [Source:HGNC Symbol;A
11	ILMN_165303	1.4	−1.48	0.44		
12	ILMN_170014	1.38	−1.08	0.5	VPREB3	pre−B lymphocyte 3 [Source:HGNC Symbol;Acc:HGNC:1271
13	ILMN_169022	1.38	−0.68	0.4	CNTNAP2	contactin associated protein−like 2 [Source:HGNC Symbol;A
14	ILMN_236621	1.34	−1.34	0.55	CD79B	CD79b molecule [Source:HGNC Symbol;Acc:HGNC:1699]
15	ILMN_171513	1.34	−1.58	0.84	CCR7	C−C motif chemokine receptor 7 [Source:HGNC Symbol;Acc:
16	ILMN_230275	1.33	−1.08	0.53	FCGBP	Fc fragment of IgG binding protein [Source:HGNC Symbol;A
17	ILMN_177554	1.28	−1.27	0.86	FCMR	Fc fragment of IgM receptor [Source:HGNC Symbol;Acc:HG
18	ILMN_178543	1.28	−0.95	0.48	CD79B	CD79b molecule [Source:HGNC Symbol;Acc:HGNC:1699]
19	ILMN_172646	1.26	−1.1	0.76	RPL14	ribosomal protein L14 [Source:HGNC Symbol;Acc:HGNC:10
20	ILMN_170042	1.24	−0.89	0.45		

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	6e−42	42 / 132	Refer	Chaussabel_1,7_MHC Ribosomal proteins
2	4e−41	40 / 119	Refer	Chaussabel_2,8_T−cells
3	1e−24	23 / 65	BP	SRP−dependent cotranslational protein targeting to membrane
4	3e−24	28 / 119	Refer	Chaussabel_2,4_Ribosomal proteins
5	3e−23	21 / 56	GSEA	REACTOME_PEPTIDE_CHAIN_ELONGATION
6	4e−22	23 / 81	BP	viral transcription
7	1e−21	24 / 96	BP	translational initiation
8	3e−21	21 / 68	GSEA	REACTOME_INFLUENZA_VIRAL_RNA_TRANSCRIPTION_AND_REPLIC
9	5e−21	21 / 69	GSEA	REACTOME_3_UTR_MEDIATED_TRANSLATIONAL_REGULATION
10	2e−20	16 / 32	Lifest	Marjolein_ageing−genes_DN
11	2e−20	21 / 74	GSEA	REACTOME_SRP_DEPENDENT_COTRANSLATIONAL_PROTEIN_TARG
12	3e−20	28 / 163	BP	rRNA processing
13	5e−20	22 / 87	BP	nuclear−transcribed mRNA catabolic process, nonsense−mediated decay
14	7e−20	19 / 58	GSEA	KEGG_RIBOSOME
15	9e−20	23 / 101	GSEA	REACTOME_TRANSLATION
16	6e−19	20 / 74	GSEA	REACTOME_NONSENSE_MEDIATED_DECAY_ENHANCED_BY_THE_E
17	1e−18	22 / 99	GSEA	REACTOME_INFLUENZA_LIFE_CYCLE
18	8e−17	33 / 317	GSEA	HSIAO_HOUSEKEEPING_GENES
19	9e−17	53 / 831	Colon	Pentrack_CRC_TCGA_group.over_C_normal_DN
20	1e−16	26 / 184	BP	translation
21	3e−16	15 / 44	GSEA	BILANGES_SERUM_AND_RAPAMYCIN_SENSITIVE_GENES
22	5e−16	26 / 196	GSEA	REACTOME_METABOLISM_OF_RNA
23	2e−15	23 / 155	GSEA	REACTOME_METABOLISM_OF_MRNA
24	5e−15	56 / 1013	MF	poly(A) RNA binding
25	1e−14	22 / 151	GSEA	JISON_SICKLE_CELL_DISEASE_DN
26	1e−14	23 / 169	MF	structural constituent of ribosome
27	7e−12	49 / 965	Colon	Pentrack_CRC_TCGA_corr_R_normal_DN
28	7e−12	35 / 529	GSEA	CAIRO_HEPATOBLASTOMA_CLASSES_UP
29	8e−12	12 / 45	CC	cytosolic large ribosomal subunit
30	2e−11	28 / 354	GSEA	REACTOME_METABOLISM_OF_PROTEINS
31	2e−11	10 / 28	CC	cytosolic small ribosomal subunit
32	1e−10	11 / 43	GSEA	TIEN_INTESTINE_PROBIOTICS_6HR_UP
33	2e−10	11 / 46	GSEA	LEE_EARLY_T_LYMPHOCYTE_DN
34	3e−10	10 / 36	GSEA	CHNG_MULTIPLE_MYELOMA_HYPERPLOID_UP
35	5e−10	9 / 28	GSEA	REACTOME_FORMATION_OF_THE_TERNARY_COMPLEX_AND_SUBS
36	7e−10	11 / 51	Refer	Chaussabel_1,3_B−cells
37	1e−09	27 / 402	GSEA	SMID_BREAST_CANCER_NORMAL_LIKE_UP
38	2e−09	16 / 139	Lymp	Hopp_June14_MMML937 tumors+controls_group.overexpression_F_FL_to
39	2e−09	16 / 141	Lymp	WIRTH_lymphoma937_spot F
40	5e−09	9 / 35	GSEA	REACTOME_ACTIVATION_OF_THE_MRNA_UPON_BINDING_OF_THE_

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.04	5 / 111	HORVATH_aging_genes meth DOWN
2	0.70	2 / 142	HORVATH_aging_genes meth UP
3	1.00	0 / 58	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	1e−24	23 / 65	SRP−dependent cotranslational protein targeting to membrane
2	4e−22	23 / 81	viral transcription
3	1e−21	24 / 96	translational initiation
4	3e−20	28 / 163	rRNA processing
5	5e−20	22 / 87	nuclear−transcribed mRNA catabolic process, nonsense−mediated decay
6	1e−16	26 / 184	translation
7	2e−06	5 / 14	ribosomal small subunit biogenesis
8	8e−06	6 / 29	B cell receptor signaling pathway
9	4e−05	4 / 12	maturation of LSU−rRNA
10	4e−05	4 / 12	maturation of SSU−rRNA
11	9e−05	7 / 63	T cell costimulation
12	5e−04	3 / 10	ribosomal small subunit assembly
13	9e−04	4 / 26	maturation of SSU−rRNA from tricistronic rRNA transcript (SSU−rRNA, 5.8S r
14	1e−03	4 / 28	T cell differentiation in thymus
15	2e−03	13 / 293	immune response

Brain

Rank	p−value	#in/all	Geneset
1	3e−06	14 / 180	Overlap_fetal_midbrain_Het
2	2e−04	28 / 796	Overlap_fetal_midbrain_ZNF
3	6e−02	22 / 906	Fetal_HetRpts
4	1e−01	19 / 818	Mid_Frontal_Lobe_Het
5	2e−01	9 / 386	Fetal_ZNF
6	2e−01	59 / 3164	Mid_Frontal_Lobe_ZNF
7	4e−01	21 / 1171	Fetal_EnhP
8	5e−01	47 / 2709	Mid_Frontal_Lobe_HetRpts
9	5e−01	46 / 2654	Fetal_Quies
10	7e−01	23 / 1506	Mid_Frontal_Lobe_Quies
11	8e−01	26 / 1728	Fetal_ReprPCWk
12	8e−01	153 / 9504	Overlap_fetal_midbrain_K9K27me3
13	8e−01	4 / 328	Fetal_Het
14	8e−01	8 / 630	Mid_Frontal_Lobe_EnhP
15	8e−01	1 / 110	Overlap_fetal_midbrain_Tx

Cancer

Rank	p−value	#in/all	Geneset
1	1e−04	4 / 16	GENTLES_modul11
2	5e−04	5 / 39	ZHANG_MM up
3	1e−03	3 / 13	GENTLES_modul18
4	2e−02	2 / 13	GENTLES_modul12
5	3e−02	2 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
6	5e−02	15 / 554	Lembcke_Colonic Inflammation
7	6e−02	0 / 13	RHODES_CANCER_META_SIGNATURE
8	1e−01	1 / 6	ZHANG_MGUS up
9	1e−01	2 / 36	PanCan_HK_geneset_nanostring
10	1e−01	1 / 9	GENTLES_modul5
11	2e−01	1 / 13	WANG_ER_DN
12	2e−01	1 / 13	GENTLES_modul6
13	2e−01	1 / 14	LIU_COMMON_CANCER_GENES
14	2e−01	1 / 14	BEN−PORATH_UP
15	2e−01	1 / 14	GENTLES_modul13

CC

Rank	p−value	#in/all	Geneset
1	8e−12	12 / 45	cytosolic large ribosomal subunit
2	2e−11	10 / 28	cytosolic small ribosomal subunit
3	7e−08	9 / 46	ribosome
4	9e−08	34 / 721	nucleolus
5	7e−06	60 / 1979	membrane
6	1e−05	19 / 352	focal adhesion
7	2e−05	5 / 21	U4/U6 x U5 tri−snRNP complex
8	5e−05	9 / 101	intracellular ribonucleoprotein complex
9	1e−04	4 / 16	small nuclear ribonucleoprotein complex
10	2e−04	4 / 17	T cell receptor complex
11	3e−04	75 / 2979	cytosol
12	6e−04	10 / 167	external side of plasma membrane
13	9e−04	3 / 12	small ribosomal subunit
14	2e−03	4 / 30	immunological synapse
15	2e−03	3 / 15	U5 snRNP

Chr

Rank	p−value	#in/all	Geneset
1	0.09	27 / 1211	Chr 6
2	0.09	26 / 1160	Chr 12
3	0.09	29 / 1318	Chr 17
4	0.13	26 / 1217	Chr 3
5	0.26	21 / 1060	Chr 5
6	0.29	9 / 422	Chr 13
7	0.33	19 / 994	Chr X
8	0.35	42 / 2323	Chr 1
9	0.36	6 / 289	Chr 21
10	0.54	13 / 769	Chr 15
11	0.56	9 / 536	Chr 22
12	0.60	10 / 619	Chr 20
13	0.61	19 / 1170	Chr 7
14	0.74	14 / 954	Chr 9
15	0.76	12 / 836	Chr 8

Chromatin states

Rank	p−value	#in/all	Geneset
1	1e−05	21 / 416	4_TxTrans_Neuronal_Progenitor
2	6e−04	54 / 2028	4_TxTrans_Melanocytes
3	1e−02	75 / 3450	4_TxTrans_Fibroblasts
4	1e−02	31 / 1206	6_EnhG_Neuronal_Progenitor
5	1e−01	91 / 4795	6_EnhG_Fibroblasts
6	1e−01	106 / 5699	6_EnhG_Melanocytes
7	5e−01	119 / 6970	5_Tx_Neuronal_Progenitor
8	1e+00	192 / 12298	2_TssA_Melanocytes
9	1e+00	12 / 1154	11_K9K27me3_Neuronal_Progenitor
10	1e+00	14 / 1324	13_HetRpts_Fibroblasts
11	1e+00	21 / 1846	14_ZNF_Melanocytes
12	1e+00	179 / 11836	3_TssF_Melanocytes
13	1e+00	82 / 5956	3_TssF_Neuronal_Progenitor
14	1e+00	126 / 8771	5_Tx_Melanocytes
15	1e+00	140 / 9635	3_TssF_Fibroblasts

Colon Cancer

Rank	p−value	#in/all	Geneset
1	9e−17	53 / 831	Pentrack_CRC_TCGA_group.over_C_normal_DN
2	7e−12	49 / 965	Pentrack_CRC_TCGA_corr_R_normal_DN
3	9e−06	32 / 810	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
4	3e−05	13 / 193	Kosinski_lower−crypt−long−list
5	2e−03	25 / 789	TxEnhG2_Colon
6	1e−02	2 / 11	Juehling−MSI−enriched−in−7
7	1e−02	145 / 7354	TssF_Colon
8	2e−02	48 / 2073	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
9	3e−02	36 / 1547	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
10	6e−02	59 / 2845	TxEnhG1_Colon
11	6e−02	28 / 1216	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_
12	7e−02	17 / 676	Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN
13	7e−02	13 / 489	K9acLow_Colon
14	8e−02	11 / 398	Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN
15	1e−01	3 / 76	Pentrack_CRC_TCGA_corr_N_msi−h_DN

Glio

Rank	p−value	#in/all	Geneset
1	0.006	2 / 7	Donson−adaptive−immunity−associated with LTS in HGA
2	0.026	2 / 15	WILLSCHER_GBM_Verhaak−PN (mut&wt)_up (I)
3	0.036	3 / 43	Noushmehr_Pron_GCIMP_hypermeth_DN
4	0.066	2 / 25	Sturm_GBM_Meth_overexpression_H_K27_UP
5	0.107	2 / 33	Shaw_responders_down_in_oligo_glioma
6	0.128	1 / 8	Donson−migration tethering and rolling−associated with LTS in HGA
7	0.128	5 / 157	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
8	0.145	10 / 401	Down_b
9	0.171	1 / 11	VERHAAK_Brain
10	0.195	2 / 48	Vishal_subnetwork signature of survival in GBM
11	0.207	2 / 50	WILLSCHER_GBM_proteomics_wtOnly_SpotG
12	0.209	3 / 93	Hopp_Sturm_GBM_Epi3_C2_adult_fetus_DN
13	0.220	2 / 52	OL vs. OPC
14	0.226	1 / 15	WILLSCHER_GBM_STSwt_proteomics−O_UP
15	0.279	4 / 158	Hopp_Sturm_GBM_Epi3_D_adult_fetus_IDH_UP

GSEA C2

Rank	p−value	#in/all	Geneset
1	3e−23	21 / 56	REACTOME_PEPTIDE_CHAIN_ELONGATION
2	3e−21	21 / 68	REACTOME_INFLUENZA_VIRAL_RNA_TRANSCRIPTION_AND_REPLICAT
3	5e−21	21 / 69	REACTOME_3_UTR_MEDIATED_TRANSLATIONAL_REGULATION
4	2e−20	21 / 74	REACTOME_SRP_DEPENDENT_COTRANSLATIONAL_PROTEIN_TARGET
5	7e−20	19 / 58	KEGG_RIBOSOME
6	9e−20	23 / 101	REACTOME_TRANSLATION
7	6e−19	20 / 74	REACTOME_NONSENSE_MEDIATED_DECAY_ENHANCED_BY_THE_EXC
8	1e−18	22 / 99	REACTOME_INFLUENZA_LIFE_CYCLE
9	8e−17	33 / 317	HSIAO_HOUSEKEEPING_GENES
10	3e−16	15 / 44	BILANGES_SERUM_AND_RAPAMYCIN_SENSITIVE_GENES
11	5e−16	26 / 196	REACTOME_METABOLISM_OF_RNA
12	2e−15	23 / 155	REACTOME_METABOLISM_OF_MRNA
13	1e−14	22 / 151	JISON_SICKLE_CELL_DISEASE_DN
14	7e−12	35 / 529	CAIRO_HEPATOBLASTOMA_CLASSES_UP
15	2e−11	28 / 354	REACTOME_METABOLISM_OF_PROTEINS

HM

Rank	p−value	#in/all	Geneset
1	3e−08	16 / 170	HALLMARK_MYC_TARGETS_V1
2	4e−06	13 / 162	HALLMARK_ALLOGRAFT_REJECTION
3	8e−03	6 / 103	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
4	1e−02	8 / 186	HALLMARK_ESTROGEN_RESPONSE_EARLY
5	2e−02	6 / 130	HALLMARK_DNA_REPAIR
6	6e−02	3 / 54	HALLMARK_MYC_TARGETS_V2
7	7e−02	6 / 173	HALLMARK_E2F_TARGETS
8	8e−02	6 / 177	HALLMARK_MITOTIC_SPINDLE
9	1e−01	2 / 37	HALLMARK_PANCREAS_BETA_CELLS
10	2e−01	5 / 186	HALLMARK_ESTROGEN_RESPONSE_LATE
11	2e−01	5 / 186	HALLMARK_IL2_STAT5_SIGNALING
12	3e−01	4 / 167	HALLMARK_OXIDATIVE_PHOSPHORYLATION
13	4e−01	4 / 183	HALLMARK_APICAL_JUNCTION
14	4e−01	1 / 29	HALLMARK_NOTCH_SIGNALING
15	4e−01	3 / 138	HALLMARK_FATTY_ACID_METABOLISM

Lifestyle

Rank	p−value	#in/all	Geneset
1	2e−20	16 / 32	Marjolein_ageing−genes_DN
2	1e−06	13 / 147	Homuth_BMI−associated−genes_UP
3	3e−02	2 / 17	DUMEAUX_High bmi enriched genes
4	4e−01	1 / 31	DUMEAUX_Fasting enriched genes
5	5e−01	2 / 94	DUMEAUX_Smoking enriched genes
6	1e+00	1 / 211	Homuth_BMI−associated−genes_DN
7	1e+00	0 / 10	DUMEAUX_Smoking literature genes up
8	1e+00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
9	1e+00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
10	1e+00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
11	1e+00	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
12	1e+00	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
13	1e+00	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
14	1e+00	0 / 10	DUMEAUX_Women normal BMI literature genes up
15	1e+00	0 / 18	Huan_blood−pressure_SBP−signature

Lymphoma

Rank	p−value	#in/all	Geneset
1	2e−09	16 / 139	Hopp_June14_MMML937 tumors+controls_group.overexpression_F_FL_tons
2	2e−09	16 / 141	WIRTH_lymphoma937_spot F
3	6e−07	23 / 408	TARTE_Mature plasma cell signature
4	2e−04	8 / 94	Sha_BL UP
5	8e−04	118 / 5356	HOPP_Txn_transition
6	2e−03	8 / 134	DAVE_BL−vs−DLBCL
7	3e−03	4 / 35	TARTE_B−cell signature
8	4e−03	12 / 286	ZHANG_DLBCL mutated
9	4e−03	6 / 88	WIRTH_lymphoma937_spot A
10	4e−03	13 / 331	SPANG_CD40 6hrs UP
11	5e−03	4 / 40	Monti_BCR_cluster
12	5e−03	6 / 92	Hopp_June14_MMML937 tumors+controls_group.overexpression_A_mBL_ce
13	7e−03	16 / 472	Hopp_June14_MMML937 tumors+controls_group.overexpression_J_GC−B−c
14	1e−02	16 / 493	WIRTH_lymphoma937_spot J
15	1e−02	6 / 109	ROSOLOWSKI_blue total

Melanoma

Rank	p−value	#in/all	Geneset
1	1	0 / 30	Hugo_melanoma−all−MET_UP
2	1	0 / 54	Hugo_melanoma−all−MET_DN
3	1	0 / 43	Hugo_melanoma−BRAFmut−MET_UP
4	1	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
5	1	0 / 27	Hugo_melanoma−all−LEF1_UP
6	1	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

MF

Rank	p−value	#in/all	Geneset
1	5e−15	56 / 1013	poly(A) RNA binding
2	1e−14	23 / 169	structural constituent of ribosome
3	6e−05	19 / 399	RNA binding
4	1e−04	5 / 29	rRNA binding
5	9e−04	3 / 12	pseudouridine synthase activity
6	3e−03	14 / 350	protein kinase binding
7	6e−03	11 / 265	cadherin binding involved in cell−cell adhesion
8	1e−02	3 / 28	tumor necrosis factor receptor binding
9	1e−02	2 / 11	RNA polymerase I activity
10	2e−02	2 / 14	channel activity
11	2e−02	2 / 14	MHC class II protein complex binding
12	2e−02	2 / 14	protein kinase A catalytic subunit binding
13	3e−02	2 / 16	amino acid binding
14	3e−02	4 / 70	ATPase binding
15	4e−02	2 / 18	snoRNA binding

miRNA Disease

Rank	p−value	#in/all	Geneset
1	1	0 / 7	Thyroid carcinoma, papillary
2	1	0 / 123	Pancreatic cancer
3	1	0 / 68	Glioblastoma multiforme, somatic
4	1	0 / 63	Gastrointestinal
5	1	0 / 3	Pituitary adenoma
6	1	0 / 116	Cancer
7	1	0 / 95	Colorectal cancer
8	1	0 / 2	Adenomas, multiple colorectal
9	1	0 / 124	Prostate cancer
10	1	0 / 48	Alzheimer disease, susceptibility to
11	1	0 / 7	Schizophrenia, susceptibility to
12	1	0 / 20	Parkinson disease
13	1	0 / 65	Hepatocellular carcinoma
14	1	0 / 3	Down syndrome, risk of
15	1	0 / 127	Melanoma and neural system tumor syndrome

miRNA target

Rank	p−value	#in/all	Geneset
1	0.02	4 / 58	hsa−miR−193a−3p
2	0.03	4 / 70	hsa−miR−193b
3	0.08	2 / 28	hsa−miR−597
4	0.08	3 / 61	hsa−miR−296−3p
5	0.09	4 / 100	hsa−miR−516b
6	0.09	4 / 100	hsa−miR−525−5p
7	0.10	2 / 31	hsa−miR−617
8	0.12	2 / 35	hsa−miR−892b
9	0.12	3 / 71	hsa−miR−1266
10	0.12	3 / 72	hsa−miR−935
11	0.14	3 / 77	hsa−miR−422a
12	0.16	1 / 10	hsa−miR−887
13	0.16	1 / 10	hsa−miR−1306
14	0.17	2 / 44	hsa−miR−660
15	0.17	1 / 11	hsa−miR−1180

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.2	1 / 12	BENTINK_ras.1
2	1.0	0 / 14	GUSTAFSON_PI3K_UP
3	1.0	0 / 15	GUSTAFSON_PI3K_DN
4	1.0	0 / 13	BENTINK_e2f3.1
5	1.0	0 / 13	BENTINK_e2f3.2
6	1.0	0 / 13	BENTINK_myc.1
7	1.0	0 / 11	BENTINK_ras.4
8	1.0	0 / 14	BENTINK_ras.6
9	1.0	0 / 13	BENTINK_src.10
10	1.0	0 / 12	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Reference Signatures

Rank	p−value	#in/all	Geneset
1	6e−42	42 / 132	Chaussabel_1,7_MHC Ribosomal proteins
2	4e−41	40 / 119	Chaussabel_2,8_T−cells
3	3e−24	28 / 119	Chaussabel_2,4_Ribosomal proteins
4	7e−10	11 / 51	Chaussabel_1,3_B−cells
5	2e−07	28 / 535	PROTEINATLAS_spleen
6	2e−07	24 / 412	WIRTH_Immune system
7	3e−05	37 / 1063	PROTEINATLAS_tonsil
8	5e−05	28 / 724	PROTEINATLAS_lymph node
9	1e−03	30 / 960	PROTEINATLAS_cerebellum
10	2e−03	34 / 1194	PROTEINATLAS_stomach
11	3e−03	21 / 639	PROTEINATLAS_breast
12	3e−03	25 / 816	PROTEINATLAS_endometrium
13	6e−03	34 / 1268	PROTEINATLAS_colon
14	6e−03	31 / 1138	PROTEINATLAS_small intestine
15	7e−03	28 / 1003	PROTEINATLAS_appendix

Telomeres

Rank	p−value	#in/all	Geneset
1	1	0 / 13	Alternative lengthening of telomeres
2	1	0 / 27	Nabetani_alt len telomeres_genes_ko
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	1e−06	45 / 1231	KIM_MYC targets
2	4e−05	4 / 12	MYC_Protein synthesis degradation UP
3	4e−05	7 / 55	MYC_Targets UP
4	3e−03	3 / 18	MYC_Metabolism UP
5	4e−03	39 / 1478	ICGC_Myc_targets
6	4e−03	44 / 1723	HEBENSTREIT_high expression TF
7	8e−02	1 / 5	MYC_TF and cofactors
8	1e−01	112 / 5961	ICGC_Pol24_targets
9	1e−01	35 / 1669	ICGC_P300_targets
10	1e−01	43 / 2133	ICGC_Mef2_targets
11	1e−01	1 / 9	MYC_Targets DOWN
12	2e−01	41 / 2087	ICGC_Cebpbsc150_targets
13	2e−01	30 / 1501	ICGC_Usf1_targets
14	2e−01	92 / 5067	ICGC_Taf1_targets
15	3e−01	88 / 4881	ICGC_Atf2_targets

K−Means Cluster

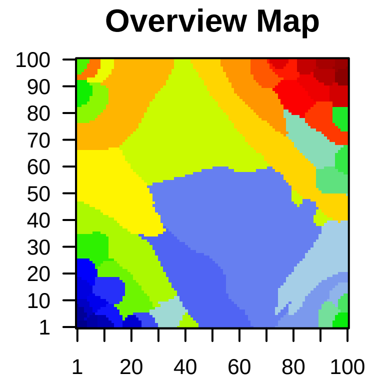
Spot Summary: R1

metagenes = 21
genes = 383

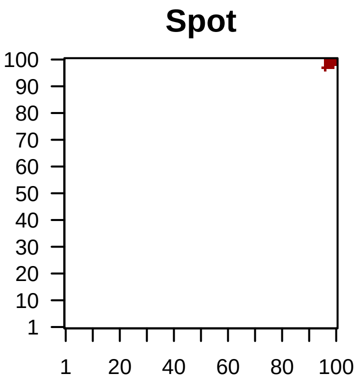
<r> metagenes = 0.98
<r> genes = 0.6
beta: r2= 96.93 / log p= −Inf

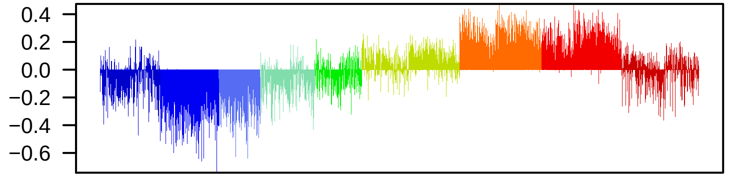
samples with spot = 1006 (29.7 %)
A * : 13 (3.8 %)
A F * : 4 (1.3 %)
C F * : 13 (4.9 %)
F * : 169 (30.5 %)
F J * : 423 (91.4 %)
J * : 341 (76.3 %)
N * : 43 (9.7 %)

Overview Map



Spot





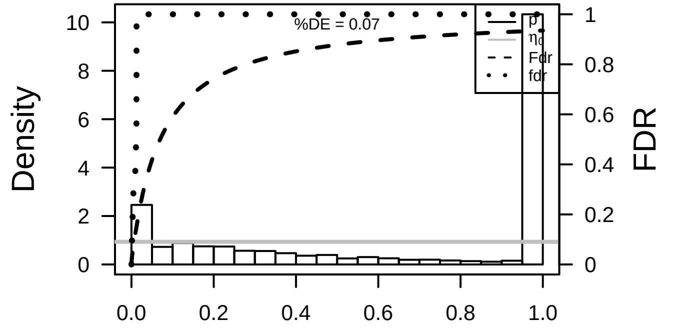
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_210544	2.45	−1.45	0.34	JCHAIN	joining chain of multimeric IgA and IgM [Source:HGNC Symb
2	ILMN_165219	2.24	−1.63	0.3		
3	ILMN_173950	2.08	−1.34	0.34		
4	ILMN_324037	2.04	−1.35	0.39		immunoglobulin kappa variable 1D−17 [Source:HGNC Symbo
5	ILMN_324966	1.89	−1.85	0.36		
6	ILMN_169921	1.89	−1.18	0.33		
7	ILMN_178810	1.79	−0.92	0.38		BLOC1S5−TXNDC5 readthrough (NMD candidate) [Source:H
8	ILMN_180840	1.68	−1.68	0.39	HLA−DQA1	major histocompatibility complex, class II, DQ alpha 1 [Source
9	ILMN_171073	1.39	−1.44	0.51	GZMK	granzyme K [Source:HGNC Symbol;Acc:HGNC:4711]
10	ILMN_170496	1.38	−1.61	0.54		
11	ILMN_166708	1.34	−1.65	0.66	CCND2	cyclin D2 [Source:HGNC Symbol;Acc:HGNC:1583]
12	ILMN_234257	1.32	−1.58	0.61	IL7R	interleukin 7 receptor [Source:HGNC Symbol;Acc:HGNC:602
13	ILMN_207965	1.24	−1.4	0.6	KLRB1	killer cell lectin like receptor B1 [Source:HGNC Symbol;Acc:H
14	ILMN_206765	1.22	−1.32	0.72	CCND2	cyclin D2 [Source:HGNC Symbol;Acc:HGNC:1583]
15	ILMN_176037	1.22	−0.81	0.48	CD8A	CD8a molecule [Source:HGNC Symbol;Acc:HGNC:1706]
16	ILMN_187303	1.2	−1.66	0.81		
17	ILMN_328411	1.18	−0.87	0.83		nucleophosmin 1 pseudogene 25 [Source:HGNC Symbol;Acc
18	ILMN_330772	1.18	−1.05	0.51	CXXC5	CXXC finger protein 5 [Source:HGNC Symbol;Acc:HGNC:26
19	ILMN_172413	1.15	−1.15	0.72	TMEM123	transmembrane protein 123 [Source:HGNC Symbol;Acc:HGN
20	ILMN_167918	1.15	−1.53	0.8	LEF1	lymphoid enhancer binding factor 1 [Source:HGNC Symbol;A

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	6e−28	78 / 1417	GSEA	PUJANA_BRCA1_PCC_NETWORK
2	8e−26	27 / 119	Refer	Chaussabel_2,4_Ribosomal proteins
3	2e−23	67 / 1241	GSEA	PUJANA_ATM_PCC_NETWORK
4	6e−21	47 / 669	GSEA	PUJANA_CHEK2_PCC_NETWORK
5	6e−21	52 / 831	Colon	Pentrack_CRC_TCGA_group.over_C_normal_DN
6	1e−20	24 / 132	Refer	Chaussabel_1,7_MHC Ribosomal proteins
7	4e−17	137 / 5356	Lympl	HOPP_Txn_transition
8	3e−16	28 / 291	GSEA	WONG_EMBRYONIC_STEM_CELL_CORE
9	3e−16	34 / 455	GSEA	ZHENG_BOUND_BY_FOXP3
10	1e−15	21 / 151	GSEA	JISON_SICKLE_CELL_DISEASE_DN
11	2e−15	28 / 317	GSEA	HSIAO_HOUSEKEEPING_GENES
12	4e−15	162 / 7275	Lympl	HOPP_Txn_elongation
13	1e−14	21 / 170	HM	HALLMARK_MYC_TARGETS_V1
14	4e−14	46 / 965	Colon	Pentrack_CRC_TCGA_corr_R_normal_DN
15	1e−13	16 / 95	GSEA	HAHTOLA_MYCOSIS_FUNGOIDES_CD4_DN
16	2e−13	171 / 8226	Lympl	HOPP_Active_promoter
17	2e−13	46 / 1013	MF	poly(A) RNA binding
18	5e−12	27 / 402	GSEA	SMID_BREAST_CANCER_NORMAL_LIKE_UP
19	7e−12	61 / 1797	GSEA	PILON_KLF1_TARGETS_DN
20	7e−12	24 / 316	GSEA	RHEIN_ALL_GLUCOCORTICOID_THERAPY_DN
21	6e−11	15 / 119	Refer	Chaussabel_2,8_T−cells
22	6e−11	32 / 622	GSEA	SCHLOSSER_SERUM_RESPONSE_DN
23	7e−11	14 / 101	GSEA	REACTOME_TRANSLATION
24	7e−11	35 / 737	GSEA	ACEVEDO_LIVER_TUMOR_VS_NORMAL_ADJACENT_TISSUE_UP
25	7e−11	16 / 142	GSEA	SCHLOSSER_MYC_TARGETS_REPRESSED_BY_SERUM
26	1e−10	29 / 529	GSEA	CAIRO_HEPATOBLASTOMA_CLASSES_UP
27	1e−10	46 / 1216	Colon	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP
28	1e−10	47 / 1265	GSEA	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
29	2e−10	34 / 724	Refer	PROTEINATLAS_lymph node
30	4e−10	13 / 96	BP	translational initiation
31	7e−10	45 / 1239	Refer	PROTEINATLAS_testis
32	8e−10	41 / 1063	Refer	PROTEINATLAS_tonsil
33	9e−10	16 / 168	GSEA	LEE_DIFFERENTIATING_T_LYMPHOCYTE
34	1e−09	30 / 623	Refer	PROTEINATLAS_seminal vesicle
35	1e−09	158 / 8098	Lympl	HOPP_Weak_promoter
36	2e−09	41 / 1098	GSEA	BLALOCK_ALZHEIMERS_DISEASE_DN
37	3e−09	42 / 1161	GSEA	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
38	3e−09	9 / 42	GSEA	MENSSEN_MYC_TARGETS
39	4e−09	34 / 816	Refer	PROTEINATLAS_endometrium
40	5e−09	14 / 139	Lympl	Hopp_June14_MMML937 tumors+controls_group.overexpression_F_FL_to

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.4	2 / 111	HORVATH_aging_genes meth DOWN
2	0.5	1 / 58	TESCHENDORFF_age_hypermethylated
3	0.6	2 / 142	HORVATH_aging_genes meth UP
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Cancer

Rank	p−value	#in/all	Geneset
1	6e−05	2 / 13	RHODES_CANCER_META_SIGNATURE
2	7e−04	3 / 14	GENTLES_modul1
3	1e−03	3 / 16	GENTLES_modul16
4	6e−03	6 / 125	PanCan_CC+Apop_geneset_nanostring
5	7e−03	5 / 91	PanCan_TXmisReg_geneset_nanostring
6	7e−03	15 / 554	Lembcke_Colonic Inflammation
7	1e−02	2 / 13	GENTLES_modul18
8	1e−02	2 / 14	GENTLES_modul10
9	1e−02	3 / 39	ZHANG_MM up
10	2e−02	2 / 15	WOLFER_overlap genes
11	2e−02	2 / 16	GENTLES_modul7
12	2e−02	2 / 16	GENTLES_modul11
13	2e−02	4 / 82	PanCan_JAK−ST_geneset_nanostring
14	5e−02	8 / 301	SPANG_BCL6−index2
15	8e−02	1 / 6	ZHANG_MGUS up

Chromatin states

Rank	p−value	#in/all	Geneset
1	1e−04	123 / 6970	5_Tx_Neuronal_Progenitor
2	2e−03	177 / 11455	2_TssA_Fibroblasts
3	3e−03	140 / 8771	5_Tx_Melanocytes
4	1e−02	182 / 12298	2_TssA_Melanocytes
5	2e−02	122 / 7854	5_Tx_Fibroblasts
6	4e−02	89 / 5699	6_EnhG_Melanocytes
7	5e−02	186 / 12983	2_TssA_Neuronal_Progenitor
8	7e−02	132 / 8990	15_Quies_Fibroblasts
9	8e−02	22 / 1206	6_EnhG_Neuronal_Progenitor
10	2e−01	62 / 4237	14_ZNF_Neuronal_Progenitor
11	4e−01	150 / 11130	15_Quies_Melanocytes
12	4e−01	166 / 12393	15_Quies_Neuronal_Progenitor
13	4e−01	28 / 2028	4_TxTrans_Melanocytes
14	4e−01	129 / 9635	3_TssF_Fibroblasts
15	5e−01	6 / 416	4_TxTrans_Neuronal_Progenitor

GSEA C2

Rank	p−value	#in/all	Geneset
1	6e−28	78 / 1417	PUJANA_BRCA1_PCC_NETWORK
2	2e−23	67 / 1241	PUJANA_ATM_PCC_NETWORK
3	6e−21	47 / 669	PUJANA_CHEK2_PCC_NETWORK
4	3e−16	28 / 291	WONG_EMBRYONIC_STEM_CELL_CORE
5	3e−16	34 / 455	ZHENG_BOUND_BY_FOXP3
6	1e−15	21 / 151	JISON_SICKLE_CELL_DISEASE_DN
7	2e−15	28 / 317	HSIAO_HOUSEKEEPING_GENES
8	1e−13	16 / 95	HAHTOLA_MYCOSIS_FUNGOIDES_CD4_DN
9	5e−12	27 / 402	SMID_BREAST_CANCER_NORMAL_LIKE_UP
10	7e−12	61 / 1797	PILON_KLF1_TARGETS_DN
11	7e−12	24 / 316	RHEIN_ALL_GLUCOCORTICOID_THERAPY_DN
12	6e−11	32 / 622	SCHLOSSER_SERUM_RESPONSE_DN
13	7e−11	14 / 101	REACTOME_TRANSLATION
14	7e−11	35 / 737	ACEVEDO_LIVER_TUMOR_VS_NORMAL_ADJACENT_TISSUE_UP
15	7e−11	16 / 142	SCHLOSSER_MYC_TARGETS_REPRESSED_BY_SERUM

Lymphoma

Rank	p−value	#in/all	Geneset
1	4e−17	137 / 5356	HOPP_Txn_transition
2	4e−15	162 / 7275	HOPP_Txn_elongation
3	2e−13	171 / 8226	HOPP_Active_promoter
4	1e−09	158 / 8098	HOPP_Weak_promoter
5	5e−09	14 / 139	Hopp_June14_MMML937 tumors+controls_group.overexpression_F_FL_tons
6	6e−09	14 / 141	WIRTH_lymphoma937_spot F
7	8e−09	6 / 13	Care_Polarized immune response
8	4e−08	144 / 7448	HOPP_Strong_enhancer
9	3e−05	5 / 28	DAVE_Immune response 1
10	2e−04	5 / 40	Monti_BCR_cluster
11	2e−03	28 / 1169	SPANG_BCR DN
12	2e−03	3 / 19	DAVE_BL Inter
13	2e−03	3 / 19	DAVE_c−myc BL UP
14	2e−03	7 / 134	DAVE_BL−vs−DLBCL
15	2e−03	4 / 43	Monti_OxPhos_cluster

miRNA Disease

Rank	p−value	#in/all	Geneset
1	1	0 / 7	Thyroid carcinoma, papillary
2	1	0 / 123	Pancreatic cancer
3	1	0 / 68	Glioblastoma multiforme, somatic
4	1	0 / 63	Gastrointestinal
5	1	0 / 3	Pituitary adenoma
6	1	0 / 116	Cancer
7	1	0 / 95	Colorectal cancer
8	1	0 / 2	Adenomas, multiple colorectal
9	1	0 / 124	Prostate cancer
10	1	0 / 48	Alzheimer disease, susceptibility to
11	1	0 / 7	Schizophrenia, susceptibility to
12	1	0 / 20	Parkinson disease
13	1	0 / 65	Hepatocellular carcinoma
14	1	0 / 3	Down syndrome, risk of
15	1	0 / 127	Melanoma and neural system tumor syndrome

Reference Signatures

Rank	p−value	#in/all	Geneset
1	8e−26	27 / 119	Chaussabel_2,4_Ribosomal proteins
2	1e−20	24 / 132	Chaussabel_1,7_MHC Ribosomal proteins
3	6e−11	15 / 119	Chaussabel_2,8_T−cells
4	2e−10	34 / 724	PROTEINATLAS_lymph node
5	7e−10	45 / 1239	PROTEINATLAS_testis
6	8e−10	41 / 1063	PROTEINATLAS_tonsil
7	1e−09	30 / 623	PROTEINATLAS_seminal vesicle
8	4e−09	34 / 816	PROTEINATLAS_endometrium
9	1e−08	31 / 726	PROTEINATLAS_cervix, uterine
10	4e−08	22 / 412	WIRTH_Immune system
11	1e−07	34 / 933	PROTEINATLAS_adrenal gland
12	1e−07	39 / 1167	PROTEINATLAS_gallbladder
13	1e−07	30 / 759	PROTEINATLAS_epididymis
14	2e−07	27 / 650	PROTEINATLAS_hippocampus
15	6e−07	33 / 963	PROTEINATLAS_pancreas

BP

Rank	p−value	#in/all	Geneset
1	4e−10	13 / 96	translational initiation
2	2e−06	12 / 163	rRNA processing
3	2e−05	8 / 87	nuclear−transcribed mRNA catabolic process, nonsense−mediated decay
4	3e−05	5 / 28	regulation of translational initiation
5	4e−05	4 / 15	formation of translation preinitiation complex
6	8e−05	17 / 435	negative regulation of apoptotic process
7	8e−05	4 / 18	cytoplasmic translation
8	2e−04	10 / 184	translation
9	2e−04	6 / 65	SRP−dependent cotranslational protein targeting to membrane
10	2e−04	5 / 43	T cell activation
11	5e−04	4 / 29	B cell proliferation
12	5e−04	4 / 29	positive regulation of telomere maintenance via telomerase
13	6e−04	5 / 52	humoral immune response
14	7e−04	6 / 81	viral transcription
15	8e−04	4 / 32	tRNA aminoacylation for protein translation

CC

Rank	p−value	#in/all	Geneset
1	1e−07	65 / 2535	nucleoplasm
2	4e−07	28 / 721	nucleolus
3	2e−06	7 / 45	cytosolic large ribosomal subunit
4	3e−06	9 / 90	chromatin
5	6e−05	8 / 101	intracellular ribonucleoprotein complex
6	1e−04	12 / 248	extracellular matrix
7	4e−04	89 / 4822	cytoplasm
8	5e−04	3 / 12	eukaryotic translation initiation factor 3 complex
9	6e−04	3 / 13	Sin3 complex
10	6e−04	88 / 4828	nucleus
11	8e−04	51 / 2464	extracellular exosome
12	8e−04	43 / 1979	membrane
13	9e−04	59 / 2979	cytosol
14	9e−04	3 / 15	endocytic vesicle lumen
15	1e−03	6 / 88	melanosome

Colon Cancer

Rank	p−value	#in/all	Geneset
1	6e−21	52 / 831	Pentrack_CRC_TCGA_group.over_C_normal_DN
2	4e−14	46 / 965	Pentrack_CRC_TCGA_corr_R_normal_DN
3	1e−10	46 / 1216	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_
4	8e−08	47 / 1547	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
5	9e−08	172 / 9555	TssA_Colon
6	2e−07	56 / 2073	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
7	3e−06	159 / 9054	Tx_Colon
8	4e−06	152 / 8568	TxWk_Colon
9	3e−05	181 / 10999	TssWk_Colon
10	6e−05	148 / 8678	Quies3_Colon
11	8e−05	80 / 4034	TssD1_Colon
12	1e−03	9 / 193	Kosinski_lower−crypt−long−list
13	1e−03	22 / 810	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
14	7e−03	2 / 10	KIM_MSI−in−EC
15	2e−02	29 / 1468	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo

HM

Rank	p−value	#in/all	Geneset
1	1e−14	21 / 170	HALLMARK_MYC_TARGETS_V1
2	1e−07	11 / 103	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
3	1e−05	11 / 162	HALLMARK_ALLOGRAFT_REJECTION
4	2e−03	8 / 176	HALLMARK_KRAS_SIGNALING_UP
5	3e−03	8 / 186	HALLMARK_ESTROGEN_RESPONSE_EARLY
6	3e−03	8 / 186	HALLMARK_IL2_STAT5_SIGNALING
7	6e−03	4 / 54	HALLMARK_MYC_TARGETS_V2
8	8e−03	7 / 173	HALLMARK_E2F_TARGETS
9	1e−02	6 / 137	HALLMARK_UV_RESPONSE_UP
10	1e−02	7 / 185	HALLMARK_MTORC1_SIGNALING
11	1e−02	7 / 187	HALLMARK_COMPLEMENT
12	1e−02	7 / 191	HALLMARK_INFLAMMATORY_RESPONSE
13	2e−02	3 / 40	HALLMARK_WNT_BETA_CATENIN_SIGNALING
14	4e−02	5 / 138	HALLMARK_FATTY_ACID_METABOLISM
15	4e−02	6 / 185	HALLMARK_TNFA_SIGNALING_VIA_NFKB

Melanoma

Rank	p−value	#in/all	Geneset
1	0.3	1 / 30	Hugo_melanoma−all−MET_UP
2	1.0	0 / 54	Hugo_melanoma−all−MET_DN
3	1.0	0 / 43	Hugo_melanoma−BRAFmut−MET_UP
4	1.0	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
5	1.0	0 / 27	Hugo_melanoma−all−LEF1_UP
6	1.0	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

miRNA target

Rank	p−value	#in/all	Geneset
1	6e−07	12 / 146	hsa−miR−518a−5p
2	7e−07	12 / 149	hsa−miR−527
3	2e−06	16 / 293	hsa−miR−34c−5p
4	3e−06	12 / 172	hsa−miR−548k
5	5e−06	12 / 180	hsa−miR−1
6	6e−06	8 / 74	hsa−miR−657
7	7e−06	13 / 216	hsa−miR−520g
8	1e−05	15 / 295	hsa−miR−561
9	1e−05	11 / 164	hsa−miR−153
10	2e−05	8 / 85	hsa−miR−1265
11	2e−05	14 / 272	hsa−miR−30d
12	2e−05	9 / 113	hsa−miR−154
13	3e−05	14 / 283	hsa−miR−320a
14	3e−05	10 / 147	hsa−miR−506
15	3e−05	10 / 148	hsa−miR−409−3p

Telomeres

Rank	p−value	#in/all	Geneset
1	0.2	1 / 13	Alternative lengthening of telomeres
2	1.0	0 / 27	Nabetani_alt len telomeres_genes_ko
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Brain

Rank	p−value	#in/all	Geneset
1	2e−07	119 / 5936	Overlap_fetal_midbrain_HetRpts
2	1e−06	171 / 9815	Overlap_fetal_midbrain_ReprPC
3	8e−06	27 / 796	Overlap_fetal_midbrain_ZNF
4	3e−05	11 / 180	Overlap_fetal_midbrain_Het
5	3e−04	156 / 9504	Overlap_fetal_midbrain_K9K27me3
6	2e−03	13 / 386	Fetal_ZNF
7	1e−02	10 / 328	Fetal_Het
8	2e−02	24 / 1162	Fetal_Enh
9	2e−02	149 / 9917	Overlap_fetal_midbrain_ReprPCWk
10	2e−01	16 / 937	Fetal_EnhG
11	2e−01	19 / 1171	Fetal_EnhP
12	2e−01	15 / 906	Fetal_HetRpts
13	3e−01	18 / 1213	Fetal_TssP
14	4e−01	141 / 10430	Overlap_fetal_midbrain_Quies
15	5e−01	36 / 2654	Fetal_Quies

Chr

Rank	p−value	#in/all	Geneset
1	0.005	22 / 904	Chr 10
2	0.021	24 / 1160	Chr 12
3	0.024	29 / 1492	Chr 2
4	0.034	24 / 1217	Chr 3
5	0.071	20 / 1060	Chr 5
6	0.091	17 / 902	Chr 4
7	0.299	6 / 342	Chr 18
8	0.338	18 / 1211	Chr 6
9	0.438	11 / 769	Chr 15
10	0.533	4 / 289	Chr 21
11	0.564	10 / 768	Chr 14
12	0.582	30 / 2323	Chr 1
13	0.658	5 / 422	Chr 13
14	0.667	12 / 994	Chr X
15	0.687	14 / 1170	Chr 7

Glio

Rank	p−value	#in/all	Geneset
1	6e−04	3 / 13	Donson−immune cell intra signaling−associated with LTS in HGA
2	2e−03	43 / 2043	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
3	2e−02	34 / 1777	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
4	3e−02	9 / 316	WILLSCHER_GBM_Verhaak−PNwt & CL_up
5	4e−02	3 / 55	Stuehler_Proteins_up_in_STS
6	9e−02	9 / 401	Down_b
7	9e−02	1 / 7	Donson−cytotoxic effectors−associated with LTS in HGA
8	1e−01	1 / 8	Donson−migration tethering and rolling−associated with LTS in HGA
9	1e−01	1 / 9	Sturm_GBM_Meth_overexpression_G_IDH_UP
10	1e−01	3 / 92	Weller_LGG_A_vs_O_DOWN
11	1e−01	2 / 47	Donson−innate immunity−associated with LTS in HGA
12	1e−01	2 / 48	Vishal_subnetwork signature of survival in GBM
13	1e−01	1 / 11	Mukasa_UP_in_Oligodendroglioma_with_1intact
14	2e−01	1 / 15	VERHAAK_CL subtype
15	2e−01	1 / 15	VERHAAK_MES subtype

Lifestyle

Rank	p−value	#in/all	Geneset
1	3e−05	12 / 211	Homuth_BMI−associated−genes_DN
2	6e−05	5 / 32	Marjolein_ageing−genes_DN
3	5e−02	5 / 147	Homuth_BMI−associated−genes_UP
4	7e−01	1 / 94	DUMEAUX_Smoking enriched genes
5	1e+00	0 / 10	DUMEAUX_Smoking literature genes up
6	1e+00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
7	1e+00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
8	1e+00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
9	1e+00	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
10	1e+00	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
11	1e+00	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
12	1e+00	0 / 10	DUMEAUX_Women normal BMI literature genes up
13	1e+00	0 / 17	DUMEAUX_High bmi enriched genes
14	1e+00	0 / 31	DUMEAUX_Fasting enriched genes
15	1e+00	0 / 18	Huan_blood−pressure_SBP−signature

MF

Rank	p−value	#in/all	Geneset
1	2e−13	46 / 1013	poly(A) RNA binding
2	1e−05	6 / 39	translation initiation factor activity
3	3e−05	17 / 399	RNA binding
4	9e−05	149 / 8818	protein binding
5	3e−04	5 / 45	tRNA binding
6	4e−04	12 / 283	nucleotide binding
7	8e−04	6 / 82	unfolded protein binding
8	1e−03	11 / 274	transcription factor binding
9	1e−03	5 / 60	transcriptional repressor activity, RNA polymerase II transcription regulatory r
10	1e−03	3 / 17	metalloaminopeptidase activity
11	1e−03	3 / 17	phosphatidylcholine binding
12	1e−03	3 / 17	promoter−specific chromatin binding
13	2e−03	31 / 1329	ATP binding
14	2e−03	8 / 169	structural constituent of ribosome
15	3e−03	12 / 355	chromatin binding

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.01	2 / 12	BENTINK_src.2
2	0.16	1 / 13	BENTINK_e2f3.2
3	0.16	1 / 13	BENTINK_myc.1
4	0.17	1 / 14	BENTINK_ras.6
5	1.00	0 / 14	GUSTAFSON_PI3K_UP
6	1.00	0 / 15	GUSTAFSON_PI3K_DN
7	1.00	0 / 13	BENTINK_e2f3.1
8	1.00	0 / 12	BENTINK_ras.1
9	1.00	0 / 11	BENTINK_ras.4
10	1.00	0 / 13	BENTINK_src.10
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	2e−08	42 / 1231	KIM_MYC targets
2	7e−05	38 / 1478	ICGC_Myc_targets
3	2e−04	47 / 2087	ICGC_Cebpbsc150_targets
4	8e−04	5 / 55	MYC_Targets UP
5	4e−03	43 / 2133	ICGC_Mef2_targets
6	5e−03	32 / 1498	ICGC_Ets1_targets
7	8e−03	98 / 5961	ICGC_Pol24_targets
8	9e−03	43 / 2255	ICGC_SrfV0416101_targets
9	2e−02	32 / 1669	ICGC_P300_targets
10	3e−02	1 / 2	MYC_Chromatin_modification UP
11	3e−02	44 / 2497	ICGC_Bcl11_targets
12	3e−02	47 / 2704	ICGC_Pbx3_targets
13	3e−02	28 / 1466	ICGC_NrsfPcr1_targets
14	4e−02	80 / 5067	ICGC_Taf1_targets
15	5e−02	53 / 3194	ICGC_Irf4_targets

K−Means Cluster

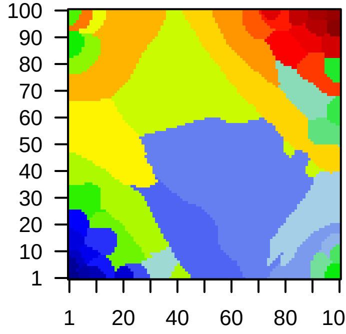
Spot Summary: S1

metagenes = 45
genes = 644

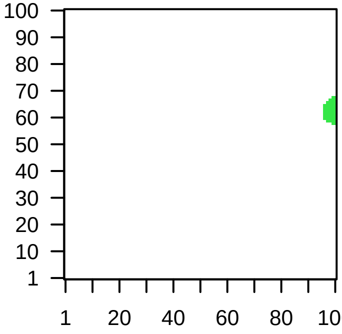
<r> metagenes = 0.84
<r> genes = 0.17
beta: r2= 4.14 / log p= −Inf

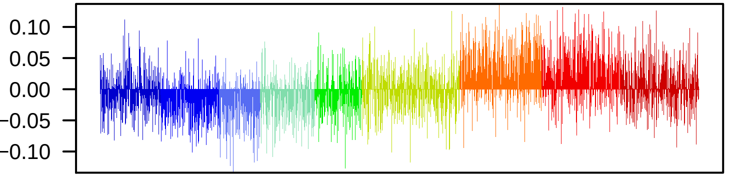
samples with spot = 17 (0.5 %)
A * : 1 (0.3 %)
F * : 1 (0.2 %)
F J * : 7 (1.5 %)
J * : 7 (1.6 %)
N * : 1 (0.2 %)

Overview Map



Spot





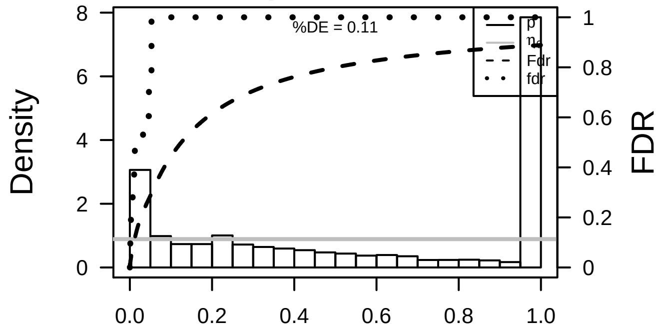
Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_324359	1.46	−0.55	0.25		
2	ILMN_167657	1.42	−1.17	0.36	IKZF1	IKAROS family zinc finger 1 [Source:HGNC Symbol;Acc:HGN
3	ILMN_234913	1.35	−0.37	0.33	CDC42SE1	CDC42 small effector 1 [Source:HGNC Symbol;Acc:HGNC:1
4	ILMN_177798	1.34	−0.35	0.14	USF1	upstream transcription factor 1 [Source:HGNC Symbol;Acc:H
5	ILMN_166813	0.93	−0.56	0.13	GSTM1	glutathione S−transferase mu 1 [Source:HGNC Symbol;Acc:H
6	ILMN_166092	0.92	−0.81	0.28	LOC554223	major histocompatibility complex, class I, V (pseudogene) [So
7	ILMN_180478	0.87	−0.92	0.59	CCAR2	cell cycle and apoptosis regulator 2 [Source:HGNC Symbol;A
8	ILMN_166703	0.85	−0.74	0.21	PDPR	pyruvate dehydrogenase phosphatase regulatory subunit [So
9	ILMN_323500	0.81	−0.62	0.38	LINC00869	long intergenic non−protein coding RNA 869 [Source:HGNC
10	ILMN_176225	0.8	−0.41	0.1	GSTM1	glutathione S−transferase mu 1 [Source:HGNC Symbol;Acc:H
11	ILMN_173842	0.8	−0.65	0.29	CDC42	cell division cycle 42 [Source:HGNC Symbol;Acc:HGNC:1736
12	ILMN_237582	0.79	−0.86	0.36	CD37	CD37 molecule [Source:HGNC Symbol;Acc:HGNC:1666]
13	ILMN_174282	0.78	−0.67	0.29	SPATA13	spermatogenesis associated 13 [Source:HGNC Symbol;Acc:I
14	ILMN_168010	0.77	−0.56	0.32	COL4A3BP	collagen type IV alpha 3 binding protein [Source:HGNC Symb
15	ILMN_235777	0.73	−0.64	0.29	TCEA1	transcription elongation factor A1 [Source:HGNC Symbol;Acc
16	ILMN_175710	0.73	−0.58	0.43	MARCH6	membrane associated ring−CH−type finger 6 [Source:HGNC
17	ILMN_177315	0.7	−0.71	0.26		
18	ILMN_225213	0.7	−0.49	0.51	YWHAE	tyrosine 3−monooxygenase/tryptophan 5−monooxygenase ac
19	ILMN_168831	0.7	−0.7	0.22		FSHD region gene 1 family member B, pseudogene [Source:I
20	ILMN_172728	0.69	−0.63	0.22	CD4	CD4 molecule [Source:HGNC Symbol;Acc:HGNC:1678]

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	8e−73	304 / 5356	Lympl	HOPP_Txn_transition
2	7e−70	350 / 7275	Lympl	HOPP_Txn_elongation
3	9e−67	386 / 9054	Colon	Tx_Colon
4	3e−64	372 / 8568	Colon	TxWk_Colon
5	9e−64	355 / 7854	Chror	5_Tx_Fibroblasts
6	6e−58	367 / 8771	Chror	5_Tx_Melanocytes
7	4e−56	381 / 9555	Colon	TssA_Colon
8	8e−51	426 / 12298	Chror	2_TssA_Melanocytes
9	1e−48	283 / 5936	Brain	Overlap_fetal_midbrain_HetRpts
10	2e−45	402 / 11455	Chror	2_TssA_Fibroblasts
11	8e−45	333 / 8226	Lympl	HOPP_Active_promoter
12	2e−44	302 / 6970	Chror	5_Tx_Neuronal_Progenitor
13	4e−39	420 / 12983	Chror	2_TssA_Neuronal_Progenitor
14	1e−38	332 / 8678	Colon	Quies3_Colon
15	2e−38	233 / 4795	Chror	6_EnhG_Fibroblasts
16	3e−36	296 / 7354	Colon	TssF_Colon
17	6e−36	393 / 11836	Chror	3_TssF_Melanocytes
18	7e−36	253 / 5699	Chror	6_EnhG_Melanocytes
19	6e−35	343 / 9504	Brain	Overlap_fetal_midbrain_K9K27me3
20	1e−33	347 / 9815	Brain	Overlap_fetal_midbrain_ReprPC
21	4e−33	359 / 10430	Brain	Overlap_fetal_midbrain_Quies
22	1e−32	291 / 7448	Lympl	HOPP_Strong_enhancer
23	6e−29	362 / 10999	Colon	TssWk_Colon
24	3e−24	328 / 9917	Brain	Overlap_fetal_midbrain_ReprPCWk
25	1e−23	135 / 2535	CC	nucleoplasm
26	4e−23	377 / 12393	Chror	15_Quies_Neuronal_Progenitor
27	4e−23	109 / 1797	GSEA	PILON_KLF1_TARGETS_DN
28	5e−23	208 / 5067	TF	ICGC_Taf1_targets
29	9e−23	343 / 10779	Colon	Enh_Colon
30	2e−20	277 / 8098	Lympl	HOPP_Weak_promoter
31	2e−20	138 / 2845	Colon	TxEnhG1_Colon
32	2e−19	180 / 4362	TF	ICGC_Creb1_targets
33	2e−19	286 / 8613	Chror	7_Enh_Fibroblasts
34	7e−19	373 / 12741	Chror	7_Enh_Melanocytes
35	9e−19	289 / 8818	MF	protein binding
36	2e−18	190 / 4828	CC	nucleus
37	2e−18	204 / 5373	Colon	EnhWk1_Colon
38	2e−17	289 / 8990	Chror	15_Quies_Fibroblasts
39	1e−16	85 / 1468	Colon	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse c
40	1e−16	75 / 1194	Refer	PROTEINATLAS_stomach

p−values



Aging

Rank	p−value	#in/all	Geneset
1	0.2	4 / 111	HORVATH_aging_genes meth DOWN
2	1.0	0 / 142	HORVATH_aging_genes meth UP
3	1.0	0 / 58	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Cancer

Rank	p−value	#in/all	Geneset
1	0.001	9 / 117	PanCan_Driver_Gene_geneset_nanostring
2	0.005	3 / 16	GENTLES_modul14
3	0.032	2 / 13	GENTLES_modul2
4	0.036	19 / 554	Lembcke_Colonic Inflammation
5	0.049	5 / 91	PanCan_TXmisReg_geneset_nanostring
6	0.053	3 / 39	ZHANG_MM up
7	0.110	6 / 150	PanCan_MAPK_geneset_nanostring
8	0.124	10 / 301	SPANG_BCL6−index2
9	0.138	5 / 125	PanCan_CC+Apop_geneset_nanostring
10	0.230	3 / 76	PanCan_Wnt_geneset_nanostring
11	0.249	1 / 13	WANG_ER_DN
12	0.249	1 / 13	GENTLES_modul12
13	0.249	1 / 13	GENTLES_modul18
14	0.265	1 / 14	LIU_PROSTATE_CANCER_UP
15	0.281	1 / 15	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN

Chromatin states

Rank	p−value	#in/all	Geneset
1	9e−64	355 / 7854	5_Tx_Fibroblasts
2	6e−58	367 / 8771	5_Tx_Melanocytes
3	8e−51	426 / 12298	2_TssA_Melanocytes
4	2e−45	402 / 11455	2_TssA_Fibroblasts
5	2e−44	302 / 6970	5_Tx_Neuronal_Progenitor
6	4e−39	420 / 12983	2_TssA_Neuronal_Progenitor
7	2e−38	233 / 4795	6_EnhG_Fibroblasts
8	6e−36	393 / 11836	3_TssF_Melanocytes
9	7e−36	253 / 5699	6_EnhG_Melanocytes
10	4e−23	377 / 12393	15_Quies_Neuronal_Progenitor
11	2e−19	286 / 8613	7_Enh_Fibroblasts
12	7e−19	373 / 12741	7_Enh_Melanocytes
13	2e−17	289 / 8990	15_Quies_Fibroblasts
14	6e−16	299 / 9635	3_TssF_Fibroblasts
15	7e−15	328 / 11130	15_Quies_Melanocytes

GSEA C2

Rank	p−value	#in/all	Geneset
1	4e−23	109 / 1797	PILON_KLF1_TARGETS_DN
2	5e−15	86 / 1601	GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_DN
3	3e−14	82 / 1535	BLALOCK_ALZHEIMERS_DISEASE_UP
4	3e−11	34 / 411	GARY_CD5_TARGETS_UP
5	1e−08	28 / 368	OSMAN_BLADDER_CANCER_UP
6	2e−08	14 / 95	SCHLOSSER_SERUM_RESPONSE_AUGMENTED_BY_MYC
7	6e−08	23 / 281	GINESTIER_BREAST_CANCER_ZNF217_AMPLIFIED_DN
8	2e−07	57 / 1265	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
9	2e−07	30 / 471	SCHAEFFER_PROSTATE_DEVELOPMENT_6HR_DN
10	2e−07	18 / 190	CHANDRAN_METASTASIS_UP
11	2e−07	39 / 723	LASTOWSKA_NEUROBLASTOMA_COPY_NUMBER_DN
12	2e−07	41 / 783	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
13	9e−07	28 / 454	SENESE_HDAC3_TARGETS_UP
14	1e−06	29 / 483	MARTORIATI_MDM4_TARGETS_FETAL_LIVER_DN
15	1e−06	26 / 407	SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_UP

Lymphoma

Rank	p−value	#in/all	Geneset
1	8e−73	304 / 5356	HOPP_Txn_transition
2	7e−70	350 / 7275	HOPP_Txn_elongation
3	8e−45	333 / 8226	HOPP_Active_promoter
4	1e−32	291 / 7448	HOPP_Strong_enhancer
5	2e−20	277 / 8098	HOPP_Weak_promoter
6	4e−13	67 / 1169	SPANG_BCR DN
7	2e−11	212 / 6559	HOPP_Weak_txn
8	1e−09	35 / 493	WIRTH_lymphoma937_spot J
9	1e−09	34 / 472	Hopp_June14_MMML937 tumors+controls_group.overexpression_J_GC−B−c
10	2e−07	205 / 6959	HOPP_Weak_enhancer
11	8e−05	49 / 1270	SPANG_BCR UP
12	1e−04	87 / 2701	HOPP_Repetitive
13	2e−04	6 / 40	Monti_BCR_cluster
14	5e−04	22 / 455	SPANG_CD40 6hrs DN
15	7e−03	13 / 272	SPANG_IL21 DN

miRNA Disease

Rank	p−value	#in/all	Geneset
1	1	0 / 7	Thyroid carcinoma, papillary
2	1	0 / 123	Pancreatic cancer
3	1	0 / 68	Glioblastoma multiforme, somatic
4	1	0 / 63	Gastrointestinal
5	1	0 / 3	Pituitary adenoma
6	1	0 / 116	Cancer
7	1	0 / 95	Colorectal cancer
8	1	0 / 2	Adenomas, multiple colorectal
9	1	0 / 124	Prostate cancer
10	1	0 / 48	Alzheimer disease, susceptibility to
11	1	0 / 7	Schizophrenia, susceptibility to
12	1	0 / 20	Parkinson disease
13	1	0 / 65	Hepatocellular carcinoma
14	1	0 / 3	Down syndrome, risk of
15	1	0 / 127	Melanoma and neural system tumor syndrome

Reference Signatures

Rank	p−value	#in/all	Geneset
1	1e−16	75 / 1194	PROTEINATLAS_stomach
2	1e−15	68 / 1063	PROTEINATLAS_tonsil
3	9e−13	57 / 912	PROTEINATLAS_urinary bladder
4	1e−12	20 / 119	Chaussabel_2,11_Replication
5	2e−12	66 / 1173	PROTEINATLAS_rectum
6	4e−12	65 / 1167	PROTEINATLAS_gallbladder
7	6e−12	68 / 1268	PROTEINATLAS_colon
8	8e−12	57 / 963	PROTEINATLAS_pancreas
9	1e−11	55 / 912	PROTEINATLAS_fallopian tube
10	3e−11	46 / 695	PROTEINATLAS_bone marrow
11	4e−11	61 / 1118	PROTEINATLAS_placenta
12	1e−10	46 / 724	PROTEINATLAS_lymph node
13	1e−10	56 / 1003	PROTEINATLAS_appendix
14	2e−10	46 / 740	PROTEINATLAS_esophagus
15	2e−10	53 / 933	PROTEINATLAS_adrenal gland

BP

Rank	p−value	#in/all	Geneset
1	1e−10	77 / 1643	transcription, DNA−templated
2	2e−08	35 / 550	positive regulation of transcription, DNA−templated
3	2e−07	21 / 254	cell−cell adhesion
4	4e−07	30 / 486	negative regulation of transcription, DNA−templated
5	7e−07	24 / 346	transcription from RNA polymerase II promoter
6	1e−06	55 / 1272	regulation of transcription, DNA−templated
7	1e−05	40 / 889	positive regulation of transcription from RNA polymerase II promoter
8	4e−05	7 / 43	substantia nigra development
9	7e−05	14 / 189	intracellular protein transport
10	2e−04	10 / 115	regulation of signal transduction by p53 class mediator
11	2e−04	22 / 434	protein phosphorylation
12	4e−04	29 / 671	negative regulation of transcription from RNA polymerase II promoter
13	4e−04	9 / 103	covalent chromatin modification
14	5e−04	22 / 457	regulation of transcription from RNA polymerase II promoter
15	7e−04	6 / 49	regulation of circadian rhythm

CC

Rank	p−value	#in/all	Geneset
1	1e−23	135 / 2535	nucleoplasm
2	2e−18	190 / 4828	nucleus
3	3e−11	89 / 1979	membrane
4	8e−09	159 / 4822	cytoplasm
5	6e−07	22 / 295	cell−cell adherens junction
6	1e−06	9 / 49	transcriptional repressor complex
7	1e−06	103 / 2979	cytosol
8	4e−06	36 / 721	nucleolus
9	9e−06	15 / 179	nuclear speck
10	1e−05	37 / 788	endoplasmic reticulum membrane
11	1e−05	7 / 37	mitotic spindle
12	2e−05	24 / 422	protein complex
13	3e−05	5 / 18	exon−exon junction complex
14	4e−04	12 / 173	nuclear chromatin
15	5e−04	8 / 85	integral component of endoplasmic reticulum membrane

Colon Cancer

Rank	p−value	#in/all	Geneset
1	9e−67	386 / 9054	Tx_Colon
2	3e−64	372 / 8568	TxWk_Colon
3	4e−56	381 / 9555	TssA_Colon
4	1e−38	332 / 8678	Quies3_Colon
5	3e−36	296 / 7354	TssF_Colon
6	6e−29	362 / 10999	TssWk_Colon
7	9e−23	343 / 10779	Enh_Colon
8	2e−20	138 / 2845	TxEnhG1_Colon
9	2e−18	204 / 5373	EnhWk1_Colon
10	1e−16	85 / 1468	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
11	9e−15	213 / 6138	TssD2_Colon
12	1e−12	66 / 1168	LaPointe_mucosa−position_kmeans_O_transverse colon_UP_
13	3e−11	73 / 1470	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
14	5e−11	75 / 1547	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
15	1e−10	112 / 2810	EnhA_Colon

HM

Rank	p−value	#in/all	Geneset
1	7e−04	6 / 50	HALLMARK_TGF_BETA_SIGNALING
2	3e−03	4 / 29	HALLMARK_NOTCH_SIGNALING
3	2e−02	9 / 177	HALLMARK_MITOTIC_SPINDLE
4	2e−02	6 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING
5	4e−02	5 / 87	HALLMARK_PROTEIN_SECRETION
6	4e−02	8 / 179	HALLMARK_G2M_CHECKPOINT
7	5e−02	7 / 151	HALLMARK_APOPTOSIS
8	5e−02	5 / 91	HALLMARK_PEROXISOME
9	5e−02	8 / 185	HALLMARK_P53_PATHWAY
10	5e−02	8 / 186	HALLMARK_IL2_STAT5_SIGNALING
11	6e−02	3 / 40	HALLMARK_WNT_BETA_CATENIN_SIGNALING
12	7e−02	6 / 130	HALLMARK_DNA_REPAIR
13	8e−02	6 / 137	HALLMARK_UV_RESPONSE_UP
14	1e−01	7 / 191	HALLMARK_INFLAMMATORY_RESPONSE
15	1e−01	4 / 91	HALLMARK_ANDROGEN_RESPONSE

Melanoma

Rank	p−value	#in/all	Geneset
1	0.5	1 / 30	Hugo_melanoma−all−MET_UP
2	0.6	1 / 43	Hugo_melanoma−BRAFmut−MET_UP
3	1.0	0 / 54	Hugo_melanoma−all−MET_DN
4	1.0	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
5	1.0	0 / 27	Hugo_melanoma−all−LEF1_UP
6	1.0	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

miRNA target

Rank	p−value	#in/all	Geneset
1	2e−11	30 / 315	hsa−miR−30e
2	8e−11	24 / 217	hsa−miR−185
3	1e−10	34 / 433	hsa−miR−19b
4	7e−10	33 / 438	hsa−miR−19a
5	2e−09	25 / 272	hsa−miR−101
6	2e−09	25 / 274	hsa−miR−1244
7	2e−09	20 / 178	hsa−miR−300
8	3e−09	37 / 561	hsa−miR−20b
9	3e−09	20 / 181	hsa−miR−381
10	4e−09	29 / 374	hsa−miR−144
11	4e−09	36 / 546	hsa−miR−93
12	7e−09	26 / 314	hsa−miR−340
13	8e−09	18 / 154	hsa−miR−139−5p
14	8e−09	24 / 272	hsa−miR−30d
15	1e−08	32 / 463	hsa−miR−301a

Telomeres

Rank	p−value	#in/all	Geneset
1	1	0 / 13	Alternative lengthening of telomeres
2	1	0 / 27	Nabetani_alt len telomeres_genes_ko
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Brain

Rank	p−value	#in/all	Geneset
1	1e−48	283 / 5936	Overlap_fetal_midbrain_HetRpts
2	6e−35	343 / 9504	Overlap_fetal_midbrain_K9K27me3
3	1e−33	347 / 9815	Overlap_fetal_midbrain_ReprPC
4	4e−33	359 / 10430	Overlap_fetal_midbrain_Quies
5	3e−24	328 / 9917	Overlap_fetal_midbrain_ReprPCWk
6	2e−13	130 / 3164	Mid_Frontal_Lobe_ZNF
7	6e−09	45 / 796	Overlap_fetal_midbrain_ZNF
8	1e−03	57 / 1728	Fetal_ReprPCWk
9	3e−03	40 / 1162	Fetal_Enh
10	4e−03	30 / 818	Mid_Frontal_Lobe_Het
11	4e−03	26 / 681	Overlap_fetal_midbrain_EnhP
12	6e−03	39 / 1171	Fetal_EnhP
13	1e−02	31 / 937	Fetal_EnhG
14	2e−02	30 / 906	Fetal_HetRpts
15	3e−02	13 / 328	Fetal_Het

Chr

Rank	p−value	#in/all	Geneset
1	0.007	33 / 959	Chr 16
2	0.021	65 / 2323	Chr 1
3	0.111	32 / 1170	Chr 7
4	0.170	28 / 1060	Chr 5
5	0.175	34 / 1318	Chr 17
6	0.282	21 / 836	Chr 8
7	0.314	28 / 1160	Chr 12
8	0.315	11 / 422	Chr 13
9	0.386	13 / 536	Chr 22
10	0.602	20 / 954	Chr 9
11	0.604	6 / 289	Chr 21
12	0.635	31 / 1492	Chr 2
13	0.655	29 / 1411	Chr 11
14	0.700	12 / 619	Chr 20
15	0.763	17 / 902	Chr 4

Glio

Rank	p−value	#in/all	Geneset
1	5e−07	23 / 316	WILLSCHER_GBM_Verhaak−PNwt & CL_up
2	1e−05	74 / 2043	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
3	3e−05	37 / 820	Sturm_GBM_Meth_overexpression_E_G34_UP
4	8e−04	59 / 1777	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
5	3e−03	5 / 44	WILLSCHER_GBM_Verhaak−PNwt_up
6	4e−03	6 / 69	WILLSCHER_GBM_Verhaak−PNwt & MES_up
7	1e−02	14 / 315	Up
8	2e−02	2 / 9	WILLSCHER_GBM_LTSmut_proteomics−A_UP
9	2e−02	4 / 50	WILLSCHER_GBM_proteomics_wtOnly_SpotG
10	4e−02	2 / 15	VERHAAK_NL subtype
11	5e−02	5 / 94	Weller_LGG_A_vs_O_UP
12	6e−02	7 / 157	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
13	6e−02	5 / 96	Weller_LGG_1p19qDel−vs−intact_DOWN
14	1e−01	2 / 24	Martinez_Glio_hypermeth
15	1e−01	3 / 55	Stuehler_Proteins_up_in_STS

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.2	2 / 32	Marjolein_ageing−genes_DN
2	0.2	7 / 211	Homuth_BMI−associated−genes_DN
3	0.4	4 / 147	Homuth_BMI−associated−genes_UP
4	1.0	0 / 94	DUMEAUX_Smoking enriched genes
5	1.0	0 / 10	DUMEAUX_Smoking literature genes up
6	1.0	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
7	1.0	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
8	1.0	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
9	1.0	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
10	1.0	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
11	1.0	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
12	1.0	0 / 10	DUMEAUX_Women normal BMI literature genes up
13	1.0	0 / 17	DUMEAUX_High bmi enriched genes
14	1.0	0 / 31	DUMEAUX_Fasting enriched genes
15	1.0	0 / 18	Huan_blood−pressure_SBP−signature

MF

Rank	p−value	#in/all	Geneset
1	9e−19	289 / 8818	protein binding
2	2e−15	66 / 1013	poly(A) RNA binding
3	2e−07	22 / 274	transcription factor binding
4	4e−07	21 / 265	cadherin binding involved in cell−cell adhesion
5	5e−07	10 / 59	RNA polymerase II distal enhancer sequence−specific DNA binding
6	6e−07	19 / 227	transcription coactivator activity
7	2e−06	60 / 1475	DNA binding
8	4e−06	47 / 1065	zinc ion binding
9	1e−05	22 / 355	chromatin binding
10	2e−05	6 / 26	thyroid hormone receptor binding
11	2e−05	16 / 215	transcription regulatory region DNA binding
12	1e−04	37 / 877	transcription factor activity, sequence−specific DNA binding
13	1e−04	13 / 173	ubiquitin protein ligase activity
14	2e−04	9 / 92	histone deacetylase binding
15	2e−04	18 / 315	protein serine/threonine kinase activity

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.2	1 / 12	BENTINK_src.2
2	0.3	1 / 14	GUSTAFSON_PI3K_UP
3	0.3	1 / 14	BENTINK_ras.6
4	1.0	0 / 15	GUSTAFSON_PI3K_DN
5	1.0	0 / 13	BENTINK_e2f3.1
6	1.0	0 / 13	BENTINK_e2f3.2
7	1.0	0 / 13	BENTINK_myc.1
8	1.0	0 / 12	BENTINK_ras.1
9	1.0	0 / 11	BENTINK_ras.4
10	1.0	0 / 13	BENTINK_src.10
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	5e−23	208 / 5067	ICGC_Taf1_targets
2	2e−19	180 / 4362	ICGC_Creb1_targets
3	2e−16	186 / 4890	ICGC_Bclaf101388_targets
4	3e−16	174 / 4468	ICGC_Egr1_targets
5	5e−16	201 / 5518	ICGC_Stat5_targets
6	8e−16	184 / 4881	ICGC_Atf2_targets
7	8e−16	197 / 5383	ICGC_Sp1_targets
8	4e−15	197 / 5466	ICGC_Nficsc81335_targets
9	4e−15	193 / 5312	ICGC_Tcf12_targets
10	1e−14	195 / 5442	ICGC_Pmlsc71910_targets
11	2e−14	160 / 4131	ICGC_Nfatc1_targets
12	3e−14	193 / 5410	ICGC_Foxm1_targets
13	7e−14	221 / 6578	ICGC_Pou2_targets
14	9e−14	213 / 6267	ICGC_Yy1_targets
15	2e−13	102 / 2215	ICGC_GabpPcr2_targets

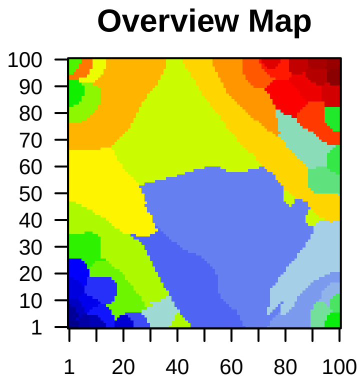
K−Means Cluster

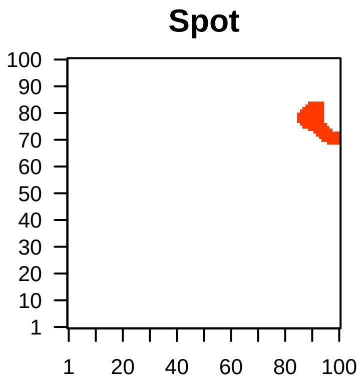
Spot Summary: T1

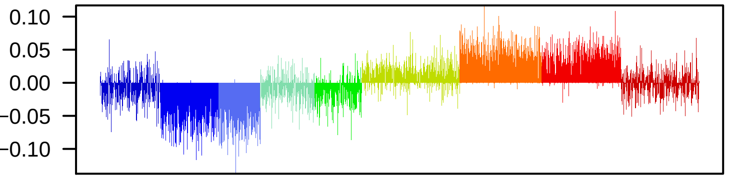
metagenes = 138
genes = 967

<r> metagenes = 0.9
<r> genes = 0.2
beta: r2= 4.56 / log p= −Inf

samples with spot = 1 (0 %)
F J * : 1 (0.2 %)





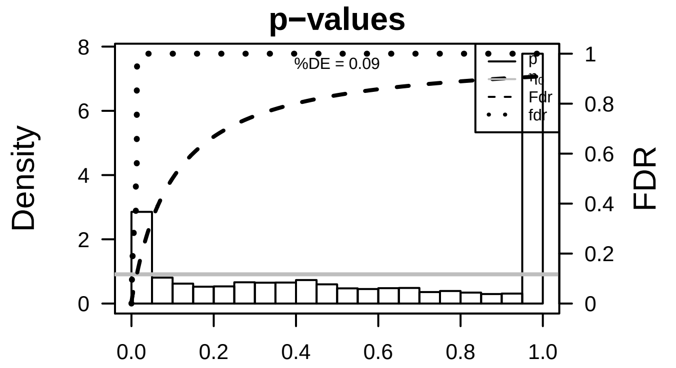


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_208306	1.69	−0.7	0.17		immunoglobulin lambda like polypeptide 3, pseudogene [Sour
2	ILMN_180460	1.38	−0.59	0.22		
3	ILMN_240396	1.27	−0.58	0.41		
4	ILMN_167422	1.18	−0.67	0.21		
5	ILMN_229476	1.15	−0.77	0.25	AMY1A	amylase, alpha 1A (salivary) [Source:HGNC Symbol;Acc:HGI
6	ILMN_176801	1.09	−0.44	0.4	TNFRSF17	TNF receptor superfamily member 17 [Source:HGNC Symbol
7	ILMN_170744	0.93	−0.49	0.21	CDK12	cyclin dependent kinase 12 [Source:HGNC Symbol;Acc:HGN
8	ILMN_166339	0.85	−0.34	0.28	CDC20	cell division cycle 20 [Source:HGNC Symbol;Acc:HGNC:1723
9	ILMN_167885	0.84	−0.34	0.11		immunoglobulin lambda variable 8−61 [Source:HGNC Symbo
10	ILMN_171375	0.82	−0.58	0.14	UBE2J1	ubiquitin conjugating enzyme E2 J1 [Source:HGNC Symbol;A
11	ILMN_223378	0.8	−0.38	0.3	CD38	CD38 molecule [Source:HGNC Symbol;Acc:HGNC:1667]
12	ILMN_172429	0.78	−0.57	0.26	KDELR2	KDEL endoplasmic reticulum protein retention receptor 2 [Sou
13	ILMN_175316	0.77	−0.9	0.17	IPO8	importin 8 [Source:HGNC Symbol;Acc:HGNC:9853]
14	ILMN_178460	0.75	−0.58	0.18		
15	ILMN_180675	0.75	−0.33	0.34	GLDC	glycine decarboxylase [Source:HGNC Symbol;Acc:HGNC:43
16	ILMN_235202	0.71	−0.97	0.07	DSTYK	dual serine/threonine and tyrosine protein kinase [Source:HG
17	ILMN_173718	0.7	−0.44	0.42	CDCA7	cell division cycle associated 7 [Source:HGNC Symbol;Acc:H
18	ILMN_171906	0.68	−0.47	0.17	KCTD10	potassium channel tetramerization domain containing 10 [Sou
19	ILMN_167148	0.66	−0.49	0.19	GALM	galactose mutarotase [Source:HGNC Symbol;Acc:HGNC:240
20	ILMN_323269	0.66	−0.54	0.15		dihydrofolate reductase pseudogene 2 [Source:HGNC Symbo

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	6e−95	608 / 9815	Brain	Overlap_fetal_midbrain_ReprPC
2	8e−91	549 / 8226	Lympl	HOPP_Active_promoter
3	8e−91	651 / 11455	Chror	2_TssA_Fibroblasts
4	4e−86	507 / 7275	Lympl	HOPP_Txn_elongation
5	3e−81	661 / 12298	Chror	2_TssA_Melanocytes
6	6e−80	551 / 8771	Chror	5_Tx_Melanocytes
7	9e−78	515 / 7854	Chror	5_Tx_Fibroblasts
8	1e−72	667 / 12983	Chror	2_TssA_Neuronal_Progenitor
9	1e−60	544 / 9555	Colon	TssA_Colon
10	2e−60	590 / 10999	Colon	TssWk_Colon
11	6e−56	505 / 8678	Colon	Quies3_Colon
12	3e−55	483 / 8098	Lympl	HOPP_Weak_promoter
13	3e−53	528 / 9504	Brain	Overlap_fetal_midbrain_K9K27me3
14	2e−52	509 / 8990	Chror	15_Quies_Fibroblasts
15	4e−52	394 / 5936	Brain	Overlap_fetal_midbrain_HetRpts
16	7e−52	493 / 8568	Colon	TxWk_Colon
17	5e−48	502 / 9054	Colon	Tx_Colon
18	6e−48	426 / 6970	Chror	5_Tx_Neuronal_Progenitor
19	1e−46	152 / 1222	GSEA	DODD_NASOPHARYNGEAL_CARCINOMA_DN
20	1e−43	583 / 11836	Chror	3_TssF_Melanocytes
21	4e−41	140 / 1161	GSEA	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
22	8e−41	346 / 5356	Lympl	HOPP_Txn_transition
23	4e−39	551 / 11130	Chror	15_Quies_Melanocytes
24	3e−35	502 / 9917	Brain	Overlap_fetal_midbrain_ReprPCWk
25	1e−34	106 / 800	GSEA	JOHNSTONE_PARVB_TARGETS_3_DN
26	3e−34	579 / 12393	Chror	15_Quies_Neuronal_Progenitor
27	1e−33	103 / 777	Lympl	WIRTH_lymphoma937_spot D
28	4e−33	49 / 162	GSEA	GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP
29	2e−32	101 / 772	Lympl	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell li
30	6e−32	584 / 12741	Chror	7_Enh_Melanocytes
31	6e−32	44 / 132	Glio	WILLSCHER_GBM_Verhaak−CL_up (C)
32	2e−30	35 / 80	GSEA	GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
33	4e−30	84 / 581	GSEA	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_UP
34	2e−29	55 / 249	GSEA	ZHANG_TLX_TARGETS_60HR_DN
35	2e−27	153 / 1797	GSEA	PILON_KLF1_TARGETS_DN
36	2e−27	39 / 124	GSEA	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
37	3e−27	103 / 926	GSEA	NUYTTEN_EZH2_TARGETS_DN
38	4e−27	84 / 641	GSEA	MARSON_BOUND_BY_E2F4_UNSTIMULATED
39	3e−26	74 / 518	GSEA	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
40	2e−25	253 / 4034	Colon	TssD1_Colon



Aging

Rank	p−value	#in/all	Geneset
1	0.3	6 / 142	HORVATH_aging_genes meth UP
2	0.5	4 / 111	HORVATH_aging_genes meth DOWN
3	1.0	0 / 58	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	4e−11	36 / 300	cell division
2	2e−08	98 / 1643	transcription, DNA−templated
3	1e−07	25 / 219	mitotic nuclear division
4	1e−07	18 / 122	G2/M transition of mitotic cell cycle
5	3e−07	22 / 185	cell cycle
6	8e−07	22 / 196	mRNA splicing, via spliceosome
7	3e−06	74 / 1272	regulation of transcription, DNA−templated
8	3e−06	14 / 94	G1/S transition of mitotic cell cycle
9	2e−05	7 / 26	DNA replication initiation
10	2e−05	7 / 27	mitotic spindle assembly
11	4e−05	6 / 20	regulation of transcription involved in G1/S transition of mitotic cell cycle
12	4e−05	5 / 13	spindle organization
13	6e−05	18 / 187	DNA repair
14	7e−05	15 / 139	RNA splicing
15	1e−04	14 / 130	DNA replication

Brain

Rank	p−value	#in/all	Geneset
1	6e−95	608 / 9815	Overlap_fetal_midbrain_ReprPC
2	3e−53	528 / 9504	Overlap_fetal_midbrain_K9K27me3
3	4e−52	394 / 5936	Overlap_fetal_midbrain_HetRpts
4	3e−35	502 / 9917	Overlap_fetal_midbrain_ReprPCWk
5	2e−24	489 / 10430	Overlap_fetal_midbrain_Quies
6	2e−06	70 / 1171	Fetal_EnhP
7	9e−06	56 / 906	Fetal_HetRpts
8	6e−05	43 / 681	Overlap_fetal_midbrain_EnhP
9	2e−04	53 / 937	Fetal_EnhG
10	7e−04	26 / 386	Fetal_ZNF
11	1e−03	70 / 1436	Fetal_K9K27me3
12	3e−03	114 / 2654	Fetal_Quies
13	7e−03	55 / 1162	Fetal_Enh
14	2e−02	38 / 796	Overlap_fetal_midbrain_ZNF
15	6e−02	55 / 1329	Overlap_fetal_midbrain_Enh

Cancer

Rank	p−value	#in/all	Geneset
1	9e−23	6 / 12	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
2	1e−11	51 / 527	Lembcke_Normal vs Adenoma
3	3e−06	4 / 14	RHODES_UNDIFFERENTIATED_CANCER
4	1e−04	4 / 9	GENTLES_modul3
5	7e−04	9 / 73	SHAUGHNESSY_MM high risk
6	2e−03	1 / 13	RHODES_CANCER_META_SIGNATURE
7	8e−03	5 / 38	KUIPER_MM good survival
8	9e−03	6 / 54	KUIPER_MM poor survival
9	1e−02	3 / 14	BEN−PORATH_UP
10	3e−02	9 / 125	PanCan_CC+Apop_geneset_nanostring
11	3e−02	4 / 36	PanCan_HK_geneset_nanostring
12	6e−02	1 / 14	LIU_COMMON_CANCER_GENES
13	7e−02	1 / 2	GENTLES_modul8
14	7e−02	2 / 13	GENTLES_modul6
15	2e−01	0 / 14	LIU_PROSTATE_CANCER_UP

CC

Rank	p−value	#in/all	Geneset
1	1e−23	181 / 2535	nucleoplasm
2	6e−21	273 / 4828	nucleus
3	6e−10	39 / 379	centrosome
4	6e−08	152 / 2979	cytosol
5	8e−08	223 / 4822	cytoplasm
6	5e−07	51 / 721	nucleolus
7	3e−06	20 / 179	nuclear speck
8	2e−05	72 / 1304	mitochondrion
9	4e−05	7 / 29	small−subunit processome
10	6e−05	9 / 53	chromosome, centromeric region
11	6e−05	11 / 79	spliceosomal complex
12	1e−04	13 / 116	midbody
13	2e−04	6 / 26	condensed chromosome
14	8e−04	10 / 89	centriole
15	9e−04	11 / 107	spindle

Chr

Rank	p−value	#in/all	Geneset
1	0.002	26 / 422	Chr 13
2	0.036	16 / 289	Chr 21
3	0.054	37 / 836	Chr 8
4	0.064	45 / 1060	Chr 5
5	0.102	49 / 1211	Chr 6
6	0.170	57 / 1492	Chr 2
7	0.181	86 / 2323	Chr 1
8	0.267	34 / 902	Chr 4
9	0.271	45 / 1217	Chr 3
10	0.283	29 / 768	Chr 14
11	0.286	29 / 769	Chr 15
12	0.291	43 / 1170	Chr 7
13	0.478	31 / 904	Chr 10
14	0.521	39 / 1160	Chr 12
15	0.601	11 / 342	Chr 18

Chromatin states

Rank	p−value	#in/all	Geneset
1	8e−91	651 / 11455	2_TssA_Fibroblasts
2	3e−81	661 / 12298	2_TssA_Melanocytes
3	6e−80	551 / 8771	5_Tx_Melanocytes
4	9e−78	515 / 7854	5_Tx_Fibroblasts
5	1e−72	667 / 12983	2_TssA_Neuronal_Progenitor
6	2e−52	509 / 8990	15_Quies_Fibroblasts
7	6e−48	426 / 6970	5_Tx_Neuronal_Progenitor
8	1e−43	583 / 11836	3_TssF_Melanocytes
9	4e−39	551 / 11130	15_Quies_Melanocytes
10	3e−34	579 / 12393	15_Quies_Neuronal_Progenitor
11	6e−32	584 / 12741	7_Enh_Melanocytes
12	2e−21	417 / 8613	7_Enh_Fibroblasts
13	3e−17	438 / 9635	3_TssF_Fibroblasts
14	3e−16	234 / 4237	14_ZNF_Neuronal_Progenitor
15	6e−13	121 / 1846	14_ZNF_Melanocytes

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−60	544 / 9555	TssA_Colon
2	2e−60	590 / 10999	TssWk_Colon
3	6e−56	505 / 8678	Quies3_Colon
4	7e−52	493 / 8568	TxWk_Colon
5	5e−48	502 / 9054	Tx_Colon
6	2e−25	253 / 4034	TssD1_Colon
7	1e−18	121 / 1547	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
8	1e−11	335 / 7354	TssF_Colon
9	2e−10	78 / 1083	ZNF_Colon
10	2e−10	93 / 1404	LaPointe_mucosa−position_kmeans_D_transverse colon_UP_
11	8e−09	118 / 2073	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
12	4e−08	24 / 193	Kosinski_lower−crypt−long−list
13	9e−08	88 / 1468	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
14	1e−07	76 / 1216	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_
15	4e−07	63 / 965	Pentrack_CRC_TCGA_corr_R_normal_DN

Glio

Rank	p−value	#in/all	Geneset
1	6e−32	44 / 132	WILLSCHER_GBM_Verhaak−CL_up (C)
2	1e−21	153 / 2043	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
3	1e−15	125 / 1777	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
4	1e−13	72 / 820	Sturm_GBM_Meth_overexpression_E_G34_UP
5	3e−11	18 / 74	Weller_LGG_gradeII−vs−III_DOWN
6	2e−07	12 / 55	developing astrocytes
7	7e−05	25 / 316	WILLSCHER_GBM_Verhaak−PNwt & CL_up
8	1e−02	19 / 315	Up
9	2e−02	6 / 65	cultured astroglia vs. in vivo astrocytes
10	3e−02	5 / 50	WILLSCHER_GBM_proteomics_wtOnly_SpotG
11	3e−02	2 / 9	WILLSCHER_GBM_LTSmut_proteomics−A_UP
12	4e−02	6 / 76	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
13	8e−02	4 / 48	Vishal_subnetwork signature of survival in GBM
14	2e−01	1 / 5	Phillips Prolif up vs PN & MES
15	2e−01	3 / 43	Noushmehr_Pron_GCIMP_hypermeth_DN

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−46	152 / 1222	DODD_NASOPHARYNGEAL_CARCINOMA_DN
2	4e−41	140 / 1161	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
3	1e−34	106 / 800	JOHNSTONE_PARVB_TARGETS_3_DN
4	4e−33	49 / 162	GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP
5	2e−30	35 / 80	GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
6	4e−30	84 / 581	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_UP
7	2e−29	55 / 249	ZHANG_TLX_TARGETS_60HR_DN
8	2e−27	153 / 1797	PILON_KLF1_TARGETS_DN
9	2e−27	39 / 124	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
10	3e−27	103 / 926	NUYTTEN_EZH2_TARGETS_DN
11	4e−27	84 / 641	MARSON_BOUND_BY_E2F4_UNSTIMULATED
12	3e−26	74 / 518	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
13	2e−24	39 / 145	WINNEPENNINCKX_MELANOMA_METASTASIS_UP
14	7e−24	47 / 228	KOBAYASHI_EGFR_SIGNALING_24HR_DN
15	1e−23	125 / 1417	PUJANA_BRCA1_PCC_NETWORK

HM

Rank	p−value	#in/all	Geneset
1	6e−17	34 / 173	HALLMARK_E2F_TARGETS
2	5e−14	31 / 179	HALLMARK_G2M_CHECKPOINT
3	6e−07	21 / 177	HALLMARK_MITOTIC_SPINDLE
4	1e−03	12 / 130	HALLMARK_DNA_REPAIR
5	2e−03	11 / 116	HALLMARK_SPERMATOGENESIS
6	5e−03	13 / 170	HALLMARK_MYC_TARGETS_V1
7	1e−02	10 / 132	HALLMARK_UV_RESPONSE_DN
8	7e−02	3 / 29	HALLMARK_NOTCH_SIGNALING
9	7e−02	6 / 87	HALLMARK_PROTEIN_SECRETION
10	1e−01	9 / 167	HALLMARK_OXIDATIVE_PHOSPHORYLATION
11	1e−01	6 / 103	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
12	1e−01	6 / 103	HALLMARK_BILE_ACID_METABOLISM
13	2e−01	9 / 185	HALLMARK_MTORC1_SIGNALING
14	2e−01	9 / 185	HALLMARK_P53_PATHWAY
15	2e−01	9 / 186	HALLMARK_ESTROGEN_RESPONSE_LATE

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.1	11 / 211	Homuth_BMI−associated−genes_DN
2	0.3	1 / 10	DUMEAUX_Smoking literature genes up
3	0.8	2 / 94	DUMEAUX_Smoking enriched genes
4	0.9	3 / 147	Homuth_BMI−associated−genes_UP
5	1.0	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
6	1.0	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
7	1.0	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
8	1.0	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
9	1.0	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
10	1.0	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
11	1.0	0 / 10	DUMEAUX_Women normal BMI literature genes up
12	1.0	0 / 17	DUMEAUX_High bmi enriched genes
13	1.0	0 / 31	DUMEAUX_Fasting enriched genes
14	1.0	0 / 18	Huan_blood−pressure_SBP−signature
15	1.0	0 / 16	Huan_blood−pressure_DBP−signature

Lymphoma

Rank	p−value	#in/all	Geneset
1	8e−91	549 / 8226	HOPP_Active_promoter
2	4e−86	507 / 7275	HOPP_Txn_elongation
3	3e−55	483 / 8098	HOPP_Weak_promoter
4	8e−41	346 / 5356	HOPP_Txn_transition
5	1e−33	103 / 777	WIRTH_lymphoma937_spot D
6	2e−32	101 / 772	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell line_
7	3e−24	351 / 6559	HOPP_Weak_txn
8	1e−23	364 / 6959	HOPP_Weak_enhancer
9	4e−13	38 / 283	TARTE_Plasmablast signature
10	4e−13	94 / 1270	SPANG_BCR UP
11	1e−10	334 / 7448	HOPP_Strong_enhancer
12	6e−08	75 / 1169	SPANG_BCR DN
13	2e−05	13 / 94	Sha_BL UP
14	7e−05	10 / 66	TARTE_Plasma cell signature
15	3e−04	15 / 158	WIRTH_lymphoma937_spot C

Melanoma

Rank	p−value	#in/all	Geneset
1	0.2	2 / 27	Hugo_melanoma−all−LEF1_UP
2	0.8	1 / 43	Hugo_melanoma−BRAFmut−MET_UP
3	1.0	0 / 30	Hugo_melanoma−all−MET_UP
4	1.0	0 / 54	Hugo_melanoma−all−MET_DN
5	1.0	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
6	1.0	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

MF

Rank	p−value	#in/all	Geneset
1	6e−19	416 / 8818	protein binding
2	3e−10	74 / 1013	poly(A) RNA binding
3	6e−09	103 / 1717	metal ion binding
4	1e−06	84 / 1475	DNA binding
5	4e−05	30 / 399	RNA binding
6	4e−05	72 / 1329	ATP binding
7	6e−05	52 / 877	transcription factor activity, sequence−specific DNA binding
8	3e−04	11 / 92	histone deacetylase binding
9	3e−04	6 / 29	repressing transcription factor binding
10	5e−04	11 / 99	mRNA binding
11	6e−04	22 / 301	ubiquitin−protein transferase activity
12	1e−03	4 / 14	RNA polymerase II carboxy−terminal domain kinase activity
13	1e−03	8 / 63	protein transporter activity
14	2e−03	5 / 26	Ran GTPase binding
15	2e−03	5 / 28	DNA−dependent ATPase activity

miRNA Disease

Rank	p−value	#in/all	Geneset
1	1	0 / 7	Thyroid carcinoma, papillary
2	1	0 / 123	Pancreatic cancer
3	1	0 / 68	Glioblastoma multiforme, somatic
4	1	0 / 63	Gastrointestinal
5	1	0 / 3	Pituitary adenoma
6	1	0 / 116	Cancer
7	1	0 / 95	Colorectal cancer
8	1	0 / 2	Adenomas, multiple colorectal
9	1	0 / 124	Prostate cancer
10	1	0 / 48	Alzheimer disease, susceptibility to
11	1	0 / 7	Schizophrenia, susceptibility to
12	1	0 / 20	Parkinson disease
13	1	0 / 65	Hepatocellular carcinoma
14	1	0 / 3	Down syndrome, risk of
15	1	0 / 127	Melanoma and neural system tumor syndrome

miRNA target

Rank	p−value	#in/all	Geneset
1	6e−09	38 / 394	hsa−miR−301b
2	4e−08	24 / 194	hsa−miR−568
3	7e−08	35 / 379	hsa−miR−454
4	1e−07	19 / 134	hsa−miR−656
5	2e−07	39 / 463	hsa−miR−301a
6	2e−07	29 / 291	hsa−miR−186
7	6e−07	18 / 135	hsa−miR−488
8	1e−06	22 / 198	hsa−miR−221
9	1e−06	26 / 263	hsa−miR−449a
10	1e−06	17 / 125	hsa−miR−508−3p
11	1e−06	29 / 317	hsa−miR−559
12	1e−06	33 / 389	hsa−miR−519a
13	1e−06	23 / 218	hsa−miR−181a
14	1e−06	32 / 374	hsa−miR−144
15	2e−06	36 / 455	hsa−miR−130a

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.06	2 / 12	BENTINK_ras.1
2	0.07	2 / 13	BENTINK_e2f3.2
3	0.08	2 / 14	BENTINK_ras.6
4	0.31	1 / 11	BENTINK_ras.4
5	0.34	1 / 12	BENTINK_src.2
6	0.36	1 / 13	BENTINK_src.10
7	0.38	1 / 14	GUSTAFSON_PI3K_UP
8	0.40	1 / 15	GUSTAFSON_PI3K_DN
9	1.00	0 / 13	BENTINK_e2f3.1
10	1.00	0 / 13	BENTINK_myc.1
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Reference Signatures

Rank	p−value	#in/all	Geneset
1	4e−11	24 / 139	Chaussabel_1,8_Metabolism Biosynthesis
2	8e−10	30 / 242	Chaussabel_3,9_Kinases
3	1e−08	32 / 302	Chaussabel_3,4_Protein phosphatases
4	2e−06	23 / 221	Chaussabel_3,8_Enzymes
5	4e−06	24 / 248	Chaussabel_3,6_Mitochondrial ribosomal proteins
6	6e−06	15 / 113	Chaussabel_1,4_Replication
7	7e−06	59 / 963	PROTEINATLAS_pancreas
8	7e−06	25 / 275	Chaussabel_3,7_Spliceosome
9	1e−05	58 / 959	PROTEINATLAS_nasopharynx
10	2e−05	49 / 782	PROTEINATLAS_thyroid gland
11	5e−05	68 / 1239	PROTEINATLAS_testis
12	9e−05	65 / 1194	PROTEINATLAS_stomach
13	1e−04	68 / 1268	PROTEINATLAS_colon
14	1e−04	64 / 1176	PROTEINATLAS_duodenum
15	1e−04	48 / 816	PROTEINATLAS_endometrium

Telomeres

Rank	p−value	#in/all	Geneset
1	0.4	1 / 13	Alternative lengthening of telomeres
2	1.0	0 / 27	Nabetani_alt len telomeres_genes_ko
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	4e−20	280 / 5067	ICGC_Taf1_targets
2	2e−13	229 / 4362	ICGC_Creb1_targets
3	4e−12	267 / 5466	ICGC_Nficsc81335_targets
4	4e−12	266 / 5442	ICGC_Pmlsc71910_targets
5	1e−11	101 / 1498	ICGC_Ets1_targets
6	3e−11	98 / 1452	ICGC_Six5_targets
7	6e−11	240 / 4890	ICGC_Bclaf101388_targets
8	3e−10	237 / 4881	ICGC_Atf2_targets
9	4e−10	107 / 1723	HEBENSTREIT_high expression TF
10	1e−09	286 / 6267	ICGC_Yy1_targets
11	2e−09	257 / 5518	ICGC_Stat5_targets
12	2e−09	126 / 2215	ICGC_GabpPcr2_targets
13	2e−08	247 / 5383	ICGC_Sp1_targets
14	2e−08	79 / 1231	KIM_MYC targets
15	3e−08	290 / 6578	ICGC_Pou2_targets

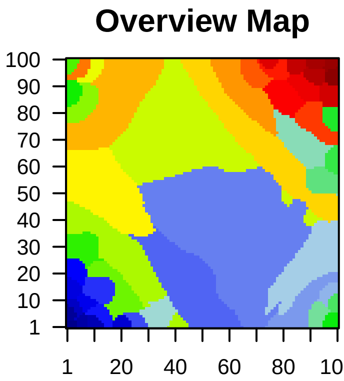
K−Means Cluster

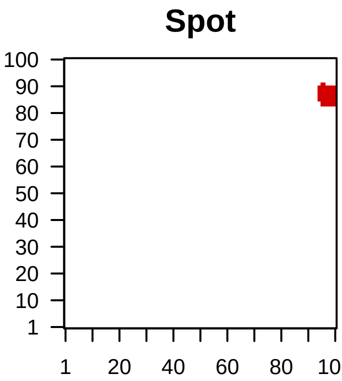
Spot Summary: U1

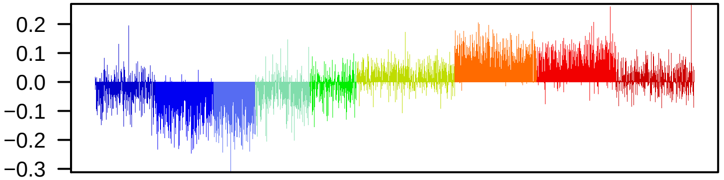
metagenes = 56
genes = 703

<r> metagenes = 0.96
<r> genes = 0.35
beta: r2= 19.11 / log p= −Inf

samples with spot = 194 (5.7 %)
A * : 2 (0.6 %)
A F * : 3 (1 %)
F * : 3 (0.5 %)
F J * : 106 (22.9 %)
J * : 77 (17.2 %)
N * : 3 (0.7 %)





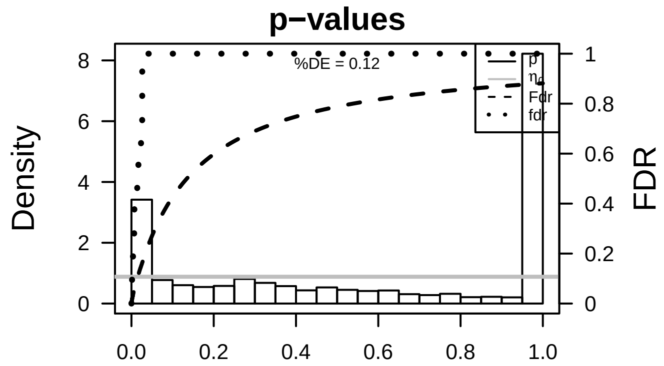


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_169749	5.33	−1.74	0.09	HLA−DRB5	major histocompatibility complex, class II, DR beta 5 [Source:
2	ILMN_171516	4.62	−2.25	0.09		
3	ILMN_179817	2.09	−1.22	0.17	CHURC1	churchill domain containing 1 [Source:HGNC Symbol;Acc:HG
4	ILMN_321438	1.33	−1.23	0.24		
5	ILMN_224608	1.32	−1.59	0.13	CCZ1B	CCZ1 homolog B, vacuolar protein trafficking and biogenesis
6	ILMN_231390	1.03	−0.92	0.3	PAM	peptidylglycine alpha−amidating monooxygenase [Source:HG
7	ILMN_219840	0.97	−1.14	0.24		
8	ILMN_208622	0.94	−0.81	0.22	WDR11	WD repeat domain 11 [Source:HGNC Symbol;Acc:HGNC:13
9	ILMN_172449	0.88	−0.84	0.53	LYSMD2	LysM domain containing 2 [Source:HGNC Symbol;Acc:HGNC
10	ILMN_176173	0.87	−0.81	0.44	HLA−DMB	major histocompatibility complex, class II, DM beta [Source:H
11	ILMN_166464	0.84	−0.6	0.37	MED4	mediator complex subunit 4 [Source:HGNC Symbol;Acc:HGN
12	ILMN_165936	0.82	−0.62	0.21		
13	ILMN_222100	0.82	−1.13	0.31		
14	ILMN_177672	0.79	−0.51	0.45	PHF11	PHD finger protein 11 [Source:HGNC Symbol;Acc:HGNC:17
15	ILMN_167584	0.79	−0.69	0.53	MYL12A	myosin light chain 12A [Source:HGNC Symbol;Acc:HGNC:16
16	ILMN_239016	0.78	−0.62	0.49	PHF11	PHD finger protein 11 [Source:HGNC Symbol;Acc:HGNC:17
17	ILMN_238414	0.77	−0.42	0.36		
18	ILMN_167249	0.76	−0.58	0.49	DNAJA1	DnaJ heat shock protein family (Hsp40) member A1 [Source:
19	ILMN_234181	0.75	−1.21	0.3	TFG	TRK−fused gene [Source:HGNC Symbol;Acc:HGNC:11758]
20	ILMN_180713	0.73	−0.66	0.39		ciliary rootlet coiled−coil, rootletin pseudogene 2 [Source:HG

Geneset Overrepresentation

Rank	p−value	#in/all		Geneset
1	1e−99	489 / 8226	Lympl	HOPP_Active_promoter
2	1e−99	461 / 7275	Lympl	HOPP_Txn_elongation
3	1e−99	508 / 9555	Colon	TssA_Colon
4	1e−99	521 / 9815	Brain	Overlap_fetal_midbrain_ReprPC
5	1e−99	480 / 8771	Chror	5_Tx_Melanocytes
6	2e−98	551 / 12298	Chror	2_TssA_Melanocytes
7	3e−98	535 / 11455	Chror	2_TssA_Fibroblasts
8	4e−90	460 / 8568	Colon	TxWk_Colon
9	2e−89	462 / 8678	Colon	Quies3_Colon
10	2e−87	469 / 9054	Colon	Tx_Colon
11	5e−87	437 / 7854	Chror	5_Tx_Fibroblasts
12	1e−86	551 / 12983	Chror	2_TssA_Neuronal_Progenitor
13	2e−85	378 / 5936	Brain	Overlap_fetal_midbrain_HetRpts
14	3e−79	469 / 9504	Brain	Overlap_fetal_midbrain_K9K27me3
15	8e−74	425 / 8098	Lympl	HOPP_Weak_promoter
16	2e−71	493 / 10999	Colon	TssWk_Colon
17	3e−70	337 / 5356	Lympl	HOPP_Txn_transition
18	2e−65	436 / 8990	Chror	15_Quies_Fibroblasts
19	2e−65	380 / 6970	Chror	5_Tx_Neuronal_Progenitor
20	1e−59	450 / 9917	Brain	Overlap_fetal_midbrain_ReprPCWk
21	4e−55	507 / 12741	Chror	7_Enh_Melanocytes
22	2e−53	485 / 11836	Chror	3_TssF_Melanocytes
23	4e−51	465 / 11130	Chror	15_Quies_Melanocytes
24	2e−44	482 / 12393	Chror	15_Quies_Neuronal_Progenitor
25	7e−44	145 / 1547	Colon	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP
26	9e−44	435 / 10430	Brain	Overlap_fetal_midbrain_Quies
27	2e−39	150 / 1797	GSEA	PILON_KLF1_TARGETS_DN
28	1e−37	317 / 6559	Lympl	HOPP_Weak_txn
29	6e−37	374 / 8613	Chror	7_Enh_Fibroblasts
30	1e−35	119 / 1265	GSEA	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
31	1e−34	322 / 6959	Lympl	HOPP_Weak_enhancer
32	8e−34	65 / 388	GSEA	SHEN_SMARCA2_TARGETS_UP
33	3e−32	369 / 8818	MF	protein binding
34	1e−31	257 / 5067	TF	ICGC_Taf1_targets
35	5e−31	90 / 841	GSEA	ACEVEDO_LIVER_CANCER_UP
36	1e−27	129 / 1777	Glio	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
37	2e−27	63 / 465	GSEA	MILI_PSEUDOPODIA_HAPTOTAXIS_UP
38	6e−27	82 / 800	GSEA	JOHNSTONE_PARVB_TARGETS_3_DN
39	2e−26	138 / 2043	Glio	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
40	5e−24	68 / 622	GSEA	SCHLOSSER_SERUM_RESPONSE_DN



Aging

Rank	p−value	#in/all	Geneset
1	0.07	6 / 111	HORVATH_aging_genes meth DOWN
2	0.88	2 / 142	HORVATH_aging_genes meth UP
3	1.00	0 / 58	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Cancer

Rank	p−value	#in/all	Geneset
1	5e−04	6 / 39	ZHANG_MM up
2	5e−04	7 / 54	KUIPER_MM poor survival
3	2e−03	12 / 178	SPANG_LPS−index2
4	4e−03	3 / 13	GENTLES_modul6
5	5e−03	16 / 301	SPANG_BCL6−index2
6	1e−02	8 / 117	PanCan_Driver_Gene_geneset_nanostring
7	1e−02	6 / 76	PanCan_Wnt_geneset_nanostring
8	2e−02	2 / 14	RHODES_UNDIFFERENTIATED_CANCER
9	4e−02	2 / 12	LIU_BREAST_CANCER
10	4e−02	2 / 13	RHODES_CANCER_META_SIGNATURE
11	6e−02	2 / 15	WOLFER_overlap genes
12	1e−01	3 / 46	PanCan_TGF−B_geneset_nanostring
13	2e−01	1 / 9	GENTLES_modul5
14	2e−01	5 / 125	PanCan_CC+Apop_geneset_nanostring
15	2e−01	2 / 36	PanCan_HK_geneset_nanostring

Chromatin states

Rank	p−value	#in/all	Geneset
1	1e−99	480 / 8771	5_Tx_Melanocytes
2	2e−98	551 / 12298	2_TssA_Melanocytes
3	3e−98	535 / 11455	2_TssA_Fibroblasts
4	5e−87	437 / 7854	5_Tx_Fibroblasts
5	1e−86	551 / 12983	2_TssA_Neuronal_Progenitor
6	2e−65	436 / 8990	15_Quies_Fibroblasts
7	2e−65	380 / 6970	5_Tx_Neuronal_Progenitor
8	4e−55	507 / 12741	7_Enh_Melanocytes
9	2e−53	485 / 11836	3_TssF_Melanocytes
10	4e−51	465 / 11130	15_Quies_Melanocytes
11	2e−44	482 / 12393	15_Quies_Neuronal_Progenitor
12	6e−37	374 / 8613	7_Enh_Fibroblasts
13	3e−21	205 / 4237	14_ZNF_Neuronal_Progenitor
14	9e−19	244 / 5699	6_EnhG_Melanocytes
15	5e−16	346 / 9635	3_TssF_Fibroblasts

GSEA C2

Rank	p−value	#in/all	Geneset
1	2e−39	150 / 1797	PILON_KLF1_TARGETS_DN
2	1e−35	119 / 1265	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
3	8e−34	65 / 388	SHEN_SMARCA2_TARGETS_UP
4	5e−31	90 / 841	ACEVEDO_LIVER_CANCER_UP
5	2e−27	63 / 465	MILI_PSEUDOPODIA_HAPTOTAXIS_UP
6	6e−27	82 / 800	JOHNSTONE_PARVB_TARGETS_3_DN
7	5e−24	68 / 622	SCHLOSSER_SERUM_RESPONSE_DN
8	1e−22	90 / 1098	BLALOCK_ALZHEIMERS_DISEASE_DN
9	4e−22	92 / 1161	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
10	6e−22	60 / 532	SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_DN
11	7e−22	103 / 1417	PUJANA_BRCA1_PCC_NETWORK
12	1e−20	92 / 1222	DODD_NASOPHARYNGEAL_CARCINOMA_DN
13	4e−19	69 / 783	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
14	1e−18	58 / 581	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_UP
15	2e−18	53 / 498	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR_UP

Lymphoma

Rank	p−value	#in/all	Geneset
1	1e−99	489 / 8226	HOPP_Active_promoter
2	1e−99	461 / 7275	HOPP_Txn_elongation
3	8e−74	425 / 8098	HOPP_Weak_promoter
4	3e−70	337 / 5356	HOPP_Txn_transition
5	1e−37	317 / 6559	HOPP_Weak_txn
6	1e−34	322 / 6959	HOPP_Weak_enhancer
7	1e−23	309 / 7448	HOPP_Strong_enhancer
8	7e−12	72 / 1169	SPANG_BCR DN
9	5e−06	60 / 1270	SPANG_BCR UP
10	9e−06	29 / 455	SPANG_CD40 6hrs DN
11	1e−05	11 / 84	ROSOLOWSKI_green UP
12	2e−05	21 / 283	TARTE_Plasmablast signature
13	7e−05	39 / 777	WIRTH_lymphoma937_spot D
14	1e−04	38 / 772	Hopp_June14_MMML937 tumors+controls_group.overexpression_D_cell line
15	2e−04	11 / 115	ROSOLOWSKI_green total

miRNA Disease

Rank	p−value	#in/all	Geneset
1	1	0 / 7	Thyroid carcinoma, papillary
2	1	0 / 123	Pancreatic cancer
3	1	0 / 68	Glioblastoma multiforme, somatic
4	1	0 / 63	Gastrointestinal
5	1	0 / 3	Pituitary adenoma
6	1	0 / 116	Cancer
7	1	0 / 95	Colorectal cancer
8	1	0 / 2	Adenomas, multiple colorectal
9	1	0 / 124	Prostate cancer
10	1	0 / 48	Alzheimer disease, susceptibility to
11	1	0 / 7	Schizophrenia, susceptibility to
12	1	0 / 20	Parkinson disease
13	1	0 / 65	Hepatocellular carcinoma
14	1	0 / 3	Down syndrome, risk of
15	1	0 / 127	Melanoma and neural system tumor syndrome

Reference Signatures

Rank	p−value	#in/all	Geneset
1	5e−19	42 / 302	Chaussabel_3,4_Protein phosphatases
2	9e−16	34 / 242	Chaussabel_3,9_Kinases
3	1e−14	76 / 1118	PROTEINATLAS_placenta
4	1e−14	33 / 248	Chaussabel_3,6_Mitochondrial ribosomal proteins
5	2e−13	24 / 139	Chaussabel_1,8_Metabolism Biosynthesis
6	3e−11	61 / 933	PROTEINATLAS_adrenal gland
7	3e−10	60 / 963	PROTEINATLAS_pancreas
8	6e−10	70 / 1239	PROTEINATLAS_testis
9	8e−10	67 / 1167	PROTEINATLAS_gallbladder
10	2e−09	44 / 619	PROTEINATLAS_salivary gland
11	2e−09	58 / 959	PROTEINATLAS_nasopharynx
12	2e−09	62 / 1063	PROTEINATLAS_tonsil
13	2e−09	66 / 1173	PROTEINATLAS_rectum
14	5e−09	55 / 912	PROTEINATLAS_urinary bladder
15	3e−08	55 / 960	PROTEINATLAS_cerebellum

BP

Rank	p−value	#in/all	Geneset
1	2e−05	16 / 181	proteasome−mediated ubiquitin−dependent protein catabolic process
2	2e−05	15 / 163	protein polyubiquitination
3	2e−05	23 / 335	protein transport
4	5e−05	8 / 51	stem cell population maintenance
5	5e−05	13 / 134	transcription initiation from RNA polymerase II promoter
6	5e−05	22 / 330	protein ubiquitination
7	5e−05	6 / 27	vesicle organization
8	7e−05	27 / 457	regulation of transcription from RNA polymerase II promoter
9	1e−04	8 / 57	COPII vesicle coating
10	2e−04	5 / 21	nucleotide−excision repair, DNA damage recognition
11	2e−04	7 / 46	protein K48−linked ubiquitination
12	2e−04	4 / 12	regulation of acetyl−CoA biosynthetic process from pyruvate
13	2e−04	16 / 219	mitotic nuclear division
14	2e−04	5 / 22	SCF−dependent proteasomal ubiquitin−dependent protein catabolic process
15	4e−04	7 / 52	ER−associated ubiquitin−dependent protein catabolic process

CC

Rank	p−value	#in/all	Geneset
1	1e−15	148 / 2979	cytosol
2	2e−14	204 / 4828	nucleus
3	2e−14	129 / 2535	nucleoplasm
4	4e−11	21 / 134	myelin sheath
5	2e−10	74 / 1304	mitochondrion
6	4e−10	114 / 2464	extracellular exosome
7	4e−08	180 / 4822	cytoplasm
8	3e−07	88 / 1979	membrane
9	6e−06	26 / 374	mitochondrial inner membrane
10	8e−06	18 / 207	lysosome
11	1e−05	33 / 561	intracellular membrane−bounded organelle
12	1e−05	19 / 234	lysosomal membrane
13	3e−05	38 / 721	nucleolus
14	1e−04	38 / 777	Golgi apparatus
15	4e−04	28 / 539	Golgi membrane

Colon Cancer

Rank	p−value	#in/all	Geneset
1	1e−99	508 / 9555	TssA_Colon
2	4e−90	460 / 8568	TxWk_Colon
3	2e−89	462 / 8678	Quies3_Colon
4	2e−87	469 / 9054	Tx_Colon
5	2e−71	493 / 10999	TssWk_Colon
6	7e−44	145 / 1547	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
7	1e−15	183 / 4034	TssD1_Colon
8	3e−15	281 / 7354	TssF_Colon
9	1e−14	74 / 1069	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
10	1e−14	90 / 1468	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
11	5e−12	361 / 10779	Enh_Colon
12	6e−12	106 / 2073	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
13	6e−06	60 / 1281	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv
14	1e−05	57 / 1216	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_
15	3e−05	10 / 76	Pentrack_CRC_TCGA_corr_N_msi−h_DN

HM

Rank	p−value	#in/all	Geneset
1	2e−09	21 / 167	HALLMARK_OXIDATIVE_PHOSPHORYLATION
2	5e−07	18 / 170	HALLMARK_MYC_TARGETS_V1
3	2e−06	18 / 185	HALLMARK_MTORC1_SIGNALING
4	2e−06	12 / 87	HALLMARK_PROTEIN_SECRETION
5	2e−04	14 / 177	HALLMARK_MITOTIC_SPINDLE
6	3e−03	10 / 138	HALLMARK_FATTY_ACID_METABOLISM
7	6e−03	11 / 176	HALLMARK_ADIPOGENESIS
8	7e−03	11 / 179	HALLMARK_G2M_CHECKPOINT
9	7e−03	9 / 132	HALLMARK_UV_RESPONSE_DN
10	1e−02	11 / 189	HALLMARK_HYPOXIA
11	1e−02	7 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING
12	3e−02	6 / 91	HALLMARK_ANDROGEN_RESPONSE
13	4e−02	3 / 29	HALLMARK_NOTCH_SIGNALING
14	5e−02	9 / 183	HALLMARK_GLYCOLYSIS
15	5e−02	6 / 103	HALLMARK_UNFOLDED_PROTEIN_RESPONSE

Melanoma

Rank	p−value	#in/all	Geneset
1	0.7	1 / 43	Hugo_melanoma−BRAFmut−MET_UP
2	1.0	0 / 30	Hugo_melanoma−all−MET_UP
3	1.0	0 / 54	Hugo_melanoma−all−MET_DN
4	1.0	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
5	1.0	0 / 27	Hugo_melanoma−all−LEF1_UP
6	1.0	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

miRNA target

Rank	p−value	#in/all	Geneset
1	6e−15	38 / 321	hsa−miR−590−3p
2	7e−14	40 / 382	hsa−let−7c
3	9e−14	35 / 299	hsa−miR−548c−3p
4	1e−13	42 / 425	hsa−let−7b
5	2e−13	42 / 429	hsa−miR−548n
6	2e−13	39 / 374	hsa−miR−144
7	2e−13	33 / 272	hsa−miR−101
8	2e−13	33 / 274	hsa−miR−1244
9	2e−13	34 / 291	hsa−miR−186
10	2e−13	29 / 212	hsa−miR−196a
11	3e−13	34 / 295	hsa−miR−561
12	4e−13	38 / 366	hsa−let−7d
13	5e−13	35 / 317	hsa−miR−559
14	3e−12	41 / 449	hsa−miR−130b
15	6e−12	45 / 540	hsa−miR−17

Telomeres

Rank	p−value	#in/all	Geneset
1	0.5	1 / 27	Nabetani_alt len telomeres_genes_ko
2	1.0	0 / 13	Alternative lengthening of telomeres
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Brain

Rank	p−value	#in/all	Geneset
1	1e−99	521 / 9815	Overlap_fetal_midbrain_ReprPC
2	2e−85	378 / 5936	Overlap_fetal_midbrain_HetRpts
3	3e−79	469 / 9504	Overlap_fetal_midbrain_K9K27me3
4	1e−59	450 / 9917	Overlap_fetal_midbrain_ReprPCWk
5	9e−44	435 / 10430	Overlap_fetal_midbrain_Quies
6	2e−07	52 / 937	Fetal_EnhG
7	3e−06	57 / 1162	Fetal_Enh
8	1e−05	46 / 906	Fetal_HetRpts
9	8e−05	24 / 386	Fetal_ZNF
10	2e−04	34 / 681	Overlap_fetal_midbrain_EnhP
11	3e−03	46 / 1171	Fetal_EnhP
12	1e−02	51 / 1436	Fetal_K9K27me3
13	1e−02	26 / 630	Mid_Frontal_Lobe_EnhP
14	2e−02	31 / 796	Overlap_fetal_midbrain_ZNF
15	8e−02	13 / 328	Fetal_Het

Chr

Rank	p−value	#in/all	Geneset
1	2e−05	51 / 1060	Chr 5
2	5e−05	44 / 902	Chr 4
3	3e−04	24 / 422	Chr 13
4	2e−02	34 / 904	Chr 10
5	4e−02	13 / 289	Chr 21
6	4e−02	30 / 836	Chr 8
7	1e−01	39 / 1217	Chr 3
8	1e−01	26 / 768	Chr 14
9	2e−01	44 / 1492	Chr 2
10	2e−01	35 / 1170	Chr 7
11	3e−01	11 / 342	Chr 18
12	3e−01	34 / 1211	Chr 6
13	5e−01	30 / 1160	Chr 12
14	8e−01	54 / 2323	Chr 1
15	9e−01	12 / 619	Chr 20

Glio

Rank	p−value	#in/all	Geneset
1	1e−27	129 / 1777	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
2	2e−26	138 / 2043	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
3	1e−14	63 / 820	Sturm_GBM_Meth_overexpression_E_G34_UP
4	5e−11	32 / 316	WILLSCHER_GBM_Verhaak−PNwt & CL_up
5	1e−05	15 / 157	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
6	3e−05	22 / 315	Up
7	8e−05	8 / 55	Stuehler_Proteins_up_in_STS
8	1e−03	8 / 84	GIEZELT_GBM_WT_down_VS_mut
9	2e−03	6 / 50	WILLSCHER_GBM_proteomics_wtOnly_SpotG
10	4e−03	4 / 25	Sturm_GBM_Meth_overexpression_H_K27_UP
11	6e−03	3 / 15	WILLSCHER_GBM_STSwt_proteomics−O_UP
12	9e−03	19 / 401	Down_b
13	9e−03	6 / 69	WILLSCHER_GBM_Verhaak−PNwt & MES_up
14	1e−02	4 / 37	WILLSCHER_GBM_proteomics_wtOnly_SpotH
15	2e−02	2 / 8	Sturm_GBM_Meth_overexpression_C_G34_UP

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.09	7 / 147	Homuth_BMI−associated−genes_UP
2	0.34	1 / 16	Huan_blood−pressure_DBP−signature
3	0.36	1 / 17	DUMEAUX_High bmi enriched genes
4	0.38	1 / 18	Huan_blood−pressure_SBP−signature
5	0.46	6 / 211	Homuth_BMI−associated−genes_DN
6	0.56	1 / 31	DUMEAUX_Fasting enriched genes
7	0.91	1 / 94	DUMEAUX_Smoking enriched genes
8	1.00	0 / 10	DUMEAUX_Smoking literature genes up
9	1.00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
10	1.00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
11	1.00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
12	1.00	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
13	1.00	0 / 8	DUMEAUX_Monocytes in smokers literature genes up
14	1.00	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
15	1.00	0 / 10	DUMEAUX_Women normal BMI literature genes up

MF

Rank	p−value	#in/all	Geneset
1	3e−32	369 / 8818	protein binding
2	2e−17	77 / 1013	poly(A) RNA binding
3	1e−06	24 / 301	ubiquitin−protein transferase activity
4	5e−05	15 / 173	ubiquitin protein ligase activity
5	5e−05	11 / 99	mRNA binding
6	3e−04	16 / 227	transcription coactivator activity
7	4e−04	8 / 70	ATPase binding
8	1e−03	17 / 283	nucleotide binding
9	1e−03	28 / 580	identical protein binding
10	2e−03	21 / 399	RNA binding
11	2e−03	10 / 133	ATPase activity
12	3e−03	4 / 24	transmembrane transporter activity
13	5e−03	50 / 1329	ATP binding
14	6e−03	6 / 63	phosphatidylinositol binding
15	6e−03	3 / 15	ATPase activator activity

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.005	3 / 14	BENTINK_ras.6
2	0.270	1 / 12	BENTINK_src.2
3	0.288	1 / 13	BENTINK_e2f3.1
4	0.288	1 / 13	BENTINK_e2f3.2
5	0.288	1 / 13	BENTINK_myc.1
6	0.307	1 / 14	GUSTAFSON_PI3K_UP
7	0.325	1 / 15	GUSTAFSON_PI3K_DN
8	1.000	0 / 12	BENTINK_ras.1
9	1.000	0 / 11	BENTINK_ras.4
10	1.000	0 / 13	BENTINK_src.10
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	1e−31	257 / 5067	ICGC_Taf1_targets
2	6e−23	217 / 4468	ICGC_Egr1_targets
3	7e−23	230 / 4881	ICGC_Atf2_targets
4	2e−22	229 / 4890	ICGC_Bclaf101388_targets
5	3e−22	246 / 5442	ICGC_Pmlsc71910_targets
6	9e−22	247 / 5518	ICGC_Stat5_targets
7	2e−20	207 / 4362	ICGC_Creb1_targets
8	8e−20	240 / 5466	ICGC_Nficsc81335_targets
9	8e−20	264 / 6267	ICGC_Yy1_targets
10	2e−18	123 / 2087	ICGC_Cebpbsc150_targets
11	2e−18	129 / 2255	ICGC_SrfV0416101_targets
12	2e−18	231 / 5312	ICGC_Tcf12_targets
13	6e−18	250 / 5984	ICGC_Mta3_targets
14	3e−17	230 / 5383	ICGC_Sp1_targets
15	9e−17	196 / 4345	ICGC_Zeb1_targets

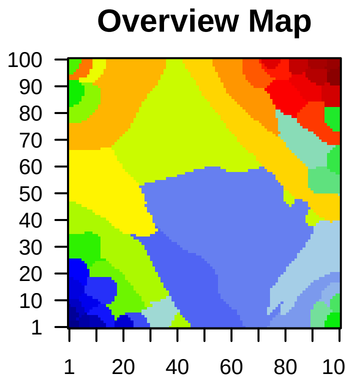
K−Means Cluster

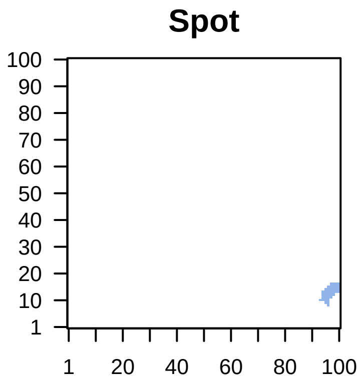
Spot Summary: V1

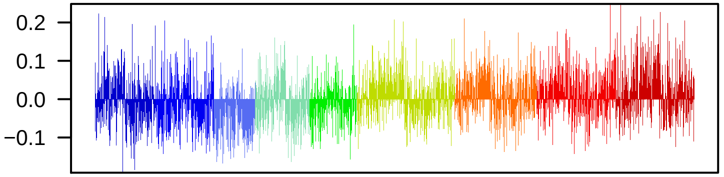
metagenes = 38
genes = 378

<r> metagenes = 0.9
<r> genes = 0.21
beta: r2= 9.78 / log p= −Inf

samples with spot = 137 (4 %)
A * : 13 (3.8 %)
A C * : 13 (4 %)
A C F * : 1 (0.4 %)
A F * : 9 (2.9 %)
C F * : 4 (1.5 %)
F * : 14 (2.5 %)
F J * : 16 (3.5 %)
J * : 22 (4.9 %)
N * : 45 (10.2 %)





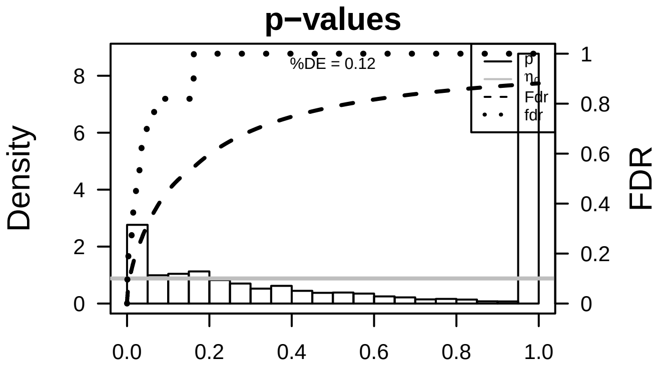


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_239946	1.66	−1.47	0.08	VAV3	vav guanine nucleotide exchange factor 3 [Source:HGNC Syr
2	ILMN_168292	1.2	−1	0.72	CPVL	carboxypeptidase, vitellogenic like [Source:HGNC Symbol;Ac
3	ILMN_240075	1.2	−1.07	0.72	CPVL	carboxypeptidase, vitellogenic like [Source:HGNC Symbol;Ac
4	ILMN_174202	1.1	−0.56	0.25	OLFM1	olfactomedin 1 [Source:HGNC Symbol;Acc:HGNC:17187]
5	ILMN_166386	1.04	−0.97	0.71	TGFBI	transforming growth factor beta induced [Source:HGNC Symb
6	ILMN_176989	0.97	−0.8	0.7		
7	ILMN_177476	0.97	−0.82	0.71	CCR2	C−C motif chemokine receptor 2 [Source:HGNC Symbol;Acc:
8	ILMN_178053	0.95	−0.84	0.38	RNASE6	ribonuclease A family member k6 [Source:HGNC Symbol;Acc
9	ILMN_169034	0.95	−0.77	0.59	LTA4H	leukotriene A4 hydrolase [Source:HGNC Symbol;Acc:HGNC:
10	ILMN_237964	0.92	−0.88	0.45	CD74	CD74 molecule [Source:HGNC Symbol;Acc:HGNC:1697]
11	ILMN_178086	0.89	−0.68	0.39	METRNL	meteorin like, glial cell differentiation regulator [Source:HGNC
12	ILMN_204110	0.87	−0.74	0.44		
13	ILMN_167089	0.86	−0.59	0.47	FBN2	fibrillin 2 [Source:HGNC Symbol;Acc:HGNC:3604]
14	ILMN_168877	0.85	−0.7	0.39	METRNL	meteorin like, glial cell differentiation regulator [Source:HGNC
15	ILMN_208501	0.84	−0.5	0.21		
16	ILMN_169496	0.84	−0.57	0.48	ASGR2	asialoglycoprotein receptor 2 [Source:HGNC Symbol;Acc:HG
17	ILMN_177660	0.84	−0.6	0.5	RNASE4	ribonuclease A family member 4 [Source:HGNC Symbol;Acc:
18	ILMN_235516	0.83	−0.62	0.69	MGST1	microsomal glutathione S−transferase 1 [Source:HGNC Symb
19	ILMN_323155	0.83	−0.38	0.21		
20	ILMN_175692	0.83	−0.81	0.63	RTN1	reticulon 1 [Source:HGNC Symbol;Acc:HGNC:10467]

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	4e−30	27 / 84	Refer	Chaussabel_2,10_Immune related cell surface molecules
2	5e−27	36 / 240	Refer	Chaussabel_3,3_Inflammation II
3	2e−22	233 / 10999	Colon	TssWk_Colon
4	5e−20	209 / 9555	Colon	TssA_Colon
5	8e−19	236 / 11836	Chror	3_TssF_Melanocytes
6	4e−18	198 / 9054	Colon	Tx_Colon
7	7e−18	192 / 8678	Colon	Quies3_Colon
8	8e−18	174 / 7448	Lympl	HOPP_Strong_enhancer
9	1e−17	205 / 9635	Chror	3_TssF_Fibroblasts
10	1e−17	185 / 8226	Lympl	HOPP_Active_promoter
11	2e−17	228 / 11455	Chror	2_TssA_Fibroblasts
12	8e−17	188 / 8568	Colon	TxWk_Colon
13	9e−17	218 / 10779	Colon	Enh_Colon
14	1e−16	242 / 12741	Chror	7_Enh_Melanocytes
15	1e−15	19 / 113	Refer	Chaussabel_1,5_Myeloid lineage
16	6e−15	51 / 1081	GSEA	CHEN_METABOLIC_SYNDROM_NETWORK
17	1e−14	176 / 8098	Lympl	HOPP_Weak_promoter
18	2e−14	185 / 8771	Chror	5_Tx_Melanocytes
19	8e−14	181 / 8613	Chror	7_Enh_Fibroblasts
20	2e−13	28 / 366	GSEA	RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_UP
21	2e−13	229 / 12298	Chror	2_TssA_Melanocytes
22	3e−13	27 / 346	GSEA	MULLIGHAN_MLL_SIGNATURE_1_UP
23	3e−13	53 / 1281	Colon	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_trar
24	3e−13	161 / 7354	Colon	TssF_Colon
25	3e−13	130 / 5373	Colon	EnhWk1_Colon
26	1e−12	77 / 2464	CC	extracellular exosome
27	3e−12	27 / 382	GSEA	MULLIGHAN_MLL_SIGNATURE_2_UP
28	4e−12	28 / 416	GSEA	FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN
29	5e−12	55 / 1470	Colon	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon
30	7e−12	181 / 8990	Chror	15_Quies_Fibroblasts
31	7e−12	23 / 282	GSEA	RUTELLA_RESPONSE_TO_CSF2RB_AND_IL4_DN
32	2e−11	163 / 7854	Chror	5_Tx_Fibroblasts
33	3e−11	38 / 810	Colon	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
34	5e−11	44 / 1069	Colon	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
35	7e−11	25 / 376	GSEA	REN_ALVEOLAR_RHABDOMYOSARCOMA_DN
36	9e−11	18 / 187	GSEA	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
37	2e−10	59 / 1797	GSEA	PILON_KLF1_TARGETS_DN
38	2e−10	206 / 11130	Chror	15_Quies_Melanocytes
39	5e−10	188 / 9917	Brain	Overlap_fetal_midbrain_ReprPCWk
40	6e−10	228 / 12983	Chror	2_TssA_Neuronal_Progenitor



Aging

Rank	p−value	#in/all	Geneset
1	0.4	2 / 111	HORVATH_aging_genes meth DOWN
2	0.5	1 / 58	TESCHENDORFF_age_hypermethylated
3	1.0	0 / 142	HORVATH_aging_genes meth UP
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	5e−07	17 / 292	positive regulation of apoptotic process
2	2e−06	9 / 86	Wnt signaling pathway, planar cell polarity pathway
3	1e−05	9 / 103	activation of MAPK activity
4	1e−05	8 / 80	ephrin receptor signaling pathway
5	2e−05	8 / 86	response to organic substance
6	3e−05	4 / 14	positive regulation of NIK/NF−kappaB signaling
7	9e−05	4 / 18	positive regulation of dendritic spine development
8	2e−04	5 / 39	positive regulation of stress fiber assembly
9	2e−04	8 / 118	chemotaxis
10	2e−04	14 / 336	inflammatory response
11	3e−04	6 / 66	Fc−gamma receptor signaling pathway involved in phagocytosis
12	3e−04	6 / 66	vascular endothelial growth factor receptor signaling pathway
13	3e−04	3 / 10	bleb assembly
14	4e−04	4 / 26	positive regulation of cytokine secretion
15	4e−04	4 / 26	proteolysis involved in cellular protein catabolic process

Brain

Rank	p−value	#in/all	Geneset
1	5e−10	188 / 9917	Overlap_fetal_midbrain_ReprPCWk
2	1e−08	182 / 9815	Overlap_fetal_midbrain_ReprPC
3	2e−08	190 / 10430	Overlap_fetal_midbrain_Quies
4	1e−05	86 / 4112	Mid_Frontal_Lobe_ReprPC
5	2e−05	165 / 9504	Overlap_fetal_midbrain_K9K27me3
6	1e−04	59 / 2709	Mid_Frontal_Lobe_HetRpts
7	2e−04	109 / 5936	Overlap_fetal_midbrain_HetRpts
8	2e−04	32 / 1213	Fetal_TssP
9	3e−04	63 / 3046	Fetal_TssA
10	7e−04	56 / 2700	Fetal_TxTrans
11	2e−03	53 / 2630	Fetal_TssF
12	4e−03	38 / 1784	Mid_Frontal_Lobe_ReprPCWk
13	7e−03	31 / 1436	Fetal_K9K27me3
14	9e−03	22 / 937	Fetal_EnhG
15	9e−03	58 / 3164	Mid_Frontal_Lobe_ZNF

Cancer

Rank	p−value	#in/all	Geneset
1	1e−09	21 / 301	SPANG_BCL6−index2
2	2e−08	15 / 178	SPANG_LPS−index2
3	3e−03	4 / 46	PanCan_TGF−B_geneset_nanostring
4	9e−03	15 / 554	Lembcke_Colonic Inflammation
5	2e−02	4 / 76	PanCan_Wnt_geneset_nanostring
6	5e−02	5 / 150	PanCan_MAPK_geneset_nanostring
7	8e−02	0 / 15	LIU_PROSTATE_CANCER_DN
8	1e−01	4 / 136	PanCan_RAS_geneset_nanostring
9	2e−01	1 / 13	LIU_LIVER_CANCER
10	2e−01	1 / 15	WANG_ER_UP
11	2e−01	3 / 117	PanCan_Driver_Gene_geneset_nanostring
12	2e−01	3 / 125	PanCan_CC+Apop_geneset_nanostring
13	3e−01	2 / 73	SHAUGHNESSY_MM high risk
14	3e−01	0 / 14	LIU_PROSTATE_CANCER_UP
15	4e−01	1 / 38	KUIPER_MM good survival

CC

Rank	p−value	#in/all	Geneset
1	1e−12	77 / 2464	extracellular exosome
2	5e−07	72 / 2979	cytosol
3	2e−06	82 / 3662	plasma membrane
4	7e−06	8 / 74	lysosomal lumen
5	2e−05	26 / 775	endoplasmic reticulum
6	3e−05	71 / 3291	integral component of membrane
7	1e−04	47 / 1979	membrane
8	1e−04	11 / 207	lysosome
9	2e−04	34 / 1304	mitochondrion
10	3e−04	19 / 561	intracellular membrane−bounded organelle
11	3e−04	10 / 194	membrane raft
12	7e−04	5 / 53	clathrin−coated vesicle
13	1e−03	22 / 777	Golgi apparatus
14	1e−03	11 / 273	neuron projection
15	1e−03	10 / 234	lysosomal membrane

Chr

Rank	p−value	#in/all	Geneset
1	0.003	24 / 954	Chr 9
2	0.059	16 / 768	Chr 14
3	0.101	15 / 769	Chr 15
4	0.102	25 / 1411	Chr 11
5	0.130	19 / 1060	Chr 5
6	0.291	19 / 1217	Chr 3
7	0.329	20 / 1318	Chr 17
8	0.353	5 / 289	Chr 21
9	0.401	17 / 1160	Chr 12
10	0.415	17 / 1170	Chr 7
11	0.558	31 / 2323	Chr 1
12	0.564	12 / 902	Chr 4
13	0.589	7 / 536	Chr 22
14	0.682	4 / 342	Chr 18
15	0.725	18 / 1492	Chr 2

Chromatin states

Rank	p−value	#in/all	Geneset
1	8e−19	236 / 11836	3_TssF_Melanocytes
2	1e−17	205 / 9635	3_TssF_Fibroblasts
3	2e−17	228 / 11455	2_TssA_Fibroblasts
4	1e−16	242 / 12741	7_Enh_Melanocytes
5	2e−14	185 / 8771	5_Tx_Melanocytes
6	8e−14	181 / 8613	7_Enh_Fibroblasts
7	2e−13	229 / 12298	2_TssA_Melanocytes
8	7e−12	181 / 8990	15_Quies_Fibroblasts
9	2e−11	163 / 7854	5_Tx_Fibroblasts
10	2e−10	206 / 11130	15_Quies_Melanocytes
11	6e−10	228 / 12983	2_TssA_Neuronal_Progenitor
12	4e−08	120 / 5699	6_EnhG_Melanocytes
13	5e−08	207 / 11847	7_Enh_Neuronal_Progenitor
14	3e−07	103 / 4795	6_EnhG_Fibroblasts
15	7e−07	210 / 12393	15_Quies_Neuronal_Progenitor

Colon Cancer

Rank	p−value	#in/all	Geneset
1	2e−22	233 / 10999	TssWk_Colon
2	5e−20	209 / 9555	TssA_Colon
3	4e−18	198 / 9054	Tx_Colon
4	7e−18	192 / 8678	Quies3_Colon
5	8e−17	188 / 8568	TxWk_Colon
6	9e−17	218 / 10779	Enh_Colon
7	3e−13	53 / 1281	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv
8	3e−13	161 / 7354	TssF_Colon
9	3e−13	130 / 5373	EnhWk1_Colon
10	5e−12	55 / 1470	LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a
11	3e−11	38 / 810	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
12	5e−11	44 / 1069	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
13	1e−07	125 / 6138	TssD2_Colon
14	2e−07	57 / 2073	LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t
15	2e−05	84 / 4018	EnhWk2_Colon

Glio

Rank	p−value	#in/all	Geneset
1	8e−10	20 / 267	WILLSCHER_GBM_Verhaak−CL & MES_up
2	2e−05	9 / 113	GIEZELT_GBM_WT_up_VS_mut
3	1e−04	14 / 315	Up
4	4e−03	4 / 47	Donson−innate immunity−associated with LTS in HGA
5	6e−03	4 / 53	mature astrocytes
6	1e−02	2 / 12	Mukasa_UP_in_Astroglioma
7	1e−02	3 / 37	Christensen_hypomethylated_in_ependymoma
8	2e−02	2 / 15	Donson−chemokines/cytokines−associated with LTS in HGA
9	2e−02	2 / 15	WILLSCHER_GBM_STSwt_proteomics−O_UP
10	4e−02	4 / 94	Weller_LGG_A_vs_O_UP
11	5e−02	27 / 1417	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
12	5e−02	5 / 147	Christensen_hypermethylated_in_grade2_oligodendroglioma
13	5e−02	2 / 28	KIM prognostic signature LTS vs. STS
14	6e−02	3 / 65	cultured astroglia vs. in vivo astrocytes
15	6e−02	2 / 29	Christensen_hypomethylated_in_grade3_astrocytoma

GSEA C2

Rank	p−value	#in/all	Geneset
1	6e−15	51 / 1081	CHEN_METABOLIC_SYNDROM_NETWORK
2	2e−13	28 / 366	RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_UP
3	3e−13	27 / 346	MULLIGHAN_MLL_SIGNATURE_1_UP
4	3e−12	27 / 382	MULLIGHAN_MLL_SIGNATURE_2_UP
5	4e−12	28 / 416	FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN
6	7e−12	23 / 282	RUTELLA_RESPONSE_TO_CSF2RB_AND_IL4_DN
7	7e−11	25 / 376	REN_ALVEOLAR_RHABDOMYOSARCOMA_DN
8	9e−11	18 / 187	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
9	2e−10	59 / 1797	PILON_KLF1_TARGETS_DN
10	2e−09	10 / 53	HAHTOLA_MYCOSIS_FUNGOIDES_CD4_UP
11	3e−09	23 / 381	RUTELLA_RESPONSE_TO_HGF_UP
12	3e−09	17 / 203	VERHAAK_GLIOBLASTOMA_MESENCHYMAL
13	3e−09	21 / 319	WANG_RESPONSE_TO_GSK3_INHIBITOR_SB216763_UP
14	3e−09	38 / 960	NUYTTEN_EZH2_TARGETS_UP
15	4e−09	30 / 642	CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_3

HM

Rank	p−value	#in/all	Geneset
1	5e−05	11 / 185	HALLMARK_MTORC1_SIGNALING
2	5e−05	11 / 185	HALLMARK_P53_PATHWAY
3	7e−05	10 / 162	HALLMARK_ALLOGRAFT_REJECTION
4	1e−03	9 / 189	HALLMARK_HYPOXIA
5	1e−03	9 / 191	HALLMARK_INFLAMMATORY_RESPONSE
6	3e−03	8 / 176	HALLMARK_ADIPOGENESIS
7	4e−03	8 / 183	HALLMARK_GLYCOLYSIS
8	4e−03	8 / 185	HALLMARK_TNFA_SIGNALING_VIA_NFKB
9	4e−03	8 / 187	HALLMARK_COMPLEMENT
10	7e−03	5 / 87	HALLMARK_PROTEIN_SECRETION
11	9e−03	7 / 172	HALLMARK_INTERFERON_GAMMA_RESPONSE
12	1e−02	7 / 175	HALLMARK_XENOBIOTIC_METABOLISM
13	1e−02	5 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING
14	1e−02	7 / 186	HALLMARK_IL2_STAT5_SIGNALING
15	3e−02	6 / 167	HALLMARK_OXIDATIVE_PHOSPHORYLATION

Lifestyle

Rank	p−value	#in/all	Geneset
1	0.008	2 / 10	DUMEAUX_Smoking literature genes up
2	0.025	7 / 211	Homuth_BMI−associated−genes_DN
3	0.066	1 / 5	DUMEAUX_Estrogen related in smokers literature genes up
4	0.103	1 / 8	DUMEAUX_Monocytes in smokers literature genes up
5	0.135	3 / 94	DUMEAUX_Smoking enriched genes
6	0.139	4 / 147	Homuth_BMI−associated−genes_UP
7	0.196	1 / 16	Huan_blood−pressure_DBP−signature
8	0.217	1 / 18	Huan_blood−pressure_SBP−signature
9	1.000	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
10	1.000	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
11	1.000	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
12	1.000	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
13	1.000	0 / 10	DUMEAUX_Women normal BMI literature genes up
14	1.000	0 / 17	DUMEAUX_High bmi enriched genes
15	1.000	0 / 31	DUMEAUX_Fasting enriched genes

Lymphoma

Rank	p−value	#in/all	Geneset
1	8e−18	174 / 7448	HOPP_Strong_enhancer
2	1e−17	185 / 8226	HOPP_Active_promoter
3	1e−14	176 / 8098	HOPP_Weak_promoter
4	4e−08	144 / 7275	HOPP_Txn_elongation
5	2e−07	18 / 300	Hopp_June14_MMML937 tumors+controls_group.overexpression_E_GC−B−
6	2e−07	137 / 6959	HOPP_Weak_enhancer
7	2e−07	18 / 306	WIRTH_lymphoma937_spot E
8	1e−06	37 / 1169	SPANG_BCR DN
9	2e−06	127 / 6559	HOPP_Weak_txn
10	4e−04	57 / 2701	HOPP_Repetitive
11	2e−03	95 / 5356	HOPP_Txn_transition
12	2e−03	10 / 244	LENZ_Stromal signature 1
13	4e−03	9 / 226	Hopp_Lymphoma_Epi1_no_zentr_6_MCL_DN
14	4e−03	14 / 455	SPANG_CD40 6hrs DN
15	4e−03	5 / 78	Sha_DLBCL UP

Melanoma

Rank	p−value	#in/all	Geneset
1	0.4	1 / 43	Hugo_melanoma−BRAFmut−MET_UP
2	0.5	1 / 54	Hugo_melanoma−all−MET_DN
3	1.0	0 / 30	Hugo_melanoma−all−MET_UP
4	1.0	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
5	1.0	0 / 27	Hugo_melanoma−all−LEF1_UP
6	1.0	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

MF

Rank	p−value	#in/all	Geneset
1	2e−07	164 / 8818	protein binding
2	5e−04	3 / 12	serine−type carboxypeptidase activity
3	6e−04	3 / 13	ribonuclease activity
4	1e−03	4 / 33	endonuclease activity
5	1e−03	18 / 580	identical protein binding
6	3e−03	3 / 21	zinc ion transmembrane transporter activity
7	3e−03	12 / 350	protein kinase binding
8	3e−03	3 / 22	glutathione transferase activity
9	3e−03	10 / 265	cadherin binding involved in cell−cell adhesion
10	4e−03	3 / 24	calcium channel regulator activity
11	5e−03	5 / 81	protease binding
12	8e−03	2 / 10	regulatory region DNA binding
13	9e−03	2 / 11	NADPH binding
14	1e−02	2 / 12	activin binding
15	1e−02	2 / 12	phosphate ion binding

miRNA Disease

Rank	p−value	#in/all	Geneset
1	0.2	1 / 17	Bladder cancer
2	0.3	1 / 30	Systemic lupus erythematosus (SLE)
3	0.8	1 / 113	Ovarian cancer
4	0.8	1 / 116	Cancer
5	1.0	0 / 7	Thyroid carcinoma, papillary
6	1.0	0 / 123	Pancreatic cancer
7	1.0	0 / 68	Glioblastoma multiforme, somatic
8	1.0	0 / 63	Gastrointestinal
9	1.0	0 / 3	Pituitary adenoma
10	1.0	0 / 95	Colorectal cancer
11	1.0	0 / 2	Adenomas, multiple colorectal
12	1.0	0 / 124	Prostate cancer
13	1.0	0 / 48	Alzheimer disease, susceptibility to
14	1.0	0 / 7	Schizophrenia, susceptibility to
15	1.0	0 / 20	Parkinson disease

miRNA target

Rank	p−value	#in/all	Geneset
1	4e−04	16 / 449	hsa−miR−130b
2	7e−04	14 / 379	hsa−miR−454
3	9e−04	8 / 146	hsa−miR−518a−5p
4	1e−03	8 / 149	hsa−miR−527
5	1e−03	9 / 186	hsa−miR−520d−5p
6	1e−03	14 / 394	hsa−miR−301b
7	1e−03	11 / 272	hsa−miR−30d
8	1e−03	11 / 274	hsa−miR−30b
9	2e−03	11 / 283	hsa−miR−30c
10	2e−03	12 / 328	hsa−miR−367
11	2e−03	8 / 167	hsa−miR−374b
12	3e−03	5 / 74	hsa−miR−1254
13	4e−03	7 / 144	hsa−miR−140−5p
14	4e−03	3 / 23	hsa−miR−662
15	4e−03	10 / 267	hsa−miR−30a

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.2	1 / 13	BENTINK_e2f3.1
2	0.2	1 / 14	BENTINK_ras.6
3	0.2	1 / 15	GUSTAFSON_PI3K_DN
4	1.0	0 / 14	GUSTAFSON_PI3K_UP
5	1.0	0 / 13	BENTINK_e2f3.2
6	1.0	0 / 13	BENTINK_myc.1
7	1.0	0 / 12	BENTINK_ras.1
8	1.0	0 / 11	BENTINK_ras.4
9	1.0	0 / 13	BENTINK_src.10
10	1.0	0 / 12	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Reference Signatures

Rank	p−value	#in/all	Geneset
1	4e−30	27 / 84	Chaussabel_2,10_Immune related cell surface molecules
2	5e−27	36 / 240	Chaussabel_3,3_Inflammation II
3	1e−15	19 / 113	Chaussabel_1,5_Myeloid lineage
4	4e−05	10 / 150	Chaussabel_2,6_Myeloid lineage
5	5e−04	11 / 242	Chaussabel_3,2_Inflammation I
6	3e−03	16 / 535	PROTEINATLAS_spleen
7	6e−03	18 / 681	PROTEINATLAS_lung
8	1e−02	4 / 64	VAQUERIZAS_Lung_TF
9	1e−02	2 / 14	JONGENEEL_Peripheral Blood Lymphocytes
10	2e−02	3 / 43	VAQUERIZAS_Placenta_TF
11	4e−02	2 / 24	VAQUERIZAS_Trachea_TF
12	5e−02	24 / 1239	PROTEINATLAS_testis
13	7e−02	1 / 5	VAQUERIZAS_Appendix_TF
14	8e−02	1 / 6	JONGENEEL_SpinalCord
15	9e−02	22 / 1194	PROTEINATLAS_stomach

Telomeres

Rank	p−value	#in/all	Geneset
1	1	0 / 13	Alternative lengthening of telomeres
2	1	0 / 27	Nabetani_alt len telomeres_genes_ko
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	2e−05	73 / 3348	ICGC_BatfPcr1_targets
2	3e−05	94 / 4735	ICGC_Pu1_targets
3	1e−04	56 / 2497	ICGC_Bcl11_targets
4	2e−04	102 / 5466	ICGC_Nficsc81335_targets
5	6e−04	47 / 2133	ICGC_Mef2_targets
6	6e−04	39 / 1669	ICGC_P300_targets
7	7e−04	46 / 2087	ICGC_Cebpbsc150_targets
8	7e−04	31 / 1231	KIM_MYC targets
9	8e−04	56 / 2704	ICGC_Pbx3_targets
10	9e−04	5 / 55	MYC_Targets UP
11	1e−03	19 / 631	ICGC_RxraPcr1_targets
12	2e−03	93 / 5188	ICGC_Ebfsc137065_targets
13	2e−03	34 / 1466	ICGC_NrsfPcr1_targets
14	2e−03	77 / 4131	ICGC_Nfatc1_targets
15	2e−03	123 / 7247	ICGC_Runx3_targets

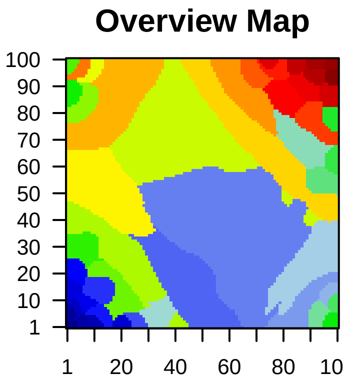
K−Means Cluster

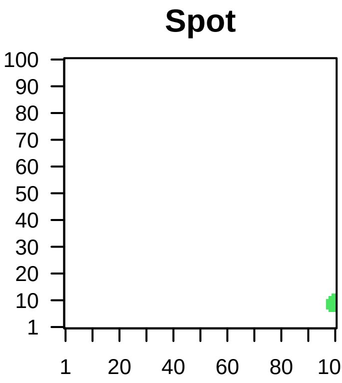
Spot Summary: W1

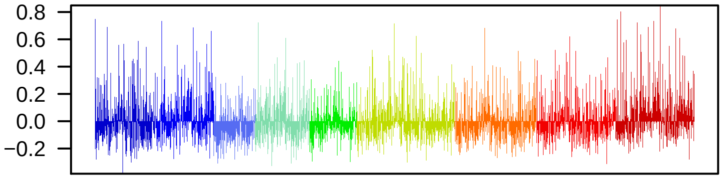
metagenes = 24
genes = 275

<r> metagenes = 0.93
<r> genes = 0.32
beta: r2= 41.4 / log p= −Inf

samples with spot = 569 (16.8 %)
A * : 63 (18.3 %)
A C * : 69 (21 %)
A C F * : 23 (9.8 %)
A F * : 52 (16.9 %)
C F * : 28 (10.6 %)
F * : 88 (15.9 %)
F J * : 65 (14 %)
J * : 73 (16.3 %)
N * : 108 (24.4 %)





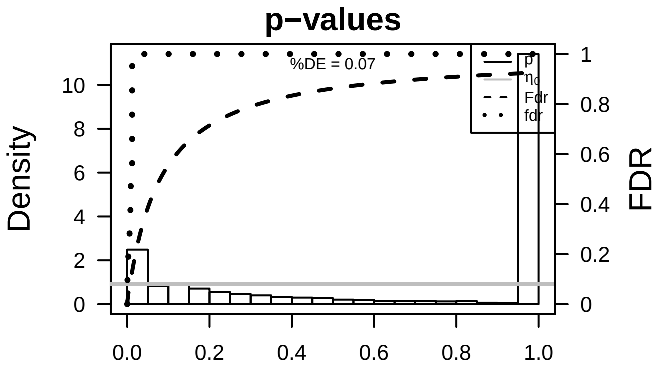


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_170769	2.95	−1.6	0.78	IFIT1	interferon induced protein with tetratricopeptide repeats 1 [So
2	ILMN_205878	2.77	−0.73	0.47	IFI27	interferon alpha inducible protein 27 [Source:HGNC Symbol;A
3	ILMN_180575	2.64	−2.03	0.62	IFITM3	interferon induced transmembrane protein 3 [Source:HGNC S
4	ILMN_172391	2.52	−1.06	0.79	IFI44L	interferon induced protein 44 like [Source:HGNC Symbol;Acc
5	ILMN_170178	2.51	−1.31	0.79	IFIT3	interferon induced protein with tetratricopeptide repeats 3 [So
6	ILMN_165787	2.46	−0.83	0.8	RSAD2	radical S−adenosyl methionine domain containing 2 [Source:I
7	ILMN_205401	2.34	−1	0.71	ISG15	ISG15 ubiquitin−like modifier [Source:HGNC Symbol;Acc:HG
8	ILMN_172974	2.3	−1.14	0.76	HERC5	HECT and RLD domain containing E3 ubiquitin protein ligase
9	ILMN_238854	2.22	−1.39	0.8	EPSTI1	epithelial stromal interaction 1 (breast) [Source:HGNC Symbo
10	ILMN_174539	2.13	−1.15	0.8	OAS3	2'−5'−oligoadenylate synthetase 3 [Source:HGNC Symbol;Ac
11	ILMN_166235	2.12	−1.32	0.71	MX1	MX dynamin like GTPase 1 [Source:HGNC Symbol;Acc:HGN
12	ILMN_176006	2.1	−1.07	0.78	IFI44	interferon induced protein 44 [Source:HGNC Symbol;Acc:HG
13	ILMN_166314	1.94	−1.51	0.19	CLEC12A	C−type lectin domain family 12 member A [Source:HGNC Sy
14	ILMN_168738	1.93	−1.08	0.73	IFI6	interferon alpha inducible protein 6 [Source:HGNC Symbol;Ac
15	ILMN_173942	1.91	−1.24	0.8	IFIT2	interferon induced protein with tetratricopeptide repeats 2 [So
16	ILMN_324306	1.85	−2.53	0.26	SIGLEC14	sialic acid binding Ig like lectin 14 [Source:HGNC Symbol;Acc
17	ILMN_167481	1.79	−0.91	0.72	OASL	2'−5'−oligoadenylate synthetase like [Source:HGNC Symbol;A
18	ILMN_169540	1.74	−1.31	0.5	LY6E	lymphocyte antigen 6 complex, locus E [Source:HGNC Symb
19	ILMN_211456	1.71	−1.04	0.61		
20	ILMN_170111	1.7	−1.09	0.74	GBP1	guanylate binding protein 1 [Source:HGNC Symbol;Acc:HGN

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	3e−99	59 / 96	Refer	Chaussabel_3,1_Interferon−inducible
2	5e−80	93 / 810	Colon	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
3	2e−79	59 / 172	HM	HALLMARK_INTERFERON_GAMMA_RESPONSE
4	3e−73	46 / 85	HM	HALLMARK_INTERFERON_ALPHA_RESPONSE
5	1e−72	46 / 87	GSEA	HECKER_IFNB1_TARGETS
6	1e−58	62 / 416	GSEA	FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN
7	4e−58	35 / 58	GSEA	BROWNE_INTERFERON_RESPONSIVE_GENES
8	3e−57	46 / 161	GSEA	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_3D_UP
9	2e−54	27 / 29	GSEA	MOSERLE_IFNA_RESPONSE
10	5e−47	32 / 73	GSEA	BOSCO_INTERFERON_INDUCED_ANTIVIRAL_MODULE
11	5e−46	27 / 42	GSEA	DAUER_STAT3_TARGETS_DN
12	1e−43	46 / 300	Lympl	Hopp_June14_MMML937 tumors+controls_group.overexpression_E_GC−E
13	3e−43	46 / 306	Lympl	WIRTH_lymphoma937_spot E
14	1e−40	66 / 960	GSEA	NUYTTEN_EZH2_TARGETS_UP
15	2e−38	36 / 180	GSEA	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_10D_UP
16	3e−37	26 / 64	GSEA	SANA_RESPONSE_TO_IFNG_UP
17	8e−37	25 / 57	BP	type I interferon signaling pathway
18	2e−34	38 / 272	Lympl	SPANG_IL21 DN
19	2e−34	19 / 26	GSEA	BENNETT_SYSTEMIC_LUPUS_ERYTHEMATOSUS
20	3e−34	37 / 253	GSEA	WALLACE_PROSTATE_CANCER_RACE_UP
21	5e−34	30 / 132	GSEA	REACTOME_INTERFERON_SIGNALING
22	2e−33	31 / 153	BP	defense response to virus
23	4e−32	17 / 21	GSEA	ZHANG_INTERFERON_RESPONSE
24	7e−32	18 / 26	GSEA	EINAV_INTERFERON_SIGNATURE_IN_CANCER
25	2e−31	34 / 235	GSEA	REACTOME_CYTOKINE_SIGNALING_IN_IMMUNE_SYSTEM
26	4e−31	52 / 774	GSEA	REACTOME_IMMUNE_SYSTEM
27	1e−30	23 / 69	GSEA	SEITZ_NEOPLASTIC_TRANSFORMATION_BY_8P_DELETION_UP
28	6e−30	49 / 704	GSEA	NUYTTEN_NIPP1_TARGETS_UP
29	6e−30	21 / 53	GSEA	REACTOME_INTERFERON_ALPHA_BETA_SIGNALING
30	1e−29	29 / 162	GSEA	JISON_SICKLE_CELL_DISEASE_UP
31	1e−29	20 / 46	GSEA	RADAEVA_RESPONSE_TO_IFNA1_UP
32	2e−29	24 / 88	GSEA	DER_IFN_BETA_RESPONSE_UP
33	2e−29	28 / 147	GSEA	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_8D_UP
34	3e−28	21 / 62	GSEA	DER_IFN_ALPHA_RESPONSE_UP
35	9e−28	24 / 102	BP	response to virus
36	1e−26	24 / 113	Refer	Chaussabel_1,5_Myeloid lineage
37	2e−26	13 / 14	GSEA	BOWIE_RESPONSE_TO_TAMOXIFEN
38	2e−26	18 / 43	GSEA	STAMBOLSKY_TARGETS_OF_MUTATED_TP53_DN
39	2e−25	27 / 182	GSEA	MARKEY_RB1_ACUTE_LOF_UP
40	8e−25	27 / 190	GSEA	GRAESSMANN_RESPONSE_TO_MC_AND_SERUM_DEPRIVATION_UP



Aging

Rank	p−value	#in/all	Geneset
1	0.3	2 / 111	HORVATH_aging_genes meth DOWN
2	1.0	0 / 142	HORVATH_aging_genes meth UP
3	1.0	0 / 58	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	8e−37	25 / 57	type I interferon signaling pathway
2	2e−33	31 / 153	defense response to virus
3	9e−28	24 / 102	response to virus
4	6e−20	14 / 37	negative regulation of viral genome replication
5	3e−18	15 / 60	interferon−gamma−mediated signaling pathway
6	3e−17	26 / 335	innate immune response
7	9e−11	6 / 10	response to interferon−alpha
8	1e−09	18 / 336	inflammatory response
9	1e−08	11 / 123	adaptive immune response
10	4e−08	6 / 23	response to interferon−gamma
11	1e−07	10 / 122	positive regulation of NF−kappaB transcription factor activity
12	1e−07	11 / 155	positive regulation of I−kappaB kinase/NF−kappaB signaling
13	2e−07	19 / 511	apoptotic process
14	4e−07	14 / 293	immune response
15	5e−07	5 / 19	positive regulation of interleukin−1 beta secretion

Brain

Rank	p−value	#in/all	Geneset
1	3e−11	76 / 4112	Mid_Frontal_Lobe_ReprPC
2	4e−09	38 / 1506	Mid_Frontal_Lobe_Quies
3	1e−07	31 / 1213	Fetal_TssP
4	1e−07	39 / 1784	Mid_Frontal_Lobe_ReprPCWk
5	1e−06	41 / 2127	Mid_Frontal_Lobe_K9K27me3
6	2e−05	45 / 2700	Fetal_TxTrans
7	6e−04	44 / 3046	Fetal_TssA
8	7e−04	40 / 2709	Mid_Frontal_Lobe_HetRpts
9	8e−04	39 / 2630	Fetal_TssF
10	1e−03	18 / 924	Mid_Frontal_Lobe_TssF
11	1e−02	11 / 578	Fetal_Tx
12	9e−02	17 / 1360	Mid_Frontal_Lobe_TssP
13	2e−01	19 / 1728	Fetal_ReprPCWk
14	3e−01	2 / 110	Overlap_fetal_midbrain_Tx
15	3e−01	11 / 1012	Mid_Frontal_Lobe_Enh

Cancer

Rank	p−value	#in/all	Geneset
1	3e−17	25 / 301	SPANG_BCL6−index2
2	1e−14	29 / 554	Lembcke_Colonic Inflammation
3	6e−11	15 / 178	SPANG_LPS−index2
4	2e−02	4 / 117	PanCan_Driver_Gene_geneset_nanostring
5	4e−02	3 / 82	PanCan_JAK−ST_geneset_nanostring
6	4e−02	1 / 15	LIU_PROSTATE_CANCER_DN
7	5e−02	3 / 91	PanCan_TXmisReg_geneset_nanostring
8	5e−02	1 / 6	ZHANG_MGUS up
9	9e−02	0 / 14	RHODES_UNDIFFERENTIATED_CANCER
10	1e−01	1 / 13	WANG_ER_DN
11	1e−01	2 / 73	SHAUGHNESSY_MM high risk
12	3e−01	1 / 38	KUIPER_MM good survival
13	3e−01	2 / 125	PanCan_CC+Apop_geneset_nanostring
14	4e−01	0 / 13	RHODES_CANCER_META_SIGNATURE
15	4e−01	1 / 54	KUIPER_MM poor survival

CC

Rank	p−value	#in/all	Geneset
1	1e−14	69 / 2979	cytosol
2	2e−09	80 / 4822	cytoplasm
3	4e−06	44 / 2464	extracellular exosome
4	1e−05	17 / 571	perinuclear region of cytoplasm
5	5e−05	6 / 74	lysosomal lumen
6	1e−04	9 / 207	lysosome
7	2e−04	8 / 172	endosome membrane
8	2e−04	9 / 234	lysosomal membrane
9	5e−04	51 / 3662	plasma membrane
10	6e−04	32 / 1979	membrane
11	8e−04	21 / 1101	extracellular space
12	2e−03	13 / 561	intracellular membrane−bounded organelle
13	2e−03	22 / 1249	extracellular region
14	2e−03	7 / 200	nuclear membrane
15	2e−03	12 / 512	cell surface

Chr

Rank	p−value	#in/all	Geneset
1	0.06	13 / 902	Chr 4
2	0.18	11 / 904	Chr 10
3	0.18	16 / 1411	Chr 11
4	0.18	14 / 1211	Chr 6
5	0.19	15 / 1318	Chr 17
6	0.31	23 / 2323	Chr 1
7	0.33	12 / 1160	Chr 12
8	0.33	10 / 954	Chr 9
9	0.34	15 / 1492	Chr 2
10	0.39	12 / 1217	Chr 3
11	0.47	6 / 619	Chr 20
12	0.47	3 / 289	Chr 21
13	0.51	5 / 536	Chr 22
14	0.52	7 / 768	Chr 14
15	0.58	3 / 342	Chr 18

Chromatin states

Rank	p−value	#in/all	Geneset
1	5e−07	147 / 12741	7_Enh_Melanocytes
2	1e−06	138 / 11836	3_TssF_Melanocytes
3	7e−06	107 / 8613	7_Enh_Fibroblasts
4	3e−04	110 / 9635	3_TssF_Fibroblasts
5	5e−04	125 / 11455	2_TssA_Fibroblasts
6	2e−03	130 / 12298	2_TssA_Melanocytes
7	3e−03	37 / 2620	1_TssP_Neuronal_Progenitor
8	8e−03	116 / 11130	15_Quies_Melanocytes
9	1e−02	96 / 8990	15_Quies_Fibroblasts
10	4e−02	62 / 5699	6_EnhG_Melanocytes
11	2e−01	76 / 7854	5_Tx_Fibroblasts
12	2e−01	24 / 2297	10_ReprPC_Neuronal_Progenitor
13	2e−01	37 / 3691	9_ReprPCWk_Neuronal_Progenitor
14	2e−01	83 / 8771	5_Tx_Melanocytes
15	3e−01	109 / 11847	7_Enh_Neuronal_Progenitor

Colon Cancer

Rank	p−value	#in/all	Geneset
1	5e−80	93 / 810	Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
2	8e−25	33 / 338	Pentrack_CRC_TCGA_group.over_B_msi−h_UP
3	6e−23	31 / 328	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
4	1e−17	15 / 64	Marisa_CRC−cluster−g
5	1e−13	149 / 10999	TssWk_Colon
6	2e−10	37 / 1281	LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv
7	3e−10	33 / 1069	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
8	5e−10	128 / 9555	TssA_Colon
9	1e−09	138 / 10779	Enh_Colon
10	5e−09	121 / 9054	Tx_Colon
11	8e−08	114 / 8678	Quies3_Colon
12	3e−07	111 / 8568	TxWk_Colon
13	5e−07	87 / 6138	TssD2_Colon
14	4e−06	96 / 7354	TssF_Colon
15	4e−05	3 / 8	Marisa_CRC−C2

Glio

Rank	p−value	#in/all	Geneset
1	3e−15	22 / 267	WILLSCHER_GBM_Verhaak−CL & MES_up
2	8e−09	8 / 47	Donson−innate immunity−associated with LTS in HGA
3	6e−08	5 / 13	Donson−immune cell intra signaling−associated with LTS in HGA
4	2e−07	9 / 96	Weller_LGG_1p19qDel−vs−intact_DOWN
5	3e−07	6 / 32	Donson−Misc immune function−associated with LTS in HGA
6	1e−06	10 / 158	Hopp_Sturm_GBM_Epi3_D_adult_fetus_IDH_UP
7	1e−03	5 / 94	Weller_LGG_A_vs_O_UP
8	8e−03	2 / 15	Donson−chemokines/cytokines−associated with LTS in HGA
9	2e−02	3 / 65	cultured astroglia vs. in vivo astrocytes
10	2e−02	3 / 65	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
11	2e−02	7 / 315	Up
12	3e−02	3 / 74	Weller_LGG_gradeII−vs−III_DOWN
13	3e−02	36 / 2988	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
14	4e−02	2 / 35	Colman_survival_associated
15	5e−02	3 / 90	GIEZELT_GBM_STSwt_down_VS_LTSwt

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−72	46 / 87	HECKER_IFNB1_TARGETS
2	1e−58	62 / 416	FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN
3	4e−58	35 / 58	BROWNE_INTERFERON_RESPONSIVE_GENES
4	3e−57	46 / 161	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_3D_UP
5	2e−54	27 / 29	MOSERLE_IFNA_RESPONSE
6	5e−47	32 / 73	BOSCO_INTERFERON_INDUCED_ANTIVIRAL_MODULE
7	5e−46	27 / 42	DAUER_STAT3_TARGETS_DN
8	1e−40	66 / 960	NUYTTEN_EZH2_TARGETS_UP
9	2e−38	36 / 180	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_10D_UP
10	3e−37	26 / 64	SANA_RESPONSE_TO_IFNG_UP
11	2e−34	19 / 26	BENNETT_SYSTEMIC_LUPUS_ERYTHEMATOSUS
12	3e−34	37 / 253	WALLACE_PROSTATE_CANCER_RACE_UP
13	5e−34	30 / 132	REACTOME_INTERFERON_SIGNALING
14	4e−32	17 / 21	ZHANG_INTERFERON_RESPONSE
15	7e−32	18 / 26	EINAV_INTERFERON_SIGNATURE_IN_CANCER

HM

Rank	p−value	#in/all	Geneset
1	2e−79	59 / 172	HALLMARK_INTERFERON_GAMMA_RESPONSE
2	3e−73	46 / 85	HALLMARK_INTERFERON_ALPHA_RESPONSE
3	2e−08	13 / 191	HALLMARK_INFLAMMATORY_RESPONSE
4	2e−08	12 / 162	HALLMARK_ALLOGRAFT_REJECTION
5	5e−08	9 / 82	HALLMARK_IL6_JAK_STAT3_SIGNALING
6	6e−08	12 / 176	HALLMARK_KRAS_SIGNALING_UP
7	9e−07	11 / 187	HALLMARK_COMPLEMENT
8	2e−04	8 / 185	HALLMARK_TNFA_SIGNALING_VIA_NFKB
9	3e−04	8 / 186	HALLMARK_IL2_STAT5_SIGNALING
10	2e−03	6 / 151	HALLMARK_APOPTOSIS
11	5e−03	6 / 175	HALLMARK_XENOBIOTIC_METABOLISM
12	6e−03	6 / 183	HALLMARK_APICAL_JUNCTION
13	6e−03	6 / 185	HALLMARK_MTORC1_SIGNALING
14	6e−03	6 / 185	HALLMARK_P53_PATHWAY
15	8e−03	5 / 138	HALLMARK_FATTY_ACID_METABOLISM

Lifestyle

Rank	p−value	#in/all	Geneset
1	4e−07	4 / 8	DUMEAUX_Monocytes in smokers literature genes up
2	3e−03	2 / 10	DUMEAUX_Smoking literature genes up
3	4e−02	1 / 5	DUMEAUX_Estrogen related in smokers literature genes up
4	1e−01	1 / 17	DUMEAUX_High bmi enriched genes
5	3e−01	3 / 211	Homuth_BMI−associated−genes_DN
6	4e−01	2 / 147	Homuth_BMI−associated−genes_UP
7	6e−01	1 / 94	DUMEAUX_Smoking enriched genes
8	1e+00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
9	1e+00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
10	1e+00	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
11	1e+00	0 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
12	1e+00	0 / 10	DUMEAUX_Women normal BMI literature genes up
13	1e+00	0 / 31	DUMEAUX_Fasting enriched genes
14	1e+00	0 / 18	Huan_blood−pressure_SBP−signature
15	1e+00	0 / 16	Huan_blood−pressure_DBP−signature

Lymphoma

Rank	p−value	#in/all	Geneset
1	1e−43	46 / 300	Hopp_June14_MMML937 tumors+controls_group.overexpression_E_GC−B−
2	3e−43	46 / 306	WIRTH_lymphoma937_spot E
3	2e−34	38 / 272	SPANG_IL21 DN
4	4e−18	126 / 7448	HOPP_Strong_enhancer
5	2e−15	13 / 57	Monti_Host_response_cluster
6	1e−10	21 / 408	TARTE_Mature plasma cell signature
7	1e−09	115 / 8226	HOPP_Active_promoter
8	4e−08	82 / 5356	HOPP_Txn_transition
9	5e−08	16 / 331	SPANG_CD40 6hrs UP
10	2e−07	107 / 8098	HOPP_Weak_promoter
11	5e−07	5 / 19	DAVE_Immune response 2
12	2e−05	93 / 7275	HOPP_Txn_elongation
13	3e−05	5 / 40	ROSOLOWSKI_blue DOWN
14	5e−05	88 / 6959	HOPP_Weak_enhancer
15	1e−04	7 / 121	SPANG_LPS 6hrs UP

Melanoma

Rank	p−value	#in/all	Geneset
1	0.3	1 / 43	Hugo_melanoma−BRAFmut−MET_UP
2	1.0	0 / 30	Hugo_melanoma−all−MET_UP
3	1.0	0 / 54	Hugo_melanoma−all−MET_DN
4	1.0	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
5	1.0	0 / 27	Hugo_melanoma−all−LEF1_UP
6	1.0	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

MF

Rank	p−value	#in/all	Geneset
1	9e−13	128 / 8818	protein binding
2	1e−09	9 / 54	double−stranded RNA binding
3	2e−05	5 / 36	single−stranded RNA binding
4	4e−05	9 / 182	signal transducer activity
5	5e−05	5 / 46	helicase activity
6	9e−05	8 / 160	carbohydrate binding
7	1e−04	3 / 12	proteoglycan binding
8	2e−04	6 / 94	double−stranded DNA binding
9	2e−04	9 / 232	ligase activity
10	3e−04	25 / 1329	ATP binding
11	6e−04	3 / 19	NAD+ ADP−ribosyltransferase activity
12	7e−04	14 / 580	identical protein binding
13	2e−03	9 / 311	enzyme binding
14	2e−03	3 / 28	tumor necrosis factor receptor binding
15	3e−03	7 / 213	GTPase activity

miRNA Disease

Rank	p−value	#in/all	Geneset
1	1	0 / 7	Thyroid carcinoma, papillary
2	1	0 / 123	Pancreatic cancer
3	1	0 / 68	Glioblastoma multiforme, somatic
4	1	0 / 63	Gastrointestinal
5	1	0 / 3	Pituitary adenoma
6	1	0 / 116	Cancer
7	1	0 / 95	Colorectal cancer
8	1	0 / 2	Adenomas, multiple colorectal
9	1	0 / 124	Prostate cancer
10	1	0 / 48	Alzheimer disease, susceptibility to
11	1	0 / 7	Schizophrenia, susceptibility to
12	1	0 / 20	Parkinson disease
13	1	0 / 65	Hepatocellular carcinoma
14	1	0 / 3	Down syndrome, risk of
15	1	0 / 127	Melanoma and neural system tumor syndrome

miRNA target

Rank	p−value	#in/all	Geneset
1	0.03	6 / 263	hsa−miR−449a
2	0.06	2 / 44	hsa−miR−660
3	0.07	5 / 250	hsa−miR−548l
4	0.07	3 / 110	hsa−miR−190b
5	0.08	3 / 113	hsa−miR−154
6	0.08	2 / 54	hsa−miR−504
7	0.08	1 / 10	hsa−miR−1306
8	0.10	2 / 59	hsa−miR−526b*
9	0.10	2 / 61	hsa−miR−627
10	0.11	2 / 63	hsa−miR−1243
11	0.11	1 / 13	hsa−miR−744
12	0.11	1 / 13	hsa−miR−452*
13	0.12	6 / 377	hsa−miR−373
14	0.13	2 / 71	hsa−miR−578
15	0.13	6 / 389	hsa−miR−519a

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.004	2 / 11	BENTINK_ras.4
2	0.109	1 / 13	BENTINK_src.10
3	1.000	0 / 14	GUSTAFSON_PI3K_UP
4	1.000	0 / 15	GUSTAFSON_PI3K_DN
5	1.000	0 / 13	BENTINK_e2f3.1
6	1.000	0 / 13	BENTINK_e2f3.2
7	1.000	0 / 13	BENTINK_myc.1
8	1.000	0 / 12	BENTINK_ras.1
9	1.000	0 / 14	BENTINK_ras.6
10	1.000	0 / 12	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Reference Signatures

Rank	p−value	#in/all	Geneset
1	3e−99	59 / 96	Chaussabel_3,1_Interferon−inducible
2	1e−26	24 / 113	Chaussabel_1,5_Myeloid lineage
3	2e−23	20 / 84	Chaussabel_2,10_Immune related cell surface molecules
4	1e−07	11 / 150	Chaussabel_2,6_Myeloid lineage
5	2e−07	13 / 240	Chaussabel_3,3_Inflammation II
6	3e−05	4 / 21	VAQUERIZAS_Tonsil_TF
7	1e−04	4 / 30	VAQUERIZAS_Lymph node_TF
8	3e−04	5 / 66	VAQUERIZAS_Whole blood_TF
9	3e−04	12 / 412	WIRTH_Immune system
10	4e−04	16 / 681	PROTEINATLAS_lung
11	1e−03	13 / 535	PROTEINATLAS_spleen
12	2e−03	4 / 64	VAQUERIZAS_Lung_TF
13	5e−03	2 / 12	WIRTH_Lymphocytes
14	5e−03	14 / 724	PROTEINATLAS_lymph node
15	2e−02	12 / 695	PROTEINATLAS_bone marrow

Telomeres

Rank	p−value	#in/all	Geneset
1	0.2	1 / 27	Nabetani_alt len telomeres_genes_ko
2	1.0	0 / 13	Alternative lengthening of telomeres
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	6e−05	41 / 2497	ICGC_Bcl11_targets
2	5e−04	46 / 3194	ICGC_Irf4_targets
3	9e−04	61 / 4735	ICGC_Pu1_targets
4	3e−03	83 / 7247	ICGC_Runx3_targets
5	4e−03	31 / 2133	ICGC_Mef2_targets
6	5e−03	70 / 5984	ICGC_Mta3_targets
7	5e−03	26 / 1723	HEBENSTREIT_high expression TF
8	5e−03	30 / 2087	ICGC_Cebpbsc150_targets
9	7e−03	64 / 5466	ICGC_Nficsc81335_targets
10	8e−03	58 / 4881	ICGC_Atf2_targets
11	8e−03	61 / 5188	ICGC_Ebfsc137065_targets
12	1e−02	63 / 5442	ICGC_Pmlsc71910_targets
13	1e−02	71 / 6322	ICGC_Tcf3_targets
14	1e−02	67 / 5961	ICGC_Pol24_targets
15	2e−02	35 / 2759	ICGC_Bcl3_targets

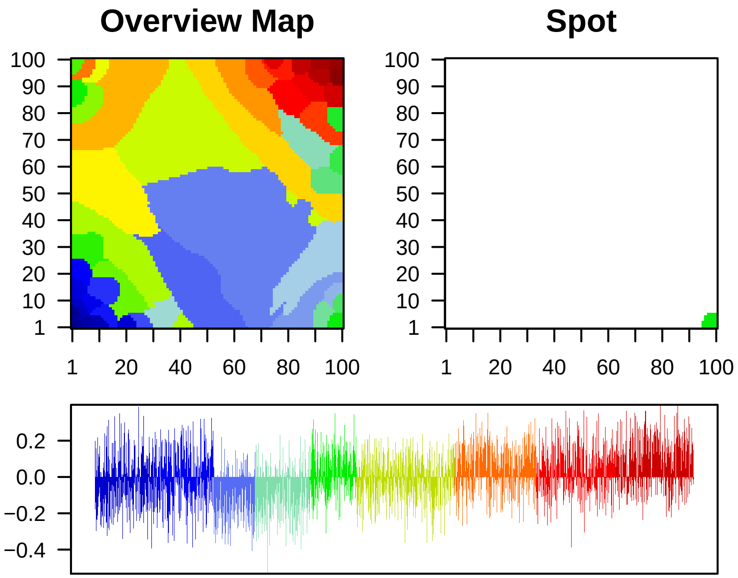
K−Means Cluster

Spot Summary: X1

metagenes = 32
genes = 506

<r> metagenes = 0.93
<r> genes = 0.38
beta: r2= 50.75 / log p= −Inf

samples with spot = 710 (21 %)
A * : 53 (15.4 %)
A C * : 71 (21.6 %)
A C F * : 7 (3 %)
A F * : 15 (4.9 %)
C F * : 63 (23.8 %)
F * : 79 (14.2 %)
F J * : 144 (31.1 %)
J * : 109 (24.4 %)
N * : 169 (38.1 %)

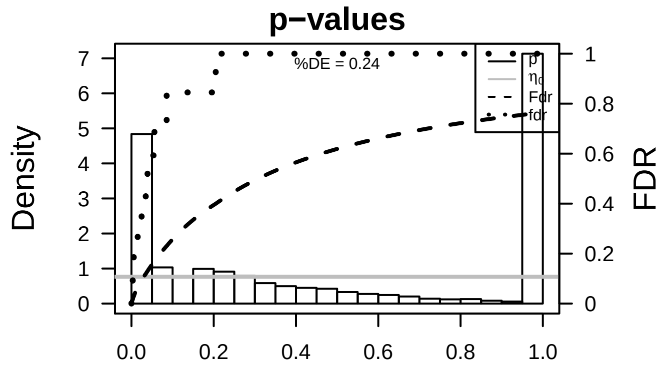


Spot Genelist

Rank	ID	max e	min e	r	Symbol	Description
1	ILMN_181520	2.38	−5.09	0.25		
2	ILMN_324640	2.08	−1.52	0.48	HNRNPH1	heterogeneous nuclear ribonucleoprotein H1 (H) [Source:HGI
3	ILMN_172311	1.86	−0.84	0.3	AMFR	autocrine motility factor receptor [Source:HGNC Symbol;Acc:
4	ILMN_166043	1.74	−1.19	0.53	HSPA1B	heat shock protein family A (Hsp70) member 1B [Source:HGI
5	ILMN_180439	1.74	−1.24	0.62	IRF2BPL	interferon regulatory factor 2 binding protein like [Source:HGN
6	ILMN_168231	1.7	−1.19	0.64		
7	ILMN_218437	1.61	−1.4	0.36	CXCL8	C−X−C motif chemokine ligand 8 [Source:HGNC Symbol;Acc
8	ILMN_167870	1.61	−1.35	0.42	TAF15	TATA−box binding protein associated factor 15 [Source:HGNC
9	ILMN_328909	1.6	−0.76	0.61		
10	ILMN_234779	1.53	−0.57	0.42	IFI6	interferon alpha inducible protein 6 [Source:HGNC Symbol;Ac
11	ILMN_238959	1.51	−2.92	0.18	PRKAR1A	protein kinase cAMP−dependent type I regulatory subunit alp
12	ILMN_175311	1.45	−1.67	0.75	NAMPT	nicotinamide phosphoribosyltransferase [Source:HGNC Symb
13	ILMN_209565	1.43	−0.84	0.24	AFMID	arylformamidase [Source:HGNC Symbol;Acc:HGNC:20910]
14	ILMN_330896	1.42	−0.59	0.27	ND6	mitochondrially encoded NADH:ubiquinone oxidoreductase c
15	ILMN_210192	1.41	−0.75	0.5		
16	ILMN_239376	1.39	−1.23	0.6	ARPC4−TTLL3	ARPC4−TTLL3 readthrough [Source:HGNC Symbol;Acc:HGI
17	ILMN_172165	1.36	−0.96	0.56		ubiquitin conjugating enzyme E2 H pseudogene 1 [Source:HC
18	ILMN_176605	1.31	−1.01	0.45	ABCA1	ATP binding cassette subfamily A member 1 [Source:HGNC S
19	ILMN_324364	1.31	−0.56	0.39		
20	ILMN_169333	1.29	−1.28	0.4	CYP1B1	cytochrome P450 family 1 subfamily B member 1 [Source:HG

Geneset Overrepresentation

Rank	p−value	#in/all	Geneset	
1	8e−56	321 / 9555	Colon	TssA_Colon
2	1e−55	280 / 7275	Lympl	HOPP_Txn_elongation
3	2e−52	308 / 9054	Colon	Tx_Colon
4	9e−49	334 / 10999	Colon	TssWk_Colon
5	1e−47	131 / 1797	GSEA	PILON_KLF1_TARGETS_DN
6	1e−46	291 / 8568	Colon	TxWk_Colon
7	2e−45	291 / 8678	Colon	Quies3_Colon
8	4e−45	310 / 9815	Brain	Overlap_fetal_midbrain_ReprPC
9	2e−43	265 / 7448	Lympl	HOPP_Strong_enhancer
10	5e−42	219 / 5356	Lympl	HOPP_Txn_transition
11	6e−42	331 / 11455	Chror	2_TssA_Fibroblasts
12	3e−41	276 / 8226	Lympl	HOPP_Active_promoter
13	1e−40	285 / 8771	Chror	5_Tx_Melanocytes
14	5e−39	339 / 12298	Chror	2_TssA_Melanocytes
15	5e−36	260 / 7854	Chror	5_Tx_Fibroblasts
16	3e−35	220 / 5936	Brain	Overlap_fetal_midbrain_HetRpts
17	6e−35	295 / 9917	Brain	Overlap_fetal_midbrain_ReprPCWk
18	6e−33	300 / 10430	Brain	Overlap_fetal_midbrain_Quies
19	3e−32	338 / 12983	Chror	2_TssA_Neuronal_Progenitor
20	8e−32	270 / 8818	MF	protein binding
21	5e−30	317 / 11836	Chror	3_TssF_Melanocytes
22	1e−29	269 / 8990	Chror	15_Quies_Fibroblasts
23	2e−28	328 / 12741	Chror	7_Enh_Melanocytes
24	5e−28	55 / 498	GSEA	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR_UP
25	6e−28	249 / 8098	Lympl	HOPP_Weak_promoter
26	1e−27	274 / 9504	Brain	Overlap_fetal_midbrain_K9K27me3
27	2e−26	198 / 5699	Chror	6_EnhG_Melanocytes
28	2e−26	224 / 6970	Chror	5_Tx_Neuronal_Progenitor
29	1e−25	42 / 301	Cance	SPANG_BCL6−index2
30	6e−25	63 / 763	GSEA	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP
31	1e−24	295 / 11130	Chror	15_Quies_Melanocytes
32	2e−24	63 / 783	GSEA	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
33	5e−24	52 / 532	GSEA	SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_DN
34	3e−23	55 / 622	GSEA	SCHLOSSER_SERUM_RESPONSE_DN
35	9e−23	127 / 2979	CC	cytosol
36	2e−22	71 / 1069	Colon	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
37	3e−22	246 / 8613	Chror	7_Enh_Fibroblasts
38	1e−21	52 / 602	miRN	hsa−miR−20a
39	2e−21	76 / 1265	GSEA	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
40	4e−21	48 / 520	miRN	hsa−miR−106a



Aging

Rank	p−value	#in/all	Geneset
1	0.6	2 / 111	HORVATH_aging_genes meth DOWN
2	0.7	2 / 142	HORVATH_aging_genes meth UP
3	1.0	0 / 58	TESCHENDORFF_age_hypermethylated
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

BP

Rank	p−value	#in/all	Geneset
1	8e−10	29 / 434	protein phosphorylation
2	6e−07	18 / 254	cell−cell adhesion
3	8e−07	24 / 435	negative regulation of apoptotic process
4	8e−06	9 / 77	movement of cell or subcellular component
5	2e−05	11 / 128	actin cytoskeleton organization
6	4e−05	23 / 511	apoptotic process
7	4e−05	4 / 12	negative regulation of interleukin−12 production
8	4e−05	10 / 118	protein stabilization
9	5e−05	6 / 38	positive regulation of autophagy
10	8e−05	5 / 26	regulation of transcription from RNA polymerase II promoter in response to hy
11	1e−04	10 / 131	cell cycle arrest
12	1e−04	5 / 28	cellular response to nerve growth factor stimulus
13	1e−04	23 / 550	positive regulation of transcription, DNA−templated
14	1e−04	17 / 342	intracellular signal transduction
15	2e−04	6 / 47	phagocytosis

Brain

Rank	p−value	#in/all	Geneset
1	4e−45	310 / 9815	Overlap_fetal_midbrain_ReprPC
2	3e−35	220 / 5936	Overlap_fetal_midbrain_HetRpts
3	6e−35	295 / 9917	Overlap_fetal_midbrain_ReprPCWk
4	6e−33	300 / 10430	Overlap_fetal_midbrain_Quies
5	1e−27	274 / 9504	Overlap_fetal_midbrain_K9K27me3
6	9e−06	87 / 3164	Mid_Frontal_Lobe_ZNF
7	7e−05	17 / 328	Fetal_Het
8	9e−05	40 / 1213	Fetal_TssP
9	3e−04	11 / 180	Overlap_fetal_midbrain_Het
10	4e−04	37 / 1171	Fetal_EnhP
11	1e−03	29 / 906	Fetal_HetRpts
12	7e−03	24 / 796	Overlap_fetal_midbrain_ZNF
13	8e−03	32 / 1162	Fetal_Enh
14	2e−02	13 / 386	Fetal_ZNF
15	2e−02	25 / 937	Fetal_EnhG

Cancer

Rank	p−value	#in/all	Geneset
1	1e−25	42 / 301	SPANG_BCL6−index2
2	9e−15	24 / 178	SPANG_LPS−index2
3	6e−07	28 / 554	Lembcke_Colonic Inflammation
4	1e−04	4 / 16	GENTLES_modul14
5	4e−04	9 / 125	PanCan_CC+Apop_geneset_nanostring
6	1e−03	3 / 13	GENTLES_modul12
7	3e−03	6 / 82	PanCan_JAK−ST_geneset_nanostring
8	8e−03	4 / 46	PanCan_TGF−B_geneset_nanostring
9	1e−02	5 / 76	PanCan_Wnt_geneset_nanostring
10	1e−02	4 / 54	KUIPER_MM poor survival
11	2e−02	6 / 117	PanCan_Driver_Gene_geneset_nanostring
12	5e−02	6 / 150	PanCan_MAPK_geneset_nanostring
13	7e−02	2 / 24	PanCan_Notch_geneset_nanostring
14	8e−02	4 / 91	PanCan_TXmisReg_geneset_nanostring
15	1e−01	1 / 6	ZHANG_MGUS up

CC

Rank	p−value	#in/all	Geneset
1	9e−23	127 / 2979	cytosol
2	2e−18	161 / 4822	cytoplasm
3	1e−16	101 / 2464	extracellular exosome
4	3e−12	79 / 1979	membrane
5	1e−08	83 / 2535	nucleoplasm
6	2e−08	24 / 352	focal adhesion
7	6e−08	130 / 4828	nucleus
8	1e−07	36 / 777	Golgi apparatus
9	2e−07	17 / 208	actin cytoskeleton
10	4e−07	15 / 172	endosome membrane
11	1e−06	19 / 295	cell−cell adherens junction
12	3e−06	10 / 88	melanosome
13	1e−05	9 / 83	ruffle
14	2e−05	25 / 561	intracellular membrane−bounded organelle
15	6e−05	12 / 173	nuclear chromatin

Chr

Rank	p−value	#in/all	Geneset
1	0.008	39 / 1492	Chr 2
2	0.053	26 / 1060	Chr 5
3	0.079	10 / 342	Chr 18
4	0.113	21 / 902	Chr 4
5	0.122	27 / 1217	Chr 3
6	0.222	25 / 1211	Chr 6
7	0.225	24 / 1160	Chr 12
8	0.319	9 / 422	Chr 13
9	0.448	24 / 1318	Chr 17
10	0.475	14 / 768	Chr 14
11	0.476	14 / 769	Chr 15
12	0.503	17 / 954	Chr 9
13	0.571	5 / 289	Chr 21
14	0.572	17 / 994	Chr X
15	0.603	14 / 836	Chr 8

Chromatin states

Rank	p−value	#in/all	Geneset
1	6e−42	331 / 11455	2_TssA_Fibroblasts
2	1e−40	285 / 8771	5_Tx_Melanocytes
3	5e−39	339 / 12298	2_TssA_Melanocytes
4	5e−36	260 / 7854	5_Tx_Fibroblasts
5	3e−32	338 / 12983	2_TssA_Neuronal_Progenitor
6	5e−30	317 / 11836	3_TssF_Melanocytes
7	1e−29	269 / 8990	15_Quies_Fibroblasts
8	2e−28	328 / 12741	7_Enh_Melanocytes
9	2e−26	198 / 5699	6_EnhG_Melanocytes
10	2e−26	224 / 6970	5_Tx_Neuronal_Progenitor
11	1e−24	295 / 11130	15_Quies_Melanocytes
12	3e−22	246 / 8613	7_Enh_Fibroblasts
13	9e−21	307 / 12393	15_Quies_Neuronal_Progenitor
14	2e−16	250 / 9635	3_TssF_Fibroblasts
15	9e−10	267 / 11847	7_Enh_Neuronal_Progenitor

Colon Cancer

Rank	p−value	#in/all	Geneset
1	8e−56	321 / 9555	TssA_Colon
2	2e−52	308 / 9054	Tx_Colon
3	9e−49	334 / 10999	TssWk_Colon
4	1e−46	291 / 8568	TxWk_Colon
5	2e−45	291 / 8678	Quies3_Colon
6	2e−22	71 / 1069	LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN
7	4e−20	279 / 10779	Enh_Colon
8	3e−16	167 / 5373	EnhWk1_Colon
9	2e−12	196 / 7354	TssF_Colon
10	2e−12	68 / 1547	LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a
11	1e−10	96 / 2845	TxEnhG1_Colon
12	4e−09	24 / 328	Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN
13	5e−09	58 / 1468	LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo
14	5e−08	49 / 1216	LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_
15	9e−08	113 / 4034	TssD1_Colon

Glio

Rank	p−value	#in/all	Geneset
1	1e−15	32 / 315	Up
2	9e−15	31 / 316	WILLSCHER_GBM_Verhaak−PNwt & CL_up
3	7e−11	24 / 267	WILLSCHER_GBM_Verhaak−CL & MES_up
4	2e−08	71 / 2043	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
5	1e−06	59 / 1777	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
6	3e−06	34 / 820	Sturm_GBM_Meth_overexpression_E_G34_UP
7	2e−03	2 / 4	WILLSCHER_GBM_Verhaak−CL_up (E)
8	1e−02	4 / 48	Vishal_subnetwork signature of survival in GBM
9	3e−02	3 / 37	WILLSCHER_GBM_proteomics_wtOnly_SpotH
10	3e−02	2 / 16	Donson−chemokine/cytokine−receptors−associated with LTS in HGA
11	3e−02	10 / 290	Hopp_Sturm_GBM_Epi3_C_IDH_UP
12	3e−02	5 / 101	Hopp_Sturm_GBM_Epi3_D1_IDH_UP_adult_fetus_DN
13	4e−02	34 / 1417	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN
14	5e−02	1 / 3	WILLSCHER_GBM_STSwt_proteomics−L_UP
15	6e−02	6 / 157	WILLSCHER_GBM_proteomics_wtOnly_Differencelist

GSEA C2

Rank	p−value	#in/all	Geneset
1	1e−47	131 / 1797	PILON_KLF1_TARGETS_DN
2	5e−28	55 / 498	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR_UP
3	6e−25	63 / 763	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP
4	2e−24	63 / 783	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
5	5e−24	52 / 532	SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_DN
6	3e−23	55 / 622	SCHLOSSER_SERUM_RESPONSE_DN
7	2e−21	76 / 1265	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
8	9e−21	74 / 1241	PUJANA_ATM_PCC_NETWORK
9	1e−20	63 / 924	MARSON_BOUND_BY_FOXP3_STIMULATED
10	6e−19	30 / 208	THEILGAARD_NEUTROPHIL_AT_SKIN_WOUND_DN
11	6e−18	65 / 1104	MARSON_BOUND_BY_FOXP3_UNSTIMULATED
12	5e−17	53 / 794	NUYTTEN_NIPP1_TARGETS_DN
13	6e−17	52 / 770	CUI_TCF21_TARGETS_2_DN
14	1e−16	54 / 841	ACEVEDO_LIVER_CANCER_UP
15	3e−16	39 / 455	ZHENG_BOUND_BY_FOXP3

HM

Rank	p−value	#in/all	Geneset
1	2e−07	16 / 185	HALLMARK_TNFA_SIGNALING_VIA_NFKB
2	7e−05	11 / 151	HALLMARK_APOPTOSIS
3	1e−04	8 / 87	HALLMARK_PROTEIN_SECRETION
4	4e−04	9 / 127	HALLMARK_COAGULATION
5	4e−04	11 / 185	HALLMARK_MTORC1_SIGNALING
6	5e−04	11 / 187	HALLMARK_COMPLEMENT
7	6e−04	11 / 191	HALLMARK_INFLAMMATORY_RESPONSE
8	2e−03	5 / 50	HALLMARK_TGF_BETA_SIGNALING
9	3e−03	8 / 137	HALLMARK_UV_RESPONSE_UP
10	5e−03	6 / 91	HALLMARK_PEROXISOME
11	5e−03	9 / 185	HALLMARK_HEME_METABOLISM
12	6e−03	9 / 186	HALLMARK_IL2_STAT5_SIGNALING
13	6e−03	9 / 189	HALLMARK_HYPOXIA
14	1e−02	7 / 138	HALLMARK_FATTY_ACID_METABOLISM
15	1e−02	8 / 172	HALLMARK_INTERFERON_GAMMA_RESPONSE

Lifestyle

Rank	p−value	#in/all	Geneset
1	2e−11	22 / 211	Homuth_BMI−associated−genes_DN
2	1e−08	7 / 18	Huan_blood−pressure_SBP−signature
3	5e−05	3 / 5	Huan_blood−pressure_HTN−signature
4	1e−04	4 / 16	Huan_blood−pressure_DBP−signature
5	2e−01	1 / 10	DUMEAUX_Smoking literature genes up
6	2e−01	1 / 10	DUMEAUX_Women normal BMI literature genes up
7	2e−01	1 / 15	DUMEAUX_Red blood cells in non smokers literature genes up
8	3e−01	1 / 17	DUMEAUX_High bmi enriched genes
9	4e−01	1 / 31	DUMEAUX_Fasting enriched genes
10	5e−01	2 / 94	DUMEAUX_Smoking enriched genes
11	7e−01	2 / 147	Homuth_BMI−associated−genes_UP
12	1e+00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
13	1e+00	0 / 5	DUMEAUX_Estrogen related in smokers literature genes up
14	1e+00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
15	1e+00	0 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up

Lymphnoma

Rank	p−value	#in/all	Geneset
1	1e−55	280 / 7275	HOPP_Txn_elongation
2	2e−43	265 / 7448	HOPP_Strong_enhancer
3	5e−42	219 / 5356	HOPP_Txn_transition
4	3e−41	276 / 8226	HOPP_Active_promoter
5	6e−28	249 / 8098	HOPP_Weak_promoter
6	2e−18	197 / 6559	HOPP_Weak_txn
7	3e−17	202 / 6959	HOPP_Weak_enhancer
8	2e−14	61 / 1169	SPANG_BCR DN
9	3e−09	22 / 272	SPANG_IL21 DN
10	5e−08	22 / 318	Hopp_June14_MMML937 tumors+controls_group.overexpression_H_GC−B−
11	1e−07	22 / 331	WIRTH_lymphoma937_spot H
12	2e−07	27 / 493	WIRTH_lymphoma937_spot J
13	3e−07	26 / 472	Hopp_June14_MMML937 tumors+controls_group.overexpression_J_GC−B−
14	4e−07	21 / 331	SPANG_CD40 6hrs UP
15	1e−06	10 / 78	Sha_DLBCL UP

Melanoma

Rank	p−value	#in/all	Geneset
1	0.04	3 / 43	Hugo_melanoma−BRAFmut−MET_UP
2	0.38	1 / 27	Hugo_melanoma−all−LEF1_UP
3	0.41	1 / 30	Hugo_melanoma−all−MET_UP
4	1.00	0 / 54	Hugo_melanoma−all−MET_DN
5	1.00	0 / 9	Hugo_melanoma−BRAFmut−MET_DN
6	1.00	0 / 8	Hugo_melanoma−BRAFmut−LEF1_UP
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

MF

Rank	p−value	#in/all	Geneset
1	8e−32	270 / 8818	protein binding
2	4e−08	22 / 315	protein serine/threonine kinase activity
3	2e−07	19 / 265	cadherin binding involved in cell−cell adhesion
4	7e−07	20 / 311	enzyme binding
5	3e−06	15 / 204	protein domain specific binding
6	7e−06	15 / 217	protein kinase activity
7	2e−05	7 / 48	receptor signaling protein serine/threonine kinase activity
8	3e−05	14 / 213	GTPase activity
9	8e−05	43 / 1329	ATP binding
10	1e−04	35 / 1013	poly(A) RNA binding
11	2e−04	25 / 646	protein homodimerization activity
12	2e−04	13 / 232	ligase activity
13	3e−04	6 / 51	GDP binding
14	3e−04	5 / 35	RNA polymerase II activating transcription factor binding
15	5e−04	7 / 81	protease binding

miRNA Disease

Rank	p−value	#in/all	Geneset
1	1	0 / 7	Thyroid carcinoma, papillary
2	1	0 / 123	Pancreatic cancer
3	1	0 / 68	Glioblastoma multiforme, somatic
4	1	0 / 63	Gastrointestinal
5	1	0 / 3	Pituitary adenoma
6	1	0 / 116	Cancer
7	1	0 / 95	Colorectal cancer
8	1	0 / 2	Adenomas, multiple colorectal
9	1	0 / 124	Prostate cancer
10	1	0 / 48	Alzheimer disease, susceptibility to
11	1	0 / 7	Schizophrenia, susceptibility to
12	1	0 / 20	Parkinson disease
13	1	0 / 65	Hepatocellular carcinoma
14	1	0 / 3	Down syndrome, risk of
15	1	0 / 127	Melanoma and neural system tumor syndrome

miRNA target

Rank	p−value	#in/all	Geneset
1	1e−21	52 / 602	hsa−miR−20a
2	4e−21	48 / 520	hsa−miR−106a
3	7e−21	39 / 336	hsa−miR−142−5p
4	1e−20	49 / 561	hsa−miR−20b
5	2e−20	43 / 429	hsa−miR−548n
6	3e−20	48 / 546	hsa−miR−93
7	3e−19	41 / 416	hsa−miR−372
8	7e−19	34 / 281	hsa−miR−570
9	3e−18	44 / 513	hsa−miR−106b
10	4e−18	45 / 540	hsa−miR−17
11	4e−18	35 / 317	hsa−miR−18a
12	1e−17	31 / 250	hsa−miR−548l
13	2e−17	33 / 292	hsa−miR−18b
14	5e−17	40 / 455	hsa−miR−130a
15	2e−16	38 / 428	hsa−miR−519d

Pathw Act

Rank	p−value	#in/all	Geneset
1	0.02	2 / 11	BENTINK_ras.4
2	0.02	2 / 12	BENTINK_ras.1
3	0.20	1 / 13	BENTINK_src.10
4	0.22	1 / 14	GUSTAFSON_PI3K_UP
5	0.23	1 / 15	GUSTAFSON_PI3K_DN
6	1.00	0 / 13	BENTINK_e2f3.1
7	1.00	0 / 13	BENTINK_e2f3.2
8	1.00	0 / 13	BENTINK_myc.1
9	1.00	0 / 14	BENTINK_ras.6
10	1.00	0 / 12	BENTINK_src.2
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

Reference Signatures

Rank	p−value	#in/all	Geneset
1	3e−20	42 / 412	WIRTH_Immune system
2	4e−20	33 / 240	Chaussabel_3,3_Inflammation II
3	4e−17	30 / 242	Chaussabel_3,2_Inflammation I
4	3e−12	20 / 153	Chaussabel_2,9_Cytosceleton
5	4e−10	51 / 1118	PROTEINATLAS_placenta
6	8e−10	24 / 302	Chaussabel_3,4_Protein phosphatases
7	1e−08	35 / 681	PROTEINATLAS_lung
8	6e−08	15 / 150	Chaussabel_2,6_Myeloid lineage
9	1e−07	36 / 782	PROTEINATLAS_thyroid gland
10	2e−07	47 / 1194	PROTEINATLAS_stomach
11	2e−07	10 / 66	VAQUERIZAS_Whole blood_TF
12	3e−07	18 / 242	Chaussabel_3,9_Kinases
13	1e−06	27 / 535	PROTEINATLAS_spleen
14	2e−06	30 / 650	PROTEINATLAS_hippocampus
15	2e−06	32 / 724	PROTEINATLAS_lymph node

Telomeres

Rank	p−value	#in/all	Geneset
1	0.2	1 / 13	Alternative lengthening of telomeres
2	0.4	1 / 27	Nabetani_alt len telomeres_genes_ko
3	NA	0 / 0	
4	NA	0 / 0	
5	NA	0 / 0	
6	NA	0 / 0	
7	NA	0 / 0	
8	NA	0 / 0	
9	NA	0 / 0	
10	NA	0 / 0	
11	NA	0 / 0	
12	NA	0 / 0	
13	NA	0 / 0	
14	NA	0 / 0	
15	NA	0 / 0	

TF

Rank	p−value	#in/all	Geneset
1	1e−15	159 / 5067	ICGC_Taf1_targets
2	2e−13	140 / 4468	ICGC_Egr1_targets
3	2e−13	161 / 5466	ICGC_Nficsc81335_targets
4	4e−13	148 / 4881	ICGC_Atf2_targets
5	1e−12	73 / 1723	HEBENSTREIT_high expression TF
6	2e−12	83 / 2133	ICGC_Mef2_targets
7	5e−12	145 / 4890	ICGC_Bclaf101388_targets
8	9e−12	141 / 4735	ICGC_Pu1_targets
9	2e−11	127 / 4131	ICGC_Nfatc1_targets
10	4e−11	155 / 5518	ICGC_Stat5_targets
11	8e−11	152 / 5410	ICGC_Foxm1_targets
12	9e−11	78 / 2087	ICGC_Cebpbsc150_targets
13	2e−10	151 / 5442	ICGC_Pmlsc71910_targets
14	3e−10	148 / 5312	ICGC_Tcf12_targets
15	4e−10	128 / 4362	ICGC_Creb1_targets