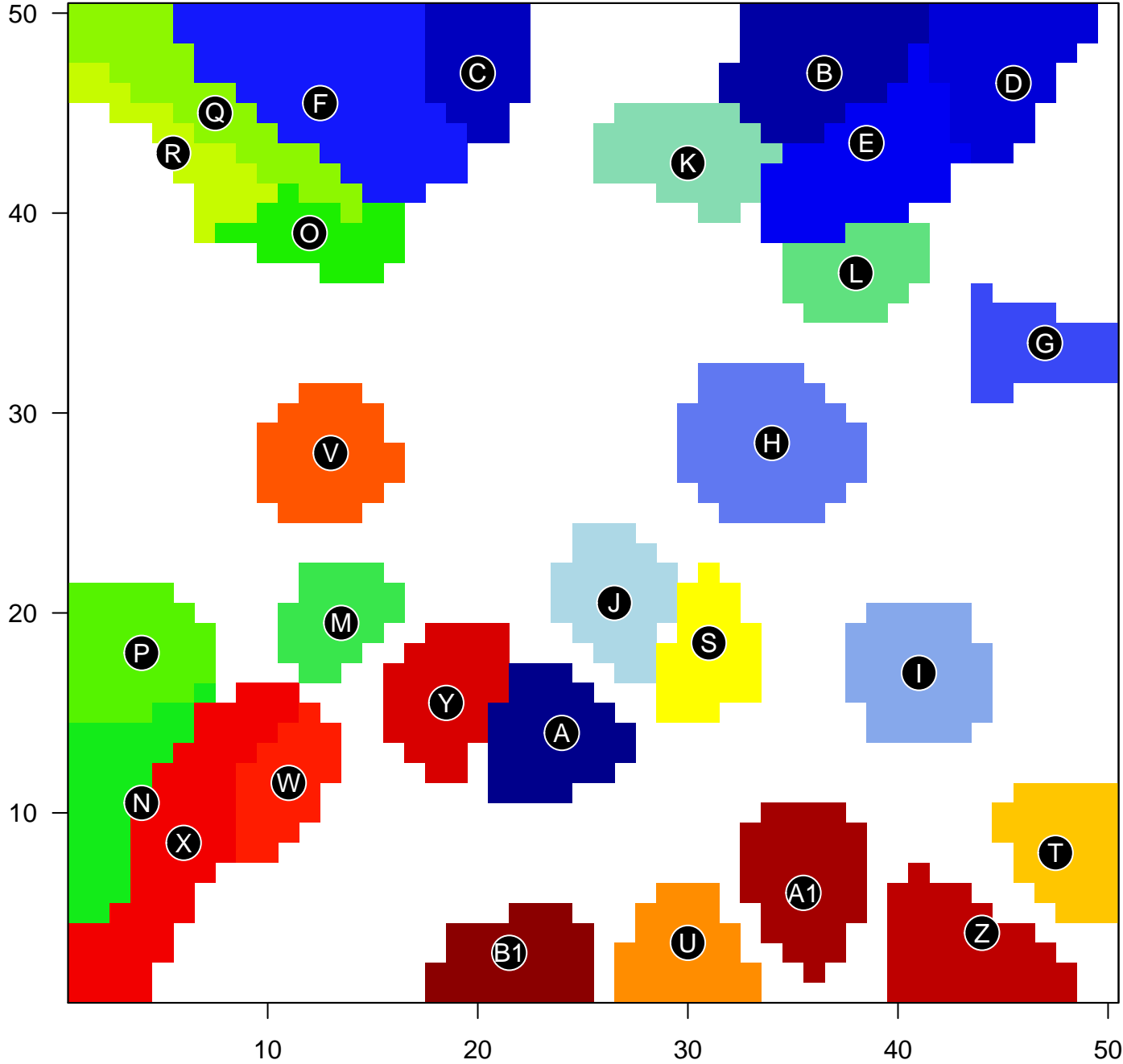


Correlation Cluster

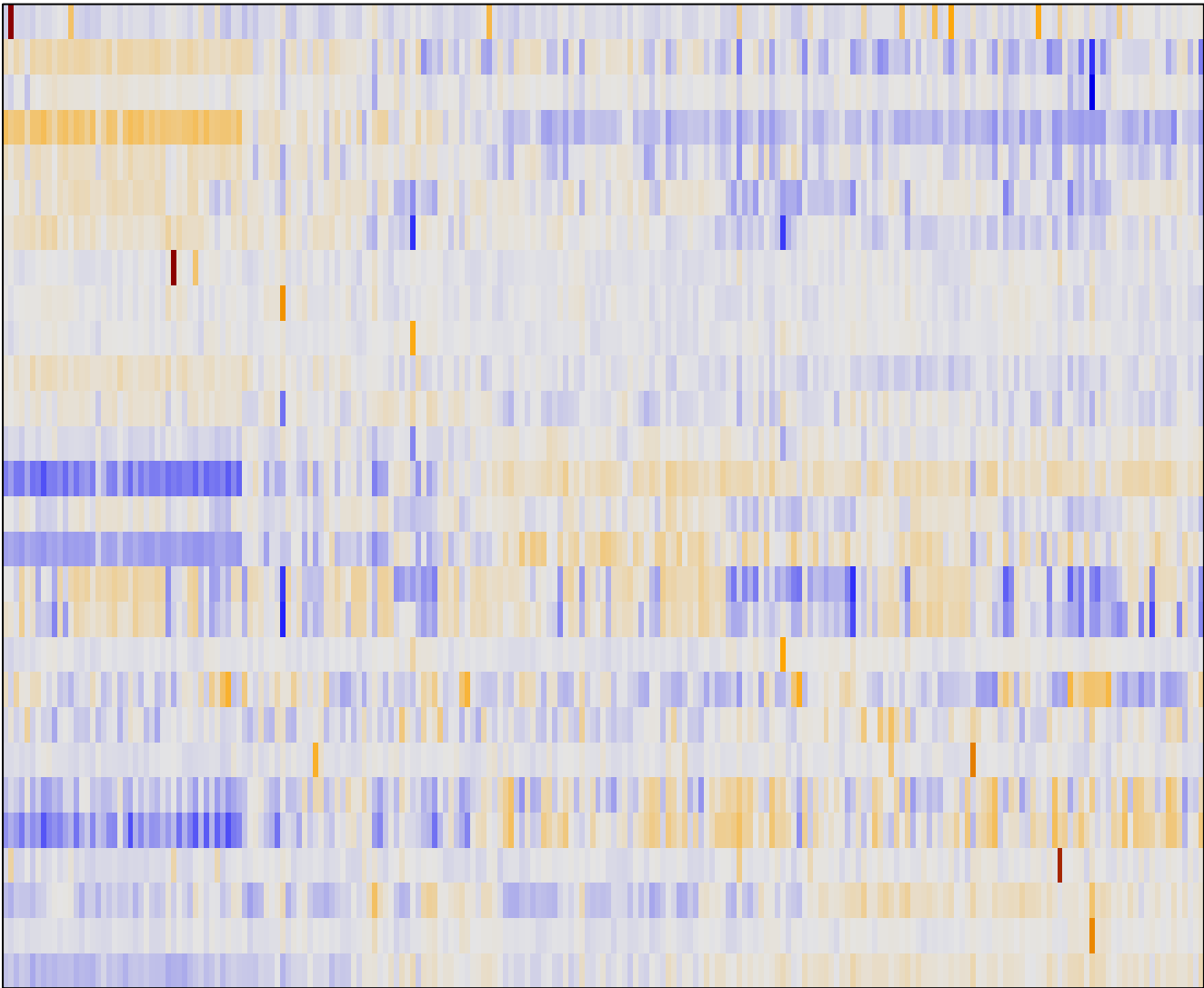
annotation



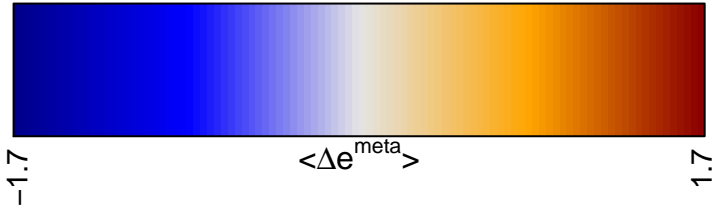
- A ■ WIRTH_Mucosa
JAEGER_METASTASIS_DN
- B ■ WILLSCHER_GBM_Verhaak-CL_up (C)
Gerber_wt/wt_melanoma-cells-SpotA
- C ■ HOPP_Txn_elongation
HOPP_Active_promoter
- D ■ HUMMEL_BURKITTTS_LYMPHOMA_UP
Sha_BL UP
- E ■ KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
RNA binding
- F ■ T CD8+ naive cells peripheral blood_4_Tx
HOPP_Txn_elongation
- G ■ HOPP_Txn_elongation
T CD8+ naive cells peripheral blood_4_Tx
- H ■ WIRTH_Liver
HSIAO_LIVER_SPECIFIC_GENES
- I ■ T CD8+ naive cells peripheral blood_14_ReprPCWk
Thelper cells peripheral blood_14_ReprPCWk
- J ■ LaPointe_mucosa-position_kmeans_F_cecum_colon_trans
Tcells peripheral blood_13_ReprPC
- K ■ BLALOCK_ALZHEIMERS_DISEASE_DN
HOPP_Txn_elongation
- L ■ Bcells peripheral blood_2_TssAFlnk
Bcells peripheral blood_1_TssA
- M ■ BLALOCK_ALZHEIMERS_DISEASE_DN
monocytes peripheral blood_1_TssA
- N ■ SPANG_BCL6-index2
Sha_DLBCL UP
- O ■ hsa-miR-576-3p
YANAGIHARA_ESX1_TARGETS
- P ■ Bcells peripheral blood_6_EnhG
HOPP_Strong_enhancer
- Q ■ WILLSCHER_GBM_Verhaak-PNwt & CL_up
Chaussabel_2,9_Cytoskeleton
- R ■ Tcells peripheral blood_6_EnhG
natural killer cells peripheral blood_6_EnhG
- S ■ Tcells peripheral blood_13_ReprPC
monocytes peripheral blood_13_ReprPC
- T ■ LaPointe_mucosa-position_kmeans_E_transverse_colon_U
Chaussabel_3,8_Enzymes
- U ■ WIRTH_post GC B-cells
WIRTH_pre+post GC B-cells
- V ■ 13_HetRpts_Melanocytes
natural killer cells peripheral blood_9_Het
- W ■ Lembcke_TCGA-expr_kmeans_E_CIMP.H_UP_Cluster4_D
WALLACE_PROSTATE_CANCER_RACE UP



A
B
C
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G
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Q
R
S
T
U
V
W
X
Y
Z
A1
B1



WIRTH_MUCOSA_STASIS_DN
ONDER_CDH1_TARGETS_2_DN
WILLSCHEER_GBM_Verhaak_CL_up (C)
Gambetta_WHM_melanoma_Cls_up
KINSEY_TARGETS_OF_EWSRT_FLI1_FUSION_UP
HOBBS_Txn_elongation
Bcells_peripheral_blood_1_TssA
HUMMEL_BURKITT'S_LYMPHOMA_UP
SPANG_HIP
SPANG_BCR_UP
KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
Tcells_peripheral_blood_2_TssAFlnk
TCD8+naive_cells_peripheral_blood_4_Tx
HOBBS_Txn_elongation
Tcells_peripheral_blood_4_Tx
HOBBS_Txn_elongation_peripheral_blood_4_Tx
Bcells_peripheral_blood_4_Tx
WIRTH_Liver_SPECIFIC_GENES
SPANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_DN
TCD8+naive_cells_peripheral_blood_14_ReprPCWk
HSC_14_ReprPCWk
LaPointe_mucosa_position_kmeans_F_cecum_colon_transverse_colon_UP_
Tcells_peripheral_blood_13_ReprPC
BLALOCK_ALZHEIMERS_DISEASE_DN
HALLMARK_OXIDATIVE_PHOSPHORYLATION
Bcells_peripheral_blood_7_TssAFlnk
6x_ERHG_Fibroblasts
BLALOCK_ALZHEIMERS_DISEASE_DN
HSC_1_TssA
SPANG_BCL6_index2
SPANG_LPS_index2
hsa-miR-576-3p-x1_TARGETS
REACTOME_IMMUNE_SYSTEM
Bcells_peripheral_blood_6_EnhG
SPANG_BCL6_index2
WILLSCHEER_GBM_Verhaak-PNwt & CL_up
Bcells_peripheral_blood_4_Tx
Tcells_peripheral_blood_6_EnhG
Bcells_peripheral_blood_6_EnhG
Tcells_peripheral_blood_13_ReprPC
LaPointe_mucosa_position_kmeans_F_cecum_colon_transverse_colon_UP_
Chavakis_3_8_EnhG
natural_killer_cells_peripheral_blood_4_Tx
WIRTH_post_GC_B_cells
EHRW14_Colon
13_HetRpis_Melanocytes
VeharASUBRAMANIAN_PROSTATE_CANCER
Lembcke_TCGA_expr_kmeans_E_CIMP_H_UP_Cluster4_DN
FULCHER_INFLAMMATORY_RESPONSE_LLECTIN_VS_LPS_DN
Lembcke_TCGA_expr_kmeans_E_CIMP_H_UP_Cluster4_DN
WIRTH_EBV_B_cells
LaPointe_mucosa_position_kmeans_L_transverse_colon_cecum_colon_DN
Lembcke_TCGA_expr_kmeans_M_CIMP_H_DN
MOREAUX_MULTIPLE_MYELOMA_BY_TACI_UP
6x_ERHG_Fibroblasts
WIRTH_pre_post_GC_B_cells
LaPointe_mucosa_position_kmeans_F_cecum_colon_transverse_colon_UP_
4_TxTrans_Fibroblasts
6x_ERHG_Fibroblasts



Correlation Cluster

Spot Summary: A

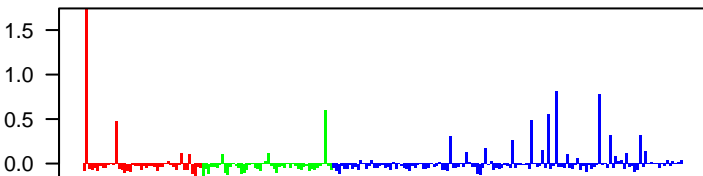
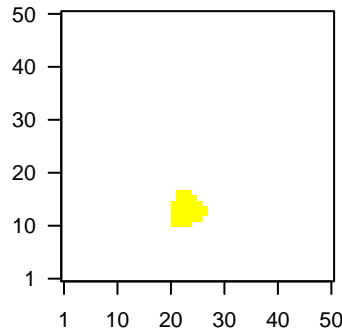
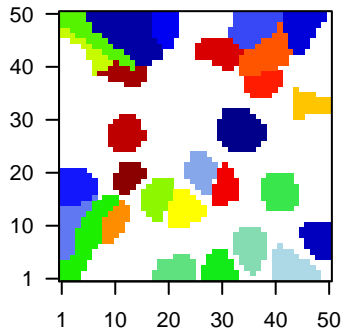
metagenes = 37
genes = 168

<r> metagenes = 0.93
<r> genes = 0.23
beta: r2= 1.46 / log p= -Inf

samples with spot = 13 (5.9 %)
mBL : 2 (4.5 %)
intermediate : 1 (2.1 %)
non-mBL : 10 (7.8 %)

Overview Map

Spot

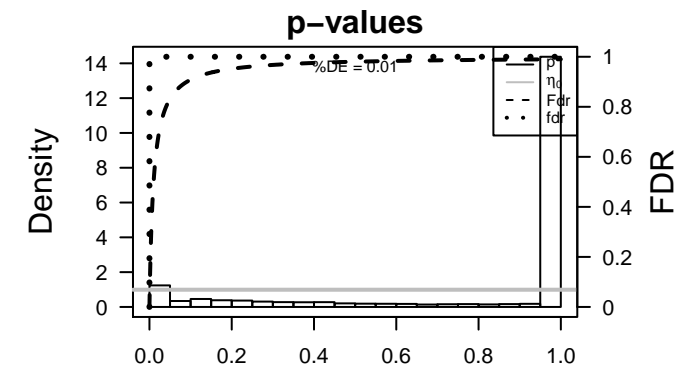


Spot Genelist

Rank	ID	max e	r	min e	Description
1	209351_at	3.74	-0.88	0.79	KRT14 keratin 14 [Source:HGNC Symbol;Acc:HGNC:6416]
2	207935_s_at	3.59	-0.75	0.81	KRT13 keratin 13 [Source:HGNC Symbol;Acc:HGNC:6415]
3	209125_at	3.52	-0.85	0.81	KRT6A keratin 6A [Source:HGNC Symbol;Acc:HGNC:6443]
4	213796_at	3.5	-0.56	0.86	SPRR1A small proline rich protein 1A [Source:HGNC Symbol;Acc:HGNC:6442]
5	214580_x_at	3.41	-0.74	0.79	KRT6A keratin 6A [Source:HGNC Symbol;Acc:HGNC:6443]
6	213240_s_at	3.27	-0.54	0.73	KRT4 keratin 4 [Source:HGNC Symbol;Acc:HGNC:6441]
7	209126_x_at	3.19	-0.85	0.83	KRT6B keratin 6B [Source:HGNC Symbol;Acc:HGNC:6444]
8	218990_s_at	3.14	-0.5	0.8	SPRR3 small proline rich protein 3 [Source:HGNC Symbol;Acc:HGNC:6440]
9	205064_at	3.11	-0.84	0.8	SPRR1B small proline rich protein 1B [Source:HGNC Symbol;Acc:HGNC:6439]
10	204268_at	3.09	-0.94	0.83	S100A2 S100 calcium binding protein A2 [Source:HGNC Symbol;Acc:HGNC:9023]
11	213680_at	2.96	-0.86	0.79	KRT6B keratin 6B [Source:HGNC Symbol;Acc:HGNC:6444]
12	208539_x_at	2.91	-0.65	0.75	SPRR2D small proline rich protein 2D [Source:HGNC Symbol;Acc:HGNC:6441]
13	221854_at	2.91	-0.82	0.55	PKP1 plakophilin 1 [Source:HGNC Symbol;Acc:HGNC:9023]
14	211639_x_at	2.89	-1.23	0.18	immunoglobulin heavy variable 4-34 [Source:HGNC Symbol;Acc:HGNC:9023]
15	205916_at	2.87	-0.49	0.65	S100A7S100 calcium binding protein A7A [Source:HGNC Symbol;Acc:HGNC:9023]
16	205185_at	2.83	-0.74	0.76	SPINK5 serine peptidase inhibitor, Kazal type 5 [Source:HGNC Symbol;Acc:HGNC:6427]
17	205157_s_at	2.82	-0.57	0.73	KRT17 keratin 17 [Source:HGNC Symbol;Acc:HGNC:6427]
18	202504_at	2.8	-1.08	0.69	TRIM29 tripartite motif containing 29 [Source:HGNC Symbol;Acc:HGNC:6427]
19	205595_at	2.76	-0.98	0.7	DSG3 desmoglein 3 [Source:HGNC Symbol;Acc:HGNC:3050]
20	202286_s_at	2.75	-0.69	0.78	TACSTD2 tumor associated calcium signal transducer 2 [Source:HGNC Symbol;Acc:HGNC:6427]

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	1e-99	73 / 105	Refer WIRTH_Mucosa
2	1e-83	67 / 248	GSE/ JAEGER_METASTASIS_DN
3	5e-66	68 / 453	GSE/ ONDER_CDH1_TARGETS_2_DN
4	2e-41	30 / 78	BP cornification
5	1e-38	28 / 72	BP keratinization
6	3e-28	24 / 93	GSE/ CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_UP
7	7e-28	18 / 35	CC cornified envelope
8	1e-26	20 / 57	GSE/ ONDER_CDH1_TARGETS_3_DN
9	1e-25	37 / 422	GSE/ DELYS_THYROID_CANCER_UP
10	4e-25	18 / 46	GSE/ BOSCO_EPITHELIAL_DIFFERENTIATION_MODULE
11	1e-24	21 / 82	GSE/ LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
12	4e-24	18 / 51	GSE/ HUPER_BREAST_BASAL_VS_LUMINAL_UP
13	4e-24	25 / 152	GSE/ COLDREN_GEFITINIB_RESISTANCE_DN
14	4e-23	50 / 1029	GSE/ DODD_NASOPHARYNGEAL_CARCINOMA_UP
15	6e-23	40 / 608	GSE/ SMID_BREAST_CANCER_BASAL_UP
16	7e-22	26 / 208	GSE/ RICKMAN_METASTASIS_DN
17	4e-21	17 / 59	Melan TCGA_melanoma_keratin_high
18	3e-20	58 / 1652	Gliom Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
19	4e-20	20 / 113	GSE/ SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_DN
20	1e-19	27 / 282	GSE/ SMID_BREAST_CANCER_RELAPSE_IN_BONE_DN
21	5e-19	22 / 169	MF structural molecule activity
22	2e-18	22 / 178	GSE/ WU_CELL_MIGRATION
23	2e-18	33 / 516	GSE/ SMID_BREAST_CANCER_LUMINAL_B_DN
24	1e-17	16 / 74	BP epidermis development
25	3e-16	24 / 282	GSE/ RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_DN
26	3e-16	13 / 46	BP keratinocyte differentiation
27	1e-15	19 / 163	GSE/ ONDER_CDH1_TARGETS_1_DN
28	2e-15	28 / 448	Color Lembcke_TCGA_meth_kmeans_J_CIMP_H_DN
29	5e-15	10 / 23	CC desmosome
30	7e-15	23 / 294	GSE/ LEL_MYB_TARGETS
31	8e-15	13 / 58	GSE/ RICKMAN_HEAD_AND_NECK_CANCER_E
32	1e-14	59 / 2239	CC extracellular exosome
33	2e-14	25 / 374	GSE/ CHARAFE_BREAST_CANCER_LUMINAL_VS_BASAL_DN
34	2e-14	12 / 47	GSE/ CROMER_TUMORIGENESIS_DN
35	2e-14	27 / 452	Color Lembcke_TCGA-expr_kmeans_L_CIMP_H_UP_Cluster4_DN
36	2e-14	10 / 26	GSE/ AIGNER_ZEB1_TARGETS
37	4e-14	32 / 677	Refer PROTEINATLAS_esophagus
38	5e-14	14 / 83	GSE/ RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATELY_DN
39	6e-14	10 / 28	BP peptide cross-linking
40	6e-14	17 / 148	GSE/ TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_DUCTAL_NORMAL



Rank	p-value	#in/all	Geneset
1	0.6	1 / 92	HPRVATH_aging_genes_meth_DOWN
2	0.6	1 / 107	TORVATH_aging_genes_meth_UP
3	1.0	0 / 47	HESCHENDORFF_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-41	30 / 78	cornification
2	1e-38	28 / 72	keratinization
3	1e-17	16 / 74	epidermis development
4	3e-16	13 / 46	keratinocyte differentiation
5	6e-14	10 / 28	peptide cross-linking
6	3e-08	5 / 11	hemidesmosome assembly
7	6e-07	9 / 78	negative regulation of peptidase activity
8	7e-07	9 / 104	cell-cell adhesion
9	7e-06	17 / 500	cell adhesion
10	2e-05	4 / 17	hair follicle morphogenesis
11	2e-05	5 / 36	skin development
12	5e-05	15 / 469	proteolysis
13	9e-05	8 / 146	cytoskeleton organization
14	1e-04	6 / 78	wound healing
15	1e-04	3 / 11	thyroid hormone generation

Cancer Rank	p-value	#in/all	Geneset
1	2e-08	1 / 44	LIU_PROSTATE_CANCER_DN
2	6e-04	12 / 409	Lembcke_Normal_vs_Adenoma
3	2e-02	10 / 480	Lembcke_Colonc_Inflammation
4	1e-01	4 / 187	PanCan_Pi3K_geneset_nanostring
5	1e-01	1 / 14	BENTINK_ras6
6	1e-01	3 / 134	PanCan_RAS_geneset_nanostring
7	3e-01	2 / 113	PanCan_Driver_Geneset_nanostring
8	4e-01	1 / 45	KUIPER_MM_poor_survival
9	4e-01	1 / 47	PanCan_TGF-B_geneset_nanostring
10	7e-01	1 / 130	PanCan_CC+Apop_geneset_nanostring
11	8e-01	1 / 147	PanCan_MAPK_geneset_nanostring
12	1e+00	0 / 15	RHODES_CANCER_META_SIGNATURE
13	1e+00	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
14	1e+00	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
15	1e+00	0 / 14	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP

CC Rank	p-value	#in/all	Geneset
1	7e-28	18 / 35	cornified envelope
2	5e-15	10 / 23	desmosome
3	1e-14	15 / 2239	extracellular exosome
4	3e-13	13 / 76	intermediate filament
5	2e-10	43 / 1611	extracellular region
6	6e-08	22 / 595	cell junction
7	2e-07	6 / 27	keratin filament
8	1e-06	56 / 3210	plasma membrane
9	5e-06	37 / 1090	extracellular space
10	9e-05	4 / 25	basal plasma membrane
11	6e-04	4 / 41	intermediate filament cytoskeleton
12	1e-03	3 / 22	anchored component of plasma membrane
13	3e-03	6 / 146	cell-cell junction
14	4e-03	4 / 66	basement membrane
15	5e-03	4 / 73	cell-cell adhesion junction

Chr Rank	p-value	#in/all	Geneset
1	4e-04	8 / 184	Chr 18
2	8e-03	22 / 1325	Chr 1
3	1e-09	15 / 819	Chr 19
4	1e-01	11 / 776	Chr 17
5	1e-01	6 / 369	Chr 20
6	4e-01	9 / 832	Chr 2
7	4e-01	6 / 548	Chr 16
8	5e-01	7 / 661	Chr 6
9	5e-01	7 / 480	Chr 4
10	6e-01	7 / 756	Chr 11
11	7e-01	2 / 242	Chr 13
12	7e-01	4 / 492	Chr 9
13	8e-01	3 / 343	Chr 14
14	8e-01	3 / 437	Chr 8
15	9e-01	3 / 490	Chr 10

Chromatin states Rank	p-value	#in/all	Geneset
1	6e-13	75 / 3734	Tcells_peripheral_blood_13_ReprPC
2	4e-11	52 / 2148	10_ReprPC_Skeletal_Muscle
3	1e-09	6 / 1824	10_ReprPC_Melanocytes
4	2e-09	52 / 2375	10_ReprPC_Fibroblasts
5	2e-09	44 / 1813	8_EnhP_Fibroblasts
6	8e-09	49 / 2254	10_ReprPC_MSC_Adipocyte
7	8e-09	69 / 3318	Tcells_peripheral_blood_14_ReprPCWk
8	3e-06	50 / 2417	8_ReprPCWk_Melanocytes
9	5e-08	65 / 3724	Tcells_peripheral_blood_12_EnhBiv
10	1e-07	54 / 2867	9_ReprPCWk_MSC_Adipocyte
11	2e-07	27 / 922	Overlap_fetal_midbrain_TxTrans
12	2e-07	48 / 2405	Bcells_peripheral_blood_13_ReprPC
13	3e-07	55 / 3011	Bcells_peripheral_blood_14_ReprPCWk
14	3e-07	50 / 2602	natural_killer_cells_peripheral_blood_12_EnhBiv
15	3e-06	23 / 808	Mid_Frontal_Lobe_TssP

Colon Cancer Rank	p-value	#in/all	Geneset
1	2e-15	28 / 448	Lembcke_TCGA_meth_kmeans_J_CIMP_H_DN
2	2e-14	27 / 452	Lembcke_TCGA_epr_kmeans_L_CIMP_H_UP_Cluster4_DN
3	9e-07	18 / 483	Lembcke_TCGA_epr_kmeans_H_CIMP_H_UP_Cluster3_DN
4	7e-06	12 / 255	Kosinski_top_crypt-long-list
5	5e-05	3 / 35	Ang_CRC_Hypermethylated
6	1e-02	9 / 376	Lembcke_TCGA_epr_kmeans_M_CIMP_H_DN
7	2e-02	9 / 397	Pentrack_CRC_TCGA_corr_C_normal_UP
8	2e-02	2 / 20	Kosinski_top_crypt-short-list
9	2e-02	18 / 1083	LaPointe_mucosa-position_kmeans_J_cecum_colon_ascending_colon_transv
10	3e-02	7 / 137	Pentrack_CRC_TCGA_group_over_B_msi-h_UP
11	7e-02	1 / 7	Budinska_C_CIMP-H-like_UP
12	8e-02	1 / 8	Marisa_CRC-C3
13	9e-02	4 / 172	Pentrack_CRC_TCGA_corr_U_msi-h_UP
14	9e-02	1 / 10	Budinska_E_Mixed_UP
15	2e-01	4 / 221	Lembcke_TCGA_meth_kmeans_A_Cluster4_DN

Glioma Rank	p-value	#in/all	Geneset
1	3e-20	58 / 1652	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
2	5e-10	21 / 414	Hopp_Sturm_GBM_Epi3_A_adult_fetus_UP_G34_DN
3	1e-09	17 / 273	Hopp_Sturm_GBM_Epi3_B_adult_UP_G34_DN
4	5e-07	7 / 50	Christensen_hypermethylated_in_primary_glioblastoma
5	1e-06	6 / 36	Christensen_hypermethylated_in_ependymoma
6	3e-05	6 / 61	Christensen_hypermethylated_in_secondary_glioblastoma
7	8e-05	8 / 144	Christensen_hypermethylated_in_grade2_oligodendroglioma
8	1e-03	5 / 85	Scov_O_999_Sturm_E2_IDH_DN
9	2e-03	5 / 87	Christensen_hypermethylated_in_secondary_glioblastoma
10	2e-03	5 / 132	Christensen_hypermethylated_in_grade3_oligoastrocytoma
11	5e-03	5 / 114	Christensen_hypermethylated_in_grade2_oligoastrocytoma
12	7e-03	3 / 41	Hopp_Sturm_GBM_Epi3_C1_IDH_UP_fetus_DN
13	8e-03	4 / 82	laffaire_hypermeth_LGG_vs_control
14	1e-02	4 / 86	Sturm_GBM_Meth_overexpression_B_adult_UP
15	1e-02	3 / 53	Christensen_hypermethylated_in_primary_glioblastoma

GSEA C2 Rank	p-value	#in/all	Geneset
1	1e-83	67 / 248	JAEGER_METASTASIS_DN
2	5e-66	68 / 453	ONDER_CDH1_TARGETS_2_DN
3	3e-28	24 / 93	CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_UP
4	1e-26	20 / 57	CDH1_TARGETS_3_DN
5	3e-25	37 / 422	DELVS_THYROID_CANCER_UP
6	4e-25	18 / 46	BOSCO_EPITHELIAL_DIFFERENTIATION_MODULE
7	1e-24	21 / 82	LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
8	4e-24	18 / 51	HUPPER_BREAST_BASAL_VS_LUMINAL_UP
9	4e-24	25 / 152	COLDREN_GEFITINIB_RESISTANCE_DN
10	4e-23	40 / 1029	ODDER_NASOPHARYNGEAL_CARCINOMA_UP
11	6e-23	40 / 608	SMID_BREAST_CANCER_BASAL_UP
12	7e-22	26 / 208	RICKMAN_METASTASIS_DN
13	4e-20	20 / 113	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_DN
14	1e-19	27 / 282	SMID_BREAST_CANCER_RELAPSE_IN_BONE_DN
15	2e-18	22 / 178	WU_CELL_MIGRATION

LM Rank	p-value	#in/all	Geneset
1	5e-08	13 / 193	HALLMARK_ESTROGEN_RESPONSE_LATE
2	5e-08	13 / 195	HALLMARK_KRAS_SIGNALING_DN
3	3e-06	11 / 194	HALLMARK_ESTROGEN_RESPONSE_EARLY
4	1e-04	9 / 191	HALLMARK_P53_PATHWAY
5	2e-03	7 / 174	HALLMARK_APICAL_JUNCTION
6	1e-04	4 / 130	HALLMARK_KRAS_SIGNALING_UP
7	4e-02	4 / 130	HALLMARK_COAGULATION
8	4e-02	2 / 34	HALLMARK_APICAL_SURFACE
9	2e-01	3 / 170	HALLMARK_IL2_STATS_SIGNALING
10	2e-01	2 / 187	HALLMARK_BILE_ACID_METABOLISM
11	3e-01	3 / 181	HALLMARK_XENOBIOTIC_METABOLISM
12	3e-01	3 / 182	HALLMARK_GLYCOLYSIS
13	3e-01	1 / 34	HALLMARK_ANGIOGENESIS
14	3e-01	3 / 196	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
15	4e-01	2 / 139	HALLMARK_FATTY_ACID_METABOLISM

Immunome Rank	p-value	#in/all	Geneset
1	0.01	2 / 19	Angelova_immune-metagene-IDC
2	0.25	2 / 29	Angelova_immune-metagene-Th1
3	0.31	1 / 38	Angelova_immune-metagene-mast-cells
4	1.00	0 / 13	Angelova_immune-metagene-activated_B-cells
5	1.00	0 / 26	Angelova_immune-metagene-activated_CD4
6	1.00	0 / 19	Angelova_immune-metagene-activated_CD8
7	1.00	0 / 21	Angelova_immune-metagene-central_memory_CD4
8	1.00	0 / 17	Angelova_immune-metagene-central_memory_CD8
9	1.00	0 / 7	Angelova_immune-metagene-cytotoxic_cells
10	1.00	0 / 25	Angelova_immune-metagene-DC
11	1.00	0 / 12	Angelova_immune-metagene-effector_memory_CD4
12	1.00	0 / 32	Angelova_immune-metagene-effector_memory_CD8
13	1.00	0 / 14	Angelova_immune-metagene-eosinophil
14	1.00	0 / 13	Angelova_immune-metagene-immature_B-cells
15	1.00	0 / 11	Angelova_immune-metagene-macrophages

Lifestyle Rank	p-value	#in/all	Geneset
1	0.04	1 / 4	DUMEAUX_Exercise_in_non_smokers_literature_enriched_genes
2	0.09	1 / 10	DUMEAUX_Smoking_literature_genes_up
3	0.45	1 / 62	DUMEAUX_Smoking_enriched_genes
4	1.00	0 / 5	DUMEAUX_Estrogen_related_in_smokers_literature_genes_up
5	1.00	0 / 7	DUMEAUX_Estrogen_related_in_non_smokers_literature_genes_up
6	1.00	0 / 18	DUMEAUX_Hormon_therapy_in_non_smokers_literature_genes_up
7	1.00	0 / 9	DUMEAUX_Monocytes_in_smokers_literature_genes_up
8	1.00	0 / 16	DUMEAUX_Red_blood_cells_in_non_smokers_literature_genes_up
9	1.00	0 / 12	DUMEAUX_Women_normal_BMI_literature_genes_up
10	1.00	0 / 22	DUMEAUX_High_bmi_enriched_genes
11	1.00	0 / 22	DUMEAUX_Fasting_enriched_genes
12	1.00	0 / 150	Homuth_BMI-associated_genes_UP
13	1.00	0 / 210	Homuth_BMI-associated_genes_DN
14	1.00	0 / 14	Huan_blood-pressure_SBP-signature
15	1.00	0 / 13	Huan_blood-pressure_DBP-signature

Lymphoma Rank	p-value	#in/all	Geneset
1	3e-07	9 / 94	Hopp_Lymphoma_Epi1_with_zentr_iii_B_cell_GCB_UP
2	7e-07	56 / 3168	Jeonsson_Repressed
3	4e-05	3 / 10	Hopp_Lymphoma_Epi1_no_zentr_5_B_cell_GCB_UP
4	1e-03	4 / 46	Subero_DLBCL_hypo_meth
5	1e-03	4 / 47	Subero_B-ALL_hyper_meth
6	4e-04	4 / 54	Hopp_Lymphoma_Epi1_no_zentr_1_B_cell_DN
7	2e-03	4 / 56	Hopp_Lymphoma_Epi1_with_zentr_iv_B_cell_MM_UP
8	6e-03	33 / 2206	HOPP_Heterochrom
9	3e-02	3 / 70	Subero_FL_hyper_meth
10	3e-02	8 / 378	TARTE_Mature_plasma_cell_signature
11	4e-02	4 / 132	Subero_DLBCL_hyper_meth
12	4e-02	2 / 33	Subero_T-PILL_hypo_meth
13	5e-02	3 / 87	Hopp_Lymphoma_Epi1_with_zentr_v_B_cell_DN
14	6e-02	5 / 214	LENZ_Stromal_signature_1
15	6e-02	25 / 1894	HOPP_Poised_promoter

Melanoma Rank	p-value	#in/all	Geneset
1	4e-21	17 / 59	TCGA_melanoma_keratin_high
2	8e-13	7 / 10	Jeonsson_Melanoma_Normal_like_subtype
3	2e-09	7 / 24	Gerami_melanoma-metastatic-risk_DN
4	3e-04	8 / 171	Landsberg_dedifferentiation_up
5	4e-04	5 / 64	Harbst_melanoma_lowgrade_up
6	3e-02	4 / 119	TCGA_melanoma_MITF_low
7	3e-02	1 / 3	Gerami_melanoma-metastatic-risk_UP
8	1e-01	1 / 16	Hugo_melanoma-all_UP
9	2e-01	2 / 75	Tirosh_Endothelial-cell_specific_genes-melanoma
10	2e-01	2 / 85	Tirosh_AXL-signature
11	2e-01	4 / 249	Gerber_wt_wt_melanoma-cells-SpotE
12	3e-01	1 / 39	Tirosh_melanoma_specific_genes
13	3e-01	1 / 78	Tirosh_CAF-cell_specific_genes
14	5e-01	1 / 81	Tirosh_Genes_in_the_MITF_program
15	8e-01	1 / 185	Tirosh_genes_from_malignant_cells_in_Mel79-melanoma

MF Rank	p-value	#in/all	Geneset
1	5e-19	22 / 169	structural_molecule_activity
2	3e-09	13 / 154	serine-type_endopeptidase_activity
3	5e-08	9 / 77	peptidase_inhibitor_activity
4	6e-08	10 / 104	serine-type_peptidase_activity
5	4e-07	9 / 96	structural_constituent_of_cytoskeleton
6	2e-06	7 / 61	serine-type_endopeptidase_inhibitor_activity
7	1e-05	4 / 15	transition_metal_ion_binding
8	2e-05	14 / 374	peptidase_activity
9	9e-05	4 / 25	cysteine-type_endopeptidase_inhibitor_activity
10	1e-04	3 / 11	structural_constituent_of_epidermis
11	1e-04	15 / 517	calcium_ion_binding
12	2e-04	3 / 12	interleukin-1_receptor_binding
13	2e-04	5 / 65	chloride_channel_activity
14	7e-04	5 / 74	protein_biding_bridging
15	1e-03	5 / 86	metalloendopeptidase_activity

miRNA target Rank	p-value	#in/all	Geneset
1	0.01	2 / 18	hsa-miR-591
2	0.05	2 / 35	hsa-miR-331-5p
3	0.11	1 / 12	hsa-miR-1234
4	0.12	2 / 61	hsa-miR-939
5	0.14	1 / 15	hsa-miR-551b
6	0.16	1 / 16	hsa-miR-551a
7	0.14	1 / 16	hsa-miR-564
8	0.15	1 / 17	hsa-miR-151-5p
9	0.18	3 / 70	hsa-miR-98b
10	0.19	2 / 83	hsa-miR-513b
11	0.20	1 / 23	hsa-miR-521
12	0.20	2 / 86	hsa-miR-1259
13	0.21	2 / 88	hsa-miR-600
14	0.21	2 / 89	hsa-miR-526b

Correlation Cluster

Spot Summary: B

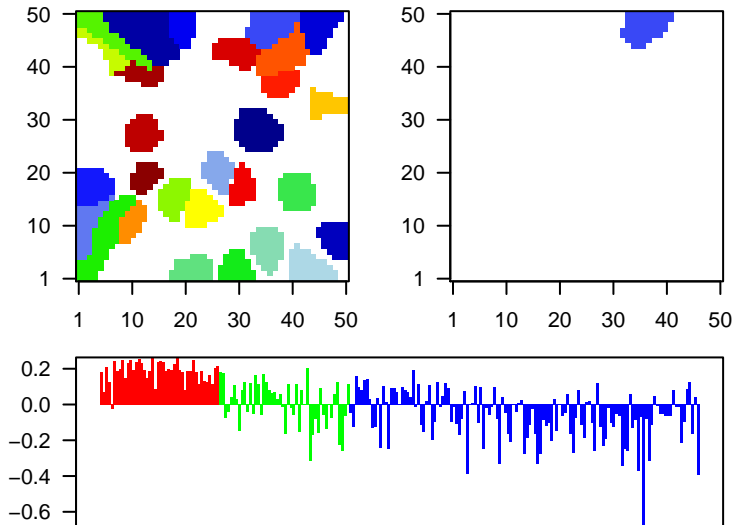
metagenes = 51
genes = 734

<r> metagenes = 0.94
<r> genes = 0.31
beta: r2= 5.75 / log p= -Inf

samples with spot = 43 (19.5 %)
mBL : 35 (79.5 %)
intermediate : 5 (10.4 %)
non-mBL : 3 (2.3 %)

Overview Map

Spot

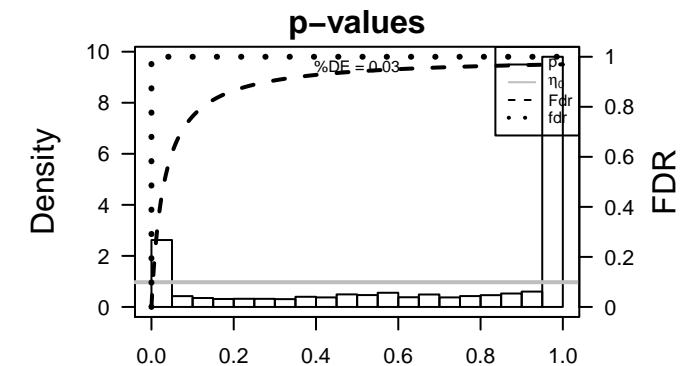


Spot Genelist

Rank	ID	max e	r	min e	Description
1	206023_at	2.55	-1.15	0.18	NMU neuromedin U [Source:HGNC Symbol;Acc:HGNC:7859]
2	205190_at	1.86	-1.09	0.49	PLS1 plastin 1 [Source:HGNC Symbol;Acc:HGNC:9090]
3	205229_s_at	1.84	-2.18	0.37	COCH cochlin [Source:HGNC Symbol;Acc:HGNC:2180]
4	209980_s_at	1.66	-1.51	0.74	SHMT1 serine hydroxymethyltransferase 1 [Source:HGNC Symbol;Acc:HGNC:10805]
5	212436_at	1.64	-1.2	0.32	TRIM33 tripartite motif containing 33 [Source:HGNC Symbol;Acc:HGNC:15512]
6	219474_at	1.6	-1.32	0.49	C3orf52 chromosome 3 open reading frame 52 [Source:HGNC Symbol;Acc:HGNC:19112]
7	206940_s_at	1.59	-0.88	0.26	POU4F1 POU class 4 homeobox 1 [Source:HGNC Symbol;Acc:HGNC:9050]
8	218507_at	1.58	-1.34	0.21	HILPDA hypoxia inducible lipid droplet associated [Source:HGNC Symbol;Acc:HGNC:19112]
9	217127_at	1.5	-1.12	0.41	CTH cystathionine gamma-lyase [Source:HGNC Symbol;Acc:HGNC:2180]
10	219733_s_at	1.48	-1.19	0.47	SLC27A5 solute carrier family 27 member 5 [Source:HGNC Symbol;Acc:HGNC:15512]
11	214519_s_at	1.47	-1.06	0.34	RLN2 relaxin 2 [Source:HGNC Symbol;Acc:HGNC:10027]
12	204720_s_at	1.4	-1.15	0.38	DNAJC6 DnaJ heat shock protein family (Hsp40) member C6 [Source:HGNC Symbol;Acc:HGNC:2180]
13	213610_s_at	1.38	-1.42	0.48	KLHL23 kelch like family member 23 [Source:HGNC Symbol;Acc:HGNC:15512]
14	219763_at	1.3	-1.3	0.34	DENND1B DENN domain containing 1B [Source:HGNC Symbol;Acc:HGNC:15512]
15	219034_at	1.29	-1.33	0.38	PARP16 poly(ADP-ribose) polymerase family member 16 [Source:HGNC Symbol;Acc:HGNC:15512]
16	204001_at	1.26	-1.33	0.38	SNAPC3 small nuclear RNA activating complex polypeptide 3 [Source:HGNC Symbol;Acc:HGNC:15512]
17	206047_at	1.24	-1.27	0.31	GNB3 G protein subunit beta 3 [Source:HGNC Symbol;Acc:HGNC:2180]
18	201791_s_at	1.24	-1.39	0.33	DHCR7 7-dehydrocholesterol reductase [Source:HGNC Symbol;Acc:HGNC:2180]
19	204430_s_at	1.22	-1.69	0.24	SLC2A5 solute carrier family 2 member 5 [Source:HGNC Symbol;Acc:HGNC:15512]
20	205164_at	1.22	-1.07	0.31	GCAT glycine C-acetyltransferase [Source:HGNC Symbol;Acc:HGNC:2180]

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	1e-99	92 / 115	Gliom WILLSCHEER_GBM_Verhaak-CL-up (C)
2	1e-99	177 / 319	Melar Gerber_wt/wt_melanoma-cells-SpotA
3	1e-99	262 / 966	GSE# KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
4	1e-99	105 / 137	GSE# ROBY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
5	1e-99	146 / 244	GSE# KOBAYASHI_EGFR_SIGNALING_24HR_DN
6	1e-99	128 / 254	GSE# DUTERTRE ESTRADIOL_RESPONSE_24HR_UP
7	1e-99	174 / 431	GSE# GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
8	4e-98	158 / 439	GSE# SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
9	6e-93	166 / 526	GSE# MARSON_BOUND_BY_E2F4_UNSTIMULATED
10	2e-91	12 / 14	Cancr SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
11	2e-91	12 / 14	Cancr SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
12	2e-90	125 / 280	GSE# MANALO_HYPOXIA_DN
13	1e-85	219 / 1052	GSE# DODD_NASOPHARYNGEAL_CARCINOMA_DN
14	1e-84	183 / 726	GSE# PUJANA_CHEK2_PCC_NETWORK
15	8e-82	97 / 174	GSE# GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP
16	2e-80	99 / 187	HM HALLMARK_E2F_TARGETS
17	1e-79	105 / 219	Refer WIRTH_GC B-cells
18	4e-79	159 / 575	GSE# CAIRO_HEPATOBLASTOMA_CLASSES_UP
19	9e-78	134 / 400	GSE# PUJANA_BRCA2_PCC_NETWORK
20	2e-76	104 / 226	GSE# ZHANG_TLX_TARGETS_60HR_DN
21	1e-74	119 / 321	GSE# BLUM_RESPONSE_TO_SALIRASIB_DN
22	5e-74	175 / 758	GSE# NUYTEN_EZH2_TARGETS_DN
23	4e-71	129 / 409	Cancr Lembcke_Normal vs Adenoma
24	4e-69	241 / 1527	GSE# PUJANA_BRCA1_PCC_NETWORK
25	1e-68	63 / 79	Melar Tirosh_core cycling genes in low- and high-proliferation melanoma
26	4e-67	161 / 703	GSE# LEE_BMP2_TARGETS_DN
27	6e-67	110 / 307	GSE# VECCHI_GASTRIC_CANCER_EARLY_UP
28	7e-66	66 / 93	GSE# CROONQUIST_IL6_DEPRIVATION_DN
29	2e-65	131 / 466	GSE# BERENJENO_TRANSFORMED_BY_RHOA_UP
30	6e-65	478 / 5529	Lymp HOPP_Txn_elongation
31	2e-63	71 / 117	GSE# CHANG_CYCLING_GENES
32	3e-63	139 / 548	GSE# BENPORATH_CYCLING_GENES
33	3e-59	101 / 294	GSE# WONG_EMBRYONIC_STEM_CELL_CORE
34	2e-58	59 / 84	GSE# GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
35	2e-56	90 / 241	GSE# BASAKI_YBX1_TARGETS_UP
36	5e-56	77 / 169	GSE# FUJII_YBX1_TARGETS_DN
37	8e-56	141 / 641	GSE# CASORELLI_ACUTE_PROMYELOCYTIC_LEUKEMIA_DN
38	8e-56	126 / 509	GSE# RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_UP
39	1e-55	53 / 70	GSE# CROONQUIST_NRAS_SIGNALING_DN
40	5e-55	81 / 195	HM HALLMARK_G2M_CHECKPOINT



Rank	p-value	#in/all	Geneset
1	0.08	9 / 107	HORVATH_aging_genes_meth_UP
2	0.83	3 / 82	HORVATH_aging_genes_meth_DOWN
3	1.00	0 / 47	TSCHEMDORFF_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	

Rank	p-value	#in/all	Geneset
1	5e-40	266 / 2541	nucleoplasm
2	5e-37	378 / 4579	nucleus
3	1e-34	67 / 324	chromosome
4	2e-21	38 / 118	chromosome, centromeric region
5	1e-19	90 / 653	nucleolus
6	7e-19	29 / 77	condensed chromosome kinetochore
7	5e-18	32 / 101	kinetochore
8	4e-15	56 / 354	cytoplasm
9	2e-14	3 / 157	spindle
10	4e-13	117 / 1221	mitochondrion
11	2e-11	263 / 3805	cytosol
12	3e-11	24 / 98	spindle pole
13	1e-09	302 / 4701	centrosome
14	2e-09	39 / 277	mitochondrial matrix
15	3e-09	40 / 292	microtubule organizing center

Rank	p-value	#in/all	Geneset
1	2e-21	47 / 184	Kosinski_lower-crypt-long-list
2	2e-17	78 / 561	Pentrack_CRC_TCGA_over_C_normal_DN
3	4e-13	73 / 602	Pentrack_CRC_TCGA_corr_R_normal_DN
4	1e-04	117 / 1729	LaPointe_mucosa-position_kmeans_G_cecum_colon_ascending_colon_UP_1t
5	3e-03	6 / 33	Kosinski_lower-crypt-short-list
6	4e-03	4 / 14	Hewish_dMMR-secondary-mutations_DNA-repair
7	4e-03	87 / 1354	LaPointe_mucosa-position_kmeans_N_cecum_colon_ascending_colon_UP_a
8	2e-02	3 / 12	Juehling-MSI-enriched-in-6
9	4e-02	36 / 539	Lembcke_TCGA_meth_kmeans_L_CIMP_H_DN
10	5e-02	3 / 16	Boland_CRC-MSI-A6-A10
11	5e-02	2 / 8	Boland_CRC-MMR-system
12	1e-01	1 / 2	Hewish_dMMR-secondary-mutations_Cell-motility
13	1e-01	1 / 2	Hewish_dMMR-secondary-mutations_Damage_signaling
14	3e-01	1 / 6	Marisa_CRC-C6
15	3e-01	62 / 1174	LaPointe_mucosa-position_kmeans_E_transverse_colon_UP_transverse_colo

Rank	p-value	#in/all	Geneset
1	2e-80	99 / 187	HALLMARK_E2F_TARGETS
2	5e-55	81 / 195	HALLMARK_G2M_CHECKPOINT
3	2e-15	40 / 190	HALLMARK_MYC_TARGETS_V1
4	6e-11	32 / 173	HALLMARK_MITOTIC_SPINDLE
5	4e-09	16 / 55	HALLMARK_MYC_TARGETS_V2
6	2e-08	14 / 133	HALLMARK_DNA_REPAIR
7	2e-06	26 / 192	HALLMARK_MTORC1_SIGNALING
8	3e-04	16 / 122	HALLMARK_SPERMATOGENESIS
9	6e-04	20 / 182	HALLMARK_GLYCOLYSIS
10	1e-02	17 / 186	HALLMARK_OXIDATIVE_PHOSPHORYLATION
11	5e-02	15 / 193	HALLMARK_ESTROGEN_RESPONSE_LATE
12	7e-02	6 / 59	HALLMARK_CHOLESTEROL_HOMEOSTASIS
13	7e-02	9 / 106	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
14	2e-01	7 / 97	HALLMARK_PEROXISOME
15	2e-01	11 / 174	HALLMARK_ADIPOGENESIS

Rank	p-value	#in/all	Geneset
1	6e-65	478 / 5529	HOPP_Txn_elongation
2	4e-52	78 / 192	Victoria_Dark_zone_signature
3	5e-51	453 / 5308	HOPP_Active_promoter
4	9e-40	83 / 305	TARTE_Plasmablast_signature
5	3e-32	350 / 4261	HOPP_Txn_transition
6	1e-12	365 / 5682	HOPP_Weak_promoter
7	3e-11	94 / 955	SPANG_BCR_UP
8	4e-9	24 / 99	Sha_BL_UP
9	9e-06	317 / 5404	HOPP_Strong_enhancer
10	3e-05	19 / 135	DAVE_BL-vs-DLBCL
11	3e-05	16 / 102	ROSLOWSKI_blue_total
12	3e-03	11 / 85	Aukema_BCL2_DN_BCL6_UP
13	1e-02	7 / 42	Mont_OxPhos_cluster
14	4e-03	7 / 40	CARO_OxPhos_in_DLBCL_UP
15	1e-02	239 / 4357	HOPP_Weak_txn

Rank	p-value	#in/all	Geneset
1	9e-05	8 / 31	hsa-miR-661
2	5e-04	10 / 59	hsa-miR-651
3	2e-03	26 / 285	hsa-miR-546b-5p
4	3e-03	17 / 167	hsa-miR-432
5	5e-03	21 / 232	hsa-miR-186
6	5e-03	5 / 24	hsa-miR-197
7	7e-03	11 / 95	hsa-miR-376a
8	7e-03	10 / 83	hsa-miR-513b
9	7e-03	7 / 47	hsa-miR-151-3p
10	7e-03	17 / 181	hsa-miR-520g
11	9e-03	8 / 61	hsa-miR-619
12	1e-02	11 / 100	hsa-miR-493
13	1e-02	7 / 50	hsa-miR-384
14	1e-02	23 / 284	hsa-miR-546b-5p
15	1e-02	8 / 64	hsa-miR-1261

Rank	p-value	#in/all	Geneset
1	0.002	6 / 27	Nabetani_all_ten_telomeres_genes_ks
2	0.003	4 / 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	

Rank	p-value	#in/all	Geneset
1	1e-41	108 / 497	cell cycle
2	2e-39	83 / 307	cell division
3	2e-35	54 / 137	DNA replication
4	4e-25	37 / 91	sister chromatid cohesion
5	1e-20	57 / 281	DNA repair
6	8e-16	15 / 21	mitotic sister chromatid segregation
7	3e-15	56 / 351	cellular response to DNA damage stimulus
8	9e-15	24 / 70	chromosome segregation
9	3e-14	14 / 21	telomere maintenance via semi-conservative replication
10	1e-13	16 / 31	DNA replication initiation
11	2e-13	27 / 101	mitotic cell cycle
12	6e-12	10 / 14	chromosome condensation
13	8e-11	14 / 32	DNA synthesis involved in DNA repair
14	3e-10	22 / 91	G1/S transition of mitotic cell cycle
15	1e-09	10 / 17	spindle organization

Rank	p-value	#in/all	Geneset
1	3e-04	35 / 382	Chr 15
2	3e-04	92 / 1325	Chr 1
3	4e-02	49 / 72	Chr 17
4	6e-02	32 / 490	Chr 10
5	8e-02	17 / 242	Chr 13
6	1e-01	33 / 548	Chr 16
7	1e-01	29 / 480	Chr 4
8	2e-01	26 / 437	Chr 8
9	2e-01	20 / 333	Chr 22
10	2e-01	42 / 756	Chr 11
11	2e-01	9 / 139	Chr 21
12	2e-01	13 / 403	Chr 14
13	3e-01	11 / 164	Chr 18
14	3e-01	27 / 492	Chr 9
15	6e-01	33 / 700	Chr 12

Rank	p-value	#in/all	Geneset
1	1e-99	92 / 115	WILLSCHER_GBM_Verhaak-CL_up (C)
2	6e-21	25 / 47	developing astrocytes
3	2e-15	24 / 66	Weller_LGG_gradIII-vs-III_DOWN
4	7e-13	136 / 1523	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
5	1e-12	124 / 1343	Hopp_Sturm_GBM_Epi3_zentr_6_fetus_UP
6	8e-04	48 / 614	Sturm_GBM_Meth_overexpression_E_G34_UP
7	7e-03	8 / 58	Stuehler_Proteins_up_in_STS
8	1e-02	8 / 64	cultured astroglia vs. in vivo astrocytes
9	8e-02	2 / 10	WILLSCHER_GBM_LTSmut_proteomics-B_UP
10	1e-02	5 / 49	OPC
11	1e-01	1 / 2	Philips Prolif up vs PN & MES
12	3e-01	2 / 21	Barbus_GBM_STS_vs_LTS
13	3e-01	2 / 22	Sturm_GBM_Meth_overexpression_H_K27_UP
14	5e-01	1 / 13	WILLSCHER_GBM_STSwt_proteomics-O_UP
15	5e-01	2 / 34	WILLSCHER_GBM_proteomics_wtOnly_SpotH

Rank	p-value	#in/all	Geneset
1	8e-22	20 / 25	Angelova Immune-metagenes-activated CD4
2	2e-05	19	Angelova Immune-metagenes-activated CD8
3	1e-01	2 / 12	Angelova Immune-metagenes-effector_memory_CD4
4	1e-01	2 / 12	Angelova Immune-metagenes-memory_B-cells
5	4e-01	1 / 10	Angelova Immune-metagenes-neutrophils
6	1e-01	2 / 38	Angelova Immune-metagenes-mast-cells
7	6e-01	1 / 18	Angelova Immune-metagenes-pDC
8	9e-01	1 / 45	Angelova Immune-metagenes-MDSC
9	1e+00	0 / 13	Angelova Immune-metagenes-activated_B-cells
10	1e+00	0 / 21	Angelova Immune-metagenes-central_memory_CD4
11	1e+00	0 / 17	Angelova Immune-metagenes-central_memory_CD8
12	1e+00	0 / 7	Angelova Immune-metagenes-cytotoxic_cells
13	1e+00	0 / 25	Angelova Immune-metagenes-DC
14	1e+00	0 / 32	Angelova Immune-metagenes-effector_memory_CD8
15	1e+00	0 / 14	Angelova Immune-metagenes-eosinophil

Rank	p-value	#in/all	Geneset
1	1e-99	177 / 319	Gerber_wtwt_melanoma-cells-SpotA
2	1e-68	63 / 79	Tirosh_core_cycling_genes_in_low- and high-proliferation melanoma
3	1e-48	40 / 44	Tirosh_top50 correlated genes PC2
4	3e-38	36 / 47	Tirosh_G2/M phase specific genes
5	6e-31	29 / 38	Tirosh_G1/S phase specific genes
6	1e-15	24 / 65	Harbst_melanoma_highgrade_up
7	5e-04	27 / 276	Gerber_wtwt_melanoma-cells-SpotB
8	2e-04	8 / 46	Tirosh_top50 correlated genes PC5
9	2e-01	1 / 4	Melanoma Epi-Enzyme Cluster 3
10	2e-01	1 / 4	Melanoma Epi-Enzyme Cluster 5
11	6e-01	2 / 38	Tirosh_top50 correlated genes PC1
12	6e-01	4 / 81	Tirosh_Genes_in the MITF program
13	1e-01	4 / 107	Tirosh_Exhaustion program in Met/5
14	8e-01	10 / 249	Gerber_wtwt_melanoma-cells-SpotE
15	8e-01	3 / 85	Tirosh_AXL-signature

Rank	p-value	#in/all	Geneset
1	0.006	14 / 135	Terre_MSV_multiple_respiratory_viruses_up
2	0.387	7 / 122	Terre_IMS_influenza_meta_signature
3	0.514	9 / 179	Terre_MSV_multiple_respiratory_viruses_dn
4	0.748	2 / 7	Burnham_timecourse
5	0.775	2 / 57	Burnham_day1_vs_5_UP
6	0.926	1 / 52	Burnham_day1_vs_5_DN
7	0.943	1 / 57	Burnham_viral_UP
8	0.972	1 / 71	Burnham_cap_fp_vs_con_UP
9	0.008	0 / 68	Burnham_sep_vs_con_UP
10	1.000	0 / 56	Burnham_sep_vs_con_DN
11	1.000	0 / 48	Burnham_cap_fp_vs_con_DN
12	1.000	0 / 48	Burnham_viral_DN
13	1.000	0 / 18	Scicluna_UP
14	1.000	0 / 41	Scicluna_DN
15	1.000	0 / 37	Sweeney_viral_up

Rank	p-value	#in/all	Geneset
1	1e-22	141 / 1241	KIM_MYC_targets
2	7e-16	266 / 3564	ICGC_Taf1_targets
3	1e-14	239 / 3150	ICGC_Creb1_targets
4	7e-12	106 / 1107	ICGC_Myc_targets
5	2e-10	258 / 3796	ICGC_Nficsb1335_targets
6	3e-10	256 / 3769	ICGC_Pmlsc71910_targets
7	2e-09	245 / 3630	ICGC_Sp1_targets
8	2e-09	254 / 3804	ICGC_Stat5_targets
9	2e-08	239 / 3608	ICGC_Tcf12_targets
10	2e-08	244 / 3703	ICGC_Foxm1_targets
11	1e-08	18 / 62	MYC_targets_UP
12	6e-08	289 / 4602	ICGC_Elf1_targets
13	1e-07	92 / 1089	ICGC_Ets1_targets
14	1e-07	227 / 3451	ICGC_Atf2_targets
15	1e-07	225 / 3420	ICGC_Bclaf101388_targets

Rank	p-value	#in/all	Geneset
1	2e-91	12 / 14	SOTTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
2	4e-71	129 / 409	Lembcke_Normal_vs_Adenoma
3	4e-24	7 / 15	RHODES_UNDIFFERENTIATED_CANCER
4	3e-13	12 / 16	WOLFER_overlap_genes
5	4e-09	14 / 41	PanCan_DNARepair_geneset_nanostring
6	1e-08	16 / 58	SHUAUJHNESSY_MM_high_risk
7	1e-07	13 / 45	KUIPER_poor_survival
8	2e-05	1 / 15	RHODES_CANCER_META_SIGNATURE
9	5e-05	6 / 15	GENTLES_modul2
10	2e-04	17 / 130	PanCan_CC+Apop_geneset_nanostring
11	9e-04	4 / 10	GENTLES_modul3
12	9e-04	4 / 10	GENTLES_modul5
13	3e-03	4 / 13	GENTLES_modul1
14	5e-03	4 / 15	BEN-PORATH_UP
15	6e-03	4 / 16	GENTLES_modul6

Rank	p-value	#in/all	Geneset
1	5e-74	589 / 7957	Tcells_peripheral_blood_2_TssAFink
2	5e-72	595 / 8200	monocytes_peripheral_blood_2_TssAFink
3	5e-72	593 / 8245	regulatory_cells_peripheral_blood_2_TssAFink
4	3e-69	598 / 8406	Bcells_peripheral_blood_2_TssAFink
5	1e-67	595 / 8370	natural_killer_cells_peripheral_blood_2_TssAFink
6	3e-65	574 / 7833	Bcells_peripheral_blood_1_Tssa
7	1e-64	566 / 7635	monocytes_peripheral_blood_1_Tssa
8	3e-64	576 / 7430	regulatory_cells_peripheral_blood_1_Tssa
9	2e-63	604 / 8816	Thelper_cells_peripheral_blood_2_TssAFink
10	1e-62	591 / 8431	T_CD8+_naive_cells_peripheral_blood_2_TssAFink
11	3e-62	587 / 8322	T_CD8+_naive_cells_peripheral_blood_1_Tssa
12	5e-61	498 / 6099	HSC_4_Tx
13	5e-59	13 / 6068	Thelper_cells_peripheral_blood_1_Tssa
14	3e-57	560 / 775	natural_killer_cells_peripheral_blood_1_Tssa
15	2e-55	593 / 8766	2_Tssa_Melanocytes

Rank	p-value	#in/all	Geneset
1	1e-99	262 / 966	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
2	1e-99	105 / 137	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
3	1e-99	146 / 244</	

Correlation Cluster

Spot Summary: C

metagenes = 30
genes = 155

<r> metagenes = 0.96
<r> genes = 0.19
beta: r2= 1.13 / log p= -Inf

samples with spot = 0 (0 %)

Spot Genelist

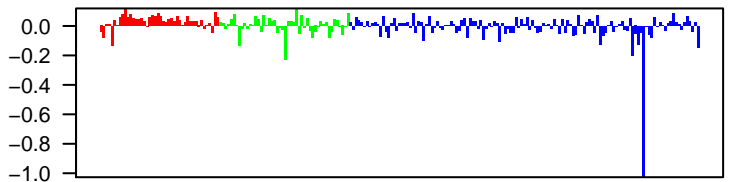
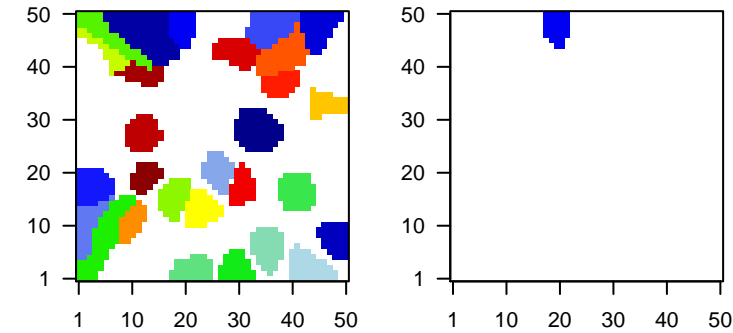
Rank	ID	max e	r	min e	Description
1	205414_s_at	1.45	-0.96	0.25	ARHGAP40 GTPase activating protein 44 [Source:HGNC Symbol;Acc:HGNC:2419]
2	203067_at	1.41	-0.69	0.36	PDHX pyruvate dehydrogenase complex component X [Source:HGNC Symbol;Acc:HGNC:2419]
3	32128_at	1.12	-1.78	0.32	CCL18 C-C motif chemokine ligand 18 [Source:HGNC Symbol;Acc:HGNC:2419]
4	209924_at	1.04	-2.14	0.37	CCL18 C-C motif chemokine ligand 18 [Source:HGNC Symbol;Acc:HGNC:2419]
5	200862_at	1.02	-1.6	0.21	DHCR2424-dehydrocholesterol reductase [Source:HGNC Symbol;Acc:HGNC:2419]
6	222209_s_at	1.01	-1.35	0.41	TMEM138 transmembrane protein 135 [Source:HGNC Symbol;Acc:HGNC:2419]
7	213189_at	0.97	-1.21	0.42	RIOX2 ribosomal oxygenase 2 [Source:HGNC Symbol;Acc:HGNC:2419]
8	221189_s_at	0.92	-1.05	0.37	TARS2 threonyl-tRNA synthetase 2, mitochondrial [Source:HGNC Symbol;Acc:HGNC:2419]
9	201937_s_at	0.84	-1.7	0.41	DNPEP aspartyl aminopeptidase [Source:HGNC Symbol;Acc:HGNC:2419]
10	202950_at	0.82	-1.51	0.33	CRYZ crystallin zeta [Source:HGNC Symbol;Acc:HGNC:2419]
11	201523_x_at	0.75	-1.53	0.62	UBE2N ubiquitin conjugating enzyme E2 N [Source:HGNC Symbol;Acc:HGNC:2419]
12	218361_at	0.75	-1.59	0.43	GOLPH3 golgi phosphoprotein 3 like [Source:HGNC Symbol;Acc:HGNC:2419]
13	202584_at	0.74	-1.16	0.25	NFX1 nuclear transcription factor, X-box binding 1 [Source:HGNC Symbol;Acc:HGNC:2419]
14	204808_s_at	0.73	-1.3	0.34	RXYLT1 ribitol xylosyltransferase 1 [Source:HGNC Symbol;Acc:HGNC:2419]
15	212407_at	0.72	-1.18	0.52	METTL13 methyltransferase like 13 [Source:HGNC Symbol;Acc:HGNC:2419]
16	220949_s_at	0.72	-0.8	0.25	C7orf49 chromosome 7 open reading frame 49 [Source:HGNC Symbol;Acc:HGNC:2419]
17	212103_at	0.7	-1.32	0.3	KPNA6 karyopherin subunit alpha 6 [Source:HGNC Symbol;Acc:HGNC:2419]
18	218176_at	0.7	-1.4	0.26	MAGEF1 MAGE family member F1 [Source:HGNC Symbol;Acc:HGNC:2419]
19	201524_x_at	0.7	-0.28	0.3	UBE2N ubiquitin conjugating enzyme E2 N [Source:HGNC Symbol;Acc:HGNC:2419]
20	208898_at	0.7	-1.49	0.53	ATP6V1D ATPase H+ transporting V1 subunit D [Source:HGNC Symbol;Acc:HGNC:2419]

Geneset Overrepresentation

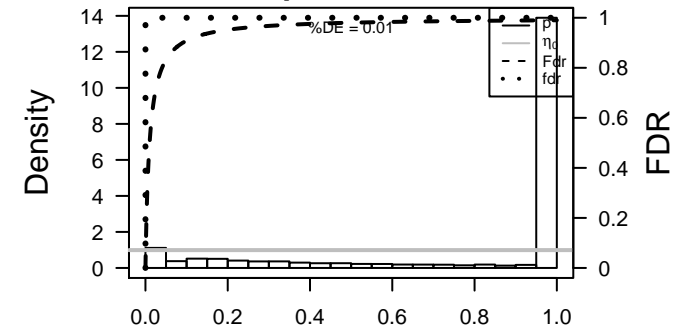
Rank	p-value	#in/all	Geneset
1	8e-21	115 / 5529	Lympi HOPP_Txn_elongation
2	3e-20	118 / 5908	Lympi HOPP_Active_promoter
3	4e-14	48 / 1354	Colon LaPointe_mucosa-position_kmeans_N_pecum_colon_ascending_colon_UP
4	7e-13	29 / 540	GSE/ TIEN_INTESTINE_PROBIOTICS_24HR_UP
5	9e-13	88 / 4261	Lympi HOPP_Txn_transition
6	3e-10	99 / 5682	Lympi HOPP_Weak_promoter
7	5e-09	34 / 1044	TF ICGC_Six5_targets
8	4e-08	35 / 1190	GSE/ BLALOCK_ALZHEIMERS_DISEASE_DN
9	1e-07	12 / 156	GSE/ REACTOME_ANTIGEN_PROCESSING_UBIQUITINATION_PROTEASOM
10	1e-07	12 / 156	GSE/ TIEN_INTESTINE_PROBIOTICS_6HR_DN
11	1e-07	19 / 417	GSE/ SHEN_SMARCA2_TARGETS_UP
12	7e-07	12 / 182	GSE/ REACTOME_CLASS_I_MHC_MEDIATED_ANTIGEN_PROCESSING_PR
13	7e-07	33 / 1221	CC mitochondrion
14	8e-07	11 / 152	Refer Chaussabel_3.6_Mitochondrial_ribosomal_proteins
15	1e-06	38 / 1550	GSE/ PILON_KLF1_TARGETS_DN
16	1e-06	33 / 1241	TF KIM_MYC_targets
17	2e-06	35 / 1387	TF HEBENSTREIT_high_expression_TF
18	2e-06	30 / 1083	Color LaPointe_mucosa-position_kmeans_J_pecum_colon_ascending_colon_tra
19	2e-06	21 / 590	GSE/ GRAESSMANN_RESPONSE_TO_MC_AND_DOXORUBICIN_DN
20	2e-06	16 / 361	GSE/ GARY_CD5_TARGETS_DN
21	2e-06	17 / 406	GSE/ MOOTHA_HUMAN_MITODB_6_2002
22	3e-06	28 / 1007	Refer PROTEINATLAS_kidney
23	5e-06	36 / 1527	GSE/ PUJANA_BRCA1_PCC_NETWORK
24	5e-06	33 / 1338	GSE/ DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
25	7e-06	22 / 699	GSE/ BENPORATH_MYC_MAX_TARGETS
26	1e-05	36 / 1578	TF ICGC_GabpPcr2_targets
27	1e-05	10 / 167	BP protein polyubiquitination
28	1e-05	16 / 422	GSE/ MOOTHA_MITOCHONDRIA
29	2e-05	65 / 3805	CC cytosol
30	2e-05	19 / 594	Refer PROTEINATLAS_parathyroid_gland
31	2e-05	10 / 178	GSE/ PENG_LEUCINE_DEPRIVATION_DN
32	3e-05	14 / 352	GSE/ MULLIGHAN_MLL_SIGNATURE_1_UP
33	3e-05	6 / 56	CC proteasome complex
34	4e-05	23 / 840	Refer PROTEINATLAS_urinary_bladder
35	4e-05	15 / 408	GSE/ REACTOME_ADAPTIVE_IMMUNE_SYSTEM
36	5e-05	61 / 3564	TF ICGC_Taf1_targets
37	5e-05	5 / 37	GSE/ KEGG_PROTEASOME
38	5e-05	12 / 277	CC mitochondrial_matrix
39	5e-05	19 / 630	GSE/ KIM_BIPOLAR_DISORDER_OLIGODENDROCYTE_DENSITY_CORR_UP
40	6e-05	5 / 39	GSE/ REACTOME_CROSS_PRESENTATION_OF_SOLUBLE_EXOGENOUS_A

Overview Map

Spot



p-values



Aging Rank	p-value	#in/all	Geneset
1	1	0/ 92	HORVATH_aging_genes_meth_DOWN
2	1	0/ 107	HORVATH_aging_genes_meth_UP
3	0.04	0/ 47	TSCHEMDORFF_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	10 / 167	protein polyubiquitination
2	7e-04	4 / 17	mitochondrial translation
3	1e-04	3 / 10	negative regulation of viral transcription
4	2e-04	5 / 49	regulation of cellular amino acid metabolic process
5	4e-04	5 / 56	negative regulation of G2/M transition of mitotic cell cycle
6	5e-04	6 / 91	interleukin-1-mediated signaling pathway
7	7e-04	7 / 64	NIK/NF-kappaB signaling
8	7e-04	5 / 65	negative regulation of ubiquitin-protein ligase activity involved in mitotic cell c
9	7e-04	5 / 65	SCF-dependent proteasomal ubiquitin-dependent protein catabolic process
10	8e-04	3 / 17	positive regulation of ubiquitin-protein transferase activity
11	9e-04	5 / 69	antigen processing and presentation of exogenous peptide antigen via MHC c
12	9e-04	5 / 69	positive regulation of ubiquitin-protein ligase activity involved in regulation of t
13	1e-03	5 / 70	regulation of transcription from RNA polymerase II promoter in response to hy
14	1e-03	9 / 232	translation
15	1e-03	6 / 105	stimulatory C-type lectin receptor signaling pathway

Cancer Rank	p-value	#in/all	Geneset
1	0.02	0 / 15	RHODES_CANCER_META_SIGNATURE
2	0.03	3 / 58	SHAUGHNESSY_MM_high_risk
3	0.04	2 / 28	PanCan_HK_geneset_nanostring
4	0.10	1 / 10	GENTLES_modu5
5	0.14	1 / 14	BENTINK_src2
6	0.15	1 / 15	GENTLES_modu7
7	0.35	2 / 13	PanCan_Driver_Gene_geneset_nanostring
8	0.36	1 / 41	PanCan_DNARepair_geneset_nanostring
9	0.40	0 / 14	LIU_COMMON_CANCER_GENES
10	0.44	0 / 16	SOTRIOU_BREAST_CANCER_GRADE_1_VS_3D
11	0.46	5 / 409	Lambcke_Normal_vs_Adenoma
12	0.51	0 / 15	RHODES_UNDIFFERENTIATED_CANCER
13	0.56	0 / 11	LIU_PROSTATE_CANCER_UP
14	0.80	0 / 14	SOTRIOU_BREAST_CANCER_GRADE_1_VS_3P
15	0.80	1 / 147	PanCan_MAPK_geneset_nanostring

CC Rank	p-value	#in/all	Geneset
1	7e-07	33 / 1221	mitochondrion
2	2e-05	65 / 3805	cytosol
3	3e-05	6 / 56	proteasome complex
4	5e-05	12 / 277	mitochondrial matrix
5	7e-05	4 / 21	mitochondrial small ribosomal subunit
6	3e-04	12 / 330	mitochondrial inner membrane
7	7e-04	44 / 2541	nucleoplasm
8	8e-04	3 / 17	proteasome regulatory particle, base subcomplex
9	8e-04	3 / 17	retromer complex
10	2e-03	4 / 46	peroxisomal membrane
11	2e-03	67 / 4579	nucleus
12	4e-03	3 / 30	small-subunit processome
13	7e-03	2 / 12	proteasome regulatory particle, base subcomplex
14	8e-03	3 / 37	mitochondrial respiratory chain complex I
15	8e-03	4 / 73	ubiquitin ligase complex

Chr Rank	p-value	#in/all	Geneset
1	0.04	15 / 832	Chr 2
2	0.04	13 / 700	Chr 12
3	0.07	13 / 756	Chr 11
4	0.07	12 / 689	Chr 3
5	0.15	7 / 403	Chr 14
6	0.17	8 / 492	Chr 9
7	0.39	7 / 548	Chr 16
8	0.43	6 / 480	Chr 4
9	0.49	3 / 242	Chr 13
10	0.57	6 / 554	Chr 5
11	0.59	14 / 1325	Chr 1
12	0.71	3 / 333	Chr 22
13	0.73	5 / 583	Chr 7
14	0.79	4 / 490	Chr 10
15	0.79	3 / 382	Chr 15

Chromatin states Rank	p-value	#in/all	Geneset
1	3e-20	134 / 7833	Bcells_peripheral_blood_1_TssA
2	1e-18	133 / 7930	Regulatory_cells_peripheral_blood_1_TssA
3	3e-18	117 / 6099	ISC_4_Tx
4	6e-18	100 / 4528	T_CD8+_naive_cells_peripheral_blood_4_Tx
5	1e-17	128 / 7420	Tcells_peripheral_blood_1_TssA
6	3e-17	130 / 7751	natural_killer_cells_peripheral_blood_1_TssA
7	6e-17	132 / 8068	Thelper_cells_peripheral_blood_1_TssA
8	2e-16	128 / 7635	monocytes_peripheral_blood_1_TssA
9	3e-16	133 / 8322	T_CD8+_naive_cells_peripheral_blood_1_TssA
10	3e-16	121 / 6839	T_CD8+_naive_cells_peripheral_blood_5_TxWk
11	4e-16	119 / 6637	Tcells_peripheral_blood_5_TxWk
12	8e-16	110 / 5753	Tcells_peripheral_blood_4_Tx
13	1e-16	133 / 8406	Bcells_peripheral_blood_2_TssAFlnk
14	7e-15	122 / 7116	Tx_Color
15	1e-14	130 / 8200	monocytes_peripheral_blood_2_TssAFlnk

Colon Cancer Rank	p-value	#in/all	Geneset
1	4e-14	48 / 1354	LaPointe_mucosa-position_kmeans_N_cecum_colon_ascending_colon_UP_a
2	2e-06	30 / 1083	LaPointe_mucosa-position_kmeans_J_cecum_colon_ascending_colon_transv
3	9e-04	16 / 602	Pentrack_CRC_TCGA_corr_R_normal_DN
4	3e-03	14 / 561	Pentrack_CRC_TCGA_group_over_C_normal_DN
5	9e-02	18 / 1174	LaPointe_mucosa-position_kmeans_E_transverse_colon_UP_transverse_colo
6	1e-01	1 / 14	Hewish_dMMR-secondary-mutations_DNA-repair
7	2e-01	14 / 958	LaPointe_mucosa-position_kmeans_D_transverse_colon_UP_
8	2e-01	1 / 18	Boland_CRC-MSI-A6-A10
9	2e-01	2 / 83	Manisa_CRC-cluster-d
10	3e-01	3 / 172	Pentrack_CRC_TCGA_corr_U_msi-h_UP
11	4e-01	11 / 883	LaPointe_mucosa-position_kmeans_L_transverse_colon_cecum_colon_DN
12	4e-01	12 / 1001	LaPointe_mucosa-position_kmeans_H_cecum_colon_ascending_colon_UP_
13	4e-01	1 / 49	Pentrack_CRC_TCGA_corr_N_msi-h_DN
14	4e-01	6 / 492	LaPointe_mucosa-position_kmeans_C_cecum_colon_ascending_colon_trans
15	6e-01	9 / 854	LaPointe_mucosa-position_kmeans_A_ascending_colon_UP_

Glioma Rank	p-value	#in/all	Geneset
1	8e-05	33 / 1523	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
2	1e-03	27 / 1343	Hopp_Sturm_GBM_Epi3_no_zentr6_fetus_UP
3	4e-03	4 / 58	Stuehler_Proteins_up_in_STS
4	2e-02	5 / 139	WILLSCHER_GBM_proteomics_wtOnly_Differencelst
5	9e-02	6 / 282	WILLSCHER_GBM_verhaak-PNwt & CL_up
6	9e-02	2 / 46	WILLSCHER_GBM_proteomics_wtOnly_SpotG
7	1e-01	1 / 10	WILLSCHER_GBM_LTSmut_proteomics-B_UP
8	1e-01	10 / 614	Sturm_GBM_Meth_overexpression_E_G34_UP
9	1e-01	2 / 59	GIEZELT_GBM_STS_up_VS_LTS
10	1e-01	6 / 300	Up
11	2e-01	1 / 22	Sturm_GBM_Meth_overexpression_H_K27_UP
12	3e-01	2 / 100	WILLSCHER_GBM_proteomics_wtOnly_SpotB
13	3e-01	6 / 421	Down_b
14	3e-01	1 / 34	WILLSCHER_GBM_proteomics_wtOnly_SpotH
15	5e-01	1 / 58	GIEZELT_GBM_STSwt_down_VS_LTSwt

GSEA C2 Rank	p-value	#in/all	Geneset
1	7e-13	29 / 540	TIEN_INTESTINE_PROBIOTICS_24HR_UP
2	4e-08	36 / 1190	BLALOCK_ALZHEIMERS_DISEASE_DN
3	1e-07	12 / 156	REACTOME_ANTIGEN_PROCESSING_UBIQUITINATION_PROTEASOME
4	1e-07	12 / 156	TIEN_INTESTINE_PROBIOTICS_6HR_DN
5	1e-07	19 / 417	SHEN_SMARCA2_TARGETS_UP
6	7e-07	12 / 182	REACTOME_CLASS_I_MHC_MEDIATED_ANTIGEN_PROCESSING_PRES
7	1e-06	38 / 1550	PILON_KLF1_TARGETS_DN
8	2e-06	21 / 590	GRAESSMANN_RESPONSE_TO_MC_AND_DOXORUBICIN_DN
9	2e-06	16 / 361	GARY_CD5_TARGETS_DN
10	2e-06	17 / 406	MOOHA_HUMAN_MITODB_6_2002
11	5e-06	36 / 1527	PUJANA_BRCA1_PCC_NETWORK
12	5e-06	33 / 1338	DIAZ_CHRONIC_MEYLOGNEOUS_LEUKEMIA_UP
13	7e-06	22 / 699	BENPORATH_MYC_MAX_TARGETS
14	1e-05	16 / 422	MOOHA_MITOCHONDRIA
15	2e-05	10 / 178	PENG_LEUCINE_DEPRIVATION_DN

LM Rank	p-value	#in/all	Geneset
1	3e-04	9 / 192	HALLMARK_MTORC1_SIGNALING
2	6e-04	7 / 133	HALLMARK_DNA_REPAIR
3	1e-03	8 / 186	HALLMARK_OXIDATIVE_PHOSPHORYLATION
4	2e-02	5 / 139	HALLMARK_FATTY_ACID_METABOLISM
5	3e-02	4 / 106	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
6	3e-02	3 / 96	HALLMARK_ANDROGEN_RESPONSE
7	1e-01	4 / 182	HALLMARK_GLYCOLYSIS
8	2e-01	4 / 190	HALLMARK_MYC_TARGETS_V1
9	2e-01	2 / 76	HALLMARK_INTERFERON_ALPHA_RESPONSE
10	3e-01	3 / 166	HALLMARK_INTERFERON_GAMMA_RESPONSE
11	3e-01	2 / 87	HALLMARK_BILE_ACID_METABOLISM
12	3e-01	2 / 97	HALLMARK_PEROXISOME
13	3e-01	3 / 174	HALLMARK_ADIPOGENESIS
14	3e-01	1 / 39	HALLMARK_PANCREAS_BETA_CELLS
15	5e-01	1 / 55	HALLMARK_MYC_TARGETS_V2

Immunome Rank	p-value	#in/all	Geneset
1	0.05	1 / 5	Angelova Immune-metagenome-NK56_bright
2	0.12	1 / 12	Angelova Immune-metagenome-NK56_dim
3	0.19	1 / 19	Angelova Immune-metagenome-activated_CD8
4	0.25	1 / 26	Angelova Immune-metagenome-activated_CD4
5	0.37	1 / 42	Angelova Immune-metagenome-TGD
6	0.03	0 / 13	Angelova Immune-metagenome-activated_B-cells
7	1.00	0 / 21	Angelova Immune-metagenome-central_memory_CD4
8	1.00	0 / 17	Angelova Immune-metagenome-central_memory_CD8
9	1.00	0 / 7	Angelova Immune-metagenome-cytotoxic_cells
10	1.00	0 / 25	Angelova Immune-metagenome-DC
11	1.00	0 / 12	Angelova Immune-metagenome-effector_memory_CD4
12	1.00	0 / 32	Angelova Immune-metagenome-effector_memory_CD8
13	1.00	0 / 14	Angelova Immune-metagenome-eosinophil
14	1.00	0 / 19	Angelova Immune-metagenome-IDC
15	1.00	0 / 13	Angelova Immune-metagenome-immature_B-cells

Lifestyle Rank	p-value	#in/all	Geneset
1	0.8	1 / 150	Homuth_BMI-associated-genes_UP
2	0.9	1 / 210	Homuth_BMI-associated-genes_DN
3	1.0	0 / 62	DUMEAUX_Smoking enriched genes
4	1.0	0 / 10	DUMEAUX_Smoking literature genes up
5	1.0	0 / 4	DUMEAUX_Exercise 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 / 7	DUMEAUX_Hormon therapy in non smokers literature genes up
9	1.0	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
10	1.0	0 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
11	1.0	0 / 12	DUMEAUX_Women normal BMI literature genes up
12	1.0	0 / 22	DUMEAUX_High bmi enriched genes
13	1.0	0 / 22	DUMEAUX_Fasting enriched genes
14	1.0	0 / 14	Huan_blood-pressure_SBP-signature
15	1.0	0 / 13	Huan_blood-pressure_DBP-signature

Lymphoma Rank	p-value	#in/all	Geneset
1	8e-21	115 / 5529	HOPP_Txn_elongation
2	3e-20	118 / 5908	HOPP_Active_promoter
3	9e-13	88 / 4261	HOPP_Txn_transition
4	3e-10	99 / 5682	HOPP_Weak_promoter
5	2e-03	77 / 5404	HOPP_Strong_enhancer
6	2e-03	67 / 4559	HOPP_Weak_enhancer
7	4e-03	63 / 4357	HOPP_Weak_txn
8	6e-03	19 / 955	SPANG_BCR_UP
9	1e-02	3 / 42	Monti_OxPhos_cluster
10	7e-02	1 / 7	CARO_OxPhos_vs_BCR_UP
11	8e-02	31 / 2206	HOPP_Heterochrom
12	8e-02	1 / 8	MASCOUIN_GCB_UP
13	9e-02	7 / 353	SPANG_CD40_glns_DN
14	1e-01	6 / 305	TARTE_Plasmaablast_signature
15	1e-01	1 / 13	Hopp_Lymphoma_Epi1_with_zentr_ii_MCL_mBL_UP

Melanoma Rank	p-value	#in/all	Geneset
1	0.04	1 / 4	Melanoma Epi-Enzyme Cluster 5
2	0.08	6 / 276	Gerber_wtwt_melanoma-cells-SpotB
3	0.10	5 / 222	Gerber_wtwt_melanoma-cells-SpotF
4	0.11	2 / 51	Tirosh_genes from CD8 T-cells in Mel79-melanoma
5	0.11	5 / 230	Gerber_wtwt_melanoma-cells-SpotC
6	0.22	2 / 81	Tirosh_Genes in the MITF program
7	0.24	2 / 85	Tirosh_AXL-signature
8	0.26	4 / 236	Gerber_wtwt_group3-specific
9	0.29	4 / 249	Gerber_wtwt_melanoma-cells-SpotE
10	0.33	3 / 185	Tirosh_genes from malignant cells in Mel79-melanoma
11	0.34	1 / 38	Tirosh_top50 correlated genes PC1
12	0.36	1 / 41	Tirosh_top50 correlated genes PC3
13	0.58	1 / 58	Tirosh_nousekeeping_genes
14	0.58	1 / 79	Tirosh_core cycling genes in low- and high-proliferation melanoma
15	0.61	2 / 189	Tirosh_genes preferentially expressed by Tregs

MF Rank	p-value	#in/all	Geneset
1	0.001	6 / 106	ligase activity
2	0.001	7 / 148	ubiquitin protein ligase activity
3	0.004	23 / 1161	RNA binding
4	0.004	8 / 237	ubiquitin-protein transferase activity
5	0.005	3 / 32	aminoacyl-tRNA ligase activity
6	0.005	3 / 33	NADH dehydrogenase (ubiquinone) activity
7	0.007	5 / 109	structural constituent of ribosome
8	0.010	4 / 78	endopeptidase activity
9	0.016	2 / 18	threonine-type endopeptidase activity
10	0.017	4 / 90	unfolded protein binding
11	0.017	23 / 1329	transferase activity
12	0.018	2 / 19	metalloaminopeptidase activity
13	0.021	8 / 32	enzyme binding
14	0.032	6 / 217	lipid binding
15	0.037	2 / 28	aminopeptidase activity

mikNA target Rank	p-value	#in/all	Geneset
1	0.004	8 / 236	hsa-miR-34a
2	0.005	6 / 145	hsa-miR-607
3	0.009	3 / 39	hsa-miR-362-3p
4	0.012	5 / 125	hsa-miR-512-3p
5	0.015	4 / 87	hsa-miR-501-5p
6	0.016	4 / 89	hsa-miR-146a
7	0.017	6 / 189	hsa-miR-27a
8	0.019	5 / 140	hsa-miR-520f
9	0.019	3 / 248	hsa-miR-520c-3p
10	0.023	3 / 56	hsa-miR-182b
11	0.025	3 / 58	hsa-miR-331-3p
12	0.030	2 / 25	hsa-miR-892b
13	0.030	2 / 25	hsa-miR-17*

Correlation Cluster

Spot Summary: D

metagenes = 44
genes = 569

<r> metagenes = 0.96

<r> genes = 0.29

beta: r2= 11.99 / log p= -Inf

samples with spot = 52 (23.5 %)

mBL : 42 (95.5 %)

intermediate : 10 (20.8 %)

Spot Genelist

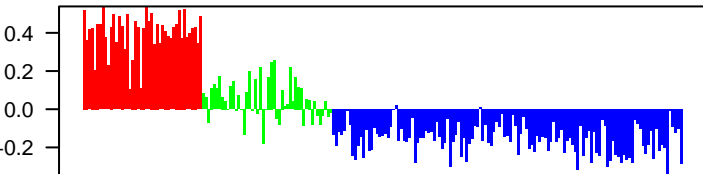
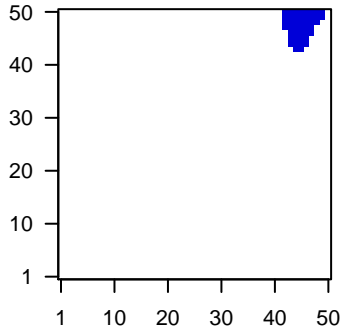
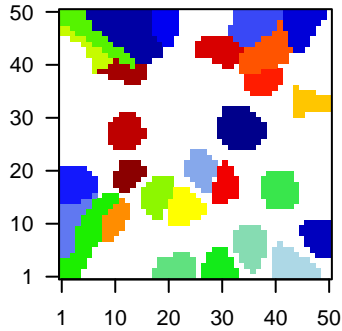
Rank	ID	max e	r	min e	Description
					Symbol
1	206660_at	2.83	-0.99	0.5	IGLL1 immunoglobulin lambda like polypeptide 1 [Source:HGNC Sym
2	221349_at	2.76	-0.89	0.71	VPREB1 V-set pre-B cell surrogate light chain 1 [Source:HGNC Symt
3	206413_s_at	2.76	-1.22	0.37	TCL1B T cell leukemia/lymphoma 1B [Source:HGNC Symbol;Acc:HC
4	203980_at	2.41	-1.55	0.3	FABP4 fatty acid binding protein 4 [Source:HGNC Symbol;Acc:HGNC
5	205123_s_at	2.4	-0.7	0.56	TMEFF1 transmembrane protein with EGF like and two follistatin like d
6	204914_s_at	2.24	-0.89	0.66	SOX11 SRY-box 11 [Source:HGNC Symbol;Acc:HGNC:11191]
7	213920_at	2.19	-1.02	0.51	CUX2 cut like homeobox 2 [Source:HGNC Symbol;Acc:HGNC:1934
8	219855_at	2.18	-0.78	0.45	NUDT11 nudix hydrolase 11 [Source:HGNC Symbol;Acc:HGNC:18011
9	213674_x_at	2.16	-1.9	0.35	immunoglobulin heavy constant delta [Source:HGNC Symbol
10	38037_at	2.16	-1.11	0.57	HBEGF heparin binding EGF like growth factor [Source:HGNC Symbc
11	204915_s_at	2.16	-0.86	0.59	SOX11 SRY-box 11 [Source:HGNC Symbol;Acc:HGNC:11191]
12	209598_at	2.13	-0.99	0.22	PNMA2 PNMA family member 2 [Source:HGNC Symbol;Acc:HGNC:9
13	209590_at	2.09	-1.32	0.78	BMP7 bone morphogenetic protein 7 [Source:HGNC Symbol;Acc:H
14	210244_at	2.07	-1.33	0.36	CAMP cathelicidin antimicrobial peptide [Source:HGNC Symbol;Acc:
15	203821_at	2.07	-1.19	0.52	HBEGF heparin binding EGF like growth factor [Source:HGNC Symbc
16	219737_s_at	2.07	-1.48	0.68	PCDH9 protocadherin 9 [Source:HGNC Symbol;Acc:HGNC:8661]
17	204913_s_at	2.07	-1.11	0.64	SOX11 SRY-box 11 [Source:HGNC Symbol;Acc:HGNC:11191]
18	214930_at	2.05	-0.71	0.63	SLITRK5SLIT and NTRK like family member 5 [Source:HGNC Symbol
19	205122_at	2	-1	0.61	TMEFF1 transmembrane protein with EGF like and two follistatin like d
20	209469_at	1.96	-1.84	0.47	GPM6A glycoprotein M6A [Source:HGNC Symbol;Acc:HGNC:4460]

Geneset Overrepresentation

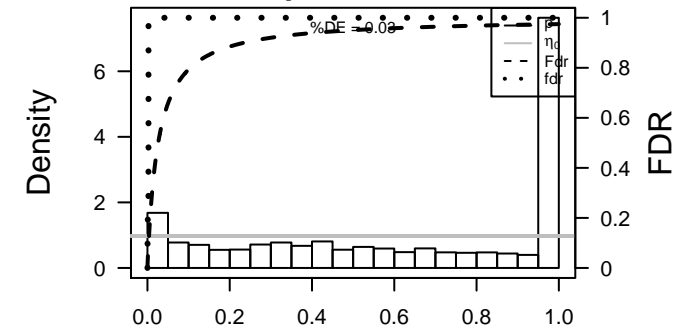
Rank	p-value	#in/all	Geneset
1	5e-52	38 / 42	GSE/ HUMMEL_BURKITTs_LYMPHOMA_UP
2	7e-33	40 / 99	Lympi Sha_BL_UP
3	1e-29	108 / 955	Lympi SPANG_BCR_UP
4	2e-22	42 / 192	Lympi Victora_Dark zone signature
5	8e-18	13 / 15	Lympi BENTINK_mBL_UP
6	8e-18	40 / 227	Lympi SPANG_IL21_UP
7	8e-16	71 / 728	GSE/ KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
8	5e-15	111 / 1527	GSE/ PUJANA_BRCA1_PCC_NETWORK
9	9e-14	27 / 135	Lympi DAVE_BL-vs-DLBCL
10	1e-13	10 / 12	Canci BENTINK_e2f3.2
11	6e-13	59 / 615	GSE/ BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_DN
12	8e-13	65 / 726	GSE/ PUJANA_CHEK2_PCC_NETWORK
13	9e-13	37 / 275	GSE/ HADDAD_B_LYMPHOCYTE_PROGENITOR
14	1e-12	36 / 263	Lymp SPANG_CD40_6hrs_UP
15	4e-12	275 / 5908	Lymp HOPP_Active_promoter
16	6e-12	59 / 651	GSE/ KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
17	1e-11	54 / 575	GSE/ CAIRO_HEPATOBLASTOMA_CLASSES_UP
18	2e-10	53 / 602	Color Pentrack_CRC_TCGA_corr_R_normal_DN
19	1e-09	140 / 2541	CC nucleoplasm
20	2e-09	6 / 6	Lymp MASCQUE_mBL_UP
21	2e-09	70 / 966	GSE/ KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
22	2e-09	32 / 280	GSE/ MANALO_HYPOXIA_DN
23	4e-09	29 / 240	GSE/ MITSIADES_RESPONSE_TO_APLIDIN_DN
24	4e-09	73 / 1052	GSE/ DODD_NASOPHARYNGEAL_CARCINOMA_DN
25	1e-08	38 / 400	GSE/ PUJANA_BRCA2_PCC_NETWORK
26	1e-08	14 / 61	GSE/ BILBAN_B_CLL_LPL_UP
27	1e-08	14 / 61	GSE/ BASSO_CD40_SIGNALING_DN
28	4e-08	7 / 12	Canci BENTINK_ras.1
29	4e-08	252 / 5682	Lymp HOPP_Weak_promoter
30	6e-08	24 / 195	GSE/ HOLLMANN_APOPTOSIS_VIA_CD40_UP
31	8e-08	33 / 340	GSE/ RHEIN_ALL_GLUCOCORTICOID_THERAPY_DN
32	1e-07	14 / 72	GSE/ SCHUHMACHER_MYC_TARGETS_UP
33	1e-07	26 / 234	GSE/ HOLLMANN_APOPTOSIS_VIA_CD40_DN
34	2e-07	210 / 4579	CC nucleus
35	2e-07	38 / 439	GSE/ SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
36	4e-07	49 / 669	GSE/ JOHNSTONE_PARVB_TARGETS_3_DN
37	9e-07	78 / 1312	GSE/ PUJANA_ATM_PCC_NETWORK
38	1e-06	71 / 1161	MF RNA binding
39	2e-06	34 / 409	Canci Lembcke_Normal vs Adenoma
40	3e-06	31 / 361	GSE/ GARY_CD5_TARGETS_DN

Overview Map

Spot



p-values



Aging Rank	p-value	#in/all	Geneset
1	0.2	5 / 92	HORVATH_aging_genes_meth_DOWN
2	0.3	5 / 107	HORVATH_aging_genes_meth_UP
3	0.8	1 / 47	TSCHEINDORFF_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-05	31 / 414	negative regulation of transcription, DNA-templated
2	1e-04	15 / 144	methylation
3	3e-04	6 / 27	DNA biosynthetic process
4	5e-04	7 / 42	response to ionizing radiation
5	7e-04	21 / 281	DNA repair
6	1e-03	15 / 174	rRNA processing
7	0 / 0	11 / 110	translational initiation
8	3e-03	5 / 29	protein localization to nucleus
9	4e-03	4 / 19	translational elongation
10	4e-03	19 / 281	mRNA processing
11	4e-03	3 / 10	stratum development
12	4e-03	4 / 20	negative regulation of cell cycle arrest
13	4e-03	4 / 20	negative regulation of cyclin-dependent protein serine/threonine kinase activi
14	4e-03	4 / 20	tRNA modification
15	5e-03	6 / 46	double-strand break repair

Cancer Rank	p-value	#in/all	Geneset
1	1e-13	10 / 12	BENTINK_e2f3_2
2	4e-08	7 / 12	BENTINK_gas.1
3	2e-06	363 / 409	Lembcke_Normal vs Adenoma
4	4e-04	7 / 41	PanCan_DNARepair_geneset_nanostring
5	1e-03	4 / 14	BENTINK_src.10
6	2e-03	15 / 186	SPANG_LPS-index2
7	4e-03	3 / 10	GENTLES_modu3
8	5e-03	11 / 130	PanCan_CC+Apop_geneset_nanostring
9	1e-02	3 / 14	BENTINK_myc.1
10	7e-02	2 / 13	GENTLES_modu11
11	8e-02	4 / 47	PanCan_TGF-B_geneset_nanostring
12	9e-02	2 / 14	LIU_COMMON_CANCER_GENES
13	9e-02	2 / 15	RHODES_UNDIFFERENTIATED_CANCER
14	9e-02	2 / 15	GENTLES_modu4
15	9e-02	2 / 15	GENTLES_modu7

CC Rank	p-value	#in/all	Geneset
1	1e-09	140 / 2541	nucleoplasm
2	2e-07	210 / 4579	nucleus
3	1e-04	22 / 258	intracellular ribonucleoprotein complex
4	5e-04	11 / 98	spindle pole
5	2e-03	7 / 50	lateral plasma membrane
6	2e-03	192 / 4701	cytoplasm
7	2e-03	227 / 326	nuclear speck
8	3e-03	48 / 936	cytoskeleton
9	5e-03	3 / 11	Fanconi anaemia nuclear complex
10	6e-03	35 / 653	nucleolus
11	6e-03	12 / 157	spindle
12	9e-03	5 / 38	mitochondrial nucleoid
13	1e-02	4 / 25	condensed chromosome
14	1e-02	5 / 39	centrosome
15	1e-02	21 / 354	centrosome

Chr Rank	p-value	#in/all	Geneset
1	0.002	18 / 242	Chr 13
2	0.015	26 / 480	Chr 4
3	0.039	21 / 403	Chr 4
4	0.048	22 / 437	Chr 8
5	0.051	4 / 41	Chr Y
6	0.134	24 / 548	Chr 16
7	0.174	15 / 333	Chr 22
8	0.228	28 / 70	Chr 12
9	0.286	28 / 689	Chr 6
10	0.373	48 / 1325	Chr 1
11	0.392	14 / 369	Chr 20
12	0.421	30 / 832	Chr 2
13	0.421	18 / 130	Chr 10
14	0.428	18 / 482	Chr 9
15	0.633	18 / 554	Chr 5

Chromatin states Rank	p-value	#in/all	Geneset
1	8e-23	382 / 8406	Bcells_peripheral_blood_2_TssAFInk
2	2e-21	363 / 7833	Bcells_peripheral_blood_1_TssA
3	1e-20	375 / 8322	T_CD8_naive_cells_peripheral_blood_1_TssA
4	6e-19	364 / 8068	Thelper_cells_peripheral_blood_1_TssA
5	3e-18	393 / 9160	2_TssA_Neuronal_Progenitor
6	1e-16	380 / 8816	Thelper_cells_peripheral_blood_2_TssAFInk
7	3e-16	399 / 9544	HSC_2_TssAFInk
8	5e-16	377 / 8766	2_TssA_Melanocytes
9	9e-16	363 / 8370	natural_killer_cells_peripheral_blood_2_TssAFInk
10	1e-15	362 / 8275	2_TssA_Fibroblasts
11	2e-15	322 / 6997	Overlap_fetal_midbrain_K9K27me3
12	2e-15	380 / 8918	1_TssA_ESC_Mesoderm
13	3e-15	345 / 7751	natural_killer_cells_peripheral_blood_1_TssA
14	1e-14	327 / 7225	Overlap_fetal_midbrain_ReprPC
15	2e-14	267 / 5456	5_Tx_Neuronal_Progenitor

Colon Cancer Rank	p-value	#in/all	Geneset
1	2e-10	53 / 602	Pentrack_CRC_TCGA_corr_R_normal_DN
2	6e-05	58 / 1001	LaPointe_mucosa-position_kmeans_H_cecum_colon_ascending_colon_UP
3	4e-04	85 / 1729	LaPointe_mucosa-position_kmeans_G_cecum_colon_ascending_colon_UP
4	5e-04	35 / 561	Pentrack_CRC_TCGA_group_over_C_normal_DN
5	2e-03	50 / 958	LaPointe_mucosa-position_kmeans_D_transverse_colon_UP
6	2e-02	3 / 16	Budinska_B_Lower_crypt-like_UP
7	2e-02	241 / 6368	LaPointe_mucosa-position_kmeans_F_cecum_colon_transverse_colon_UP
8	3e-02	2 / 8	KIM_MSI_in-EC
9	3e-02	2 / 8	Boland_CRC_MMR-system
10	3e-02	25 / 738	Lembcke_TCGA_expr_kmeans_N_CIMP_H_DN
11	4e-02	39 / 848	LaPointe_mucosa-position_kmeans_O_transverse_colon_UP
12	5e-02	11 / 184	Kosinski_lower_crypt-long-list
13	6e-02	18 / 349	Lembcke_TCGA_meth_kmeans_F_CIMP_H_UP
14	7e-02	6 / 83	Marisa_CRC_cluster-d
15	8e-02	2 / 14	Hewish_dMMR-secondary-mutations_DNA-repair

Glioma Rank	p-value	#in/all	Geneset
1	0.005	71 / 1523	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
2	0.023	4 / 32	WIRTH_PN_subtype
3	0.045	8 / 115	WILLSCHEER_GBM_Verhaak-CL_up (C)
4	0.052	5 / 59	GIZELT_GBM_STS_up_VS_LTS
5	0.055	57 / 1343	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
6	0.057	11 / 186	Hopp_Sturm_GBM_Epi3_C_IDH_UP
7	0.083	3 / 30	Shaw_responders_down_in_oidigo_glioma
8	0.090	20 / 421	Down_b
9	0.096	3 / 32	Shaw_down_in_1p19q
10	0.103	4 / 52	GIZELT_GBM_WT_down_VS_mut
11	0.103	3 / 33	Sturm_GBM_Meth_overexpression_F_IDH_UP
12	0.109	41 / 979	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_up_fetus_adult_DN
13	0.166	3 / 41	Hopp_Sturm_GBM_Epi3_C1_IDH_UP_fetus_DN
14	0.187	2 / 23	Christensen_hypermethylated_in_grade3_astrocytoma
15	0.189	1 / 6	Donson-adaptive-immunity-associated with LTS in HGA

GSEA C2 Rank	p-value	#in/all	Geneset
1	5e-52	38 / 42	HUMMEL_BURKITTS_LYMPHOMA_UP
2	8e-16	71 / 728	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
3	6e-15	111 / 1527	PUJANA_BRCA1_PCC_NETWORK
4	5e-15	59 / 615	BIFERTER_PHOTODYNAMIC_THERAPY_STRESS_DN
5	6e-15	65 / 726	PUJANA_CHEK2_PCC_NETWORK
6	9e-13	37 / 275	HADDAD_B_LYMPHOCYTE_PROGENITOR
7	6e-12	59 / 651	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
8	1e-11	54 / 575	CAIRO_HEPATOBLASTOMA_CLASSES_UP
9	2e-09	70 / 966	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
10	2e-09	32 / 280	MANALO_HYPOND_DN
11	4e-09	29 / 240	MITSIADES_RESPONSE_TO_APLIDIN_DN
12	4e-09	73 / 1052	DODD_NASOPHARYNGEAL_CARINOMA_DN
13	1e-08	38 / 400	PUJANA_BRCA2_PCC_NETWORK
14	1e-08	14 / 61	BILBAN_B_CLL_LPL_UP
15	1e-08	14 / 61	BASSO_CD40_SIGNALING_DN

BM Rank	p-value	#in/all	Geneset
1	4e-05	19 / 195	HALLMARK_G2M_CHECKPOINT
2	7e-04	16 / 187	HALLMARK_E2F_TARGETS
3	2e-03	15 / 190	HALLMARK_MYC_TARGETS_V1
4	9e-03	5 / 38	HALLMARK_WNT_BETA_CATENIN_SIGNALING
5	1e-02	6 / 55	HALLMARK_MYC_TARGETS_V2
6	1e-02	12 / 194	HALLMARK_ESTROGEN_RESPONSE_EARLY
7	5e-02	9 / 141	HALLMARK_UV_RESPONSE_DN
8	7e-02	11 / 193	HALLMARK_ESTROGEN_RESPONSE_LATE
9	1e-01	4 / 51	HALLMARK_TGF_BETA_SIGNALING
10	1e-01	9 / 173	HALLMARK_MITOTIC_SPINDLE
11	1e-01	9 / 174	HALLMARK_ADIPOGENESIS
12	3e-01	7 / 149	HALLMARK_UV_RESPONSE_UP
13	3e-01	8 / 176	HALLMARK_ALLOGRAFT_REJECTION
14	3e-01	2 / 29	HALLMARK_NOTCH_SIGNALING
15	3e-01	2 / 35	HALLMARK_HEDGEHOG_SIGNALING

Immunome Rank	p-value	#in/all	Geneset
1	0.2	2 / 25	Angelova_immune-metagene-DC
2	0.3	10	Angelova_immune-metagene-neutrophils
3	0.3	1 / 12	Angelova_immune-metagene-memory_B-cells
4	0.4	1 / 13	Angelova_immune-metagene-activated_B-cells
5	0.4	1 / 13	Angelova_immune-metagene-immature_B-cells
6	0.4	1 / 17	Angelova_immune-metagene-central_memory_CD8
7	0.5	1 / 18	Angelova_CRC_immunostimulators
8	0.5	1 / 19	Angelova_immune-metagene-activated_CD8
9	0.5	1 / 21	Angelova_immune-metagene-central_memory_CD4
10	0.6	1 / 23	Angelova_immune-metagene-Th2
11	0.6	1 / 23	Angelova_immune-metagene-Treg
12	0.6	1 / 26	Angelova_immune-metagene-activated_CD4
13	0.8	1 / 45	Angelova_immune-metagene-MDSC
14	0.9	1 / 67	Angelova_immune-metagene-T-cells
15	1.0	0 / 7	Angelova_immune-metagene-cytotoxic_cells

Lifestyle Rank	p-value	#in/all	Geneset
1	0.004	5 / 32	Marjolein_ageing_genes_DN
2	0.146	8 / 150	Homuth_BMI-associated_genes_UP
3	0.270	1 / 9	DUMEAUX_Monocytes_in_smokers_literature_genes_up
4	0.435	8 / 210	Homuth_BMI-associated_genes_DN
5	0.537	1 / 22	DUMEAUX_Fasting_enriched_genes
6	0.836	1 / 62	DUMEAUX_Smoking_enriched_genes
7	1.000	0 / 0	DUMEAUX_Smoking_literature_genes_up
8	1.000	0 / 4	DUMEAUX_Exercise_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 / 7	DUMEAUX_Hormon_therapy_in_non_smokers_literature_genes_up
12	1.000	0 / 16	DUMEAUX_Red_blood_cells_in_non_smokers_literature_genes_up
13	1.000	0 / 12	DUMEAUX_Women_normal_BMI_literature_genes_up
14	1.000	0 / 22	DUMEAUX_High_bmi_enriched_genes
15	1.000	0 / 14	Huan_blood-pressure_SBP-signature

Lymphoma Rank	p-value	#in/all	Geneset
1	7e-33	40 / 99	Sha_BL_UP
2	1e-29	108 / 955	SPANG_BCR_UP
3	2e-22	42 / 192	Victoria_Dark_zone_signature
4	8e-18	13 / 15	BENTINK_mBL_UP
5	8e-18	40 / 227	SPANG_IL21_UP
6	9e-14	27 / 135	DAVE_BL-vs-DLBCL
7	1e-12	36 / 263	SPANG_CD40_Shrs_UP
8	4e-12	27 / 5908	HOPP_Active_promoter
9	2e-09	6 / 6	MASCQUE_mBL_UP
10	4e-08	252 / 5682	HOPP_Weak_promoter
11	5e-06	5 / 9	DAVE_BL_UP
12	7e-06	236 / 5529	HOPP_Txn_elongation
13	6e-05	9 / 183	DAVE_mBL_UP
14	4e-05	227 / 5404	HOPP_Strong_enhancer
15	6e-05	21 / 234	Hopp_Lymphoma_Epi1_no_zentr_6_MCL_DN

Melanoma Rank	p-value	#in/all	Geneset
1	0.002	22 / 319	Gerber_w/wt_melanoma-cells-SpotA
2	0.009	7 / 68	Tirosh_housekeeping_genes
3	0.068	4 / 12	Melanoma_Epi-Enzym_Cluster 6
4	0.131	1 / 4	Melanoma_Epi-Enzyme_Cluster 5
5	0.136	5 / 79	Tirosh_core_cycling_genes_in_low_and_high-proliferation_melanoma
6	0.157	5 / 83	TCGA_melanoma_immune_high
7	0.185	4 / 65	Harbst_melanoma_highgrade_up
8	0.192	3 / 44	Tirosh_core_correlated_genes_Pc2
9	0.219	3 / 47	Tirosh_G2/M_phase_specific_genes
10	0.243	12 / 276	Gerber_w/wt_melanoma-cells-SpotB
11	0.258	4 / 75	Tirosh_Endothelial-cell_specific_genes-melanoma
12	0.269	10 / 230	Gerber_w/wt_melanoma-cells-SpotC
13	0.303	8 / 30	Tirosh_genes_from_malignant_cells_in_Mel79-melanoma
14	0.350	19 / 497	Gerber_w/wt_melanoma-cells-SpotD
15	0.473	2 / 46	Tirosh_top50_correlated_genes_Pc5

MF Rank	p-value	#in/all	Geneset
1	1e-06	71 / 1161	RNA binding
2	2e-05	83 / 1541	DNA binding
3	5e-04	5 / 20	dynein complex binding
4	6e-04	13 / 132	methyltransferase activity
5	2e-03	9 / 81	single-stranded DNA binding
6	2e-03	19 / 268	transcription factor binding
7	3e-03	4 / 18	translation elongation factor activity
8	4e-03	44 / 852	nucleic acid binding
9	5e-03	7 / 61	nucleotidyltransferase activity
10	5e-03	3 / 11	DNA-(apurinic or apyrimidinic site) lyase activity
11	7e-03	3 / 12	protein kinase A catalytic subunit binding
12	7e-03	3 / 12	S-adenosylmethionine-dependent methyltransferase activity
13	9e-03	16 / 239	protein domain specific binding
14	1e-02	9 / 107	mRNA binding
15	1e-02	4 / 28	Ran GTPase binding

miRNA target Rank	p-value	#in/all	Geneset
1	4e-04	3 / 5	hsa-miR-937
2	8e-04	10 / 87	hsa-miR-449b
3	2e-03	18 / 244	hsa-miR-34c-5p
4	2e-03	14 / 171	hsa-miR-203
5	3e-03	6 / 42	hsa-miR-549
6	3e-03	6 / 42	hsa-miR-411
7	3e-03	17 / 236	hsa-miR-34a
8	4e-03	5 / 31	hsa-miR-661
9	5e-03	7 / 23	hsa-miR-205
10	1e-02	4 / 26	hsa-miR-934
11	1e-02	9 / 107	hsa-miR-24
12	1e-02	11 / 145	hsa-miR-607
13	1e-02	10 / 126	hsa-miR-33b-3p
14	1e-02	10 / 126	hsa-miR-548b
15	1e-02	8 / 92	hsa-miR-500

Correlation Cluster

Spot Summary: E

metagenes = 54
genes = 581

<r> metagenes = 0.93
<r> genes = 0.22
beta: r2= 2.68 / log p= -Inf

samples with spot = 15 (6.8 %)
mBL : 14 (31.8 %)
non-mBL : 1 (0.8 %)

Spot Genelist

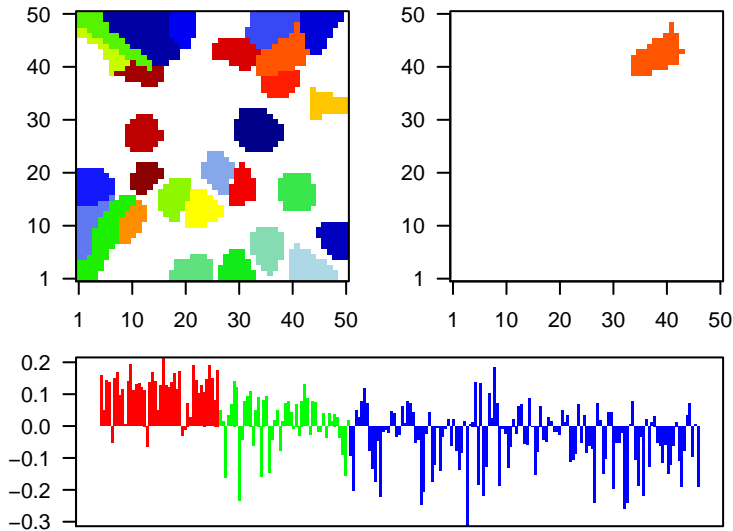
Rank	ID	max e	r	min e	Description
					Symbol
1	209859_at	1.78	-0.9	0.18	TRIM9 tripartite motif containing 9 [Source:HGNC Symbol;Acc:HGNC:10000]
2	220051_at	1.68	-0.94	0.19	PRSS21 serine protease 21 [Source:HGNC Symbol;Acc:HGNC:9485]
3	208502_s_at	1.64	-1.55	0.38	PITX1 paired like homeodomain 1 [Source:HGNC Symbol;Acc:HGNC:10000]
4	204993_at	1.61	-1.23	0.28	GNAZ G protein subunit alpha z [Source:HGNC Symbol;Acc:HGNC:10000]
5	221591_s_at	1.45	-0.81	0.25	PIMREG PICALM interacting mitotic regulator [Source:HGNC Symbol;Acc:HGNC:10000]
6	206264_at	1.45	-0.76	0.41	GPLD1 glycosylphosphatidylinositol specific phospholipase D1 [Source:HGNC Symbol;Acc:HGNC:10000]
7	41037_at	1.43	-0.89	0.27	TEAD4 TEA domain transcription factor 4 [Source:HGNC Symbol;Acc:HGNC:10000]
8	221967_at	1.41	-0.93	0.28	NXP4H neurexophilin 4 [Source:HGNC Symbol;Acc:HGNC:8078]
9	215379_x_at	1.41	-2.47	0.2	immunoglobulin lambda constant 2 [Source:HGNC Symbol;Acc:HGNC:10000]
10	215946_x_at	1.37	-1.38	0.25	immunoglobulin lambda like polypeptide 3, pseudogene [Source:HGNC Symbol;Acc:HGNC:10000]
11	221239_s_at	1.35	-1.87	0.38	FCRL2 Fc receptor like 2 [Source:HGNC Symbol;Acc:HGNC:14875]
12	207396_s_at	1.29	-1.19	0.39	ALG3 ALG3, alpha-1,3- mannosyltransferase [Source:HGNC Symbol;Acc:HGNC:10000]
13	220004_at	1.28	-0.61	0.27	DDX43 DEAD-box helicase 43 [Source:HGNC Symbol;Acc:HGNC:10000]
14	205262_at	1.28	-0.6	0.4	KCNH2 potassium voltage-gated channel subfamily H member 2 [Source:HGNC Symbol;Acc:HGNC:10000]
15	204123_at	1.22	-1.08	0.38	LIG3 DNA ligase 3 [Source:HGNC Symbol;Acc:HGNC:6600]
16	205155_s_at	1.22	-0.87	0.35	SPTBN2 spectrin beta, non-erythrocytic 2 [Source:HGNC Symbol;Acc:HGNC:10000]
17	218296_x_at	1.2	-1.56	0.62	MSTO1 misato 1, mitochondrial distribution and morphology regulator [Source:HGNC Symbol;Acc:HGNC:10000]
18	206777_s_at	1.2	-0.95	0.44	CRYBB2 crystallin beta B2 [Source:HGNC Symbol;Acc:HGNC:2398]
19	219189_at	1.19	-0.73	0.32	FBXL6 F-box and leucine rich repeat protein 6 [Source:HGNC Symbol;Acc:HGNC:10000]
20	213259_s_at	1.17	-0.63	0.29	SARM1 sterile alpha and TIR motif containing 1 [Source:HGNC Symbol;Acc:HGNC:10000]

Geneset Overrepresentation

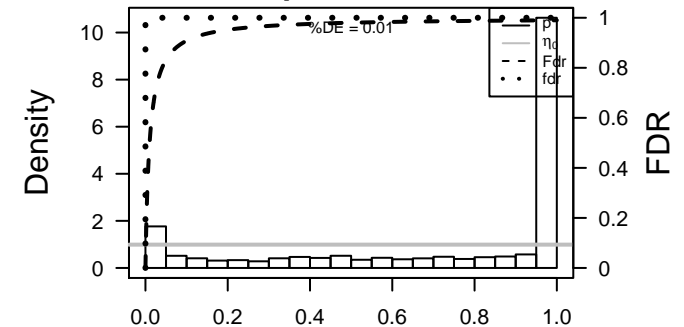
Rank	p-value	#in/all	Geneset
1	1e-51	130 / 728	GSE/ KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
2	9e-46	156 / 1161	MF RNA binding
3	8e-38	168 / 1527	GSE/ PUJANA_BRCA1_PCC_NETWORK
4	5e-34	101 / 651	GSE/ KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
5	6e-32	104 / 726	GSE/ PUJANA_CHEK2_PCC_NETWORK
6	9e-32	68 / 314	GSE/ PENG_GLUTAMINE_DEPRIVATION_DN
7	5e-31	97 / 653	CC nucleolus
8	2e-30	90 / 575	GSE/ CAIRO_HEPATOBLASTOMA_CLASSES_UP
9	1e-29	62 / 280	GSE/ MANALO_HYPOXIA_DN
10	3e-29	304 / 4579	CC nucleus
11	2e-27	205 / 2541	CC nucleoplasm
12	1e-25	46 / 174	BP rRNA processing
13	6e-24	90 / 703	GSE/ LEE_BMP2_TARGETS_DN
14	2e-22	26 / 55	HM HALLMARK_MYC_TARGETS_V2
15	1e-21	272 / 4261	Lymp HOPP_Txn_transition
16	4e-21	43 / 190	HM HALLMARK_MYC_TARGETS_V1
17	2e-20	74 / 561	Color Pentrack_CRC_TCGA_group.over_C_normal_DN
18	8e-20	38 / 158	GSE/ BILD_MYC_ONCOGENIC_SIGNATURE
19	4e-18	73 / 602	Color Pentrack_CRC_TCGA_corr_R_normal_DN
20	1e-17	84 / 776	Refer PROTEINATLAS_skin
21	2e-17	47 / 281	BP mRNA processing
22	4e-17	312 / 5529	Lymp HOPP_Txn_elongation
23	5e-17	39 / 198	BP mRNA splicing, via spliceosome
24	1e-16	101 / 1081	Refer PROTEINATLAS_testis
25	2e-16	42 / 239	GSE/ GINESTIER_BREAST_CANCER_ZNF217_AMPLIFIED_DN
26	2e-16	100 / 1076	Refer PROTEINATLAS_stomach
27	6e-16	64 / 527	Refer PROTEINATLAS_oral_mucosa
28	9e-16	86 / 866	Refer PROTEINATLAS_cerebellum
29	2e-15	29 / 120	GSE/ REACTOME_PROCESSING_OF_CAPPED_INTRON_CONTAINING_PRE
30	3e-15	33 / 159	GSE/ SANSOM_APC_TARGETS_REQUIRE_MYC
31	3e-15	40 / 233	BP RNA splicing
32	3e-15	73 / 677	Refer PROTEINATLAS_esophagus
33	3e-15	96 / 1048	Refer PROTEINATLAS_rectum
34	3e-15	84 / 852	MF nucleic acid binding
35	7e-15	83 / 848	Refer PROTEINATLAS_adrenal_gland
36	1e-14	101 / 1161	Refer PROTEINATLAS_colon
37	1e-14	42 / 268	GSE/ MUELLER_PLURINET
38	2e-14	66 / 595	Refer PROTEINATLAS_breast
39	6e-14	29 / 136	GSE/ REACTOME_MRNA_PROCESSING
40	8e-14	24 / 92	GSE/ REACTOME_MRNA_SPLICING

Overview Map

Spot



p-values



Rank	p-value	#in/all	Geneset
1	0.5	4 / 92	HORVATH_aging_genes_meth_DOWN
2	1.0	1 / 107	HORVATH_aging_genes_meth_UP
3	1.0	0 / 47	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-25	46 / 174	RNA processing
2	2e-17	47 / 281	mRNA processing
3	5e-17	39 / 198	RNA splicing, via spliceosome
4	3e-15	40 / 233	RNA splicing
5	9e-14	22 / 76	ribosome biogenesis
6	2e-09	24 / 144	methylation
7	0 / 0	12 / 39	RNA secondary structure unwinding
8	1e-07	9 / 23	RNA splicing, via transesterification reactions
9	2e-07	12 / 47	mRNA 3'-end processing
10	2e-07	13 / 56	termination of RNA polymerase II transcription
11	2e-07	16 / 86	mRNA export from nucleus
12	2e-07	13 / 67	mRNA processing
13	2e-06	7 / 17	negative regulation of mRNA splicing, via spliceosome
14	2e-06	11 / 49	RNA export from nucleus
15	6e-06	8 / 27	maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S r

Cancer Rank	p-value	#in/all	Geneset
1	4e-07	7 / 14	BENTINK_myc.1
2	8e-05	33 / 409	Lembcke_Normal vs Adenoma
3	1e-03	43 / 13	GENTLES_modul1
4	2e-03	3 / 15	RHODES_CANCER_META_SIGNATURE
5	3e-03	4 / 16	GENTLES_modul6
6	2e-02	3 / 15	GENTLES_modul2
7	2e-02	3 / 16	WOLFPER_overlay_genes
8	3e-02	6 / 58	SHAUGHNESSY_MM_high_risk
9	4e-02	1 / 15	RHODES_UNDIFFERENTIATED_CANCER
10	4e-02	3 / 20	PanCan_ChromMod_geneset_nanostring
11	5e-02	4 / 36	ZHANG_MM_up
12	5e-02	2 / 10	GENTLES_modul3
13	8e-02	4 / 41	PanCan_DNARepair_geneset_nanostring
14	1e-01	2 / 15	GENTLES_modul4
15	1e-01	2 / 15	GENTLES_modul7

CC Rank	p-value	#in/all	Geneset
1	5e-31	97 / 653	nucleolus
2	3e-29	304 / 4579	nucleus
3	2e-27	205 / 2541	nucleoplasm
4	3e-11	25 / 128	spliceosomal complex
5	7e-10	92 / 1221	mitochondrion
6	6e-09	33 / 268	intracellular ribonucleoprotein complex
7	9e-09	11 / 30	small-subunit processome
8	2e-07	33 / 326	nuclear speck
9	2e-06	237 / 4701	cytoplasm
10	5e-06	6 / 13	exosome (RNase complex)
11	1e-05	27 / 277	mitochondrial matrix
12	3e-05	6 / 17	U1 snRNP
13	5e-05	12 / 77	catalytic step 2 spliceosome
14	5e-05	6 / 18	U12-type spliceosomal complex
15	6e-05	5 / 12	integrator complex

Chr Rank	p-value	#in/all	Geneset
1	2e-06	61 / 833	Chr 19
2	1e-04	40 / 548	Chr 16
3	2e-02	24 / 369	Chr 20
4	1e-02	22 / 333	Chr 22
5	8e-02	22 / 403	Chr 14
6	1e-01	37 / 756	Chr 11
7	2e-01	24 / 492	Chr 9
8	3e-01	7 / 139	Chr 2
9	4e-01	11 / 242	Chr 13
10	4e-01	29 / 700	Chr 12
11	5e-01	28 / 689	Chr 3
12	5e-01	53 / 1325	Chr 1
13	5e-01	31 / 776	Chr 17
14	7e-01	6 / 184	Chr 18
15	8e-01	1 / 41	Chr Y

Chromatin states Rank	p-value	#in/all	Geneset
1	1e-42	454 / 7957	Tcells_peripheral_blood_2_TssAFlnk
2	2e-42	450 / 7833	Bcells_peripheral_blood_1_TssA
3	3e-42	326 / 4585	6_EnhG_Melanocytes
4	3e-37	458 / 8370	natural_killer_cells_peripheral_blood_2_TssAFlnk
5	3e-37	459 / 8406	Bcells_peripheral_blood_2_TssAFlnk
6	4e-37	454 / 8245	Tregulatory_cells_peripheral_blood_2_TssAFlnk
7	4e-36	451 / 8200	monocytes_peripheral_blood_2_TssAFlnk
8	2e-35	425 / 7420	Tcells_peripheral_blood_1_TssA
9	5e-34	229 / 2701	4_TxTrans_Fibroblasts
10	1e-34	440 / 7930	Tregulatory_cells_peripheral_blood_1_TssA
11	3e-34	455 / 8431	T_CD8+_naive_cells_peripheral_blood_2_TssAFlnk
12	3e-34	299 / 4208	Tcells_peripheral_blood_6_EnhG
13	7e-34	451 / 8322	T_CD8+_naive_cells_peripheral_blood_1_TssA
14	1e-33	413 / 7165	Tx_Colon
15	2e-33	465 / 8816	Thelper_cells_peripheral_blood_2_TssAFlnk

Colon Cancer Rank	p-value	#in/all	Geneset
1	2e-20	74 / 561	Pentrack_CRC_TCGA_group.over_C_normal_DN
2	4e-18	73 / 602	Pentrack_CRC_TCGA_corr_R_normal_DN
3	2e-09	88 / 1174	LaPointe_mucosa-position_kmeans_E_transverse_colon_UP_transverse_colo
4	3e-05	93 / 1354	LaPointe_mucosa-position_kmeans_N_cecum_colon_ascending_colon_UP_a
5	1e-03	17 / 184	Kosinski_lower_crypt-long-list
6	4e-02	2 / 8	KIM_MSI-in-EC
7	9e-02	79 / 1729	LaPointe_mucosa-position_kmeans_G_cecum_colon_ascending_colon_UP_t
8	1e-01	6 / 83	Marisa_CRC_cluster-d
9	2e-01	1 / 6	Marisa_CRC-C6
10	2e-01	2 / 24	Pentrack_CRC_TCGA_corr_H_mss_UP_msi-h_DN
11	2e-01	1 / 7	TCGA_Mutated-in-CRC_mismatch-repair_genes
12	3e-01	1 / 8	Marisa_CRC-C1
13	3e-01	1 / 10	KIM_CRC-MSI-regulated_DN
14	4e-01	1 / 12	Juehling_HNPCC-mutated-in-4
15	4e-01	1 / 12	Juehling-MSI-enriched-in-6

Glioma Rank	p-value	#in/all	Geneset
1	2e-07	11 / 38	WILLSCHER_GBM_Verhaak-PNwt_up
2	5e-07	15 / 81	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
3	7e-04	41 / 614	Sturm_GBM_Meth_overexpression_E_G34_UP
4	2e-03	82 / 1523	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
5	3e-03	3 / 24	WILLSCHER_GBM_LTSmut_proteomics-A_UP
6	1e-02	70 / 1343	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
7	7e-02	2 / 11	WILLSCHER_GBM_Verhaak-PN (mut&wt)_up (I)
8	7e-02	2 / 11	WILLSCHER_GBM_LTSwt_proteomics-C_UP
9	1e-01	4 / 50	Vishal_subnetwork_signature_of_survival_in_GBM
10	1e-01	3 / 33	Sturm_GBM_Meth_overexpression_F_IDH_up
11	2e-01	4 / 58	Stuehler_Proteins_up_in_STS
12	2e-01	4 / 59	WILLSCHER_GBM_Verhaak-PNwt & MES_up
13	2e-01	16 / 330	Up
14	3e-01	4 / 69	Hopp_Sturm_GBM_Epi3_D1_IDH_UP_adult_fetus_DN
15	3e-01	1 / 10	WILLSCHER_GBM_LTSmut_proteomics-B_UP

GSEA C2 Rank	p-value	#in/all	Geneset
1	1e-51	130 / 728	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
2	8e-38	168 / 1527	PJUAN_ABRCA1_PCC_NETWORK
3	5e-34	101 / 625	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
4	6e-32	104 / 761	PJUAN_ABRCA1_PCC_NETWORK
5	9e-32	68 / 314	PENG_GLUTAMINE_DEPRIVATION_DN
6	2e-30	90 / 575	CAIRO_HEPATOBLASTOMA_CLASSES_UP
7	1e-29	62 / 280	MANALO_HYPOXIA_DN
8	6e-24	90 / 703	LEE_BMP2_TARGETS_DN
9	8e-20	38 / 158	BUILD_MYC_ONCOGENIC_SIGNATURE
10	2e-16	42 / 239	GINESTIER_BREST_CANCER_ZNF217_AMPLIFIED_DN
11	2e-15	29 / 120	REACTOME_PROCESSING_OF_CAPPED_INTRON_CONTAINING_PRE_M
12	3e-15	33 / 159	SANSOM_APC_TARGETS_REQUIRE_MYC
13	1e-14	42 / 268	MUELLER_PLURINET
14	6e-14	29 / 136	REACTOME_MRNA_PROCESSING
15	8e-14	24 / 92	REACTOME_MRNA_SPLICING

LM Rank	p-value	#in/all	Geneset
1	2e-22	26 / 55	HALLMARK_MYC_TARGETS_V2
2	4e-21	43 / 190	HALLMARK_MYC_TARGETS_V1
3	2e-07	18 / 106	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
4	5e-06	22 / 187	HALLMARK_E2F_TARGETS
5	3e-05	21 / 195	HALLMARK_G2M_CHECKPOINT
6	2e-05	11 / 33	HALLMARK_DNA_REPAIR
7	7e-02	10 / 149	HALLMARK_UV_RESPONSE_UP
8	8e-02	12 / 192	HALLMARK_MTORC1_SIGNALING
9	2e-01	10 / 186	HALLMARK_OXIDATIVE_PHOSPHORYLATION
10	3e-01	7 / 139	HALLMARK_FATTY_ACID_METABOLISM
11	4e-01	3 / 193	HALLMARK_ESTROGEN_RESPONSE_LATE
12	4e-01	3 / 59	HALLMARK_CHOLESTEROL_HOMEOSTASIS
13	5e-01	8 / 191	HALLMARK_P53_PATHWAY
14	5e-01	8 / 194	HALLMARK_ESTROGEN_RESPONSE_EARLY
15	5e-01	7 / 174	HALLMARK_ADIPOGENESIS

Immunome Rank	p-value	#in/all	Geneset
1	0.04	3 / 9	Angelova Immune-metagenes-activated_CD8
2	0.18	1 / 5	Angelova Immune-metagenes-NK56_bright
3	0.18	1 / 5	Angelova Immune-metagenes-NKT
4	0.27	2 / 26	Angelova Immune-metagenes-activated_CD4
5	0.38	1 / 12	Angelova Immune-metagenes-NK56_dim
6	0.41	1 / 13	Angelova Immune-metagenes-immature_B-cells
7	0.84	1 / 45	Angelova Immune-metagenes-MDSC
8	1.00	0 / 13	Angelova Immune-metagenes-activated_B-cells
9	1.00	0 / 21	Angelova Immune-metagenes-central_memory_CD4
10	1.00	0 / 17	Angelova Immune-metagenes-central_memory_CD8
11	1.00	0 / 7	Angelova Immune-metagenes-cytotoxic_cells
12	1.00	0 / 25	Angelova Immune-metagenes-DC
13	1.00	0 / 12	Angelova Immune-metagenes-effector_memory_CD4
14	1.00	0 / 32	Angelova Immune-metagenes-effector_memory_CD8
15	1.00	0 / 14	Angelova Immune-metagenes-eosinophil

Lifestyle Rank	p-value	#in/all	Geneset
1	0.04	4 / 32	Marjolein_aging_genes_DN
2	0.22	2 / 22	DUMEAUX_Fasting_enriched_genes
3	0.32	10 / 210	Homuth_BMI-associated_genes_DN
4	0.48	1 / 16	DUMEAUX_Red_blood_cells_in_non_smokers_literature_genes_up
5	0.59	1 / 22	DUMEAUX_High_bmi_enriched_genes
6	0.85	4 / 150	Homuth_BMI-associated_genes_UP
7	1.00	0 / 62	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 / 7	DUMEAUX_Hormon therapy_in_non_smokers_literature_genes_up
13	1.00	0 / 9	DUMEAUX_Monocytes_in_smokers_literature_genes_up
14	1.00	0 / 12	DUMEAUX_Women_normal_BMI_literature_genes_up
15	1.00	0 / 14	Huan_blood-pressure_SBP-signature

Lymphoma Rank	p-value	#in/all	Geneset
1	1e-21	272 / 4261	HOPP_Txn_transition
2	4e-17	312 / 5529	HOPP_Txn_elongation
3	2e-09	300 / 5908	HOPP_Active_promoter
4	5e-07	32 / 305	TARTE_Plasmablast_signature
5	5e-05	19 / 173	Victoria_Light_zone_signature
6	4e-04	5 / 121	DAVE_e-myc_BL_UP
7	1e-03	13 / 121	ROSLOWSKI_green_total
8	2e-03	54 / 906	SPANG_BCR_DN
9	2e-03	11 / 99	Sha_BL_UP
10	1e-02	9 / 97	ROSLOWSKI_red_total
11	2e-02	4 / 25	ROSLOWSKI_red_UP
12	3e-02	5 / 45	SPANG_BUFF_9hrs_DN
13	6e-02	7 / 89	ROSLOWSKI_green_UP
14	7e-02	20 / 353	SPANG_CD40_9hrs_DN
15	9e-02	9 / 135	DAVE_BL-vs-DLCL

Melanoma Rank	p-value	#in/all	Geneset
1	1e-04	25 / 276	Gerber_wt/wt_melanoma-cells-SpotB
2	3e-03	6 / 38	Tirosh_top50_correlated_genes_PC1
3	3e-02	20 / 319	Gerber_wt/wt_melanoma-cells-SpotA
4	1e-01	11 / 185	Tirosh_genes_from_malignant_cells_in_Mel79-melanoma
5	1e-01	1 / 4	Melanoma_Epi-Enzyme_Cluster_3
6	2e-01	12 / 222	Gerber_wt/wt_melanoma-cells-SpotF
7	2e-01	5 / 79	Tirosh_core_cycling_genes_in_low- and_high-proliferation_melanoma
8	2e-01	2 / 24	Tirosh_top50-associated_genes_consistent_across_tumors
9	3e-01	3 / 47	Tirosh_G2/M_phase_specific_genes
10	3e-01	11 / 236	Gerber_wt/wt_group3-specific
11	4e-01	1 / 11	Tirosh_genes_shared_by_CD8_T-cells_and_malign_cells_in_Mel79-melanoma
12	5e-01	3 / 65	Harbst_melanoma_highgrade_up
13	5e-01	1 / 23	Melanoma_Epi-Enzyme_Cluster_7
14	6e-01	1 / 24	Tirosh_B-cell_specific_genes-melanoma
15	6e-01	1 / 24	Gerami_melanoma-metastatic-risk_DN

MF Rank	p-value	#in/all	Geneset
1	9e-46	156 / 1161	RNA binding
2	3e-15	84 / 852	nucleic_acid_binding
3	9e-12	22 / 116	ATP-dependent_RNA_helicase_activity
4	8e-10	22 / 116	helicase_activity
5	1e-08	22 / 132	methyltransferase_activity
6	1e-06	7 / 16	snRNA_binding
7	2e-05	6 / 16	3'-5'-exoribonuclease_activity
8	6e-05	25 / 267	binding
9	8e-05	14 / 107	mRNA_binding
10	8e-05	7 / 28	Ran_GTPase_binding
11	2e-04	82 / 1402	nucleotide_binding
12	2e-04	7 / 32	aminoacyl-tRNA_ligase_activity
13	3e-04	13 / 106	ligase_activity
14	3e-04	9 / 55	double-stranded_RNA_binding
15	3e-04	349 / 7864	protein_binding

mikNA target Rank	p-value	#in/all	Geneset
1	1e-04	11 / 72	hsa-miR-149
2	6e-03	7 / 55	hsa-miR-637
3	7e-03	5 / 31	hsa-miR-661
4	8e-03	8 / 73	hsa-miR-423-5p
5	9e-03	8 / 75	hsa-miR-220c
6	1e-02	4 / 22	hsa-miR-1225-3p
7	1e-02	7 / 62	hsa-miR-489
8	1e-02	5 / 35	hsa-miR-532-3p
9	1e-02	9 / 94	hsa-miR-875-3p
10	2e-02	7 / 68	hsa-miR-608
11	2e-02	6 / 53	hsa-miR-485-3p
12	2e-02	7 / 69	hsa-miR-125a-5p
13	2e-02	3 / 15	hsa-miR-598
14	2e-02	6 / 55	hsa-miR-14

Correlation Cluster

Spot Summary: F

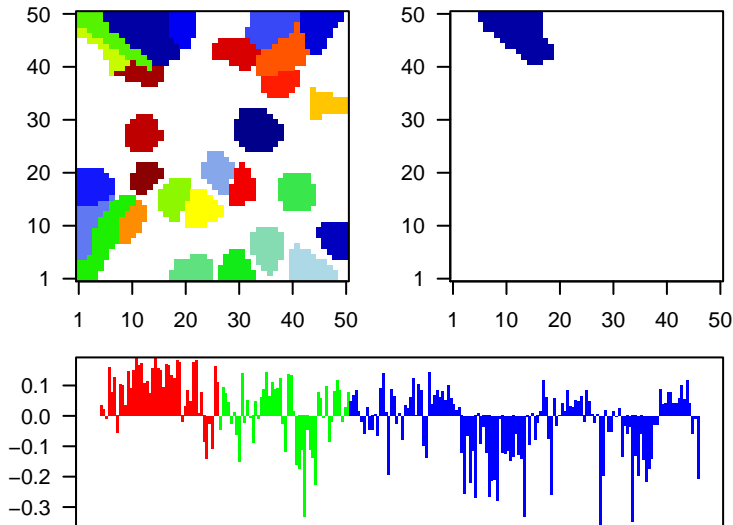
metagenes = 89
genes = 483

<r> metagenes = 0.92
<r> genes = 0.22
beta: r2= 2.97 / log p= -Inf

samples with spot = 19 (8.6 %)
mBL : 17 (38.6 %)
intermediate : 1 (2.1 %)
non-mBL : 1 (0.8 %)

Overview Map

Spot

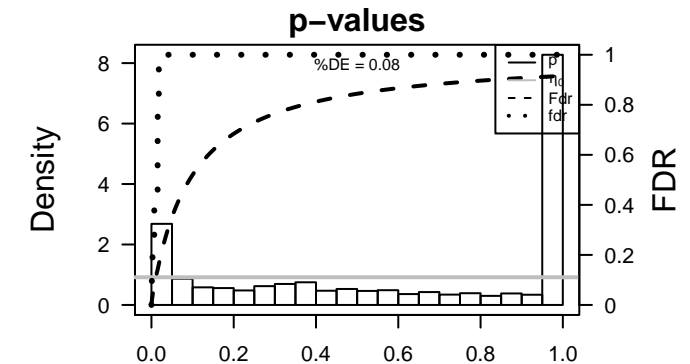


Spot Genelist

Rank	ID	max e	r	min e	Description
					Symbol
1	215489_x_at	1.98	-1.03	0.42	HOMER3 homer scaffolding protein 3 [Source:HGNC Symbol;Acc:HGNC:11168]
2	206624_at	1.74	-1.1	0.15	USP9Y ubiquitin specific peptidase 9, Y-linked [Source:HGNC Symbol;Acc:HGNC:11168]
3	214831_at	1.57	-0.86	0.51	ELK4 ELK4, ETS transcription factor [Source:HGNC Symbol;Acc:HGNC:11168]
4	220086_at	1.45	-1.15	0.5	IKZF5 IKAROS family zinc finger 5 [Source:HGNC Symbol;Acc:HGNC:11168]
5	206220_s_at	1.35	-0.91	0.32	RASA3 RAS p21 protein activator 3 [Source:HGNC Symbol;Acc:HGNC:11168]
6	208608_s_at	1.34	-0.79	0.33	SNTB1 syntrophin beta 1 [Source:HGNC Symbol;Acc:HGNC:11168]
7	221703_at	1.32	-1.12	0.63	BRIP1 BRCA1 interacting protein C-terminal helicase 1 [Source:HGNC Symbol;Acc:HGNC:11168]
8	202558_s_at	1.31	-0.89	0.49	HSPA13 heat shock protein family A (Hsp70) member 13 [Source:HGNC Symbol;Acc:HGNC:11168]
9	202479_s_at	1.28	-1.16	0.37	TRIB2 tribbles pseudokinase 2 [Source:HGNC Symbol;Acc:HGNC:11168]
10	220615_s_at	1.27	-0.69	0.1	FAR2 fatty acyl-CoA reductase 2 [Source:HGNC Symbol;Acc:HGNC:11168]
11	214012_at	1.25	-1.11	0.16	ERAP1 endoplasmic reticulum aminopeptidase 1 [Source:HGNC Symbol;Acc:HGNC:11168]
12	220342_x_at	1.25	-1.17	0.52	EDEM3 ER degradation enhancing alpha-mannosidase like protein 3 [Source:HGNC Symbol;Acc:HGNC:11168]
13	210544_s_at	1.23	-0.85	0.33	ALDH3A2 aldehyde dehydrogenase 3 family member A2 [Source:HGNC Symbol;Acc:HGNC:11168]
14	221326_s_at	1.21	-1.14	0.61	TUBD1 tubulin delta 1 [Source:HGNC Symbol;Acc:HGNC:11168]
15	205398_s_at	1.2	-1.15	0.26	SMAD3 SMAD family member 3 [Source:HGNC Symbol;Acc:HGNC:11168]
16	210349_at	1.2	-1.13	0.17	CAMK4 calcium/calmodulin dependent protein kinase IV [Source:HGNC Symbol;Acc:HGNC:11168]
17	219003_s_at	1.2	-1.08	0.53	MANEA mannosidase endo-alpha [Source:HGNC Symbol;Acc:HGNC:11168]
18	204849_at	1.19	-1.27	0.13	TCFL5 transcription factor like 5 [Source:HGNC Symbol;Acc:HGNC:11168]
19	215150_at	1.17	-0.74	0.6	YOD1 YOD1 deubiquitinase [Source:HGNC Symbol;Acc:HGNC:11168]
20	208512_at	1.15	-1.4	0.4	HSDL2 hydroxysteroid dehydrogenase like 2 [Source:HGNC Symbol;Acc:HGNC:11168]

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	4e-62	352 / 5529	Lymp HOPP_Txn_elongation
2	3e-42	335 / 5908	Lymp HOPP_Active_promoter
3	1e-38	142 / 1338	GSE# DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
4	1e-36	269 / 4261	Lymp HOPP_Txn_transition
5	2e-36	89 / 564	GSE# SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_DN
6	2e-27	103 / 966	GSE# KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
7	9e-24	127 / 1527	GSE# PUJANA_BRCA1_PCC_NETWORK
8	5e-22	115 / 1354	Colon LaPointe_mucosa-position_kmeans_N_ascending_colon_UP
9	8e-21	58 / 417	GSE# SHEN_SMARCA2_TARGETS_UP
10	2e-20	284 / 5682	Lymp HOPP_Weak_promoter
11	3e-20	121 / 1550	GSE# PILON_KLF1_TARGETS_DN
12	2e-19	47 / 297	GSE# BORCZUK_MALIGNANT_MESOTHELIOMA_UP
13	2e-18	203 / 3564	TF ICGC_Taf1_targets
14	3e-17	69 / 673	GSE# SCHLOSSER_SERUM_RESPONSE_DN
15	3e-17	97 / 1190	GSE# BLALOCK_ALZHEIMERS_DISEASE_DN
16	4e-17	43 / 282	Gliom WILLSCHER_GBM_Verhaak-PNwt & CL_up
17	4e-16	70 / 726	GSE# PUJANA_CHEK2_PCC_NETWORK
18	7e-16	29 / 136	Refer Chaussabel_2_9_Cytoskeleton
19	7e-15	42 / 310	Refer Chaussabel_3_4_Protein_phosphatases
20	1e-14	66 / 703	GSE# LEE_BMP2_TARGETS_DN
21	3e-14	199 / 3769	TF ICGC_Pmlsc71910_targets
22	4e-14	42 / 327	GSE# ZHANG_BREAST_CANCER_PROGENITORS_UP
23	5e-14	185 / 3420	TF ICGC_Bclaf101388_targets
24	8e-14	108 / 1578	TF ICGC_GabpPcr2_targets
25	9e-14	195 / 3703	TF ICGC_Foxm1_targets
26	2e-13	197 / 3778	TF ICGC_Poi24_targets
27	4e-13	197 / 3804	TF ICGC_Stat5_targets
28	4e-13	52 / 509	GSE# RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_UP
29	5e-13	95 / 1343	Gliom Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
30	5e-13	224 / 4559	Lymp HOPP_Weak_enhancer
31	6e-13	183 / 3451	TF ICGC_Atf2_targets
32	7e-13	103 / 1523	Gliom Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
33	1e-12	82 / 1089	TF ICGC_Ets1_targets
34	5e-12	193 / 3796	TF ICGC_Nfics81335_targets
35	5e-12	29 / 189	GSE# BIDUS_METASTASIS_UP
36	6e-12	144 / 2541	CC nucleoplasm
37	6e-12	167 / 3121	TF ICGC_Egr1_targets
38	9e-12	68 / 848	Refer PROTEINATLAS_adrenal_gland
39	1e-11	78 / 1052	GSE# DODD_NASOPHARYNGEAL_CARCINOMA_DN
40	1e-11	90 / 1312	GSE# PUJANA_ATM_PCC_NETWORK



Rank	p-value	#in/all	Geneset
1	0.03	7 / 92	HORVATH_aging_genes_meth_DOWN
2	0.07	1 / 107	HORVATH_aging_genes_meth_UP
3	1.00	0 / 47	TSCHEENDORFF_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	

Rank	p-value	#in/all	Geneset
1	6e-12	144 / 2541	nucleoplasm
2	2e-10	216 / 4579	nucleus
3	1e-03	13 / 3805	cytosol
4	7e-04	9 / 73	ubiquitin ligase complex
5	8e-04	7 / 46	peroxisomal membrane
6	9e-04	6 / 35	cytoplasmic stress granule
7	2e-03	186 / 4701	cytoplasm
8	2e-03	5 / 28	microtubule associated complex
9	2e-03	8 / 70	nuclear pore
10	2e-03	10 / 103	nuclear chromosome, telomeric region
11	3e-03	21 / 326	nuclear speck
12	4e-03	11 / 128	spliceosomal complex
13	5e-03	5 / 34	peroxisomal matrix
14	5e-03	5 / 34	spindle microtubule
15	8e-03	5 / 38	mitochondrial nucleoid

Rank	p-value	#in/all	Geneset
1	5e-22	115 / 1354	LaPointe_mucosa-position_kmeans_N_cecum_colon_ascending_colon_UP_a
2	3e-11	108 / 1729	LaPointe_mucosa-position_kmeans_G_cecum_colon_ascending_colon_UP_t
3	3e-08	65 / 958	LaPointe_mucosa-position_kmeans_D_transverse_colon_UP_
4	5e-06	40 / 561	Pentrack_CRC_TCGA_group_our_C_normal_DN
5	1e-04	38 / 602	Pentrack_CRC_TCGA_corr_R_normal_DN
6	4e-04	57 / 1083	LaPointe_mucosa-position_kmeans_J_cecum_colon_ascending_colon_transv
7	7e-04	46 / 848	LaPointe_mucosa-position_kmeans_O_transverse_colon_UP_
8	9e-04	59 / 1174	LaPointe_mucosa-position_kmeans_E_transverse_colon_UP_transverse_colo
9	9e-04	4 / 14	TCGA_Mutated-in-CRC_hypermethylated
10	9e-04	4 / 14	TCGA_Mutated-in-CRC_non-hypermethylated
11	2e-03	4 / 16	Vilar_non-hypermethylated-in-CRC
12	3e-03	44 / 854	LaPointe_mucosa-position_kmeans_A_ascending_colon_UP_
13	4e-03	49 / 1001	LaPointe_mucosa-position_kmeans_H_cecum_colon_ascending_colon_UP_
14	5e-03	55 / 1166	LaPointe_mucosa-position_kmeans_K_transverse_colon_UP_cecum_colon_a
15	1e-02	3 / 14	Hewish_dMMR-secondary-mutations_DNA-repair

Rank	p-value	#in/all	Geneset
1	4e-07	22 / 190	HALLMARK_MYC_TARGETS_V1
2	9e-05	18 / 195	HALLMARK_G2M_CHECKPOINT
3	2e-04	17 / 192	HALLMARK_MTORC1_SIGNALING
4	1e-03	7 / 51	HALLMARK_TGF_BETA_SIGNALING
5	1e-03	10 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING
6	9e-03	9 / 106	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
7	1e-02	13 / 186	HALLMARK_OXIDATIVE_PHOSPHORYLATION
8	1e-02	12 / 173	HALLMARK_MITOTIC_SPINDLE
9	1e-02	10 / 133	HALLMARK_DNA_REPAIR
10	4e-02	7 / 96	HALLMARK_ANDROGEN_RESPONSE
11	4e-02	9 / 130	HALLMARK_FATTY_ACID_METABOLISM
12	6e-02	11 / 193	HALLMARK_HEME_METABOLISM
13	9e-02	6 / 94	HALLMARK_PROTEIN_SECRETION
14	1e-01	7 / 122	HALLMARK_SPERMATOGENESIS
15	1e-01	9 / 174	HALLMARK_ADIPOGENESIS

Rank	p-value	#in/all	Geneset
1	4e-62	352 / 5529	HOPP_Txn_elongation
2	2e-40	335 / 5908	HOPP_Active_promoter
3	1e-36	283 / 4281	HOPP_Txn_transition
4	3e-20	284 / 5682	HOPP_Weak_promoter
5	5e-13	224 / 4559	HOPP_Weak_enhancer
6	7e-09	202 / 4357	HOPP_Weak_txn
7	1e-06	229 / 5404	HOPP_Strong_enhancer
8	4e-06	27 / 305	TARTE_Plastidb_signature
9	9e-05	54 / 955	SPANG_BCR_UP
10	9e-04	48 / 906	SPANG_BCR_DN
11	1e-02	78 / 1814	HOPP_Repetitive
12	1e-02	5 / 40	CARO_OxPhos_in_DLBCL_UP
13	1e-02	20 / 353	SPANG_CD40_genes_DN
14	2e-02	14 / 227	SPANG_IL21_UP
15	7e-02	6 / 88	ROSLOWSKI_green_UP

Rank	p-value	#in/all	Geneset
1	1e-11	43 / 405	hsa-miR-107
2	9e-11	23 / 134	hsa-miR-141
3	2e-10	41 / 404	hsa-miR-103
4	3e-04	31 / 275	hsa-miR-330-3p
5	5e-09	36 / 364	hsa-miR-548n
6	5e-09	29 / 251	hsa-miR-548l
7	1e-08	17 / 95	hsa-miR-361-5p
8	2e-08	20 / 133	hsa-miR-495
9	2e-08	9 / 160	hsa-miR-330-5p
10	2e-08	32 / 315	hsa-miR-144
11	2e-08	30 / 284	hsa-miR-548d-3p
12	6e-08	25 / 216	hsa-miR-548l
13	9e-08	29 / 285	hsa-miR-548b-5p
14	2e-07	33 / 363	hsa-miR-195
15	2e-07	33 / 369	hsa-miR-15b

Rank	p-value	#in/all	Geneset
1	0.06	3 / 27	Nabetani_alt_len_telomeres_genes_ko
2	0.07	2 / 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	

Rank	p-value	#in/all	Geneset
1	3e-06	21 / 198	mRNA splicing, via spliceosome
2	7e-05	15 / 140	protein folding
3	7e-05	23 / 281	DNA repair
4	7e-05	23 / 281	mRNA processing
5	9e-05	10 / 69	regulation of cellular response to heat
6	1e-04	20 / 233	RNA splicing
7	1e-04	16 / 166	ubiquitin-dependent protein catabolic process
8	2e-04	8 / 50	response to oxidated protein
9	3e-04	9 / 64	transcription-coupled nucleotide-excision repair
10	3e-04	6 / 28	nucleotide-excision repair, preincision complex assembly
11	4e-04	5 / 20	nucleotide-excision repair, preincision complex stabilization
12	5e-04	9 / 21	nucleotide-excision repair, DNA incision, 3' to 5' lesion
13	6e-04	6 / 32	regulation of cholesterol biosynthetic process
14	7e-04	4 / 13	regulation of transcription from RNA polymerase III promoter
15	1e-03	5 / 25	developmental growth

Rank	p-value	#in/all	Geneset
1	4e-04	34 / 554	Chr 5
2	6e-03	35 / 669	Chr 6
3	9e-03	13 / 184	Chr 18
4	9e-03	22 / 382	Chr 15
5	3e-02	38 / 832	Chr 2
6	3e-02	24 / 480	Chr 4
7	1e-01	18 / 403	Chr 14
8	2e-01	3 / 41	Chr Y
9	2e-01	30 / 1325	Chr 1
10	3e-01	10 / 242	Chr 13
11	3e-01	17 / 437	Chr 8
12	4e-01	18 / 490	Chr 10
13	4e-01	27 / 176	Chr 17
14	5e-01	23 / 689	Chr 3
15	6e-01	22 / 700	Chr 12

Rank	p-value	#in/all	Geneset
1	4e-17	43 / 282	WILLSCHER_GBM_Verhaak-PNwt & CL_up
2	5e-13	95 / 1343	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
3	7e-13	103 / 1523	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
4	7e-04	36 / 614	Sturm_GBM_Meth_overexpression_E_G34_UP
5	3e-03	7 / 58	Sturm_Proteins_up_in_STS
6	1e-02	6 / 65	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
7	1e-02	19 / 330	WILLSCHER_GBM_Verhaak-CL_up (E)
8	3e-02	5 / 52	GIEZELT_GBM_WT_down_VS_mut
9	1e-01	2 / 16	VERHAAK_PN_subtype
10	1e-01	1 / 4	WILLSCHER_GBM_Verhaak-CL_up (E)
11	2e-01	7 / 139	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
12	2e-01	3 / 50	Vishal_subnetwork_signature_of_survival_in_GBM
13	2e-01	1 / 8	WILLSCHER_GBM_LTSmut_proteomics-A_UP
14	3e-01	1 / 11	WILLSCHER_GBM_LTSwt_proteomics-C_UP
15	3e-01	1 / 11	Sturm_GBM_Meth_overexpression_G_IDH_UP

Rank	p-value	#in/all	Geneset
1	0.003	4 / 8	Angelova Immune-metagenes-pDC
2	0.288	1 / 10	Angelova Immune-metagenes-TFH
3	0.334	1 / 12	Angelova Immune-metagenes-effector_memory_CD4
4	0.399	1 / 15	Angelova Immune-metagenes-NK
5	0.475	1 / 19	Angelova Immune-metagenes-activated_CD8
6	0.510	1 / 21	Angelova Immune-metagenes-central_memory_CD4
7	0.542	1 / 23	Angelova Immune-metagenes-monocytes
8	0.542	1 / 23	Angelova Immune-metagenes-Th2
9	0.586	1 / 26	Angelova Immune-metagenes-activated_CD4
10	0.626	1 / 29	Angelova Immune-metagenes-Th1
11	0.662	1 / 32	Angelova Immune-metagenes-effector_memory_CD8
12	0.897	1 / 32	Angelova Immune-metagenes-T-cells
13	1.000	0 / 13	Angelova Immune-metagenes-activated_B-cells
14	1.000	0 / 17	Angelova Immune-metagenes-central_memory_CD8
15	1.000	0 / 7	Angelova Immune-metagenes-cytotoxic_cells

Rank	p-value	#in/all	Geneset
1	0.003	16 / 222	Gerber_wtwt_melanoma-cells-SpotF
2	0.010	15 / 230	Gerber_wtwt_melanoma-cells-SpotC
3	0.021	12 / 185	Tirosh_genes_from_malignant_cells_in_Mel79-melanoma
4	0.037	4 / 38	Tirosh_top50 correlated genes PC1
5	0.044	15 / 276	Gerber_wtwt_melanoma-cells-SpotB
6	0.285	5 / 107	Tirosh_Exhaustion program in Mel75
7	0.311	1 / 11	Tirosh_genes shared by CD8 T-cells and malign cells in Mel79-melanoma
8	0.319	8 / 249	Gerber_wtwt_melanoma-cells-SpotE
9	0.363	2 / 38	Hugo_melanoma-BRAFmut-MET_UP
10	0.363	2 / 38	Tirosh_G1/S phase specific genes
11	0.419	1 / 16	Hugo_melanoma-all-LEF1_UP
12	0.511	2 / 51	Tirosh_genes from CD8 T-cells in Mel79-melanoma
13	0.511	1 / 41	Tirosh_top50 correlated genes PC3
14	0.757	2 / 81	Tirosh_Genes in the MITF program
15	0.790	1 / 46	Tirosh_top50 correlated genes PC5

Rank	p-value	#in/all	Geneset
1	0.2	8 / 179	Terre_MSIV_multiple_respiratory_viruses_dn
2	0.5	2 / 48	Burnham_viral_DN
3	0.5	2 / 54	Burnham_timecourse
4	0.7	4 / 125	Terre_MSIV_multiple_respiratory_viruses_up
5	0.7	1 / 33	Sweeney_viral_dn
6	0.8	3 / 122	Terre_IMS_influenza_meta_signature
7	0.8	1 / 48	Burnham_cap_fp_vs_con_DN
8	0.8	1 / 52	Burnham_day1_vs_5_DN
9	0.9	1 / 56	Burnham_sep_vs_con_DN
10	0.9	1 / 71	Burnham_cap_fp_vs_con_UP
11	1.0	0 / 68	Burnham_sep_vs_con_UP
12	1.0	0 / 57	Burnham_viral_UP
13	1.0	0 / 57	Burnham_day1_vs_5_UP
14	1.0	0 / 18	SciCluna_UP
15	1.0	0 / 41	SciCluna_DN

Rank	p-value	#in/all	Geneset
1	2e-18	203 / 3564	ICGC_Taf1_targets
2	3e-14	199 / 3769	ICGC_Pmlsc71910_targets
3	5e-14	185 / 3420	ICGC_Bclaf101388_targets
4	8e-14	108 / 1578	ICGC_GabpPcr2_targets
5	9e-14	195 / 3703	ICGC_Foxm1_targets
6	2e-13	197 / 3778	ICGC_Polr24_targets
7	4e-13	197 / 3804	ICGC_Stat5_targets
8	6e-13	183 / 3451	ICGC_Atf2_targets
9	1e-12	82 / 1089	ICGC_Ets1_targets
10	5e-12	193 / 3796	ICGC_Mics081335_targets
11	1e-11	187 / 3121	ICGC_Egr1_targets
12	2e-11	201 / 4072	ICGC_Mia3_targets
13	6e-11	165 / 3150	ICGC_Creb1_targets
14	6e-11	207 / 4278	ICGC_Yy1_targets
15	1e-10	181 / 3608	ICGC_Tcf12_targets

Rank	p-value	#in/all	Geneset
1	0.01	7 / 72	PanCan_Wint_geneset_nanostring
2	0.02	5 / 46	KUIPER_MM_poor_survival
3	0.08	7 / 113	PanCan_Driver_Gene_geneset_nanostring
4	0.09	2 / 15	BEN-PORATH_UP
5	0.09	2 / 15	GENTLES_mod4
6	0.09	2 / 15	GENTLES_mod7
7	0.10	2 / 16	WOLFNER_overlap_genes
8	0.10	2 / 16	GENTLES_mod6
9	0.12	3 / 36	ZHANG_MM_up
10	0.14	7 / 130	PanCan_CC+Apop_geneset_nanostring
11	0.21	1 / 14	LIU_COMMON_CANCER_GENES
12	0.21	3 / 47	PanCan_TGF-B_geneset_nanostring
13	0.24	2 / 28	PanCan_HK_geneset_nanostring
14	0.26	1 / 9	WANG_ER_DN
15	0.29	2 / 32	KUIPER_MM_good_survival

Rank	p-value	#in/all	Geneset
1	8e-69	328 / 4528	T CD8+ naive cells peripheral blood_4_Tx
2	1e-60	357 / 5753	Tcells peripheral blood_4_Tx
3	7e-57	53 / 527	Regulatory cells peripheral blood_4_Tx
4	1e-59	400 / 7420	Tcells peripheral blood_1_TssA
5	1e-55	349 / 5716	Bcells peripheral blood_4_Tx
6	8e-54	343 / 5601	Thelper cells peripheral blood_4_Tx
7	8e-54	358 / 6099	HSC_4_Tx
8	2e-53	378 / 6839	T CD8+ naive cells peripheral blood_5_TxWk
9	4e-52	401 / 7833	Bcells peripheral blood_1_TssA
10	5e-51	344 / 5766	natural killer cells peripheral blood_4_Tx
11	6e-51	395 / 7635	monocytes peripheral blood_1_TssA
12	2e-49	396 / 7751	natural killer cells peripheral blood_1_TssA
13	8e-48	404 / 8322	T CD8+ naive cells peripheral blood_1_TssA
14	1e-48	399 / 7930	Regulatory cells peripheral blood_1_TssA
15	5e-47	365 / 6679	5_Tx_Melanocytes

Rank	p-value	#in/all	Geneset
1	1e-38	142 / 1338	DIAPZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP

Correlation Cluster

Spot Summary: G

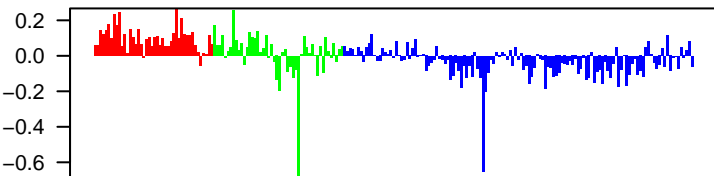
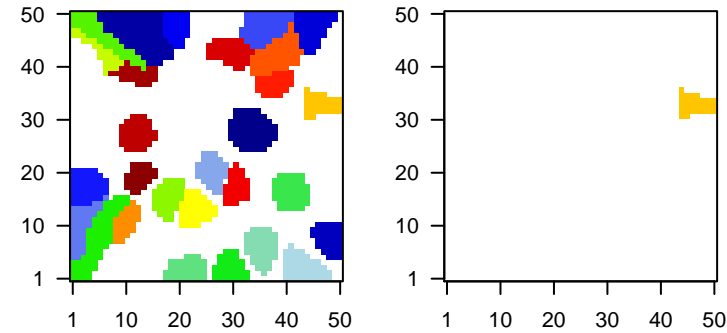
metagenes = 28
genes = 331

<r> metagenes = 0.95
<r> genes = 0.24
beta: r2= 2.61 / log p= -Inf

samples with spot = 11 (5 %)
mBL : 9 (20.5 %)
intermediate : 2 (4.2 %)

Overview Map

Spot

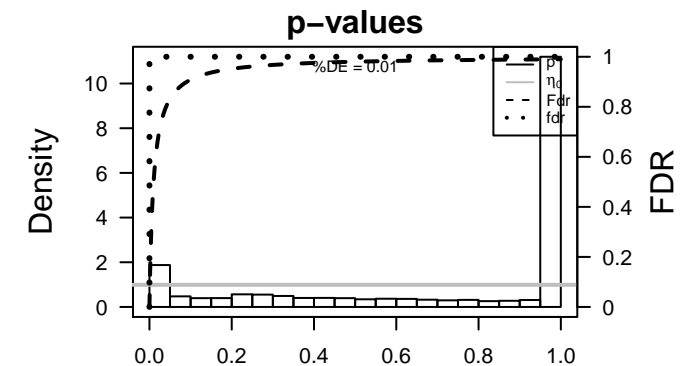


Spot Genelist

Rank	ID	max e	r	min e	Description
1	206233_at	1.81	-0.95	0.19	B4GALT6beta-1,4-galactosyltransferase 6 [Source:HGNC Symbol;Acc:HGNC:1184]
2	213489_at	1.67	-1.75	0.29	MAPRE2microtubule associated protein RP/EB family member 2 [Source:HGNC Symbol;Acc:HGNC:1184]
3	202661_at	1.39	-1.1	0.28	
4	204547_at	1.34	-1.13	0.28	RAB40B RAB40B, member RAS oncogene family [Source:HGNC Symbol;Acc:HGNC:1184]
5	220181_x_at	1.3	-1.03	0.45	SLC30A5solute carrier family 30 member 5 [Source:HGNC Symbol;Acc:HGNC:1184]
6	210379_s_at	1.17	-1.36	0.23	TLK1 tousel like kinase 1 [Source:HGNC Symbol;Acc:HGNC:1184]
7	218911_at	1.14	-0.76	0.65	YEATS4 YEATS domain containing 4 [Source:HGNC Symbol;Acc:HGNC:1184]
8	203298_s_at	1.07	-1.25	0.15	JARID2 jumonji and AT-rich interaction domain containing 2 [Source:HGNC Symbol;Acc:HGNC:1184]
9	221575_at	1.06	-0.97	0.32	SCLY selenocysteine lyase [Source:HGNC Symbol;Acc:HGNC:1184]
10	219342_at	1.03	-1.01	0.43	CASD1 CAS1 domain containing 1 [Source:HGNC Symbol;Acc:HGNC:1184]
11	216713_at	0.99	-1.62	0.59	KRIT1 KRIT1, ankyrin repeat containing [Source:HGNC Symbol;Acc:HGNC:1184]
12	218247_s_at	0.98	-1.28	0.59	MEX3C mex-3 RNA binding family member C [Source:HGNC Symbol;Acc:HGNC:1184]
13	202259_s_at	0.98	-1.04	0.42	N4BP2L2NEDD4 binding protein 2 like 2 [Source:HGNC Symbol;Acc:HGNC:1184]
14	202314_at	0.96	-1.51	0.35	CYP51A1cytochrome P450 family 51 subfamily A member 1 [Source:HGNC Symbol;Acc:HGNC:1184]
15	213391_at	0.95	-0.98	0.5	DPY19L4dpy-19 like 4 [Source:HGNC Symbol;Acc:HGNC:27829]
16	218871_x_at	0.95	-2.17	0.48	CSGALNAC1chondroitin sulfate N-acetylgalactosaminyltransferase 2 [Source:HGNC Symbol;Acc:HGNC:1184]
17	217559_at	0.94	-1.26	0.3	RPL10L ribosomal protein L10 like [Source:HGNC Symbol;Acc:HGNC:1184]
18	205281_s_at	0.93	-1.24	0.41	PIGA phosphatidylinositol glycan anchor biosynthesis class A [Source:HGNC Symbol;Acc:HGNC:1184]
19	210054_at	0.91	-1.27	0.36	HAUS3 HAUS augmin like complex subunit 3 [Source:HGNC Symbol;Acc:HGNC:1184]
20	214130_s_at	0.91	-1.18	0.24	PDE4DIPphosphodiesterase 4D interacting protein [Source:HGNC Symbol;Acc:HGNC:1184]

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	3e-50	256 / 5529	Lymp HOPP_Txn_elongation
2	4e-46	67 / 310	Refer Chaussabel_3.4_Protein phosphatases
3	3e-42	254 / 5908	Lymp HOPP_Active_promoter
4	5e-33	50 / 245	Refer Chaussabel_3.9_Kinases
5	8e-27	191 / 4261	Lymp HOPP_Txn_transition
6	2e-26	77 / 830	GSE/ DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
7	3e-22	217 / 5682	Lymp HOPP_Weak_promoter
8	7e-21	54 / 516	GSE/ HAMAI_APOPTOSIS_VIA_TRAIL_UP
9	2e-20	89 / 1338	GSE/ DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
10	3e-20	48 / 417	GSE/ SHEN_SMARCA2_TARGETS_UP
11	8e-16	54 / 669	GSE/ JOHNSTONE_PARVB_TARGETS_3_DN
12	2e-15	47 / 528	GSE/ FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR_UP
13	7e-15	168 / 4357	Lymp HOPP_Weak_txn
14	1e-14	43 / 469	GSE/ DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN
15	2e-14	52 / 673	GSE/ SCHLOSSER_SERUM_RESPONSE_DN
16	2e-14	85 / 1550	GSE/ PILON_KLF1_TARGETS_DN
17	4e-14	41 / 442	GSE/ KIM_WT1_TARGETS_DN
18	8e-14	66 / 1052	GSE/ DODD_NASOPHARYNGEAL_CARCINOMA_DN
19	1e-12	22 / 139	GSE/ MOREAUX_MULTIPLE_MYELOMA_BY_TACI_DN
20	1e-12	74 / 1343	Gliom Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
21	3e-12	31 / 297	GSE/ BORCZUK_MALIGNANT_MESOTHELIOMA_UP
22	5e-12	79 / 1527	GSE/ PUJANA_BRCA1_PCC_NETWORK
23	6e-12	73 / 1354	Color LaPointe_mucosa-position_kmeans_N_cecum_colon_ascending_colon_UP
24	1e-11	35 / 398	GSE/ MILL_PSEUDOPODIA_HAPTOTAXIS_UP
25	3e-11	77 / 1523	Gliom Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
26	5e-11	163 / 4579	CC nucleus
27	7e-11	57 / 966	GSE/ KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
28	7e-11	162 / 4559	Lymp HOPP_Weak_enhancer
29	2e-10	47 / 726	GSE/ PUJANA_CHEK2_PCC_NETWORK
30	2e-10	14 / 65	GSE/ GAZDA_DIAMOND_BLACKFAN_ANEMIA_PROGENITOR_DN
31	4e-10	31 / 361	GSE/ GARY_CD5_TARGETS_DN
32	9e-10	29 / 330	Gliom Up
33	1e-09	39 / 564	GSE/ RODRIGUES_THYROID_CARCINOMA_ANAPLASTIC_UP
34	2e-09	27 / 298	GSE/ DEBIAS1_APOPTOSIS_BY_REOVIRUS_INFECTON_UP
35	2e-09	30 / 364	miRN hsa-miR-548n
36	4e-09	65 / 1312	GSE/ PUJANA_ATM_PCC_NETWORK
37	7e-09	25 / 275	miRN hsa-miR-590-3p
38	1e-08	14 / 87	GSE/ SEIDEN_ONCOGENESIS_BY_MET
39	2e-08	33 / 468	GSE/ ENK_UV_RESPONSE_KERATINOCYTE_DN
40	2e-08	19 / 171	miRN hsa-miR-203



Rank	p-value	#in/all	Geneset
1	0.9	1 / 92	HORVATH_aging_genes_meth_DOWN
2	1.0	0 / 107	HORVATH_aging_genes_meth_UP
3	1.0	0 / 47	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-05	65 / 1655	transcription, DNA-templated
2	2e-05	20 / 497	cell cycle
3	4e-05	67 / 1764	regulation of transcription, DNA-templated
4	4e-04	21 / 391	protein ubiquitination
5	6e-04	12 / 166	ubiquitin-dependent protein catabolic process
6	1e-03	24 / 520	positive regulation of transcription, DNA-templated
7	2e-03	23 / 502	protein transport
8	2e-03	4 / 24	chromosome organization
9	2e-03	16 / 307	cell division
10	4e-03	24 / 569	regulation of transcription from RNA polymerase II promoter
11	4e-03	5 / 46	regulation of circadian rhythm
12	6e-03	6 / 68	protein sumoylation
13	6e-03	7 / 91	mRNA transport
14	6e-03	7 / 91	sister chromatid cohesion
15	6e-03	4 / 31	tRNA export from nucleus

Cancer Rank	p-value	#in/all	Geneset
1	2e-05	7 / 36	ZHANG_MM_up
2	2e-03	3 / 11	GENTLES_modul14
3	4e-03	3 / 14	BENTINK_src.2
4	6e-03	3 / 16	GENTLES_modul6
5	3e-02	3 / 28	PanCan_HK_geneset_nanostring
6	3e-02	2 / 12	GENTLES_modul12
7	3e-02	1 / 7	GENTLES_modul8
8	2e-01	3 / 58	SHAUGHNESSY_MM_high_risk
9	2e-01	1 / 10	GENTLES_modul3
10	2e-01	1 / 12	BENTINK_ras.1
11	3e-01	1 / 13	GENTLES_modul1
12	3e-01	1 / 14	GENTLES_modul10
13	3e-01	1 / 15	RHODES_CANCER_META_SIGNATURE
14	3e-01	1 / 15	WANG_ER_UP
15	3e-01	1 / 15	BEN-PORATH_UP

CC Rank	p-value	#in/all	Geneset
1	5e-11	163 / 4579	nucleus
2	4e-07	96 / 2541	nucleoplasm
3	2e-04	19 / 324	chromosome
4	3e-04	140 / 4701	cytoplasm
5	3e-04	30 / 653	nucleolus
6	9e-04	15 / 251	microtubule
7	1e-03	7 / 70	nuclear pore
8	1e-03	3 / 10	nuclear pore outer ring
9	2e-03	3 / 173	ubiquitin ligase complex
10	3e-03	8 / 101	kinetochore
11	3e-03	10 / 149	nuclear envelope
12	3e-03	8 / 103	nuclear chromosome, telomeric region
13	3e-03	3 / 13	Ada2/Gen5/Ada3 transcription activator complex
14	3e-03	3 / 13	COPII vesicle coat
15	3e-03	4 / 27	mediator complex

Chr Rank	p-value	#in/all	Geneset
1	0.004	32 / 832	Chr 2
2	0.060	10 / 242	Chr 13
3	0.064	19 / 564	Chr 5
4	0.069	8 / 184	Chr 18
5	0.094	14 / 403	Chr 14
6	0.147	18 / 585	Chr 7
7	0.149	21 / 700	Chr 12
8	0.149	14 / 437	Chr 8
9	0.160	20 / 689	Chr 6
10	0.239	14 / 480	Chr 4
11	0.263	14 / 490	Chr 10
12	0.387	33 / 1325	Chr 1
13	0.544	9 / 542	Chr 15
14	0.555	16 / 689	Chr 3
15	0.762	11 / 556	Chr X

Chromatin states Rank	p-value	#in/all	Geneset
1	6e-50	233 / 4528	T CD8+ naive cells peripheral blood_4_Tx
2	1e-48	256 / 5716	Bcells peripheral blood_4_Tx
3	3e-47	256 / 5716	TSC_4_Tx
4	3e-47	257 / 5753	Tcells peripheral blood_4_Tx
5	6e-45	251 / 5601	Thelper cells peripheral blood_4_Tx
6	4e-43	247 / 5527	Tregulatory cells peripheral blood_4_Tx
7	1e-42	251 / 5738	monocytes peripheral blood_4_Tx
8	9e-41	218 / 5766	natural killer cells peripheral blood_4_Tx
9	5e-38	277 / 7420	Tcells peripheral blood_1_TssA
10	3e-37	219 / 4683	Overlap_fetal_midbrain_HetRpts
11	7e-36	280 / 7751	natural killer cells peripheral blood_1_TssA
12	3e-35	263 / 6839	T CD8+ naive cells peripheral blood_5_TXWk
13	3e-35	259 / 6637	Tcells peripheral blood_5_TXWk
14	5e-35	277 / 7635	monocytes peripheral blood_1_TssA
15	1e-33	256 / 6590	Tregulatory cells peripheral blood_5_TXWk

Colon Cancer Rank	p-value	#in/all	Geneset
1	7e-12	73 / 1354	LaPointe_mucosa-position_kmeans_N_cecum_colon_ascending_colon_UP_a
2	7e-10	50 / 958	LaPointe_mucosa-position_kmeans_D_transverse_colon_UP
3	2e-06	39 / 1174	LaPointe_mucosa-position_kmeans_E_transverse_colon_UP_transverse_colo
4	5e-06	68 / 1729	LaPointe_mucosa-position_kmeans_G_cecum_colon_ascending_colon_UP_t
5	2e-04	39 / 1729	LaPointe_mucosa-position_kmeans_O_transverse_colon_UP
6	1e-03	23 / 492	LaPointe_mucosa-position_kmeans_C_cecum_colon_ascending_colon_trans
7	2e-03	34 / 854	LaPointe_mucosa-position_kmeans_A_ascending_colon_UP
8	2e-03	26 / 602	Pentrack_CRC_TCGA_corr_R_normal_DN
9	3e-03	3 / 13	Vilar_hypermethylation-in-CRC
10	6e-03	5 / 49	Pentrack_CRC_TCGA_corr_N_msi-h_DN
11	1e-02	40 / 1166	LaPointe_mucosa-position_kmeans_K_transverse_colon_UP_cecum_colon_a
12	1e-02	2 / 7	Juehling-MSI-enriched-in-7
13	1e-02	22 / 561	Pentrack_CRC_TCGA_group_over_C_normal_DN
14	1e-02	21 / 532	LaPointe_mucosa-position_kmeans_B_ascending_colon_transverse_colon_U
15	2e-02	34 / 1001	LaPointe_mucosa-position_kmeans_H_cecum_colon_ascending_colon_UP_

Glioma Rank	p-value	#in/all	Geneset
1	1e-12	74 / 1343	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
2	3e-11	77 / 1523	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
3	9e-10	29 / 330	Up
4	8e-07	22 / 282	WILLSCHER_GBM_Verhaak-PNwt & CL_up
5	3e-03	6 / 59	WILLSCHER_GBM_Verhaak-PNwt & MES_up
6	5e-03	25 / 614	Sturm_GBM_Meth_overexpression_E_G34_UP
7	3e-02	4 / 52	GIEZELT_GBM_WT_down_VS_mut
8	7e-02	4 / 66	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
9	1e-01	1 / 6	Donson-adaptive-immunity-associated with LTS in HGA
10	3e-01	2 / 43	Patel_01
11	3e-01	2 / 47	GIEZELT_GBM_STSwt_up_VS_LTSwt
12	4e-01	2 / 55	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
13	4e-01	2 / 55	Hopp_Sturm_GBM_Epi3_C2_adult_fetus_DN
14	4e-01	1 / 21	Barbus_GBM_STS_vs_LTS
15	4e-01	2 / 58	Stuehler_Proteins_up_in_STS

GSEA C2 Rank	p-value	#in/all	Geneset
1	2e-26	77 / 830	DACOSTA_VL_RESPONSE_VIA_ERCC3_DN
2	7e-21	54 / 516	HAMAI_APOPTOSIS_VIA_TRAIL_UP
3	2e-20	89 / 1338	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
4	3e-20	48 / 417	SEN_SMARCA2_TARGETS_UP
5	8e-18	54 / 669	JOHNSTONE_PARVB_TARGETS_3_DN
6	2e-15	47 / 528	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR_UP
7	1e-14	43 / 469	DACOSTA_VL_RESPONSE_VIA_ERCC3_COMMON_DN
8	2e-14	52 / 673	SCHLOSSER_SERUM_RESPONSE_DN
9	2e-14	85 / 1570	PAN_CNF1_TARGETS_DN
10	4e-14	41 / 442	KIM_WTT_TARGETS_DN
11	8e-14	66 / 1052	DODD_NASOPHARYNGEAL_CARCINOMA_DN
12	1e-12	22 / 139	MOREAUX_MULTIPLE_MYELOMA_BY_TACI_DN
13	3e-12	31 / 297	BORCZUK_MALIGNANT_MESOTHELIOMA_UP
14	5e-12	79 / 1527	PUJANA_BRCA1_PCC_NETWORK
15	1e-11	35 / 398	MILI_PSEUDOPODIA_HAPTOTAXIS_UP

LM Rank	p-value	#in/all	Geneset
1	0.002	12 / 195	HALLMARK_G2M_CHECKPOINT
2	0.160	7 / 190	HALLMARK_MYC_TARGETS_V1
3	0.166	7 / 192	HALLMARK_MTORC1_SIGNALING
4	0.222	6 / 173	HALLMARK_MITOTIC_SPINDLE
5	0.372	2 / 55	HALLMARK_MYC_TARGETS_V2
6	0.456	3 / 104	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
7	0.587	3 / 174	HALLMARK_ADIPOGENESIS
8	0.596	4 / 176	HALLMARK_ALLOGRAFT_REJECTION
9	0.638	3 / 139	HALLMARK_FATTY_ACID_METABOLISM
10	0.639	4 / 186	HALLMARK_OXIDATIVE_PHOSPHORYLATION
11	0.663	3 / 196	HALLMARK_ANDROGEN_RESPONSE
12	0.668	4 / 193	HALLMARK_HEME_METABOLISM
13	0.669	2 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING
14	0.669	2 / 97	HALLMARK_PEROXISOME
15	0.672	4 / 194	HALLMARK_KRAS_SIGNALING_UP

Immunome Rank	p-value	#in/all	Geneset
1	0.2	1 / 12	Angelova Immune-metagenes-effector_memory_CD4
2	0.4	1 / 21	Angelova Immune-metagenes-central_memory_CD4
3	0.5	1 / 32	Angelova Immune-metagenes-effector_memory_CD8
4	0.6	1 / 38	Angelova Immune-metagenes-mast_cells
5	0.7	1 / 45	Angelova Immune-metagenes-MDSC
6	0.8	0 / 7	Angelova Immune-metagenes-T_cells
7	1.0	0 / 13	Angelova Immune-metagenes-activated_B_cells
8	1.0	0 / 26	Angelova Immune-metagenes-activated_CD4
9	1.0	0 / 19	Angelova Immune-metagenes-activated_CD8
10	1.0	0 / 17	Angelova Immune-metagenes-central_memory_CD8
11	1.0	0 / 7	Angelova Immune-metagenes-cytotoxic_cells
12	1.0	0 / 25	Angelova Immune-metagenes-DC
13	1.0	0 / 14	Angelova Immune-metagenes-eosinophil
14	1.0	0 / 19	Angelova Immune-metagenes-IDC
15	1.0	0 / 13	Angelova Immune-metagenes-immature_B_cells

Lifestyle Rank	p-value	#in/all	Geneset
1	0.4	6 / 210	Homuth_BMI-associated_genes_DN
2	0.4	1 / 22	DUMEAUX_Fasting_enriched_genes
3	1.0	0 / 62	DUMEAUX_Smoking_enriched_genes
4	1.0	0 / 10	DUMEAUX_Smoking_literature_genes
5	1.0	0 / 4	DUMEAUX_Exercise_non_smoker_literature_genes
6	1.0	0 / 7	DUMEAUX_Exercise_smoker_literature_genes
7	1.0	0 / 9	DUMEAUX_Estrogen_related_in_smokers_literature_genes_up
8	1.0	0 / 7	DUMEAUX_Hormon_therapy_in_non_smokers_literature_genes_up
9	1.0	0 / 9	DUMEAUX_Monocytes_in_smokers_literature_genes_up
10	1.0	0 / 16	DUMEAUX_Red_blood_cells_in_non_smokers_literature_genes_up
11	1.0	0 / 12	DUMEAUX_Women_normal_BMI_literature_genes_up
12	1.0	0 / 22	DUMEAUX_High_bmi_enriched_genes
13	1.0	0 / 150	Homuth_BMI-associated_genes_UP
14	1.0	0 / 14	Huan_blood-pressure_SBP-signature
15	1.0	0 / 13	Huan_blood-pressure_DBP-signature

Lymphoma Rank	p-value	#in/all	Geneset
1	3e-50	256 / 5529	HOPP_Txn_elongation
2	3e-47	254 / 5908	HOPP_Active_promoter
3	3e-22	191 / 4261	HOPP_Txn_transition
4	3e-22	217 / 5682	HOPP_Weak_promoter
5	7e-15	168 / 4357	HOPP_Weak_txn
6	7e-11	162 / 4559	HOPP_Weak_enhancer
7	1e-06	45 / 906	SPANG_BCR_DN
8	1e-03	38 / 855	SPANG_BCR_UP
9	1e-03	8 / 88	ROSLOWSKI_green_UP
10	3e-03	151 / 5404	HOPP_Strong_enhancer
11	3e-03	8 / 121	ROSLOWSKI_green_total
12	9e-03	7 / 97	ROSLOWSKI_red_total
13	1e-02	53 / 1814	HOPP_Repetitive
14	7e-02	3 / 41	ROSLOWSKI_blue_DOWN
15	9e-02	9 / 227	SPANG_IL21_UP

Melanoma Rank	p-value	#in/all	Geneset
1	0.008	12 / 230	Gerber_wtwt_melanoma-cells-SpotC
2	0.037	10 / 222	Gerber_wtwt_melanoma-cells-SpotF
3	0.107	5 / 107	Tirosh_Exhaustion_program_in_MelF5
4	0.146	7 / 185	Tirosh_genes_for_malignant_cells_in_MelT9-melanoma
5	0.218	10 / 319	Gerber_wtwt_melanoma-cells-SpotA
6	0.421	1 / 23	Melanoma_Epi-Enzyme_Cluster_7
7	0.435	1 / 24	Tirosh_exhaustion-associated_genes_consistent_across_tumors
8	0.532	6 / 349	Gerber_wtwt_melanom-cells-SpotE
9	0.605	1 / 39	Tirosh_melanoma_specific_genes
10	0.665	1 / 46	Tirosh_top50_correlated_genes_PC5
11	0.673	1 / 47	Tirosh_G2/M_phase_specific_genes
12	0.736	10 / 497	Gerber_wtwt_melanoma-cells-SpotD
13	0.765	1 / 65	Hartsch_melanoma_highgrade_up
14	0.802	1 / 68	Tirosh_housekeeping_genes
15	0.855	1 / 81	Tirosh_Genes_in_the_MITF_program

MF Rank	p-value	#in/all	Geneset
1	5e-07	226 / 7864	protein binding
2	6e-05	18 / 267	binding
3	1e-04	38 / 852	nucleic acid binding
4	2e-04	47 / 1161	RNA binding
5	3e-04	15 / 225	transcription coactivator activity
6	3e-03	10 / 148	ubiquitin protein ligase activity
7	4e-03	13 / 237	ubiquitin-protein transferase activity
8	5e-03	5 / 48	translation initiation factor activity
9	7e-03	3 / 17	lysine-acetylated histone binding
10	1e-02	3 / 20	dynein complex binding
11	1e-02	3 / 21	transcription factor activity, transcription factor binding
12	2e-02	2 / 10	G-rich strand telomeric DNA binding
13	2e-02	2 / 10	MAP kinase kinase kinase activity
14	3e-02	2 / 11	cAMP response element binding
15	3e-02	2 / 11	long-chain fatty acid-CoA ligase activity

mikNA target Rank	p-value	#in/all	Geneset
1	2e-09	30 / 364	hsa-miR-548n
2	7e-09	25 / 275	hsa-miR-590-3p
3	2e-08	19 / 171	hsa-miR-203
4	5e-08	19 / 111	hsa-miR-656
5	5e-08	23 / 260	hsa-miR-561
6	5e-08	23 / 261	hsa-miR-559
7	6e-08	20 / 202	hsa-miR-26b
8	7e-08	14 / 99	hsa-miR-543
9	1e-07	15 / 314	hsa-miR-17
10	1e-07	15 / 193	hsa-miR-26a
11	2e-07	21 / 236	hsa-miR-18b
12	2e-07	20 / 216	hsa-miR-548l
13	4e-07	21 / 248	hsa-miR-520c-3p
14	4e-07	24 / 315	hsa-miR-144
15	7e-07	20 / 234	hsa-m

Correlation Cluster

Spot Summary: H

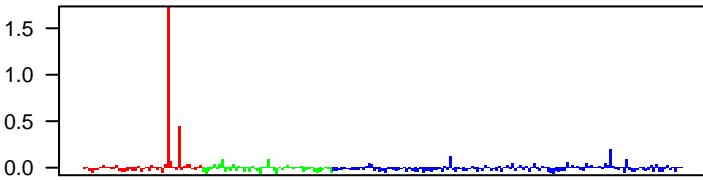
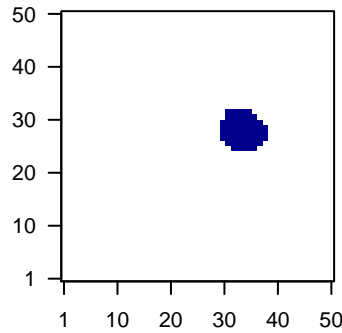
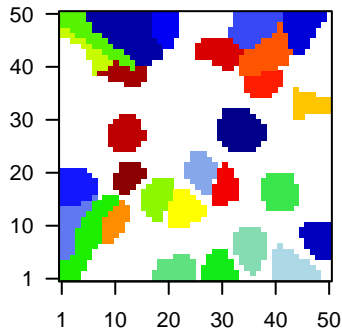
metagenes = 58
genes = 289

<r> metagenes = 0.97
<r> genes = 0.19
beta: r2= 1.51 / log p= -Inf

samples with spot = 3 (1.4 %)
mBL : 2 (4.5 %)
non-mBL : 1 (0.8 %)

Overview Map

Spot

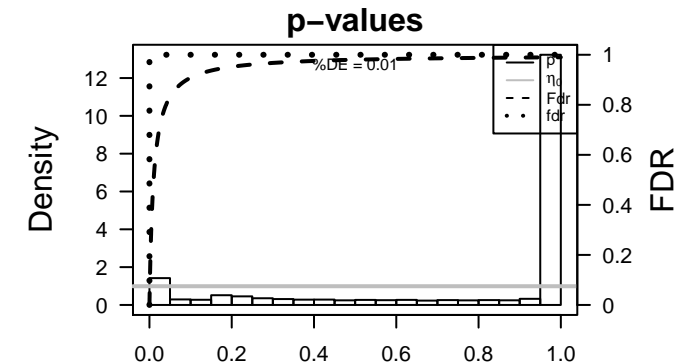


Spot Genelist

Rank	ID	max e	r	min e	Description
1	219465_at	3.55	-0.52	0.78	APOA2 apolipoprotein A2 [Source:HGNC Symbol;Acc:HGNC:601]
2	208470_s_at	3.52	-0.84	0.61	HPR haptoglobin-related protein [Source:HGNC Symbol;Acc:HGN
3	219466_s_at	3.5	-0.5	0.8	APOA2 apolipoprotein A2 [Source:HGNC Symbol;Acc:HGNC:601]
4	211298_s_at	3.41	-0.62	0.76	ALB albumin [Source:HGNC Symbol;Acc:HGNC:399]
5	203400_s_at	3.34	-0.63	0.73	TF transferrin [Source:HGNC Symbol;Acc:HGNC:11740]
6	217238_s_at	3.3	-0.55	0.7	ALDOB aldolase, fructose-bisphosphate B [Source:HGNC Symbol;Ac
7	205820_s_at	3.27	-0.63	0.68	APOC3 apolipoprotein C3 [Source:HGNC Symbol;Acc:HGNC:610]
8	206697_s_at	3.26	-0.73	0.55	HP haptoglobin [Source:HGNC Symbol;Acc:HGNC:5141]
9	204988_at	3.25	-0.63	0.69	FGB fibrinogen beta chain [Source:HGNC Symbol;Acc:HGNC:366
10	205892_s_at	3.21	-0.45	0.68	FABP1 fatty acid binding protein 1 [Source:HGNC Symbol;Acc:HGNC
11	204965_at	3.18	-0.53	0.74	GC GC, vitamin D binding protein [Source:HGNC Symbol;Acc:HC
12	209937_at	3.14	-0.36	0.77	TM4SF4 transmembrane 4 L six family member 4 [Source:HGNC Sym
13	208383_s_at	3.1	-0.64	0.6	PCK1 phosphoenolpyruvate carboxykinase 1 [Source:HGNC Symb
14	219140_s_at	3.1	-0.66	0.68	RBP4 retinol binding protein 4 [Source:HGNC Symbol;Acc:HGNC:9
15	206226_at	3.08	-0.56	0.69	HRG histidine rich glycoprotein [Source:HGNC Symbol;Acc:HGNC
16	210929_s_at	3.08	-0.82	0.67	AHSG alpha 2-HS glycoprotein [Source:HGNC Symbol;Acc:HGNC::
17	214063_s_at	3.07	-0.61	0.73	TF transferrin [Source:HGNC Symbol;Acc:HGNC:11740]
18	205650_s_at	3.06	-0.63	0.68	FGA fibrinogen alpha chain [Source:HGNC Symbol;Acc:HGNC:36
19	219612_s_at	3.01	-0.47	0.73	FGG fibrinogen gamma chain [Source:HGNC Symbol;Acc:HGNC::
20	216238_s_at	2.97	-0.52	0.72	FGB fibrinogen beta chain [Source:HGNC Symbol;Acc:HGNC:366

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	1e-99	73 / 94	Refer WIRTH_Liver
2	1e-99	115 / 218	GSE# HSIAO_LIVER_SPECIFIC_GENES
3	3e-56	52 / 147	GSE# CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_DN
4	7e-46	51 / 208	GSE# CAIRO_LIVER_DEVELOPMENT_DN
5	1e-44	32 / 52	GSE# SU_LIVER
6	9e-43	52 / 250	GSE# CAIRO_HEPATOBLASTOMA_DN
7	4e-41	42 / 144	GSE# LEE_LIVER_CANCER_SURVIVAL_UP
8	7e-41	50 / 243	GSE# HOSHIDA_LIVER_CANCER_SUBCLASS_S3
9	3e-37	58 / 421	GSE# ACEVEDO_LIVER_CANCER_DN
10	6e-37	30 / 64	GSE# KEGG_COMPLEMENT_AND_COAGULATION_CASCADES
11	6e-35	35 / 116	CC blood microparticle
12	7e-33	32 / 100	GSE# OHGUCHI_LIVER_HNF4A_TARGETS_DN
13	7e-32	96 / 1611	CC extracellular region
14	1e-29	77 / 1090	CC extracellular space
15	2e-27	31 / 130	HM HALLMARK_COAGULATION
16	8e-27	30 / 124	GSE# SERVITJA_LIVER_HNF1A_TARGETS_DN
17	2e-26	47 / 410	GSE# PILON_KLF1_TARGETS_UP
18	3e-26	24 / 67	GSE# YAMASHITA_LIVER_CANCER_STEM_CELL_DN
19	1e-24	24 / 77	GSE# WOO_LIVER_CANCER_RECURRENCE_DN
20	7e-22	83 / 1652	Gliom Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
21	1e-21	30 / 181	HM HALLMARK_XENOBIOTIC_METABOLISM
22	2e-21	97 / 2239	CC extracellular exosome
23	2e-21	19 / 51	BP hemostasis
24	2e-21	19 / 51	GSE# KEGG_DRUG_METABOLISM_CYTOCHROME_P450
25	6e-21	42 / 429	Refer PROTEINATLAS_liver
26	5e-20	29 / 189	GSE# NABA_ECM_REGULATORS
27	6e-19	17 / 47	GSE# KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_P450
28	6e-19	21 / 88	BP negative regulation of endopeptidase activity
29	1e-18	30 / 229	GSE# ACEVEDO_LIVER_TUMOR_VS_NORMAL_ADJACENT_TISSUE_DN
30	1e-18	16 / 41	GSE# KEGG_RETINOL_METABOLISM
31	2e-18	35 / 337	GSE# BOCHKIS_FOXA2_TARGETS
32	3e-18	15 / 35	GSE# LEE_LIVER_CANCER
33	2e-17	14 / 31	GSE# REACTOME_FORMATION_OF_FIBRIN_CLOT_CLOTTING_CASCADE
34	2e-17	21 / 103	GSE# REACTOME_BIOLOGICAL_OXIDATIONS
35	3e-17	19 / 79	CC organelle membrane
36	6e-17	27 / 205	GSE# CAIRO_HEPATOBLASTOMA_CLASSES_DN
37	1e-16	18 / 73	GSE# LEE_LIVER_CANCER_DENA_DN
38	4e-16	12 / 23	GSE# BIOCAPTA_INTRINSIC_PATHWAY
39	5e-16	34 / 376	Color Lembcke_TCGA-expr_kmeans_M_CIMP_H_DN
40	9e-16	16 / 58	GSE# REACTOME_PHASE1_FUNCTIONALIZATION_OF_COMPOUNDS



Rank	p-value	#in/all	Geneset
1	0.8	1 / 92	HORVATH_aging_genes_meth_DOWN
2	1.0	1 / 107	HORVATH_aging_genes_meth_UP
3	1.0	0 / 47	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	

Rank	p-value	#in/all	Geneset
1	6e-35	35 / 116	blood microparticle
2	7e-32	96 / 1611	extracellular region
3	1e-30	1 / 1040	extracellular space
4	2e-21	97 / 22339	extracellular exosome
5	3e-17	19 / 79	organelle membrane
6	9e-11	22 / 241	endoplasmic reticulum lumen
7	3e-10	8 / 19	high-density lipoprotein particle
8	8e-8	1 / 63	platelet alpha granule lumen
9	3e-07	29 / 604	intracellular membrane-bounded organelle
10	9e-07	5 / 12	chylomicron
11	5e-06	5 / 16	very-low-density lipoprotein particle
12	3e-05	27 / 683	endoplasmic reticulum membrane
13	3e-05	21 / 462	cell surface
14	4e-05	35 / 1035	endoplasmic reticulum
15	5e-05	4 / 13	endocytic vesicle lumen

Rank	p-value	#in/all	Geneset
1	5e-16	34 / 376	Lembcke_TCGA-expr_kmeans_M_CIMP_H_DN
2	4e-12	32 / 452	Lembcke_TCGA-expr_kmeans_L_CIMP_H_UP_Cluster4_DN
3	2e-07	144 / 6368	LaPointe_mucosa-position_kmeans_F_ascending_colon_transverse_colon_UP
4	6e-06	22 / 448	Lembcke_TCGA_meth_kmeans_J_CIMP_H_DN
5	3e-03	12 / 230	Lembcke_TCGA_meth_kmeans_O_CIMP_H_DN
6	1e-02	10 / 255	Kosinski_top_crypt-long-list
7	3e-02	3 / 38	Marisa_CRC-cluster-e
8	4e-02	2 / 20	Kosinski_top_crypt-short-list
9	6e-02	14 / 532	LaPointe_mucosa-position_kmeans_B_ascending_colon_transverse_colon_UP
10	7e-02	11 / 37	Pentrack_CRC_TCGA_corr_C_normal_UP
11	1e-01	17 / 738	Lembcke_TCGA-expr_kmeans_N_CIMP_H_DN
12	2e-01	3 / 82	Pentrack_CRC_TCGA_group_over_A_normal_UP
13	2e-01	3 / 92	Marisa_CRC-cluster-h
14	3e-01	17 / 854	LaPointe_mucosa-position_kmeans_A_ascending_colon_UP
15	3e-01	4 / 164	Lembcke_TCGA_meth_kmeans_B_Cluster4_DN

Rank	p-value	#in/all	Geneset
1	2e-27	31 / 130	HALLMARK_COAGULATION
2	1e-21	30 / 181	HALLMARK_XENOBIOTIC_METABOLISM
3	7e-08	12 / 97	HALLMARK_BILE_ACID_METABOLISM
4	3e-03	9 / 178	HALLMARK_COMPLEMENT
5	2e-02	8 / 193	HALLMARK_ESTROGEN_RESPONSE_LATE
6	2e-02	3 / 34	HALLMARK_ANGIOGENESIS
7	2e-02	3 / 97	HALLMARK_PEROXISOME
8	4e-02	7 / 194	HALLMARK_KRAS_SIGNALING_UP
9	2e-01	5 / 194	HALLMARK_ESTROGEN_RESPONSE_EARLY
10	4e-01	4 / 182	HALLMARK_GLYCOLYSIS
11	4e-01	4 / 186	HALLMARK_HYPOXIA
12	4e-01	4 / 193	HALLMARK_HEME_METABOLISM
13	4e-01	4 / 194	HALLMARK_MYOGENESIS
14	4e-01	4 / 195	HALLMARK_KRAS_SIGNALING_DN
15	4e-01	3 / 139	HALLMARK_FATTY_ACID_METABOLISM

Rank	p-value	#in/all	Geneset
1	1e-14	84 / 2206	HOPP_Heterochrom
2	2e-07	9 / 53	LENZ_Stromal_signature_2
3	6e-06	82 / 3168	HOPP_Repressed
4	2e-02	12 / 378	TARTE_Mature_plasma_cell_signature
5	2e-01	4 / 130	Hopp_Lymphoma_Epi1_no_zentr_5_B.cell_GCB_UP
6	2e-01	2 / 45	Subero_INT_hypo_meth
7	2e-01	1 / 12	Subero_MM_hypo_meth
8	2e-01	6 / 237	ZHANG_DLBCL_mutated
9	2e-01	3 / 94	Hopp_Lymphoma_Epi1_with_zentr_iii_B.cell_GCB_UP
10	3e-01	2 / 70	Subero_FL_hyper_meth
11	5e-01	2 / 102	ROSLOWSKI_blue_total
12	5e-01	1 / 46	Subero_DLBCL_hypo_meth
13	5e-01	1 / 47	Subero_B-ALL_hyper_meth
14	5e-01	31 / 1894	HOPP_Poised_promoter
15	7e-01	1 / 66	Hopp_Lymphoma_Epi1_with_zentr_i_B.cell_DN

Rank	p-value	#in/all	Geneset
1	0.3	2 / 64	hsa-miR-569
2	0.3	1 / 23	hsa-miR-99b
3	0.3	1 / 25	hsa-miR-635
4	0.3	1 / 26	hsa-miR-982b
5	0.4	1 / 26	hsa-miR-934
6	0.4	1 / 29	hsa-miR-215
7	0.4	1 / 29	hsa-miR-647
8	0.4	2 / 84	hsa-miR-377
9	0.4	1 / 32	hsa-miR-525-3p
10	0.4	1 / 32	hsa-miR-450a
11	0.4	2 / 89	hsa-miR-146a
12	0.5	1 / 40	hsa-miR-524-3p
13	0.5	1 / 41	hsa-miR-519e
14	0.5	1 / 41	hsa-miR-331-3p
15	0.5	1 / 41	hsa-miR-519b-5p

Rank	p-value	#in/all	Geneset
1	0.13	0 / 13	Alternative lengthening of telomeres
2	NA	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	

Rank	p-value	#in/all	Geneset
1	2e-21	19 / 51	hemostasis
2	1e-19	21 / 88	negative regulation of endopeptidase activity
3	1e-15	13 / 32	acute-phase response
4	1e-14	23 / 172	blood coagulation
5	4e-13	10 / 21	fibrinolysis
6	4e-12	21 / 185	cellular protein metabolic process
7	4e-12	34 / 542	oxidation-reduction process
8	4e-11	16 / 110	platelet degranulation
9	5e-11	12 / 53	regulation of complement activation
10	7e-11	15 / 98	steroid metabolic process
11	1e-10	8 / 17	epoxygenase P450 pathway
12	8e-10	8 / 18	blood coagulation, intrinsic pathway
13	2e-10	8 / 18	drug metabolic process
14	5e-10	13 / 78	negative regulation of peptidase activity
15	7e-10	11 / 52	complement activation, classical pathway

Rank	p-value	#in/all	Geneset
1	5e-06	23 / 440	Chr 4
2	4e-02	14 / 480	Chr 10
3	4e-02	4 / 689	Chr 3
4	5e-02	30 / 1325	Chr 1
5	2e-01	15 / 700	Chr 12
6	2e-01	12 / 554	Chr 5
7	4e-01	15 / 832	Chr 2
8	5e-01	10 / 385	Chr 7
9	7e-01	6 / 403	Chr 14
10	7e-01	8 / 548	Chr 16
11	8e-01	5 / 382	Chr 15
12	8e-01	4 / 333	Chr 22
13	8e-01	10 / 376	Chr 17
14	8e-01	8 / 669	Chr 6
15	9e-01	9 / 756	Chr 11

Rank	p-value	#in/all	Geneset
1	7e-22	83 / 1652	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
2	5e-11	29 / 414	Hopp_Sturm_GBM_Epi3_A_adult_fetus_UP_G34_DN
3	1e-09	5 / 5	WILLSCHER_GBM_LTSwt_proteomics-M_UP
4	6e-04	7 / 86	Sturm_GBM_Meth_overexpression_B_adult_UP
5	6e-04	19 / 496	Hopp_Sturm_GBM_Epi3_no_zentr_1_G34_DN
6	7e-04	13 / 273	Hopp_Sturm_GBM_Epi3_B_adult_UP_G34_DN
7	2e-03	4 / 31	WILLSCHER_GBM_proteomics_wtOnly_SpotC
8	1e-02	5 / 82	laffaire_hypermeth_LGG_vs_control
9	2e-02	4 / 58	GIZELT_GBM_STSwt_down_VS_LTSwt
10	1e-02	7 / 12	VERHAAK_Brain
11	2e-02	2 / 12	Sturm_GBM_Meth_overexpression_J_RTK II 'classic'_UP
12	3e-02	2 / 15	Gorovets_LGG_NB_subclass
13	3e-02	1 / 2	WILLSCHER_GBM_Verhaak-PN (mut&wt)_up (L)
14	5e-02	2 / 21	Hopp_Sturm_GBM_Epi3_B1_G34_DN
15	5e-02	1 / 3	WILLSCHER_GBM_Verhaak-PNmwt_up (N)

Rank	p-value	#in/all	Geneset
1	0.2	1 / 12	Angelova Immune-metagenes-NK56_dim
2	0.2	1 / 16	Angelova Immune-metagenes-Th17
3	0.3	1 / 23	Angelova Immune-metagenes-Treg
4	0.5	1 / 45	Angelova Immune-metagenes-MDSC
5	1.0	0 / 13	Angelova Immune-metagenes-activated_B-cells
6	1.0	0 / 26	Angelova Immune-metagenes-activated_CD4
7	1.0	0 / 19	Angelova Immune-metagenes-activated_CD8
8	1.0	0 / 21	Angelova Immune-metagenes-central_memory_CD4
9	1.0	0 / 17	Angelova Immune-metagenes-central_memory_CD8
10	1.0	0 / 7	Angelova Immune-metagenes-cytotoxic_cells
11	1.0	0 / 25	Angelova Immune-metagenes-DC
12	1.0	0 / 12	Angelova Immune-metagenes-effector_memory_CD4
13	1.0	0 / 32	Angelova Immune-metagenes-effector_memory_CD8
14	1.0	0 / 14	Angelova Immune-metagenes-eosinophil
15	1.0	0 / 19	Angelova Immune-metagenes-IDC

Rank	p-value	#in/all	Geneset
1	7e-04	6 / 64	Harbst_melanoma_lowgrade_spot
2	6e-02	8 / 249	Gerber_wtwt_melanoma-cells-SpotE
3	1e-01	2 / 41	Tirosh_top50_correlated_genes_PC3
4	2e-01	1 / 16	Hugo_melanoma-all-LEF1_UP
5	3e-01	3 / 119	TCGA_melanoma_MITF_low
6	3e-01	1 / 24	Gerami_melanoma-metastatic-risk_DN
7	5e-01	1 / 38	Hugo_melanoma-BRAFmut-MET_UP
8	5e-01	1 / 39	Tirosh_melanoma_specific_genes
9	5e-01	4 / 230	Gerber_wtwt_melanoma-cells-SpotC
10	7e-01	3 / 204	Landsberg_dedifferentiation_down
11	7e-01	1 / 75	Tirosh_Endothelial-cell_specific_genes-melanoma
12	7e-01	1 / 78	Tirosh_CAF-cell_specific_genes
13	7e-01	2 / 236	Gerber_wtwt_group3-specific_genes
14	9e-01	1 / 171	Landsberg_dedifferentiation_up
15	1e+00	1 / 185	Tirosh_genes_from_malignant_cells_in_Mel79-melanoma

Rank	p-value	#in/all	Geneset
1	0.2	2 / 48	Burnham_viral_DN
2	0.3	1 / 18	Sciicluna_UP
3	0.3	2 / 68	Burnham_sep_vs_con_UP
4	0.3	2 / 71	Burnham_sep_fp_vs_con_UP
5	0.6	1 / 52	Burnham_day1_vs_5_DN
6	0.6	1 / 57	Burnham_day1_vs_5_UP
7	0.9	1 / 122	Terre_IMS_influenza_meta_signature
8	1.0	0 / 56	Burnham_sep_vs_con_DN
9	1.0	0 / 48	Burnham_sep_fp_vs_con_DN
10	1.0	0 / 57	Burnham_viral_UP
11	1.0	0 / 54	Burnham_timecourse
12	1.0	0 / 41	Sciicluna_DN
13	1.0	0 / 37	Sweeney_viral_up
14	1.0	0 / 33	Sweeney_viral_dn
15	1.0	0 / 179	Terre_MSX_multiple_respiratory_viruses_dn

Rank	p-value	#in/all	Geneset
1	1e-07	44 / 1148	HEBENSTREIT_low_expression_TF
2	8e-01	14 / 1041	ICGC_P300_targets
3	9e-01	4 / 415	ICGC_RxraPcr1_targets
4	1e+00	3 / 485	ICGC_NrsIPcr2_targets
5	1e+00	26 / 2321	ICGC_Rad21_targets
6	1e+00	2 / 522	ICGC_SRFcr2_targets
7	1e+00	14 / 1636	ICGC_Bcl11_targets
8	1e+00	6 / 1032	ICGC_Usf1_targets
9	1e+00	41 / 3778	ICGC_Pol24_targets
10	1e+00	5 / 1107	ICGC_Myc_targets
11	1e+00	4 / 1025	ICGC_NrsPcr1_targets
12	1e+00	4 / 1089	ICGC_Ets1_targets
13	1e+00	43 / 4264	ICGC_Pax5_targets
14	1e+00	28 / 3213	ICGC_Pu1_targets
15	1e+00	5 / 1241	KIM_MYC_targets

Rank	p-value	#in/all	Geneset
1	0.002	3 / 16	LIU_LIVER_CANCER
2	0.106	12 / 480	Lembcke_ColonInflammation
3	0.183	1 / 12	LIU_BREAST_CANCER
4	0.196	1 / 13	GENTLES_modul17
5	0.196	1 / 13	BENTINK_e2f3.1
6	0.210	1 / 14	LIU_PROSTATE_CANCER_DN
7	0.210	1 / 14	GENTLES_modul13
8	0.236	1 / 16	GENTLES_modul6
9	0.286	1 / 20	PanCan_ChromMod_geneset_nanostring
10	0.386	2 / 80	PanCan_JAK-ST_geneset_nanostring
11	0.454	1 / 36	ZHANG_MM_up
12	0.606	3 / 187	PanCan_PIK_geneset_nanostring
13	0.717	0 / 11	LIU_PROSTATE_CANCER_UP
14	0.802	1 / 96	PanCan_TXmisReg_geneset_nanostring
15	0.816	5 / 409	Lembcke_Normal_vs_Adenoma

Rank	p-value	#in/all	Geneset
1	1e-16	124 / 3918	Tcells_peripheral_blood_14_ReprPCWk
2	1e-14	116 / 3734	Tcells_peripheral_blood_13_ReprPC
3	5e-03	81 / 2667	ReprPCWk_MSC_Adipocytes
4	9e-10	84 / 2700	Thelper_cells_peripheral_blood_14_ReprPCWk
5	9e-10	78 / 2417	9_ReprPCWk_Melanocytes
6	1e-09	77 / 2374	9_ReprPCWk_Fibroblasts
7	1e-08	75 / 2408	9_ReprPCWk_Skeletal_Muscle
8	1e-08	74 / 2375	10_ReprPC_Fibroblasts
9	1e-07	105 / 4079	15_Quies_ESC_Endoderm
10	1e-06	81 / 2984	natural_killer_cells_peripheral_blood_14_ReprPCWk
11	1e-06	73 / 2600	HSC_14_ReprPCWk
12	2e-06	86 / 3272	monocytes_peripheral_blood_14_ReprPCWk
13	4e-06	81 / 3069	Tregulatory_cells_peripheral_blood_14_ReprPCWk
14	2e-06	61 / 2173	HSC_13_ReprPC
15	2e-05	77 / 3001	Bcells_peripheral_blood_14_ReprPCWk

Rank	p-value	#in/all	Geneset
1	1e-99	115 / 218	HSIAO_LIVER_SPECIFIC_GENES
2	3e-56	52 / 147	CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_DN
3	7e-46	51 / 208	CAIRO_LIVER_DEVELOPMENT_DN
4	1e-44	32 / 52	SL_LIVER
5	9e-250	52 / 250	CAIRO_HEPATOBLASTOMA_DN
6			

Correlation Cluster

Spot Summary: I

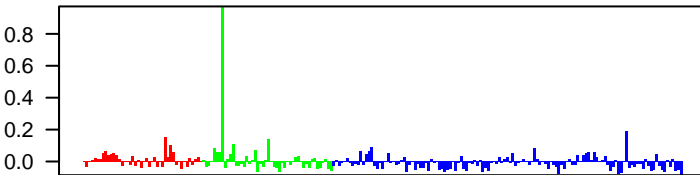
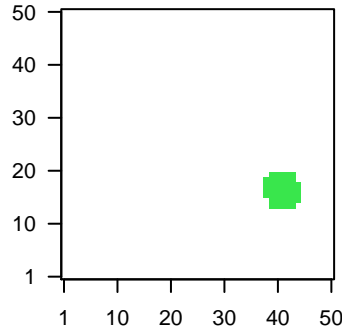
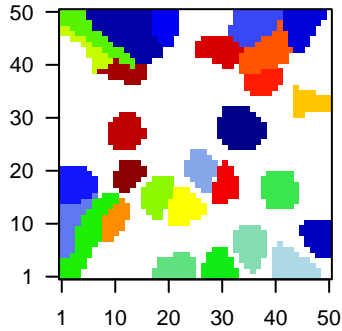
metagenes = 43
genes = 384

<r> metagenes = 0.95
<r> genes = 0.1
beta: r2= 0.54 / log p= -Inf

samples with spot = 4 (1.8 %)
mBL : 1 (2.3 %)
intermediate : 2 (4.2 %)
non-mBL : 1 (0.8 %)

Overview Map

Spot

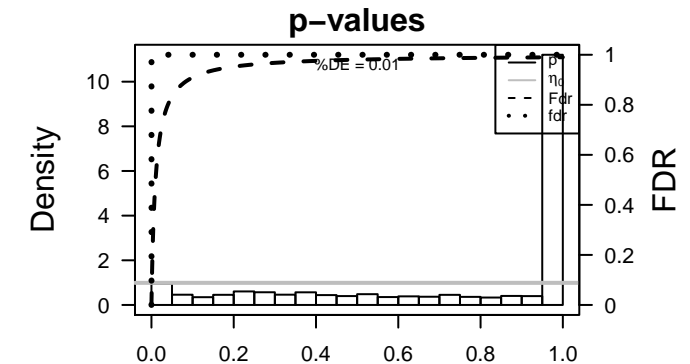


Spot Genelist

Rank	ID	max e	r	min e	Description
1	209888_s_at	2.71	-0.65	0.48	MYL1 myosin light chain 1 [Source:HGNC Symbol;Acc:HGNC:7582
2	204865_at	2.65	-0.72	0.52	CA3 carbonic anhydrase 3 [Source:HGNC Symbol;Acc:HGNC:137
3	206793_at	2.56	-0.94	0.26	PNMT phenylethanolamine N-methyltransferase [Source:HGNC Syr
4	205363_at	2.4	-0.69	0.39	BBOX1 gamma-butyrobetaine hydroxylase 1 [Source:HGNC Symbol;
5	206045_s_at	2.39	-0.93	0.29	NOL4 nucleolar protein 4 [Source:HGNC Symbol;Acc:HGNC:7870]
6	209840_s_at	2.32	-0.65	0.41	LRRN3 leucine rich repeat neuronal 3 [Source:HGNC Symbol;Acc:HC
7	205388_at	2.24	-0.82	0.34	TNNC2 troponin C2, fast skeletal type [Source:HGNC Symbol;Acc:HC
8	205951_at	2.23	-0.46	0.46	MYH1 myosin heavy chain 1 [Source:HGNC Symbol;Acc:HGNC:756
9	219692_at	2.17	-1.61	0.1	KREMEN3 single containing transmembrane protein 2 [Source:HGNC S
10	209841_s_at	2.16	-0.89	0.39	LRRN3 leucine rich repeat neuronal 3 [Source:HGNC Symbol;Acc:HC
11	206502_s_at	2.15	-0.97	0.18	INSM1 INSM transcriptional repressor 1 [Source:HGNC Symbol;Acc:
12	205529_s_at	2.09	-0.74	0.16	RUNX1T1 RUNX1 translocation partner 1 [Source:HGNC Symbol;Acc:H
13	205347_s_at	1.97	-1.15	0.15	TMSB15A thymosin beta 15a [Source:HGNC Symbol;Acc:HGNC:30744;
14	209757_s_at	1.94	-0.99	0.26	MYCN MYCN proto-oncogene, bHLH transcription factor [Source:HC
15	207445_s_at	1.92	-0.85	0.34	CCR9 C-C motif chemokine receptor 9 [Source:HGNC Symbol;Acc:
16	206318_at	1.84	-0.63	0.6	EPPIN epididymal peptidase inhibitor [Source:HGNC Symbol;Acc:HC
17	213894_at	1.84	-0.59	0.39	THSD7A thrombospondin type 1 domain containing 7A [Source:HGNC
18	214920_at	1.79	-0.73	0.41	THSD7A thrombospondin type 1 domain containing 7A [Source:HGNC
19	206404_at	1.78	-0.73	0.34	FGF9 fibroblast growth factor 9 [Source:HGNC Symbol;Acc:HGNC:.
20	220027_s_at	1.72	-0.81	0.02	RASIP1 Ras interacting protein 1 [Source:HGNC Symbol;Acc:HGNC:.

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	7e-13	123 / 3168	Lymp/ HOPP_Repressed
2	2e-09	57 / 1148	TF HEBENSTREIT_low expression TF
3	3e-09	187 / 6368	Colon LaPointe_mucosa-position_kmeans_F_cecum colon_transverse colon_UP
4	1e-07	18 / 184	Chr Chr 18
5	6e-07	45 / 958	Colon LaPointe_mucosa-position_kmeans_D_transverse colon_UP_
6	2e-06	64 / 1652	Gliom Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
7	2e-05	34 / 730	GSE/ BENPORATH_ES_WITH_H3K27ME3
8	3e-05	6 / 29	GSE/ KEGG_REGULATION_OF_AUTOPHAGY
9	3e-05	5 / 18	BP positive regulation of peptidyl-serine phosphorylation of STAT protein
10	4e-05	66 / 1894	Lymp/ HOPP_Poised_promoter
11	7e-05	25 / 492	Colon LaPointe_mucosa-position_kmeans_C_cecum colon_ascending colon_tra
12	8e-05	12 / 146	GSE/ LEE_NEURAL_CREST_STEM_CELL_UP
13	8e-05	7 / 49	GSE/ EBAUER_MYOGENIC_TARGETS_OF_PAX3_FOXO1_FUSION
14	1e-04	31 / 697	GSE/ BENPORATH_SUZ12_TARGETS
15	2e-04	5 / 25	BP gastrulation
16	2e-04	4 / 14	MF type I interferon receptor binding
17	2e-04	4 / 14	GSE/ REACTOME_SIGNALING_BY_NODAL
18	2e-04	4 / 14	GSE/ NIELSEN_LIPOSARCOMA_DN
19	2e-04	13 / 185	GSE/ KONDO_EZH2_TARGETS
20	2e-04	4 / 15	GSE/ LIN_TUMOR_ESCAPE_FROM_IMMUNE_ATTACK
21	3e-04	13 / 194	HM HALLMARK_MYOGENESIS
22	3e-04	4 / 16	BP natural killer cell activation involved in immune response
23	4e-04	13 / 198	GSE/ EBAUER_TARGETS_OF_PAX3_FOXO1_FUSION_UP
24	4e-04	4 / 17	BP embryonic pattern specification
25	4e-04	8 / 83	Refer WIRTH_Muscle
26	4e-04	34 / 854	Color LaPointe_mucosa-position_kmeans_A_ascending colon_UP_
27	5e-04	16 / 284	GSE/ MIKKELSEN_MCV6_HCP_WITH_H3K27ME3
28	5e-04	5 / 31	BP cellular response to BMP stimulus
29	5e-04	5 / 31	GSE/ BONOME_OVARIAN_CANCER_POOR_SURVIVAL_UP
30	5e-04	4 / 18	BP T cell activation involved in immune response
31	5e-04	4 / 18	GSE/ HUMMERICH_BENIGN_SKIN_TUMOR_DN
32	6e-04	5 / 32	Gliom WIRTH_PN subtype
33	7e-04	5 / 33	CC myofibril
34	7e-04	20 / 414	Gliom Hopp_Sturm_GBM_Epi3_A_adult_fetus_UP_G34_DN
35	1e-03	6 / 53	Lymp LENZ_Stromal signature 2
36	1e-03	4 / 22	MF cytokine receptor binding
37	1e-03	9 / 120	GSE/ MARTORIATI_MDM4_TARGETS_NEUROEPITHELIUM_DN
38	1e-03	3 / 11	GSE/ DELASERNA_TARGETS_OF_MYOD_AND_SMARCA4
39	2e-03	4 / 24	BP outflow tract septum morphogenesis
40	2e-03	18 / 382	CC synapse



Rank	p-value	#in/all	Geneset
1	0.03	6 / 107	HORVATH_aging_genes_meth_UP
2	0.27	18 / 382	TESCHENDORFF_age_hypermethylated
3	0.60	2 / 92	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	3e-05	5 / 18	positive regulation of peptidyl-serine phosphorylation of STAT protein
2	3e-04	5 / 25	gastrulation
3	3e-04	4 / 16	natural killer cell activation involved in immune response
4	4e-04	4 / 17	embryonic pattern specification
5	5e-04	5 / 31	cellular response to BMP stimulus
6	5e-04	4 / 18	T cell activation involved in immune response
7	5e-04	4 / 24	outflow tract septum morphogenesis
8	2e-03	7 / 80	lung development
9	3e-03	4 / 27	B cell proliferation
10	3e-03	4 / 27	regulation of type I interferon-mediated signaling pathway
11	3e-03	3 / 14	activin receptor signaling pathway
12	3e-03	3 / 14	regulation of transforming growth factor beta receptor signaling pathway
13	3e-03	4 / 29	response to exogenous dsRNA
14	3e-03	5 / 47	regulation of cardiac conduction
15	4e-03	25 / 646	cell differentiation

Cancer Rank	p-value	#in/all	Geneset
1	0.003	5 / 47	PanCan_TGF-B_geneset_nanostring
2	0.015	8 / 147	PanCan_MAPK_geneset_nanostring
3	0.027	2 / 12	BEN-PORATH_DN
4	0.152	2 / 32	KUIPER_MM_good_survival
5	0.166	5 / 134	PanCan_RAS_geneset_nanostring
6	0.181	1 / 14	LIU_PROSTATE_CANCER_DN
7	0.222	0 / 16	LIU_PROSTATE_CANCER_UP
8	0.231	0 / 12	HLA2_signature
9	0.264	1 / 14	GUSTAFSON_PI3K_DN
10	0.280	1 / 15	BEN-PORATH_UP
11	0.280	1 / 15	GENTLES_modul4
12	0.286	1 / 16	LIU_LIVER_CANCER
13	0.296	1 / 16	GENTLES_modul16
14	0.311	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
15	0.326	1 / 18	PanCan_Notch_geneset_nanostring

CC Rank	p-value	#in/all	Geneset
1	7e-04	5 / 33	myofibril
2	2e-03	18 / 382	synapse
3	2e-03	7 / 8	sarcolemma
4	8e-03	4 / 37	T-tubule
5	1e-02	3 / 21	muscle myosin complex
6	1e-02	7 / 113	receptor complex
7	1e-02	36 / 1128	integral component of plasma membrane
8	4 / 43	2 / 10	intercalated disc
9	2e-02	2 / 10	apical junction complex
10	2e-02	11 / 254	axon
11	2e-02	3 / 29	histone deacetylase complex
12	3e-02	2 / 13	somatodendritic compartment
13	4e-02	3 / 19	dystrophin-associated glycoprotein complex
14	5e-02	82 / 3210	plasma membrane
15	6e-02	2 / 18	myosin filament

Chr Rank	p-value	#in/all	Geneset
1	1e-07	18 / 184	Chr 18
2	8e-02	6 / 139	Chr 21
3	2e-01	14 / 490	Chr 10
4	2e-01	11 / 369	Chr 20
5	2e-01	14 / 492	Chr 9
6	3e-01	14 / 554	Chr 5
7	3e-01	19 / 776	Chr 17
8	3e-01	11 / 437	Chr 8
9	3e-01	20 / 833	Chr 19
10	4e-01	6 / 242	Chr 13
11	5e-01	9 / 403	Chr 14
12	6e-01	17 / 832	Chr 2
13	7e-01	14 / 230	Chr 12
14	7e-01	11 / 556	Chr X
15	7e-01	13 / 669	Chr 6

Chromatin states Rank	p-value	#in/all	Geneset
1	2e-14	110 / 2535	T CD8+ naive cells peripheral blood_14_ReprPCWk
2	7e-14	113 / 2700	Thelper cells peripheral blood_14_ReprPCWk
3	9e-14	113 / 2684	HSC_14_ReprPCWk
4	7e-13	121 / 3089	Regulatory cells peripheral blood_14_ReprPCWk
5	1e-12	99 / 2300	Thelper cells peripheral blood_13_ReprPC
6	1e-12	125 / 3272	monocytes peripheral blood_14_ReprPCWk
7	2e-12	95 / 2173	HSC_13_ReprPC
8	2e-12	117 / 2684	natural killer cells peripheral blood_14_ReprPCWk
9	2e-12	111 / 2765	Regulatory cells peripheral blood_13_ReprPC
10	4e-12	140 / 3918	Tcells peripheral blood_14_ReprPCWk
11	5e-12	135 / 3734	Tcells peripheral blood_13_ReprPC
12	2e-11	82 / 1799	T CD8+ naive cells peripheral blood_13_ReprPC
13	2e-11	98 / 2405	Bcells peripheral blood_13_ReprPC
14	2e-11	88 / 2015	ReprPC_Color
15	2e-11	80 / 1744	ReprPCWk_Color

Colon Cancer Rank	p-value	#in/all	Geneset
1	3e-09	187 / 6368	LaPointe_mucosa-position_kmeans_F_cecum_colon_transverse_colon_UP_
2	6e-07	45 / 958	LaPointe_mucosa-position_kmeans_D_transverse_colon_UP
3	7e-05	25 / 492	LaPointe_mucosa-position_kmeans_C_cecum_colon_ascending_colon_trans
4	4e-04	34 / 854	LaPointe_mucosa-position_kmeans_A_ascending_colon_UP_
5	3e-03	17 / 376	Lembcke_TCGA_expr_kmeans_M_CIMPH_DN
6	4e-03	15 / 318	Lembcke_TCGA_meth_kmeans_E_CIMPH_UP
7	6e-03	21 / 532	LaPointe_mucosa-position_kmeans_B_ascending_colon_transverse_colon_U
8	2e-02	3 / 25	Ang_CRC-CIMPH-vs-L_hypo
9	3e-02	8 / 164	Lembcke_TCGA_meth_kmeans_B_Cluster4_DN
10	4e-02	2 / 14	TCGA_Mutated-in-CRC_non-hypermethylated
11	4e-02	3 / 35	Ang_CRC_Hypomethylated
12	5e-02	2 / 16	Vilar_mutated-in-CRC-Camp
13	5e-02	2 / 16	Vilar_non-hypermethylated-in-CRC
14	6e-02	15 / 448	Lembcke_TCGA_meth_kmeans_J_CIMPH_DN
15	1e-01	10 / 290	Lembcke_TCGA_meth_kmeans_O_CIMPH_DN

Glioma Rank	p-value	#in/all	Geneset
1	2e-06	64 / 1652	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
2	6e-04	5 / 32	WIRTH_PN_subtype
3	7e-04	20 / 414	Hopp_Sturm_GBM_Epi3_A_adult_fetus_UP_G34_DN
4	2e-03	13 / 239	Scov_0_001_Sturm_M3_RTK_II_Classic_DN
5	3e-03	11 / 191	Scov_0_5_Sturm_G2_RTK_I_PDGFR_A_DN
6	9e-03	3 / 20	Mukasa_UP_in_Oligodendrogloma_with_1pLOH
7	1e-02	3 / 21	Barbus_GBM_STS_vs_STS
8	1e-02	5 / 61	Christensen_hypomethylated_in_secondary_glioblastoma
9	1e-02	5 / 67	Weiler_LGG_tp19Del-vs-intact_UP
10	2e-02	12 / 296	Hopp_Sturm_GBM_Epi3_no_zentr_4_IDH_UP_adult_fetus_K27_DN
11	2e-02	2 / 11	WILLSCHER_GBM_Verhaak-PN (mut&wt)_up (I)
12	4e-02	2 / 15	neurons_glio
13	5e-02	6 / 121	Hopp_Sturm_GBM_Epi3_F_RTK_II_UP_adult_fetus_K27_DN
14	6e-02	10 / 264	Hopp_Sturm_GBM_Epi3_no_zentr_3_RTK_II_UP_adult_fetus_K27_DN
15	7e-02	5 / 102	WILLSCHER_GBM_Verhaak-PN (mut&wt)_up (MES&L down)

GSEA C2 Rank	p-value	#in/all	Geneset
1	2e-05	34 / 730	BENPORATH_ES_WITH_H3K27ME3
2	3e-05	6 / 29	KEGG_REGULATION_OF_AUTOPIAGY
3	8e-05	12 / 146	LEE_NEURAL_CREST_STEM_CELL_UP
4	8e-05	7 / 49	GENESET_MYOGENIC_TARGETS_OF_PAX3_FOXO1_FUSION
5	1e-04	31 / 697	BENPORATH_SUIZ12_TARGETS
6	2e-04	4 / 14	REACTOME_SIGNALING_BY_NODAL
7	2e-04	4 / 14	NIELSEN_LIPOSARCOMA_DN
8	2e-04	13 / 185	KONDO_E2H2_TARGETS
9	2e-04	4 / 15	LIU_TUMOR_PCAPAFE_FROM_IMMUNE_ATTACK
10	4e-04	13 / 305	EBAUER_TARGETS_OF_PAX3_FOXO1_FUSION_UP
11	5e-04	16 / 284	MIKKELSEN_MCV6_HCP_WITH_H3K27ME3
12	5e-04	5 / 31	BONOME_OVARIAN_CANCER_POOR_SURVIVAL_UP
13	5e-04	4 / 18	HUMMERTICH_BENIGN_SKIN_TUMOR_DN
14	1e-03	9 / 120	MANTORIATTI_MDMA4_TARGETS_TUMOR_EPITHELIUM_DN
15	1e-03	3 / 11	DELASERNA_TARGETS_OF_MYOD_AND_SMARCA4

LM Rank	p-value	#in/all	Geneset
1	3e-04	13 / 194	HALLMARK_MYOGENESIS
2	4e-02	3 / 35	HALLMARK_HEDGEHOG_SIGNALING
3	5e-02	3 / 39	HALLMARK_PANCREAS_BETA_CELLS
4	9e-02	6 / 141	HALLMARK_UV_RESPONSE_DN
5	1e-01	7 / 194	HALLMARK_KRAS_SIGNALING_UP
6	1e-01	4 / 23	HALLMARK_NOTCH_SIGNALING
7	2e-01	2 / 34	HALLMARK_ANGIOGENESIS
8	2e-01	6 / 195	HALLMARK_KRAS_SIGNALING_DN
9	3e-01	6 / 196	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
10	4e-01	3 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING
11	4e-01	5 / 187	HALLMARK_XENOBIOTIC_METABOLISM
12	4e-01	5 / 187	HALLMARK_INFLAMMATORY_RESPONSE
13	6e-01	1 / 38	HALLMARK_WNT_BETA_CATENIN_SIGNALING
14	6e-01	4 / 188	HALLMARK_HYPOXIA
15	6e-01	4 / 194	HALLMARK_ESTROGEN_RESPONSE_EARLY

Immunome Rank	p-value	#in/all	Geneset
1	0.09	2 / 23	Angelova Immune-metagenes-Th2
2	0.10	2 / 25	Angelova Immune-metagenes-Dc
3	0.20	2 / 38	Angelova Immune-metagenes-mast-cells
4	0.37	1 / 21	Angelova Immune-metagenes-central_memory_CD4
5	1.00	0 / 13	Angelova Immune-metagenes-activated_B-cells
6	1.00	0 / 26	Angelova Immune-metagenes-activated_CD4
7	1.00	0 / 19	Angelova Immune-metagenes-activated_CD8
8	1.00	0 / 17	Angelova Immune-metagenes-central_memory_CD8
9	1.00	0 / 7	Angelova Immune-metagenes-cytotoxic_cells
10	1.00	0 / 12	Angelova Immune-metagenes-effector_memory_CD4
11	1.00	0 / 32	Angelova Immune-metagenes-effector_memory_CD8
12	1.00	0 / 14	Angelova Immune-metagenes-eosinophil
13	1.00	0 / 19	Angelova Immune-metagenes-iDC
14	1.00	0 / 13	Angelova Immune-metagenes-immature_B-cells
15	1.00	0 / 11	Angelova Immune-metagenes-macrophages

Lifestyle Rank	p-value	#in/all	Geneset
1	0.01	5 / 52	DUMEAUX_Smoking enriched genes
2	0.14	1 / 6	DUMEAUX_Hormon therapy in non smokers literature genes up
3	0.30	1 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
4	0.50	1 / 32	Marjolein_ageing-genes_DN
5	0.94	2 / 210	Horuth_BMI-associated-genes_DN
6	0.96	1 / 150	Horuth_BMI-associated-genes_UP
7	1.00	0 / 10	DUMEAUX_Smoking literature genes up
8	1.00	0 / 4	DUMEAUX_Exercise 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 / 9	DUMEAUX_Monocytes in smokers literature genes up
12	1.00	0 / 12	DUMEAUX_Women related BMI literature genes up
13	1.00	0 / 22	DUMEAUX_High bmi enriched genes
14	1.00	0 / 22	DUMEAUX_Fasting enriched genes
15	1.00	0 / 14	Huan_blood-pressure_SBP_signature

Lymphoma Rank	p-value	#in/all	Geneset
1	7e-13	123 / 3168	HOPP_Repressed
2	4e-05	66 / 1894	HOPP_Poised_promoter
3	1e-03	3 / 53	LENZ_Stromal_signature_2
4	2e-02	7 / 130	Hopp_Lymphoma_Epi1_no_zentr_5_B.cell_GCB_UP
5	3e-02	4 / 54	Hopp_Lymphoma_Epi1_no_zentr_1_B.cell_DN
6	4e-02	3 / 35	Subero_MM_hyper_meth
7	4e-02	5 / 87	Hopp_Lymphoma_Epi1_with_zentr_v_B.cell_DN
8	5e-02	5 / 87	HOPP_Heterochrom
9	5e-02	5 / 94	Hopp_Lymphoma_Epi1_with_zentr_iii_B.cell_GCB_UP
10	8e-02	3 / 46	Subero_DLBCL_hypo_meth
11	8e-02	48 / 1814	HOPP_Repetitive
12	9e-02	2 / 23	Subero_mBL_hypo_meth
13	2e-01	3 / 70	Subero_FL_hyper_meth
14	2e-01	1 / 10	MASCOUE_ABC_UP
15	2e-01	1 / 12	Subero_MM_hypo_meth

Melanoma Rank	p-value	#in/all	Geneset
1	0.04	1 / 2	Melanoma Epi-Enzyme Cluster 2
2	0.07	3 / 37	Hugo_melanoma-all-MET_DN
3	0.20	2 / 38	Hugo_melanoma-BRAFmut-MET_UP
4	0.23	7 / 230	Gerber_wtwt_melanoma-cells-SpotC
5	0.31	1 / 17	Hugo_melanoma-all-MET_UP
6	0.31	5 / 171	Landsberg_dedifferentiation_up
7	0.39	7 / 276	Gerber_wtwt_melanoma-cells-SpotB
8	0.41	2 / 65	Harbst_melanoma_lowgrade_up
9	0.41	2 / 65	Harbst_melanoma_highgrade_up
10	0.49	2 / 75	Tirosh_Endothelial-cell specific genes-melanoma
11	0.51	2 / 78	Tirosh_CAF-cell specific genes
12	0.57	1 / 39	Tirosh_top50 correlated genes PC4
13	0.57	1 / 39	Tirosh_top50 correlated genes PC5
14	0.64	1 / 46	Tirosh_top50 correlated genes PCs
15	0.73	1 / 59	TCGA_melanoma_keratin_high

MF Rank	p-value	#in/all	Geneset
1	2e-04	4 / 14	type I interferon receptor binding
2	1e-03	4 / 22	cytokine receptor binding
3	3e-03	16 / 337	g-protein coupled receptor activity
4	8e-03	4 / 37	growth factor binding
5	1e-02	14 / 329	RNA polymerase II proximal promoter sequence-specific DNA binding
6	1e-02	3 / 23	alpha-tubulin binding
7	2e-02	6 / 94	ion channel binding
8	2e-02	4 / 46	SH3/SH2 adaptor activity
9	2e-02	2 / 10	ATPase-coupled anion transmembrane transporter activity
10	2e-02	2 / 10	I-SMAD binding
11	2e-02	2 / 11	tropomyosin binding
12	2e-02	18 / 500	signal transducer activity
13	3e-02	3 / 30	histone-lysine N-methyltransferase activity
14	3e-02	2 / 12	actin binding
15	3e-02	2 / 12	calcium-transporting ATPase activity

miRNA target Rank	p-value	#in/all	Geneset
1	0.03	6 / 107	hsa-miR-24
2	0.05	2 / 17	hsa-miR-609
3	0.06	4 / 68	hsa-miR-505
4	0.06	3 / 42	hsa-miR-28-3p
5	0.06	2 / 19	hsa-miR-596
6	0.06	2 / 19	hsa-miR-632
7	0.07	3 / 44	hsa-miR-455-5p
8	0.08	2 / 22	hsa-miR-941
9	0.10	3 / 45	hsa-miR-892b
10	0.11	4 / 85	hsa-miR-499-5p
11	0.13	4 / 89	hsa-miR-1248
12	0.13	4 / 89	hsa-miR-624
13	0.16	3 / 63	hsa-miR-30a*
14	0.16	5 / 133	hsa-miR-298

Correlation Cluster

Spot Summary: J

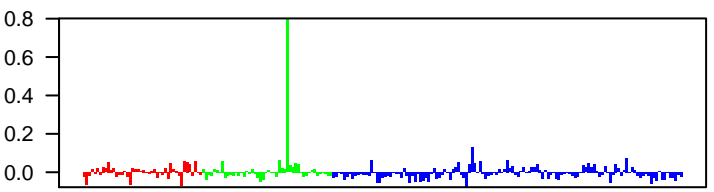
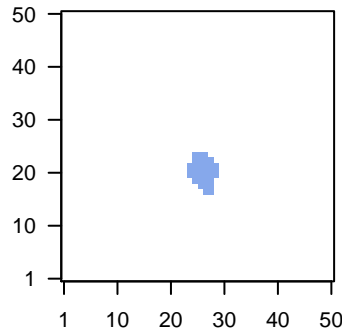
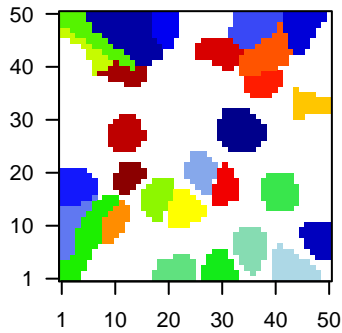
metagenes = 34
genes = 377

<r> metagenes = 0.94
<r> genes = 0.07
beta: r2= 0.12 / log p= -6.94

samples with spot = 1 (0.5 %)
intermediate : 1 (2.1 %)

Overview Map

Spot

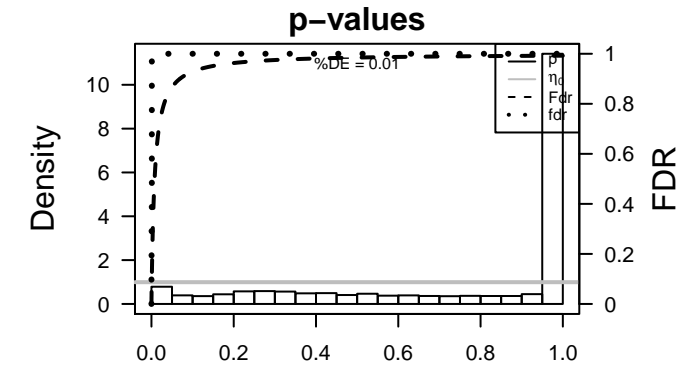


Spot Genelist

Rank	ID	max e	r	min e	Description
1	203215_s_at	2.09	-0.79	0.16	MYO6 myosin VI [Source:HGNC Symbol;Acc:HGNC:7605]
2	205177_at	2.03	-0.59	0.49	TNNI1 troponin I1, slow skeletal type [Source:HGNC Symbol;Acc:HC
3	220179_at	1.97	-0.73	0.11	DPEP3 dipeptidase 3 [Source:HGNC Symbol;Acc:HGNC:23029]
4	216573_at	1.88	-0.75	0.15	
5	219578_s_at	1.76	-0.64	0.31	CPEB1 cytoplasmic polyadenylation element binding protein 1 [Sourc
6	206569_at	1.6	-0.7	0.27	IL24 interleukin 24 [Source:HGNC Symbol;Acc:HGNC:11346]
7	210094_s_at	1.58	-0.67	0.18	PARD3 par-3 family cell polarity regulator [Source:HGNC Symbol;Ac
8	208491_s_at	1.57	-0.57	0.42	PGM5 phosphoglucomutase 5 [Source:HGNC Symbol;Acc:HGNC:8]
9	211781_x_at	1.55	-0.85	0.25	
10	216293_at	1.47	-1.03	0.4	
11	214954_at	1.47	-0.61	0.18	SUSD5 sushi domain containing 5 [Source:HGNC Symbol;Acc:HGNC
12	202588_at	1.46	-1.05	0.16	AK1 adenylate kinase 1 [Source:HGNC Symbol;Acc:HGNC:361]
13	218537_at	1.44	-1.31	0.23	HCFC1R1 host cell factor C1 regulator 1 [Source:HGNC Symbol;Acc:HC
14	207442_at	1.42	-0.88	0.38	CSF3 colony stimulating factor 3 [Source:HGNC Symbol;Acc:HGNC
15	210400_at	1.42	-0.63	0.44	GRIN2C glutamate ionotropic receptor NMDA type subunit 2C [Source
16	205426_s_at	1.39	-1.12	0.12	HIP1 huntingtin interacting protein 1 [Source:HGNC Symbol;Acc:Hi
17	211690_at	1.37	-0.72	0.37	
18	205522_at	1.36	-0.56	0.34	
19	217230_at	1.33	-0.82	0.22	
20	216936_at	1.33	-0.9	0.17	

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	2e-13	194 / 6368	Colon LaPointe_mucosa-position_kmeans_F_ Cecum colon_transverse colon_UP
2	3e-07	104 / 3168	LympI HOPP_Repressed
3	1e-06	49 / 1148	TF HEBENSTREIT_low expression TF
4	6e-05	7 / 48	BP bone development
5	2e-04	19 / 352	Refer WIRTH_Nervous System
6	2e-04	15 / 240	GSE# KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERACTION
7	2e-04	3 / 6	GSE# REACTOME_OPSINS
8	2e-04	4 / 15	MF extracellularly glutamate-gated ion channel activity
9	2e-04	4 / 15	MF ionotropic glutamate receptor activity
10	3e-04	17 / 311	GSE# SHEN_SMARCA2_TARGETS_DN
11	4e-04	19 / 373	GSE# MIKKELSEN_MEF_HCP_WITH_H3K27ME3
12	4e-04	61 / 1894	Lymp HOPP_Poised_promoter
13	4e-04	9 / 105	Gliom WIRTH_Normal Brain
14	4e-04	6 / 46	BP retinoid metabolic process
15	5e-04	4 / 18	BP ionotropic glutamate receptor signaling pathway
16	5e-04	7 / 67	Gliom Weller_LGG_1p19qDel-vs-intact_UP
17	5e-04	6 / 49	BP regulation of protein stability
18	7e-04	40 / 1128	CC integral component of plasma membrane
19	8e-04	17 / 337	MF G-protein coupled receptor activity
20	1e-03	13 / 225	BP ion transmembrane transport
21	1e-03	4 / 22	BP phototransduction
22	1e-03	4 / 23	GSE# LOPES_METHYLATED_IN_COLON_CANCER_UP
23	1e-03	90 / 3210	CC plasma membrane
24	1e-03	3 / 11	BP suckling behavior
25	1e-03	9 / 126	Gliom ScoV_0.999_Sturm_E5_RTK II 'Classic'_UP_RTK I 'PDGFRA'_DN
26	1e-03	6 / 59	CC adherens junction
27	1e-03	4 / 24	BP outflow tract septum morphogenesis
28	2e-03	3 / 12	CC Golgi-associated vesicle membrane
29	2e-03	3 / 12	BP negative regulation of microtubule polymerization
30	2e-03	5 / 43	Refer WIRTH_Placenta
31	2e-03	6 / 65	BP excitatory postsynaptic potential
32	2e-03	15 / 310	CC dendrite
33	3e-03	5 / 46	CC clathrin-coated vesicle membrane
34	3e-03	14 / 284	GSE# MIKKELSEN_MCV6_HCP_WITH_H3K27ME3
35	3e-03	3 / 14	MF tau protein binding
36	3e-03	13 / 254	CC axon
37	3e-03	17 / 382	CC synapse
38	3e-03	18 / 417	GSE# REACTOME_GPCR_DOWNSTREAM_SIGNALING
39	3e-03	8 / 117	GSE# REACTOME_NEUROTRANSMITTER_RECEPTOR_BINDING_AND_DOW
40	3e-03	3 / 15	BP response to peptide



Rank	p-value	#in/all	Geneset
1	0.08	3 / 47	TESCHENDORFF_age_hypermethylated
2	0.39	3 / 107	HORVATH_aging_genes_meth UP
3	0.58	2 / 92	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	

Rank	p-value	#in/all	Geneset
1	7e-04	40 / 1128	integral component of plasma membrane
2	1e-03	90 / 3210	plasma membrane
3	1e-03	6 / 58	adherens junction
4	2e-03	3 / 12	Golgi-associated vesicle membrane
5	2e-03	15 / 310	dendrite
6	3e-03	5 / 46	clathrin-coated vesicle membrane
7	3e-03	13 / 254	axon
8	3e-03	17 / 382	synapse
9	5e-03	6 / 75	apical part of cell
10	8e-03	3 / 20	excitatory synapse
11	1e-02	4 / 40	chloride channel complex
12	1e-02	21 / 595	cell junction
13	2e-02	2 / 10	STAGA complex
14	2e-02	6 / 101	endomembrane system
15	2e-02	4 / 50	terminal bouton

Rank	p-value	#in/all	Geneset
1	2e-13	194 / 6368	LaPointe_mucosa-position_kmeans_F_cecum_colon_transverse_colon_UP
2	7e-03	29 / 854	LaPointe_mucosa-position_kmeans_A_ascending_colon_UP
3	3e-02	17 / 492	LaPointe_mucosa-position_kmeans_C_cecum_colon_ascending_colon_trans
4	3e-02	26 / 848	LaPointe_mucosa-position_kmeans_O_transverse_colon_UP
5	4e-02	12 / 318	Lembcke_TCGA_meth_kmeans_E_CIMP_H_UP
6	9e-02	10 / 290	Lembcke_TCGA_meth_kmeans_O_CIMP_H_DN
7	9e-02	2 / 24	Pentrack_CRC_TCGA_corr_S_normal_DN
8	1e-01	8 / 221	Lembcke_TCGA_meth_kmeans_A_Cluster4_DN
9	1e-01	26 / 958	LaPointe_mucosa-position_kmeans_D_transverse_colon_UP
10	1e-01	6 / 104	Lembcke_TCGA_meth_kmeans_B_Cluster4_DN
11	1e-01	9 / 278	Lembcke_TCGA_meth_kmeans_H_CIMP_L_UP_CIMP_H_DN
12	1e-01	14 / 532	LaPointe_mucosa-position_kmeans_B_ascending_colon_transverse_colon_U
13	3e-01	1 / 16	Budinska_B_Lower_crypt-like_UP
14	3e-01	12 / 483	Lembcke_TCGA-expr_kmeans_H_CIMP_H_UP_Cluster3_DN
15	3e-01	1 / 20	Kosinski_top-crypt-short-list

Rank	p-value	#in/all	Geneset
1	0.1	7 / 187	HALLMARK_INFLAMMATORY_RESPONSE
2	0.1	7 / 193	HALLMARK_HEME_METABOLISM
3	0.2	6 / 191	HALLMARK_P53_PATHWAY
4	0.3	4 / 122	HALLMARK_SPERMATOGENESIS
5	0.5	4 / 176	HALLMARK_ALLOGRAFT_REJECTION
6	0.5	3 / 34	HALLMARK_ANGIOGENESIS
7	0.5	1 / 35	HALLMARK_HEDGEHOG_SIGNALING
8	0.6	4 / 194	HALLMARK_KRAS_SIGNALING_UP
9	0.6	4 / 195	HALLMARK_KRAS_SIGNALING_DN
10	0.7	3 / 173	HALLMARK_MITOTIC_SPINDLE
11	0.7	3 / 174	HALLMARK_APICAL_JUNCTION
12	0.7	3 / 174	HALLMARK_XENOBIOTIC_METABOLISM
13	0.8	3 / 188	HALLMARK_HYPOXIA
14	0.8	2 / 130	HALLMARK_COAGULATION
15	0.8	2 / 133	HALLMARK_DNA_REPAIR

Rank	p-value	#in/all	Geneset
1	3e-07	104 / 3168	HOPP_Repressed
2	4e-04	61 / 1894	HOPP_Poised_promoter
3	5e-02	48 / 1814	HOPP_Repetitive
4	8e-02	3 / 49	LEE_Developmental_regulators
5	1e-01	5 / 118	Subero_INT_hyper_meth
6	1e-01	3 / 54	Hopp_Lymphoma_Epi1_no_zentr_1_B.cell_DN
7	2e-01	11 / 378	TARTE_Mature_plasma_cell_signature
8	2e-01	3 / 70	Subero_FL_hyper_meth
9	2e-01	1 / 13	Hopp_Lymphoma_Epi1_with_zentr_ii_MCL_mBL_UP
10	3e-01	1 / 14	Subero_B-ALL_hypo_meth
11	3e-01	2 / 47	Subero_B-ALL_hyper_meth
12	3e-01	3 / 87	Hopp_Lymphoma_Epi1_with_zentr_v_B.cell_DN
13	3e-01	3 / 91	Subero_T-ALL_hyper_meth
14	3e-01	4 / 132	Hopp_DLBCL_hyper_meth
15	3e-01	1 / 19	Subero_MCL_hypo_meth

Rank	p-value	#in/all	Geneset
1	0.02	3 / 25	hsa-miR-635
2	0.02	3 / 28	hsa-miR-296-5p
3	0.04	2 / 15	hsa-miR-542-5p
4	0.04	4 / 61	hsa-miR-942-5p
5	0.04	5 / 92	hsa-miR-491-3p
6	0.05	3 / 40	hsa-miR-642
7	0.08	2 / 22	hsa-miR-663
8	0.09	3 / 50	hsa-miR-409-5p
9	0.09	3 / 51	hsa-miR-648
10	0.09	3 / 51	hsa-miR-126*
11	0.13	3 / 60	hsa-miR-1321
12	0.14	1 / 7	hsa-miR-1180
13	0.16	1 / 8	hsa-miR-202*
14	0.17	1 / 9	hsa-miR-687
15	0.18	2 / 36	hsa-miR-412

Rank	p-value	#in/all	Geneset
1	0.13	0 / 13	Alternative lengthening of telomeres
2	NA	0 / 27	Nabetai_n1_letn_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	

Rank	p-value	#in/all	Geneset
1	6e-05	7 / 48	bone development
2	4e-04	6 / 46	retinoid metabolic process
3	5e-04	4 / 18	ionotropic glutamate receptor signaling pathway
4	5e-04	6 / 49	regulation of protein stability
5	1e-03	13 / 225	ion transmembrane transport
6	1e-03	4 / 22	phototransduction
7	1e-03	3 / 11	suckling behavior
8	1e-03	4 / 24	outflow tract septum morphogenesis
9	2e-03	3 / 12	negative regulation of microtubule polymerization
10	2e-03	6 / 65	excitatory postsynaptic potential
11	3e-03	3 / 15	response to peptide
12	4e-03	9 / 145	response to stimulus
13	4e-03	6 / 72	activation of cysteine-type endopeptidase activity involved in apoptotic proces
14	4e-03	3 / 16	synaptic vesicle endocytosis
15	4e-03	4 / 32	hair follicle development

Rank	p-value	#in/all	Geneset
1	0.005	17 / 403	Chr 14
2	0.111	23 / 833	Chr 19
3	0.171	18 / 659	Chr 7
4	0.252	15 / 585	Chr 7
5	0.281	19 / 776	Chr 17
6	0.370	13 / 548	Chr 16
7	0.390	13 / 556	Chr X
8	0.458	11 / 490	Chr 10
9	0.517	8 / 389	Chr 20
10	0.545	4 / 184	Chr 18
11	0.556	7 / 333	Chr 22
12	0.557	8 / 382	Chr 15
13	0.564	3 / 150	Chr 21
14	0.580	5 / 242	Chr 13
15	0.591	10 / 492	Chr 9

Rank	p-value	#in/all	Geneset
1	4e-04	9 / 105	WIRTH_Normal_Brain
2	5e-04	7 / 67	Weller_LGG_ip19qDel-vs-intact_UP
3	1e-03	9 / 126	Scov_0_999_Sturm_E5_RTK_II_Classic_UP_RTK_I_PDGFR_A_DN
4	6e-03	7 / 102	MULLSCHERER_BM_Verhaak-PN(mut&wt)_up_(MES&C_down)
5	7e-03	10 / 191	Scov_0_Sturm_C2_RTK_I_PDGFR_A_DN
6	8e-03	5 / 59	GIEZELI_GBM_STS_up_VS_LTS
7	1e-02	5 / 64	Weller_LGG_A_vs_O_DOWN
8	3e-02	5 / 81	GIEZELI_GBM_MGMTmethyl_up_VS_nonmethyl
9	3e-02	15 / 423	Down_a
10	3e-02	16 / 386	Hopp_Sturm_GBM_Epi3_no_zentr_4_IDH_UP_adult_fetus_K27_DN
11	4e-02	6 / 121	Hopp_Sturm_GBM_Epi3_F_RTK_II_UP_adult_fetus_K27_DN
12	6e-02	14 / 414	Hopp_Sturm_GBM_Epi3_A_adult_fetus_UP_G34_DN
13	8e-02	43 / 1652	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
14	8e-02	3 / 49	OPC
15	1e-01	9 / 264	Hopp_Sturm_GBM_Epi3_no_zentr_3_RTK_II_UP_adult_fetus_K27_DN

Rank	p-value	#in/all	Geneset
1	0.03	2 / 12	Angelova Immune-metagenes-NK56_dim
2	0.19	10	DUMEAUX Immune-metagenes-neutrophils
3	0.21	1 / 11	Angelova Immune-metagenes-macrophages
4	0.26	1 / 14	Angelova Immune-metagenes-eosinophil
5	0.27	1 / 15	Angelova Immune-metagenes-NK
6	0.33	1 / 39	Angelova Immune-metagenes-IDC
7	0.56	1 / 38	Angelova Immune-metagenes-mast-cells
8	0.76	1 / 67	Angelova Immune-metagenes-T-cells
9	1.00	0 / 13	Angelova Immune-metagenes-activated_B-cells
10	1.00	0 / 26	Angelova Immune-metagenes-activated_CD4
11	1.00	0 / 19	Angelova Immune-metagenes-activated_CD8
12	1.00	0 / 21	Angelova Immune-metagenes-central_memory_CD4
13	1.00	0 / 17	Angelova Immune-metagenes-central_memory_CD8
14	1.00	0 / 7	Angelova Immune-metagenes-cytotoxic_cells
15	1.00	0 / 25	Angelova Immune-metagenes-DC

Rank	p-value	#in/all	Geneset
1	0.01	4 / 41	Tirosh_top50 correlated genes PC3
2	0.07	8 / 204	Landisberg_dedifferentiation_down
3	0.17	3 / 68	Tirosh_housekeeping_genes
4	0.20	2 / 39	Tirosh_top50 correlated genes PC4
5	0.20	2 / 39	Tirosh_melanoma specific genes
6	0.24	4 / 119	TCGA_melanoma_MITF_low
7	0.25	13 / 497	Gerber_wt/wt_melanoma-cells-SpotD
8	0.34	1 / 34	Harbst_melanoma_lowgrade_up
9	0.44	2 / 71	Tirosh_Macrophage specific genes-melanoma
10	0.47	2 / 75	Tirosh_Endothelial-cell specific genes-melanoma
11	0.50	5 / 222	Gerber_wt/wt_melanoma-cells-SpotF
12	0.51	2 / 81	Tirosh_Genes in the MITF program
13	0.58	1 / 58	Hugo_melanoma-BRAFmut-MET_UP
14	0.61	5 / 249	Gerber_wt/wt_melanoma-cells-SpotE
15	0.72	4 / 230	Gerber_wt/wt_melanoma-cells-SpotC

Rank	p-value	#in/all	Geneset
1	0.3	1 / 18	Scicluna_UP
2	0.4	2 / 68	Burnham_sep_vs_con_UP
3	0.4	2 / 71	Burnham_cap_ip_vs_con_UP
4	0.6	1 / 48	Burnham_viral_DN
5	0.7	3 / 179	Terre_MSV_multiple_respiratory_viruses_dn
6	0.9	1 / 135	Terre_MSV_multiple_respiratory_viruses_up
7	1.0	0 / 56	Burnham_sep_vs_con_DN
8	1.0	0 / 48	Burnham_cap_ip_vs_con_DN
9	1.0	0 / 57	Burnham_viral_UP
10	1.0	0 / 57	Burnham_day1_vs_5_UP
11	1.0	0 / 52	Burnham_day1_vs_5_DN
12	1.0	0 / 54	Burnham_timecourse
13	1.0	0 / 41	Scicluna_DN
14	1.0	0 / 37	Sweeney_viral_up
15	1.0	0 / 33	Sweeney_viral_dn

Rank	p-value	#in/all	Geneset
1	1e-06	49 / 1148	HEBENSTREIT_low expression TF
2	1e-01	1 / 5	MYC_TFs
3	1e-01	14 / 485	ICGC_NrsIPcr2_targets
4	2e-01	1 / 12	NOWICK_TF
5	3e-01	14 / 549	ICGC_Atl3_targets
6	1e-01	1 / 16	MYC_Protein synthesis degradation UP
7	5e-01	50 / 2321	ICGC_Rad21_targets
8	6e-01	40 / 1941	ICGC_Bcl3_targets
9	7e-01	1 / 62	MYC_Targets UP
10	8e-01	28 / 1508	ICGC_Mel2_targets
11	NA	18 / 1032	ICGC_Usf1_targets
12	9e-01	8 / 522	ICGC_SrfPcr2_targets
13	9e-01	39 / 2150	ICGC_Irf4_targets
14	9e-01	5 / 415	ICGC_RxraPcr1_targets
15	9e-01	55 / 3121	ICGC_Egr1_targets

Rank	p-value	#in/all	Geneset
1	0.04	2 / 15	WANG_ER_UP
2	0.07	2 / 20	PanCan_ChromMod_geneset_nanostring
3	0.09	5 / 113	PanCan_Driver_Geneset_nanostring
4	0.12	3 / 58	SHAUGHNESSY_MM_high risk
5	0.20	6 / 187	PanCan_Pi3K_geneset_nanostring
6	0.21	1 / 11	GENTLES_modul4
7	0.24	3 / 80	PanCan_JAK-STAT_geneset_nanostring
8	0.25	1 / 14	LIU_PROSTATE_CANCER_DN
9	0.29	1 / 16	LIU_LIVER_CANCER
10	0.31	4 / 134	PanCan_RAS_geneset_nanostring
11	0.41	1 / 25	PanCan_HHT_geneset_nanostring
12	0.52	3 / 130	PanCan_CC+Apopt_geneset_nanostring
13	0.54	1 / 36	ZHANG_MM_up
14	0.60	3 / 147	PanCan_MAPK_geneset_nanostring
15	0.60	2 / 96	PanCan_TXmisReg_geneset_nanostring

Rank	p-value	#in/all	Geneset
1	4e-13	135 / 3734	Tcells_peripheral_blood_13_ReprPC
2	8e-12	103 / 2600	HSC_14_ReprPCWk
3	3e-11	107 / 2765	Regulatory cells_peripheral_blood_13_ReprPC
4	6e-11	85 / 2015	ReprPC_Colon
5	8e-11	77 / 1744	ReprPCWk_Colon
6	5e-10	131 / 3918	Tcells_peripheral_blood_14_ReprPCWk
7	6e-10	89 / 2254	10_ReprPC_MSC_Adipocyte
8	6e-10	112 / 3150	monocytes_peripheral_blood_13_ReprPC
9	9e-10	110 / 3089	Regulatory cells_peripheral_blood_14_ReprPCWk
10	1e-09	86 / 2173	HSC_13_ReprPC
11	2e-09	75 / 1799	T_CD8+ naive cells_peripheral_blood_13_ReprPC
12	3e-09	106 / 2984	natural killer cells_peripheral_blood_14_ReprPCWk
13	3e-09	113 / 3272	monocytes_peripheral_blood_14_ReprPCWk
14	4e-09	94 / 2535	T_CD8+ naive cells_peripheral_blood_14_ReprPCWk
15	6e-09	123 / 3724	Tcells_peripheral_blood_12_EnhBiv

Rank	p-value	#in/all	Geneset
1	2e-04	15 / 240	KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERACTION
2	2e-04	3 / 6	REACTOME_OPSINS
3	3e-04	17 / 311	SHEN_SMACA2_TARGETS_DN
4	4e-04	19 / 373	MIKKELEN_MEF_HCP_WITH_H3K27ME3
5	4e-03	4 / 23	

Correlation Cluster

Spot Summary: K

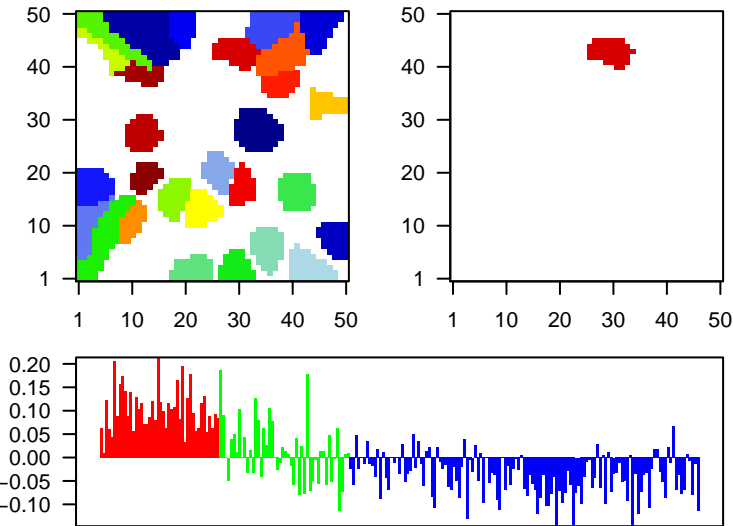
metagenes = 38
genes = 219

<r> metagenes = 0.94
<r> genes = 0.18
beta: r2= 0.83 / log p= -Inf

samples with spot = 10 (4.5 %)
mBL : 8 (18.2 %)
intermediate : 2 (4.2 %)

Overview Map

Spot



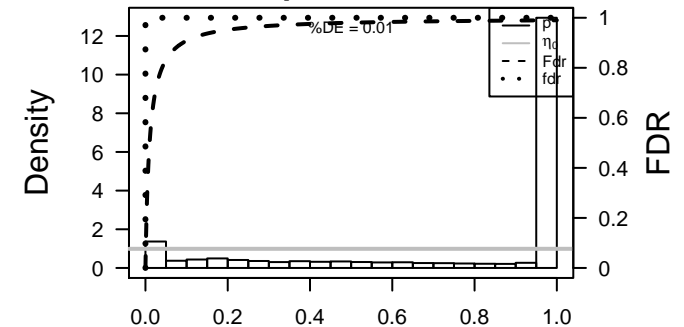
Spot Genelist

Rank	ID	max e	r	min e	Description
1	208496_x_at	1.86	-0.87	0.24	HIST1H3 histone cluster 1 H3 family member g [Source:HGNC Symbol]
2	220158_at	1.85	-0.68	0.21	LGALS1 galactin 14 [Source:HGNC Symbol;Acc:HGNC:30054]
3	205888_s_at	1.79	-0.75	0.44	JAKMIP2 janus kinase and microtubule interacting protein 2 [Source:HGNC Symbol]
4	203770_s_at	1.76	-0.79	0.23	STS steroid sulfatase [Source:HGNC Symbol;Acc:HGNC:11425]
5	219370_at	1.67	-0.85	0.08	RPRM reprimin 1, TP53 dependent G2 arrest mediator homolog [Source:HGNC Symbol]
6	214554_at	1.64	-0.71	0.45	HIST1H2A histone cluster 1 H2A family member I [Source:HGNC Symbol]
7	212816_s_at	1.56	-0.7	0.22	CBSL1 cystathionine-beta-synthase like [Source:HGNC Symbol;Acc:HGNC:11425]
8	214534_at	1.46	-0.71	0.54	HIST1H1B histone cluster 1 H1 family member b [Source:HGNC Symbol]
9	203811_s_at	1.43	-1.13	0.4	DNAJB4 DnaJ heat shock protein family (Hsp40) member B4 [Source:HGNC Symbol]
10	219208_at	1.42	-0.79	0.62	FBXO11 F-box protein 11 [Source:HGNC Symbol;Acc:HGNC:13590]
11	210991_s_at	1.37	-0.62	0.24	RIMS3 regulating synaptic membrane exocytosis 3 [Source:HGNC Symbol]
12	209032_s_at	1.3	-0.92	0.22	CADM1 cell adhesion molecule 1 [Source:HGNC Symbol;Acc:HGNC:11425]
13	214562_at	1.29	-0.66	0.33	HIST1H4B histone cluster 1 H4 family member I [Source:HGNC Symbol]
14	219842_at	1.28	-0.65	0.36	ARL15 ADP ribosylation factor like GTPase 15 [Source:HGNC Symbol]
15	204757_s_at	1.26	-0.79	0.12	C2CD2L C2CD2 like [Source:HGNC Symbol;Acc:HGNC:29000]
16	205938_at	1.25	-0.71	0.32	PPM1E protein phosphatase, Mg2+/Mn2+ dependent 1E [Source:HGNC Symbol]
17	217405_x_at	1.23	-1.12	0.45	GPLD1 glycosylphosphatidylinositol specific phospholipase D1 [Source:HGNC Symbol]
18	216698_x_at	1.22	-0.84	0.31	OR51E2 olfactory receptor family 7 subfamily E member 12 pseudogene [Source:HGNC Symbol]
19	208547_at	1.18	-0.62	0.33	HIST1H2BB histone cluster 1 H2B family member b [Source:HGNC Symbol]
20	208575_at	1.17	-0.51	0.45	HIST1H3A histone cluster 1 H3 family member a [Source:HGNC Symbol]

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	5e-16	59 / 1190	GSE# BLALOCK_ALZHEIMERS_DISEASE_DN
2	3e-14	141 / 5529	Lymp# HOPP_Txn_elongation
3	2e-13	22 / 186	HM# HALLMARK_OXIDATIVE_PHOSPHORYLATION
4	1e-12	16 / 95	GSE# KEGG_OXIDATIVE_PHOSPHORYLATION
5	2e-12	143 / 5908	Lymp# HOPP_Active_promoter
6	2e-12	27 / 330	CC# mitochondrial inner membrane
7	4e-12	38 / 669	GSE# JOHNSTONE_PARVB_TARGETS_3_DN
8	1e-11	14 / 77	GSE# MOOTHA_VOXPPOS
9	3e-11	13 / 67	GSE# REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_SYNTHASE
10	1e-10	53 / 1338	GSE# DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
11	5e-10	110 / 4261	Lymp# HOPP_Txn_transition
12	5e-10	14 / 100	GSE# REACTOME_TCA_CYCLE_AND_RESPIRATORY_ELECTRON_TRANSPORT
13	5e-10	18 / 181	GSE# WONG_MITOCHONDRIA_GENE_MODULE
14	7e-10	56 / 1527	GSE# PUJANA_BRCA1_PCC_NETWORK
15	3e-09	35 / 726	GSE# PUJANA_CHEK2_PCC_NETWORK
16	6e-09	25 / 406	GSE# MOOTHA_HUMAN_MITODB_6_2002
17	6e-09	7 / 18	CC# mitochondrial proton-transporting ATP synthase complex
18	6e-09	50 / 1354	Color# LaPointe_mucosa-position_kmeans_N_cecum_colon_ascending_colon_UP
19	9e-09	47 / 1241	TF# KIM_MYC_targets
20	1e-08	45 / 1161	MF# RNA binding
21	1e-08	43 / 1081	Refer# PROTEINATLAS_testis
22	1e-08	25 / 422	GSE# MOOTHA_MITOCHONDRIA
23	1e-08	12 / 88	BP# regulation of hematopoietic stem cell differentiation
24	3e-08	12 / 96	GSE# KEGG_PARKINSONS_DISEASE
25	4e-08	24 / 417	GSE# SHEN_SMARCA2_TARGETS_UP
26	9e-08	10 / 67	BP# regulation of gene silencing by miRNA
27	1e-07	27 / 540	GSE# TIEN_INTESTINE_PROBIOTICS_24HR_UP
28	2e-07	24 / 455	Refer# PROTEINATLAS_heart muscle
29	2e-07	40 / 1072	Refer# PROTEINATLAS_duodenum
30	2e-07	126 / 5682	Lymp# HOPP_Weak_promoter
31	2e-07	71 / 2541	CC# nucleoplasm
32	3e-07	28 / 604	Refer# PROTEINATLAS_hippocampus
33	3e-07	14 / 164	GSE# REACTOME_TRANSCRIPTION
34	3e-07	39 / 1044	TF# ICGC_Six5_targets
35	3e-07	22 / 398	GSE# MILL_PSEUDOPODIA_HAPTOTAXIS_UP
36	4e-07	43 / 1221	CC# mitochondrion
37	4e-07	13 / 143	GSE# KEGG_HUNTINGTONS_DISEASE
38	4e-07	28 / 616	GSE# WEI_MYCN_TARGETS_WITH_E_BOX
39	5e-07	9 / 62	GSE# REACTOME_RNA_POL_I_TRANSCRIPTION
40	9e-07	6 / 22	BP# telomere organization

p-values



Aging Rank	p-value	#in/all	Geneset
1	0.0	2 / 92	HORVATH_aging_genes_meth_DOWN
2	1.0	0 / 107	HORVATH_aging_genes_meth_UP
3	1.0	0 / 47	TSCHEMDORFF_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	

CC Rank	p-value	#in/all	Geneset
1	2e-12	27 / 330	mitochondrial inner membrane
2	6e-09	7 / 78	mitochondrial proton-transporting ATP synthase complex
3	2e-07	71 / 2541	nucleoplasm
4	4e-07	43 / 1221	mitochondrion
5	1e-06	9 / 70	nucleosome
6	5e-06	7 / 44	nuclear chromosome
7	5e-06	7 / 44	chromatin
8	8e-06	6 / 31	nuclear nucleosome
9	1e-05	4 / 10	proton-transporting ATP synthase complex, coupling factor F(o)
10	1e-05	17 / 324	chromosome
11	2e-05	6 / 37	mitochondrial respiratory chain complex I
12	4e-05	100 / 4579	nucleus
13	2e-04	4 / 19	proteasome core complex
14	2e-04	6 / 56	proteasome complex
15	3e-04	23 / 653	nucleolus

Colon Cancer Rank	p-value	#in/all	Geneset
1	6e-09	50 / 1354	LaPointe_mucosa-position_kmeans_N_ascending_colon_UP_a
2	3e-05	24 / 602	Pentrack_CRC_TCGA_corr_R_normal_DN
3	6e-04	20 / 561	Pentrack_CRC_TCGA_group_over_C_normal_DN
4	3e-02	27 / 1174	LaPointe_mucosa-position_kmeans_E_transverse_colon_UP
5	5e-02	36 / 1729	LaPointe_mucosa-position_kmeans_G_ascending_colon_UP_t
6	9e-02	1 / 6	Hewish_dMMR-secondary-mutations_Transcriptional_regulation
7	1e-01	1 / 7	Boland_CRC-MSI-TGC
8	2e-01	1 / 12	Juehling-MSI-enriched-in-6
9	2e-01	2 / 49	Pentrack_CRC_TCGA_corr_N_msi-h_DN
10	4e-01	2 / 82	Pentrack_CRC_TCGA_group_over_A_normal_UP
11	4e-01	2 / 83	Marisa_CRC-cluster-d
12	4e-01	1 / 31	Marisa_CRC-cluster-c
13	4e-01	17 / 1001	LaPointe_mucosa-position_kmeans_H_ascending_colon_UP_
14	4e-01	16 / 958	LaPointe_mucosa-position_kmeans_D_transverse_colon_UP
15	4e-01	18 / 1083	LaPointe_mucosa-position_kmeans_J_ascending_colon_transv

LM Rank	p-value	#in/all	Geneset
1	2e-13	22 / 186	HALLMARK_OXIDATIVE_PHOSPHORYLATION
2	5e-05	12 / 190	HALLMARK_MYC_TARGETS_V1
3	1e-02	8 / 195	HALLMARK_G2M_CHECKPOINT
4	7e-02	4 / 97	HALLMARK_PEROXISOME
5	1e-01	5 / 174	HALLMARK_ADIPOGENESIS
6	2e-01	5 / 183	HALLMARK_DNA_REPAIR
7	2e-01	5 / 187	HALLMARK_E2F_TARGETS
8	2e-01	4 / 139	HALLMARK_FATTY_ACID_METABOLISM
9	2e-01	5 / 192	HALLMARK_MTORC1_SIGNALING
10	2e-01	3 / 96	HALLMARK_ANDROGEN_RESPONSE
11	2e-01	2 / 80	HALLMARK_CHOLESTEROL_HOMEOSTASIS
12	5e-01	2 / 97	HALLMARK_BILE_ACID_METABOLISM
13	6e-01	1 / 51	HALLMARK_TGF_BETA_SIGNALING
14	6e-01	1 / 55	HALLMARK_MYC_TARGETS_V2
15	8e-01	2 / 173	HALLMARK_MITOTIC_SPINDLE

Lymphoma Rank	p-value	#in/all	Geneset
1	3e-14	141 / 5529	HOPP_Txn_elongation
2	2e-12	143 / 5908	HOPP_Active_promoter
3	5e-10	110 / 4261	HOPP_Txn_transition
4	2e-07	126 / 5682	HOPP_Weak_promoter
5	4e-06	7 / 42	Monti_OxPhos_cluster
6	3e-05	16 / 305	TARTE_PlasmaBlast_signature
7	4e-04	5 / 40	CARO_OxPhos_in_DLCL_UP
8	7e-03	3 / 25	ROSLOWSKI_red_UP
9	2e-02	87 / 4559	HOPP_Weak_enhancer
10	5e-02	4 / 85	Aukema_BCL2_DN_BCL6_UP
11	5e-02	4 / 88	ROSLOWSKI_green_UP
12	1e-01	19 / 906	SPANG_BCR_DN
13	1e-01	12 / 83	ROSLOWSKI_green_total
14	2e-01	76 / 4357	HOPP_Weak_txn
15	2e-01	3 / 97	ROSLOWSKI_red_total

mikNA target Rank	p-value	#in/all	Geneset
1	0.001	14 / 350	hsa-miR-424
2	0.002	4 / 32	hsa-miR-758
3	0.002	7 / 111	hsa-miR-656
4	0.003	11 / 107	hsa-miR-200a
5	0.003	14 / 378	hsa-miR-16
6	0.003	6 / 91	hsa-miR-211
7	0.003	6 / 91	hsa-miR-579
8	0.003	4 / 39	hsa-miR-555-3p
9	0.009	11 / 269	hsa-miR-548a-3p
10	0.005	7 / 134	hsa-miR-141
11	0.006	13 / 369	hsa-miR-15b
12	0.006	7 / 137	hsa-miR-190
13	0.006	5 / 74	hsa-miR-496
14	0.006	6 / 105	hsa-miR-105
15	0.007	6 / 107	hsa-miR-204

Telomeres Rank	p-value	#in/all	Geneset
1	0.3	1 / 27	Nabetani_all_ten_telomeres_genes_ks
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	

BP Rank	p-value	#in/all	Geneset
1	1e-08	12 / 89	regulation of hematopoietic stem cell differentiation
2	9e-08	10 / 67	regulation of gene silencing by miRNA
3	9e-07	6 / 22	telomere organization
4	3e-06	6 / 26	DNA replication-dependent nucleosome assembly
5	3e-06	6 / 27	chromatin silencing at rDNA
6	4e-06	7 / 42	protein heterotetramerization
7	4e-06	18 / 44	mitochondrial respiratory chain complex I assembly
8	7e-06	5 / 18	ATP synthesis coupled proton transport
9	9e-06	5 / 19	mitochondrial ATP synthesis coupled proton transport
10	1e-05	7 / 49	positive regulation of gene expression, epigenetic
11	2e-05	4 / 11	regulation of gene silencing
12	2e-05	6 / 36	mitochondrial electron transport, NADH to ubiquinone
13	2e-05	6 / 37	negative regulation of gene expression, epigenetic
14	3e-05	8 / 78	nucleosome assembly
15	4e-05	5 / 25	ATP biosynthetic process

Chr Rank	p-value	#in/all	Geneset
1	0.003	24 / 832	Chr 2
2	0.009	32 / 1325	Chr 1
3	0.019	18 / 619	Chr 6
4	0.067	10 / 369	Chr 20
5	0.078	12 / 480	Chr 5
6	0.089	17 / 756	Chr 11
7	0.258	11 / 554	Chr 5
8	0.275	3 / 139	Chr 15
9	0.397	7 / 382	Chr 9
10	0.536	7 / 437	Chr 8
11	0.548	11 / 700	Chr 12
12	0.614	6 / 403	Chr 14
13	0.682	7 / 322	Chr 9
14	0.685	11 / 776	Chr 17
15	0.898	2 / 242	Chr 13

Glioma Rank	p-value	#in/all	Geneset
1	0.004	34 / 1343	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
2	0.008	36 / 1523	UP_fetus_UP_fetus_DN
3	0.016	3 / 34	WILLSCHER_GBM_proteomics_wtOnly_SpotH
4	0.036	3 / 46	WILLSCHER_GBM_proteomics_wtOnly_SpotG
5	0.056	3 / 55	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
6	0.063	3 / 58	Stuehler_Proteins_up_in_STS
7	0.069	5 / 139	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
8	0.106	14 / 614	Sturm_GBM_Meth_overexpression_E_G34_UP
9	0.119	1 / 8	WILLSCHER_GBM_LTSmut_proteomics-A_UP
10	0.169	2 / 47	developing astrocytes
11	0.186	2 / 50	Vishal_subnetwork signature of survival in GBM
12	0.187	1 / 13	Mukasa_UP_in_Astrogloma
13	0.187	1 / 13	WILLSCHER_GBM_STSwt_proteomics-O_UP
14	0.220	9 / 421	Down_b
15	0.225	1 / 16	Shinawi_with_increased_methylation_in_STS

Immunome Rank	p-value	#in/all	Geneset
1	0.2	1 / 12	Angelova Immune-metagenome-effector_memory_CD4
2	0.2	1 / 18	Angelova Immune-metagenome-pDC
3	0.3	1 / 19	Angelova Immune-metagenome-activated_CD8
4	0.5	1 / 45	Angelova Immune-metagenome-MDSC
5	1.0	0 / 13	Angelova Immune-metagenome-activated_B-cells
6	1.0	0 / 26	Angelova Immune-metagenome-activated_CD4
7	1.0	0 / 21	Angelova Immune-metagenome-central_memory_CD4
8	1.0	0 / 17	Angelova Immune-metagenome-central_memory_CD8
9	1.0	0 / 7	Angelova Immune-metagenome-cytotoxic_cells
10	1.0	0 / 25	Angelova Immune-metagenome-DC
11	1.0	0 / 32	Angelova Immune-metagenome-effector_memory_CD8
12	1.0	0 / 14	Angelova Immune-metagenome-endothelial
13	1.0	0 / 19	Angelova Immune-metagenome-iDC
14	1.0	0 / 13	Angelova Immune-metagenome-immature_B-cells
15	1.0	0 / 11	Angelova Immune-metagenome-macrophages

Melanoma Rank	p-value	#in/all	Geneset
1	0.02	3 / 38	Tirosh_G1/S phase specific genes
2	0.03	9 / 276	Gerber_wt/wt_melanoma-cells-SpotB
3	0.13	8 / 319	Gerber_wt/wt_melanoma-cells-SpotA
4	0.15	1 / 10	Joensson_Melanoma Normal like subtype
5	0.17	5 / 185	Tirosh_genes from malignant cells in Mel179-melanoma
6	0.45	1 / 38	Tirosh_top50 correlated genes PC1
7	0.46	1 / 39	Tirosh_melanoma specific genes
8	0.49	4 / 20	Gerber_wt/wt_melanoma-SpotC
9	0.50	1 / 44	Tirosh_top50 correlated genes PC2
10	0.52	1 / 46	Tirosh_top50 correlated genes PC5
11	0.64	1 / 65	Harbst_melanoma_highgrade_up
12	0.68	3 / 222	Gerber_wt/wt_melanoma-cells-SpotF
13	0.72	1 / 73	Tirosh_core cycling genes in low- and high-proliferation melanoma
14	0.72	1 / 81	Tirosh_Genes in the MITF program
15	0.74	1 / 85	Tirosh_AXL-signature

Pneumonia Rank	p-value	#in/all	Geneset
1	0.4	1 / 33	Sweeney_viral_dn
2	0.6	1 / 54	Burnham_timecourse
3	0.6	2 / 135	Terre_MSV_multiple_respiratory_viruses_up
4	0.9	1 / 10	Terre_ILM5_influenza_meth_signature
5	0.9	1 / 179	Terre_MSV_multiple_respiratory_viruses_dn
6	0.68	0 / 68	Burnham_sep_vs_con_UP
7	1.0	0 / 56	Burnham_sep_vs_con_DN
8	1.0	0 / 48	Burnham_cap_ip_vs_con_DN
9	1.0	0 / 71	Burnham_cap_ip_vs_con_UP
10	1.0	0 / 48	Burnham_viral_DN
11	1.0	0 / 57	Burnham_viral_UP
12	1.0	0 / 57	Burnham_day1_vs_5_UP
13	1.0	0 / 52	Burnham_day1_vs_5_DN
14	1.0	0 / 18	Scicluna_UP
15	1.0	0 / 41	Scicluna_DN

TF Rank	p-value	#in/all	Geneset
1	9e-09	47 / 1241	KIM_MYC_targets
2	3e-07	39 / 1044	ICGC_Six5_targets
3	5e-04	40 / 1494	ICGC_Cebpbsc150_targets
4	9e-04	31 / 1089	ICGC_Ets1_targets
5	2e-03	73 / 3403	ICGC_Atl2_targets
6	5e-03	78 / 3703	ICGC_Foxm1_targets
7	6e-03	73 / 3564	ICGC_Taf1_targets
8	9e-03	76 / 3796	ICGC_Nficsc81335_targets
9	1e-02	36 / 1578	ICGC_GabpPcr2_targets
10	2e-02	68 / 3420	ICGC_Bclaf101388_targets
11	2e-02	74 / 3805	ICGC_Staf1_targets
12	2e-02	36 / 1630	ICGC_Srfv0416101_targets
13	2e-02	73 / 3769	ICGC_Pmlsc71910_targets
14	3e-02	45 / 2150	ICGC_Irf4_targets
15	3e-02	26 / 1107	ICGC_Myc_targets

Cancer Rank	p-value	#in/all	Geneset
1	4e-04	3 / 10	GENTLES_modu5
2	8e-03	0 / 14	SOTTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
3	2e-02	2 / 14	GENTLES_modu10
4	3e-02	1 / 2	GENTLES_modu8
5	9e-02	2 / 32	KUIPER_MM_good_survival
6	2e-01	1 / 11	LIU_PROSTATE_CANCER_UP
7	2e-01	1 / 15	GENTLES_modu11
8	2e-01	1 / 14	LIU_COMMON_CANCER_GENES
9	2e-01	1 / 14	GUSTAFSON_Pi3K_UP
10	2e-01	1 / 14	BENTINK_ras6
11	2e-01	1 / 15	RHODES_UNDIFFERENTIATED_CANCER
12	2e-01	1 / 15	WANG_ER_UP
13	2e-01	1 / 15	GENTLES_modu4
14	2e-01	1 / 16	GENTLES_modu6
15	4e-01	1 / 28	PanCan_HK_geneset_nanostring

Chromatin states Rank	p-value	#in/all	Geneset
1	5e-13	166 / 7420	Tcells_peripheral_blood_1_TssA
2	8e-12	119 / 4528	T_CD8+ naive cells_peripheral_blood_4_Tx
3	1e-11	153 / 3331	153a_Colon
4	2e-11	108 / 3938	Thelper_cells_peripheral_blood_6_EnhG
5	1e-10	168 / 7930	Regulatory_cells_peripheral_blood_1_TssA
6	6e-10	165 / 7833	Bcells_peripheral_blood_1_TssA
7	1e-09	162 / 7635	monocytes_peripheral_blood_1_TssA
8	1e-09	98 / 3524	Regulatory_cells_peripheral_blood_6_EnhG
9	2e-09	167 / 8068	Thelper_cells_peripheral_blood_1_TssA
10	3e-09	165 / 7957	Tcells_peripheral_blood_2_TssAFink
11	3e-09	162 / 7751	natural killer cells_peripheral_blood_1_TssA
12	8e-09	67 / 2144	T_CD8+ naive cells_peripheral_blood_6_EnhG
13	1e-08	148 / 6725	Overlap_fetal_midbrain_RepPC
14	4e-08	143 / 6537	Tcells_peripheral_blood_5_TxWk
15	4e-08	166 / 8245	Regulatory_cells_peripheral_blood_2_TssAFink

GSEA C2 Rank	p-value	#in/all	Geneset
1	5e-16	59 / 1190	BLALOCK_ALZHEIMERS_DISEASE_DN
2	1e-12	16 / 95	KEGG_OXIDATIVE_PHOSPHORYLATION
3	4e-12	38 / 669	JOHNSTONE_PARVUS_TARGETS_3_DN
4	1e-11	14 / 77	MOOHA_VOXPHOS
5	3e-		

Correlation Cluster

Spot Summary: L

metagenes = 28
genes = 203

<r> metagenes = 0.93
<r> genes = 0.17
beta: r2= 1.22 / log p= -Inf

samples with spot = 3 (1.4 %)
intermediate : 2 (4.2 %)
non-mBL : 1 (0.8 %)

Spot Genelist

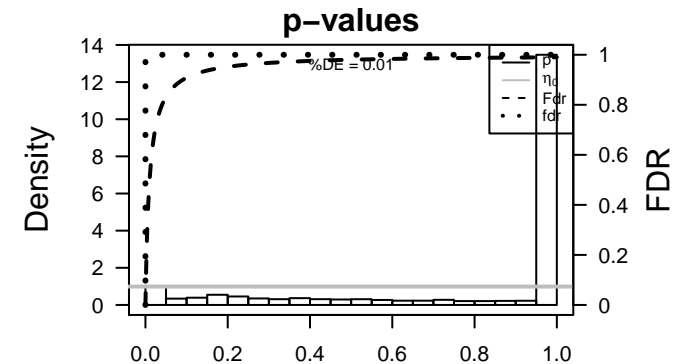
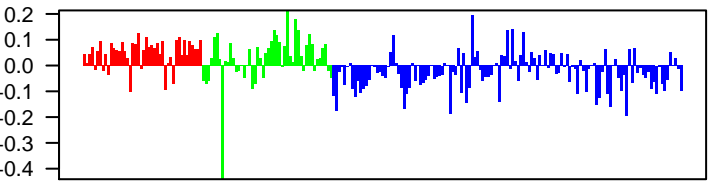
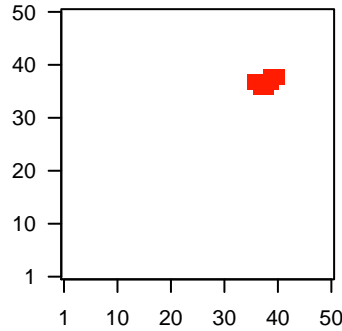
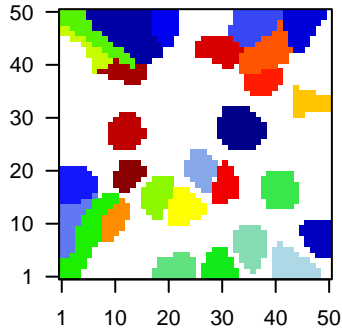
Rank	ID	max e	r	min e	Description
1	204550_x_at	2.33	-1.15	0.25	GSTM4 glutathione S-transferase mu 4 [Source:HGNC Symbol;Acc:...
2	204281_at	2.28	-1.06	0.28	TEAD4 TEA domain transcription factor 4 [Source:HGNC Symbol;Acc:...
3	215333_x_at	2.19	-1.28	0.26	GSTM4 glutathione S-transferase mu 4 [Source:HGNC Symbol;Acc:...
4	204418_x_at	2.18	-1.41	0.25	GSTM4 glutathione S-transferase mu 4 [Source:HGNC Symbol;Acc:...
5	218745_x_at	1.23	-1.09	0.46	TMEM1616 transmembrane protein 161A [Source:HGNC Symbol;Acc:HGNC:...
6	219522_at	1.23	-0.88	0.2	FJX1 four jointed box 1 [Source:HGNC Symbol;Acc:HGNC:17166]
7	218812_s_at	1.07	-1.04	0.39	ORAI2 ORAI calcium release-activated calcium modulator 2 [Source:...
8	203456_at	1.07	-0.98	0.32	PRAF2 PRA1 domain family member 2 [Source:HGNC Symbol;Acc:...
9	203682_s_at	1.06	-0.82	0.25	IVD isovaleryl-CoA dehydrogenase [Source:HGNC Symbol;Acc:...
10	202203_s_at	0.99	-1.47	0.16	AMFR autocrine motility factor receptor [Source:HGNC Symbol;Acc:...
11	204545_at	0.97	-0.81	0.34	PEX6 peroxisomal biogenesis factor 6 [Source:HGNC Symbol;Acc:...
12	218161_s_at	0.97	-0.52	0.36	
13	204483_at	0.93	-0.87	0.24	ENO3 enolase 3 [Source:HGNC Symbol;Acc:HGNC:3354]
14	220707_s_at	0.92	-0.95	0.34	FOXRED1 FOXRED1 dependent oxidoreductase domain containing 2 [Source:...
15	221876_at	0.91	-1.1	0.29	ZNF783 zinc finger family member 783 [Source:HGNC Symbol;Acc:HGNC:...
16	206587_at	0.88	-0.93	0.28	CCT6B chaperonin containing TCP1 subunit 6B [Source:HGNC Symbol;Acc:...
17	209256_s_at	0.88	-1.18	0.24	KLHDC14 kelch domain containing 10 [Source:HGNC Symbol;Acc:HGNC:...
18	218608_at	0.88	-1.05	0.23	ATP13A2 ATPase 13A2 [Source:HGNC Symbol;Acc:HGNC:30213]
19	213363_at	0.87	-0.63	0.4	carbonic anhydrase 5B pseudogene 1 [Source:HGNC Symbol;Acc:...
20	206949_s_at	0.86	-0.71	0.3	RUSC1 RUN and SH3 domain containing 1 [Source:HGNC Symbol;Acc:...

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	1e-11	45 / 1107	TF ICGC_Myc_targets
2	3e-10	19 / 232	BP translation
3	8e-10	86 / 3564	TF ICGC_Taf1_targets
4	2e-09	20 / 287	GSE/ DAIRKEE_TERT_TARGETS_UP
5	4e-09	95 / 4261	Lympi HOPP_Txn_transition
6	4e-09	113 / 5529	Lympi HOPP_Txn_elongation
7	5e-09	77 / 3121	TF ICGC_Egr1_targets
8	2e-08	40 / 1161	Refer PROTEINATLAS_colon
9	3e-08	29 / 675	GSE/ GRADE_COLON_CANCER_UP
10	4e-08	18 / 277	CC mitochondrial matrix
11	6e-08	43 / 1354	Color LaPointe_mucosa-position_kmeans_N_cecum_colon_ascending_colon_UP
12	2e-07	91 / 4319	TF ICGC_Pou2_targets
13	3e-07	39 / 1221	CC mitochondrion
14	3e-07	88 / 4131	TF ICGC_Tcf3_targets
15	4e-07	80 / 3630	TF ICGC_Sp1_targets
16	5e-07	17 / 294	GSE/ WONG_EMBRYONIC_STEM_CELL_CORE
17	5e-07	30 / 819	Refer PROTEINATLAS_bronchus
18	5e-07	21 / 442	GSE/ SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_UP
19	6e-07	20 / 406	GSE/ MOOTHA_HUMAN_MITODB_6_2002
20	6e-07	37 / 1161	MF RNA binding
21	6e-07	7 / 38	CC mitochondrial nucleoid
22	7e-07	35 / 1072	Refer PROTEINATLAS_duodenum
23	7e-07	27 / 700	GSE/ KIM_ALL_DISORDERS_OLIGODENDROCYTE_NUMBER_CORR_UP
24	8e-07	35 / 1076	Refer PROTEINATLAS_stomach
25	1e-06	81 / 3769	TF ICGC_Pmlsc71910_targets
26	1e-06	34 / 1048	Refer PROTEINATLAS_rectum
27	1e-06	93 / 4602	TF ICGC_Elf1_targets
28	1e-06	26 / 677	Refer PROTEINATLAS_esophagus
29	1e-06	30 / 861	Refer PROTEINATLAS_nasopharynx
30	2e-06	30 / 866	Refer PROTEINATLAS_cerebellum
31	2e-06	79 / 3703	TF ICGC_Foxm1_targets
32	2e-06	23 / 569	Refer PROTEINATLAS_salivary_gland
33	3e-06	30 / 893	Refer PROTEINATLAS_pancreas
34	3e-06	80 / 3804	TF ICGC_Stat5_targets
35	4e-06	33 / 1048	Refer PROTEINATLAS_gallbladder
36	4e-06	26 / 716	Refer PROTEINATLAS_epididymis
37	4e-06	19 / 422	GSE/ MOOTHA_MITOCHONDRIA
38	6e-06	69 / 3150	TF ICGC_Creb1_targets
39	6e-06	83 / 4072	TF ICGC_Mta3_targets
40	7e-06	23 / 604	Refer PROTEINATLAS_hippocampus

Overview Map

Spot



Rank	p-value	#in/all	Geneset
1	0.1	3 / 92	HOPVATH_aging_genes_meth_DOWN
2	0.4	2 / 107	HOEVATH_aging_genes_meth_UP
3	1.0	0 / 47	TSCHEMDORFF_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	

Rank	p-value	#in/all	Geneset
1	4e-08	18 / 277	mitochondrial matrix
2	3e-07	39 / 1221	mitochondrion
3	6e-07	7 / 38	mitochondrial nucleoid
4	4e-05	4 / 15	eukaryotic translation initiation factor 3 complex
5	2e-04	85 / 4579	nucleus
6	2e-04	54 / 2541	nucleoplasm
7	5e-04	3 / 12	aminoacyl-tRNA synthetase multienzyme complex
8	5e-04	15 / 330	mitochondrial inner membrane
9	5e-04	72 / 3805	cytosol
10	1e-03	11 / 268	intracellular ribonucleoprotein complex
11	2e-03	4 / 41	cytosolic large ribosomal subunit
12	8e-03	2 / 10	RISC complex
13	6e-03	6 / 131	myelin sheath
14	1e-02	6 / 139	ribosome
15	1e-02	2 / 13	mRNA cleavage and polyadenylation specificity factor complex

Rank	p-value	#in/all	Geneset
1	6e-08	43 / 1354	LaPointe_mucosa-position_kmeans_N_pecum_colon_ascending_colon_UP_a
2	1e-03	18 / 602	Pentrack_CRC_TCGA_corr_R_normal_DN
3	2e-03	17 / 561	Pentrack_CRC_TCGA_group_over_C_normal_DN
4	1e-02	34 / 1729	LaPointe_mucosa-position_kmeans_G_pecum_colon_ascending_colon_UP_t
5	1e-02	25 / 1174	LaPointe_mucosa-position_kmeans_E_transverse_colon_UP_transverse_colo
6	3e-02	22 / 1083	LaPointe_mucosa-position_kmeans_J_pecum_colon_ascending_colon_transv
7	6e-02	12 / 539	Lembcke_TCGA_meth_kmeans_L_CIMP_H_DN
8	8e-02	1 / 6	Hewish_dMMR-secondary-mutations_Transcriptional_regulation
9	9e-02	1 / 7	TCGA_Mutated-in-CRC_mismatch-repair-genes
10	1e-01	1 / 8	LaPointe_CRC-MMR-system
11	2e-01	1 / 12	Juehling_HNPCC-mutated-in-4
12	2e-01	1 / 12	Juehling-MSI-enriched-in-6
13	2e-01	1 / 14	Hewish_dMMR-secondary-mutations_DNA-repair
14	2e-01	1 / 18	Boland_CRC-MSI-A6-A10
15	4e-01	17 / 1166	LaPointe_mucosa-position_kmeans_K_transverse_colon_UP_pecum_colon_a

Rank	p-value	#in/all	Geneset
1	8e-06	12 / 186	HALLMARK_OXIDATIVE_PHOSPHORYLATION
2	3e-04	10 / 190	HALLMARK_MYC_TARGETS_V1
3	6e-02	4 / 106	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
4	1e-01	4 / 133	HALLMARK_DNA_REPAIR
5	1e-01	5 / 192	HALLMARK_MTORC1_SIGNALING
6	1e-01	4 / 103	HALLMARK_FATTY_ACID_METABOLISM
7	1e-01	3 / 97	HALLMARK_PEROXISOME
8	2e-01	2 / 59	HALLMARK_CHOLESTEROL_HOMEOSTASIS
9	2e-01	3 / 122	HALLMARK_SPERMATOGENESIS
10	2e-01	4 / 181	HALLMARK_XENOBIOTIC_METABOLISM
11	3e-01	4 / 103	HALLMARK_G2M_CHECKPOINT
12	3e-01	2 / 78	HALLMARK_INTERFERON_ALPHA_RESPONSE
13	4e-01	2 / 97	HALLMARK_BILE_ACID_METABOLISM
14	5e-01	3 / 194	HALLMARK_MYOGENESIS
15	5e-01	1 / 55	HALLMARK_MYC_TARGETS_V2

Rank	p-value	#in/all	Geneset
1	4e-09	95 / 4261	HOPP_Txn_transition
2	4e-09	113 / 5529	HOPP_Txn_elongation
3	2e-03	4 / 40	CARO_OxPhos_in_DLBLCL_UP
4	2e-03	99 / 5908	HOPP_Active_promoter
5	2e-02	2 / 15	DAVE_BL_Inter
6	5e-02	84 / 5404	HOPP_Strong_enhancer
7	9e-02	1 / 7	CARO_OxPhos_vs_BCR_UP
8	1e-01	1 / 9	DAVE_BL_UP
9	2e-01	83 / 5682	HOPP_Weak_promoter
10	2e-01	4 / 173	Victoria_Light_zone_signature
11	2e-01	6 / 305	TARTE_PlasmaBlast_signature
12	3e-01	14 / 906	SPANIG_BCR_DN
13	4e-01	2 / 85	SPANIG_BCR_UP
14	4e-01	1 / 42	Monti_OxPhos_cluster
15	5e-01	2 / 121	ROSLOWSKI_green_total

Rank	p-value	#in/all	Geneset
1	0.01	3 / 36	hsa-miR-423-3p
2	0.01	9 / 278	hsa-let-7d
3	0.02	3 / 41	hsa-miR-346
4	0.03	4 / 89	hsa-miR-376c
5	0.04	6 / 189	hsa-miR-214
6	0.05	3 / 60	hsa-miR-1321
7	0.05	2 / 26	hsa-miR-558
8	0.06	6 / 194	hsa-miR-124
9	0.06	2 / 120	hsa-miR-1231
10	0.06	4 / 108	hsa-miR-421
11	0.06	5 / 155	hsa-miR-129-5p
12	0.06	6 / 205	hsa-miR-1252
13	0.07	5 / 160	hsa-miR-330-3p
14	0.07	3 / 72	hsa-miR-149
15	0.08	3 / 73	hsa-miR-299-3p

Rank	p-value	#in/all	Geneset
1	0.3	1 / 27	Nabetani_alt_len_telomeres_genes_ks
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	

Rank	p-value	#in/all	Geneset
1	3e-10	19 / 232	translation
2	1e-09	5 / 36	IRNA-aminocyclization_for_protein_translation
3	1e-04	8 / 110	translational_initiation
4	8e-04	4 / 31	protein_targeting_to_mitochondrion
5	1e-03	3 / 17	branched-chain_amino_acid_catabolic_process
6	2e-03	4 / 42	RNA_metabolic_process
7	0	6 / 25	ATP_hydrolysis_coupled_cation_transmembrane_transport
8	8e-03	2 / 10	cellular_response_to_interferon-beta
9	8e-03	2 / 10	IRES-dependent_viral_translational_initiation
10	8e-03	2 / 10	regulation_of_mitochondrion_organization
11	8e-03	5 / 91	mRNA_transport
12	9e-03	3 / 32	regulation_of_cholesterol_biosynthetic_process
13	9e-03	2 / 11	iron-sulfur_cluster_assembly
14	9e-03	2 / 11	maturation_of_LSU-rRNA
15	1e-02	4 / 62	positive_regulation_of_translation

Rank	p-value	#in/all	Geneset
1	5e-05	26 / 833	Chr 19
2	9e-04	18 / 585	Chr 7
3	3e-03	19 / 70	Chr 12
4	7e-03	15 / 548	Chr 16
5	8e-02	8 / 333	Chr 22
6	3e-01	20 / 1325	Chr 1
7	4e-01	12 / 776	Chr 17
8	4e-01	6 / 369	Chr 20
9	6e-01	5 / 403	Chr 14
10	6e-01	3 / 242	Chr 13
11	7e-01	5 / 437	Chr 8
12	8e-01	4 / 382	Chr 15
13	8e-01	6 / 554	Chr 5
14	9e-01	4 / 490	Chr 10
15	9e-01	4 / 492	Chr 9

Rank	p-value	#in/all	Geneset
1	0.002	4 / 38	WILLSCHER_GBM_Verhaak-PNwt_up
2	0.019	2 / 16	VERHAAK_CL_subtype
3	0.030	3 / 50	Vishal_subnetwork_signature_of_survival_in_GBM
4	0.037	26 / 1343	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
5	0.040	1 / 23	WILLSCHER_GBM_LTSmut_proteomics-E_UP
6	0.043	3 / 58	Stuehler_Proteins_up_in_STS
7	0.045	3 / 59	WILLSCHER_GBM_Verhaak-PNwt & MES_up
8	0.054	28 / 1523	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
9	0.072	13 / 614	Sturm_GBM_Meth_overexpression_E_G34_UP
10	0.119	1 / 19	WILLSCHER_GBM_LTSmut_proteomics-wtOnly_Differencel
11	0.170	2 / 55	WILLSCHER_GBM_proteomics_wtOnly_SpotJ
12	0.209	8 / 421	Down_b
13	0.377	3 / 163	ScovV_0.999_Sturm_E1_IDH_DN
14	0.379	1 / 35	Garovets_LGG_EPL_subclass
15	0.465	1 / 46	WILLSCHER_GBM_proteomics_wtOnly_SpotG

Rank	p-value	#in/all	Geneset
1	0.2	1 / 19	Angelova_immune-metagenes-activated_CD8
2	0.0	0 / 13	Angelova_immune-metagenes-activated_B-cells
3	1.0	0 / 26	Angelova_immune-metagenes-activated_CD4
4	1.0	0 / 21	Angelova_immune-metagenes-central_memory_CD4
5	1.0	0 / 17	Angelova_immune-metagenes-central_memory_CD8
6	1.0	0 / 7	Angelova_immune-metagenes-cytotoxic_cells
7	1.0	0 / 25	Angelova_immune-metagenes-DC
8	1.0	0 / 12	Angelova_immune-metagenes-effector_memory_CD4
9	1.0	0 / 32	Angelova_immune-metagenes-effector_memory_CD8
10	1.0	0 / 14	Angelova_immune-metagenes-eosinophil
11	1.0	0 / 19	Angelova_immune-metagenes-IDC
12	1.0	0 / 13	Angelova_immune-metagenes-immature_B-cells
13	1.0	0 / 11	Angelova_immune-metagenes-macrophages
14	1.0	0 / 38	Angelova_immune-metagenes-mast-cells
15	1.0	0 / 8	Angelova_immune-metagenes-mDC

Rank	p-value	#in/all	Geneset
1	0.002	4 / 38	Tirosh_top50_correlated_genes_PC1
2	0.004	10 / 276	Gerber_wiwt_melanoma-cells-SpotB
3	0.064	3 / 68	Tirosh_housekeeping_genes
4	0.103	1 / 8	Hugo_melanoma-BRAFmut-LEF1_UP
5	0.214	5 / 236	Gerber_wiwt_group3-specific
6	0.251	4 / 189	Tirosh_genes_preferentially_expressed_by_Tregs
7	0.268	1 / 23	Melanoma_Epi-Enzyme_Cluster_7
8	0.376	4 / 230	Gerber_wiwt_melanoma-cells-SpotC
9	0.457	3 / 185	Tirosh_genes_from_malignant_cells_in_Mel79-melanoma
10	0.521	3 / 204	Landsberg_dedifferentiation_down
11	0.656	3 / 249	Gerber_wiwt_melanoma-cells-SpotE
12	0.767	1 / 107	Tirosh_Exhaustion_program_in_Mel75
13	0.803	2 / 222	Gerber_wiwt_melanoma-cells-SpotF
14	0.903	1 / 171	Landsberg_dedifferentiation_up
15	0.988	1 / 319	Gerber_wiwt_melanoma-cells-SpotA

Rank	p-value	#in/all	Geneset
1	0.2	4 / 179	Terre_MSV_multiple_respiratory_viruses_dn
2	0.4	1 / 33	Sweeney_viral_dn
3	0.4	1 / 41	Sciduna_DN
4	0.5	1 / 54	Burnham_timecourse
5	0.5	1 / 57	Burnham_viral_UP
6	0.5	1 / 57	Burnham_day1_vs_5_UP
7	0.8	1 / 122	Terre_IMS_influenza_meta_signature
8	0.8	1 / 135	Terre_MSV_multiple_respiratory_viruses_up
9	1.0	0 / 9	Burnham_sep_vs_con_UP
10	1.0	0 / 56	Burnham_sep_vs_con_DN
11	1.0	0 / 48	Burnham_cap_fp_vs_con_DN
12	1.0	0 / 71	Burnham_cap_fp_vs_con_UP
13	1.0	0 / 48	Burnham_viral_DN
14	1.0	0 / 52	Burnham_day1_vs_5_DN
15	1.0	0 / 18	Sciduna_UP

Rank	p-value	#in/all	Geneset
1	1e-11	45 / 1107	ICGC_Myc_targets
2	8e-10	86 / 3564	ICGC_Taf1_targets
3	5e-09	77 / 3121	ICGC_Egr1_targets
4	2e-07	91 / 4319	ICGC_Pou2_targets
5	3e-07	88 / 4131	ICGC_Tcf3_targets
6	4e-07	80 / 3630	ICGC_Sp1_targets
7	1e-06	81 / 3769	ICGC_Pmlsc7f910_targets
8	1e-06	93 / 4602	ICGC_Elf1_targets
9	2e-06	79 / 3703	ICGC_Foxm1_targets
10	3e-06	80 / 3804	ICGC_Stat5_targets
11	4e-06	69 / 3150	ICGC_Creb1_targets
12	6e-06	83 / 4072	ICGC_Mta3_targets
13	9e-06	43 / 1630	ICGC_SrfV0416101_targets
14	1e-05	78 / 3796	ICGC_Nficc81335_targets
15	1e-05	64 / 2899	ICGC_Nfatc1_targets

Rank	p-value	#in/all	Geneset
1	8e-04	3 / 144	GENTLES_modul10
2	1e-01	9 / 409	Lembcke_Normal_vs_Adenoma
3	1e-01	1 / 10	GENTLES_modul5
4	1e-01	1 / 11	LIU_PROSTATE_CANCER_UP
5	2e-01	1 / 12	LIU_BREAST_CANCER
6	2e-01	1 / 12	BENTINK_e2f5.2
7	2e-01	1 / 14	BENTINK_src.2
8	2e-01	1 / 15	WANG_ER_UP
9	2e-01	1 / 16	LIU_LIVER_CANCER
10	2e-01	1 / 16	GENTLES_modul6
11	3e-01	0 / 14	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
12	3e-01	1 / 28	PanCan_HK_geneset_nanostring
13	4e-01	1 / 36	ZHANG_MM_UP
14	5e-01	2 / 130	PanCan_CC+Apop_geneset_nanostring
15	5e-01	1 / 58	SHAUGHNESSY_MM_higheset

Rank	p-value	#in/all	Geneset
1	2e-20	166 / 8406	Bcells_peripheral_blood_2_TssAFlnk
2	8e-19	160 / 7833	Bcells_peripheral_blood_1_TssA
3	1.09 / 3803	6_EnhG_Fibroblasts	
4	6e-19	160 / 7957	Tcells_peripheral_blood_2_TssAFlnk
5	1e-17	158 / 7930	Regulatory_cells_peripheral_blood_1_TssA
6	2e-17	87 / 2704	4_TxTrans_Fibroblasts
7	3e-17	131 / 5620	TssF_Color
8	4e-17	160 / 8200	monocytes_peripheral_blood_2_TssAFlnk
9	1e-16	116 / 4535	6_EnhG_Melanocytes
10	1e-16	110 / 4208	Tcells_peripheral_blood_6_EnhG
11	3e-16	161 / 8431	T_CD8+_naive_cells_peripheral_blood_2_TssAFlnk
12	3e-16	148 / 7165	Tx_Color
13	4e-16	159 / 8245	Regulatory_cells_peripheral_blood_2_TssAFlnk
14	5e-16	160 / 8370	natural_killer_cells_peripheral_blood_2_TssAFlnk
15	1e-15	162 / 8641	1_TssA_ESC_Endoderm

Rank	p-value	#in/all	Geneset
1	2e-09	20 / 287	DAIRKEE_TERT_TARGETS_UP
2	3e-08	29 / 675	GRADE_COLORECTAL_CANCER_UP
3	5e-07	17 / 294	WONG_EMBRYONIC_STEM_CELL_CORE
4	5e-07	21 / 442	SULLERMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_UP
5			

Correlation Cluster

Spot Summary: M

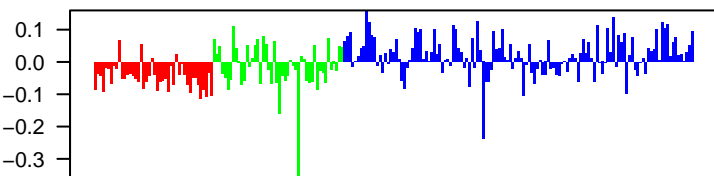
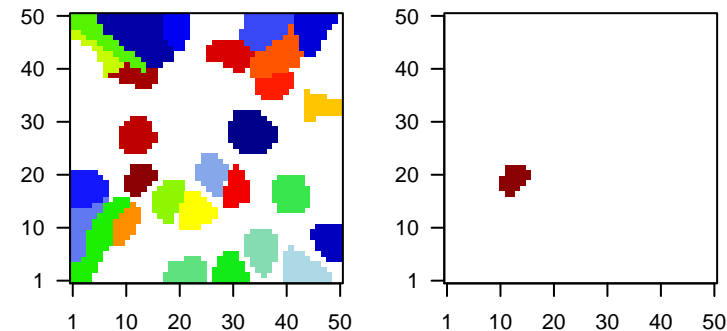
metagenes = 26
genes = 130

<r> metagenes = 0.91
<r> genes = 0.15
beta: r2= 0.41 / log p= -Inf

samples with spot = 1 (0.5 %)
non-mBL : 1 (0.8 %)

Overview Map

Spot

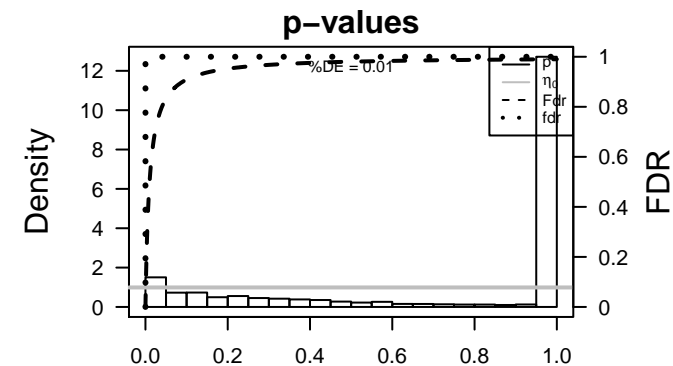


Spot Genelist

Rank	ID	max e	r	min e	Description
1	205445_at	2.65	-0.7	0.19	PRL prolactin [Source:HGNC Symbol;Acc:HGNC:9445]
2	211828_s_at	2.43	-0.94	0.42	TNIK TRAF2 and NCK interacting kinase [Source:HGNC Symbol;A
3	206412_at	2.4	-0.99	0.26	FER FER tyrosine kinase [Source:HGNC Symbol;Acc:HGNC:3655]
4	210127_at	2.14	-0.79	0.3	RAB6B RAB6B, member RAS oncogene family [Source:HGNC Symb
5	220234_at	1.99	-0.62	0.27	CA8 carbonic anhydrase 8 [Source:HGNC Symbol;Acc:HGNC:138
6	206489_s_at	1.83	-0.43	0.33	DLGAP1 DLG associated protein 1 [Source:HGNC Symbol;Acc:HGNC
7	212686_at	1.74	-0.85	0.26	PPM1H protein phosphatase, Mg2+/Mn2+ dependent 1H [Source:HG
8	206490_at	1.73	-0.74	0.31	DLGAP1 DLG associated protein 1 [Source:HGNC Symbol;Acc:HGNC
9	213107_at	1.63	-1.03	0.35	TNIK TRAF2 and NCK interacting kinase [Source:HGNC Symbol;A
10	214156_at	1.5	-0.79	0.21	MYRIP myosin VIIA and Rab interacting protein [Source:HGNC Symt
11	211499_s_at	1.36	-0.68	0.26	MAPK11 mitogen-activated protein kinase 11 [Source:HGNC Symbol;
12	219295_s_at	1.24	-0.9	0.27	PCOLCEprocollagen C-endopeptidase enhancer 2 [Source:HGNC Sy
13	219885_at	1.21	-0.72	0.32	SLFN12 schlafen family member 12 [Source:HGNC Symbol;Acc:HGNC
14	203662_s_at	1.17	-0.77	0.4	TMOD1 tropomodulin 1 [Source:HGNC Symbol;Acc:HGNC:11871]
15	205103_at	1.11	-1.01	0.29	C1orf61 chromosome 1 open reading frame 61 [Source:HGNC Symbc
16	204101_at	1.08	-0.83	0.25	MTM1 myotubularin 1 [Source:HGNC Symbol;Acc:HGNC:7448]
17	203671_at	1.04	-0.89	0.36	TPMT thiopurine S-methyltransferase [Source:HGNC Symbol;Acc:G
18	203840_at	0.92	-0.81	0.45	BLZF1 basic leucine zipper nuclear factor 1 [Source:HGNC Symbol;
19	204901_at	0.77	-0.69	0.17	BTRC beta-transducin repeat containing E3 ubiquitin protein ligase
20	212530_at	0.77	-0.81	0.57	NEK7 NIMA related kinase 7 [Source:HGNC Symbol;Acc:HGNC:13

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	1e-11	35 / 1190	GSE/ BLALOCK_ALZHEIMERS_DISEASE_DN
2	2e-10	20 / 417	GSE/ SHEN_SMARCA2_TARGETS_UP
3	2e-10	63 / 3805	CC cytosol
4	1e-09	34 / 1338	GSE/ DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
5	9e-09	26 / 883	Colon LaPointe_mucosa-position_kmeans_L_transverse colon_cecum colon_DN
6	2e-08	22 / 673	GSE/ SCHLOSSER_SERUM_RESPONSE_DN
7	3e-07	72 / 5529	Lymph HOPP_Txn_elongation
8	3e-07	75 / 5908	Lymph HOPP_Active_promoter
9	1e-06	15 / 405	miRN hsa-miR-107
10	2e-06	6 / 44	GSE/ TIEN_INTESTINE_PROBIOTICS_6HR_UP
11	2e-06	31 / 1550	GSE/ PILON_KLF1_TARGETS_DN
12	2e-06	20 / 726	GSE/ REACTOME_IMMUNE_SYSTEM
13	2e-06	63 / 4701	CC cytoplasm
14	3e-06	28 / 1354	Colon LaPointe_mucosa-position_kmeans_N_cecum colon_ascending colon_UP
15	3e-06	9 / 147	GSE/ WANG_CLIM2_TARGETS_DN
16	7e-06	16 / 528	GSE/ FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR_UP
17	8e-06	11 / 256	miRN hsa-miR-548c-3p
18	1e-05	57 / 4261	Lymph HOPP_Txn_transition
19	1e-05	5 / 37	GSE/ PID_FAS_PATHWAY
20	2e-05	9 / 180	CC actin cytoskeleton
21	3e-05	13 / 404	miRN hsa-miR-103
22	3e-05	8 / 148	MF ubiquitin protein ligase activity
23	3e-05	13 / 408	GSE/ REACTOME_ADAPTIVE_IMMUNE_SYSTEM
24	3e-05	12 / 350	miRN hsa-miR-424
25	4e-05	7 / 114	GSE/ KEGG_UBIQUITIN_MEDIATED_PROTEOLYSIS
26	5e-05	8 / 157	miRN hsa-miR-206
27	5e-05	4 / 25	GSE/ BURTON_ADIPOGENESIS_10
28	5e-05	11 / 310	Refer Chaussabel_3.4_Protein phosphatases
29	6e-05	26 / 1402	MF nucleotide binding
30	6e-05	3 / 10	BP regulation of lamellipodium assembly
31	6e-05	25 / 1329	MF transferase activity
32	7e-05	9 / 213	GSE/ THEILGAARD_NEUTROPHIL_AT_SKIN_WOUND_DN
33	7e-05	4 / 27	GSE/ ST_TUMOR_NECROSIS_FACTOR_PATHWAY
34	7e-05	5 / 52	miRN hsa-miR-514
35	8e-05	35 / 2239	CC extracellular exosome
36	8e-05	67 / 5682	Lymph HOPP_Weak_promoter
37	9e-05	5 / 55	CC brush border
38	9e-05	4 / 29	GSE/ PID_CD40_PATHWAY
39	9e-05	12 / 391	BP protein ubiquitination
40	1e-04	17 / 739	GSE/ ACEVEDO_LIVER_CANCER_UP



Aging Rank	p-value	#in/all	Geneset
1	0.5	1 / 92	HORVATH_aging_genes_meth_DOWN
2	0.3	1 / 107	HORVATH_aging_genes_meth_UP
3	1.0	0 / 47	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-05	3 / 10	regulation of lamellipodium assembly
2	6e-05	12 / 391	ubiquitin ubiquitination
3	1e-04	3 / 13	barbed-end actin filament capping
4	1e-04	3 / 13	regulation of centrosome duplication
5	2e-04	6 / 101	mitotic cell cycle
6	2e-04	13 / 502	protein transport
7	3e-04	14 / 578	phosphorylation
8	6e-04	7 / 173	proteasome-mediated ubiquitin-dependent protein catabolic process
9	7e-04	6 / 129	Fc-epsilon receptor signaling pathway
10	8e-04	5 / 87	antigen processing and presentation of exogenous peptide antigen via MHC c
11	8e-04	4 / 51	retrograde transport, endosome to Golgi
12	9e-04	9 / 307	cell division
13	1e-03	3 / 26	endosome organization
14	2e-03	3 / 28	mitotic metaphase plate congression
15	2e-03	4 / 64	Golgi organization

Cancer Rank	p-value	#in/all	Geneset
1	0.02	5 / 186	SPANG_LPS-index2
2	0.05	6 / 317	SPANG_BCL6-index2
3	0.07	1 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
4	0.12	1 / 15	BEN-PORATH_UP
5	0.12	3 / 147	PanCan_MAPK_geneset_nanostring
6	0.23	1 / 32	KUJPER_MM_good_survival
7	0.26	1 / 36	ZHANG_MM_UP
8	0.29	1 / 41	PanCan_DNARepair_geneset_nanostring
9	0.45	1 / 72	PanCan_Wnt_geneset_nanostring
10	0.46	0 / 11	LIU_PROSTATE_CANCER_UP
11	0.49	1 / 80	PanCan_JAK-ST_geneset_nanostring
12	0.52	1 / 130	PanCan_CC+Apopt_geneset_nanostring
13	0.67	1 / 134	PanCan_RAS_geneset_nanostring
14	0.70	0 / 14	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
15	0.79	1 / 187	PanCan_PI3K_geneset_nanostring

CC Rank	p-value	#in/all	Geneset
1	2e-10	63 / 3805	cytosol
2	2e-06	63 / 4701	cytoplasm
3	2e-05	9 / 180	actin cytoskeleton
4	8e-05	35 / 2239	extracellular exosome
5	9e-05	5 / 55	brush border
6	1e-04	11 / 345	focal adhesion
7	5e-04	55 / 4579	nucleus
8	8e-04	18 / 936	cytoskeleton
9	9e-04	3 / 23	cortical cytoskeleton
10	1e-03	5 / 100	late endosome
11	2e-03	4 / 60	actin filament
12	3e-03	11 / 494	endosome
13	3e-03	2 / 10	XY body
14	3e-03	4 / 74	secretory granule membrane
15	6e-03	4 / 86	PML body

Chr Rank	p-value	#in/all	Geneset
1	0.03	11 / 689	Chr 3
2	0.09	8 / 556	Chr X
3	0.15	6 / 157	Chr 5
4	0.17	7 / 554	Chr 5
5	0.21	5 / 382	Chr 15
6	0.30	4 / 333	Chr 22
7	0.32	2 / 139	Chr 21
8	0.32	3 / 242	Chr 13
9	0.36	4 / 369	Chr 20
10	0.38	5 / 492	Chr 9
11	0.45	2 / 184	Chr 18
12	0.46	7 / 776	Chr 17
13	0.52	6 / 700	Chr 12
14	0.54	11 / 1325	Chr 1
15	0.56	4 / 480	Chr 4

Chromatin states Rank	p-value	#in/all	Geneset
1	2e-11	95 / 7635	monocytes peripheral blood_1_TssA
2	4e-11	96 / 7835	HSC_1_TssA
3	2e-10	96 / 7835	Bcells_peripheral blood_1_TssA
4	2e-10	91 / 7225	Overlap_fetal_midbrain_ReprPC
5	3e-10	92 / 7420	Tcells_peripheral blood_1_TssA
6	4e-10	96 / 8068	Thelper cells peripheral blood_1_TssA
7	4e-10	94 / 7751	natural killer cells peripheral blood_1_TssA
8	4e-10	95 / 7930	regulatory cells peripheral blood_1_TssA
9	6e-10	82 / 6099	HSC_4_Tx
10	1e-09	77 / 5527	regulatory cells peripheral blood_4_Tx
11	2e-09	68 / 4528	T CD8+ naive cells peripheral blood_4_Tx
12	3e-09	78 / 5753	Tcells_peripheral blood_4_Tx
13	3e-09	88 / 7331	TssA_Color
14	9e-09	68 / 4683	Overlap_fetal_midbrain_HetRpts
15	1e-08	93 / 7957	Tcells_peripheral blood_2_TssAFlnk

Colon Cancer Rank	p-value	#in/all	Geneset
1	9e-09	26 / 883	LaPointe_mucosa-position_kmeans_L_transverse_colon_cecum_colon_DN
2	3e-06	28 / 1354	LaPointe_mucosa-position_kmeans_N_cecum_colon_ascending_colon_UP_a
3	7e-03	17 / 1083	LaPointe_mucosa-position_kmeans_J_cecum_colon_ascending_colon_transv
4	8e-03	3 / 49	Pentrack_CRC_TCGA_corr_N_msi-h_DN
5	4e-02	1 / 5	Hewish_MMIR-secondary-mutations_Apoptosis
6	5e-02	13 / 958	LaPointe_mucosa-position_kmeans_D_transverse_colon_UP
7	7e-02	20 / 1729	LaPointe_mucosa-position_kmeans_G_cecum_colon_ascending_colon_UP_t
8	1e-01	6 / 397	Pentrack_CRC_TCGA_corr_C_normal_UP
9	1e-01	1 / 16	Budinska_B_Lower_cryp-like_UP
10	1e-01	1 / 18	Bolander-CRC-MSI-A6-A10
11	2e-01	11 / 1001	LaPointe_mucosa-position_kmeans_H_cecum_colon_ascending_colon_UP
12	4e-01	11 / 1174	LaPointe_mucosa-position_kmeans_E_transverse_colon_UP_transverse_colo
13	4e-01	5 / 532	LaPointe_mucosa-position_kmeans_B_ascending_colon_UP_transverse_colon_U
14	5e-01	1 / 83	Marisa_CRC-cluster-d
15	5e-01	10 / 1166	LaPointe_mucosa-position_kmeans_K_transverse_colon_UP_cecum_colon_a

Glioma Rank	p-value	#in/all	Geneset
1	0.003	21 / 1343	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
2	0.012	11 / 614	Sturm_GBM_Meth_overexpression_E_G34_UP
3	0.033	1 / 4	WILLSCHER_GBM_Verhaak-CL_up (E)
4	0.033	1 / 4	WILLSCHER_GBM_STSwT_proteomics-L_UP
5	0.049	2 / 43	Patel_stemness_signatures
6	0.056	6 / 330	Up
7	0.064	2 / 50	Vishal_subnetwork_signature_of_survival_in_GBM
8	0.085	2 / 59	WILLSCHER_GBM_Verhaak-PNwt & MES_up
9	0.102	1 / 13	WILLSCHER_GBM_STSwT_proteomics-O_UP
10	0.121	17 / 1523	Willschur_GBM_Epi3_E1_fetus_UP_fetus_DN
11	0.124	1 / 16	VERHAAK_CL_subtype
12	0.124	1 / 16	Shinawi_with_increased_methylation_in_STS
13	0.160	1 / 21	KIM deleted & downregulated in LTS
14	0.167	1 / 22	Sturm_GBM_Meth_overexpression_H_K27_UP
15	0.199	3 / 186	Hopp_Sturm_GBM_Epi3_C_IDH_UP

GSEA C2 Rank	p-value	#in/all	Geneset
1	1e-11	35 / 1190	BLALOCK_ALZHEIMERS_DISEASE_DN
2	2e-10	20 / 417	SHEN_SMARCA2_TARGETS_UP
3	1e-09	34 / 1338	DLAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
4	2e-08	22 / 673	WILLISER_SERUM_RESPONSE_DN
5	2e-08	6 / 44	TIEN_INTSTINE_PROBIOTICS_gHR_UP
6	2e-06	31 / 1550	PILON_KLF1_TARGETS_DN
7	2e-06	20 / 726	REACTOME_IMMUNE_SYSTEM
8	3e-06	9 / 147	WANG_CLIM2_TARGETS_DN
9	7e-06	16 / 528	FISCHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR_UP
10	1e-05	5 / 37	IFB_PATHWAY
11	3e-05	13 / 408	REACTOME_ADAPTIVE_IMMUNE_SYSTEM
12	4e-05	7 / 114	KEGG_UBIQUITIN_MEDIATED_PROTEOLYSIS
13	5e-05	4 / 25	BURTON_ADIPOGENESIS_10
14	7e-05	9 / 213	THEILGAARD_NEUTROPHIL_AT_SKIN_WOUND_DN
15	7e-05	4 / 27	ST_TUMOR_NECROSIS_FACTOR_PATHWAY

LM Rank	p-value	#in/all	Geneset
1	0.008	4 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING
2	0.028	4 / 139	HALLMARK_FATTY_ACID_METABOLISM
3	0.043	3 / 94	HALLMARK_PROTEIN_SECRETION
4	0.046	3 / 97	HALLMARK_PEROXISOME
5	0.056	4 / 174	HALLMARK_APICAL_JUNCTION
6	0.173	3 / 173	HALLMARK_MITOTIC_SPINDLE
7	0.174	3 / 174	HALLMARK_ADIPOGENESIS
8	0.182	3 / 178	HALLMARK_COMPLEMENT
9	0.199	3 / 186	HALLMARK_OXIDATIVE_PHOSPHORYLATION
10	0.209	3 / 191	HALLMARK_P53_PATHWAY
11	0.344	1 / 44	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
12	0.352	2 / 150	HALLMARK_APOPTOSIS
13	0.388	1 / 59	HALLMARK_CHOLESTEROL_HOMEOSTASIS
14	0.428	2 / 176	HALLMARK_ALLOGRAFT_REJECTION
15	0.445	2 / 182	HALLMARK_GLYCOLYSIS

Immunome Rank	p-value	#in/all	Geneset
1	0.06	1 / 8	Angelova_immune-metagenome-MDC
2	0.09	1 / 12	Angelova_immune-metagenome-effector_memory_CD4
3	0.17	1 / 23	Angelova_immune-metagenome-monocytes
4	0.31	1 / 45	Angelova_immune-metagenome-MDC5
5	1.00	0 / 13	Angelova_immune-metagenome-activated_B-cells
6	1.00	0 / 26	Angelova_immune-metagenome-activated_CD8
7	1.00	0 / 19	Angelova_immune-metagenome-activated_CD8
8	1.00	0 / 21	Angelova_immune-metagenome-central_memory_CD4
9	1.00	0 / 17	Angelova_immune-metagenome-central_memory_CD8
10	1.00	0 / 7	Angelova_immune-metagenome-cytotoxic_cells
11	1.00	0 / 25	Angelova_immune-metagenome-DC
12	1.00	0 / 32	Angelova_immune-metagenome-effector_memory_CD8
13	1.00	0 / 14	Angelova_immune-metagenome-eosinophil
14	1.00	0 / 19	Angelova_immune-metagenome-IDC
15	1.00	0 / 13	Angelova_immune-metagenome-immature_B-cells

Lifestyle Rank	p-value	#in/all	Geneset
1	0.008	6 / 210	Homuth_BMI-associated-genes_DN
2	0.036	4 / 150	Homuth_BMI-associated-genes_UP
3	0.110	1 / 14	Huan_blood-pressure_SBP-signature
4	1.000	0 / 62	DUMEAUX_Smoking_enriched_genes
5	1.000	0 / 10	DUMEAUX_Smoking_literature_genes_up
6	1.000	0 / 13	DUMEAUX_Exercising_non_smoker_literature_enriched_genes
7	1.000	0 / 5	DUMEAUX_Estrogen_related_in_smokers_literature_genes_up
8	1.000	0 / 7	DUMEAUX_Estrogen_related_in_non_smokers_literature_genes_up
9	1.000	0 / 7	DUMEAUX_Hormon_thrapy_in_non_smokers_literature_genes_up
10	1.000	0 / 9	DUMEAUX_Monocytes_in_smokers_literature_genes_up
11	1.000	0 / 11	DUMEAUX_Red_blood_cells_in_non_smokers_literature_genes_up
12	1.000	0 / 12	DUMEAUX_Women_normal_BMI_literature_genes_up
13	1.000	0 / 22	DUMEAUX_High_bmi_enriched_genes
14	1.000	0 / 22	DUMEAUX_Fasting_enriched_genes
15	1.000	0 / 13	Huan_blood-pressure_DBP-signature

Lymphoma Rank	p-value	#in/all	Geneset
1	3e-07	72 / 5529	HOPP_Txn_elongation
2	3e-07	75 / 5908	HOPP_Active_promoter
3	1e-05	57 / 4261	HOPP_Txn_transition
4	8e-05	67 / 5682	HOPP_Weak_promoter
5	1e-04	6 / 97	ROSLOWSKI_red_total
6	1e-03	61 / 5404	HOPP_Strong_enhancer
7	2e-03	51 / 4357	HOPP_Weak_txn
8	2e-03	48 / 4559	HOPP_Weak_transcancer
9	7e-02	12 / 906	SPANG_BCR_DN
10	7e-02	1 / 9	YAMANE_AICDA_targets_nonrecruited
11	8e-02	2 / 57	SPANG_LPS_6hrs_DN
12	1e-01	5 / 305	TARTE_PlasmaBst_signature
13	1e-01	18 / 1814	HOPP_Receptor_DN
14	3e-01	3 / 213	SPANG_IL21_DN
15	3e-01	3 / 237	ZHANG_DLCLC_mutated

Melanoma Rank	p-value	#in/all	Geneset
1	0.005	6 / 189	Tirosh_genes_preferentially_expressed_by_Tregs
2	0.008	2 / 17	Hugo_melanoma-all_MET_UP
3	0.038	2 / 38	Tirosh_top50_correlated_genes_PC1
4	0.042	5 / 230	Gerber_wt/wt_melanoma-cells-SpotC
5	0.072	1 / 9	Joensuu_Melanoma_Pigmentation_subtype
6	0.112	4 / 222	Gerber_wt/wt_melanoma-cells-SpotF
7	0.228	6 / 487	Gerber_wt/wt_melanoma-cells-SpotD
8	0.238	3 / 234	Landberg_dedifferentiation_down
9	0.271	1 / 38	Hugo_melanoma-BRAFmut-MET_UP
10	0.309	3 / 236	Gerber_wt/wt_group3-specific
11	0.339	3 / 249	Gerber_wt/wt_melanoma-cells-SpotE
12	0.432	1 / 68	Tirosh_housekeeping_genes
13	0.483	2 / 185	Tirosh_genes_from_melanoma_aligned_cells_in_Mel79-melanoma
14	0.477	1 / 78	Tirosh_expression_higher_in_CAFs_than_in_T-cells
15	0.493	3 / 319	Gerber_wt/wt_melanoma-cells-SpotA

MF Rank	p-value	#in/all	Geneset
1	3e-05	8 / 148	ubiquitin protein ligase activity
2	6e-05	26 / 1402	nucleotide binding
3	6e-05	25 / 1329	transferase activity
4	1e-04	9 / 237	ubiquitin-protein transferase activity
5	2e-04	3 / 15	cysteine-type endopeptidase activator activity involved in apoptotic process
6	2e-04	22 / 1185	ATP binding
7	3e-04	14 / 573	kinase activity
8	4e-04	10 / 331	protein serine/threonine kinase activity
9	9e-04	81 / 7864	protein binding
10	3e-03	10 / 437	protein kinase activity
11	4e-03	2 / 12	phosphatidylinositol-3,5-bisphosphate 3-phosphatase activity
12	5e-03	7 / 249	ubiquitin protein ligase binding
13	5e-03	2 / 13	MAP kinase activity
14	5e-03	5 / 135	actin filament binding
15	5e-03	7 / 256	cadherin binding

mikNA target Rank	p-value	#in/all	Geneset
1	1e-06	15 / 405	hsa-miR-107
2	8e-06	11 / 256	hsa-miR-548c-3p
3	3e-05	13 / 404	hsa-miR-103
4	3e-04	12 / 450	hsa-miR-424
5	5e-05	8 / 157	hsa-miR-206
6	7e-05	5 / 52	hsa-miR-514
7	1e-04	9 / 235	hsa-miR-30e
8	2e-04	8 / 194	hsa-miR-124
9	2e-04	5 / 68	hsa-miR-505
10	3e-04	7 / 155	hsa-miR-586
11	3e-04	6 / 112	hsa-miR-218
12	4e-04	7 / 164	hsa-miR-548d-3p
13	8e-04	6 / 134	hsa-miR-141
14	8e-04	7 / 185	hsa-miR-182
15	1e-03	3 / 27	

Correlation Cluster

Spot Summary: N

metagenes = 39
genes = 483

<r> metagenes = 0.96

<r> genes = 0.32

beta: r2= 10.64 / log p= -Inf

samples with spot = 76 (34.4 %)

intermediate : 3 (6.2 %)

non-mBL : 73 (56.6 %)

Spot Genelist

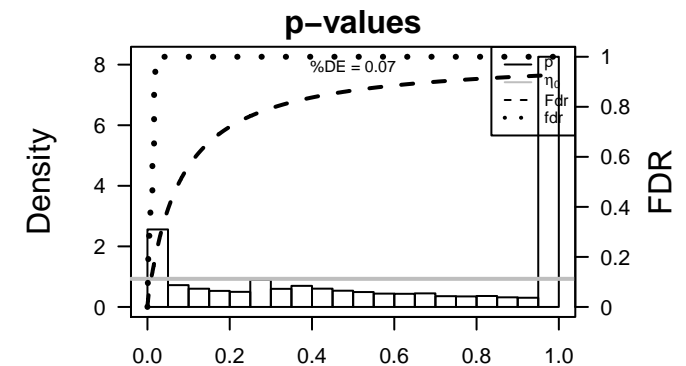
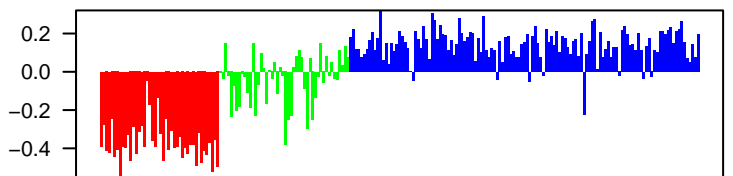
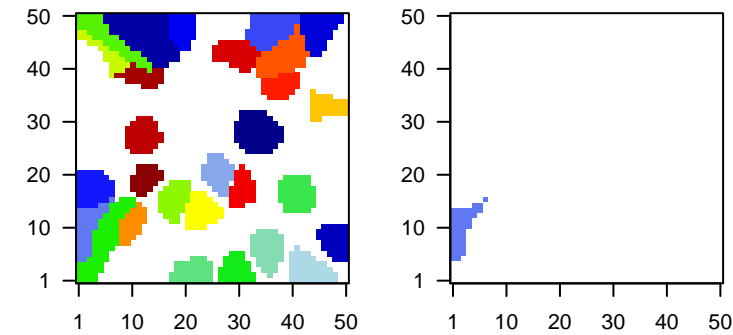
Rank	ID	max e	r	min e	Description
					Symbol
1	209728_at	2.5	-1.71	0.23	HLA-DRB1 major histocompatibility complex, class II, DR beta 4 [Source:Ensembl]
2	216615_s_at	2.49	-1.56	0.41	HTR3A 5-hydroxytryptamine receptor 3A [Source:HGNC Symbol;Acc:NCBI]
3	207245_at	2.21	-1.2	0.45	UGT2B17 UDP glucuronosyltransferase family 2 member B17 [Source:Ensembl]
4	202274_at	1.93	-2	0.45	ACTG2 actin, gamma 2, smooth muscle, enteric [Source:HGNC Symbol;Acc:NCBI]
5	210517_s_at	1.9	-1.34	0.32	AKAP12 A-kinase anchoring protein 12 [Source:HGNC Symbol;Acc:NCBI]
6	210437_at	1.88	-1.26	0.42	MAGEA9 MAGE family member A9B [Source:HGNC Symbol;Acc:NCBI]
7	205613_at	1.78	-1.32	0.21	SYT17 synaptotagmin 17 [Source:HGNC Symbol;Acc:HGNC:24119]
8	210916_s_at	1.78	-1.66	0.77	CD44 CD44 molecule (Indian blood group) [Source:HGNC Symbol;Acc:NCBI]
9	219799_s_at	1.78	-1.76	0.57	DHRS9 dehydrogenase/reductase 9 [Source:HGNC Symbol;Acc:NCBI]
10	204489_s_at	1.76	-2.02	0.78	CD44 CD44 molecule (Indian blood group) [Source:HGNC Symbol;Acc:NCBI]
11	203404_at	1.73	-1.41	0.48	ARMCX2 armadillo repeat containing, X-linked 2 [Source:HGNC Symbol;Acc:NCBI]
12	206337_at	1.72	-2.11	0.73	CCR7 C-C motif chemokine receptor 7 [Source:HGNC Symbol;Acc:NCBI]
13	203562_at	1.7	-1.4	0.55	FEZ1 fasciculation and elongation protein zeta 1 [Source:HGNC Symbol;Acc:NCBI]
14	222043_at	1.7	-1.38	0.53	CLU clusterin [Source:HGNC Symbol;Acc:HGNC:2095]
15	203835_at	1.7	-1.1	0.41	LRRC32 leucine rich repeat containing 32 [Source:HGNC Symbol;Acc:NCBI]
16	217966_s_at	1.67	-0.98	0.56	FAM129A family with sequence similarity 129 member A [Source:HGNC Symbol;Acc:NCBI]
17	219424_at	1.67	-2.01	0.79	EBI3 Epstein-Barr virus induced 3 [Source:HGNC Symbol;Acc:NCBI]
18	211194_s_at	1.66	-1.3	0.45	TP63 tumor protein p63 [Source:HGNC Symbol;Acc:HGNC:15979]
19	220358_at	1.64	-1.04	0.59	BATF3 basic leucine zipper ATF-like transcription factor 3 [Source:HGNC Symbol;Acc:NCBI]
20	205997_at	1.63	-1.62	0.63	ADAM28 ADAM metallopeptidase domain 28 [Source:HGNC Symbol;Acc:NCBI]

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	4e-48	75 / 317	Cancer SPANG_BCL6-index2
2	8e-38	39 / 85	Lymph Sha_DLBCL UP
3	5e-36	51 / 186	Cancer SPANG_LPS-index2
4	3e-34	271 / 5404	Lymph HOPP_Strong_enhancer
5	7e-32	46 / 173	Lymph Victora_Light zone signature
6	6e-31	35 / 90	GSE/ BASSO_CD40_SIGNALING_UP
7	1e-30	61 / 353	Lymph SPANG_CD40 6hrs DN
8	7e-21	20 / 40	BP antigen processing and presentation
9	9e-21	39 / 213	Lymph SPANG_IL21 DN
10	1e-19	31 / 135	Lymph DAVE_BL-vs-DLBCL
11	3e-19	255 / 5908	Lymph HOPP_Active_promoter
12	6e-19	14 / 18	CC MHC class II protein complex
13	7e-19	52 / 431	BP immune system process
14	2e-18	77 / 906	Lymph SPANG_BCR DN
15	2e-18	15 / 23	CC integral component of luminal side of endoplasmic reticulum membrane
16	4e-18	22 / 66	BP interferon-gamma-mediated signaling pathway
17	4e-18	46 / 353	GSE/ JOHNSTONE_PARVB_TARGETS_3_UP
18	7e-18	37 / 229	GSE/ QI_PLASMACYTOMA_UP
19	2e-17	13 / 17	BP antigen processing and presentation of peptide or polysaccharide antigen via
20	2e-17	12 / 14	GSE/ HUMMEL_BURKITTIS_LYMPHOMA_DN
21	5e-17	14 / 22	MF peptide antigen binding
22	2e-16	44 / 355	Refer WIRTH_Immune system
23	1e-14	44 / 397	GSE/ REN_ALVEOLAR_RHABDOMYOSARCOMA_DN
24	2e-14	10 / 12	Lymph BENTINK_mBL DOWN
25	7e-14	16 / 46	GSE/ MORI_IMMATURE_B_LYMPHOCYTE_UP
26	4e-13	38 / 336	BP immune response
27	4e-13	16 / 51	GSE/ MORI_LARGE_PRE_BII_LYMPHOCYTE_DN
28	5e-13	189 / 4261	Lymph HOPP_Txn_transition
29	7e-13	50 / 560	GSE/ KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP
30	1e-12	18 / 72	GSE/ MORI_MATURE_B_LYMPHOCYTE_UP
31	1e-12	26 / 166	HM HALLMARK_INTERFERON_GAMMA_RESPONSE
32	2e-12	16 / 55	GSE/ DIRMEIER_LMP1_RESPONSE_EARLY
33	2e-12	16 / 55	GSE/ DIRMEIER_LMP1_RESPONSE_LATE_UP
34	2e-12	36 / 321	GSE/ PHONG_TNF_RESPONSE_NOT_VIA_P38
35	3e-12	43 / 447	Glioma ScoV_0.999_Sturm_E4_Mesenchymal_RTK_I_PDGFR_A_DN
36	3e-12	65 / 902	GSE/ CHEN_METABOLIC_SYNDROM_NETWORK
37	4e-12	50 / 589	Color Lemboke_TCGA-expr_kmeans_E_CIMP_H_UP_Cluster4_DN
38	5e-12	11 / 22	Lymph DAVE_NFKB BL DN
39	5e-12	15 / 50	GSE/ LINDSTEDT_DENDRITIC_CELL_MATURATION_B
40	3e-11	226 / 5682	Lymph HOPP_Weak_promoter

Overview Map

Spot



Rank	p-value	#in/all	Geneset
1	0.4	2 / 47	TESCHENDORFF_age_hypermethylated
2	0.7	3 / 32	HORVATH_aging_genes_meth_DOWN
3	0.8	2 / 107	HORVATH_aging_genes_meth
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	

Rank	p-value	#in/all	Geneset
1	6e-19	14 / 18	MHC class II protein complex
2	2e-18	15 / 23	Integral component of luminal side of endoplasmic reticulum membrane
3	1e-10	41 / 51	ER to Golgi transport vesicle membrane
4	3e-10	146 / 3210	plasma membrane
5	7e-10	14 / 58	phagocytic vesicle membrane
6	4e-08	27 / 281	lysosome
7	7e-08	30 / 345	focal adhesion
8	4e-07	154 / 3905	cytosol
9	8e-07	8 / 25	clathrin-coated endocytic vesicle membrane
10	1e-06	21 / 219	lysosomal membrane
11	1e-06	33 / 462	cell surface
12	6e-06	8 / 36	transport vesicle membrane
13	2e-05	41 / 938	Golgi apparatus
14	2e-05	96 / 2239	extracellular exosome
15	4e-05	31 / 494	endosome

Rank	p-value	#in/all	Geneset
1	4e-12	50 / 589	Lembcke_TCGA_expr_kmeans_E_CIMP_H_UP_Cluster4_DN
2	4e-09	29 / 288	Pentrack_CRC_TCGA_corr_J_msi-h_UP_mss_DN
3	1e-07	27 / 297	Pentrack_CRC_TCGA_group_over_B_msi-h_UP
4	1e-05	48 / 883	LaPointe_mucosa-position_kmeans_L_transverse_colon_cecum_colon_DN
5	4e-05	54 / 1063	LaPointe_mucosa-position_kmeans_J_cecum_colon_ascending_colon_transv
6	9e-05	56 / 1166	LaPointe_mucosa-position_kmeans_K_transverse_colon_UP_cecum_colon_UP
7	2e-03	70 / 1729	LaPointe_mucosa-position_kmeans_G_cecum_colon_ascending_colon_UP_t
8	2e-03	28 / 539	Lembcke_TCGA_meth_kmeans_L_CIMP_H_DN
9	3e-03	25 / 483	Lembcke_TCGA_expr_kmeans_E_CIMP_H_UP_Cluster3_DN
10	5e-03	21 / 397	Pentrack_CRC_TCGA_corr_C_normal_UP
11	2e-02	2 / 7	Boland_CRC_MSI-TGC
12	2e-02	2 / 8	Marisa_CRC-C3
13	3e-02	10 / 172	Pentrack_CRC_TCGA_corr_U_msi-h_UP
14	5e-02	38 / 1001	LaPointe_mucosa-position_kmeans_H_cecum_colon_ascending_colon_UP_
15	6e-02	1 / 2	Hewish_dMMR-secondary-mutations_Cell-motility

Rank	p-value	#in/all	Geneset
1	1e-12	26 / 166	HALLMARK_INTERFERON_GAMMA_RESPONSE
2	2e-10	25 / 190	HALLMARK_TNFA_SIGNALING_VIA_NFKB
3	1e-05	17 / 176	HALLMARK_ALLOGRAFT_REJECTION
4	3e-05	11 / 85	HALLMARK_IL6_JAK_STAT3_SIGNALING
5	6e-05	10 / 76	HALLMARK_INTERFERON_ALPHA_RESPONSE
6	1e-04	15 / 187	HALLMARK_INFLAMMATORY_RESPONSE
7	4e-04	13 / 150	HALLMARK_APOPTOSIS
8	4e-04	14 / 170	HALLMARK_IL2_STATS_SIGNALING
9	5e-04	14 / 174	HALLMARK_APICAL_JUNCTION
10	1e-03	14 / 188	HALLMARK_HYPOXIA
11	2e-03	13 / 178	HALLMARK_COMPLEMENT
12	7e-03	6 / 59	HALLMARK_CHOLESTEROL_HOMEOSTASIS
13	9e-03	12 / 191	HALLMARK_P53_PATHWAY
14	1e-02	12 / 194	HALLMARK_KRAS_SIGNALING_UP
15	2e-02	11 / 193	HALLMARK_HEME_METABOLISM

Rank	p-value	#in/all	Geneset
1	8e-38	39 / 85	Sha_DLBC_LUP
2	3e-34	27 / 5404	HOPP_Strong_enhancer
3	7e-32	46 / 173	Victoria_Light_zone_signature
4	1e-30	61 / 353	SPANG_CD40_6hrs_DN
5	9e-21	39 / 213	SPANG_IL21_DN
6	1e-19	31 / 135	DAVE_BL-vs-DLBC
7	3e-19	255 / 5908	HOPP_Active_promoter
8	2e-18	27 / 906	SPANG_BCR_DN
9	2e-14	10 / 12	BENTINK_mBL_DOWN
10	5e-13	189 / 4261	HOPP_Txn_transition
11	5e-12	11 / 22	DAVE_NFKB_BL_DN
12	3e-11	220 / 5682	HOPP_Weak_promoter
13	4e-11	15 / 57	SPANG_LPS_6hrs_DN
14	1e-10	220 / 5529	HOPP_Txn_elongation
15	5e-10	6 / 6	DAVE_MHCII_BL_DN

Rank	p-value	#in/all	Geneset
1	8e-04	11 / 122	hsa-miR-506
2	1e-03	14 / 194	hsa-miR-124
3	1e-02	6 / 64	hsa-miR-1261
4	1e-04	6 / 64	hsa-miR-890
5	2e-02	12 / 205	hsa-miR-1252
6	2e-02	6 / 71	hsa-miR-188-3p
7	2e-02	5 / 53	hsa-miR-518c
8	2e-02	4 / 36	hsa-miR-129-3p
9	2e-02	7 / 39	hsa-miR-518a-3p
10	2e-02	3 / 22	hsa-miR-24-1*
11	3e-02	5 / 59	hsa-miR-361-3p
12	4e-02	6 / 87	hsa-miR-449b
13	4e-02	5 / 66	hsa-miR-567
14	4e-02	12 / 237	hsa-miR-302c
15	4e-02	2 / 12	hsa-miR-191*

Rank	p-value	#in/all	Geneset
1	0.5	1 / 27	Nabeta1n1_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	

Rank	p-value	#in/all	Geneset
1	7e-21	20 / 40	antigen processing and presentation
2	7e-19	52 / 431	immune system process
3	4e-18	22 / 66	interferon-gamma-mediated signaling pathway
4	2e-17	13 / 17	antigen processing and presentation of peptide or polysaccharide antigen via
5	4e-13	38 / 336	immune response
6	1e-09	10 / 26	antigen processing and presentation of peptide antigen via MHC class I
7	6e-07	11 / 60	T cell costimulation
8	4e-06	15 / 127	positive regulation of NF-kappaB transcription factor activity
9	6e-06	29 / 407	viral process
10	2e-05	15 / 143	positive regulation of I-kappaB kinase/NF-kappaB signaling
11	2e-05	13 / 113	regulation of immune response
12	2e-05	26 / 367	innate immune response
13	9e-05	10 / 69	antigen processing and presentation of exogenous peptide antigen via MHC c
14	4e-05	11 / 87	antigen processing and presentation of exogenous peptide antigen via MHC c
15	4e-05	27 / 403	neutrophil degranulation

Rank	p-value	#in/all	Geneset
1	0.005	37 / 832	Chr 2
2	0.006	31 / 669	Chr 2
3	0.018	32 / 756	Chr 11
4	0.031	24 / 556	Chr X
5	0.125	28 / 776	Chr 17
6	0.173	21 / 585	Chr 7
7	0.437	15 / 490	Chr 10
8	0.527	16 / 554	Chr 5
9	0.542	20 / 700	Chr 12
10	0.662	10 / 382	Chr 15
11	0.712	14 / 548	Chr 16
12	0.782	34 / 1325	Chr 1
13	0.856	8 / 616	Chr 20
14	0.896	15 / 689	Chr 3
15	0.920	4 / 242	Chr 13

Rank	p-value	#in/all	Geneset
1	3e-12	43 / 447	Scov_0.999_Sturm_E4_Mesenchymal_RTK_I_PDGFR_A_DN
2	9e-07	24 / 269	Scov_0.5_Sturm_C3_Mesenchymal_DN
3	8e-06	7 / 27	Donson-Misc immune function-associated with LTS in HGA
4	3e-05	21 / 268	Scov_0.001_Sturm_M2_Mesenchymal_RTK_I_PDGFR_A_DN
5	5e-05	50 / 479	Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_tetus_adult_DN
6	8e-05	23 / 330	Up
7	1e-04	18 / 231	WILLSCHER_GBM_Verhaak-C & MES_up
8	2e-04	18 / 242	Scov_0.5_Sturm_C1_IDH_DN
9	3e-03	8 / 83	Scov_0.999_Sturm_E3_RTK_I_PDGFR_A_DN
10	5e-03	5 / 38	10 vs OPC
11	5e-03	15 / 246	Scov_0.001_Sturm_M1_IDH_RTK_I_PDGFR_A_DN
12	9e-03	10 / 144	Christensen_hypermethylated_in_grade2_oligodendroglioma
13	9e-03	5 / 45	Donson-innate immunity-associated with LTS in HGA
14	2e-02	8 / 112	Christensen_hypermethylated_in_grade3_astrocytoma
15	2e-02	3 / 22	Martinez_Glio_hypermeth

Rank	p-value	#in/all	Geneset
1	1e-06	5 / 8	Immunity_HLA-class-II
2	2e-05	6 / 21	AngeloVA immune-metagenes-central_memory_CD4
3	1e-04	4 / 10	AngeloVA immune-metagenes-TFH
4	8e-04	3 / 7	AngeloVA immune-metagenes-cytotoxic_cells
5	1e-03	5 / 29	AngeloVA immune-metagenes-TH1
6	2e-03	6 / 45	AngeloVA immune-metagenes-MDSC
7	2e-03	6 / 32	AngeloVA immune-metagenes-effector_memory_CD8
8	5e-03	2 / 4	AngeloVA_CRC_MHC_class_II
9	1e-02	3 / 17	AngeloVA immune-metagenes-central_memory_CD8
10	1e-02	3 / 18	AngeloVA_CRC_immunostimulators
11	3e-02	4 / 42	AngeloVA immune-metagenes-TCD
12	7e-02	2 / 15	AngeloVA immune-metagenes-NK
13	8e-02	1 / 3	AngeloVA_CRC_MHC_class_I
14	1e-01	4 / 67	AngeloVA immune-metagenes-T_cells
15	1e-01	1 / 5	AngeloVA immune-metagenes-NKT

Rank	p-value	#in/all	Geneset
1	4e-07	15 / 107	Tirosh_Exhaustion program in Mel75
2	2e-06	19 / 189	Tirosh_genes preferentially expressed by Tregs
3	3e-06	11 / 85	Tirosh_IL4-signature
4	5e-03	25 / 497	Gerber_wt_wt_melanoma-cells-SpotD
5	6e-03	13 / 204	Landsberg_dedifferentiation_down
6	2e-02	5 / 51	Tirosh_genes from CD8 T-cells in Mel79-melanoma
7	2e-02	11 / 185	Tirosh_genes from malignant cells in Mel79-melanoma
8	2e-02	4 / 41	Tirosh_top50 correlated genes PC3
9	3e-02	12 / 230	Gerber_wt_wt_melanoma-cells-SpotC
10	6e-02	9 / 171	Landsberg_dedifferentiation_up
11	7e-02	3 / 33	Tirosh_T-cell specific genes-melanoma
12	8e-02	2 / 16	Gerber_melanoma-all_LEF1_UP
13	1e-01	1 / 5	Hugo_melanoma-BRAFmut-MET_DN
14	2e-01	11 / 276	Gerber_wt_wt_melanoma-cells-SpotB
15	3e-01	2 / 37	Hugo_melanoma-all_MET_DN

Rank	p-value	#in/all	Geneset
1	2e-07	10 / 41	Scicluna_DN
2	2e-04	8 / 56	Burnham_sep_vs_con_DN
3	4e-04	7 / 48	Burnham_cap_ip_vs_con_DN
4	7e-04	7 / 57	Burnham_viral_UP
5	1e-02	11 / 179	Terre_MS_V_multiple_respiratory_viruses_dn
6	9e-02	7 / 135	Terre_MS_V_multiple_respiratory_viruses_up
7	1e-01	6 / 122	Terre_IMS_influenza_meta_signature
8	2e-01	2 / 33	Sweeney_viral_dn
9	2e-01	2 / 37	Sweeney_viral_up
10	4e-01	1 / 18	Scicluna_UP
11	4e-01	2 / 52	Burnham_day1_vs_5_DN
12	6e-01	2 / 68	Burnham_sep_vs_con_UP
13	8e-01	1 / 48	Burnham_viral_DN
14	8e-01	1 / 54	Burnham_timecourse
15	9e-01	1 / 71	Burnham_cap_ip_vs_con_UP

Rank	p-value	#in/all	Geneset
1	1e-07	78 / 1508	ICGC_Mel2_targets
2	3e-06	89 / 1941	ICGC_Bcl3_targets
3	3e-06	73 / 1494	ICGC_Cebpbsc150_targets
4	6e-06	77 / 1636	ICGC_Bcl11_targets
5	2e-04	92 / 2254	ICGC_BatfP1_targets
6	7e-04	120 / 3213	ICGC_Pu1_targets
7	7e-04	110 / 2899	ICGC_Nr1c1_targets
8	9e-04	126 / 3435	ICGC_Ebfc137065_targets
9	1e-03	111 / 2994	ICGC_Zeb1_targets
10	2e-03	124 / 3420	ICGC_Bcl1f101388_targets
11	3e-03	83 / 2150	ICGC_Irf3_targets
12	3e-03	133 / 3769	ICGC_Pmlsc71910_targets
13	3e-03	134 / 3804	ICGC_Stat5_targets
14	3e-03	128 / 3608	ICGC_Tcf12_targets
15	4e-03	72 / 1848	ICGC_Pbx3_targets

Rank	p-value	#in/all	Geneset
1	4e-48	75 / 317	SPANG_BCL6-index2
2	5e-38	51 / 186	SPANG_LPS-index2
3	4e-08	37 / 480	Lembcke_Colonc Inflammation
4	1e-07	6 / 10	BENTINK_ras_4
5	4e-07	6 / 12	HLA2_signature
6	5e-04	4 / 14	BENTINK_sirc.10
7	8e-04	2 / 12	HLA1_signature
8	4e-03	3 / 12	GENTLES_modul12
9	5e-03	3 / 13	GENTLES_modul11
10	1e-02	10 / 147	PanCan_MAPK_geneset_nanostring
11	2e-02	2 / 12	LIU_BREAST_CANCER
12	6e-02	2 / 14	LIU_PROSTATE_CANCER_DN
13	8e-02	2 / 16	GENTLES_modul16
14	1e-01	5 / 96	PanCan_TXMisReg_geneset_nanostring
15	2e-01	1 / 6	ZHANG_MGUS_up

Rank	p-value	#in/all	Geneset
1	3e-24	321 / 3767	Bcells_peripheral_blood_6_EnhG
2	9e-21	202 / 8406	Bcells_peripheral_blood_2_TssAFlnk
3	1e-20	100 / 3682	natural killer cells peripheral blood_5_EnhG
4	5e-20	173 / 3223	monocytes_peripheral_blood_6_EnhG
5	1e-18	313 / 8200	monocytes_peripheral_blood_2_TssAFlnk
6	1e-18	304 / 7833	Bcells_peripheral_blood_1_TssA
7	3e-18	66 / 693	Bcells_peripheral_blood_3_TxFlnk
8	6e-18	305 / 7930	Regulatory cells peripheral blood_1_TssA
9	3e-17	314 / 8370	natural killer cells peripheral blood_2_TssAFlnk
10	3e-16	174 / 3524	Regulatory cells peripheral blood_6_EnhG
11	4e-16	196 / 4208	Tcells_peripheral_blood_6_EnhG
12	6e-16	293 / 7635	monocytes_peripheral_blood_1_TssA
13	2e-15	307 / 8245	Regulatory cells peripheral blood_2_TssAFlnk
14	3e-15	294 / 775	natural killer cells peripheral blood_1_TssA
15	4e-15	308 / 8322	T CD8+ naive cells peripheral blood_1_TssA

Rank	p-value	#in/all	Geneset
1	6e-3		

Correlation Cluster

Spot Summary: O

metagenes = 26
genes = 54

<r> metagenes = 0.94
<r> genes = 0.13
beta: r2= 0.23 / log p= -13.65

samples with spot = 5 (2.3 %)
non-mBL : 5 (3.9 %)

Spot Genelist

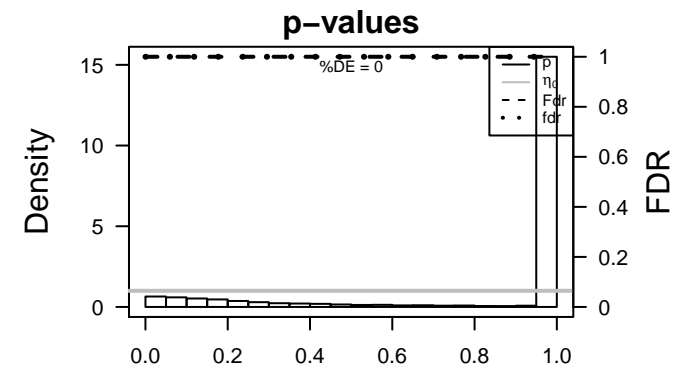
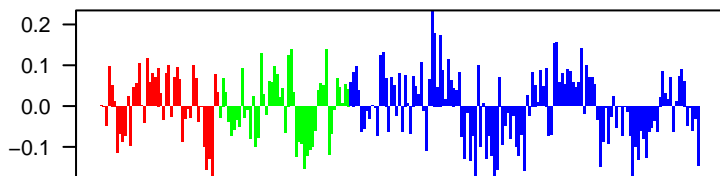
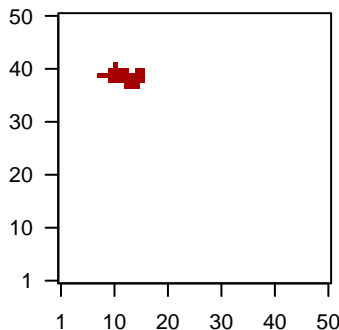
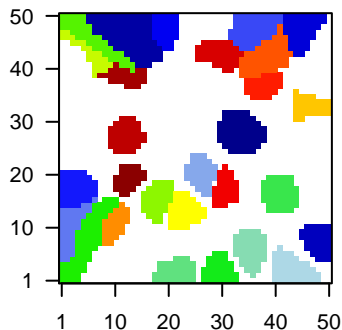
Rank	ID	max e	r	min e	Description
1	216676_x_at	2.15	-0.68	0.11	KIR3DL3 killer cell immunoglobulin like receptor, three Ig domains and
2	207638_at	2.02	-0.79	-0.01	TMPRSS3 transmembrane serine protease 15 [Source:HGNC Symbol;Acc:HGNC:1315]
3	205149_s_at	1.57	-0.85	0.65	CLCN4 chloride voltage-gated channel 4 [Source:HGNC Symbol;Acc:HGNC:1315]
4	211823_s_at	1.43	-0.78	0.58	PXN paxillin [Source:HGNC Symbol;Acc:HGNC:9718]
5	211199_s_at	1.4	-1.02	0.36	LOC102723996
6	217556_at	1.35	-0.88	0.45	CLCN4 chloride voltage-gated channel 4 [Source:HGNC Symbol;Acc:HGNC:1315]
7	212853_at	1.2	-0.83	0.53	DCUN1D defective in cullin neddylation 1 domain containing 4 [Source:HGNC Symbol;Acc:HGNC:11424]
8	211884_s_at	1.19	-0.58	0.65	CIITA class II major histocompatibility complex transactivator [Source:HGNC Symbol;Acc:HGNC:1315]
9	214901_at	1.15	-0.87	0.35	ZNF8 zinc finger protein 8 [Source:HGNC Symbol;Acc:HGNC:1315]
10	202485_s_at	1.14	-1.08	0.4	MBD2 methyl-CpG binding domain protein 2 [Source:HGNC Symbol;Acc:HGNC:1315]
11	210688_s_at	0.97	-0.77	0.27	CPT1A carnitine palmitoyltransferase 1A [Source:HGNC Symbol;Acc:HGNC:1315]
12	205520_at	0.96	-0.76	0.55	STRN striatin [Source:HGNC Symbol;Acc:HGNC:11424]
13	208423_s_at	0.93	-0.78	0.34	MSR1 macrophage scavenger receptor 1 [Source:HGNC Symbol;Acc:HGNC:1315]
14	214462_at	0.81	-0.74	0.39	SOCS6 suppressor of cytokine signaling 6 [Source:HGNC Symbol;Acc:HGNC:1315]
15	204399_s_at	0.79	-0.78	0.44	EML2 echinoderm microtubule associated protein like 2 [Source:HGNC Symbol;Acc:HGNC:1315]
16	207566_at	0.78	-0.63	0.47	MR1 major histocompatibility complex, class I-related [Source:HGNC Symbol;Acc:HGNC:1315]
17	214716_at	0.78	-0.85	0.25	BMP2K BMP2 inducible kinase [Source:HGNC Symbol;Acc:HGNC:1315]
18	221287_at	0.75	-0.81	0.57	RNASEL ribonuclease L [Source:HGNC Symbol;Acc:HGNC:10050]
19	206890_at	0.73	-1	0.35	IL12RB1 interleukin 12 receptor subunit beta 1 [Source:HGNC Symbol;Acc:HGNC:1315]
20	1773_at	0.73	-0.72	0.45	CHURC1 CHURC1-FNTB readthrough [Source:HGNC Symbol;Acc:HGNC:1315]

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	3e-05	5 / 103	miRN hsa-miR-576-3p
2	1e-04	3 / 28	GSE/ YANAGIHARA_ESX1_TARGETS
3	2e-04	10 / 726	GSE/ REACTOME_IMMUNE_SYSTEM
4	3e-04	8 / 468	GSE/ ENK_UV_RESPONSE KERATINOCYTE_DN
5	3e-04	15 / 1550	GSE/ PILON_KLF1_TARGETS_DN
6	6e-04	9 / 673	GSE/ SCHLOSSER_SERUM_RESPONSE_DN
7	8e-04	14 / 1527	GSE/ PUJANA_BRCA1_PCC_NETWORK
8	8e-04	13 / 1354	Colon LaPointe_mucosa-position_kmeans_N_ascending_colon_UP
9	9e-04	5 / 209	Refer Chaussabel_2.5_Immune related molecules
10	1e-03	3 / 59	Refer Chaussabel_2.10_Immune related cell surface molecules
11	2e-03	2 / 16	BP regulation of mitotic spindle assembly
12	2e-03	8 / 621	BP negative regulation of transcription from RNA polymerase II promoter
13	2e-03	9 / 785	GSE/ GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_DN
14	2e-03	3 / 72	GSE/ MUNSHI_MULTIPLE_MYELOMA_UP
15	2e-03	3 / 73	CC ubiquitin ligase complex
16	2e-03	3 / 73	miRN hsa-miR-423-5p
17	3e-03	3 / 75	BP cellular response to interferon-gamma
18	3e-03	2 / 24	CC membrane coat
19	3e-03	2 / 24	GSE/ CHEOK_RESPONSE_TO_HD_MTX_DN
20	3e-03	8 / 699	GSE/ BENPORATH_MYC_MAX_TARGETS
21	3e-03	6 / 408	GSE/ REACTOME_ADAPTIVE_IMMUNE_SYSTEM
22	3e-03	25 / 4261	Lymp HOPP_Txn_transition
23	3e-03	10 / 1032	Refer PROTEINATLAS_small intestine
24	4e-03	2 / 25	GSE/ MORI_PLASMA_CELL_DN
25	4e-03	6 / 415	GSE/ BAELDE_DIABETIC_NEPHROPATHY_DN
26	4e-03	2 / 26	BP antigen processing and presentation of peptide antigen via MHC class I
27	4e-03	4 / 179	Pneui Terre_MSIV_multiple_respiratory_viruses_dn
28	4e-03	7 / 564	GSE/ SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_DN
29	4e-03	31 / 5908	Lymp HOPP_Active_promoter
30	5e-03	2 / 28	CC microtubule associated complex
31	5e-03	2 / 28	miRN hsa-miR-342-5p
32	5e-03	2 / 28	GSE/ PID_IGF1_PATHWAY
33	5e-03	29 / 5404	Lymp HOPP_Strong_enhancer
34	5e-03	2 / 30	GSE/ PID_INTEGRIN_A4B1_PATHWAY
35	5e-03	2 / 30	GSE/ BANDRES_RESPONSE_TO_CARMUSTIN_MGMT_24HR_DN
36	6e-03	3 / 99	BP regulation of mRNA stability
37	6e-03	3 / 100	miRN hsa-miR-625
38	6e-03	9 / 935	GSE/ MARSON_BOUND_BY_FOXP3_UNSTIMULATED
39	6e-03	3 / 103	GSE/ NOUZOVA_TRETINOIN_AND_H4_ACETYLATION
40	6e-03	2 / 33	GSE/ GUTIERREZ_MULTIPLE_MYELOMA_DN

Overview Map

Spot



Rank	p-value	#in/all	Geneset
1	1	0/92	HORVATH_aging_genes_meth_DOWN
2	1	0/107	HORVATH_aging_genes_meth_UP
3	0.007	0/47	TSCHEENDORFF_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	

Rank	p-value	#in/all	Geneset
1	0.002	3/73	ubiquitin ligase complex
2	0.003	2/24	membrane coat
3	0.004	0/28	microtubule associated complex
4	0.009	3/118	cytoplasmic vesicle membrane
5	0.015	2/52	mitotic spindle
6	0.018	2/57	cytoplasmic ribonucleoprotein granule
7	0.019	3/157	spindle
8	0.034	3/196	nuclear membrane
9	0.036	1/10	nuclear inclusion body
10	0.036	4/345	focal adhesion
11	0.038	2/85	late endosome membrane
12	0.039	1/11	basal part of cell
13	0.041	1/12	low-density lipoprotein particle
14	0.048	2/96	melanosome
15	0.050	1/14	integral component of peroxisomal membrane

Rank	p-value	#in/all	Geneset
1	8e-04	13/1354	LaPointe_mucosa-position_kmeans_N_cecum_colon_ascending_colon_UP_a
2	9e-03	10/1174	LaPointe_mucosa-position_kmeans_E_transverse_colon_UP_transverse_colo
3	1e-02	2/49	Pentrack_CRC_TCGA_corr_N_msi-H_DN
4	3e-02	7/348	LaPointe_mucosa-position_kmeans_O_transverse_colon_UP
5	4e-02	7/883	LaPointe_mucosa-position_kmeans_L_transverse_colon_cecum_colon_DN
6	5e-02	1/14	Hewish_dMMR-secondary-mutations_DNA-repair
7	5e-02	1/15	TCGA-CRC_lesss-aggressive-disease-markers
8	6e-02	1/16	Vilar_mutated-in-CRC-Camp
9	1e-01	4/492	LaPointe_mucosa-position_kmeans_C_cecum_colon_ascending_colon_trans
10	1e-01	7/166	LaPointe_mucosa-position_kmeans_K_transverse_colon_UP_cecum_colon_a
11	1e-01	1/43	Marisa_CRC-cluster-f
12	2e-01	27/6368	LaPointe_mucosa-position_kmeans_F_cecum_colon_transverse_colon_UP
13	2e-01	9/1729	LaPointe_mucosa-position_kmeans_G_cecum_colon_ascending_colon_UP_t
14	3e-01	1/83	Marisa_CRC-cluster-d
15	3e-01	3/532	LaPointe_mucosa-position_kmeans_B_descending_colon_transverse_colon_U

Rank	p-value	#in/all	Geneset
1	0.1	2/166	HALLMARK_INTERFERON_GAMMA_RESPONSE
2	0.2	2/193	HALLMARK_HEME_METABOLISM
3	0.3	1/85	HALLMARK_IL6_JAK_STAT3_SIGNALING
4	0.3	1/96	HALLMARK_ANDROGEN_RESPONSE
5	0.3	1/97	HALLMARK_PI3K_AKT_MTOR_SIGNALING
6	0.3	1/107	HALLMARK_PEROXISOME
7	0.3	1/106	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
8	0.4	1/139	HALLMARK_FATTY_ACID_METABOLISM
9	0.4	1/150	HALLMARK_APOPTOSIS
10	0.5	1/173	HALLMARK_MITOTIC_SPINDLE
11	0.5	1/176	HALLMARK_ALLOGRAFT_REJECTION
12	0.5	1/186	HALLMARK_OXIDATIVE_PHOSPHORYLATION
13	0.5	1/187	HALLMARK_INFLAMMATORY_RESPONSE
14	0.5	1/190	HALLMARK_MYC_TARGETS_V1
15	0.5	1/192	HALLMARK_MTORC1_SIGNALING

Rank	p-value	#in/all	Geneset
1	0.003	25/4261	HOPP_Txn_transition
2	0.004	31/5908	HOPP_Active_promoter
3	0.005	29/5404	HOPP_Strong_enhancer
4	0.007	29/5529	HOPP_Txn_elongation
5	0.010	2/42	Monti_OxPhos_cluster
6	0.029	1/8	MASCOUE_GCB_UP
7	0.04	7/906	SPANG_BCR_DN
8	0.053	1/15	DAVE_BL_Inter
9	0.053	1/15	Subero_T-ALL_hypo_meth
10	0.080	1/23	Subero_mBL_hypo_meth
11	0.113	1/33	Subero_T-PLL_hypo_meth
12	0.117	1/34	TARTE_B-cell_signature
13	0.127	3/153	SPANG_CD4s_DN
14	0.139	1/41	ROSOLOWSKI_blue_DOWN
15	0.151	1/45	Subero_INT_hypo_meth

Rank	p-value	#in/all	Geneset
1	3e-05	5/103	hsa-miR-576-3p
2	2e-03	3/73	hsa-miR-423-5p
3	5e-03	2/28	hsa-miR-342-5p
4	6e-04	3/100	hsa-miR-625
5	7e-03	1/2	hsa-miR-585
6	9e-03	2/39	hsa-miR-1308
7	1e-02	1/3	hsa-miR-1268
8	1e-02	3/128	hsa-miR-583
9	1e-02	1/45	hsa-miR-891b
10	1e-02	2/47	hsa-miR-634
11	1e-02	2/49	hsa-miR-940
12	2e-02	3/155	hsa-miR-381
13	2e-02	2/58	hsa-miR-331-3p
14	2e-02	2/59	hsa-miR-1304
15	2e-02	2/60	hsa-miR-1321

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	

Rank	p-value	#in/all	Geneset
1	0.002	2/16	regulation of mitotic spindle assembly
2	0.002	8/821	regulatory regulation of transcription from RNA polymerase II promoter
3	0.003	3/75	cellular response to interferon-gamma
4	0.004	2/26	antigen processing and presentation of peptide antigen via MHC class I
5	0.006	3/99	regulation of mRNA stability
6	0.009	2/40	thymus development
7	0.011	2/44	fatty acid beta-oxidation
8	0.011	3/129	Fc-epsilon receptor signaling pathway
9	0.017	2/55	protein import into nucleus
10	0.019	3/156	protein homooligomerization
11	0.026	2/69	antigen processing and presentation of exogenous peptide antigen via MHC c
12	0.027	2/12	regulation of transcription from RNA polymerase II promoter in response to hy
13	0.032	2/77	BMP signaling pathway
14	0.036	1/10	carmitine shuttle
15	0.036	1/10	cellular response to interferon-alpha

Rank	p-value	#in/all	Geneset
1	0.03	3/184	Chr 18
2	0.09	2/139	Chr 21
3	0.12	3/152	Chr 15
4	0.18	3/403	Chr 14
5	0.21	3/437	Chr 8
6	0.25	3/480	Chr 4
7	0.36	3/585	Chr 7
8	0.36	4/833	Chr 2
9	0.36	4/833	Chr 19
10	0.60	2/554	Chr 5
11	0.61	2/556	Chr X
12	0.72	4/1325	Chr 1
13	0.74	2/44	Chr 20
14	0.77	2/758	Chr 11
15	0.78	2/776	Chr 17

Rank	p-value	#in/all	Geneset
1	0.01	4/242	Scov_0.5_Sturm_C1_IDH_DN
2	0.06	3/246	Scov_0.001_Sturm_M1_IDH_RTK1_PDGFR_A_DN
3	0.08	3/282	WILLSCHER_GBM_Verhaak-PNwt & CL_up
4	0.11	1/31	WILLSCHER_GBM_proteomics_wtOnly_SpotC
5	0.12	1/242	Sturm_GBM_Meth_overexpression_D_G34_UP
6	0.15	1/45	Donson-innate immunity-associated with LTS in HGA
7	0.17	1/50	Christensen_hypomethylated_in_primary_glioblastoma
8	0.17	1/50	Vishal_subnetwork_signature_of_survival_in_GBM
9	0.17	1/52	GIEZELT_GBM_Wt_down_VS_mu
10	0.18	8/1523	Hopp_genes_GBM_Ep3_E1_tetus_UP_tetus_DN
11	0.19	1/58	GIEZELT_GBM_STSwt_down_VS_LTSwt
12	0.20	3/423	Down_a
13	0.20	1/61	Christensen_hypomethylated_in_secondary_glioblastoma
14	0.20	1/62	GIEZELT_GBM_STS_down_VS_LTS
15	0.20	2/231	WILLSCHER_GBM_Verhaak-CL & MES_up

Rank	p-value	#in/all	Geneset
1	0.01	1/4	Angelovt_CRC_MHC_class_II
2	0.03	1/8	Immunity_HLA-class-II
3	0.05	1/14	Angelova Immune-metagene-Eosinophil
4	0.22	1/67	Angelova Immune-metagene-T-cells
5	1.00	0/13	Angelova Immune-metagene-activated_B-cells
6	1.00	0/26	Angelova Immune-metagene-activated_CD4
7	1.00	0/19	Angelova Immune-metagene-activated_CD8
8	1.00	0/21	Angelova Immune-metagene-central_memory_CD4
9	1.00	0/17	Angelova Immune-metagene-central_memory_CD8
10	1.00	0/7	Angelova Immune-metagene-cytotoxic_cells
11	1.00	0/25	Angelova Immune-metagene-DC
12	1.00	0/12	Angelova Immune-metagene-effector_memory_CD4
13	1.00	0/32	Angelova Immune-metagene-effector_memory_CD8
14	1.00	0/19	Angelova Immune-metagene-IDC
15	1.00	0/13	Angelova Immune-metagene-immature_B-cells

Rank	p-value	#in/all	Geneset
1	0.007	1/2	Melanoma Epi-Enzyme Cluster 2
2	0.029	1/8	Hugo_melanoma-BRAFmut-LEF1_UP
3	0.058	2/107	Tirosh_Exhaustion_program_in_Mel75
4	0.126	1/37	Hugo_melanoma-all-MET_DN
5	0.129	1/38	Tirosh_top50_correlated_genes_PC5
6	0.155	1/46	Tirosh_top50_correlated_genes_PC1
7	0.170	1/51	Tirosh_genes_from_CD8_T-cells_in_Mel79-melanoma
8	0.204	2/230	Gerber_wt/wt_melanoma-cells-SpotC
9	0.220	1/68	Tirosh_housekeeping_genes
10	0.228	1/71	Tirosh_Macrophage_specific_genes-melanoma
11	0.229	2/249	Gerber_wt/wt_melanoma-cells-SpotE
12	0.466	1/171	Landsberg_dedifferentiation_up
13	0.513	1/183	Tirosh_genes_preferentially_expressed_by_Tregs
14	0.558	1/222	Gerber_wt/wt_melanoma-cells-SpotF
15	0.580	1/236	Gerber_wt/wt_group3-specific

Rank	p-value	#in/all	Geneset
1	0.004	4/179	Terre_MSV_multiple_respiratory_viruses_dn
2	0.086	2/135	Terre_MSV_multiple_respiratory_viruses_up
3	1.000	0/68	Burnham_sep_vs_con_UP
4	1.000	0/66	Burnham_sep_vs_con_DN
5	1.000	0/48	Burnham_cap_fp_vs_con_DN
6	1.000	0/71	Burnham_cap_fp_vs_con_UP
7	1.000	0/48	Burnham_viral_DN
8	1.000	0/57	Burnham_viral_UP
9	1.000	0/57	Burnham_day1_vs_5_UP
10	1.000	0/52	Burnham_day1_vs_5_DN
11	1.000	0/54	Burnham_timecourse
12	1.000	0/18	Scicluna_UP
13	1.000	0/41	Scicluna_DN
14	1.000	0/37	Sweeney_viral_up
15	1.000	0/33	Sweeney_viral_dn

Rank	p-value	#in/all	Geneset
1	0.01	11/1387	HEBENSTREIT_high_expression_TF
2	0.02	14/2150	ICGC_Irf4_targets
3	0.04	10/1508	ICGC_Mef2_targets
4	0.05	18/3420	ICGC_Bclaf101388_targets
5	0.07	19/3769	ICGC_Pm1sc71910_targets
6	0.08	18/3121	ICGC_Egr1_targets
7	0.09	9/1494	ICGC_Cebpbpc150_targets
8	0.10	7/1089	ICGC_Ets1_targets
9	0.10	18/3703	ICGC_Foxm1_targets
10	0.12	18/3804	ICGC_Stat5_targets
11	0.12	19/4073	ICGC_Mta3_targets
12	0.13	10/1848	ICGC_Pbx3_targets
13	0.13	17/3564	ICGC_Taf1_targets
14	0.15	14/2899	ICGC_Ntcf1_targets
15	0.15	15/3150	ICGC_Creb1_targets

Rank	p-value	#in/all	Geneset
1	0.04	1/12	HLA2_signature
2	0.06	1/16	GENTLES_modul16
3	0.19	1/58	SHAUGHNESSY_MM_high_risk
4	0.34	1/113	PanCan_Driver_Gene_geneset_nanostring
5	0.49	1/186	SPANG_LPS-index2
6	0.53	2/480	Lemcke_Colonc_Inflammation
7	0.69	1/117	SPANG_BCL6-index2
8	0.75	0/14	LIU_PROSTATE_CANCER_DN
9	1.00	0/15	RHODES_CANCER_META_SIGNATURE
10	1.00	0/15	RHODES_UNDIFFERENTIATED_CANCER
11	1.00	0/16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
12	1.00	0/14	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
13	1.00	0/12	LIU_BREAST_CANCER
14	1.00	0/14	LIU_COMMON_CANCER_GENES
15	1.00	0/16	LIU_LIVER_CANCER

Rank	p-value	#in/all	Geneset
1	3e-04	33/5738	monocytes_peripheral_blood_4_Tx
2	4e-04	41/8200	monocytes_peripheral_blood_2_TssAFlnk
3	5e-04	25/13767	5cells_peripheral_blood_6_EnHG
4	5e-04	39/7635	monocytes_peripheral_blood_1_TssA
5	1e-03	23/3524	Tregulatory_cells_peripheral_blood_6_EnHG
6	2e-03	40/8370	natural_killer_cells_peripheral_blood_2_TssAFlnk
7	2e-03	25/4138	6_EnHG_Skeletal_Muscle
8	3e-03	18/2555	Tregulatory_cells_peripheral_blood_3_TxFlnk
9	3e-03	32/609	HSC_4_Tx
10	4e-03	26/4528	T_CD8+_naive_cells_peripheral_blood_4_Tx
11	4e-03	36/7331	TssA_Colon
12	4e-03	38/7957	Tcells_peripheral_blood_2_TssAFlnk
13	6e-03	22/3682	natural_killer_cells_peripheral_blood_6_EnHG
14	6e-03	37/7751	natural_killer_cells_peripheral_blood_1_TssA
15	6e-03	23/3933	Thelper_cells_peripheral_blood_6_EnHG

Rank	p-value	#in/all	Geneset
1	1e-04	3/28	YANAGIHARA_ESX1_TARGETS
2	2e-04	10/726	REACTOME_IMMUNE_SYSTEM
3	3e-04	8/468	ENK_UP_RESPONSE_KERATINOCYTE_DN
4	3e-04	15/1550	PILON_KLF1_TARGETS_DN
5	6e-04	9/673	SCHLOSSER_SERUM_RESPONSE_DN
6	8e-04	14/1527	PUJANA_BRCA1_PCC_NETWORK
7	2e-03	9/785	GROBERT_OLGACENTROCYTE_DIFFERENTIATION_DN
8	2e-03	3/72	MUNSHI_MULTIPLE_MYELOMA_UP
9	3e-03	2/24	CHEOK_RESPONSE_TO_HD_MTX_DN
10	3e-03	8/939	JENPORATH_MYC_MAX_TARGETS

Correlation Cluster

Spot Summary: P

metagenes = 42
genes = 415

<r> metagenes = 0.93

<r> genes = 0.2

beta: r2= 5.61 / log p= -Inf

samples with spot = 52 (23.5 %)

intermediate : 3 (6.2 %)

non-mBL : 49 (38 %)

Spot Genelist

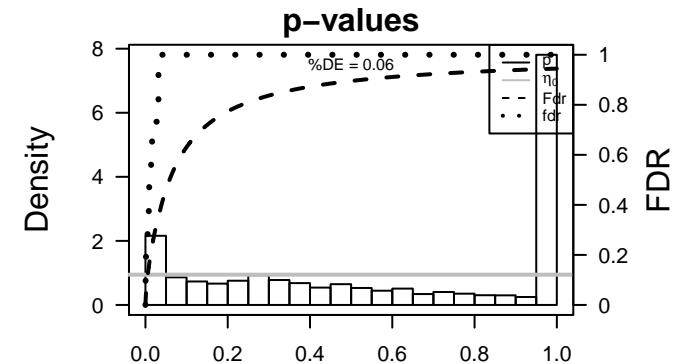
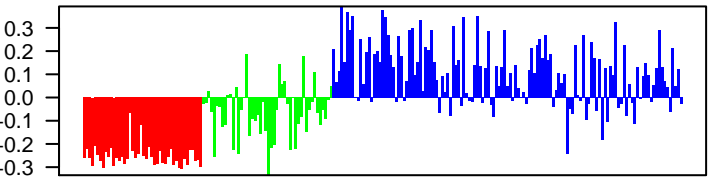
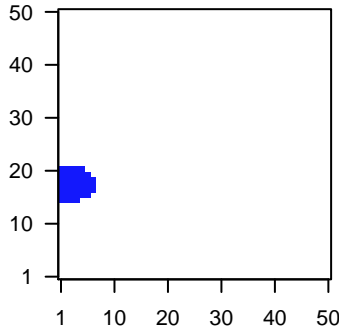
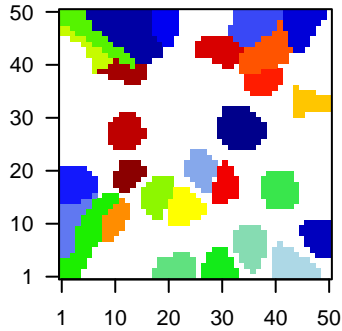
Rank	ID	max e	r	min e	Description
1	207861_at	2.76	-1.26	0.51	CCL22 C-C motif chemokine ligand 22 [Source:HGNC Symbol;Acc:U14657]
2	220635_at	2.62	-0.68	0.31	PSORS1C psoriasis susceptibility 1 candidate 2 [Source:HGNC Symbol;Acc:U14657]
3	204755_x_at	2.62	-0.62	0.48	HLF HLF, PAR bZIP transcription factor [Source:HGNC Symbol;Acc:U14657]
4	204753_s_at	2.57	-0.91	0.5	HLF HLF, PAR bZIP transcription factor [Source:HGNC Symbol;Acc:U14657]
5	201839_s_at	2.49	-1.02	0.27	EPCAM epithelial cell adhesion molecule [Source:HGNC Symbol;Acc:U14657]
6	210551_s_at	2.43	-0.93	0.51	ASMT acetylserotonin O-methyltransferase [Source:HGNC Symbol;Acc:U14657]
7	219360_s_at	2.4	-1.57	0.46	TRPM4 transient receptor potential cation channel subfamily M member 4 [Source:HGNC Symbol;Acc:U14657]
8	207534_at	2.39	-0.99	0.29	MAGEB1 MAGE family member B1 [Source:HGNC Symbol;Acc:U14657]
9	219836_at	2.38	-1.24	0.62	ZBED2 zinc finger BED-type containing 2 [Source:HGNC Symbol;Acc:U14657]
10	206881_s_at	2.3	-0.78	0.4	LILRA3 leukocyte immunoglobulin like receptor A3 [Source:HGNC Symbol;Acc:U14657]
11	218186_at	2.28	-1.29	0.38	RAB25 RAB25, member RAS oncogene family [Source:HGNC Symbol;Acc:U14657]
12	213497_at	2.23	-1.39	0.6	ABTB2 ankyrin repeat and BTB domain containing 2 [Source:HGNC Symbol;Acc:U14657]
13	217523_at	2.2	-1.4	0.73	CD44 CD44 molecule (Indian blood group) [Source:HGNC Symbol;Acc:U14657]
14	214412_at	2.18	-1.2	0.49	H2AFB2 H2A histone family member B2 [Source:HGNC Symbol;Acc:U14657]
15	219255_x_at	2.16	-1.57	0.42	IL17RB interleukin 17 receptor B [Source:HGNC Symbol;Acc:U14657]
16	221728_x_at	2.14	-1.53	0.16	X inactive specific transcript (non-protein coding) [Source:HGNC Symbol;Acc:U14657]
17	210675_s_at	2.13	-0.71	0.41	PTPRR protein tyrosine phosphatase, receptor type R [Source:HGNC Symbol;Acc:U14657]
18	206218_at	2.12	-0.98	0.36	MAGEB2 MAGE family member B2 [Source:HGNC Symbol;Acc:U14657]
19	204584_at	2.12	-1.05	0.42	L1CAM L1 cell adhesion molecule [Source:HGNC Symbol;Acc:U14657]
20	204086_at	2.11	-1.29	0.52	PRAME preferentially expressed antigen in melanoma [Source:HGNC Symbol;Acc:U14657]

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	1e-18	219 / 5404	LympI HOPP_Strong_enhancer
2	9e-18	41 / 317	Canci SPANG_BCL6-index2
3	2e-15	21 / 85	LympI Aukema_BCL2_DN_BCL6_UP
4	1e-12	28 / 213	LympI SPANG_IL21_DN
5	4e-11	69 / 1166	Colon LaPointe_mucosa-position_kmeans_K_transverse_colon_UP_cecum_colon
6	4e-09	161 / 4261	LympI HOPP_Txn_transition
7	5e-08	6 / 10	LympI Care_ABC_UP
8	1e-07	17 / 139	GSE/ BROCKE_APOPTOSIS_REVERSED_BY_IL6
9	2e-07	7 / 18	LympI WRIGHT_ABC_UP
10	2e-07	19 / 182	Refer WIRTH_post GC B-cells
11	3e-07	50 / 906	LympI SPANG_BCR_DN
12	3e-07	23 / 262	GSE/ HELLER_HDAC_TARGETS_SILENCED_BY_METHYLATION_DN
13	4e-07	27 / 348	GSE/ MARTENS_BOUND_BY_PML_RARA_FUSION
14	4e-07	75 / 1636	TF ICGC_Bcl11_targets
15	5e-07	18 / 173	LympI Victora_Light zone signature
16	7e-07	48 / 885	BP positive regulation of transcription from RNA polymerase II promoter
17	9e-07	25 / 321	GSE/ PHONG_TNF_RESPONSE_NOT_VIA_P38
18	1e-06	11 / 67	Immu Angelova_immune-metagenes-T-cells
19	2e-06	12 / 85	LympI Sha_DLBCUP
20	3e-06	34 / 558	GSE/ KRIEG_HYPOXIA_NOT_VIA_KDM3A
21	3e-06	12 / 90	GSE/ BASSO_CD40_SIGNALING_UP
22	3e-06	34 / 560	GSE/ KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP
23	4e-06	16 / 159	GSE/ KIM_WT1_TARGETS_8HR_UP
24	4e-06	35 / 589	Color Lembcke_TCGA-expr_kmeans_E_CIMP.H_UP_Cluster4_DN
25	6e-06	25 / 355	Refer WIRTH_Immune system
26	7e-06	28 / 429	GSE/ SMID_BREAST_CANCER_NORMAL_LIKE_UP
27	8e-06	19 / 229	GSE/ QI_PLASMACYTOMA_UP
28	1e-05	69 / 1602	GSE/ BLALOCK_ALZHEIMERS_DISEASE_UP
29	1e-05	31 / 520	BP positive regulation of transcription, DNA-templated
30	1e-05	31 / 521	BP transcription from RNA polymerase II promoter
31	2e-05	191 / 5908	LympI HOPP_Active_promoter
32	2e-05	24 / 353	LympI SPANG_CD40_6hrs_DN
33	2e-05	28 / 453	GSE/ FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_UP
34	2e-05	28 / 453	GSE/ ONDER_CDH1_TARGETS_2_DN
35	2e-05	29 / 480	Canci Lembcke_Colonc Inflammation
36	2e-05	20 / 269	GSE/ HELLER_HDAC_TARGETS_DN
37	3e-05	6 / 24	Melar Tirosh_B-cell specific genes-melanoma
38	3e-05	16 / 186	Canci SPANG_LPS-index2
39	3e-05	16 / 186	GSE/ PENG_RAPAMYCIN_RESPONSE_UP
40	3e-05	78 / 1941	TF ICGC_Bcl3_targets

Overview Map

Spot



Aging Rank	p-value	#in/all	Geneset
1	0.3	4 / 107	HORVATH_aging_genes_meth_UP
2	0.4	3 / 92	HORVATH_aging_genes_meth_DOWN
3	0.7	1 / 47	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	48 / 885	positive regulation of transcription from RNA polymerase II promoter
2	1e-05	31 / 520	positive regulation of transcription, DNA-templated
3	1e-05	31 / 521	transcription from RNA polymerase II promoter
4	2e-04	7 / 46	peptidyl-tyrosine autophosphorylation
5	2e-04	4 / 12	leukocyte chemotaxis
6	4e-04	13 / 169	cell migration
7	6e-04	4 / 16	negative regulation of B cell proliferation
8	6e-04	4 / 16	positive regulation of T cell differentiation
9	7e-04	8 / 76	ephrin receptor signaling pathway
10	8e-04	16 / 250	regulation of apoptotic process
11	1e-03	7 / 63	type I interferon signaling pathway
12	1e-03	27 / 553	apoptotic process
13	2e-03	3 / 10	positive regulation of T cell differentiation in thymus
14	2e-03	4 / 21	negative regulation of interleukin-6 production
15	2e-03	11 / 153	protein autophosphorylation

Cancer Rank	p-value	#in/all	Geneset
1	9e-18	41 / 317	SPANG_BCL6-index2
2	2e-05	29 / 480	Lemboke_Colonc Inflammation
3	3e-05	16 / 186	SPANG_LPS-index2
4	2e-04	9 / 80	PanCan_JAK-ST_geneset_nanostring
5	3e-03	9 / 113	PanCan_Driver_Gene_geneset_nanostring
6	4e-03	3 / 13	BENTINK_e2f1
7	5e-03	3 / 14	GUSTAFSON_P13K_UP
8	3e-02	3 / 28	PanCan_HK_geneset_nanostring
9	4e-02	1 / 11	LIU_PROSTATE_CANCER_UP
10	6e-02	2 / 15	WANG_ER_UP
11	1e-01	5 / 96	PanCan_TXN1sReg_geneset_nanostring
12	1e-01	8 / 187	PanCan_P13K_geneset_nanostring
13	1e-01	6 / 130	PanCan_CC+Apop_geneset_nanostring
14	2e-01	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
15	2e-01	6 / 147	PanCan_MAPK_geneset_nanostring

CC Rank	p-value	#in/all	Geneset
1	1e-04	130 / 3805	cytosol
2	2e-04	8 / 62	extrinsic component of cytoplasmic side of plasma membrane
3	2e-04	27 / 494	endosome
4	8e-04	30 / 623	cell projection
5	1e-03	13 / 188	endosome membrane
6	2e-03	148 / 4701	cytoplasm
7	5e-03	8 / 101	growth cone
8	7e-03	37 / 938	Golgi apparatus
9	7e-03	103 / 3210	plasma membrane
10	9e-03	26 / 604	intracellular membrane-bounded organelle
11	1e-02	8 / 118	cytoplasmic vesicle membrane
12	1e-02	12 / 219	lysosomal membrane
13	1e-02	3 / 16	mast cell granule
14	1e-02	158 / 5339	membrane
15	2e-02	35 / 936	cytoskeleton

Chr Rank	p-value	#in/all	Geneset
1	2e-04	23 / 382	Chr 15
2	5e-03	25 / 556	Chr X
3	2e-01	12 / 323	Chr 22
4	2e-01	13 / 369	Chr 20
5	2e-01	24 / 756	Chr 11
6	2e-01	22 / 689	Chr 3
7	3e-01	18 / 585	Chr 7
8	3e-01	67 / 1325	Chr 1
9	3e-01	8 / 113	Chr 18
10	5e-01	4 / 139	Chr 21
11	5e-01	22 / 832	Chr 2
12	6e-01	17 / 669	Chr 6
13	6e-01	21 / 833	Chr 19
14	6e-01	12 / 480	Chr 4
15	6e-01	12 / 492	Chr 9

Chromatin states Rank	p-value	#in/all	Geneset
1	1e-20	178 / 3767	Bcells peripheral blood_6_EnhG
2	1e-16	119 / 2203	ENH_A_Colon
3	1e-16	162 / 3223	monocytes peripheral blood_6_EnhG
4	2e-15	283 / 8406	Bcells peripheral blood_2_TssAFlnk
5	2e-15	163 / 3682	natural killer cells peripheral blood_6_EnhG
6	6e-14	56 / 693	Bcells peripheral blood_3_TxFlnk
7	2e-13	268 / 7943	Enh_Colon
8	4e-13	46 / 6906	3_TssF_Fibroblasts
9	6e-12	169 / 4219	EnhWtK1_Colon
10	9e-12	298 / 9544	HSC_2_TssAFlnk
11	5e-11	259 / 7833	Bcells peripheral blood_1_TssA
12	1e-10	280 / 8816	Thelper cells peripheral blood_2_TssAFlnk
13	3e-10	46 / 612	Thelper cells peripheral blood_3_TxFlnk
14	3e-10	262 / 8068	Thelper cells peripheral blood_1_TssA
15	3e-10	266 / 8245	Regulatory cells peripheral blood_2_TssAFlnk

Colon Cancer Rank	p-value	#in/all	Geneset
1	4e-11	69 / 1166	LaPointe_mucosa-position_kmeans_K_transverse_colon_UP_cecum_colon_a
2	4e-06	35 / 589	Lembocke_TCGA-expr_kmeans_E_CIMP_H_UP_Cluster4_DN
3	2e-03	64 / 1729	LaPointe_mucosa-position_kmeans_G_cecum_colon_ascending_colon_UP_t
4	3e-03	25 / 539	Lembocke_TCGA_meth_kmeans_O_transverse_colon_UP
5	5e-03	5 / 43	Marsa_CRC-cluster-f
6	6e-03	2 / 5	Kaneda_CIMP-group1
7	8e-03	15 / 288	Pentrack_CRC_TCGA_corr_j_msi-h_UP_mss_DN
8	2e-02	13 / 255	Kosinski_top-cript-long-list
9	3e-02	38 / 1083	LaPointe_mucosa-position_kmeans_J_cecum_colon_ascending_colon_transv
10	3e-02	30 / 840	Pentrack_CRC_TCGA_corr_kmeans_Q_transverse_colon_UP
11	5e-02	1 / 2	Hewish_dMMR-secondary-mutations_Cell-motility
12	5e-02	16 / 397	Pentrack_CRC_TCGA_corr_C_normal_UP
13	8e-02	2 / 18	Boland_CRC-MSI-A6-A10
14	1e-01	29 / 883	LaPointe_mucosa-position_kmeans_L_transverse_colon_cecum_colon_DN
15	1e-01	17 / 483	Lembocke_TCGA-expr_kmeans_H_CIMP_H_UP_Cluster3_DN

Glioma Rank	p-value	#in/all	Geneset
1	0.003	21 / 423	Down_a
2	0.005	7 / 82	laffaire_hypermeth_LGG_vs_control
3	0.006	7 / 83	Scov_0_999_Sturm_E3_RTK1_PDGFR_A_DN
4	0.012	37 / 979	Hopp_Sturm_GBM_Ep15_no_zentr_5_IDH_UP_tetus_adult_DN
5	0.022	13 / 268	Scov_0_000_Sturm_M2_Mesenchymal_RTK1_PDGFR_A_DN
6	0.024	12 / 242	Scov_0_5_Sturm_C1_IDH_DN
7	0.026	12 / 246	Scov_0_001_Sturm_M1_IDH_RTK1_PDGFR_A_DN
8	0.028	7 / 114	Christensen_hypermethylated_in_grade2_oligoastrocytoma
9	0.028	4 / 45	Donson-innate immunity-associated with LTS in HGA
10	0.033	8 / 144	Christensen_hypermethylated_in_grade2_oligodendroglioma
11	0.046	11 / 239	Scov_0_001_Sturm_M3_RTK1I_Classic_DN
12	0.049	2 / 14	Donson-chemokines/cytokines-associated with LTS in HGA
13	0.055	7 / 132	Christensen_hypermethylated_in_grade3_oligoastrocytoma
14	0.072	17 / 447	Scov_0_999_Sturm_E4_Mesenchymal_RTK1_PDGFR_A_DN
15	0.074	5 / 87	Christensen_hypermethylated_in_secondary_glioblastoma

GSEA C2 Rank	p-value	#in/all	Geneset
1	1e-07	17 / 139	BROCKE_APOPTOSIS_REVERSED_BY_IL6
2	3e-07	23 / 262	HELLER_HDAC_TARGETS_SILENCED_BY_METHYLATION_DN
3	4e-07	27 / 348	MARTENS_BOUND_BY_PML_RARA_FUSION
4	9e-07	25 / 321	SMID_BREAST_CANCER_NORMAL_LIKE_UP
5	3e-06	34 / 558	KRIEG_HYPOXIA_NOT_VIA_KDM3A
6	3e-06	12 / 90	BASSO_CD40_SIGNALING_UP
7	3e-06	34 / 560	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP
8	4e-06	16 / 159	KIM_WT1_TARGETS_8HR_UP
9	7e-06	28 / 429	SMID_BREAST_CANCER_NORMAL_LIKE_UP
10	8e-06	16 / 222	PLASMACYTOMA_UP
11	1e-05	69 / 1602	BLALOCK_ALZHEIMERS_DISEASE_UP
12	2e-05	28 / 453	FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_UP
13	2e-05	28 / 453	ONDER_CDH1_TARGETS_2_DN
14	2e-05	20 / 269	HELLER_HDAC_TARGETS_DN
15	3e-05	16 / 186	PENG_RAPAMYCIN_RESPONSE_UP

LM Rank	p-value	#in/all	Geneset
1	2e-04	14 / 176	HALLMARK_ALLOGRAFT_REJECTION
2	3e-04	9 / 85	HALLMARK_IL6_JAK_STAT3_SIGNALING
3	1e-03	11 / 141	HALLMARK_UV_RESPONSE_DN
4	1e-02	10 / 166	HALLMARK_INTERFERON_GAMMA_RESPONSE
5	1e-02	10 / 170	HALLMARK_IL2_STAT5_SIGNALING
6	2e-02	9 / 149	HALLMARK_IL17_RESPONSE_UP
7	3e-02	10 / 191	HALLMARK_P53_PATHWAY
8	3e-02	10 / 193	HALLMARK_HEME_METABOLISM
9	4e-02	8 / 150	HALLMARK_APOPTOSIS
10	5e-02	5 / 76	HALLMARK_INTERFERON_ALPHA_RESPONSE
11	3e-02	9 / 137	HALLMARK_ESTROGEN_RESPONSE_LATE
12	6e-02	9 / 194	HALLMARK_ESTROGEN_RESPONSE_EARLY
13	1e-01	8 / 190	HALLMARK_TNFA_SIGNALING_VIA_NFKB
14	1e-01	8 / 194	HALLMARK_KRAS_SIGNALING_UP
15	2e-01	6 / 139	HALLMARK_FATTY_ACID_METABOLISM

Immunome Rank	p-value	#in/all	Geneset
1	1e-06	11 / 67	Angelova Immune-metagene-T cells
2	3e-04	4 / 13	Angelova Immune-metagene-activated_B-cells
3	1e-02	3 / 18	Angelova Immune-metagene-pDC
4	3e-02	4 / 45	Angelova Immune-metagene-MDSC
5	3e-02	2 / 11	Angelova Immune-metagene-macrophages
6	3e-02	3 / 29	Angelova Immune-metagene-Th1
7	4e-02	13	Angelova Immune-metagene-immature_B-cells
8	6e-02	2 / 16	Angelova Immune-metagene-Th17
9	1e-01	1 / 4	Angelova_CRC_MSS-neoantigens
10	1e-01	2 / 23	Angelova Immune-metagene-monocytes
11	2e-01	1 / 10	Angelova_CRC_immunosuppressors
12	3e-01	1 / 12	Angelova Immune-metagene-memory_B-cells
13	4e-01	1 / 18	Angelova_CRC_immunostimulators
14	4e-01	1 / 21	Angelova Immune-metagene-central_memory_CD4
15	1e+00	0 / 26	Angelova Immune-metagene-activated_CD4

Lifestyle Rank	p-value	#in/all	Geneset
1	0.1	2 / 22	DUMEAUX_Fasting enriched genes
2	0.2	8 / 210	Homuth_BMI-associated-genes_DN
3	0.4	1 / 22	DUMEAUX_High bmi enriched genes
4	0.5	2 / 62	DUMEAUX_Smoking enriched genes
5	0.7	3 / 150	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 / 7	DUMEAUX_Hormon therapy in non smokers literature genes up
11	1.0	0 / 7	DUMEAUX_Monocytes in smokers literature genes up
12	1.0	0 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
13	1.0	0 / 12	DUMEAUX_Women normal BMI literature genes up
14	1.0	0 / 14	Huan_blood-pressure_SBP-signature
15	1.0	0 / 13	Huan_blood-pressure_DBP-signature

Lymphoma Rank	p-value	#in/all	Geneset
1	1e-18	219 / 5404	HOPP_Strong_enhancer
2	2e-15	21 / 85	Aukema_ECL2_DN_BCL6_UP
3	1e-12	28 / 213	SPANG_IL21_DN
4	4e-09	161 / 4261	HOPP_Txn_transition
5	5e-08	6 / 10	Care_ABC_UP
6	2e-07	7 / 18	WRIGHT_ABC_UP
7	3e-07	50 / 906	SPANG_BCR_DN
8	5e-07	18 / 173	Victoria_Light zone signature
9	2e-06	12 / 85	Sha_DLBCL_UP
10	2e-05	191 / 5908	HOPP_Active_promoter
11	2e-05	24 / 353	SPANG_CD40_6hrs_DN
12	7e-05	3 / 4	WRIGHT_custom_ABC-DLBCL_UP
13	2e-04	5 / 22	HOPP_NFKB_BI_DN
14	4e-04	178 / 5682	HOPP_Weak_promoter
15	8e-04	172 / 5529	HOPP_Txn_elongation

Melanoma Rank	p-value	#in/all	Geneset
1	3e-05	6 / 24	Tirosh_B-cell specific genes-melanoma
2	9e-04	15 / 230	Gerber_wtwt_melanoma-cells-SpotC
3	1e-03	13 / 189	Tirosh_genes preferentially expressed by Tregs
4	2e-02	21 / 497	Gerber_wtwt_melanoma-cells-SpotD
5	3e-02	9 / 171	Landsberg_dedifferentiation_up
6	5e-02	1 / 2	Melanoma Epi-Enzyme Cluster 1
7	6e-02	2 / 16	Hugo_melanoma-all_LEF1_UP
8	6e-02	6 / 83	TCG_melanoma Immune_high
9	7e-02	2 / 17	Hugo_melanoma-all-MET_UP
10	1e-01	1 / 5	Hugo_melanoma-BRAFmut-MET_DN
11	1e-01	1 / 5	Joensuu_Melanoma Proliferative subtype
12	1e-01	2 / 24	Tirosh_exhaustion-associated genes consistent across tumors
13	2e-01	4 / 81	Tirosh_Genes in the MITF program
14	2e-01	9 / 249	Gerber_wtwt_melanoma-cells-SpotE
15	2e-01	3 / 65	Harbst_melanoma_highgrade_up

MF Rank	p-value	#in/all	Geneset
1	5e-05	238 / 7864	protein binding
2	2e-04	7 / 46	non-membrane spanning protein tyrosine kinase activity
3	3e-04	14 / 182	RNA polymerase II regulatory region sequence-specific DNA binding
4	4e-04	11 / 125	transcriptional activator activity, RNA polymerase II transcription regulatory re
5	6e-04	22 / 393	molecular_function
6	8e-04	9 / 96	SH3 domain binding
7	1e-03	7 / 62	transcription factor activity, RNA polymerase II distal enhancer sequence-spe
8	1e-03	7 / 65	protein phosphatase binding
9	2e-03	3 / 10	profilin binding
10	2e-03	27 / 573	kinase activity
11	2e-03	47 / 1185	ATP binding
12	3e-03	13 / 206	transcription regulatory region DNA binding
13	3e-03	14 / 23	transcriptional activator activity, RNA polymerase II proximal promoter sequen
14	3e-03	57 / 1541	DNA binding
15	4e-03	31 / 722	RNA polymerase II transcription factor activity, sequence-specific DNA bindin

miRNA target Rank	p-value	#in/all	Geneset
1	3e-05	24 / 369	hsa-miR-15b
2	5e-05	24 / 378	hsa-miR-16
3	7e-05	23 / 363	hsa-miR-195
4	1e-03	23 / 350	hsa-miR-424
5	3e-04	23 / 397	hsa-miR-15a
6	8e-04	19 / 324	hsa-miR-497
7	3e-03	23 / 474	hsa-miR-20a
8	4e-03	8 / 100	hsa-miR-145
9	5e-03	19 / 128	hsa-miR-654-5p
10	6e-03	21 / 448	hsa-miR-20b
11	7e-03	17 / 336	hsa-miR-519d
12	7e-03	3 / 16	hsa-miR-891a

Correlation Cluster

Spot Summary: Q

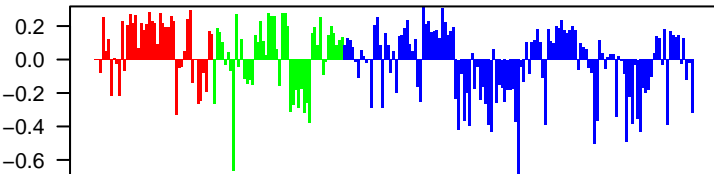
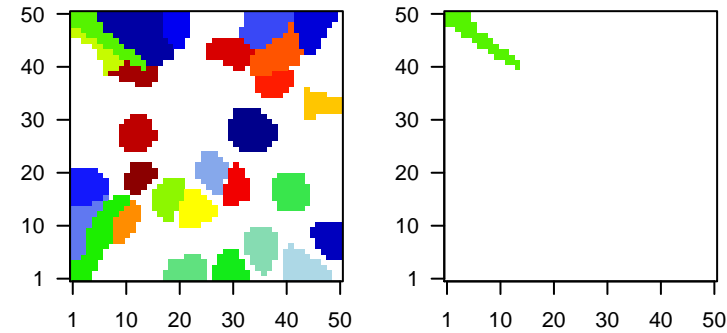
metagenes = 45
genes = 461

<r> metagenes = 0.96
<r> genes = 0.36
beta: r2= 9.33 / log p= -Inf

samples with spot = 71 (32.1 %)
mBL : 22 (50 %)
intermediate : 17 (35.4 %)
non-mBL : 32 (24.8 %)

Overview Map

Spot

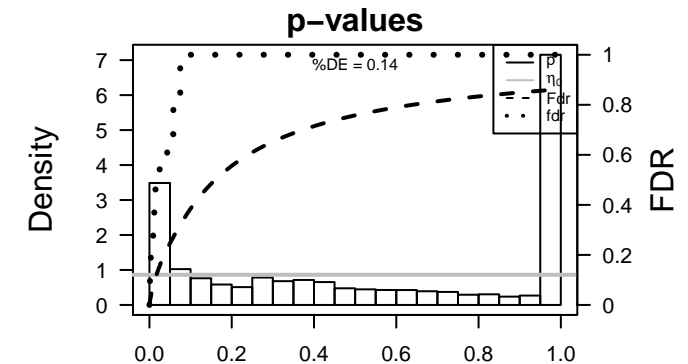


Spot Genelist

Rank	ID	max e	r	min e	Description
1	213060_s_at	1.81	-1.28	0.23	CHI3L2 chitinase 3 like 2 [Source:HGNC Symbol;Acc:HGNC:1933]
2	207686_s_at	1.62	-1.44	0.61	CASP8 caspase 8 [Source:HGNC Symbol;Acc:HGNC:1509]
3	203293_s_at	1.51	-1.49	0.6	LMAN1 lectin, mannose binding 1 [Source:HGNC Symbol;Acc:HGNC:1127]
4	211708_s_at	1.43	-1.2	0.61	SCD stearyl-CoA desaturase [Source:HGNC Symbol;Acc:HGNC:1127]
5	203294_s_at	1.4	-1.25	0.6	LMAN1 lectin, mannose binding 1 [Source:HGNC Symbol;Acc:HGNC:1127]
6	214971_s_at	1.4	-1.95	0.75	ST6GAL1ST6 beta-galactoside alpha-2,6-sialyltransferase 1 [Source:HGNC Symbol;Acc:HGNC:1127]
7	200831_s_at	1.39	-1.42	0.41	SCD stearyl-CoA desaturase [Source:HGNC Symbol;Acc:HGNC:1127]
8	211162_x_at	1.39	-1.05	0.56	SCD stearyl-CoA desaturase [Source:HGNC Symbol;Acc:HGNC:1127]
9	213562_s_at	1.35	-1.44	0.62	SQLE squalene epoxidase [Source:HGNC Symbol;Acc:HGNC:1127]
10	216986_s_at	1.32	-1.21	0.42	IRF4 interferon regulatory factor 4 [Source:HGNC Symbol;Acc:HGNC:1127]
11	204429_s_at	1.31	-2.03	0.44	SLC2A5 solute carrier family 2 member 5 [Source:HGNC Symbol;Acc:HGNC:1127]
12	204764_at	1.31	-1.23	0.64	CHURC1CHURC1-FNTB readthrough [Source:HGNC Symbol;Acc:HGNC:1127]
13	208653_s_at	1.3	-1.11	0.6	CD164 CD164 molecule [Source:HGNC Symbol;Acc:HGNC:1632]
14	201718_s_at	1.29	-1.09	0.35	EPB41L2erythrocyte membrane protein band 4.1 like 2 [Source:HGNC Symbol;Acc:HGNC:1632]
15	209629_s_at	1.29	-1.56	0.6	NXT2 nuclear transport factor 2 like export factor 2 [Source:HGNC Symbol;Acc:HGNC:1632]
16	209722_s_at	1.28	-0.69	0.33	SERPINC1serpin family B member 9 [Source:HGNC Symbol;Acc:HGNC:1632]
17	209611_s_at	1.25	-1.03	0.44	SLC1A4 solute carrier family 1 member 4 [Source:HGNC Symbol;Acc:HGNC:1632]
18	200671_s_at	1.23	-0.99	0.46	SPTBN1 spectrin beta, non-erythrocytic 1 [Source:HGNC Symbol;Acc:HGNC:1632]
19	203676_at	1.21	-1.22	0.67	GNS glucosamine (N-acetyl)-6-sulfatase [Source:HGNC Symbol;Acc:HGNC:1632]
20	203472_s_at	1.21	-0.99	0.54	SLCO2B2solute carrier organic anion transporter family member 2B1 [Source:HGNC Symbol;Acc:HGNC:1632]

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	2e-88	105 / 282	Glioni WILLSCHER_GBM_Verhaak-PNwt & CL_up
2	4e-77	74 / 136	Refer Chaussabel_2_9_Cytoskeleton
3	6e-61	327 / 5529	Lympi HOPP_Txn_elongation
4	3e-51	275 / 4261	Lympi HOPP_Txn_transition
5	5e-42	79 / 405	GSE/ SENESE_HDAC3_TARGETS_UP
6	7e-42	76 / 372	GSE/ SENESE_HDAC1_TARGETS_UP
7	8e-37	303 / 5908	Lympi HOPP_Active_promoter
8	1e-30	78 / 564	GSE/ RODRIGUES_THYROID_CARCINOMA_ANAPLASTIC_UP
9	2e-26	57 / 344	GSE/ THUM_SYSTOLIC_HEART_FAILURE_UP
10	2e-25	114 / 1338	GSE/ DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
11	8e-25	56 / 355	Refer WIRTH_Immune system
12	1e-22	269 / 5682	Lympi HOPP_Weak_promoter
13	3e-19	59 / 509	GSE/ RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_UP
14	1e-18	251 / 5404	Lympi HOPP_Strong_enhancer
15	1e-18	100 / 1312	GSE/ PUJANA_ATM_PCC_NETWORK
16	6e-18	82 / 966	GSE/ KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
17	9e-18	109 / 1550	GSE/ PILON_KLF1_TARGETS_DN
18	4e-17	276 / 6368	Color LaPointe_mucosa-position_kmeans_F_cecum_colon_transverse_colon_UP
19	5e-17	59 / 564	GSE/ SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_DN
20	5e-17	194 / 3805	CC cytosol
21	7e-17	106 / 1527	GSE/ PUJANA_BRCA1_PCC_NETWORK
22	5e-15	96 / 1390	GSE/ GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_DN
23	3e-14	22 / 92	GSE/ SENESE_HDAC2_TARGETS_UP
24	8e-14	28 / 163	GSE/ ONDER_CDH1_TARGETS_1_DN
25	1e-13	24 / 118	GSE/ AZARE_NEOPLASTIC_TRANSFORMATION_BY_STAT3_UP
26	1e-13	67 / 830	GSE/ DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
27	7e-13	26 / 152	Refer Chaussabel_3_6_Mitochondrial_ribosomal_proteins
28	1e-11	33 / 272	GSE/ LIU_SOX4_TARGETS_DN
29	2e-11	43 / 448	miRN hsa-miR-20b
30	2e-11	55 / 678	Refer PROTEINATLAS_lymph_node
31	2e-11	36 / 328	GSE/ OSMAN_BLADDER_CANCER_UP
32	5e-11	40 / 407	miRN hsa-miR-106a
33	8e-11	84 / 1343	Glioni Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
34	8e-11	59 / 785	GSE/ MARSON_BOUND_BY_FOXP3_STIMULATED
35	9e-11	43 / 469	GSE/ DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN
36	1e-10	37 / 364	miRN hsa-miR-548n
37	1e-10	84 / 1354	Color LaPointe_mucosa-position_kmeans_N_cecum_colon_ascending_colon_UP
38	2e-10	99 / 1729	Color LaPointe_mucosa-position_kmeans_G_cecum_colon_ascending_colon_UP
39	2e-10	299 / 7864	MF protein binding
40	2e-10	40 / 427	miRN hsa-miR-17



Aging Rank	p-value	#in/all	Geneset
1	0.1	5 / 92	HORVATH_aging_genes_meth_DOWN
2	0.3	2 / 107	HORVATH_aging_genes_meth_UP
3	1.0	0 / 47	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	38 / 502	protein transport
2	3e-07	38 / 507	protein phosphorylation
3	2e-06	39 / 576	phosphorylation
4	4e-06	8 / 32	regulation of cholesterol biosynthetic process
5	2e-05	23 / 281	mRNA processing
6	2e-05	12 / 91	mRNA transport
7	2e-05	33 / 437	cell cycle
8	3e-05	20 / 233	RNA splicing
9	7e-05	7 / 35	neuron apoptotic process
10	2e-04	16 / 184	intracellular protein transport
11	2e-04	5 / 19	cortical actin cytoskeleton organization
12	4e-04	9 / 12	macrophagy
13	5e-04	21 / 307	cell division
14	5e-04	7 / 47	learning or memory
15	8e-04	31 / 553	apoptotic process

Cancer Rank	p-value	#in/all	Geneset
1	9e-04	2 / 2	GENTLES_modul8
2	6e-03	10 / 130	PanCan_CC+Apop_geneset_nanostring
3	8e-03	9 / 113	PanCan_Driver_Gene_geneset_nanostring
4	8e-03	3 / 14	BENTINK_src2
5	2e-02	4 / 36	ZHANG_MM_up
6	3e-02	5 / 58	SHAUGHNESSY_MM_high_risk
7	5e-02	4 / 47	PanCan_TGF-B_geneset_nanostring
8	7e-02	2 / 14	GENTLES_modul10
9	7e-02	2 / 15	GENTLES_modul4
10	8e-02	2 / 16	GENTLES_modul16
11	1e-01	0 / 12	LIU_BREAST_CANCER
12	2e-01	5 / 96	PanCan_TXmisReg_geneset_nanostring
13	2e-01	1 / 14	LIU_COMMON_CANCER_GENES
14	3e-01	1 / 15	RHODES_CANCER_META_SIGNATURE
15	3e-01	12 / 317	SPANG_BCL6-index2

CC Rank	p-value	#in/all	Geneset
1	5e-17	194 / 3805	cytosol
2	7e-10	202 / 4701	cytoplasm
3	1e-09	198 / 4579	nucleus
4	1e-07	120 / 2541	nucleoplasm
5	6e-07	21 / 196	nuclear membrane
6	1e-05	30 / 416	macromolecular complex
7	3e-05	23 / 292	microtubule organizing center
8	2e-04	23 / 326	nuclear speck
9	3e-04	9 / 70	nuclear pore
10	9e-04	22 / 345	focal adhesion
11	1e-03	10 / 101	kinetochore
12	1e-03	28 / 494	endosome
13	2e-03	28 / 583	cytoplasmic vesicle
14	2e-03	12 / 149	nuclear envelope
15	2e-03	29 / 537	perinuclear region of cytoplasm

Chr Rank	p-value	#in/all	Geneset
1	0.03	35 / 832	Chr 2
2	0.07	18 / 403	Chr 14
3	0.09	49 / 1325	Chr 1
4	0.11	9 / 184	Chr 18
5	0.11	20 / 490	Chr 10
6	0.12	26 / 669	Chr 6
7	0.12	27 / 700	Chr 12
8	0.12	22 / 554	Chr 5
9	0.33	26 / 776	Chr 17
10	0.36	25 / 756	Chr 11
11	0.39	16 / 480	Chr 4
12	0.42	5 / 139	Chr 21
13	0.46	8 / 242	Chr 13
14	0.62	20 / 689	Chr 3
15	0.68	12 / 437	Chr 8

Chromatin states Rank	p-value	#in/all	Geneset
1	9e-67	339 / 5716	Bcells_peripheral_blood_4_Tx
2	5e-66	348 / 6099	HSC_4_Tx
3	1e-65	238 / 4528	T_CD8+naive_cells_peripheral_blood_4_Tx
4	1e-58	324 / 5527	Regulatory_cells_peripheral_blood_4_Tx
5	4e-58	330 / 5766	natural_killer_cells_peripheral_blood_4_Tx
6	4e-56	327 / 5753	Tcells_peripheral_blood_4_Tx
7	9e-52	317 / 5601	Thelper_cells_peripheral_blood_4_Tx
8	9e-51	298 / 4681	Overlap_fetal_micrbrain_HetRpis
9	6e-50	369 / 6333	Bcells_peripheral_blood_1_TssA
10	9e-50	360 / 7420	Tcells_peripheral_blood_1_TssA
11	2e-48	316 / 5738	monocytes_peripheral_blood_4_Tx
12	2e-47	362 / 7635	monocytes_peripheral_blood_1_TssA
13	2e-47	332 / 6034	5_Tx_Fibroblasts
14	3e-47	332 / 6389	5_Tx_ESC_Mesoderm
15	4e-47	364 / 7751	natural_killer_cells_peripheral_blood_1_TssA

Colon Cancer Rank	p-value	#in/all	Geneset
1	4e-17	276 / 6368	LaPointe_mucosa-position_kmeans_F_cecum_colon_transverse_colon_UP
2	1e-10	84 / 1354	LaPointe_mucosa-position_kmeans_N_cecum_colon_ascending_colon_UP
3	2e-10	99 / 1729	LaPointe_mucosa-position_kmeans_G_cecum_colon_ascending_colon_UP
4	4e-10	71 / 1083	LaPointe_mucosa-position_kmeans_J_cecum_colon_ascending_colon_transv
5	5e-09	25 / 1174	LaPointe_mucosa-position_kmeans_E_transverse_colon_UP_transverse_colo
6	2e-05	48 / 848	LaPointe_mucosa-position_kmeans_O_transverse_colon_UP
7	6e-05	47 / 854	LaPointe_mucosa-position_kmeans_A_ascending_colon_UP
8	4e-04	56 / 1166	LaPointe_mucosa-position_kmeans_K_transverse_colon_UP_cecum_colon
9	4e-04	48 / 958	LaPointe_mucosa-position_kmeans_D_transverse_colon_UP
10	2e-03	48 / 583	LaPointe_mucosa-position_kmeans_L_transverse_colon_cecum_colon_DN
11	1e-02	26 / 532	LaPointe_mucosa-position_kmeans_B_ascending_colon_transverse_colo_U
12	2e-02	3 / 18	Boland_CRC-MSI-A6-A10
13	7e-02	2 / 14	TCGA_Mutated-in-CRC_hypermutated
14	7e-02	3 / 31	Marta_CRC-cluster-c
15	7e-02	2 / 15	TCGA_CRC-less-aggressive-disease-markers

Glioma Rank	p-value	#in/all	Geneset
1	2e-88	105 / 282	WILLSCHEER_GBM_Verhaak-PNwt & CL_up
2	8e-11	84 / 1343	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
3	6e-10	89 / 1523	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
4	6e-05	37 / 614	Sturm_GBM_Meth_overexpression_E_G34_UP
5	8e-03	6 / 58	Gerber_Proteins_up_in_STS
6	2e-02	6 / 66	GIEZELI_GBM_MGMTmethyl_down_VS_nonmethyl
7	2e-02	5 / 50	Vishal_subnetwork_signature_of_survival_in_GBM
8	3e-02	9 / 139	WILLSCHEER_GBM_proteomics_wtOnly_Differencelist
9	4e-02	2 / 11	KIM_amplified & overexpressed in LTS
10	1e-02	16 / 390	Sturm_GBM_Meth_overexpression_H_K27_UP
11	1e-01	2 / 22	Sturm_GBM_Meth_overexpression_U_RTK1_PDFGRA_UP
12	1e-01	4 / 67	Hopp_Sturm_GBM_Epi3_no_zentr_4_IDH_up_adult_fetus_K27_DN
13	2e-01	12 / 286	WILLSCHEER_GBM_proteomics_wtOnly_SpotB
14	2e-01	5 / 100	Donson-Misc immune function-associated with LTS in HGA
15	2e-01	2 / 27	

GSEA C2 Rank	p-value	#in/all	Geneset
1	5e-42	79 / 405	SENSE_HDAC3_TARGETS_UP
2	7e-42	76 / 372	SENSE_HDAC1_TARGETS_UP
3	1e-30	78 / 564	RODRIGUES_THYROID_CARCINOMA_ANAPLASTIC_UP
4	2e-26	57 / 345	FLUOIN_RL1_TARGETS_DN
5	2e-26	114 / 1338	DIAGNOSTIC_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
6	3e-19	59 / 509	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_UP
7	1e-18	100 / 1312	PUJANA_ATM_PCC_NETWORK
8	6e-18	82 / 966	KINESIN_TARGETS_OF_EWSR1_FLII_FUSION_UP
9	9e-18	109 / 1550	PIELMAN_RL1_TARGETS_DN
10	2e-17	69 / 564	PIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_DN
11	7e-17	106 / 1527	PUJANA_BRCA1_PCC_NETWORK
12	5e-15	96 / 1390	GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_DN
13	3e-14	22 / 92	SENSE_HDAC2_TARGETS_UP
14	8e-14	28 / 163	ONDER_CDH1_TARGETS_DN
15	1e-13	24 / 118	AZARE_NEOPLASTIC_TRANSFORMATION_BY_STAT3_UP

BM Rank	p-value	#in/all	Geneset
1	9e-08	22 / 192	HALLMARK_MTORC1_SIGNALING
2	9e-07	14 / 94	HALLMARK_PROTEIN_SECRETION
3	1e-06	19 / 173	HALLMARK_MITOTIC_SPINDLE
4	3e-05	18 / 195	HALLMARK_G2M_CHECKPOINT
5	2e-03	7 / 59	HALLMARK_CHOLESTEROL_HOMEOSTASIS
6	4e-03	11 / 141	HALLMARK_UV_RESPONSE_DN
7	9e-03	8 / 96	HALLMARK_ANDROGEN_RESPONSE
8	1e-02	12 / 190	HALLMARK_MYC_TARGETS_V1
9	4e-02	9 / 150	HALLMARK_APOPTOSIS
10	4e-02	7 / 106	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
11	6e-02	6 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING
12	1e-01	3 / 186	HALLMARK_OXIDATIVE_PHOSPHORYLATION
13	2e-01	6 / 122	HALLMARK_SPERMATOGENESIS
14	2e-01	7 / 149	HALLMARK_UV_RESPONSE_UP
15	2e-01	8 / 187	HALLMARK_E2F_TARGETS

Immunome Rank	p-value	#in/all	Geneset
1	0.06	2 / 13	Angelova Immune-metagenome-immature_B-cells
2	0.07	2 / 14	Angelova Immune-metagenome-esoinophil
3	0.12	1 / 4	Angelova_CRC_MSS-neoantigens
4	0.19	1 / 7	Angelova_CRC_MSI-neoantigens
5	0.27	1 / 10	Angelova Immune-metagenome-TFH
6	0.33	1 / 13	Angelova_CRC_MSS-neoantigens
7	0.40	2 / 45	Angelova Immune-metagenome-MDSC
8	0.43	1 / 18	Angelova Immune-metagenome-pDC
9	0.43	1 / 18	Angelova_CRC Immunostimulators
10	0.44	1 / 19	Angelova Immune-metagenome-activated_CD8
11	0.44	1 / 19	Angelova Immune-metagenome-IDC
12	0.51	1 / 23	Angelova Immune-metagenome-Th2
13	0.63	1 / 32	Angelova Immune-metagenome-effector_memory_CD8
14	0.73	1 / 42	Angelova Immune-metagenome-TGD
15	0.87	1 / 67	Angelova Immune-metagenome-T-cells

Lifestyle Rank	p-value	#in/all	Geneset
1	2e-04	17 / 210	Homuth_BMI-associated-genes_DN
2	8e-02	2 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
3	1e-01	2 / 22	DUMEAUX_Fasting enriched genes
4	3e-01	1 / 10	DUMEAUX_Smoking literature genes up
5	4e-01	1 / 14	Huan_blood-pressure_SBP-signature
6	5e-01	1 / 14	DUMEAUX_High bmi enriched genes
7	8e-01	3 / 150	Homuth_BMI-associated-genes_UP
8	1e+00	0 / 62	DUMEAUX_Smoking enriched genes
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 / 7	DUMEAUX_Estrogen related in non smokers literature genes up
12	1e+00	0 / 7	DUMEAUX_Hormon therapy in non smokers literature genes up
13	1e+00	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
14	1e+00	0 / 12	DUMEAUX_Women normal BMI literature genes up
15	1e+00	0 / 13	Huan_blood-pressure_DBP-signature

Lymphoma Rank	p-value	#in/all	Geneset
1	6e-61	327 / 5529	HOPP_Ixn_elongation
2	3e-51	275 / 4261	HOPP_Ixn_transition
3	8e-37	303 / 5908	HOPP_Active_promoter
4	1e-22	269 / 5682	HOPP_Weak_promoter
5	1e-18	251 / 5404	HOPP_Strong_enhancer
6	1e-08	17 / 102	ROSLOWSKI_blue_total
7	1e-07	182 / 4357	HOPP_Weak_tkn
8	6e-07	180 / 306	SPANG_BCR_DN
9	2e-06	183 / 4559	HOPP_Weak_enhancer
10	3e-05	26 / 353	SPANG_CD40_hrs_DN
11	6e-05	51 / 955	SPANG_BCR_UP
12	2e-04	18 / 227	SPANG_IL21_UP
13	3e-04	180 / 1814	HOPP_Repetitive
14	1e-03	20 / 305	TARTE_PlasmaBlast_signature
15	2e-03	3 / 9	YAMANE_AICDA_targets_nonrecruited

Melanoma Rank	p-value	#in/all	Geneset
1	8e-04	7 / 51	Tirosh_genes from CD8 T-cells in Mel179-melanoma
2	3e-03	6 / 46	Tirosh_top50 correlated genes PC5
3	3e-03	15 / 222	Gerber_wt/wt_melanoma-cells_SpotF
4	5e-03	4 / 23	Melanoma Epi-Enzyme Cluster 7
5	2e-02	13 / 230	Gerber_wt/wt_melanoma-cells_SpotC
6	3e-02	4 / 38	Tirosh_top50 correlated genes PC1
7	4e-02	4 / 41	Tirosh_top50 correlated genes PC3
8	1e-01	11 / 236	Gerber_wt/wt_group5
9	1e-01	12 / 276	Gerber_wt/wt_melanoma-cells_SpotB
10	2e-01	3 / 47	Tirosh_G2/M phase specific genes
11	2e-01	13 / 319	Gerber_wt/wt_melanoma-cells_SpotA
12	2e-01	4 / 79	Tirosh_core cycling genes in low- and high-proliferation melanoma
13	2e-01	5 / 97	Tirosh Exhaustion program in Mel15
14	3e-01	18 / 497	Gerber_wt/wt_melanoma-cells_SpotD
15	3e-01	2 / 38	Hugo_melanoma-BRAFmut-MET_UP

MF Rank	p-value	#in/all	Geneset
1	2e-10	299 / 7864	protein binding
2	9e-07	66 / 1185	ATP binding
3	1e-06	28 / 331	protein serine/threonine kinase activity
4	1e-06	74 / 1402	nucleic acid binding
5	2e-06	39 / 573	kinase activity
6	4e-06	32 / 437	protein kinase activity
7	2e-05	67 / 1329	transferase activity
8	3e-05	60 / 1161	RNA binding
9	2e-04	20 / 267	binding
10	2e-04	4 / 11	RNA stem-loop binding
11	3e-04	6 / 31	disordered domain specific binding
12	3e-04	19 / 286	cadherin binding
13	3e-04	19 / 268	transcription factor binding
14	7e-04	4 / 14	protein kinase A regulatory subunit binding
15	1e-03	42 / 851	identical protein binding

miRNA target Rank	p-value	#in/all	Geneset
1	2e-11	43 / 448	hsa-miR-20b
2	5e-11	40 / 407	hsa-miR-106a
3	1e-10	37 / 364	hsa-miR-548b
4	2e-09	40 / 427	hsa-miR-15b
5	5e-10	21 / 133	hsa-miR-495
6	1e-09	28 / 240	hsa-miR-202
7	1e-09	20 / 127	hsa-miR-1297
8	2e-09	26 / 216	hsa-miR-548l
9	5e-09	36 / 397	hsa-miR-150
10	2e-08	19 / 131	hsa-miR-802
11	2e-08	37 / 435	hsa-miR-93
12	2e-08	28 / 275	hsa-miR-590-3p
13	2e-08	23 / 193	hsa-miR-26a

Correlation Cluster

Spot Summary: R

metagenes = 25
genes = 182

<r> metagenes = 0.96
<r> genes = 0.28
beta: r2= 5.8 / log p= -Inf

samples with spot = 53 (24 %)
mBL : 13 (29.5 %)
intermediate : 13 (27.1 %)
non-mBL : 27 (20.9 %)

Spot Genelist

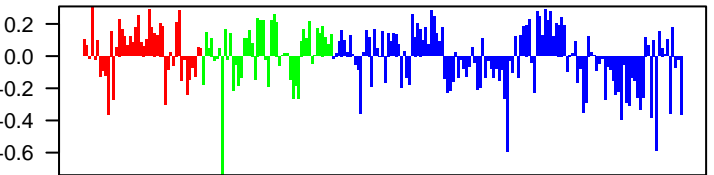
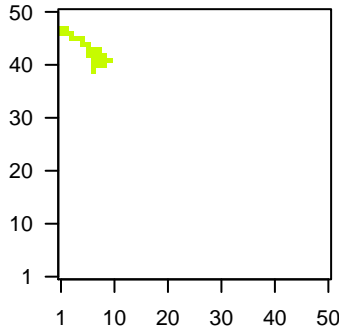
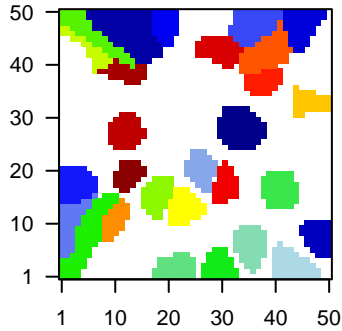
Rank	ID	max e	r	min e	Description
1	212389_at	1.62	-1.05	0.65	SBF1 SET binding factor 1 [Source:HGNC Symbol;Acc:HGNC:1054
2	215621_s_at	1.56	-1.08	0.19	immunoglobulin heavy constant delta [Source:HGNC Symbol
3	208595_s_at	1.54	-1.23	0.44	MBD1 methyl-CpG binding domain protein 1 [Source:HGNC Symbo
4	214860_at	1.52	-0.83	0.44	SLC9A7 solute carrier family 9 member A7 [Source:HGNC Symbol;Ac
5	218811_at	1.49	-1.6	0.68	ORAI2 ORAI calcium release-activated calcium modulator 2 [Source
6	214673_s_at	1.38	-1.31	0.55	HUWE1 HECT, UBA and WWE domain containing 1, E3 ubiquitin prot
7	209237_s_at	1.31	-0.87	0.31	SLC23A2solute carrier family 23 member 2 [Source:HGNC Symbol;Acc
8	210173_at	1.3	-0.76	0.58	PTPRJ protein tyrosine phosphatase, receptor type J [Source:HGNC
9	216734_s_at	1.29	-1.59	0.49	CXCR5 C-X-C motif chemokine receptor 5 [Source:HGNC Symbol;A
10	203101_s_at	1.28	-0.86	0.52	MGAT2 mannosyl (alpha-1,6-)-glycoprotein beta-1,2-N-acetylgluc
11	208536_s_at	1.24	-1.06	0.38	BCL2L11BCL2 like 11 [Source:HGNC Symbol;Acc:HGNC:994]
12	212575_at	1.22	-1.24	0.6	TMEM259transmembrane protein 259 [Source:HGNC Symbol;Acc:HGNC
13	214900_at	1.21	-0.91	0.48	ZKSCAN3zinc finger with KRAB and SCAN domains 1 [Source:HGNC S
14	208196_x_at	1.18	-1.12	0.46	NFATC1 nuclear factor of activated T cells 1 [Source:HGNC Symbol;A
15	204395_s_at	1.16	-1.06	0.44	GRK5 G protein-coupled receptor kinase 5 [Source:HGNC Symbol;
16	204543_at	1.14	-1.19	0.74	RAPGEFRap guanine nucleotide exchange factor 1 [Source:HGNC Sy
17	210350_x_at	1.11	-0.95	0.34	ING1 inhibitor of growth family member 1 [Source:HGNC Symbol;A
18	219723_x_at	1.11	-0.72	0.52	AGPAT3 1-acylglycerol-3-phosphate O-acyltransferase 3 [Source:HC
19	214530_x_at	1.1	-0.85	0.55	EPB41 erythrocyte membrane protein band 4.1 [Source:HGNC Symt
20	205196_s_at	1.09	-1.43	0.59	AP1S1 adaptor related protein complex 1 sigma 1 subunit [Source:HC

Geneset Overrepresentation

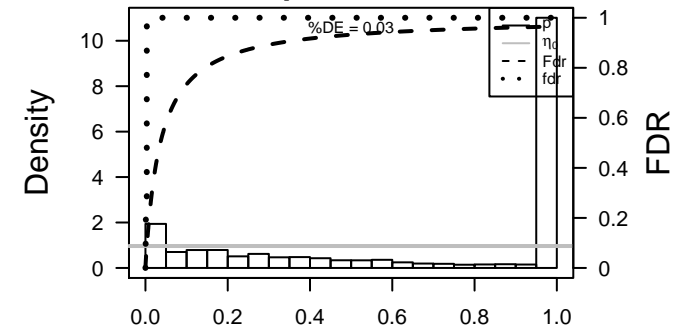
Rank	p-value	#in/all	Geneset
1	5e-22	117 / 4261	LympI HOPP_Txn_transition
2	7e-16	124 / 5529	LympI HOPP_Txn_elongation
3	3e-14	25 / 282	Gliom WILLSCHER_GBM_Verhaak-PNwt & CL_up
4	2e-13	118 / 5404	LympI HOPP_Strong_enhancer
5	2e-10	23 / 355	Refer WIRTH_Immune_system
6	3e-10	54 / 1729	Colon LaPointe_mucosa-position_kmeans_G_cecum_colon_ascending_colon_UP
7	5e-10	23 / 372	GSE/ SENESE_HDAC1_TARGETS_UP
8	2e-09	49 / 1550	GSE/ PILON_KLF1_TARGETS_DN
9	2e-09	76 / 3121	TF ICGC_Egr1_targets
10	3e-09	23 / 405	GSE/ SENESE_HDAC3_TARGETS_UP
11	8e-09	75 / 3150	TF ICGC_Creb1_targets
12	3e-08	80 / 3564	TF ICGC_Taf1_targets
13	1e-07	82 / 3796	TF ICGC_Nf1c1_targets
14	1e-07	111 / 5908	LympI HOPP_Active_promoter
15	1e-07	52 / 1941	TF ICGC_Bcl3_targets
16	3e-07	67 / 2899	TF ICGC_Nf1c1_targets
17	4e-07	19 / 376	GSE/ GARY_CD5_TARGETS_UP
18	5e-07	22 / 496	Refer PROTEINATLAS_spleen
19	5e-07	34 / 1044	TF ICGC_Six5_targets
20	6e-07	80 / 3804	TF ICGC_Stat5_targets
21	7e-07	35 / 1107	TF ICGC_Myc_targets
22	7e-07	19 / 386	GSE/ MULLIGHAN_MLL_SIGNATURE_2_UP
23	8e-07	79 / 3769	TF ICGC_Pmlsc81335_targets
24	9e-07	60 / 2541	CC nucleoplasm
25	9e-07	8 / 59	GSE/ BYSTROEM_CORRELATED_WITH_IL5_DN
26	1e-06	84 / 4131	TF ICGC_Tcf3_targets
27	1e-06	31 / 935	GSE/ MARSON_BOUND_BY_FOXP3_UNSTIMULATED
28	1e-06	7 / 43	GSE/ SIG_BCR_SIGNALING_PATHWAY
29	1e-06	37 / 1241	TF KIM_MYC_targets
30	1e-06	79 / 3805	CC cytosol
31	1e-06	34 / 1089	TF ICGC_Ets1_targets
32	1e-06	70 / 3213	TF ICGC_Pu1_targets
33	2e-06	29 / 848	Refer PROTEINATLAS_adrenal_gland
34	2e-06	73 / 3420	TF ICGC_Bclaf101388_targets
35	2e-06	25 / 671	Refer PROTEINATLAS_cervix_uterine
36	2e-06	25 / 678	Refer PROTEINATLAS_lymph_node
37	3e-06	12 / 173	HM HALLMARK_MITOTIC_SPINDLE
38	3e-06	131 / 7864	MF protein binding
39	3e-06	41 / 1508	TF ICGC_Mef2_targets
40	3e-06	11 / 146	GSE/ ELVIDGE_HYPOXIA_DN

Overview Map

Spot



p-values



Rank	p-value	#in/all	Geneset
1	0.4	2 / 107	HORVATH_aging_genes_meth_UP
2	1.0	0 / 82	HORVATH_aging_genes_meth_DOWN
3	1.0	0 / 47	TSCHEMDORFF_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-06	7 / 51	retrograde transport, endosome to Golgi
2	1.1	11 / 190	vesicle-mediated transport
3	2e-04	4 / 23	regulation of defense response to virus by virus
4	3e-04	4 / 25	homeostasis of number of cells within a tissue
5	3e-04	12 / 281	mRNA processing
6	3e-04	3 / 11	interleukin-2-mediated signaling pathway
7	3e-04	9 / 26	positive regulation of release of cytochrome c from mitochondria
8	3e-04	17 / 507	protein phosphorylation
9	4e-04	4 / 28	positive regulation of intrinsic apoptotic signaling pathway
10	4e-04	4 / 28	positive regulation of protein insertion into mitochondrial membrane involved i
11	5e-04	4 / 29	positive regulation of multicellular organism growth
12	6e-04	11 / 260	chromatin organization
13	7e-04	5 / 55	DNA damage response, signal transduction by p53 class mediator resulting in
14	8e-04	5 / 56	negative regulation of translation
15	1e-03	9 / 198	mRNA splicing, via spliceosome

Cancer Rank	p-value	#in/all	Geneset
1	9e-04	3 / 15	GENTLES_modul2
2	7e-03	6 / 130	PanCan_CC+Apop_geneset_nanostring
3	2e-02	2 / 18	PanCan_Notch_geneset_nanostring
4	9e-02	3 / 80	PanCan_JAK-ST_geneset_nanostring
5	1e-01	5 / 187	PanCan_Pi3K_geneset_nanostring
6	1e-01	4 / 134	PanCan_RAS_geneset_nanostring
7	1e-01	1 / 10	GENTLES_modul5
8	1e-01	0 / 14	LIU_COMMON_CANCER_GENES
9	1e-01	4 / 147	PanCan_MAPK_geneset_nanostring
10	1e-01	1 / 12	BENTINK_g2f3.2
11	2e-01	1 / 15	RHODES_CANCER_META_SIGNATURE
12	2e-01	2 / 58	SHAUGHNESSY_MM_high_risk
13	2e-01	2 / 72	PanCan_Wnt_geneset_nanostring
14	3e-01	0 / 11	LIU_PROSTATE_CANCER_UP
15	3e-01	1 / 28	PanCan_HK_geneset_nanostring

CC Rank	p-value	#in/all	Geneset
1	9e-07	60 / 2541	nucleoplasm
2	1e-06	79 / 3805	cytosol
2e-04	4 / 24	membrane coat	
4	4e-04	7 / 104	trans-Golgi network
5	5e-04	81 / 4579	nucleus
6	5e-04	5 / 51	clathrin-coated vesicle
7	6e-04	3 / 13	clathrin adaptor complex
8e-04	7 / 117	cell cortex	
9	1e-03	5 / 64	trans-Golgi network membrane
10	2e-03	3 / 19	exon-exon junction complex
11	2e-03	3 / 21	mitotic spindle pole
12	3e-03	13 / 416	macromolecular complex
13	3e-03	2 / 4701	cytoplasm
14	4e-03	11 / 326	nuclear speck
15	4e-03	5 / 79	ruffle membrane

Chr Rank	p-value	#in/all	Geneset
1	0.006	19 / 776	Chr 17
2	0.056	11 / 490	Chr 10
3	0.117	14 / 756	Chr 11
4	0.219	4 / 184	Chr 18
5	0.268	6 / 333	Chr 22
6	0.273	7 / 403	Chr 14
7	0.286	9 / 548	Chr 16
8	0.350	6 / 267	Chr 20
9	0.353	9 / 585	Chr 7
10	0.388	4 / 242	Chr 13
11	0.543	2 / 139	Chr 21
12	0.565	17 / 1325	Chr 1
13	0.585	9 / 726	Chr 12
14	0.623	6 / 492	Chr 9
15	0.650	10 / 832	Chr 2

Chromatin states Rank	p-value	#in/all	Geneset
1	1e-35	134 / 4208	Tcells peripheral blood_6_EnhG
2	7e-29	118 / 3682	natural killer cells peripheral blood_6_EnhG
3	1.1	111 / 6767	Tcells peripheral blood_6_EnhG
4	5e-26	118 / 3938	Thelper cells peripheral blood_6_EnhG
5	6e-25	140 / 5716	Bcells peripheral blood_4_Tx
6	8e-25	110 / 3524	Regulatory cells peripheral blood_6_EnhG
7	2e-24	140 / 5766	natural killer cells peripheral blood_4_Tx
8	3e-24	124 / 3528	T CD8+ naive cells peripheral blood_4_Tx
9	1e-23	137 / 5601	Thelper cells peripheral blood_4_Tx
10	4e-23	142 / 6099	HSC_4_Tx
11	7e-23	160 / 7957	Tcells peripheral blood_2_TssAFlnk
12	2e-22	137 / 5753	Tcells peripheral blood_4_Tx
13	2e-21	134 / 5527	Regulatory cells peripheral blood_4_Tx
14	5e-22	158 / 7833	Bcells peripheral blood_1_TssA
15	8e-22	156 / 7635	monocytes peripheral blood_1_TssA

Colon Cancer Rank	p-value	#in/all	Geneset
1	3e-10	54 / 1729	LaPointe_mucosa-position_kmeans_G_cecum_colon_ascending_colon_UP_t
2	5e-06	112 / 6368	LaPointe_mucosa-position_kmeans_F_cecum_colon_transverse_colon_UP
3	7e-06	34 / 1174	LaPointe_mucosa-position_kmeans_E_transverse_colon_UP_transverse_colo
4	1e-03	31 / 1354	LaPointe_mucosa-position_kmeans_N_cecum_colon_ascending_colon_UP_a
5	9e-03	25 / 1166	LaPointe_mucosa-position_kmeans_K_transverse_colon_UP_cecum_colon_a
6	1e-02	23 / 1083	LaPointe_mucosa-position_kmeans_J_cecum_colon_ascending_colon_transv
7	3e-02	18 / 848	LaPointe_mucosa-position_kmeans_O_transverse_colon_UP_
8	3e-02	18 / 854	LaPointe_mucosa-position_kmeans_A_ascending_colon_UP_
9	5e-02	12 / 532	LaPointe_mucosa-position_kmeans_B_ascending_colon_transverse_colon_U
10	6e-02	2 / 141	Marisa_CRC-cluster-c
11	6e-02	1 / 5	Hewish_dMMR-secondary-mutations_Apoptosis
12	9e-02	1 / 7	Boland_CRC-MSI-TGC
13	9e-02	3 / 83	Marisa_CRC-cluster-d
14	9e-02	11 / 539	Lembcke_TCGA_meth_kmeans_L_CIMP_H_DN
15	1e-01	1 / 8	Marisa_CRC-C1

Glioma Rank	p-value	#in/all	Geneset
1	3e-14	25 / 282	WILLSCHER_GBM_Verhaak-PNwt & CL_up
2	8e-03	28 / 1343	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
3	1e-02	6 / 139	WILLSCHER_GBM_proteomics_wtOnly_Differencelist
4	1e-02	4 / 71	Weller_LGG_fp19qDel-vs-intact_DOWN
5	2e-02	4 / 72	Weller_Udtf_vs_O_UP
6	3e-02	3 / 50	Vishal_subnetwork signature of survival in GBM
7	4e-02	28 / 1523	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
8	4e-02	3 / 59	WILLSCHER_GBM_Verhaak-PNwt & MES_up
9	6e-02	13 / 614	Sturm_GBM_Meth_overexpression_E_G34_UP
10	6e-02	1 / 6	WILLSCHER_GBM_LTSmut_proteomics-A_UP
11	1e-01	1 / 11	KIM amplified & overexpressed in LTS
12	1e-01	6 / 268	Scov_0_001_Sturm_M2_Mesenchymal_RTK1_PDGFRA_DN
13	1e-01	3 / 99	GIEZELT_GBM_WT_up_VS_mut
14	1e-01	3 / 100	WILLSCHER_GBM_proteomics_wtOnly_SpotB
15	2e-01	2 / 55	WILLSCHER_GBM_proteomics_wtOnly_SpotJ

GSEA C2 Rank	p-value	#in/all	Geneset
1	5e-10	23 / 372	SENSE_HDAC1_TARGETS_UP
2	2e-09	49 / 1550	PILON_KLF1_TARGETS_DN
3	3e-09	23 / 405	SENSE_HDAC3_TARGETS_UP
4	4e-07	19 / 376	GARY_CD5_TARGETS_UP
5	4e-07	12 / 386	MULLIGHAN_MLL_SIGNATURE_2_UP
6	9e-07	8 / 59	BYSTROEM_CORRELATED_WITH_IL5_DN
7	1e-06	31 / 935	MARSON_BOUND_BY_FOXP3_UNSTIMULATED
8	1e-06	7 / 43	SIG_BCR_SIGNALING_PATHWAY
9	3e-06	11 / 146	ELVDGE_HYPOXIA_DN
10	7e-06	10 / 191	REACTOME_SIGNALLING_BY_NGF
11	9e-06	15 / 300	OSMAN_BLADDER_CANCER_DN
12	1e-05	36 / 1312	PUJANA_ATM_PCC_NETWORK
13	1e-05	4 / 12	NUNODA_RESPONSE_TO_DASATINIB_IMATINIB_DN
14	1e-05	41 / 1602	BLALOCK_ALZHEIMERS_DISEASE_UP
15	1e-05	6 / 41	GALLUZZI_PERMEABILIZE_MITOCHONDRIA

LM Rank	p-value	#in/all	Geneset
1	3e-06	12 / 173	HALLMARK_MITOTIC_SPINDLE
2	4e-03	8 / 192	HALLMARK_MTORC1_SIGNALING
3	4e-03	8 / 195	HALLMARK_G2M_CHECKPOINT
4	3e-02	4 / 94	HALLMARK_PROTEIN_SECRETION
5	4e-02	6 / 187	HALLMARK_E2F_TARGETS
6	5 / 149	5 / 149	HALLMARK_UV_RESPONSE_UP
7	5e-02	5 / 150	HALLMARK_APOPTOSIS
8	5e-02	4 / 106	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
9	1e-01	5 / 193	HALLMARK_HEME_METABOLISM
10	1e-01	3 / 177	HALLMARK_PI3K_AKT_MTOR_SIGNALING
11	2e-01	4 / 174	HALLMARK_ADIPONEGENESIS
12	3e-01	3 / 141	HALLMARK_UV_RESPONSE_DN
13	4e-01	1 / 34	HALLMARK_APICAL_SURFACE
14	4e-01	2 / 97	HALLMARK_PEROXISOME
15	4e-01	3 / 170	HALLMARK_IL2_STAT5_SIGNALING

Immunome Rank	p-value	#in/all	Geneset
1	0.02	3 / 6	Angelova Immune-metagen-MDSC
2	0.06	3 / 67	Angelova Immune-metagen-T-cells
3	0.15	1 / 12	Angelova Immune-metagen-memory_B-cells
4	0.18	1 / 15	Angelova Immune-metagen-NK
5	0.20	1 / 17	Angelova Immune-metagen-central_memory_CD8
6	0.13	0 / 13	Angelova Immune-metagen-activated_B-cells
7	1.00	0 / 26	Angelova Immune-metagen-activated_CD4
8	1.00	0 / 19	Angelova Immune-metagen-activated_CD8
9	1.00	0 / 21	Angelova Immune-metagen-central_memory_CD4
10	1.00	0 / 7	Angelova Immune-metagen-cytotoxic_cells
11	0.25	0 / 25	Angelova Immune-metagen-DC
12	1.00	0 / 12	Angelova Immune-metagen-effector_memory_CD4
13	1.00	0 / 32	Angelova Immune-metagen-effector_memory_CD8
14	1.00	0 / 14	Angelova Immune-metagen-eosinophil
15	1.00	0 / 19	Angelova Immune-metagen-IDC

Lifestyle Rank	p-value	#in/all	Geneset
1	0.06	6 / 210	Homuth_BMI-associated-genes_DN
2	0.13	4 / 150	Homuth_BMI-associated-genes_UP
3	1.00	0 / 62	DUMEAUX_Smoking enriched genes
4	1.00	0 / 10	DUMEAUX_Smoking literature genes up
5	1.00	0 / 4	DUMEAUX_Exercise non smoker literature enriched genes
6	1.00	0 / 10	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 / 7	DUMEAUX_Hormon therapy in non smokers literature genes up
9	1.00	0 / 9	DUMEAUX_Monocytes in smokers literature genes up
10	1.00	0 / 16	DUMEAUX_Red blood cells in non smokers literature genes up
11	1.00	0 / 12	DUMEAUX_Women normal BMI literature genes up
12	1.00	0 / 22	DUMEAUX_High bmi enriched genes
13	1.00	0 / 22	DUMEAUX_Fasting enriched genes
14	1.00	0 / 14	Huan_blood-pressure_SBP-signature
15	1.00	0 / 13	Huan_blood-pressure_DBP-signature

Lymphoma Rank	p-value	#in/all	Geneset
1	5e-22	117 / 4261	HOPP_Txn_transition
2	7e-16	124 / 5529	HOPP_Txn_elongation
3	2e-13	118 / 5404	HOPP_Strong_enhancer
4	1e-07	111 / 5908	HOPP_Active_promoter
5	2e-05	6 / 45	Monti_BCR_cluster
6	6e-03	91 / 5682	HOPP_Weak_promoter
7	7e-03	11 / 353	SPANG_CD40_hrs_DN
8	7e-03	21 / 806	SPANG_BCR_DN
9	2e-02	3 / 45	SPANG_BAFF_hrs_DN
10	2e-02	5 / 121	ROSLOWSKI_green_tal
11	9e-02	1 / 7	Shaknovich_ABC_hypo_meth
12	1e-01	17 / 955	SPANG_BCR_UP
13	1e-01	1 / 14	YAMANE_AICDA_targets_recruited
14	2e-01	6 / 305	TARTE_Plasmablast_signature
15	3e-01	5 / 263	SPANG_CD40_hrs_UP

Melanoma Rank	p-value	#in/all	Geneset
1	0.003	9 / 230	Gerber_wtwt_melanoma-cells-SpotC
2	0.011	7 / 185	Tirosh_genes from malignant cells in Mel179-melanoma
3	0.036	2 / 23	Melanoma_Epi-Enzyme Cluster 7
4	0.051	4 / 107	Tirosh_Exhaustion program in Mel75
5	0.088	6 / 236	Gerber_wtwt_group3-specific
6	0.143	2 / 51	Tirosh_genes from CD8 T-cells in Mel179-melanoma
7	0.152	6 / 276	Gerber_wtwt_melanoma-cells-SpotB
8	0.154	9 / 222	Gerber_wtwt_melanoma-cells-SpotF
9	0.270	1 / 24	Tirosh_B-cell specific genes-melanoma
10	0.294	2 / 83	TCGA_melanoma Immune_high
11	0.304	2 / 85	Tirosh_AXL-signature
12	0.385	1 / 37	Hugo_melanoma-all-MET_DN
13	0.388	1 / 38	Tirosh_top50 correlated genes PC1
14	0.439	1 / 44	Tirosh_top50 correlated genes PC2
15	0.472	7 / 497	Gerber_wtwt_melanoma-cells-SpotD

MF Rank	p-value	#in/all	Geneset
1	3e-06	131 / 7864	protein binding
2	9e-05	34 / 1329	transferase activity
3	3e-04	8 / 130	guanyl-nucleotide exchange factor activity
4	5e-04	4 / 29	Rho GTPase binding
5	7e-04	4 / 31	disordered domain specific binding
6	9e-04	14 / 408	protein heterodimerization activity
7	1e-03	5 / 60	RNA polymerase II distal enhancer sequence-specific DNA binding
8	1e-03	12 / 331	protein serine/threonine kinase activity
9	1e-03	34 / 1541	DNA binding
10	2e-03	10 / 256	cadherin binding
11	2e-03	3 / 20	dynein complex binding
12	3e-03	6 / 107	mRNA binding
13	3e-03	27 / 1185	ATP binding
14	3e-03	16 / 573	kinase activity
15	4e-03	21 / 851	identical protein binding

miRNA target Rank	p-value	#in/all	Geneset
1	5e-05	13 / 268	hsa-miR-367
2	1e-04	6 / 59	hsa-miR-361-3p
3	3e-04	7 / 99	hsa-miR-515-5p
4	6 / 74	6 / 74	hsa-miR-142-5p
5	3e-04	5 / 47	hsa-miR-665
6	4e-04	4 / 28	hsa-miR-1237
7	5e-04	5 / 51	hsa-miR-502-5p
8	9e-04	15 / 448	hsa-miR-200b
9	1e-03	8 / 457	hsa-miR-342
10	2e-03	4 / 39	hsa-miR-362-3p
11	2e-03	8 / 169	hsa-miR-148a
12	2e-03	6 / 100	hsa-miR-145
13	2e-03	6 / 100	hsa-miR-509-3p
14	2e-03	9 / 217	hsa-miR-92
15	2e-03	4 / 43	hsa-miR-508-5p

Correlation Cluster

Spot Summary: S

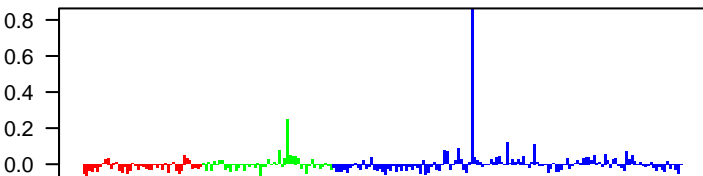
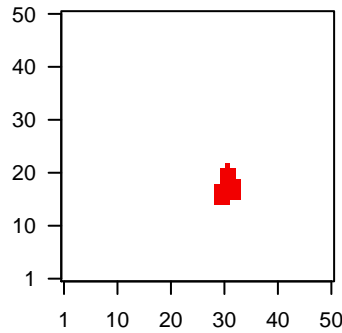
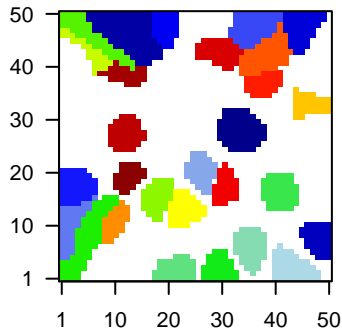
metagenes = 29
genes = 276

<r> metagenes = 0.94
<r> genes = 0.08
beta: r2= 0.27 / log p= -Inf

samples with spot = 2 (0.9 %)
intermediate : 1 (2.1 %)
non-mBL : 1 (0.8 %)

Overview Map

Spot

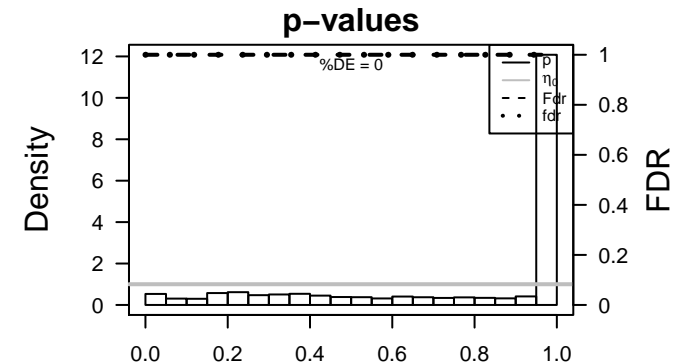


Spot Genelist

Rank	ID	max e	r	min e	Description
					Symbol
1	216430_x_at	2.85	-0.73	0.36	
2	207213_s_at	2.46	-0.66	0.43	USP2 ubiquitin specific peptidase 2 [Source:HGNC Symbol;Acc:HGNC:10887]
3	219511_s_at	2.03	-0.78	0.38	SNCAIP synuclein alpha interacting protein [Source:HGNC Symbol;Acc:HGNC:10887]
4	206001_at	2	-0.74	0.4	NPY neuropeptide Y [Source:HGNC Symbol;Acc:HGNC:7955]
5	204454_at	1.99	-0.8	0.35	LDOC1 LDOC1, regulator of NFKB signaling [Source:HGNC Symbol;Acc:HGNC:10887]
6	205817_at	1.85	-0.72	0.31	SIX1 SIX homeobox 1 [Source:HGNC Symbol;Acc:HGNC:10887]
7	203458_at	1.84	-1.13	0.3	SPR sepiapterin reductase [Source:HGNC Symbol;Acc:HGNC:112]
8	210402_at	1.83	-0.64	0.4	KCNJ1 potassium voltage-gated channel subfamily J member 1 [Source:HGNC Symbol;Acc:HGNC:1759]
9	219658_at	1.79	-0.81	0.23	PTCD2 pentatricopeptide repeat domain 2 [Source:HGNC Symbol;Acc:HGNC:10887]
10	221526_x_at	1.74	-0.59	0.26	PARD3 par-3 family cell polarity regulator [Source:HGNC Symbol;Acc:HGNC:10887]
11	203441_s_at	1.73	-0.91	0.33	CDH2 cadherin 2 [Source:HGNC Symbol;Acc:HGNC:1759]
12	219412_at	1.73	-0.59	0.34	RAB38 RAB38, member RAS oncogene family [Source:HGNC Symbol;Acc:HGNC:10887]
13	201481_s_at	1.7	-1.17	0.29	PYGB glycogen phosphorylase B [Source:HGNC Symbol;Acc:HGNC:10887]
14	214481_at	1.7	-0.74	0.19	HIST1H2A histone cluster 1 H2A family member m [Source:HGNC Symbol;Acc:HGNC:10887]
15	219527_at	1.69	-0.63	0.25	MARC2 mitochondrial amidoxime reducing component 2 [Source:HGNC Symbol;Acc:HGNC:10887]
16	206876_at	1.68	-0.46	0.4	SIM1 single-minded family bHLH transcription factor 1 [Source:HGNC Symbol;Acc:HGNC:10887]
17	205464_at	1.66	-0.64	0.38	SCNN1B sodium channel epithelial 1 beta subunit [Source:HGNC Symbol;Acc:HGNC:10887]
18	211197_s_at	1.58	-1.07	0.23	LOC102723996
19	215184_at	1.54	-0.56	0.42	DAPK2 death associated protein kinase 2 [Source:HGNC Symbol;Acc:HGNC:10887]
20	220002_at	1.54	-0.88	0.34	KIF26B kinesin family member 26B [Source:HGNC Symbol;Acc:HGNC:10887]

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	2e-06	149 / 6368	Colon LaPointe_mucosa-position_kmeans_F_cecum colon_transverse colon_UP
2	9e-06	5 / 17	BP regulation of long-term neuronal synaptic plasticity
3	1e-04	6 / 44	GSE# REACTOME_CELL_CELL_JUNCTION_ORGANIZATION
4	1e-04	7 / 63	GSE# REACTOME_CELL_CELL_JUNCTION_ORGANIZATION
5	4e-04	8 / 99	GSE# REACTOME_CELL_CELL_COMMUNICATION
6	5e-04	35 / 1092	GSE# YOSHIMURA_MAPK8_TARGETS_UP
7	6e-04	4 / 22	GSE# REACTOME_ADHERENS_JUNCTIONS_INTERACTIONS
8	7e-04	33 / 1029	GSE# DODD_NASOPHARYNGEAL_CARCINOMA_UP
9	8e-04	5 / 41	BP heterophilic cell-cell adhesion via plasma membrane cell adhesion molecules
10	8e-04	52 / 1894	Lymp# HOPP_Poised_promoter
11	1e-03	9 / 145	BP response to stimulus
12	1e-03	78 / 3210	CC plasma membrane
13	1e-03	7 / 92	Color Marisa_CRC-cluster-h
14	1e-03	79 / 3270	CC integral component of membrane
15	1e-03	3 / 13	BP striated muscle cell differentiation
16	1e-03	3 / 13	GSE# KIM_RESPONSE_TO_TSA_AND_DECITABINE_DN
17	2e-03	5 / 51	MF ubiquitin binding
18	2e-03	4 / 31	BP adherens junction organization
19	2e-03	4 / 32	BP excretion
20	3e-03	4 / 33	GSE# FIGUEROA_AML_METHYLATION_CLUSTER_5_DN
21	3e-03	9 / 164	Color Lembcke_TCGA_meth_kmeans_B_Cluster4_DN
22	3e-03	3 / 17	MF inward rectifier potassium channel activity
23	3e-03	75 / 3168	Lymp# HOPP_Repressed
24	4e-03	3 / 18	BP calcium-dependent cell-cell adhesion via plasma membrane cell adhesion molecules
25	4e-03	4 / 38	BP detection of chemical stimulus involved in sensory perception of smell
26	4e-03	4 / 38	MF olfactory receptor activity
27	4e-03	4 / 38	BP positive regulation of insulin secretion
28	5e-03	9 / 179	CC external side of plasma membrane
29	6e-03	3 / 21	BP potassium ion import
30	6e-03	3 / 21	GSE# QLSSON_E2F3_TARGETS_UP
31	7e-03	3 / 22	MF cation channel activity
32	7e-03	3 / 22	CC multivesicular body
33	7e-03	8 / 156	GSE# GAUSSMANN_MLL_AF4_FUSION_TARGETS_G_UP
34	7e-03	13 / 337	MF G-protein coupled receptor activity
35	8e-03	3 / 23	BP leukocyte cell-cell adhesion
36	8e-03	3 / 23	GSE# REACTOME_SEMA4D_INDUCED_CELL_MIGRATION_AND_GROWTH_UP
37	8e-03	5 / 70	GSE# REACTOME_POTASSIUM_CHANNELS
38	8e-03	17 / 500	BP cell adhesion
39	8e-03	2 / 8	GSE# MCCOLLUM_GELDANAMYCIN_RESISTANCE_UP
40	8e-03	6 / 99	BP homophilic cell adhesion via plasma membrane adhesion molecules



Rank	p-value	#in/all	Geneset
1	0.08	4 / 32	HORVATH_aging_genes_meth_DOWN
2	0.57	1 / 7	TESCHENDORFF_age_hypermethylated
3	0.85	1 / 107	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	

Rank	p-value	#in/all	Geneset
1	0.001	78 / 3210	plasma membrane
2	0.001	79 / 3270	integral component of membrane
3	0.003	3 / 107	external side of plasma membrane
4	0.007	3 / 22	multivesicular body
5	0.008	10 / 231	apical plasma membrane
6	0.012	3 / 27	Golgi stack
7	0.013	2 / 10	calnexin complex
8	0.017	2 / 10	cell projection membrane
9	0.015	5 / 81	synaptic vesicle
10	0.019	2 / 12	platelet alpha granule membrane
11	0.019	2 / 12	trans-Golgi network transport vesicle
12	0.019	7 / 152	basolateral plasma membrane
13	0.027	4 / 59	adherens junction
14	0.027	110 / 5339	membrane
15	0.028	4 / 65	voltage-gated potassium channel complex

Rank	p-value	#in/all	Geneset
1	2e-06	149 / 6368	LaPointe_mucosa-position_kmeans_F_cecum_colon_transverse_colon_UP_
2	1e-03	7 / 92	Marisa_CRC-cluster-h
3	3e-03	9 / 164	Lembcke_TCGA_meth_kmeans_B_Cluster4_DN
4	1e-02	11 / 278	Lembcke_TCGA_meth_kmeans_H_CIMP_L_UP_CIMP_H_DN
5	2e-02	3 / 19	TCGA_Mutated-in-CRC_non-hypermethylated
6	3e-02	2 / 16	Vilar_non-hypermethylated-in-CRC
7	5e-02	15 / 532	LaPointe_mucosa-position_kmeans_B_ascending_colon_transverse_colon_U
8	7e-02	11 / 376	Lembcke_TCGA_expr_kmeans_M_CIMP_H_DN
9	1e-01	1 / 7	Budinska_C_CIMP-h-like_UP
10	1e-01	1 / 8	Marisa_CRC-h
11	2e-01	7 / 255	Kosinski_top_crypt-long-list
12	2e-01	1 / 12	Juehling_HNPCC-mutated-in-4
13	2e-01	1 / 15	TCGA-CRC_less-aggressive-disease-markers
14	2e-01	1 / 16	Vilar_mutated-in-CRC-Camp
15	3e-01	15 / 738	Lembcke_TCGA_expr_kmeans_N_CIMP_H_DN

Rank	p-value	#in/all	Geneset
1	0.04	7 / 174	HALLMARK_ADIPOGENESIS
2	0.12	2 / 34	HALLMARK_APICAL_SURFACE
3	0.17	4 / 122	HALLMARK_SPERMATOGENESIS
4	0.17	5 / 166	HALLMARK_INTERFERON_GAMMA_RESPONSE
5	0.20	5 / 174	HALLMARK_APICAL_JUNCTION
6	0.25	3 / 19	HALLMARK_BILE_ACID_METABOLISM
7	0.26	3 / 194	HALLMARK_MYOGENESIS
8	0.27	5 / 195	HALLMARK_KRAS_SIGNALING_DN
9	0.39	2 / 76	HALLMARK_INTERFERON_ALPHA_RESPONSE
10	0.41	1 / 29	HALLMARK_NOTCH_SIGNALING
11	0.42	4 / 189	HALLMARK_OXIDATIVE_PHOSPHORYLATION
12	0.43	1 / 12	HALLMARK_INFLAMMATORY_RESPONSE
13	0.44	4 / 191	HALLMARK_P53_PATHWAY
14	0.47	1 / 35	HALLMARK_HEDGEHOG_SIGNALING
15	0.50	1 / 38	HALLMARK_WNT_BETA_CATENIN_SIGNALING

Rank	p-value	#in/all	Geneset
1	8e-04	52 / 1894	HOPP_Poised_promoter
2	3e-03	75 / 3168	HOPP_Repressed
3	6e-02	8 / 234	Hopp_Lymphoma_Epi1_no_zentr_6_MCL_DN
4	2e-01	1 / 15	DAVE_BL Inter
5	2e-01	2 / 53	LENZ_Stromal_signature2
6	4e-01	1 / 24	Hopp_Lymphoma_Epi1_no_zentr_2_B.cell_MCL_DN
7	4e-01	1 / 25	ROSLOUWSKI_red UP
8	4e-01	1 / 26	DAVE Immune response 1
9	4e-01	41 / 2206	HOPP_Heterochrom
10	5e-01	1 / 34	TARTE_B-cell signature
11	5e-01	1 / 35	Subero_MM_hyper_meth
12	5e-01	1 / 40	CARO_OxPhos_in_DLCL_UP
13	5e-01	2 / 99	Sna_BP
14	6e-01	1 / 49	LEE_Developmental_regulators
15	7e-01	4 / 263	SPANG_CD40_hrs UP

Rank	p-value	#in/all	Geneset
1	0.02	2 / 13	hsa-miR-671-3p
2	0.03	2 / 16	hsa-miR-564
3	0.04	5 / 104	hsa-miR-1272
4	0.145	2 / 145	hsa-miR-374b
5	0.12	2 / 34	hsa-miR-581
6	0.15	5 / 157	hsa-miR-374a
7	0.17	2 / 41	hsa-miR-324-3p
8	0.17	3 / 79	hsa-miR-888
9	0.17	hsa-miR-5410	
10	0.19	2 / 45	hsa-miR-379
11	0.19	1 / 12	hsa-miR-191*
12	0.21	5 / 179	hsa-miR-181d
13	0.22	1 / 14	hsa-miR-1282
14	0.22	2 / 50	hsa-miR-1285
15	0.22	2 / 50	hsa-miR-187

Rank	p-value	#in/all	Geneset
1	0.13	0 / 13	Alternative lengthening of telomeres
2	1	0 / 27	Nabeta_n1_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	

BP Rank	p-value	#in/all	Geneset
1	9e-06	5 / 17	regulation of long-term neuronal synaptic plasticity
2	5e-04	5 / 41	heterophilic cell-cell adhesion via plasma membrane cell adhesion molecules
3	1e-03	9 / 145	response to stimulus
4	1e-03	3 / 13	striated muscle cell differentiation
5	2e-03	4 / 31	adherens junction organization
6	2e-03	4 / 32	excretion
7	4e-03	3 / 18	calcium-dependent cell-cell adhesion via plasma membrane cell adhesion m
8	4e-03	4 / 38	detection of chemical stimulus involved in sensory perception of smell
9	4e-03	4 / 38	positive regulation of insulin secretion
10	6e-03	3 / 21	potassium ion import
11	8e-03	3 / 23	leukocyte cell-cell adhesion
12	8e-03	17 / 500	cell adhesion
13	8e-03	6 / 99	hemophilic cell adhesion via plasma membrane adhesion molecules
14	9e-03	3 / 24	positive regulation of blood vessel diameter
15	1e-02	19 / 595	G-protein coupled receptor signaling pathway

Chr Rank	p-value	#in/all	Geneset
1	0.02	13 / 369	Chr 20
2	0.04	11 / 333	Chr 22
3	0.05	11 / 311	Chr 11
4	0.06	20 / 776	Chr 17
5	0.27	12 / 548	Chr 16
6	0.31	17 / 833	Chr 19
7	0.52	15 / 832	Chr 2
8	0.52	1 / 41	Chr Y
9	0.53	12 / 669	Chr 6
10	0.64	3 / 184	Chr 18
11	0.65	8 / 492	Chr 9
12	0.66	9 / 556	Chr X
13	0.71	11 / 300	Chr 12
14	0.71	2 / 139	Chr 21
15	0.77	7 / 490	Chr 10

Rank	p-value	#in/all	Geneset
1	0.02	4 / 62	GIEZELT_GBM_STS_down_VS_LTS
2	0.03	3 / 37	Noushmehr_Pron_GCIMP_hypermeth_DN
3	0.07	12 / 414	Hopp_Sturm_GBM_Epi3_A_adult_fetus_UP_G34_DN
4	0.07	12 / 421	Down_b
5	0.12	2 / 23	Sturm_GBM_Meth_overexpression_F_IDH_UP
6	0.12	1 / 7	Sturm_GBM_Meth_overexpression_C_G34_UP
7	0.12	3 / 699	Hopp_Sturm_GBM_Epi3_D1_IDH_UP_adult_fetus_DN
8	0.13	6 / 191	Scov_0_5_Sturm_C2_RTK_I_PDGFR_A_DN
9	0.13	11 / 423	Down_a
10	0.13	3 / 16	Weller_LGG_A_vs_O_UP
11	0.16	1 / 10	Phillips_MES_up_vs_Prolif & PN
12	0.16	1 / 10	WILLSCHER_GBM_LTSwt_proteomics-G_UP
13	0.17	5 / 163	Scov_0_999_Sturm_E1_IDH_DN
14	0.18	1 / 11	WILLSCHER_GBM_Verhaak-PN (mut&wt)_up (l)
15	0.19	2 / 45	OL vs_MOG-OL

Rank	p-value	#in/all	Geneset
1	0.02	2 / 16	Angelova Immune-metagenes-eosinophil
2	0.05	1 / 3	Angelova_CRC_MHC_class_I
3	0.06	2 / 23	Angelova Immune-metagenes-Treg
4	0.07	1 / 4	Angelova_CRC_MHC_class_II
5	0.13	1 / 8	Immunity_HLA-class-II
6	0.14	1 / 12	Angelova Immune-metagenes-NK56_dim
7	0.24	1 / 15	Angelova Immune-metagenes-NK
8	0.29	1 / 19	Angelova Immune-metagenes-IDC
9	0.34	1 / 23	Angelova Immune-metagenes-Th2
10	0.41	1 / 29	Angelova Immune-metagenes-Th1
11	0.53	1 / 42	Angelova Immune-metagenes-TGD
12	0.55	1 / 42	Angelova Immune-metagenes-MDSC
13	1.00	0 / 13	Angelova Immune-metagenes-activated B-cells
14	1.00	0 / 26	Angelova Immune-metagenes-activated CD4
15	1.00	0 / 19	Angelova Immune-metagenes-activated CD8

Rank	p-value	#in/all	Geneset
1	0.03	4 / 64	Harbst_melanoma_lowgrade_up
2	0.10	1 / 6	Joensuu_Melanoma_high Immune response subtype
3	0.14	2 / 37	Hugo_melanoma-alm-MET_DN
4	0.15	2 / 39	Tirosh_melanoma_specific_genes
5	0.36	5 / 222	Gerber_wt/wt_melanoma-cells-SpotF
6	0.49	4 / 204	Landsberg_dedifferentiation_up
7	0.52	1 / 41	Tirosh_top50_correlated_genes_PC3
8	0.61	4 / 236	Gerber_wt/wt_groupP-specific
9	0.63	2 / 119	TCGA_melanoma_MITF_low
10	0.69	1 / 65	Harbst_melanoma_highgrade_up
11	0.74	1 / 75	Tirosh_Endothelial-cell_specific_genes-melanoma
12	0.77	1 / 81	Tirosh_Genes_in_the MITF program
13	0.78	3 / 230	Gerber_wt/wt_melanoma-cells-SpotC
14	0.78	1 / 85	Tirosh_AXL-signature
15	0.82	3 / 249	Gerber_wt/wt_melanoma-cells-SpotE

Rank	p-value	#in/all	Geneset
1	0.03	4 / 68	Burnham_sep_vs_con_UP
2	0.05	3 / 48	Burnham_viral_DN
3	0.13	3 / 71	Burnham_cap_ip_vs_con_UP
4	0.14	2 / 37	Sweeney_viral_up
5	0.24	2 / 52	Burnham_day1_vs_5_DN
6	0.27	2 / 57	Burnham_viral_UP
7	0.28	1 / 18	SciCluna_UP
8	0.37	3 / 122	Terre_IMS_influenza_meta_signature
9	0.40	4 / 140	Terre_MSV_multiple_respiratory_viruses_dn
10	0.43	3 / 135	Terre_MSV_multiple_respiratory_viruses_up
11	0.52	1 / 41	SciCluna_DN
12	0.58	1 / 48	Burnham_cap_fp_vs_con_DN
13	0.62	1 / 54	Burnham_timecourse
14	0.64	4 / 56	Burnham_sep_vs_con_DN
15	1.00	0 / 57	Burnham_day1_vs_5_UP

Rank	p-value	#in/all	Geneset
1	0.02	30 / 1148	HEBENSTREIT_low expression TF
2	0.18	13 / 549	ICGC_Atl3_targets
3	0.23	46 / 2321	ICGC_Rad21_targets
4	0.35	37 / 1941	ICGC_Bcl3_targets
5	0.36	10 / 485	ICGC_NrsfPor2_targets
6	0.57	18 / 1032	ICGC_Ustf1_targets
7	0.65	59 / 3435	ICGC_Ebfc137065_targets
8	0.71	54 / 3213	ICGC_Pu1_targets
9	0.75	22 / 1387	HEBENSTREIT_high expression TF
10	0.75	17 / 1089	ICGC_Est1_targets
11	0.81	27 / 1499	ICGC_Cetpbps50_targets
12	0.87	66 / 4131	ICGC_Tcf3_targets
13	0.88	14 / 1025	ICGC_NrsfPcr1_targets
14	0.91	67 / 4264	ICGC_Pax5_targets
15	0.91	23 / 1636	ICGC_Bcl11_targets

Rank	p-value	#in/all	Geneset
1	0.2	1 / 12	HLA2_signature
2	0.2	1 / 14	BENTINKI_cas.6
3	0.3	1 / 20	PanCan_ChromMod_geneset_nanostring
4	0.3	3 / 113	PanCan_Driver_Gene_geneset_nanostring
5	0.4	2 / 72	PanCan_Wnt_geneset_nanostring
6	0.4	1 / 32	KUIJPER_MM_good survival
7	0.5	2 / 96	PanCan_TXMRReg_geneset_nanostring
8	0.6	1 / 47	PanCan_TGF-B_geneset_nanostring
9	0.6	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
10	0.6	0 / 14	LIU_PROSTATE_CANCER_DN
11	0.7	2 / 134	PanCan_RAS_geneset_nanostring
12	0.8	1 / 80	PanCan_JAK-ST1_geneset_nanostring
13	0.8	2 / 187	PanCan_P13K_geneset_nanostring
14	0.9	5 / 409	Lembcke_Normal vs Adenoma
15	0.9	0 / 14	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP

Rank	p-value	#in/all	Geneset
1	4e-07	102 / 3734	Tcells peripheral blood_13_ReprPC
2	9e-07	89 / 3150	monocytes peripheral blood_13_ReprPC
3	3e-06	93 / 3724	Tcells peripheral blood_12_EnhBiv
4	1e-05	88 / 3272	monocytes peripheral blood_14_ReprPCWk
5	1e-05	69 / 2374	9_ReprPCWk_Fibroblasts
6	6e-05	58 / 1984	10_ReprPC_Melanocytes
7	7e-05	74 / 2747	Bcells peripheral blood_12_EnhBiv
8	2e-04	61 / 2184	monocytes peripheral blood_12_EnhBiv
9	2e-04	69 / 2602	natural killer cells peripheral blood_12_EnhBiv
10	3e-04	95 / 3918	Tcells peripheral blood_14_ReprPCWk
11	3e-04	60 / 2203	EnhA_Colon
12	4e-04	48 / 1649	13_ReprPC_ESC_Mesoderm
13	4e-04	64 / 2405	Bcells peripheral blood_13_ReprPC
14	4e-04	49 / 1700	Bcells peripheral blood_11_BivFink
15	4e-04	76 / 3001	Bcells peripheral blood_14_ReprPCWk

Rank	p-value	#in/all	Geneset
1	1e-04	6 / 44	REACTOME_CELL_CELL_JUNCTION_ORGANIZATION
2	1e-04	7 / 63	REACTOME_CELL_CELL_JUNCTION_ORGANIZATION
3	4e-04	8 / 99	REACTOME_CELL_CELL_COMMUNICATION
4	5e-04	35 / 1092	REACTOME_CELL_CELL_COMMUNICATION
5	6e-04	4 / 22	REACTOME_ADHERENS_JUNCTIONS_INTERACTIONS
6	7e-04	33 / 1029	DODD_NASOPHARYNGEAL_CARCINOMA_UP
7	1e-03	3 / 13	KIM_RESPONSE_TO_TSA_AND_DECITABINE_DN
8	3e-03	4 / 33	FIGUEROA_AML_METHYLATION_CLUSTER_5

Correlation Cluster

Spot Summary: T

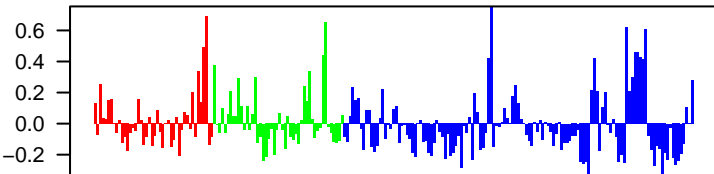
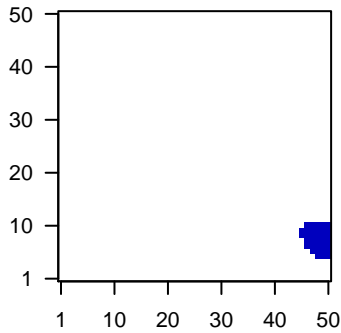
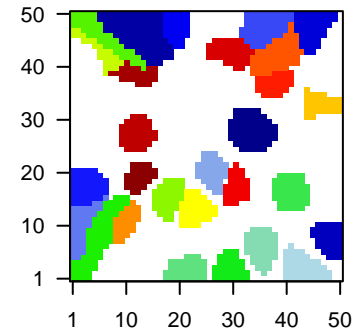
metagenes = 34
genes = 590

<r> metagenes = 0.95
<r> genes = 0.32
beta: r2= 5.7 / log p= -Inf

samples with spot = 39 (17.6 %)
mBL : 8 (18.2 %)
intermediate : 9 (18.8 %)
non-mBL : 22 (17.1 %)

Overview Map

Spot

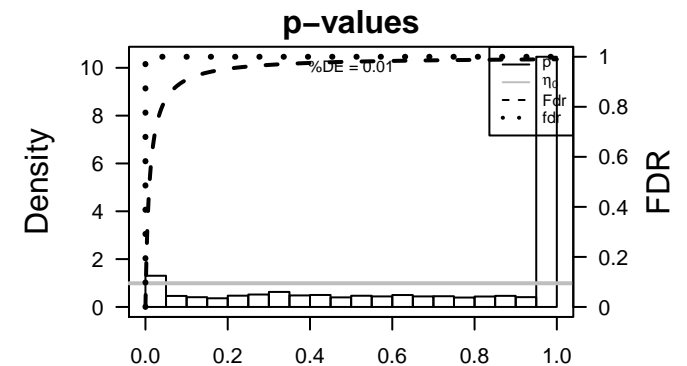


Spot Genelist

Rank	ID	max e	r	min e	Description
1	216766_at	2.26	-0.64	0.68	
2	222357_at	2.23	-0.66	0.62	ZBTB20 zinc finger and BTB domain containing 20 [Source:HGNC Syr
3	215200_x_at	2.17	-1.11	0.57	
4	222073_at	2.16	-0.87	0.38	COL4A3 collagen type IV alpha 3 chain [Source:HGNC Symbol;Acc:Hi
5	214753_at	2.14	-1.23	0.74	
6	212225_at	2.11	-0.84	0.46	EIF1 eukaryotic translation initiation factor 1 [Source:HGNC Symbc
7	207492_at	2.1	-1.01	0.76	
8	205316_at	2.09	-0.97	0.56	SLC15A2solute carrier family 15 member 2 [Source:HGNC Symbol;Acc
9	220918_at	2.03	-0.81	0.79	
10	207078_at	1.96	-0.94	0.74	MED6 mediator complex subunit 6 [Source:HGNC Symbol;Acc:HGN
11	215206_at	1.96	-0.76	0.67	
12	208268_at	1.89	-0.91	0.52	ADAM28 ADAM metallopeptidase domain 28 [Source:HGNC Symbol;A
13	215392_at	1.89	-0.68	0.78	
14	208195_at	1.84	-1.07	0.36	TTN titin [Source:HGNC Symbol;Acc:HGNC:12403]
15	222375_at	1.83	-0.72	0.69	
16	220940_at	1.83	-1.2	0.76	
17	215164_at	1.82	-1.12	0.57	
18	213931_at	1.82	-1.03	0.39	ID2 inhibitor of DNA binding 2 [Source:HGNC Symbol;Acc:HGNC
19	215768_at	1.81	-0.79	0.43	
20	217534_at	1.8	-0.88	0.76	FAM49B family with sequence similarity 49 member B [Source:HGNC :

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	4e-42	124 / 1174	Colon LaPointe_mucosa-position_kmeans_E_transverse colon_UP_transverse c
2	9e-38	52 / 188	Refer Chaussabel_3_8_Enzymes
3	1e-28	220 / 4261	Lymp HOPP_Txn_transition
4	9e-26	44 / 218	Refer WIRTH_pre+post GC B-cells
5	1e-23	247 / 5529	Lymp HOPP_Txn_elongation
6	2e-20	57 / 492	Colon LaPointe_mucosa-position_kmeans_C_cecum colon_ascending colon_tra
7	5e-20	15 / 20	Refer Chaussabel_2_7_Unknown function
8	8e-16	26 / 127	GSE/ GINESTIER_BREAST_CANCER_20Q13_AMPLIFICATION_DN
9	1e-14	18 / 59	Gliom WILLSCHER_GBM_Verhaak-PNwt & MES_up
10	6e-14	7 / 14	Cancr LIU_COMMON_CANCER_GENES
11	6e-14	7 / 14	Cancr LIU_COMMON_CANCER_GENES
12	4e-12	30 / 239	GSE/ GINESTIER_BREAST_CANCER_ZNF217_AMPLIFIED_DN
13	8e-12	23 / 143	GSE/ LEE_DIFFERENTIATING_T_LYMPHOCYTE
14	5e-11	59 / 852	MF nucleic acid binding
15	2e-10	30 / 281	BP mRNA processing
16	5e-10	22 / 159	GSE/ JISON_SICKLE_CELL_DISEASE_DN
17	3e-09	17 / 102	Lymp ROSLOWSKI_blue total
18	3e-09	219 / 5908	Lymp HOPP_Active_promoter
19	4e-09	84 / 1602	GSE/ BLALOCK_ALZHEIMERS_DISEASE_UP
20	5e-09	67 / 1161	MF RNA binding
21	5e-09	11 / 39	GSE/ BILBAN_B_CLL_LPL_DN
22	6e-09	8 / 17	GSE/ SPIRA_SMOKERS_LUNG_CANCER_DN
23	7e-09	25 / 233	BP RNA splicing
24	2e-08	147 / 3564	TF ICGC_Taf1_targets
25	3e-08	42 / 600	GSE/ RODRIGUES_THYROID_CARCIOMA_POORLY_DIFFERENTIATED_DN
26	3e-08	15 / 92	GSE/ HOEBEKE_LYMPHOID_STEM_CELL_UP
27	4e-08	18 / 136	GSE/ REACTOME_MRNA_PROCESSING
28	6e-08	176 / 4579	CC nucleus
29	7e-08	8 / 22	Refer Chaussabel_1_6_Signaling molecules
30	1e-07	35 / 477	GSE/ NAKAMURA_TUMOR_ZONE_PERIPHERAL_VS_CENTRAL_DN
31	2e-07	19 / 165	GSE/ THUM_SYSTOLIC_HEART_FAILURE_DN
32	2e-07	53 / 906	Lymp SPANG_BCR_DN
33	2e-07	16 / 120	GSE/ REACTOME_PROCESSING_OF_CAPPED_INTRON_CONTAINING_PRE
34	2e-07	68 / 1312	GSE/ PUJANA_ATM_PCC_NETWORK
35	3e-07	197 / 5404	Lymp HOPP_Strong_enhancer
36	3e-07	20 / 191	GSE/ WANG_CLIM2_TARGETS_UP
37	4e-07	45 / 730	GSE/ ONKEN_UVEAL_MELANOMA_UP
38	4e-07	129 / 3150	TF ICGC_Creb1_targets
39	6e-07	19 / 179	Pneui Terre_MSV_multiple_respiratory_viruses_dn
40	9e-07	12 / 75	GSE/ LAIHO_COLORECTAL_CANCER_SERRATED_DN



Rank	p-value	#in/all	Geneset
1	0.0	1/ 92	HORVATH_aging_genes_meth_DOWN
2	1.0	0/ 107	HORVATH_aging_genes_meth_UP
3	1.0	0/ 47	TSCHEUNDORFF_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	

Rank	p-value	#in/all	Geneset
1	6e-08	176/ 4579	nucleus
2	4e-06	25/ 326	nuclear speck
3	2e-04	98/ 2541	nucleoplasm
4	9e-04	6/ 41	cytosolic large ribosomal subunit
5	9e-04	21/ 354	centrosome
6	2e-03	9/ 101	kinetochore
7	3e-03	10/ 128	spliceosomal complex
8	3e-03	16/ 266	intracellular ribonucleoprotein complex
9	4e-03	6/ 54	axosome
10	9e-03	11/ 174	cilium
11	1e-02	3/ 18	cytoplasmic dynein complex
12	2e-02	9/ 139	ribosome
13	2e-02	8/ 118	chromosome, centromeric region
14	2e-02	6/ 77	condensed chromosome kinetochore
15	3e-02	2/ 10	azurophil granule

Rank	p-value	#in/all	Geneset
1	4e-42	124/ 1174	LaPointe_mucosa-position_kmeans_E_transverse_colon_UP_transverse_colo
2	2e-20	57/ 492	LaPointe_mucosa-position_kmeans_C_cecum_colon_ascending_colon_trans
3	2e-06	48/ 848	LaPointe_mucosa-position_kmeans_O_transverse_colon_UP
4	5e-04	208/ 6368	LaPointe_mucosa-position_kmeans_F_cecum_colon_transverse_colon_UP_
5	1e-03	39/ 854	LaPointe_mucosa-position_kmeans_A_ascending_colon_UP_
6	1e-03	5/ 31	Marisa_CRC_cluster-c
7	4e-03	3/ 12	Juehling_HNPCC-mutated-in-4
8	9e-03	64/ 1729	LaPointe_mucosa-position_kmeans_G_cecum_colon_ascending_colon_UP_t
9	1e-02	24/ 532	LaPointe_mucosa-position_kmeans_B_ascending_colon_transverse_colon_UP
10	3e-02	43/ 1166	LaPointe_mucosa-position_kmeans_K_transverse_colon_UP_cecum_colon_a
11	6e-02	2/ 14	TCGA_Mutated-in-CRC_non-hypermethylated
12	6e-02	2/ 14	Hewish_dMMR-secondary-mutations_DNA-repair
13	6e-02	35/ 958	LaPointe_mucosa-position_kmeans_D_transverse_colon_UP_
14	7e-02	2/ 16	Vilar_mutated-in-CRC-Camp
15	7e-02	2/ 16	Vilar_non-hypermethylated-in-CRC

Rank	p-value	#in/all	Geneset
1	0.1	8/ 173	HALLMARK_MITOTIC_SPINDLE
2	0.2	3/ 51	HALLMARK_TGF_BETA_SIGNALING
3	0.3	7/ 193	HALLMARK_HEME_METABOLISM
4	0.3	7/ 195	HALLMARK_G2M_CHECKPOINT
5	0.3	5/ 133	HALLMARK_DNA_REPAIR
6	0.4	6/ 144	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY
7	0.4	6/ 187	HALLMARK_E2F_TARGETS
8	0.4	6/ 190	HALLMARK_MYC_TARGETS_V1
9	0.5	3/ 97	HALLMARK_BILE_ACID_METABOLISM
10	0.6	5/ 188	HALLMARK_HYPOXIA
11	0.6	1/ 34	HALLMARK_APICAL_SURFACE
12	0.6	1/ 34	HALLMARK_ANGIOGENESIS
13	0.6	1/ 35	HALLMARK_HEDGEHOG_SIGNALING
14	0.6	5/ 194	HALLMARK_KRAS_SIGNALING_UP
15	0.7	3/ 122	HALLMARK_SPERMATOGENESIS

Rank	p-value	#in/all	Geneset
1	1e-28	220/ 4261	HOPP_Txn_transition
2	1e-23	247/ 5529	HOPP_Txn_elongation
3	3e-09	17/ 102	ROSLOWSKI_blue_total
4	3e-09	219/ 5908	HOPP_Active_promoter
5	2e-07	53/ 906	SPANG_BCR_DN
6	3e-07	197/ 5404	HOPP_Strong_enhancer
7	6e-03	8/ 99	Sha_BL_UP
8	6e-03	5/ 46	Monti_BCR_cluster
9	1e-02	2/ 6	MASCOUE_mBL_UP
10	1e-02	2/ 7	Shaknovich_ABC_hypo_meth
11	3e-02	176/ 5682	HOPP_Weak_promoter
12	6e-02	2/ 15	BENTINK_mBL_UP
13	6e-02	2/ 15	DIE_BL_Inter
14	8e-02	34/ 955	SPANG_BCR_UP
15	8e-02	60/ 1814	HOPP_Repetitive

Rank	p-value	#in/all	Geneset
1	1e-05	13/ 111	hsa-miR-656
2	5e-05	8/ 49	hsa-miR-330-5p
3	9e-05	24/ 363	hsa-miR-195
4	1e-04	24/ 378	hsa-miR-186-5p
5	3e-04	17/ 232	hsa-miR-186
6	3e-04	21/ 324	hsa-miR-497
7	5e-04	18/ 267	hsa-miR-142-5p
8	9e-04	21/ 350	hsa-miR-424
9	1e-03	8/ 78	hsa-miR-186-5p
10	1e-03	6/ 44	hsa-miR-455-5p
11	1e-03	21/ 369	hsa-miR-15b
12	2e-03	14/ 205	hsa-miR-548b
13	2e-03	5/ 33	hsa-miR-654-3p
14	3e-03	9/ 105	hsa-miR-335
15	3e-03	19/ 336	hsa-miR-519d

Rank	p-value	#in/all	Geneset
1	0.5	1/ 27	Nabetani_alt_len_telomeres_genes_ks
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	

Rank	p-value	#in/all	Geneset
1	2e-10	30/ 281	mRNA processing
2	7e-09	25/ 233	RNA splicing
3	1e-05	18/ 198	mRNA splicing, via spliceosome
4	4e-05	11/ 90	RNA processing
5	2e-04	6/ 31	regulation of alternative mRNA splicing, via spliceosome
6	3e-04	7/ 47	mRNA 3'-end processing
7	3e-04	4/ 13	alternative mRNA splicing, via spliceosome
8	4e-04	7/ 49	RNA export from nucleus
9	5e-04	9/ 83	viral transcription
10	6e-04	4/ 15	mRNA splice site selection
11	8e-04	67/ 1655	transcription, DNA-templated
12	7e-04	7/ 56	termination of RNA polymerase II transcription
13	1e-03	10/ 110	translational initiation
14	1e-03	4/ 17	negative regulation of mRNA splicing, via spliceosome
15	3e-03	8/ 86	mRNA export from nucleus

Rank	p-value	#in/all	Geneset
1	0.01	25/ 548	Chr 16
2	0.02	19/ 403	Chr 14
3	0.04	19/ 403	Chr 19
4	0.06	23/ 585	Chr 7
5	0.09	7/ 139	Chr 21
6	0.10	25/ 689	Chr 3
7	0.13	27/ 776	Chr 17
8	0.20	1/ 382	Chr 15
9	0.44	4/ 132	Chr 2
10	0.48	10/ 333	Chr 12
11	0.51	7/ 242	Chr 13
12	0.56	12/ 437	Chr 8
13	0.62	22/ 632	Chr 2
14	0.68	17/ 689	Chr 6
15	0.68	1/ 41	Chr Y

Rank	p-value	#in/all	Geneset
1	1e-14	18/ 59	WILLSCHER_GBM_Verhaak-PNwt & MES_up
2	7e-04	63/ 1523	Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
3	1e-03	3/ 8	WILLSCHER_GBM_LTSmut_proteomics-A_UP
4	2e-03	3/ 10	WILLSCHER_GBM_LTSmut_proteomics-B_UP
5	1e-02	51/ 3343	Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
6	5e-02	1/ 2	WILLSCHER_GBM_Verhaak-PN (mut&wt_up (L)
7	6e-02	2/ 15	Donson-chemokine/cytokine-receptors-associated with LTS in HGA
8	2e-01	1/ 10	Philips PN up vs MES & Prolif
9	3e-01	20/ 614	Sturm_GBM_Meth_overexpression_E_G34_UP
10	3e-01	1/ 11	Sturm_GBM_Meth_overexpression_G_IDB_UP
11	3e-01	3/ 66	Christensen_hypermethylated_in_grade2_astrocytoma
12	3e-01	3/ 66	GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
13	3e-01	4/ 100	WILLSCHER_GBM_proteomics_wtOnly_SpotB
14	3e-01	1/ 13	Christensen_hypomethylated_in_grade3_oligoastrocytoma
15	3e-01	2/ 43	Patel_stemness_signatures

Rank	p-value	#in/all	Geneset
1	0.1	1/ 5	Angelova Immune-metagenes-NKT
2	0.2	1/ 7	Angelova Immune-metagenes-cytotoxic_cells
3	0.2	1/ 10	Angelova Immune-metagenes-immatrophils
4	0.3	1/ 13	Angelova Immune-metagenes-neutrophils_B_cells
5	0.4	2/ 45	Angelova Immune-metagenes-MDSC
6	0.4	1/ 16	Angelova Immune-metagenes-pDC
7	0.4	1/ 18	Angelova_CRC_immunostimulators
8	0.5	1/ 23	Angelova Immune-metagenes-monocytes
9	1.0	0/ 13	Angelova Immune-metagenes-activated_B_cells
10	1.0	0/ 26	Angelova Immune-metagenes-activated_CD4
11	1.0	0/ 19	Angelova Immune-metagenes-activated_CD8
12	1.0	0/ 21	Angelova Immune-metagenes-central_memory_CD4
13	1.0	0/ 17	Angelova Immune-metagenes-central_memory_CD8
14	1.0	0/ 25	Angelova Immune-metagenes-DC
15	1.0	0/ 12	Angelova Immune-metagenes-effector_memory_CD4

Rank	p-value	#in/all	Geneset
1	0.03	3/ 24	Tirosh_B-cell specific genes-melanoma
2	0.04	5/ 68	Tirosh_housekeeping_genes
3	0.05	11/ 222	Gerber_wt/wt_melanoma-cells-SpotF
4	0.05	1/ 2	Melanoma Epi-Enzyme Cluster 6
5	0.11	10/ 230	Gerber_wt/wt_melanoma-cells-SpotC
6	0.13	2/ 23	Melanoma Epi-Enzyme Cluster 7
7	0.14	8/ 185	Tirosh_genes from malignant cells in MelT9-melanoma
8	0.17	12/ 319	Gerber_wt/wt_melanoma-cells-SpotA
9	0.27	1/ 11	Tirosh_genes shared by CD8 T-cells and malign cells in MelT9-melanoma
10	0.33	8/ 236	Gerber_wt/wt_group3-specific
11	0.36	1/ 16	Hugo_melanoma-all-LEF1_UP
12	0.38	2/ 47	Tirosh_G2M phase specific genes
13	0.48	1/ 24	Gerani_melanoma-metastasis-SpotA
14	0.65	7/ 276	Gerber_wt/wt_melanoma-cells-SpotB
15	0.66	1/ 38	Tirosh_top50 correlated genes PC1

Rank	p-value	#in/all	Geneset
1	6e-07	19/ 179	Terre_MS_V multiple_respiratory_viruses_dn
2	3e-01	2/ 41	SciCluna_DN
3	4e-01	2/ 54	Burnham_timecourse
4	1e+00	1/ 135	Terre_MS_V multiple_respiratory_viruses_up
5	1e+00	0/ 68	Burnham_sep_vs_con_UP
6	1e+00	0/ 56	Burnham_sep_vs_con_DN
7	1e+00	0/ 48	Burnham_cap_fp_vs_con_UP
8	1e+00	0/ 71	Burnham_cap_fp_vs_con_DN
9	1e+00	0/ 48	Burnham_viral_DN
10	1e+00	0/ 57	Burnham_viral_UP
11	1e+00	0/ 57	Burnham_day1_vs_5_UP
12	1e+00	0/ 52	Burnham_day1_vs_5_DN
13	1e+00	0/ 18	SciCluna_UP
14	1e+00	0/ 37	Sweeney_viral_UP
15	1e+00	0/ 33	Sweeney_viral_dn

Rank	p-value	#in/all	Geneset
1	2e-08	147/ 3564	ICGC_Taf1_targets
2	4e-07	129/ 3150	ICGC_Creb1_targets
3	4e-05	156/ 4319	ICGC_Pou2_targets
4	5e-05	140/ 3796	ICGC_Nficsc81335_targets
5	5e-05	140/ 3804	ICGC_Stat5_targets
6	6e-05	119/ 3121	ICGC_Egr1_targets
7	1e-04	148/ 4131	ICGC_Tcf3_targets
8	1e-04	137/ 3769	ICGC_Pmlsc71910_targets
9	2e-04	160/ 4602	ICGC_Elf1_targets
10	4e-04	149/ 4278	ICGC_Yy1_targets
11	4e-04	132/ 3703	ICGC_Foxm1_targets
12	6e-04	165/ 4851	ICGC_Runx3_targets
13	1e-03	64/ 1578	ICGC_GabpPcr2_targets
14	1e-03	122/ 3451	ICGC_Atf2_targets
15	1e-03	105/ 2899	ICGC_Nfatc1_targets

Rank	p-value	#in/all	Geneset
1	6e-14	7/ 14	LIU_COMMON_CANCER_GENES
2	5e-04	4/ 14	GUSTAFSON_PISK_DN
3	4e-02	2/ 12	LIU_BREAST_CANCER
4	6e-02	2/ 14	BENTINK_ras.6
5	7e-02	2/ 16	LIU_LIVER_CANCER
6	2e-01	1/ 10	GENTLES_modu5
7	3e-01	4/ 26	PanCan_TXMRSeq_geneset_nanostring
8	3e-01	1/ 12	BENTINK_e2f3.2
9	3e-01	5/ 134	PanCan_RAS_geneset_nanostring
10	3e-01	1/ 14	GENTLES_modu10
11	3e-01	1/ 14	BENTINK_myc.1
12	3e-01	1/ 14	BENTINK_src.2
13	4e-01	2/ 45	KUIPER_MM_poor_survival
14	4e-01	0/ 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
15	5e-01	0/ 15	RHODES_CANCER_META_SIGNATURE

Rank	p-value	#in/all	Geneset
1	2e-29	265/ 5766	natural killer cells peripheral blood_4_Tx
2	3e-29	260/ 5601	Thelper cells peripheral blood_4_Tx
3	1e-27	265/ 5716	Bcells_peripheral_blood_4_Tx
4	5e-27	260/ 5753	Tcells_peripheral_blood_4_Tx
5	5e-26	309/ 7833	Bcells_peripheral_blood_1_Tssa
6	5e-25	221/ 4528	T CD8+ naive cells peripheral blood_4_Tx
7	2e-24	297/ 7420	Tcells_peripheral_blood_1_Tssa
8	2e-23	317/ 8406	Bcells_peripheral_blood_2_TssaFlnk
9	3e-23	246/ 5527	Regulatory cells peripheral blood_4_Tx
10	3e-23	244/ 5456	5_Tx_Neural_Progenitor
11	5e-23	207/ 4208	Tcells_peripheral_blood_6_EnhG
12	6e-22	278/ 6839	T CD8+ naive cells peripheral blood_5_TxWk
13	1e-22	198/ 3682	natural killer cells peripheral blood_6_EnhG
14	7e-22	196/ 3938	Thelper cells peripheral blood_6_EnhG
15	1e-21	258/ 6099	HSC_4_Tx

Rank	p-value	#in/all	Geneset
1	8e-16	26/ 127	GINESTIER_BREAST_CANCER_20Q13_AMPLIFICATION_DN
2	6e-14	7/ 14	LIU_COMMON_CANCER_GENES
3	4e-12	30/ 239	GINESTIER_BREAST_CANCER_ZNF217_AMPLIFIED_DN
4	8e-12	23/ 143	LIU_DIFFERENTIATING_T_LY

Correlation Cluster

Spot Summary: U

metagenes = 32
genes = 182

<r> metagenes = 0.94
<r> genes = 0.12
beta: r2= 1.67 / log p= -Inf

samples with spot = 24 (10.9 %)
mBL : 1 (2.3 %)
intermediate : 6 (12.5 %)
non-mBL : 17 (13.2 %)

Spot Genelist

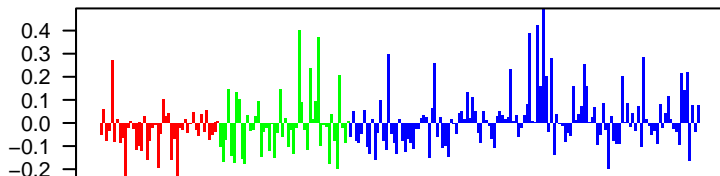
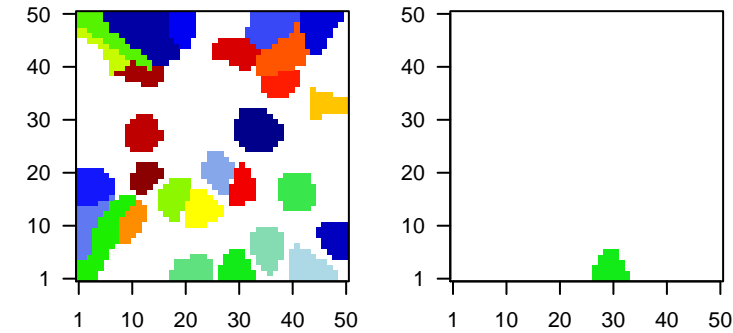
Rank	ID	max e	r	min e	Description
1	209988_s_at	3.22	-0.78	0.39	ASCL1 achaete-scute family bHLH transcription factor 1 [Source:HG
2	219463_at	3.17	-0.88	0.47	LAMP5 lysosomal associated membrane protein family member 5 [Sc
3	213768_s_at	2.71	-0.86	0.29	ASCL1 achaete-scute family bHLH transcription factor 1 [Source:HG
4	209987_s_at	2.71	-0.72	0.35	ASCL1 achaete-scute family bHLH transcription factor 1 [Source:HG
5	215118_s_at	2.52	-1.42	0.27	
6	201525_at	2.5	-0.99	0.43	APOD apolipoprotein D [Source:HGNC Symbol;Acc:HGNC:612]
7	206759_at	2.49	-0.94	0.43	FCER2 Fc fragment of IgE receptor II [Source:HGNC Symbol;Acc:HC
8	218613_at	2.4	-0.84	0.35	PSD3 pleckstrin and Sec7 domain containing 3 [Source:HGNC Syrr
9	210763_x_at	2.4	-1.08	0.18	NCR3 natural cytotoxicity triggering receptor 3 [Source:HGNC Synt
10	209695_at	2.28	-0.87	0.45	PTP4A3 protein tyrosine phosphatase type IVA, member 3 [Source:HC
11	219168_s_at	2.19	-1.1	0.46	PRR5 proline rich 5 [Source:HGNC Symbol;Acc:HGNC:31682]
12	204040_at	2.15	-0.68	0.28	RNF144A ring finger protein 144A [Source:HGNC Symbol;Acc:HGNC:2
13	210617_at	2.14	-1.06	0.35	PHEX phosphate regulating endopeptidase homolog X-linked [Sour
14	208602_x_at	2.14	-0.91	0.29	CD6 CD6 molecule [Source:HGNC Symbol;Acc:HGNC:1691]
15	206498_at	2.11	-0.99	0.28	OCA2 OCA2 melanosomal transmembrane protein [Source:HGNC S
16	214183_s_at	2.07	-0.79	0.27	TKTL1 transketolase like 1 [Source:HGNC Symbol;Acc:HGNC:1183
17	205577_at	2.01	-0.55	0.3	PYGM glycogen phosphorylase, muscle associated [Source:HGNC S
18	203355_s_at	1.96	-0.95	0.37	PSD3 pleckstrin and Sec7 domain containing 3 [Source:HGNC Syrr
19	216846_at	1.92	-0.7	0.25	
20	220146_at	1.89	-0.99	0.43	TLR7 toll like receptor 7 [Source:HGNC Symbol;Acc:HGNC:15631]

Geneset Overrepresentation

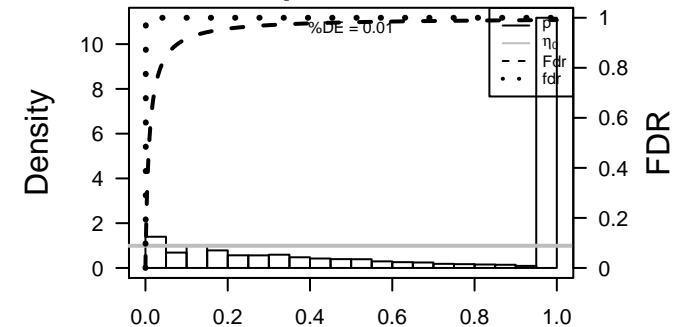
Rank	p-value	#in/all	Geneset
1	3e-12	18 / 182	Refer WIRTH_post GC B-cells
2	4e-09	16 / 218	Refer WIRTH_pre+post GC B-cells
3	6e-08	95 / 5404	Lymp HOPP_Strong_enhancer
4	3e-05	9 / 137	GSE/ VANTVEER_BREAST_CANCER_ESR1_UP
5	3e-05	12 / 249	GSE/ HUTTMANN_B CLL_POOR_SURVIVAL_UP
6	3e-05	37 / 1636	TF ICGC_Bcl11_targets
7	3e-05	35 / 1508	TF ICGC_Mef2_targets
8	6e-05	29 / 1166	Colon LaPointe_mucosa-position_kmeans_K_transverse_colon_UP_cecum_colo
9	7e-05	10 / 189	GSE/ LINDGREN_BLADDER_CANCER_CLUSTER_3_DN
10	1e-04	5 / 41	Pneur Scicluna_DN
11	1e-04	13 / 336	BP immune response
12	2e-04	11 / 251	GSE/ PEREZ_TP63_TARGETS
13	2e-04	16 / 491	GSE/ ENK_UV_RESPONSE_EPIDERMIS_DN
14	2e-04	10 / 213	GSE/ THEILGAARD_NEUTROPHIL_AT_SKIN_WOUND_DN
15	3e-04	7 / 109	BP neuron differentiation
16	3e-04	6 / 78	GSE/ RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATELY_UP
17	3e-04	20 / 741	GSE/ PEREZ_TP53_TARGETS
18	4e-04	56 / 3210	CC plasma membrane
19	4e-04	7 / 117	miRN hsa-miR-200a
20	4e-04	89 / 5908	Lymp HOPP_Active_promoter
21	4e-04	8 / 154	GSE/ MULLIGHAN_NPM1_SIGNATURE_3_DN
22	5e-04	7 / 120	GSE/ MULLIGHAN_NPM1_MUTATED_SIGNATURE_1_DN
23	5e-04	70 / 4357	Lymp HOPP_Weak_txn
24	6e-04	38 / 1941	TF ICGC_Bcl3_targets
25	7e-04	12 / 346	MF receptor binding
26	7e-04	6 / 92	BP Notch signaling pathway
27	7e-04	20 / 785	GSE/ GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_DN
28	7e-04	24 / 1029	GSE/ DODD_NASOPHARYNGEAL_CARCINOMA_UP
29	7e-04	4 / 36	BP negative regulation of cell adhesion
30	8e-04	31 / 1494	TF ICGC_Cebpbsc150_targets
31	9e-04	6 / 97	BP positive regulation of DNA binding transcription factor activity
32	9e-04	7 / 134	miRN hsa-miR-141
33	1e-03	5 / 66	BP insulin receptor signaling pathway
34	1e-03	6 / 99	GSE/ SUNG_METASTASIS_STROMA_UP
35	1e-03	9 / 220	GSE/ RUTELLA_RESPONSE_TO_HGF_DN
36	1e-03	13 / 415	GSE/ BAELDE_DIABETIC_NEPHROPATHY_DN
37	1e-03	6 / 100	Refer Chaussabel_2,8_T-cells
38	1e-03	40 / 2150	TF ICGC_Irf4_targets
39	1e-03	5 / 68	miRN hsa-miR-1265
40	1e-03	13 / 419	BP positive regulation of cell proliferation

Overview Map

Spot



p-values



Rank	p-value	#in/all	Geneset
1	0.09	2/ 107	HORVATH_aging_genes_meth_DOWN
2	0.35	2/ 107	HORVATH_aging_genes_meth_UP
3	1.00	0/ 47	TSCHEMDORFF_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	

Rank	p-value	#in/all	Geneset
1	4e-04	56/ 3210	plasma membrane
2	2e-03	5/ 77	specific granule membrane
3	2e-03	6/ 113	receptor complex
4	7e-03	2/ 11	basal part of cell
5	9e-03	2/ 12	uropod
6	1e-02	10/ 382	synapse
7	1e-02	4/ 82	transport vesicle
8	2e-02	2/ 17	T cell receptor complex
9	2e-02	3/ 48	cell periphery
10	2e-02	3/ 48	microvillus
11	2e-02	67/ 4701	cytoplasm
12	2e-02	3/ 49	RNA polymerase II transcription factor complex
13	2e-02	11/ 479	Viral_mated_CRC_Camp
14	2e-02	3/ 54	endoplasmic reticulum-Golgi intermediate compartment membrane
15	3e-02	2/ 24	sterocilium

Rank	p-value	#in/all	Geneset
1	6e-05	29/ 1166	LaPointe_mucosa-position_kmeans_K_transverse_colon_UP_cecum_colon_a
2	1e-03	15/ 539	Lembcke_TCGA_meth_kmeans_L_CIMP_H_DN
3	2e-03	25/ 1174	LaPointe_mucosa-position_kmeans_E_transverse_colon_UP_transverse_colo
4	5e-03	3/ 31	Kosinski_lower_crypt_short_list
5	1e-02	18/ 1883	LaPointe_mucosa-position_kmeans_L_transverse_colon_cecum_colon_DN
6	3e-02	11/ 492	LaPointe_mucosa-position_kmeans_C_cecum_colon_ascending_colon_trans
7	1e-01	6/ 278	Lembcke_TCGA_meth_kmeans_H_CIMP_L_UP_CIMP_H_DN
8	1e-01	4/ 164	Lembcke_TCGA_meth_kmeans_B_Cluster4_DN
9	1e-01	12/ 738	Lembcke_TCGA_expr_kmeans_N_CIMP_H_DN
10	2e-01	1/ 16	Vilar_muted_CRC_Camp
11	2e-01	15/ 1001	LaPointe_mucosa-position_kmeans_H_cecum_colon_ascending_colon_UP_
12	2e-01	2/ 72	Ang_CRC_CIMP_H_vs_L_hyper
13	2e-01	1/ 20	Kosinski_top_crypt_short_list
14	2e-01	6/ 349	Lembcke_TCGA_meth_kmeans_F_CIMP_H_UP_
15	2e-01	2/ 77	Ang_CRC_Hypermethylated

Rank	p-value	#in/all	Geneset
1	0.007	7/ 193	HALLMARK_ESTROGEN_RESPONSE_LATE
2	0.007	7/ 194	HALLMARK_ESTROGEN_RESPONSE_EARLY
3	0.007	7/ 194	HALLMARK_MYOGENESIS
4	0.009	3/ 38	HALLMARK_WNT_BETA_CATENIN_SIGNALING
5	0.022	6/ 188	HALLMARK_HYPOXIA
6	0.026	6/ 191	HALLMARK_P53_PATHWAY
7	0.024	9/ 141	HALLMARK_UV_RESPONSE_DN
8	0.051	5/ 174	HALLMARK_APICAL_JUNCTION
9	0.072	5/ 193	HALLMARK_HEME_METABOLISM
10	0.101	3/ 197	HALLMARK_PEROXISOME
11	0.158	4/ 178	HALLMARK_COPPLEMENT
12	0.158	4/ 182	HALLMARK_GLYCOLYSIS
13	0.169	4/ 187	HALLMARK_INFAMMATORY_RESPONSE
14	0.249	3/ 150	HALLMARK_APOPTOSIS
15	0.286	1/ 29	HALLMARK_NOTCH_SIGNALING

Rank	p-value	#in/all	Geneset
1	6e-08	95/ 5404	HOPP_Strong_enhancer
2	4e-04	99/ 5908	HOPP_Active_promoter
3	5e-04	70/ 4357	HOPP_Weak_txn
4	2e-03	84/ 5682	HOPP_Weak_promoter
5	6e-03	4/ 62	Monti_Host_response_cluster
6	6e-03	3/ 33	Subero_T-PLL_hypo_meth
7	6e-03	3/ 33	Care_Extended_T-cell
8	1e-02	2/ 14	Subero_B-ALL_hypo_meth
9	1e-02	8/ 263	SPANG_CD40_hrs UP
10	2e-02	7/ 234	Hopp_Lymphoma_Epi1_no_zentr_6_MCL_DN
11	4e-02	2/ 26	DAVE_Immune_response_1
12	4e-02	75/ 5529	HOPP_Txn_elongation
13	4e-02	8/ 36	Hopp_Lymphoma_Epi2_with_zentr_i_B_cell_DN
14	4e-02	63/ 4559	HOPP_Weak_enhancer
15	5e-02	3/ 70	Subero_FL_hyper_meth

Rank	p-value	#in/all	Geneset
1	4e-04	7/ 117	hsa-miR-200a
2	9e-04	7/ 134	hsa-miR-141
3	1e-03	5/ 68	hsa-miR-1265
4	2e-03	hsa-miR-421	
5	2e-03	6/ 115	hsa-miR-138
6	8e-03	5/ 106	hsa-miR-320d
7	9e-03	6/ 154	hsa-miR-944
8	1e-02	5/ 115	hsa-miR-409-3p
9	1e-02	5/ 117	hsa-miR-320f
10	1e-02	6/ 170	hsa-miR-548m
11	2e-02	3/ 46	hsa-miR-193a-3p
12	2e-02	5/ 128	hsa-miR-583
13	2e-02	4/ 85	hsa-miR-499-5p
14	2e-02	10/ 405	hsa-miR-107
15	2e-02	5/ 133	hsa-miR-320b

Rank	p-value	#in/all	Geneset
1	1	0/ 13	Alternative lengthening of telomeres
2	1	0/ 27	Nabotani_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	

Rank	p-value	#in/all	Geneset
1	1e-04	13/ 336	immune response
2	3e-04	7/ 109	neuron differentiation
3	7e-04	6/ 92	Notch signaling pathway
4	7e-04	4/ 36	negative regulation of cell adhesion
5	9e-04	6/ 97	positive regulation of DNA binding transcription factor activity
6	1e-03	5/ 66	insulin receptor signaling pathway
7	1e-03	13/ 419	positive regulation of cell proliferation
8	1e-03	3/ 19	regulation of protein binding
9	1e-03	3/ 20	regulation of axonogenesis
10	2e-03	4/ 46	peptidyl-tyrosine autophosphorylation
11	2e-03	3/ 22	positive regulation of cardiac muscle cell proliferation
12	2e-03	3/ 22	positive regulation of cell proliferation
13	2e-03	3/ 22	regulation of neurogenesis
14	2e-03	16/ 621	negative regulation of transcription from RNA polymerase II promoter
15	2e-03	3/ 23	membrane depolarization

Rank	p-value	#in/all	Geneset
1	0.03	11/ 492	Chr 9
2	0.15	7/ 382	Chr 15
3	0.18	13/ 392	Chr 12
4	0.40	10/ 776	Chr 17
5	0.42	9/ 700	Chr 12
6	0.46	7/ 554	Chr 5
7	0.46	7/ 556	Chr X
8	0.48	6/ 480	Chr 4
9	0.51	8/ 689	Chr 6
10	0.51	7/ 585	Chr 7
11	0.53	3/ 242	Chr 13
12	0.62	4/ 369	Chr 20
13	0.63	9/ 633	Chr 19
14	0.65	8/ 758	Chr 11
15	0.69	4/ 403	Chr 14

Rank	p-value	#in/all	Geneset
1	0.009	3/ 38	OL vs. OPC
2	0.011	6/ 163	Scov_0.999_Sturm_E1_IDH_DN
3	0.012	8/ 268	Scov_0.001_Sturm_M2_Mesenchymal_RTK_1_PDGFRFA'_DN
4	0.023	3/ 53	Christensen_hypermethylated_in_primary_glioblastoma
5	0.124	2/ 21	Kn1deleted& downregulated in LTS
6	0.035	3/ 62	GIEZELI_GBM_STs_DN_vs_LTS
7	0.045	1/ 4	WILLSCHER_GBM_STSwT_proteomics-L_UP
8	0.046	2/ 30	KIM prognostic signature LTS vs. STS
9	0.055	2/ 33	Sturm_GBM_Meth_overexpression_F_IDH_UP
10	0.061	3/ 78	Weller_OG_A_vs_O_U1
11	0.089	1/ 8	WILLSCHER_GBM_LTsmut_proteomics-A_UP
12	0.095	2/ 45	Donson-innate immunity-associated with LTS in HGA
13	0.095	2/ 45	OL vs. MOG- OL
14	0.099	1/ 9	Donson-migration tethering and rolling-associated with LTS in HGA
15	0.160	1/ 15	VERHAAK_Pn_Brain

Rank	p-value	#in/all	Geneset
1	0.04	2/ 29	Angelova_immune-metagenes-Th1
2	0.09	8	Angelova_immune-metagenes-MDC
3	0.19	1/ 18	Angelova_CRC_immunostimulators
4	0.23	1/ 23	Angelova_immune-metagenes-Treg
5	0.31	1/ 32	Angelova_immune-metagenes-effector_memory_CD8
6	0.45	1/ 45	Angelova_immune-metagenes-MDC
7	0.54	1/ 67	Angelova_immune-metagenes-T-cells
8	1.00	0/ 13	Angelova_immune-metagenes-activated_B-cells
9	1.00	0/ 26	Angelova_immune-metagenes-activated_CD4
10	1.00	0/ 19	Angelova_immune-metagenes-activated_CD8
11	1.00	0/ 21	Angelova_immune-metagenes-central_memory_CD4
12	1.00	0/ 17	Angelova_immune-metagenes-central_memory_CD8
13	1.00	0/ 7	Angelova_immune-metagenes-cytotoxic_cells
14	1.00	0/ 25	Angelova_immune-metagenes-DC
15	1.00	0/ 12	Angelova_immune-metagenes-effector_memory_CD4

Rank	p-value	#in/all	Geneset
1	0.006	8/ 236	Gerber_w/wt_group3-specific
2	0.006	3/ 33	Tirosh_T-cell specific genes-melanoma
3	0.021	3/ 51	Tirosh_genes from CD8+ T-cells in Mel79-melanoma
4	0.028	2/ 23	Melanoma Epi-Enzyme Cluster 7
5	0.056	1/ 5	Hugo_melanoma-BRAFmut-MET_DN
6	0.087	5/ 204	Landsberg_dedifferentiation_down
7	0.089	1/ 8	Hugo_melanoma-BRAFmut-LEF1_UP
8	0.120	4/ 497	Gerber_w/wt_melanoma-cells-SpotC
9	0.127	5/ 230	Gerber_w/wt_melanoma-cells-SpotD
10	0.248	2/ 83	TCGA_melanoma_immune_high
11	0.323	4/ 249	Gerber_w/wt_melanoma-cells-SpotE
12	0.350	2/ 107	Tirosh_Exhaustion program in Mel75
13	0.473	1/ 31	Tirosh_top50 correlated genes PC3
14	0.473	3/ 222	Gerber_w/wt_melanoma-cells-SpotF
15	0.581	1/ 75	Tirosh_Endothelial-cell specific genes-melanoma

Rank	p-value	#in/all	Geneset
1	1e-04	5/ 41	Scicluna_DN
2	3e-02	3/ 56	Burnham_sep_vs_con_DN
3	1e-01	2/ 48	Burnham_cap_fp_vs_con_DN
4	3e-01	1/ 33	Sweeney_viral_dn
5	4e-01	1/ 48	Burnham_viral_DN
6	5e-01	1/ 52	Burnham_day1_vs_5_DN
7	5e-01	1/ 54	Burnham_timecourse
8	5e-01	1/ 68	Burnham_sep_vs_con_UP
9	1e-01	2/ 179	Terre_MS_V_multiple_respiratory_viruses_dn
10	9e-01	1/ 122	Terre_IMS_influenza_meta_signature
11	1e+00	0/ 71	Burnham_cap_fp_vs_con_UP
12	1e+00	0/ 57	Burnham_viral_UP
13	1e+00	0/ 57	Burnham_day1_vs_5_UP
14	1e+00	0/ 18	Scicluna_UP
15	1e+00	0/ 37	Sweeney_viral_up

Rank	p-value	#in/all	Geneset
1	3e-05	37/ 1636	ICGC_Bcl11_targets
2	3e-05	35/ 1508	ICGC_Mef2_targets
3	6e-04	38/ 1941	ICGC_Bcl3_targets
4	8e-04	31/ 1494	ICGC_Cebpbpc150_targets
5	1e-03	40/ 2150	ICGC_Irf4_targets
6	1e-03	57/ 3493	ICGC_Eb3et37065_targets
7	1e-03	59/ 3608	ICGC_Tcf12_targets
8	2e-03	52/ 3121	ICGC_Egr1_targets
9	3e-03	66/ 4264	ICGC_Pax5_targets
10	3e-03	58/ 3630	ICGC_Sp1_targets
11	4e-03	40/ 2321	ICGC_Rad21_targets
12	5e-03	65/ 4278	ICGC_Yy1_targets
13	6e-03	33/ 1848	ICGC_Pbx3_targets
14	6e-03	51/ 3213	ICGC_Pu1_targets
15	6e-03	58/ 3769	ICGC_Pmlsc71910_targets

Rank	p-value	#in/all	Geneset
1	0.009	2/ 13	GENTLES_modul18
2	0.009	3/ 96	PanCan_TxmsReg_geneset_nanostring
3	0.102	0/ 14	LIU_COMMON_CANCER_GENES
4	0.140	1/ 13	GENTLES_modul11
5	0.140	1/ 13	BENTINK_e2f3_1
6	0.141	3/ 113	PanCan_Driver_geneset_nanostring
7	0.150	1/ 14	GENTLES_mod13
8	0.150	1/ 14	GUSTAFSON_P13K_DN
9	0.169	1/ 16	LIU_LIVER_CANCER
10	0.169	1/ 16	GENTLES_modul16
11	0.188	1/ 18	PanCan_Notch_geneset_nanostring
12	0.201	2/ 72	PanCan_Wnt_geneset_nanostring
13	0.207	1/ 20	PanCan_ChromMod_geneset_nanostring
14	0.252	1/ 25	PanCan_HH_geneset_nanostring
15	0.302	5/ 317	SPANG_BCL6-index2

Rank	p-value	#in/all	Geneset
1	1e-08	82/ 4219	EnhWk1_Colon
2	2e-07	126/ 8406	Bcels_peripheral blood_2_TssAFlnk
3	2e-07	124/ 8245	Regulatory cells peripheral blood_2_TssAFlnk
4	2e-07	72/ 3682	natural killer cells peripheral blood_6_EnhG
5	4e-07	116/ 7511	Overlap_fetal_midbrain_Quies
6	7e-07	124/ 8370	natural killer cells peripheral blood_2_TssAFlnk
7	2e-06	14/ 258	T CD8+ naive cells peripheral blood_3_TxFlnk
8	2e-06	48/ 2203	EnhA_Colon
9	2e-06	78/ 4208	cells peripheral blood_6_EnhG
10	3e-06	118/ 7930	Regulatory cells peripheral blood_1_TssA
11	3e-06	109/ 7078	Bcels_peripheral blood_5_TxWk
12	4e-06	107/ 6906	3_TssF_Fibroblasts
13	4e-06	70/ 3803	6_EnhG_Fibroblasts
14	5e-06	132/ 8440	ISC_7_Enh
15	6e-06	129/ 9142	T CD8+ naive cells peripheral blood_7_Enh

Rank	p-value	#in/all	Geneset
1	3e-05	9/ 137	VANTVEER_BREAST_CANCER_ESR1_UP
2	3e-05	12/ 249	HUTTMANN_B CLL_POOR_SURVIVAL_UP
3	7e-05	10/ 189	LINDGREN_BLADDER_CANCER_CLUSTER_3_DN
4	2e-04	11/ 251	PEREZ_TP63_TARGETS
5	1e-04	16/ 493	ENK_UV_RESPONSE_EPIDERMIS_DN
6	2e-04	10/	

Correlation Cluster

Spot Summary: V

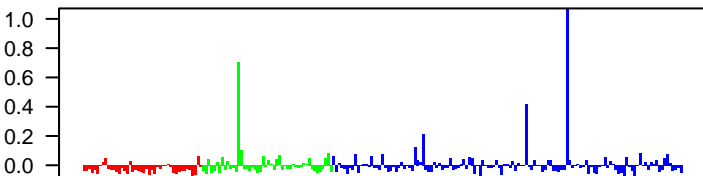
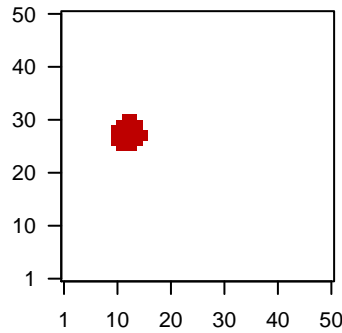
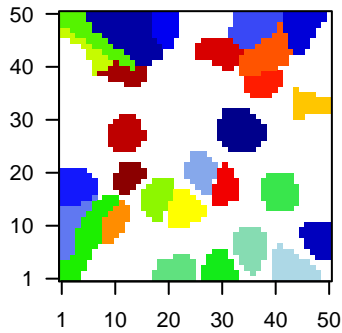
metagenes = 38
genes = 246

<r> metagenes = 0.93
<r> genes = 0.1
beta: r2= 0.82 / log p= -Inf

samples with spot = 4 (1.8 %)
intermediate : 1 (2.1 %)
non-mBL : 3 (2.3 %)

Overview Map

Spot

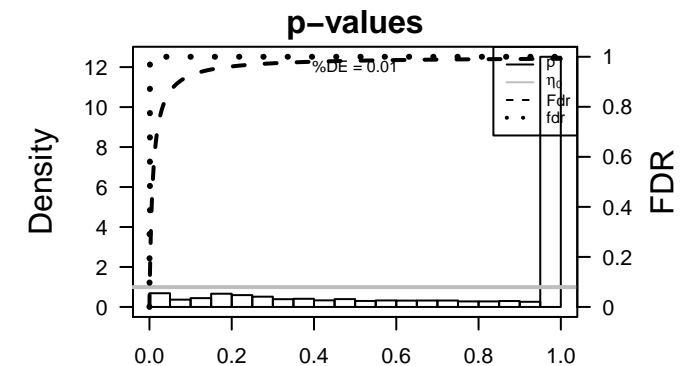


Spot Genelist

Rank	ID	max e	r	min e	Description
1	207663_x_at	3.8	-0.83	0.39	GAGE12G antigen 12J [Source:HGNC Symbol;Acc:HGNC:17778]
2	206640_x_at	3.58	-0.65	0.38	GAGE12G antigen 12J [Source:HGNC Symbol;Acc:HGNC:17778]
3	211425_x_at	3.5	-0.75	0.68	SSX family member 6, pseudogene [Source:HGNC Symbol;Acc:HGNC:17778]
4	208235_x_at	3.42	-0.72	0.31	GAGE12G antigen 12J [Source:HGNC Symbol;Acc:HGNC:17778]
5	207739_s_at	3.42	-1.01	0.39	GAGE12G antigen 12J [Source:HGNC Symbol;Acc:HGNC:17778]
6	207086_x_at	3.38	-0.68	0.38	GAGE12G antigen 12J [Source:HGNC Symbol;Acc:HGNC:17778]
7	208155_x_at	3.36	-0.82	0.38	GAGE12G antigen 12J [Source:HGNC Symbol;Acc:HGNC:17778]
8	209942_x_at	3.13	-0.71	0.59	MAGEA3MAGE family member A3 [Source:HGNC Symbol;Acc:HGNC:17778]
9	210394_x_at	3.08	-0.76	0.66	SSX family member 6, pseudogene [Source:HGNC Symbol;Acc:HGNC:17778]
10	207666_x_at	3	-0.6	0.6	SSX3 SSX family member 3 [Source:HGNC Symbol;Acc:HGNC:17778]
11	210497_x_at	3	-0.67	0.63	SSX3 SSX family member 3 [Source:HGNC Symbol;Acc:HGNC:17778]
12	214612_x_at	3	-0.72	0.61	MAGEA3MAGE family member A3 [Source:HGNC Symbol;Acc:HGNC:17778]
13	214957_at	2.96	-0.84	0.28	ACTL8 actin like 8 [Source:HGNC Symbol;Acc:HGNC:24018]
14	206626_x_at	2.85	-0.74	0.63	SSX1 SSX family member 1 [Source:HGNC Symbol;Acc:HGNC:17778]
15	207325_x_at	2.83	-0.79	0.6	MAGEA1MAGE family member A1 [Source:HGNC Symbol;Acc:HGNC:17778]
16	206834_at	2.78	-0.67	0.54	HBD hemoglobin subunit delta [Source:HGNC Symbol;Acc:HGNC:17778]
17	214254_at	2.78	-0.63	0.46	MAGEA4MAGE family member A4 [Source:HGNC Symbol;Acc:HGNC:17778]
18	217339_x_at	2.78	-0.86	0.52	CTAG1A cancer/testis antigen 1A [Source:HGNC Symbol;Acc:HGNC:17778]
19	216471_x_at	2.77	-0.78	0.6	SSX3 SSX family member 3 [Source:HGNC Symbol;Acc:HGNC:17778]
20	220062_s_at	2.72	-0.8	0.43	MAGEC2MAGE family member C2 [Source:HGNC Symbol;Acc:HGNC:17778]

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	2e-09	14 / 115	GSE/ YEGNASUBRAMANIAN_PROSTATE_CANCER
2	3e-07	12 / 119	Melar TCGA_melanoma_MITF_low
3	3e-07	26 / 556	Chr Chr X
4	9e-07	5 / 13	Immu Angelova_CRC_MSS~neointens
5	2e-06	19 / 352	Refer WIRTH_Nervous System
6	3e-06	79 / 3270	CC integral component of membrane
7	2e-05	15 / 271	GSE/ VECCHI_GASTRIC_CANCER_EARLY_DN
8	5e-05	14 / 262	GSE/ HELLER_HDAC_TARGETS_SILENCED_BY_METHYLATION_DN
9	6e-05	14 / 269	GSE/ HELLER_HDAC_TARGETS_DN
10	1e-04	3 / 7	Immu Angelova_CRC_MSI~neointens
11	2e-04	5 / 34	BP positive regulation of protein secretion
12	2e-04	3 / 8	GSE/ GALIE_TUMOR_ANGIOGENESIS
13	2e-04	17 / 412	GSE/ BOQUEST_STEM_CELL_CULTURED_VS_FRESH_UP
14	2e-04	5 / 36	GSE/ RICKMAN_HEAD_AND_NECK_CANCER_B
15	3e-04	70 / 3168	Lymph HOPP_Repressed
16	4e-04	18 / 478	GSE/ ACEVEDO_METHYLATED_IN_LIVER_CANCER_DN
17	4e-04	6 / 64	GSE/ SHAFFER_IRF4_TARGETS_IN_PLASMA_CELL_VS_MATURE_B_LYMPH
18	6e-04	7 / 95	GSE/ HELLER_SILENCED_BY_METHYLATION_DN
19	6e-04	5 / 46	GSE/ KLEIN_PRIMARY_EFFUSION_LYMPHOMA_UP
20	7e-04	8 / 126	Gliom ScoV_0.999_Sturm_E5_RTK II 'Classi' UP_RTK I 'PDGFRA' DN
21	7e-04	4 / 27	BP eye development
22	8e-04	16 / 424	GSE/ HELLER_HDAC_TARGETS_SILENCED_BY_METHYLATION_UP
23	1e-03	5 / 51	BP positive regulation of osteoblast differentiation
24	1e-03	3 / 14	BP calcium ion-regulated exocytosis of neurotransmitter
25	1e-03	3 / 14	GSE/ BIOCARTA_ERYTH_PATHWAY
26	1e-03	3 / 14	GSE/ REACTOME_PRE_NOTCH_PROCESSING_IN_GOLGI
27	1e-03	3 / 14	GSE/ MATTIOLI_MULTIPLE_MYELOMA_SUBGROUPS
28	1e-03	9 / 169	GSE/ VERHAAK_GLIOMASTOMA_PRONEURAL
29	1e-03	5 / 52	BP positive regulation of signal transduction
30	1e-03	6 / 79	BP positive regulation of peptidyl-tyrosine phosphorylation
31	1e-03	4 / 32	GSE/ ZHAN_LATE_DIFFERENTIATION_GENES_UP
32	1e-03	2 / 4	Immu Angelova_CRC_MSS~neointens
33	2e-03	6 / 83	Melar TCGA_melanoma_immune_high
34	2e-03	3 / 16	BP synaptic vesicle exocytosis
35	2e-03	10 / 216	GSE/ PASQUALUCCI_LYMPHOMA_BY_GC_STAGE_UP
36	2e-03	11 / 255	GSE/ HELLER_SILENCED_BY_METHYLATION_UP
37	2e-03	22 / 741	GSE/ PEREZ_TP53_TARGETS
38	2e-03	7 / 118	GSE/ ACEVEDO_LIVER_CANCER_WITH_H3K27ME3_DN
39	2e-03	2 / 5	GSE/ MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_1
40	2e-03	3 / 18	BP positive regulation of heart rate



Rank	p-value	#in/all	Geneset
1	0.4	2 / 92	HORVATH_aging_genes_meth_DOWN
2	0.5	2 / 107	HORVATH_aging_genes_meth_UP
3	0.5	1 / 47	TSCHEINDORFF_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	5 / 34	positive regulation of protein secretion
2	7e-04	4 / 27	eye development
3	1e-03	5 / 51	positive regulation of osteoblast differentiation
4	1e-03	3 / 14	calcium ion-regulated exocytosis of neurotransmitter
5	1e-03	5 / 52	positive regulation of signal transduction
6	1e-03	6 / 79	positive regulation of peptidyl-tyrosine phosphorylation
7	2e-03	3 / 16	synaptic vesicle exocytosis
8	2e-03	3 / 18	positive regulation of heart rate
9	3e-03	5 / 63	positive regulation of phosphatidylinositol 3-kinase signaling
10	3e-03	3 / 19	low-density lipoprotein particle clearance
11	4e-03	4 / 42	negative regulation of nucleic acid-templated transcription
12	5e-03	14 / 421	nervous system development
13	6e-03	3 / 24	endochondral ossification
14	6e-03	3 / 24	insulin secretion
15	6e-03	3 / 24	regulation of exocytosis

Rank	p-value	#in/all	Geneset
1	0.02	2 / 13	GENTLES_modul11
2	0.03	3 / 47	PanCan_TGF-B_geneset_nanostring
3	0.07	6 / 187	PanCan_P13K_geneset_nanostring
4	0.12	3 / 80	PanCan_JAK-ST_geneset_nanostring
5	0.15	4 / 134	PanCan_RAS_geneset_nanostring
6	0.15	2 / 45	KUIPER_MM_good_survival
7	0.19	4 / 147	PanCan_MAPK_geneset_nanostring
8	0.19	1 / 14	GENTLES_modul13
9	0.20	0 / 14	LIU_PROSTATE_CANCER_DN
10	0.21	1 / 15	GENTLES_modul4
11	0.39	1 / 32	KUIPER_MM_good_survival
12	0.42	1 / 36	ZHANG_MM_up
13	0.43	2 / 96	PanCan_TXmisReg_geneset_nanostring
14	0.45	8 / 480	Lembcke_Colonc_Inflammation
15	0.55	0 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN

CC Rank	p-value	#in/all	Geneset
1	3e-06	79 / 3270	integral component of membrane
2	4e-03	66 / 3210	plasma membrane
3	4e-03	100 / 5339	membrane
4	6e-03	3 / 25	presynaptic active zone
5	7e-03	28 / 1128	integral component of plasma membrane
6	8e-03	26 / 1035	endoplasmic reticulum
7	1e-02	2 / 12	trans-Golgi network transport vesicle
8	2e-02	4 / 65	collagen trimer
9	2e-02	2 / 15	pericentriolar material
10	4e-02	3 / 51	presynaptic membrane
11	5e-02	2 / 24	endoplasmic reticulum quality control compartment
12	6e-02	2 / 25	vesicle membrane
13	6e-02	16 / 683	endoplasmic reticulum membrane
14	7e-02	6 / 188	endosome membrane
15	7e-02	3 / 63	platelet alpha granule lumen

Chr Rank	p-value	#in/all	Geneset
1	3e-07	26 / 556	Chr X
2	8e-02	7 / 242	Chr 13
3	1e-03	2 / 41	Chr 3
4	3e-01	8 / 403	Chr 14
5	3e-01	11 / 585	Chr 7
6	4e-01	12 / 689	Chr 3
7	4e-01	7 / 382	Chr 15
8	5e-01	21 / 1325	Chr 1
9	9e-01	6 / 383	Chr 20
10	5e-01	13 / 833	Chr 19
11	6e-01	7 / 480	Chr 4
12	6e-01	2 / 139	Chr 21
13	7e-01	6 / 307	Chr 8
14	7e-01	11 / 832	Chr 2
15	7e-01	7 / 554	Chr 5

Rank	p-value	#in/all	Geneset
1	7e-10	48 / 1233	13_HetRpts_Melanocytes
2	1e-09	61 / 1833	natural killer cells peripheral blood_9_Het
3	6e-09	82 / 2393	monocytes peripheral blood_9_Het
4	7e-09	30 / 585	13_HetRpts_Fibroblasts
5	9e-09	76 / 2700	Thelper cells peripheral blood_14_ReprPCWk
6	2e-08	67 / 2272	13_HetRpts_MSC_Adipocyte
7	2e-08	55 / 1693	Tcells peripheral blood_9_Het
8	4e-08	80 / 3001	4celsis peripheral blood_14_ReprPCWk
9	1e-07	40 / 1098	12_Het_Melanocytes
10	2e-07	69 / 2515	natural killer cells peripheral blood_13_ReprPC
11	3e-07	92 / 3819	natural killer cells peripheral blood_15_Quies
12	3e-07	65 / 2338	Bcells peripheral blood_9_Het
13	6e-07	31 / 767	Overlap_fetal_midbrain_Enh
14	6e-07	76 / 2974	9_Het_ESC_Endoderm
15	7e-07	69 / 2600	HSC_14_ReprPCWk

Rank	p-value	#in/all	Geneset
1	2e-09	14 / 115	YEGNASUBRAMANIAN_PROSTATE_CANCER
2	2e-05	15 / 271	VECCI_GASTRIC_CANCER_EARLY_DN
3	5e-05	14 / 262	HELLER_HDAC_TARGETS_SILENCED_BY_METHYLATION_DN
4	6e-05	14 / 269	HELLER_HDAC_TARGETS_DN
5	2e-04	2 / 64	GALLIE_TUMOR_ANGIOGENESIS
6	2e-04	17 / 412	BOQUEST_STEM_CELL_CULTURED_VS_FRESH_UP
7	2e-04	5 / 36	RICKMAN_HEAD_AND_NECK_CANCER_B
8	4e-04	18 / 478	ACEVEDO_METHYLATED_IN_LIVER_CANCER_DN
9	4e-04	6 / 64	SHAFER_IRF4_TARGETS_IN_PLASMA_CELL_VS_MATURE_B_LYMPHO
10	6e-04	7 / 65	HELLER_SILENCED_BY_METHYLATION_DN
11	6e-04	5 / 46	KLEIN_PRIMARY EFFUSION_LYMPHOMA_UP
12	8e-04	16 / 424	HELLER_HDAC_TARGETS_SILENCED_BY_METHYLATION_UP
13	1e-03	3 / 14	BIOCARTA_ERYTH_PATHWAY
14	1e-03	3 / 14	REACTOME_PRE_NOTCH_PROCESSING_IN_GOLGI
15	1e-03	3 / 14	MATTIOLI_MULTIPLE_MYELOMA_SUBGROUPS

Rank	p-value	#in/all	Geneset
1	0.1	4 / 122	HALLMARK_SPERMATOGENESIS
2	0.1	5 / 181	HALLMARK_XENOBIOTIC_METABOLISM
3	0.2	5 / 187	HALLMARK_INFAMMATORY_RESPONSE
4	0.2	5 / 194	HALLMARK_MYOGENESIS
5	0.2	3 / 96	HALLMARK_ANDROGEN_RESPONSE
6	0.2	2 / 101	HALLMARK_APOPTOSIS
7	0.2	2 / 59	HALLMARK_CHOLESTEROL_HOMEOSTASIS
8	0.3	4 / 193	HALLMARK_ESTROGEN_RESPONSE_LATE
9	0.4	3 / 139	HALLMARK_FATTY_ACID_METABOLISM
10	0.4	1 / 29	HALLMARK_NOTCH_SIGNALING
11	0.4	2 / 97	HALLMARK_BILE_ACID_METABOLISM
12	0.4	1 / 38	HALLMARK_WNT_BETA_CATENIN_SIGNALING
13	0.5	2 / 106	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
14	0.6	3 / 193	HALLMARK_HEME_METABOLISM
15	0.6	3 / 194	HALLMARK_KRAS_SIGNALING_UP

Colon Cancer Rank	p-value	#in/all	Geneset
1	0.003	13 / 349	Lembcke_TCGA_meth_kmeans_F_CIMP_H_UP
2	0.006	115 / 6368	LaPointe_mucosa-position_kmeans_F_pecum_colon_transverse_colon_UP
3	0.024	10 / 318	Lembcke_TCGA_meth_kmeans_E_CIMP_H_UP
4	0.072	4 / 103	Marisa_CRC_cluster-5
5	0.081	18 / 84	LaPointe_mucosa-position_kmeans_A_ascending_colon_UP
6	0.113	12 / 532	LaPointe_mucosa-position_kmeans_B_ascending_colon_transverse_colon_UI
7	0.116	1 / 8	Marisa_CRC-C1
8	0.129	1 / 9	Marisa_CRC-C2
9	0.139	2 / 43	Marisa_CRC_cluster-f
10	0.171	2 / 49	Pentzik_CRC_TCGA_corr_N_msi-hn_DN
11	0.188	12 / 589	Lembcke_TCGA_expr_kmeans_E_CIMP_H_UP_Cluster4_DN
12	0.193	1 / 14	TCGA_Mutated-in-CRC_non-hypermethylated
13	0.206	1 / 15	TCGA-CRC_less-aggressive-disease-markers
14	0.215	8 / 376	Lembcke_TCGA_expr_kmeans_M_CIMP_H_DN
15	0.218	1 / 16	Vilar_mutated-in-CRC-Camp

Glioma Rank	p-value	#in/all	Geneset
1	7e-04	8 / 126	Scov_0_999_Sturm_E5_RTK_II_Classic_UP_RTK_I_PDGFR_A_DN
2	3e-03	5 / 64	Weller_LGG_A_vs_O_DOWN
3	7e-03	10 / 264	Hopp_Sturm_GBM_Epi3_no_zentr_3_RTK_II_UP_adult_fetus_K27_DN
4	1e-02	3 / 32	WIRTH_PN_subtype
5	2e-02	4 / 67	Weller_LGG_1p19del_vs-intact_UP
6	2e-02	5 / 105	WIRTH_Normal_Brain
7	4e-02	6 / 163	Scov_0_999_Sturm_E1_IDH_DN
8	6e-02	8 / 273	Hopp_Sturm_GBM_Epi3_B_adult_UP_G34_DN
9	7e-02	6 / 191	Scov_0_5_Sturm_C2_RTK_I_PDGFR_A_DN
10	8e-02	2 / 10	Shaw_responders_down_in_oligo_glioma
11	8e-02	3 / 66	Christensen_hypermethylated_in_grade2_astrocytoma
12	8e-02	7 / 246	Scov_0_001_Sturm_M1_IDH_RTK_I_PDGFR_A_DN
13	1e-01	10 / 423	Down_a
14	1e-01	4 / 121	Hopp_Sturm_GBM_Epi3_F_RTK_II_UP_adult_fetus_K27_DN
15	1e-01	1 / 9	Donson-migration_ithering_and_rolling-associated_with_LTS_in_HGA

Rank	p-value	#in/all	Geneset
1	9e-07	5 / 13	Angelova_CRC_MSS-neoantigens
2	1e-04	3 / 7	Angelova_CRC_MSI-neoantigens
3	1e-03	2 / 4	Angelova_CRC_MSS-neoantigens
4	1e-01	2 / 45	Angelova Immune-metagenes-MDSC
5	2e-01	1 / 11	Angelova Immune-metagenes-macrophages
6	2e-01	1 / 12	Angelova Immune-metagenes-NK66_dim
7	2e-01	1 / 16	Angelova Immune-metagenes-Th17
8	2e-01	1 / 18	Angelova_CRC_immunostimulators
9	3e-01	1 / 19	Angelova Immune-metagenes-activated_CD8
10	3e-01	1 / 21	Angelova Immune-metagenes-central_memory_CD4
11	4e-01	1 / 32	Angelova Immune-metagenes-effector_memory_CD8
12	1e+00	0 / 13	Angelova Immune-metagenes-activated_B-cells
13	1e+00	0 / 26	Angelova Immune-metagenes-activated_CD4
14	1e+00	0 / 17	Angelova Immune-metagenes-central_memory_CD8
15	1e+00	0 / 7	Angelova Immune-metagenes-cytotoxic_cells

Rank	p-value	#in/all	Geneset
1	0.6	1 / 62	DUMEAUX_Smoking_enriched_genes
2	0.9	1 / 150	Homuth_BMI-associated_genes_UP
3	1.0	0 / 10	DUMEAUX_Smoking_literature_genes_up
4	1.0	0 / 4	DUMEAUX_Exercise_in_non_smokers_literature_enriched_genes
5	1.0	0 / 5	DUMEAUX_Estrogen_related_in_smokers_literature_genes_up
6	1.0	0 / 3	DUMEAUX_Estrogen_related_in_non_smokers_literature_genes_up
7	1.0	0 / 7	DUMEAUX_Hormon therapy_in_non_smokers_literature_genes_up
8	1.0	0 / 9	DUMEAUX_Monocytes_in_smokers_literature_genes_up
9	1.0	0 / 16	DUMEAUX_Red_blood_cells_in_non_smokers_literature_genes_up
10	1.0	0 / 12	DUMEAUX_Women_normal_BMI_literature_genes_up
11	1.0	0 / 22	DUMEAUX_High_bmi_enriched_genes
12	1.0	0 / 22	DUMEAUX_Fasting_enriched_genes
13	1.0	0 / 210	Homuth_BMI-associated_genes_DN
14	1.0	0 / 14	Huan_blood-pressure_SBP-signature
15	1.0	0 / 13	Huan_blood-pressure_DBP-signature

Rank	p-value	#in/all	Geneset
1	0.003	3 / 20	hydrolase activity, acting on ester bonds
2	0.005	4 / 45	synixin binding
3	0.005	4 / 46	SH3/SH2 adaptor activity
4	0.006	16 / 517	calcium ion binding
5	0.006	7 / 141	growth factor activity
6	0.012	2 / 11	1-acylglycerol-3-phosphate O-acyltransferase activity
7	0.021	4 / 69	virus receptor activity
8	0.022	5 / 105	Ras_guanyl-nucleotide exchange factor activity
9	0.026	5 / 110	transferase activity, transferring acyl groups
10	0.027	2 / 17	low-density lipoprotein particle receptor binding
11	0.030	2 / 18	organic anion transmembrane transporter activity
12	0.033	2 / 19	metalloaminopeptidase activity
13	0.033	2 / 19	steroid binding
14	0.039	4 / 84	hormone activity
15	0.040	5 / 123	transporter activity

BM Rank	p-value	#in/all	Geneset
1	0.1	4 / 122	HALLMARK_SPERMATOGENESIS
2	0.1	5 / 181	HALLMARK_XENOBIOTIC_METABOLISM
3	0.2	5 / 187	HALLMARK_INFAMMATORY_RESPONSE
4	0.2	5 / 194	HALLMARK_MYOGENESIS
5	0.2	3 / 96	HALLMARK_ANDROGEN_RESPONSE
6	0.2	2 / 101	HALLMARK_APOPTOSIS
7	0.2	2 / 59	HALLMARK_CHOLESTEROL_HOMEOSTASIS
8	0.3	4 / 193	HALLMARK_ESTROGEN_RESPONSE_LATE
9	0.4	3 / 139	HALLMARK_FATTY_ACID_METABOLISM
10	0.4	1 / 29	HALLMARK_NOTCH_SIGNALING
11	0.4	2 / 97	HALLMARK_BILE_ACID_METABOLISM
12	0.4	1 / 38	HALLMARK_WNT_BETA_CATENIN_SIGNALING
13	0.5	2 / 106	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
14	0.6	3 / 193	HALLMARK_HEME_METABOLISM
15	0.6	3 / 194	HALLMARK_KRAS_SIGNALING_UP

Immunome Rank	p-value	#in/all	Geneset
1	9e-07	5 / 13	Angelova_CRC_MSS-neoantigens
2	1e-04	3 / 7	Angelova_CRC_MSI-neoantigens
3	1e-03	2 / 4	Angelova_CRC_MSS-neoantigens
4	1e-01	2 / 45	Angelova Immune-metagenes-MDSC
5	2e-01	1 / 11	Angelova Immune-metagenes-macrophages
6	2e-01	1 / 12	Angelova Immune-metagenes-NK66_dim
7	2e-01	1 / 16	Angelova Immune-metagenes-Th17
8	2e-01	1 / 18	Angelova_CRC_immunostimulators
9	3e-01	1 / 19	Angelova Immune-metagenes-activated_CD8
10	3e-01	1 / 21	Angelova Immune-metagenes-central_memory_CD4
11	4e-01	1 / 32	Angelova Immune-metagenes-effector_memory_CD8
12	1e+00	0 / 13	Angelova Immune-metagenes-activated_B-cells
13	1e+00	0 / 26	Angelova Immune-metagenes-activated_CD4
14	1e+00	0 / 17	Angelova Immune-metagenes-central_memory_CD8
15	1e+00	0 / 7	Angelova Immune-metagenes-cytotoxic_cells

Rank	p-value	#in/all	Geneset
1	3e-07	12 / 119	TCGA_melanoma_MITF_low
2	2e-03	6 / 83	TCGA_melanoma-immune_high
3	6e-02	7 / 204	Landsberg_dedifferentiation_down
4	1e-01	2 / 39	Tirosh_top50_correlated_genes_PC4
5	1e-01	1 / 10	Jonsson_Melanoma_Normal_like_subtype
6	2e-01	1 / 17	Hugo_melanoma-all-MET_UP
7	3e-01	2 / 65	Harbsl_melanoma_highgrade_up
8	3e-01	2 / 249	Gerber_wtwt_melanoma-cells-SpotE
9	4e-01	2 / 81	Tirosh_Genes_in_the_MITF_program
10	5e-01	1 / 46	Tirosh_top50_correlated_genes_PC5
11	6e-01	1 / 59	TCGA_melanoma_keratin_high
12	6e-01	1 / 64	Harbsl_melanoma_lowgrade_up
13	7e-01	3 / 290	Gerber_wtwt_melanoma-cells-SpotC
14	7e-01	1 / 75	Tirosh_Endothelial-cell_specific_genes-melanoma
15	7e-01	1 / 85	Tirosh_AXL-signature

Correlation Cluster

Spot Summary: W

metagenes = 26
genes = 227

<r> metagenes = 0.96
<r> genes = 0.24
beta: r2= 3.94 / log p= -Inf

samples with spot = 57 (25.8 %)
intermediate : 8 (16.7 %)
non-mBL : 49 (38 %)

Spot Genelist

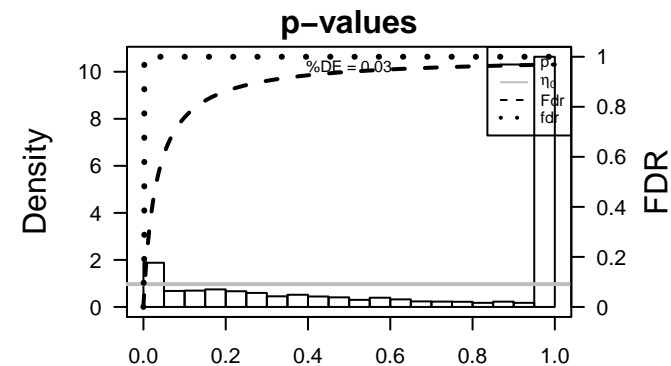
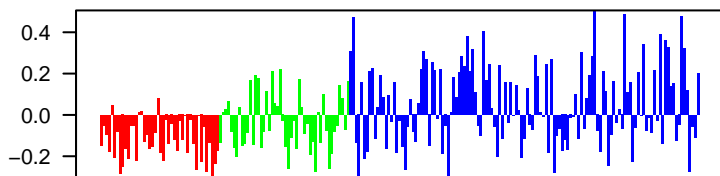
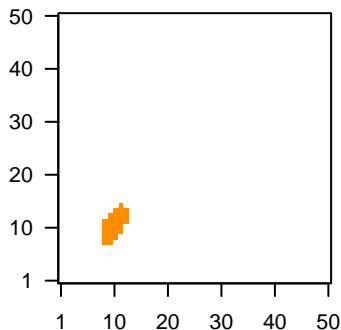
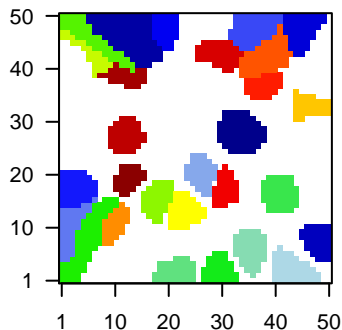
Rank	ID	max e	r	min e	Description
					Symbol
1	211861_x_at	2.6	-0.7	0.56	CD28 CD28 molecule [Source:HGNC Symbol;Acc:HGNC:1653]
2	214470_at	2.58	-1.02	0.52	KLRB1 killer cell lectin like receptor B1 [Source:HGNC Symbol;Acc:H
3	211856_x_at	2.52	-0.69	0.53	CD28 CD28 molecule [Source:HGNC Symbol;Acc:HGNC:1653]
4	210439_at	2.5	-0.93	0.55	ICOS inducible T cell costimulator [Source:HGNC Symbol;Acc:HGN
5	211395_x_at	2.46	-1.15	0.37	Fc fragment of IgG receptor IIc (gene/pseudogene) [Source:HGNC
6	204846_at	2.39	-0.88	0.51	CP ceruloplasmin [Source:HGNC Symbol;Acc:HGNC:2295]
7	214567_s_at	2.38	-1.17	0.53	XCL2 X-C motif chemokine ligand 2 [Source:HGNC Symbol;Acc:HGNC
8	206366_x_at	2.26	-1.05	0.54	XCL2 X-C motif chemokine ligand 2 [Source:HGNC Symbol;Acc:HGNC
9	211372_s_at	2.24	-1.06	0.45	IL1R2 interleukin 1 receptor type 2 [Source:HGNC Symbol;Acc:HGNC
10	213830_at	2.23	-0.76	0.48	
11	205376_at	2.19	-0.73	0.65	INPP4B inositol polyphosphate-4-phosphatase type II B [Source:HGNC
12	210992_x_at	2.15	-1.26	0.39	Fc fragment of IgG receptor IIc (gene/pseudogene) [Source:HGNC
13	216191_s_at	2.11	-0.92	0.54	T cell receptor delta constant [Source:HGNC Symbol;Acc:HGNC
14	206545_at	2.05	-0.76	0.68	CD28 CD28 molecule [Source:HGNC Symbol;Acc:HGNC:1653]
15	207509_s_at	2.04	-0.95	0.41	LAIR2 leukocyte associated immunoglobulin like receptor 2 [Source:HGNC
16	221331_x_at	2.03	-0.66	0.44	CTLA4 cytotoxic T-lymphocyte associated protein 4 [Source:HGNC
17	211209_x_at	2.03	-0.93	0.61	SH2D1A SH2 domain containing 1A [Source:HGNC Symbol;Acc:HGNC
18	209301_at	2.03	-1.21	0.31	CA2 carbonic anhydrase 2 [Source:HGNC Symbol;Acc:HGNC:137
19	206765_at	2.03	-1.12	0.47	KCNJ2 potassium voltage-gated channel subfamily J member 2 [Sou
20	210873_x_at	2.01	-0.96	0.53	APOBEC3B apolipoprotein B mRNA editing enzyme catalytic subunit 3A [

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	4e-35	60 / 589	Colon Lembcke_TCGA-expr_kmeans_E_CIMP_H_UP_Cluster4_DN
2	5e-24	35 / 265	GSE/ WALLACE_PROSTATE_CANCER_RACE_UP
3	1e-22	38 / 354	GSE/ FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_UP
4	2e-22	41 / 431	BP immune system process
5	2e-21	23 / 102	Refer WIRTH_EBV B-cells
6	2e-18	17 / 57	Pneui Burnham_viral_UP
7	7e-18	18 / 72	Refer Chaussabel_3,1_Interferon-inducible
8	2e-16	17 / 73	GSE/ HECKER_IFNB1_TARGETS
9	3e-16	16 / 62	Lymp Monti_Host_response_cluster
10	4e-15	15 / 60	GSE/ BOSCO_INTERFERON_INDUCED_ANTIVIRAL_MODULE
11	7e-15	33 / 447	Gliom ScoV_0.999_Sturm_E4_Mesenchymal_RTK_I_PDGFR_A_DN
12	3e-14	11 / 26	GSE/ MOSERL_EIFNA_RESPONSE
13	6e-14	29 / 367	BP innate immune response
14	8e-14	12 / 37	Pneui Sweeney_viral_up
15	9e-14	31 / 429	GSE/ SMID_BREAST_CANCER_NORMAL_LIKE_UP
16	2e-13	12 / 40	GSE/ FARMER_BREAST_CANCER_CLUSTER_1
17	3e-13	27 / 336	BP immune response
18	2e-12	12 / 47	GSE/ DAUER_STAT3_TARGETS_DN
19	2e-12	18 / 143	GSE/ TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_10D_UP
20	3e-12	19 / 166	HM HALLMARK_INTERFERON_GAMMA_RESPONSE
21	3e-12	21 / 211	GSE/ BOYLAN_MULTIPLE_MYELOMA_C_D_DN
22	3e-12	14 / 76	HM HALLMARK_INTERFERON_ALPHA_RESPONSE
23	3e-12	13 / 62	GSE/ BROWNE_INTERFERON_RESPONSE_GENES
24	5e-12	20 / 194	GSE/ JAATINEN_HEMATOPOIETIC_STEM_CELL_DN
25	8e-12	21 / 223	GSE/ MCLACHLAN_DENTAL_CARIES_UP
26	1e-11	15 / 99	Refer Chaussabel_1,5_Myeloid_lineage
27	1e-11	17 / 138	GSE/ TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_3D_UP
28	2e-11	16 / 122	Pneui Terre_IMS_influenza_meta_signature
29	2e-11	10 / 33	Lymp Care_Extended T-cell
30	2e-11	14 / 87	GSE/ BOSCO_TH1_CYTOTOXIC_MODULE
31	3e-11	17 / 146	BP defense response to virus
32	9e-11	18 / 178	HM HALLMARK_COMPLEMENT
33	2e-10	12 / 68	Refer Chaussabel_2,1_Cytotoxic_cells
34	2e-10	15 / 122	GSE/ TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_8D_UP
35	4e-10	13 / 88	GSE/ DER_IFN_BETA_RESPONSE_UP
36	5e-10	85 / 3210	CC plasma membrane
37	6e-10	8 / 23	GSE/ ZHANG_INTERFERON_RESPONSE
38	1e-09	12 / 78	Melar Tirosh_expression_higher_in_CAFs_than_in_T-cells
39	1e-09	10 / 48	GSE/ RADAEVA_RESPONSE_TO_IFNA1_UP
40	2e-09	23 / 355	Refer WIRTH_Immune system

Overview Map

Spot



Aging Rank	p-value	#in/all	Geneset
1	0.4	2 / 92	HORVATH_aging_genes_meth_DOWN
2	0.3	1 / 107	HORVATH_aging_genes_meth_UP
3	1.0	0 / 47	TSCHEINDORFF_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	

CC Rank	p-value	#in/all	Geneset
1	5e-10	85 / 3210	plasma membrane
2	3e-09	117 / 5339	membrane
3	2e-08	10 / 107	lysosome
4	1e-07	80 / 3270	integral component of membrane
5	2e-06	13 / 179	external side of plasma membrane
6	1e-05	35 / 1128	integral component of plasma membrane
7	3e-05	8 / 85	lysosomal lumen
8	8e-04	1 / 1019	lysosomal membrane
9	7e-04	39 / 1611	extracellular region
10	2e-03	9 / 192	membrane raft
11	3e-03	15 / 462	cell surface
12	3e-03	4 / 42	azurophil granule membrane
13	4e-03	15 / 479	Golgi membrane
14	6e-03	5 / 79	ruffle membrane
15	6e-03	6 / 113	filicolin-1-rich granule lumen

Colon Cancer Rank	p-value	#in/all	Geneset
1	4e-35	60 / 589	Lembcke_TCGA_expr_kmeans_E_CIMP_H_UP_Cluster4_DN
2	2e-07	18 / 288	Pentrack_CRC_TCGA_corr_o_msi-h_UP_mss_DN
3	6e-06	16 / 297	Pentrack_CRC_TCGA_group_over_B_msi-h_UP
4	2e-03	5 / 60	Marisa_CRC_cluster-g
5	3e-03	11 / 290	Lembocke_TCGA_meth_kmeans_O_CIMP_H_DN
6	5e-03	13 / 397	Pentrack_CRC_TCGA_corr_C_normal_UP
7	3e-03	22 / 883	LaPointe_mucosa-position_kmeans_L_transverse_colon_cecum_colon_DN
8	1e-02	36 / 1729	LaPointe_mucosa-position_kmeans_G_cecum_colon_ascending_colon_UP_t
9	2e-02	3 / 43	Marisa_CRC_cluster-l
10	4e-02	23 / 1083	LaPointe_mucosa-position_kmeans_J_cecum_colon_ascending_colon_transv
11	8e-02	1 / 6	Marisa_CRC-C6
12	1e-01	3 / 82	Pentrack_CRC_TCGA_group_over_A_normal_UP
13	1e-01	1 / 9	Marisa_CRC-C2
14	1e-01	4 / 132	Marisa_CRC_cluster-a
15	1e-01	8 / 349	Lembcke_TCGA_meth_kmeans_F_CIMP_H_UP_

LM Rank	p-value	#in/all	Geneset
1	3e-12	19 / 166	HALLMARK_INTERFERON_GAMMA_RESPONSE
2	3e-12	14 / 76	HALLMARK_INTERFERON_ALPHA_RESPONSE
3	9e-11	18 / 178	HALLMARK_COMPLEMENT
4	2e-06	13 / 176	HALLMARK_ALLOGRAFT_REJECTION
5	2e-05	12 / 187	HALLMARK_INFAMMATORY_RESPONSE
6	3e-06	11 / 170	HALLMARK_IL2_STAT3_SIGNALING
7	3e-04	9 / 149	HALLMARK_UV_RESPONSE_UP
8	1e-03	8 / 150	HALLMARK_APOPTOSIS
9	2e-03	9 / 190	HALLMARK_TNFA_SIGNALING_VIA_NFKB
10	3e-03	7 / 130	HALLMARK_COAGULATION
11	1e-02	5 / 96	HALLMARK_ANDROGEN_RESPONSE
12	2e-02	7 / 194	HALLMARK_ESTROGEN_RESPONSE_EARLY
13	3e-02	4 / 85	HALLMARK_IL6_JAK_STAT3_SIGNALING
14	5e-02	6 / 181	HALLMARK_XENOBIOTIC_METABOLISM
15	5e-02	6 / 182	HALLMARK_GLYCOLYSIS

Lymphoma Rank	p-value	#in/all	Geneset
1	3e-16	16 / 62	Monti_Host_response_cluster
2	2e-11	10 / 33	Care_Extended_T-cell
3	4e-08	3 / 15	Care_Polarized Immune response
4	2e-06	14 / 213	SPANG_IL21_DN
5	9e-06	18 / 378	TARTE_Mature plasma cell signature
6	1e-04	4 / 18	DAVE_Immune response 2
7	1e-03	99 / 5404	HOPP_Strong_enhancer
8	2e-02	2 / 14	Subero_B-CLL_hypo_meth
9	2e-02	2 / 14	Subero_B-CLL_hypo_meth
10	2e-02	79 / 4559	HOPP_Weak_enhancer
11	3e-02	2 / 19	Subero_MCL_hypo_meth
12	4e-02	8 / 263	SPANG_CD40_6hrs_UP
13	5e-02	3 / 17	Subero_PS_6hrs_DN
14	5e-02	2 / 26	DAVE_Immune response 1
15	8e-02	2 / 33	Subero_T-PLL_hypo_meth

mikRNA target Rank	p-value	#in/all	Geneset
1	0.003	5 / 68	hsa-miR-505
2	0.004	5 / 75	hsa-miR-587-4
3	0.011	4 / 61	hsa-miR-1290
4	0.016	6 / 223	hsa-miR-1214-9
5	0.016	6 / 141	hsa-miR-369-3p
6	0.024	2 / 17	hsa-miR-323-5p
7	0.025	5 / 115	hsa-miR-135a
8	0.029	4 / 81	hsa-miR-574-5p
9	0.032	6 / 33	hsa-miR-33b
10	0.034	4 / 85	hsa-miR-499-5p
11	0.035	6 / 168	hsa-miR-33a
12	0.035	3 / 50	hsa-miR-627
13	0.042	9 / 320	hsa-miR-519a
14	0.044	3 / 56	hsa-miR-618a
15	0.048	4 / 95	hsa-miR-376a

Telomeres Rank	p-value	#in/all	Geneset
1	0.13	0 / 13	Alternative lengthening of telomeres
2	NA	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	

BP Rank	p-value	#in/all	Geneset
1	2e-22	41 / 431	immune system process
2	8e-14	23 / 387	innate immune response
3	3e-13	27 / 336	immune response
4	3e-11	17 / 146	defense response to virus
5	2e-09	9 / 38	negative regulation of viral genome replication
6	2e-08	10 / 63	type I interferon signaling pathway
7	3e-07	12 / 104	response to virus
8	8e-08	14 / 161	adaptive immune response
9	7e-07	11 / 113	regulation of immune response
10	1e-06	20 / 403	neutrophil degranulation
11	6e-06	5 / 19	response to interferon-gamma
12	7e-12	7 / 60	T cell costimulation
13	2e-05	10 / 135	T cell receptor signaling pathway
14	3e-05	13 / 232	cell surface receptor signaling pathway
15	4e-05	6 / 44	proteolysis involved in cellular protein catabolic process

Chr Rank	p-value	#in/all	Geneset
1	0.01	12 / 403	Chr 14
2	0.05	5 / 139	Chr 21
3	0.05	26 / 135	Chr 17
4	0.13	15 / 756	Chr 11
5	0.17	10 / 490	Chr 10
6	0.17	10 / 492	Chr 9
7	0.37	11 / 669	Chr 6
8	0.39	8 / 480	Chr 4
9	0.42	13 / 832	Chr 2
10	0.47	6 / 382	Chr 15
11	0.53	5 / 333	Chr 22
12	0.67	9 / 689	Chr 3
13	0.68	9 / 689	Chr 12
14	0.79	9 / 776	Chr 17
15	0.81	6 / 548	Chr 16

Glioma Rank	p-value	#in/all	Geneset
1	7e-15	33 / 447	Scov_0.999_Sturm_E4_Mesenchymal_RTK_I_PDGFR_A_DN
2	1e-08	9 / 45	Donson-innate immunity-associated with LTS in HGA
3	3e-07	10 / 83	Scov_0.999_Sturm_E3_RTK_I_PDGFR_A_DN
4	9e-06	15 / 269	Scov_0.001_Sturm_G3_Mesenchymal_DN
5	2e-05	14 / 268	Scov_0.001_Sturm_M2_Mesenchymal_RTK_I_PDGFR_A_DN
6	8e-04	11 / 242	Scov_0.5_Sturm_C1_IDH_DN
7	9e-04	11 / 246	Scov_0.001_Sturm_M1_IDH_RTK_I_PDGFR_A_DN
8	2e-03	10 / 231	WILLSCHER_GBM_Verhaak-CL & MES_up
9	3e-03	5 / 66	Weller_LGG_gradef1-vs-111_DOWN
10	3e-05	6 / 29	Hopp_stem_GBM_Epi3_D_adult_fetus_IDH_UP
11	5e-03	15 / 496	Hopp_Sturm_GBM_Epi3_no_zentr_1_G34_DN
12	7e-03	2 / 9	Donson-migration tethering and rolling-associated with LTS in HGA
13	9e-03	3 / 30	Shaw_responders_down_in_oidh_glioma
14	1e-02	2 / 12	Donson-immune cell intra signaling-associated with LTS in HGA
15	2e-02	3 / 42	Sturm_GBM_Meth_overexpression_D_G34_UP

Immunogen Rank	p-value	#in/all	Geneset
1	2e-06	7 / 42	Angelova Immune-metagenes-TGD
2	5e-05	5 / 29	Angelova Immune-metagenes-Th1
3	9e-05	5 / 32	Angelova Immune-metagenes-effector_memory_CD8
4	1e-04	3 / 7	Angelova Immune-metagenes-cytotoxic_cells
5	4e-04	4 / 25	Angelova Immune-metagenes-DK
6	6e-04	2 / 3	Angelova_CRC_MHC_class_I
7	1e-03	15 / 7	Angelova Immune-metagenes-NC
8	4e-03	3 / 23	Angelova Immune-metagenes-Th2
9	2e-02	4 / 67	Angelova Immune-metagenes-T-cells
10	3e-02	2 / 18	Angelova_CRC_immunostimulators
11	2e-02	2 / 21	Angelova Immune-metagenes-central_memory_CD4
12	4e-02	2 / 23	Angelova Immune-metagenes-monocytes
13	8e-02	1 / 6	Immunity Immune-checkpoint-inhibitors
14	1e-01	1 / 8	Immunity_HLA-class-II
15	1e-01	1 / 10	Angelova_CRC_immonoinhibitors

Melanoma Rank	p-value	#in/all	Geneset
1	1e-09	12 / 78	Tiresh_expression higher in CAFs than in T-cells
2	4e-07	7 / 33	Tiresh_T-cell specific genes-melanoma
3	6e-07	14 / 189	Tiresh_genes preferentially expressed by Tregs
4	8e-07	9 / 71	Tiresh_Macrophage specific genes-melanoma
5	1e-06	13 / 171	Landsberg_dedifferentiation_up
6	7e-03	5 / 83	TCGA_melanoma Immune_high
7	2e-02	3 / 41	Tiresh_top50 correlated genes_PC3
8	2e-02	2 / 24	Tiresh_exhaustion-associated genes consistent across tumors
9	7e-02	4 / 107	Tiresh_Exhaustion program in Mel75
10	8e-02	1 / 6	Joensson_Melanoma high immune response subtype
11	1e-01	1 / 8	Hugo_melanoma-BRAFmut-LEF1_UP
12	1e-01	3 / 85	Tiresh_AXL-signature
13	1e-01	5 / 85	Tiresh_genes from malignant cells in Mel79-melanoma
14	4e-01	1 / 39	Tiresh_top50 correlated genes_PC4
15	5e-01	1 / 46	Tiresh_top50 correlated genes_PC5

Pneumonia Rank	p-value	#in/all	Geneset
1	2e-18	17 / 57	Burnham_viral_UP
2	8e-14	12 / 37	Sweeney_viral_up
3	2e-11	16 / 122	Terre_ILMS_influenza_meta_signature
4	3e-09	12 / 44	Burnham_day1_vs_5_DN
5	4e-06	11 / 135	Terre_MS_V_multiple_respiratory_viruses_up
6	2e-05	6 / 41	Scicluna_DN
7	6e-05	6 / 48	Burnham_cap_fp_vs_con_DN
8	1e-04	6 / 56	Burnham_sep_vs_con_DN
9	1e-04	2 / 18	Scicluna_UP
10	3e-02	3 / 48	Burnham_viral_DN
11	4e-02	6 / 179	Terre_MS_V_multiple_respiratory_viruses_dn
12	8e-02	2 / 33	Sweeney_viral_dn
13	3e-01	2 / 68	Burnham_sep_vs_con_UP
14	3e-01	2 / 71	Burnham_cap_fp_vs_con_UP
15	6e-01	1 / 57	Burnham_day1_vs_5_UP

TF Rank	p-value	#in/all	Geneset
1	0.03	31 / 1508	ICGC_Mef2_targets
2	0.04	22 / 1032	ICGC_Usf1_targets
3	0.04	42 / 2254	ICGC_BatfPcr1_targets
4	0.04	43 / 2321	ICGC_Rad21_targets
5	0.05	27 / 1367	HEBENS TREIT_high expression TF
6	0.10	63 / 3796	ICGC_Nficsc81335_targets
7	0.11	54 / 3213	ICGC_Pu1_targets
8	0.11	20 / 1041	ICGC_P300_targets
9	0.19	76 / 4851	ICGC_Runx3_targets
10	0.21	1 / 16	MYC Protein synthesis degradation UP
11	0.25	87 / 4319	ICGC_Pou2_targets
12	0.25	27 / 1636	ICGC_Bcl11_targets
13	0.26	54 / 3451	ICGC_Atf2_targets
14	0.26	64 / 4131	ICGC_Tcf3_targets
15	0.30	58 / 3778	ICGC_Polr24_targets

Cancer Rank	p-value	#in/all	Geneset
1	3e-06	13 / 186	SPANG_LPS-index2
2	6e-05	19 / 480	Lembcke_Colonc Inflammation
3	7e-04	13 / 317	SPANG_BCL6-index2
4	8e-04	3 / 13	GENTLES_modul11
5	1e-02	2 / 12	LIU_BREAST_CANCER
6	1e-02	2 / 13	GENTLES_modul18
7	1e-02	2 / 13	BENTINK_g213
8	2e-02	2 / 16	GENTLES_modul16
9	9e-02	2 / 36	ZHANG_MM_up
10	1e-01	2 / 45	KUIPER_MM_poor survival
11	1e-01	1 / 11	LIU_PROSTATE_CANCER_UP
12	2e-01	1 / 12	IL22_signature
13	2e-01	1 / 14	GENTLES_modul13
14	2e-01	1 / 14	BENTINK_src.10
15	3e-01	3 / 134	PanCan_RAS_geneset_nanostring

Chromatin states Rank	p-value	#in/all	Geneset
1	2e-08	29 / 626	natural killer cells peripheral blood_3_TxFlnk
2	3e-06	32 / 932	Tcells peripheral blood_3_TxFlnk
3	2e-05	24 / 642	Thelper cells peripheral blood_3_TxFlnk
4	2e-04	17 / 432	monocytes peripheral blood_3_TxFlnk
5	2e-04	131 / 7420	Tcells peripheral blood_1_TssA
6	2e-04	138 / 7957	Tcells peripheral blood_2_TssAFlnk
7	5e-04	53 / 2374	9_ReprPCWk_Fibroblasts
8	5e-04	56 / 2535	regulatory cells peripheral blood_3_TxFlnk
9	5e-04	163 / 8431	T CD8+ naive cells peripheral blood_2_TssAFlnk
10	5e-04	67 / 3223	monocytes peripheral blood_6_EnhG
11	8e-04	139 / 8143	HSC_5_TxWk
12	5e-04	62 / 2972	13_ReprPC_ESC_Endoderm
13	9e-04	46 / 2144	T CD8+ naive cells peripheral blood_6_EnhG
14	1e-03	151 / 9142	T CD8+ naive cells peripheral blood_7_Enh
15	1e-03	59 / 2825	9_Het_ESC_Mesoderm

GSEA C2 Rank	p-value	#in/all	Geneset
1	5e-24	35 / 265	WALLACE_PROSTATE_CANCER_RACE_UP
2	1e-22	38 / 354	FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN
3	2e-16	17 / 73	HECKER_IFNB1_TARGETS
4	4e-15	15 / 60</	

Correlation Cluster

Spot Summary: X

metagenes = 68
genes = 715

<r> metagenes = 0.94
<r> genes = 0.34
beta: r2= 13.53 / log p= -Inf

samples with spot = 63 (28.5 %)
intermediate : 1 (2.1 %)
non-mBL : 62 (48.1 %)

Spot Genelist

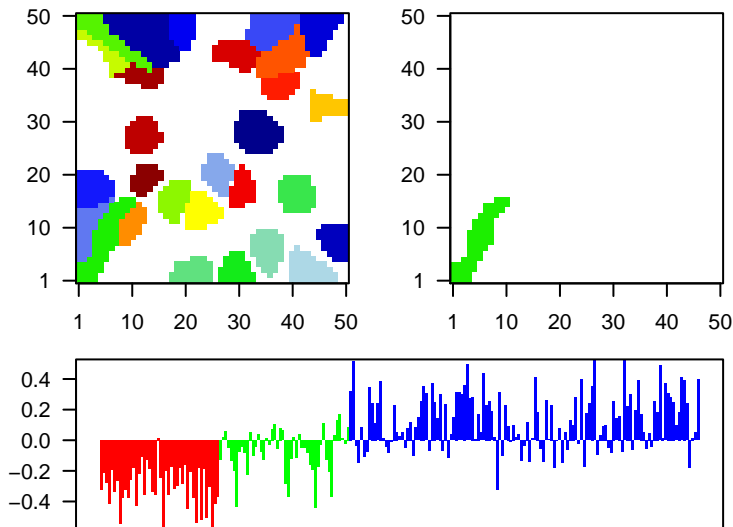
Rank	ID	max e	r	min e	Description
1	207900_at	2.93	-0.94	0.28	CCL17 C-C motif chemokine ligand 17 [Source:HGNC Symbol;Acc:...
2	217002_s_at	2.74	-1.28	0.26	HTR3A 5-hydroxytryptamine receptor 3A [Source:HGNC Symbol;Acc:...
3	211644_x_at	2.59	-1.77	0.32	immunoglobulin kappa variable 3-20 [Source:HGNC Symbol;...
4	221185_s_at	2.57	-1.49	0.54	IQCG IQ motif containing G [Source:HGNC Symbol;Acc:HGNC:252]
5	214551_s_at	2.53	-1.11	0.63	CD7 CD7 molecule [Source:HGNC Symbol;Acc:HGNC:1695]
6	207901_at	2.53	-0.61	0.23	IL12B interleukin 12B [Source:HGNC Symbol;Acc:HGNC:5970]
7	219316_s_at	2.46	-0.79	0.63	FLVCR2 feline leukemia virus subgroup C cellular receptor family merr
8	208451_s_at	2.38	-1.57	0.58	C4A complement C4A (Rodgers blood group) [Source:HGNC Sym
9	203535_at	2.34	-1.86	0.58	S100A9 S100 calcium binding protein A9 [Source:HGNC Symbol;Acc:...
10	217022_s_at	2.33	-2.54	0.44	immunoglobulin heavy constant alpha 2 (A2m marker) [Sourc
11	217546_at	2.25	-0.88	0.51	metallothionein 1M [Source:HGNC Symbol;Acc:HGNC:14296]
12	206140_at	2.21	-0.79	0.25	LHX2 LIM homeobox 2 [Source:HGNC Symbol;Acc:HGNC:6594]
13	205485_at	2.16	-1.09	0.37	RYR1 ryanodine receptor 1 [Source:HGNC Symbol;Acc:HGNC:104]
14	209791_at	2.14	-1	0.58	PADI2 peptidyl arginine deiminase 2 [Source:HGNC Symbol;Acc:HG
15	205819_at	2.09	-0.95	0.53	MARCO macrophage receptor with collagenous structure [Source:HGI
16	204836_at	2.06	-0.92	0.32	GLDC glycine decarboxylase [Source:HGNC Symbol;Acc:HGNC:43]
17	202833_s_at	2.04	-2.04	0.8	SERPINA1 serpin family A member 1 [Source:HGNC Symbol;Acc:HGNC
18	220049_s_at	2	-0.83	0.52	PCCD1L1 programmed cell death 1 ligand 2 [Source:HGNC Symbol;Acc:...
19	202357_s_at	1.99	-1.29	0.61	CFB complement factor B [Source:HGNC Symbol;Acc:HGNC:103]
20	212062_at	1.97	-1.07	0.48	ATP9A ATPase phospholipid transporting 9A (putative) [Source:HGN

Geneset Overrepresentation

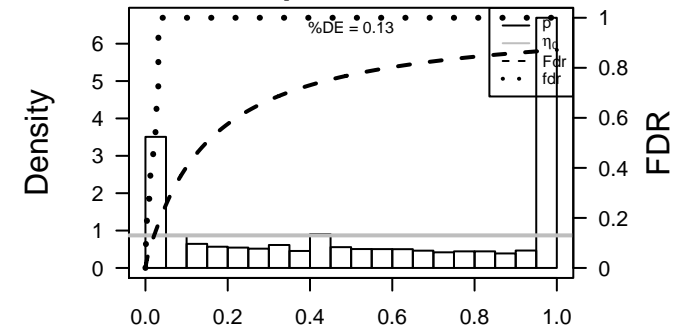
Rank	p-value	#in/all	Geneset
1	1e-85	156 / 589	Colon Lembcke_TCGA-expr_kmeans_E_CIMP_H_UP_Cluster4_DN
2	1e-70	125 / 447	Gliom ScoV_0.999_Sturm_E4_Mesenchymal_RTK_I/PDGFRA_DN
3	4e-63	64 / 102	Refer WIRTH_EBV_B-cells
4	2e-58	108 / 404	GSE/ RUTELLA_RESPONSE_TO_HGF_UP
5	2e-55	103 / 386	GSE/ RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_UP
6	8e-51	90 / 317	Canci SPANG_BCL6-index2
7	2e-46	46 / 71	Melar Tirosh_Macrophage specific genes-melanoma
8	4e-39	43 / 78	Melar Tirosh_expression higher in CAFs than in T-cells
9	1e-36	70 / 269	Gliom ScoV_0.5_Sturm_C3_Mesenchymal_DN
10	2e-36	73 / 297	GSE/ RUTELLA_RESPONSE_TO_CSF2RB_AND_IL4_DN
11	3e-36	79 / 354	GSE/ FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN
12	3e-35	58 / 186	Canci SPANG_LPS-index2
13	2e-34	63 / 231	Gliom WILLSCHER_GBM_Verhaak-CL & MES_up
14	2e-34	62 / 223	GSE/ MCLACHLAN_DENTAL_CARIES_UP
15	2e-33	123 / 902	GSE/ CHEN_METABOLIC_SYNDROM_NETWORK
16	4e-32	42 / 99	Refer Chaussabel_1.5_Myeloid lineage
17	5e-31	55 / 194	GSE/ JAATINEN_HEMATOPOIETIC_STEM_CELL_DN
18	5e-31	34 / 62	Lymp Monti_Host_response_cluster
19	5e-30	55 / 202	GSE/ VERHAAK_GLIOMASTOMA_MESENCHYMAL
20	5e-30	57 / 219	GSE/ MCLACHLAN_DENTAL_CARIES_DN
21	1e-29	76 / 403	BP neutrophil degranulation
22	7e-29	82 / 480	Canci Lembcke_Colonc Inflammation
23	7e-29	41 / 109	Refer Chaussabel_2.6_Myeloid lineage
24	6e-28	60 / 265	GSE/ WALLACE_PROSTATE_CANCER_RACE_UP
25	1e-27	48 / 166	GSE/ VERHAAK_AML_WITH_NPM1_MUTATED_UP
26	2e-26	48 / 176	HM HALLMARK_ALLOGRAFT_REJECTION
27	9e-26	35 / 88	GSE/ WIELAND_UP_BY_HBV_INFECTION
28	1e-25	50 / 198	Refer Chaussabel_3.3_Inflammation II
29	1e-25	46 / 166	HM HALLMARK_INTERFERON_GAMMA_RESPONSE
30	3e-25	64 / 336	BP immune response
31	1e-24	62 / 323	BP inflammatory response
32	3e-24	100 / 795	GSE/ NUYTEN_EZH2_TARGETS_UP
33	8e-24	36 / 105	GSE/ ICHIBA_GRAFT_VERSUS_HOST_DISEASE_35D_UP
34	1e-23	52 / 236	GSE/ LI_INDUCED_T_TO_NATURAL_KILLER_UP
35	1e-23	61 / 327	GSE/ RUTELLA_RESPONSE_TO_CSF2RB_AND_IL4_UP
36	2e-23	45 / 176	GSE/ PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
37	2e-23	44 / 169	GSE/ JISON_SICKLE_CELL_DISEASE_UP
38	4e-23	32 / 83	Melar TCGA_melanoma_immune_high
39	1e-22	56 / 288	Color Pentrack_CRC_TCGA_corr_j_msi-h_UP_mss_DN
40	2e-22	62 / 354	GSE/ RODWELL_AGING_KIDNEY_UP

Overview Map

Spot



p-values



Rank	p-value	#in/all	Geneset
1	0.3	5 / 92	HORVATH_aging_genes_meth_DOWN
2	0.8	2 / 47	TESCHENDORFF_age_hypermethylated
3	0.3	3 / 107	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	1e-29	76 / 403	neutrophil degranulation
2	64 / 336		immune response
3	1e-24	62 / 323	inflammatory response
4	6e-20	65 / 431	immune system process
5	3e-17	33 / 131	chemotaxis
6	2e-13	42 / 274	cytokine-mediated signaling pathway
7	2e-12	37 / 232	cell surface receptor signaling pathway
8	2e-12	31 / 169	response to lipopolysaccharide
9	5e-12	19 / 63	chemokine-mediated signaling pathway
10	5e-12	47 / 367	innate immune response
11	1e-10	19 / 75	cellular response to interferon-gamma
12	2e-10	16 / 156	positive regulation of ERK1 and ERK2 cascade
13	4e-09	54 / 553	apoptotic process
14	6e-09	13 / 41	positive regulation of tumor necrosis factor production
15	7e-09	21 / 113	regulation of immune response

Cancer Rank	p-value	#in/all	Geneset
1	6e-51	910 / 317	SPANG_Bcl6-index2
2	3e-35	58 / 186	SPANG_LPS-index2
3	7e-29	82 / 480	Lembcke_Colonc Inflammation
4	9e-09	8 / 13	GENTLES_modul18
5	3e-05	5 / 10	BENTINK_ras.4
6	2e-03	11 / 96	PanCan_TXmIsReg_geneset_nanostring
7	3e-03	4 / 15	WANG_ER_UP
8	6e-03	9 / 80	PanCan_JAK-ST_geneset_nanostring
9	1e-02	0 / 14	LIU_PROSTATE_CANCER_DN
10	2e-02	3 / 13	BENTINK_e2f3.1
11	4e-02	4 / 32	KUIPER_MM_good_survival
12	9e-02	2 / 12	HLA2_signature
13	1e-01	2 / 13	GENTLES_modul11
14	1e-01	2 / 14	GUSTAFSON_PI3K_UP
15	1e-01	2 / 14	BENTINK_src.10

CC Rank	p-value	#in/all	Geneset
1	8e-22	148 / 1611	extracellular region
2	3e-16	104 / 1090	extracellular space
3	1e-15	46 / 281	lysosome
4	3e-15	218 / 3270	integral component of membrane
5	2e-14	164 / 2239	extracellular exosome
6	7e-12	300 / 5339	membrane
7	1e-11	203 / 3210	plasma membrane
8	3e-11	21 / 65	lysosomal lumen
9	5e-10	15 / 48	filicolin-1-rich granule membrane
10	1e-09	28 / 179	external side of plasma membrane
11	5e-09	88 / 1128	integral component of plasma membrane
12	3e-08	51 / 537	perinuclear region of cytoplasm
13	1e-07	45 / 462	cell surface
14	1e-07	14 / 60	tertiary granule membrane
15	3e-07	15 / 74	secretory granule membrane

Chr Rank	p-value	#in/all	Geneset
1	0.04	68 / 1325	Chr 1
2	0.13	9 / 139	Chr 21
3	0.13	26 / 192	Chr 9
4	0.17	25 / 490	Chr 10
5	0.25	33 / 700	Chr 12
6	0.30	26 / 556	Chr X
7	0.36	20 / 437	Chr 8
8	0.43	36 / 832	Chr 2
9	0.45	24 / 564	Chr 5
10	0.49	32 / 756	Chr 11
11	0.52	23 / 548	Chr 16
12	0.53	14 / 333	Chr 22
13	0.71	17 / 480	Chr 4
14	0.77	13 / 389	Chr 20
15	0.81	13 / 382	Chr 15

Chromatin states Rank	p-value	#in/all	Geneset
1	2e-31	81 / 432	monocytes peripheral blood_3_TxFnk
2	249 / 3223		monocytes peripheral blood_6_EnhC
3	69 / 126		natural killer cells peripheral blood_3_TxFnk
4	4e-12	416 / 8200	monocytes peripheral blood_2_TssAFnk
5	1e-10	123 / 1676	Fetal_TxTrans
6	3e-08	156 / 2507	Mid_Frontal_Lobe_ReprPC
7	9e-07	377 / 7635	monocytes peripheral blood_1_TssA
8	4e-07	7 / 1932	Tcells peripheral blood_3_TxFnk
9	4e-07	443 / 8440	HSC_7_Enh
10	6e-07	108 / 1639	Fetal_TssF
11	1e-06	65 / 847	Fetal_TssP
12	4e-06	400 / 8370	natural killer cells peripheral blood_2_TssAFnk
13	4e-06	38 / 383	K5acLow_Colon
14	5e-06	426 / 9114	natural killer cells peripheral blood_7_Enh
15	7e-06	432 / 9298	Bcells peripheral blood_7_Enh

Colon Cancer Rank	p-value	#in/all	Geneset
1	1e-85	156 / 589	Lembcke_TCGA-expr_kmeans_E_CIMP_H_UP_Cluster4_DN
2	1e-22	56 / 288	Pentrack_CRC_TCGA_corr_J_msi-h_UP_mss_DN
3	2e-15	47 / 297	Pentrack_CRC_TCGA_group_over_B_msi-h_UP
4	1e-10	90 / 1083	LaPointe_mucosa-position_kmeans_J_cecum_colon_ascending_colon_transv
5	3e-09	44 / 197	Pentrack_CRC_TCGA_corr_C_normal_UP
6	2e-08	22 / 132	Marisa_CRC-cluster-a
7	1e-07	70 / 883	LaPointe_mucosa-position_kmeans_L_transverse_colon_cecum_colon_DN
8	3e-07	7 / 13	Budinska_B_Lower_crypt-like_DOWN
9	8e-06	10 / 43	Marisa_CRC-cluster-1
10	3e-05	28 / 290	Lembcke_TCGA_meth_kmeans_O_CIMP_H_DN
11	2e-04	10 / 60	Marisa_CRC-cluster-g
12	2e-04	101 / 1729	LaPointe_mucosa-position_kmeans_G_cecum_colon_ascending_colon_UP_t
13	3e-04	5 / 15	TCGA-CRC_less-aggressive-disease-markers
14	3e-04	18 / 172	Pentrack_CRC_TCGA_corr_U_msi-h_UP
15	7e-04	71 / 1166	LaPointe_mucosa-position_kmeans_K_transverse_colon_UP_cecum_colon_a

Glioma Rank	p-value	#in/all	Geneset
1	1e-70	125 / 447	Scov_0.999_Sturm_E4_Mesenchymal_RTK_I_PDGFR_A_DN
2	1e-36	70 / 269	Scov_0.5_Sturm_C3_Mesenchymal_DN
3	2e-34	63 / 231	WILLSCHER_GBM_Verhaak-CL & MES_up
4	1e-17	45 / 242	Scov_0.5_Sturm_C1_IDH_DN
5	2e-13	23 / 83	Scov_0.99_Sturm_E3_RTK_I_PDGFR_A_DN
6	4e-13	41 / 268	Scov_0.001_Sturm_M2_Mesenchymal_RTK_I_PDGFR_A_DN
7	2e-12	25 / 109	Hopp_Sturm_GBM_Epi3_D_adult_fetus_IDH_UP
8	2e-12	38 / 246	Scov_0.001_Sturm_M1_IDH_RTK_I_PDGFR_A_DN
9	1e-11	10 / 14	Donson-chemokines/cytokines-associated with LTS in HGA
10	2e-09	14 / 45	Donson-innate immunity-associated with LTS in HGA
11	1e-06	14 / 71	Weller_LGG_1p19qDel-vs-intact_DOWN
12	6e-05	9 / 43	Patel_stemness_signatures
13	6e-05	14 / 99	GIEZELT_GBM_WT_up_VS_mut
14	9e-05	7 / 27	Donson-Misc immune function-associated with LTS in HGA
15	9e-05	4 / 7	Donson-cytotoxic effectors-associated with LTS in HGA

GSEA C2 Rank	p-value	#in/all	Geneset
1	2e-58	108 / 404	RUTELLA_RESPONSE_TO_HGF_UP
2	2e-55	103 / 386	RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_UP
3	2e-36	73 / 297	RUTELLA_RESPONSE_TO_CSF2RB_AND_IL4_DN
4	3e-36	79 / 354	WALLACE_PROSTATE_CANCER_RESPONSE
5	6e-23	62 / 223	MCLACHLAN_DENTAL_CARIES_UP
6	2e-33	123 / 902	CHEN_METABOLIC_SYNDROM_NETWORK
7	5e-31	55 / 194	JAATINEN_HEMATOPOIETIC_STEM_CELL_DN
8	5e-30	55 / 202	VERHAAK_GLOBLASTOMA_MESENCHYMAL
9	5e-30	57 / 219	MCLACHLAN_DENTAL_CARIES_DN
10	6e-28	60 / 265	WALLACE_PROSTATE_CANCER_RACE_UP
11	1e-27	48 / 166	VERHAAK_AML_WITH_NPM1_MUTATED_UP
12	9e-26	35 / 88	WIELAND_UP_BY_HBV_INFECTION
13	3e-24	100 / 795	NUYTEN_EZH2_TARGETS_UP
14	8e-24	36 / 105	ICHIBA_GRAF_VERSUS_HOST_DISEASE_35D_UP
15	1e-23	52 / 236	LI_INDUCED_T_TO_NATURAL_KILLER_UP

LM Rank	p-value	#in/all	Geneset
1	2e-26	48 / 176	HALLMARK_ALLOGRAFT_REJECTION
2	1e-25	46 / 166	HALLMARK_INTERFERON_GAMMA_RESPONSE
3	1e-20	43 / 187	HALLMARK_INFLAMMATORY_RESPONSE
4	6e-17	39 / 190	HALLMARK_TNFA_SIGNALING_VIA_NFKB
5	1e-14	35 / 178	HALLMARK_COMPLEMENT
6	3e-12	34 / 170	HALLMARK_IL2_STAT5_SIGNALING
7	2e-10	19 / 76	HALLMARK_INTERFERON_ALPHA_RESPONSE
8	2e-10	20 / 85	HALLMARK_IL6_JAK_STAT3_SIGNALING
9	3e-07	22 / 150	HALLMARK_APOPTOSIS
10	2e-05	22 / 194	HALLMARK_KRAS_SIGNALING_UP
11	1e-04	20 / 188	HALLMARK_HYPOXIA
12	1e-04	20 / 191	HALLMARK_P53_PATHWAY
13	2e-03	7 / 44	HALLMARK_REACTIVE_OXYGEN_SPECIES_PATHWAY
14	3e-03	17 / 192	HALLMARK_MTORC1_SIGNALING
15	3e-03	8 / 59	HALLMARK_CHOLESTEROL_HOMEOSTASIS

Immunome Rank	p-value	#in/all	Geneset
1	2e-10	13 / 32	Angelova Immune-metagenes-effector_memory_CD8
2	1e-09	17 / 67	Angelova Immune-metagenes-T-cells
3	8e-09	13 / 42	Angelova Immune-metagenes-TGD
4	2e-06	9 / 29	Angelova Immune-metagenes-Th1
5	1e-05	10 / 45	Angelova Immune-metagenes-MDSC
6	3e-05	13 / 70	Angelova Immune-metagenes-monocytes
7	5e-04	6 / 25	Angelova Immune-metagenes-DC
8	7e-04	5 / 18	Angelova_CRC_immunostimulators
9	9e-04	5 / 19	Angelova Immune-metagenes-IDC
10	1e-03	3 / 6	Immunity Immune-checkpoint-inhibitors
11	5 / 23		Angelova Immune-metagenes-Treg
12	7e-03	3 / 10	Angelova_CRC_immunoinhibitors
13	1e-02	4 / 23	Angelova Immune-metagenes-Th2
14	2e-02	3 / 13	Angelova Immune-metagenes-activated_B-cells
15	2e-02	2 / 5	Angelova Immune-metagenes-NKT

Lifestyle Rank	p-value	#in/all	Geneset
1	8e-05	5 / 12	DUMEAUX_Women normal BMI literature genes up
2	2e-04	5 / 14	Huan_blood-pressure_SBP-signature
3	3e-04	4 / 9	DUMEAUX_Monocytes in smokers literature genes up
4	2e-03	4 / 13	Huan_blood-pressure_DBP-signature
5	2e-03	5 / 22	DUMEAUX_High bmi enriched genes
6	3e-03	3 / 8	Marjolein_aging_genes_UP
7	5e-03	2 / 3	Huan_blood-pressure_HTN-signature
8	2e-02	2 / 5	DUMEAUX_Estrogen related in smokers literature genes up
9	3e-02	15 / 210	Hornuth_BMI-associated-genes_DN
10	3e-01	1 / 10	DUMEAUX_Smoking literature genes up
11	4e-01	7 / 150	Hornuth_BMI-associated-genes_UP
12	5e-01	3 / 62	DUMEAUX_Smoking enriched genes
13	7e-01	1 / 32	Marjolein_aging_genes_DN
14	1e+00	0 / 4	DUMEAUX_Exercising non smoker literature enriched genes
15	1e+00	0 / 7	DUMEAUX_Estrogen related in non smokers literature genes up

Lymphoma Rank	p-value	#in/all	Geneset
1	5e-31	34 / 62	Monti_Host_response_cluster
2	2e-19	29 / 85	Sha_DLBCI_UP
3	1e-14	26 / 97	ROSLOLOWSKI_red_tcell
4	8e-13	15 / 33	Care_ExtendedT-cell
5	1e-11	82 / 906	SPANG_BCR_DN
6	4e-11	15 / 41	ROSLOLOWSKI_blue_DOWN
7	1e-09	294 / 5404	HOPF_Strong_enhancer
8	1e-09	4 / 15	Care_Polarized immune response
9	3e-09	11 / 26	DAVE_Immune response 1
10	6e-09	42 / 378	TARTE_Mature plasma cell signature
11	2e-07	27 / 213	SPANG_IL21_DN
12	3e-06	22 / 173	Victoria_Light_sina signature
13	3e-05	19 / 135	DAVE_BL-vs-DLBCI
14	4e-06	7 / 18	DAVE_Immune response 2
15	3e-05	23 / 214	LENZ_Stromal signature 1

Melanoma Rank	p-value	#in/all	Geneset
1	2e-46	46 / 71	Tirosh_Macrophage specific genes-melanoma
2	4e-39	43 / 78	Tirosh_expression higher in CAFs than in T-cells
3	4e-23	32 / 83	TCGA_melanoma Immune_high
4	3e-21	44 / 189	Tirosh_genes preferentially expressed by Tregs
5	6e-17	18 / 33	Tirosh_T-cell specific genes-melanoma
6	9e-11	29 / 171	Landsberg_dedifferentiation_up
7	1e-08	20 / 107	Tirosh_Exhaustion program in Mel75
8	2e-05	15 / 85	Tirosh_AXL-signature
9	1e-05	4 / 5	Joensuu_Melanoma Proliferative subtype
10	4e-05	22 / 204	Landsberg_dedifferentiation_down
11	9e-05	23 / 230	Gerber_wt/wt_melanoma-cells-SpotC
12	1e-04	12 / 81	Tirosh_Genes in the MITF program
13	6 / 24		Tirosh_day1_vs_5_DN
14	1e-03	8 / 51	Tirosh_genes from CD8 T-cells in Mel79-melanoma
15	6e-03	21 / 276	Gerber_wt/wt_melanoma-cells-SpotB

MF Rank	p-value	#in/all	Geneset
1	3e-09	13 / 39	chemokine activity
2	5e-08	25 / 173	cytokine activity
3	2e-06	53 / 644	protein homodimerization activity
4	1e-05	7 / 20	chemokine receptor activity
5	2e-05	23 / 205	receptor activity
6	3e-05	6 / 16	CCR chemokine receptor binding
7	1e-04	7 / 29	coreceptor activity
8	2e-04	9 / 22	amyloid-beta binding
9	3e-04	29 / 346	receptor binding
10	4e-04	6 / 24	hydrolase activity, hydrolyzing O-glycosyl compounds
11	4e-04	19 / 191	transmembrane signaling receptor activity
12	5e-04	5 / 17	MHC class I protein binding
13	5e-04	37 / 500	signal transducer activity
14	5e-04	4 / 10	serine-type carboxypeptidase activity
15	7e-04	5 / 18	cytokine binding

mikNA target Rank	p-value	#in/all	Geneset
1	0.003	26 / 344	hsa-miR-19a
2	0.005	5 / 28	hsa-miR-1274b
3	0.010	24 / 344	hsa-miR-19b
4	0.013	6 / 50	hsa-miR-513c
5	0.017	6 / 50	hsa-miR-384
6	0.018	13 / 162	hsa-miR-641
7	0.027	3 / 16	hsa-miR-563
8	0.035	5 / 44	hsa-miR-629
9	0.036	14 / 197	hsa-miR-152
10	0.037	3 / 18	hsa-miR-1228
11	0.037	3 / 18	hsa-miR-591
12	0.042	12 / 164	hsa-miR-148b
13	0.045	5 / 47	hsa-miR-191
14	0.061	4 / 36	hsa-miR-146b-3p
15	0.079	6 / 72	

Correlation Cluster

Spot Summary: Y

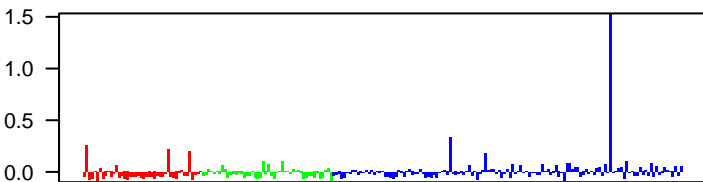
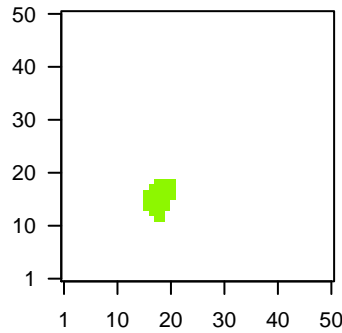
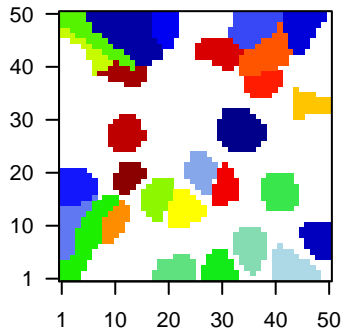
metagenes = 36
genes = 241

<r> metagenes = 0.95
<r> genes = 0.15
beta: r2= 1.39 / log p= -Inf

samples with spot = 6 (2.7 %)
mBL : 3 (6.8 %)
non-mBL : 3 (2.3 %)

Overview Map

Spot

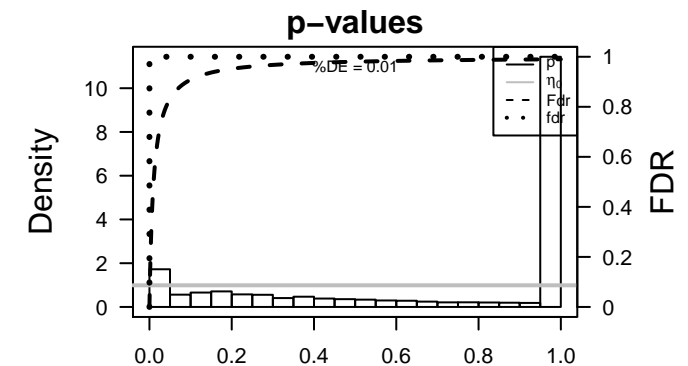


Spot Genelist

Rank	ID	max e	r	min e	Description
1	212768_s_at	3.21	-0.59	0.62	OLFM4 olfactomedin 4 [Source:HGNC Symbol;Acc:HGNC:17190]
2	203824_at	3.13	-0.55	0.67	TSPAN8 tetraspanin 8 [Source:HGNC Symbol;Acc:HGNC:11855]
3	210107_at	3.12	-1.18	0.58	CLCA1 chloride channel accessory 1 [Source:HGNC Symbol;Acc:HGNC:11855]
4	206199_at	2.96	-0.74	0.69	CEACAM7 carcinoembryonic antigen related cell adhesion molecule 7 [Source:HGNC Symbol;Acc:HGNC:11855]
5	204272_at	2.94	-0.65	0.64	LGALS4 galectin 4 [Source:HGNC Symbol;Acc:HGNC:6565]
6	206262_at	2.91	-0.55	0.66	ADH1C alcohol dehydrogenase 1C (class I), gamma polypeptide [Source:HGNC Symbol;Acc:HGNC:11855]
7	206143_at	2.89	-0.51	0.63	SLC26A3 solute carrier family 26 member 3 [Source:HGNC Symbol;Acc:HGNC:11855]
8	214142_at	2.86	-0.46	0.58	ZG16 zymogen granule protein 16 [Source:HGNC Symbol;Acc:HGNC:11855]
9	206198_s_at	2.82	-0.6	0.64	CEACAM7 carcinoembryonic antigen related cell adhesion molecule 7 [Source:HGNC Symbol;Acc:HGNC:11855]
10	201884_at	2.79	-0.93	0.6	CEACAM5 carcinoembryonic antigen related cell adhesion molecule 5 [Source:HGNC Symbol;Acc:HGNC:11855]
11	209752_at	2.77	-0.58	0.65	REG1A regenerating family member 1 alpha [Source:HGNC Symbol;Acc:HGNC:11855]
12	205009_at	2.76	-0.89	0.37	TFF1 trefoil factor 1 [Source:HGNC Symbol;Acc:HGNC:11755]
13	209847_at	2.74	-0.64	0.52	CDH17 cadherin 17 [Source:HGNC Symbol;Acc:HGNC:1756]
14	213953_at	2.71	-0.64	0.61	KRT20 keratin 20 [Source:HGNC Symbol;Acc:HGNC:20412]
15	209173_at	2.66	-0.63	0.5	AGR2 anterior gradient 2, protein disulphide isomerase family member 2 [Source:HGNC Symbol;Acc:HGNC:11855]
16	213456_at	2.65	-0.61	0.33	SOSTDC4 sclerostin domain containing 1 [Source:HGNC Symbol;Acc:HGNC:11855]
17	211848_s_at	2.64	-0.56	0.54	CEACAM7 carcinoembryonic antigen related cell adhesion molecule 7 [Source:HGNC Symbol;Acc:HGNC:11855]
18	204213_at	2.64	-0.74	0.3	PIGR polymeric immunoglobulin receptor [Source:HGNC Symbol;Acc:HGNC:11855]
19	205476_at	2.61	-0.6	0.41	CCL20 C-C motif chemokine ligand 20 [Source:HGNC Symbol;Acc:HGNC:11855]
20	203240_at	2.57	-0.63	0.42	FCGBP Fc fragment of IgG binding protein [Source:HGNC Symbol;Acc:HGNC:11855]

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	7e-40	78 / 883	Colon LaPointe_mucosa-position_kmeans_L_transverse colon_cecum colon_DN
2	3e-26	26 / 92	Colon Marisa_CRC-cluster-h
3	1e-24	42 / 376	Colon Lembcke_TCGA-expr_kmeans_M_CIMP_H_DN
4	4e-22	112 / 3168	Lymph HOPP_Repressed
5	5e-18	38 / 452	Colon Lembcke_TCGA-expr_kmeans_L_CIMP_H_UP_Cluster4_DN
6	5e-18	38 / 453	GSE/ ONDER_CDH1_TARGETS_2_DN
7	1e-16	56 / 1083	Colon LaPointe_mucosa-position_kmeans_J_ascending colon_transverse colon_DN
8	1e-15	35 / 448	Colon Lembcke_TCGA_meth_kmeans_J_CIMP_H_DN
9	2e-15	27 / 255	Colon Kosinski_top-crypt-long-list
10	5e-15	17 / 82	Colon Pentrack_CRC_TCGA_group.over_A_normal_UP
11	6e-14	31 / 397	Colon Pentrack_CRC_TCGA_corr_C_normal_UP
12	7e-14	25 / 248	GSE/ JAEGER_METASTASIS_DN
13	1e-13	50 / 1029	GSE/ DODD_NASOPHARYNGEAL_CARCIOMA_UP
14	3e-13	23 / 218	GSE/ MCBRYAN_PUBERTAL_BREAST_4_5WK_UP
15	5e-13	16 / 91	GSE/ VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_DN
16	8e-13	69 / 1894	Lymph HOPP_Poised_promoter
17	2e-12	21 / 196	GSE/ WAMUNYOKOLI_OVARIAN_CANCER_LMP_UP
18	5e-12	34 / 564	GSE/ GOZGIT_ESR1_TARGETS_DN
19	4e-11	25 / 329	GSE/ CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_UP
20	8e-11	35 / 657	GSE/ SMID_BREAST_CANCER_BASAL_DN
21	2e-10	18 / 178	GSE/ WU_CELL_MIGRATION
22	3e-09	29 / 533	GSE/ CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_3
23	3e-09	17 / 182	GSE/ SENGUPTA_NASOPHARYNGEAL_CARCIOMA_DN
24	3e-09	45 / 1148	TF HEBENSTREIT_low expression TF
25	3e-09	13 / 99	GSE/ WAMUNYOKOLI_OVARIAN_CANCER_GRADES_1_2_UP
26	7e-09	34 / 738	Colon Lembcke_TCGA-expr_kmeans_N_CIMP_H_DN
27	1e-08	29 / 565	GSE/ LEE_BMP2_TARGETS_UP
28	1e-08	42 / 1072	Refer PROTEINATLAS_duodenum
29	1e-08	15 / 152	GSE/ COLDREN_GEFITINIB_RESISTANCE_DN
30	2e-08	41 / 1048	Refer PROTEINATLAS_rectum
31	2e-08	28 / 550	GSE/ FEVR_CTNNB1_TARGETS_UP
32	3e-08	9 / 46	GSE/ BOSCO_EPITHELIAL_DIFFERENTIATION_MODULE
33	3e-08	14 / 140	GSE/ RODRIGUES_NTN1_TARGETS_DN
34	3e-08	66 / 2239	CC extracellular exosome
35	6e-08	12 / 104	GSE/ DOANE_BREAST_CANCER_ESR1_UP
36	1e-07	39 / 1032	Refer PROTEINATLAS_small intestine
37	1e-07	18 / 264	GSE/ CHEMNITZ_RESPONSE_TO_PROSTAGLANDIN_E2_DN
38	1e-07	14 / 157	GSE/ LI_AMPLIFIED_IN_LUNG_CANCER
39	2e-07	16 / 213	GSE/ SABATES_COLORECTAL_ADENOMA_DN
40	2e-07	12 / 115	GSE/ YEGNASUBRAMANIAN_PROSTATE_CANCER



Aging Rank	p-value	#in/all	Geneset
1	0.4	2 / 92	HORVATH_aging_genes_meth_DOWN
2	0.5	2 / 107	HORVATH_aging_genes_meth_UP
3	1.0	0 / 47	TSCHEINDORFF_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	

CC Rank	p-value	#in/all	Geneset
1	3e-08	66 / 2239	extracellular exosome
2	1e-06	39 / 1128	integral component of plasma membrane
3	1e-01	50 / 171	extracellular region
4	4e-06	12 / 152	basolateral plasma membrane
5	8e-06	78 / 3270	integral component of membrane
6	1e-05	7 / 50	lateral plasma membrane
7	1e-05	14 / 231	apical plasma membrane
8	2e-05	26 / 3010	plasma membrane
9	3e-04	72 / 1090	extracellular space
10	4e-04	8 / 117	cell cortex
11	1e-03	5 / 55	brush border
12	2e-03	3 / 17	apicolateral plasma membrane
13	4e-03	3 / 20	anchored component of plasma membrane
14	5e-03	5 / 73	cell-cell adherens junction
15	5e-03	100 / 5339	membrane

Colon Cancer Rank	p-value	#in/all	Geneset
1	7e-40	78 / 883	LaPointe_mucosa-position_kmeans_L_transverse_colon_cecum_colon_DN
2	3e-26	26 / 92	Marisa_CRC-cluster-h
3	1e-24	42 / 376	Lembcke_TCGA_expr_kmeans_M_CIMP_H_UP
4	5e-18	38 / 452	Lembcke_TCGA_expr_kmeans_L_CIMP_H_UP_Cluster4_DN
5	1e-18	56 / 1083	LaPointe_mucosa-position_kmeans_J_cecum_colon_ascending_colon_transv
6	1e-15	35 / 448	Lembcke_TCGA_meth_kmeans_J_CIMP_H_DN
7	2e-15	27 / 255	Kosinski_top_crypt-long-list
8	6e-15	17 / 82	Pentrack_CRC_TCGA_group_over_A_normal_UP
9	9e-14	31 / 397	Pentrack_CRC_TCGA_corr_C_normal_UP
10	7e-10	24 / 738	LaPointe_TCGA_expr_kmeans_N_CIMP_H_DN
11	4e-07	6 / 20	Kosinski_top_crypt-short-list
12	9e-07	40 / 1166	LaPointe_mucosa-position_kmeans_K_transverse_colon_UP_cecum_colon_a
13	2e-05	6 / 38	Marisa_CRC-cluster-e
14	3e-05	3 / 5	Marisa_CRC-C5
15	7e-05	3 / 6	Marisa_CRC-C6

LM Rank	p-value	#in/all	Geneset
1	2e-04	11 / 1194	HALLMARK_ESTROGEN_RESPONSE_EARLY
2	2e-03	9 / 181	HALLMARK_XENOBIOTIC_METABOLISM
3	3e-03	9 / 194	HALLMARK_KRAS_SIGNALING_UP
4	1e-02	8 / 193	HALLMARK_ESTROGEN_RESPONSE_LATE
5	1e-02	4 / 59	HALLMARK_CHOLESTEROL_HOMEOSTASIS
6	6e-02	4 / 116	HALLMARK_ANDROGEN_RESPONSE
7	7e-02	6 / 190	HALLMARK_TNFA_SIGNALING_VIA_NFKB
8	1e-01	2 / 38	HALLMARK_WNT_BETA_CATENIN_SIGNALING
9	2e-01	4 / 139	HALLMARK_FATTY_ACID_METABOLISM
10	2e-01	4 / 141	HALLMARK_UV_RESPONSE_DN
11	2e-01	3 / 94	HALLMARK_PROTEIN_SECRETION
12	2e-01	5 / 194	HALLMARK_MYOGENESIS
13	2e-01	2 / 51	HALLMARK_TGF_BETA_SIGNALING
14	2e-01	4 / 150	HALLMARK_APOPTOSIS
15	3e-01	4 / 174	HALLMARK_APICAL_JUNCTION

Lymphoma Rank	p-value	#in/all	Geneset
1	4e-22	112 / 3168	HOPP_Repressed
2	9e-13	69 / 1894	HOPP_Poised_promoter
3	4e-04	7 / 87	HOPP_Lymphoma_Epi1_with_zentr_v_B.cell_DN
4	7e-04	52 / 2206	HOPP_Heterochrom
5	7e-04	6 / 70	HOPP_Lymphoma_Epi1_no_zentr_3_B.cell_DN
6	1e-03	5 / 53	LENZ_Signature2
7	2e-03	7 / 118	Subero_INT_hyper_meth
8	3e-03	6 / 70	Subero_T-ALL_hyper_meth
9	4e-03	5 / 70	Subero_FL_hyper_meth
10	2e-02	6 / 132	Subero_DLBCL_hyper_meth
11	2e-02	4 / 66	HOPP_Lymphoma_Epi1_with_zentr_i_B.cell_DN
12	3e-02	3 / 47	Subero_B-ALL_hyper_meth
13	4e-02	2 / 20	Subero_MCL_hyper_meth
14	5e-02	2 / 23	Subero_mBL_hyper_meth
15	5e-02	3 / 54	HOPP_Lymphoma_Epi1_no_zentr_1_B.cell_DN

miRNA target Rank	p-value	#in/all	Geneset
1	0.03	4 / 74	hsa-miR-496
2	0.05	3 / 24	hsa-miR-299-5p
3	0.06	2 / 56	hsa-miR-558
4	0.07	2 / 20	hsa-miR-1274a
5	0.08	4 / 104	hsa-miR-1272
6	0.09	2 / 32	hsa-miR-885-3p
7	0.09	5 / 154	hsa-miR-944
8	0.10	3 / 72	hsa-miR-339-5p
9	0.10	1 / 7	hsa-miR-568
10	0.10	3 / 74	hsa-miR-595
11	0.10	2 / 36	hsa-miR-146b-3p
12	0.10	4 / 117	hsa-miR-522
13	0.11	5 / 167	hsa-miR-181c
14	0.11	2 / 10	hsa-miR-659
15	0.14	1 / 30	hsa-miR-487b

Telomeres Rank	p-value	#in/all	Geneset
1	1	0 / 13	Alternative lengthening of telomeres
2	1	0 / 27	Nabeta1n_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	

BP Rank	p-value	#in/all	Geneset
1	7e-07	9 / 66	epithelial cell differentiation
2	9e-07	11 / 109	animal organ morphogenesis
3	2e-05	6 / 36	antimicrobial humoral response
4	2e-05	5 / 22	digestion
5	1e-04	4 / 17	embryonic digestive tract morphogenesis
6	2e-04	4 / 20	lymphocyte chemotaxis
7	6e-04	6 / 59	chloride transport
8	4e-04	4 / 23	killing of cells of other organism
9	4e-04	3 / 10	fucosylation
10	4e-04	3 / 10	limb bud formation
11	6e-04	6 / 69	chloride transmembrane transport
12	3e-04	3 / 12	sperm capacitation
13	8e-04	10 / 193	heart development
14	8e-04	4 / 28	spleen development
15	1e-03	5 / 53	neutrophil chemotaxis

Chr Rank	p-value	#in/all	Geneset
1	0.06	5 / 139	Chr 21
2	0.12	11 / 480	Chr 4
3	0.14	17 / 334	Chr 19
4	0.22	11 / 548	Chr 16
5	0.28	11 / 585	Chr 5
6	0.35	8 / 437	Chr 8
7	0.38	22 / 1325	Chr 1
8	0.41	13 / 771	Chr 17
9	0.45	11 / 689	Chr 6
10	0.49	11 / 689	Chr 3
11	0.51	4 / 242	Chr 13
12	0.54	3 / 184	Chr 18
13	0.63	3 / 182	Chr 2
14	0.63	7 / 492	Chr 9
15	0.67	5 / 369	Chr 20

Glioma Rank	p-value	#in/all	Geneset
1	4e-07	22 / 414	Hopp_Sturm_GBM_Epi3_A_adult_fetus_UP_G34_DN
2	5e-07	51 / 1652	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
3	7e-04	3 / 12	Sturm_GBM_Meth_overexpression_J_RTK_II_classic_UP
4	1e-03	11 / 239	Sturm_GBM_Meth_overexpression_B_adult_UP
5	2e-03	6 / 96	Sturm_GBM_Meth_overexpression_B_adult_UP
6	9e-03	8 / 191	Sturm_GBM_Meth_overexpression_B_adult_UP
7	9e-03	10 / 273	Sturm_GBM_Epi3_B_adult_UP_G34_DN
8	1e-02	2 / 10	Philippis PN up vs MES & Prolif
9	1e-02	4 / 59	GIEZELT_GBM_STS_up_vs_LTS
10	2e-02	10 / 288	Sturm_GBM_Meth_overexpression_B_adult_UP
11	4e-02	6 / 163	Sturm_GBM_Meth_overexpression_B_adult_UP
12	4e-02	3 / 50	Christensen_hypermethylated_in_primary_glioblastoma
13	5e-02	5 / 132	Christensen_hypermethylated_in_grade3_oligoastrocytoma
14	7e-02	6 / 186	Hopp_Sturm_GBM_Epi3_C_IDH_UP
15	9e-02	3 / 69	Hopp_Sturm_GBM_Epi3_D1_IDH_UP_adult_fetus_DN

Immunome Rank	p-value	#in/all	Geneset
1	0.05	2 / 38	Angelova Immune-metagenome-Th2
2	0.11	2 / 38	Angelova Immune-metagenome-mast-cells
3	0.17	1 / 12	Angelova Immune-metagenome-effector_memory_CD4
4	0.32	1 / 25	Angelova Immune-metagenome-DC
5	0.65	1 / 67	Angelova Immune-metagenome-T-cells
6	0.83	0 / 13	Angelova Immune-metagenome-activated_B-cells
7	1.00	0 / 26	Angelova Immune-metagenome-activated_CD4
8	1.00	0 / 19	Angelova Immune-metagenome-activated_CD8
9	1.00	0 / 21	Angelova Immune-metagenome-central_memory_CD4
10	1.00	0 / 17	Angelova Immune-metagenome-central_memory_CD8
11	1.00	0 / 7	Angelova Immune-metagenome-cytotoxic_cells
12	1.00	0 / 32	Angelova Immune-metagenome-effector_memory_CD8
13	1.00	0 / 14	Angelova Immune-metagenome-eosinophil
14	1.00	0 / 19	Angelova Immune-metagenome-IDC
15	1.00	0 / 13	Angelova Immune-metagenome-immature_B-cells

Melanoma Rank	p-value	#in/all	Geneset
1	6e-06	8 / 64	Harbst_melanoma_lowgrade_up
2	3e-03	4 / 38	Hugo_melanoma-BRAFmut-MET_UP
3	4e-03	6 / 59	TCGA_melanoma_keratin_high
4	2e-02	14 / 497	Gerber_wt/wt_melanoma-cells-SpotD
5	2e-02	3 / 39	Tirosh_top50 correlated genes PC4
6	2e-02	3 / 39	Tirosh_melanoma specific genes
7	3e-02	2 / 17	Hugo_melanoma-all-MET_DN
8	4e-02	7 / 41	Tirosh_Genes in the MITF program
9	4e-02	8 / 249	Gerber_wt/wt_melanoma-cells-SpotE
10	6e-02	7 / 230	Gerber_wt/wt_melanoma-cells-SpotC
11	9e-02	1 / 6	Joensuu_Melanoma high immune response subtype
12	1e-01	2 / 37	Hugo_melanoma-all-MET_DN
13	1e-01	1 / 8	Joensuu_Melanoma-BRAFmut-LEF1_UP
14	1e-01	1 / 10	Joensuu_Melanoma Normal like subtype
15	2e-01	2 / 46	Tirosh_top50 correlated genes PC5

Pneumonia Rank	p-value	#in/all	Geneset
1	0.004	5 / 68	Burnham_sep_vs_con_UP
2	0.005	5 / 71	Burnham_cap_fp_vs_con_UP
3	0.167	2 / 48	Burnham_viral_DN
4	0.189	2 / 59	ICGC_Atl3_targets
5	0.217	2 / 57	Burnham_day1_vs_5_DN
6	0.524	1 / 48	Burnham_day1_vs_5_UP
7	0.579	1 / 56	Burnham_sep_vs_con_DN
8	0.849	1 / 122	Burnham_sep_vs_con_DN
9	0.938	1 / 179	Terre_IMS_influenza_meta_signature
10	1.000	0 / 57	Terre_MSX_multiple_respiratory_viruses_dn
11	1.000	0 / 54	Burnham_viral_UP
12	1.000	0 / 18	Burnham_timecourse
13	1.000	0 / 41	Scicluna_UP
14	1.000	0 / 37	Scicluna_DN
15	1.000	0 / 33	Sweeney_viral_up

TF Rank	p-value	#in/all	Geneset
1	3e-09	45 / 1148	HEBENSTREIT_low expression TF
2	8e-01	32 / 2321	ICGC_Rad21_targets
3	1e+00	10 / 1032	ICGC_Usf1_targets
4	1e+00	10 / 1041	ICGC_P300_targets
5	1e+00	4 / 549	ICGC_Atl3_targets
6	1e+00	17 / 1836	ICGC_Bcl1_targets
7	1e+00	41 / 3435	ICGC_Ebfs137065_targets
8	1e+00	22 / 2254	ICGC_BatfPcr1_targets
9	1e+00	77 / 1025	ICGC_NrfsPcr1_targets
10	1e+00	31 / 2894	ICGC_Zab1_targets
11	1e+00	12 / 1508	ICGC_Mef2_targets
12	1e+00	2 / 522	ICGC_SrfPcr2_targets
13	1e+00	7 / 1089	ICGC_Ets1_targets
14	1e+00	19 / 2150	ICGC_Irf4_targets
15	1e+00	1 / 415	ICGC_RxraPcr1_targets

Cancer Rank	p-value	#in/all	Geneset
1	2e-04	3 / 14	LIU_PROSTATE_CANCER_DN
2	6e-03	4 / 47	PanCan_TGF-B_geneset_nanostring
3	6e-03	0 / 11	LIU_PROSTATE_CANCER_UP
4	8e-03	6 / 113	PanCan_Driver_Gene_geneset_nanostring
5	8e-03	2 / 9	WANG_ER_DN
6	2e-02	5 / 96	PanCan_TXMsrReg_geneset_nanostring
7	1e-01	4 / 134	PanCan_RAS_geneset_nanostring
8	2e-01	1 / 13	GENTLES_modul17
9	2e-01	1 / 14	GENTLES_modul10
10	2e-01	1 / 18	PanCan_Notch_geneset_nanostring
11	3e-01	1 / 25	PanCan_HH_geneset_nanostring
12	3e-01	4 / 187	PanCan_PIK3_geneset_nanostring
13	4e-01	1 / 32	KUIPER_MM_good survival
14	4e-01	3 / 147	PanCan_MAPK_geneset_nanostring
15	6e-01	7 / 480	Lembcke_Colonc Inflammation

Chromatin states Rank	p-value	#in/all	Geneset
1	5e-18	92 / 2515	natural killer cells peripheral blood_13_ReprCk
2	1e-17	89 / 2405	Bcells_peripheral_blood_13_ReprCk
3	5e-17	100 / 3001	Bcells_peripheral_blood_14_ReprPCWk
4	1e-16	116 / 3918	Tcells_peripheral_blood_14_ReprPCWk
5	3e-16	112 / 3734	Tcells_peripheral_blood_13_ReprCk
6	5e-16	93 / 2747	Bcells_peripheral_blood_12_EnhBv
7	1e-14	95 / 2984	natural killer cells peripheral blood_14_ReprPCWk
8	1e-14	97 / 3089	Tregulatory cells peripheral blood_14_ReprPCWk
9	2e-14	87 / 2802	natural killer cells peripheral blood_12_EnhBv
10	9e-14	89 / 2765	Tregulatory cells peripheral blood_13_ReprCk
11	2e-13	98 / 3272	monocytes_peripheral_blood_14_ReprPCWk
12	4e-13	95 / 3150	monocytes_peripheral_blood_13_ReprCk
13	1e-12	103 / 3755	HSC_15_Quies
14	2e-12	104 / 3724	Tcells_peripheral_blood_12_EnhBv
15	3e-11	79 / 2535	T CD8+ naive cells peripheral blood_14_ReprPCWk

GSEA C2 Rank	p-value	#in/all	Geneset
1	5e-18	38 / 453	ONDER_CDH1_TARGETS_2_DN
2	7e-14	25 / 248	JAEGER_METASTASIS_DN
3	1e-13	50 / 1029	DODD_NASOPHARYNGEAL_CARCINOMA_UP
4			

Correlation Cluster

Spot Summary: Z

metagenes = 43
genes = 742

<r> metagenes = 0.94
<r> genes = 0.25
beta: r2= 4.36 / log p= -Inf

samples with spot = 30 (13.6 %)
intermediate : 8 (16.7 %)
non-mBL : 22 (17.1 %)

Spot Genelist

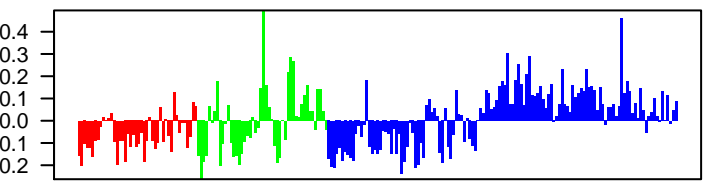
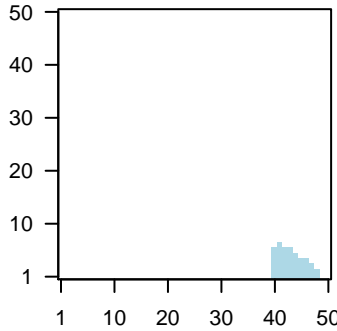
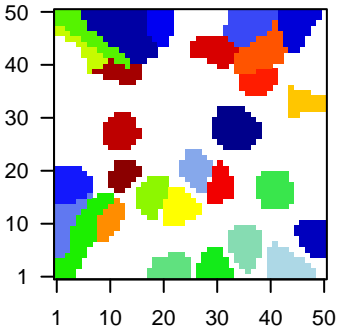
Rank	ID	max e	r	min e	Description
1	212236_x_at	2.22	-0.68	0.53	KRT17 keratin 17 [Source:HGNC Symbol;Acc:HGNC:6427]
2	205033_s_at	2.2	-0.66	0.44	DEFA1 defensin alpha 1 [Source:HGNC Symbol;Acc:HGNC:2761]
3	38691_s_at	2.17	-0.66	0.3	SFTPC surfactant protein C [Source:HGNC Symbol;Acc:HGNC:1080]
4	209800_at	2.16	-0.6	0.48	KRT16 keratin 16 [Source:HGNC Symbol;Acc:HGNC:6423]
5	202222_s_at	1.96	-0.73	0.55	DES desmin [Source:HGNC Symbol;Acc:HGNC:2770]
6	207337_at	1.83	-1.04	0.5	CTAG2 cancer/testis antigen 2 [Source:HGNC Symbol;Acc:HGNC:24
7	206012_at	1.77	-0.72	0.36	LEFTY2 left-right determination factor 2 [Source:HGNC Symbol;Acc:
8	206760_s_at	1.74	-0.74	0.47	FCER2 Fc fragment of IgE receptor II [Source:HGNC Symbol;Acc:HC
9	218687_s_at	1.71	-0.55	0.49	MUC13 mucin 13, cell surface associated [Source:HGNC Symbol;Acc
10	209957_s_at	1.66	-0.88	0.58	NPPA natriuretic peptide A [Source:HGNC Symbol;Acc:HGNC:7939
11	205334_at	1.65	-0.71	0.52	S100A1 S100 calcium binding protein A1 [Source:HGNC Symbol;Acc:
12	208607_s_at	1.55	-0.64	0.47	SAA2 serum amyloid A2 [Source:HGNC Symbol;Acc:HGNC:10514]
13	214403_x_at	1.53	-1.06	0.58	
14	205409_at	1.51	-0.76	0.47	FOSL2 FOS like 2, AP-1 transcription factor subunit [Source:HGNC :
15	217052_x_at	1.49	-0.92	0.32	
16	36829_at	1.48	-0.66	0.4	PER1 period circadian regulator 1 [Source:HGNC Symbol;Acc:HGN
17	205131_x_at	1.46	-0.62	0.43	CLEC11A C-type lectin domain containing 11A [Source:HGNC Symbol;
18	202014_at	1.44	-0.67	0.36	PPP1R15 protein phosphatase 1 regulatory subunit 15A [Source:HGNC
19	211018_at	1.43	-0.59	0.45	LSS lanosterol synthase [Source:HGNC Symbol;Acc:HGNC:6708]
20	208868_s_at	1.41	-0.86	0.36	GABARAPL1 GABA type A receptor associated protein like 1 [Source:HGN

Geneset Overrepresentation

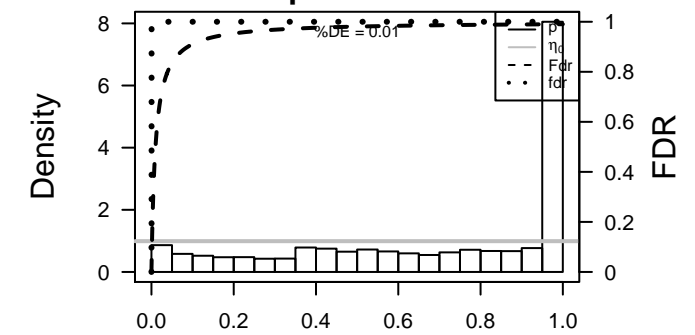
Rank	p-value	#in/all	Geneset
1	9e-30	74 / 358	GSE/ MOREAUX_MULTIPLE_MYELOMA_BY_TACI_UP
2	5e-18	384 / 6368	Colon LaPointe_mucosa-position_kmeans_F_cecum_colon_transverse_colon_UP
3	3e-13	22 / 72	GSE/ MOREAUX_B_LYMPHOCYTE_MATURATION_BY_TACI_UP
4	3e-09	52 / 483	Colon Lemboke_TCGA-expr_kmeans_H_CIMP.H_UP_Cluster3_DN
5	1e-08	38 / 311	GSE/ SHEN_SMARCA2_TARGETS_DN
6	5e-08	29 / 209	Refer Chaussabel_2.5_Immune related molecules
7	7e-08	131 / 1894	Lymp/ HOPP_Poised_promoter
8	8e-08	196 / 3168	Lymp/ HOPP_Repressed
9	4e-07	48 / 501	GSE/ MARTENS_TRETINOIN_RESPONSE_UP
10	6e-07	62 / 730	GSE/ BENPORATH_ES_WITH_H3K27ME3
11	3e-06	26 / 212	GSE/ MEISSNER_NPC_HCP_WITH_H3K4ME2_AND_H3K27ME3
12	1e-05	9 / 34	BP regulation of synaptic plasticity
13	1e-05	143 / 2321	TF ICGC_Rad21_targets
14	2e-05	26 / 239	GSE/ GINESTIER_BREAST_CANCER_ZNF217_AMPLIFIED_DN
15	2e-05	35 / 373	GSE/ MIKKELSEN_MEF_HCP_WITH_H3K27ME3
16	5e-05	103 / 1602	GSE/ BLALOCK_ALZHEIMERS_DISEASE_UP
17	9e-05	8 / 34	BP respiratory gaseous exchange
18	1e-04	104 / 1652	Gliom Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
19	2e-04	5 / 13	BP lens fiber cell differentiation
20	2e-04	21 / 198	GSE/ EBAUER_TARGETS_OF_PAX3_FOXO1_FUSION_UP
21	2e-04	39 / 485	TF ICGC_NrsfPcr2_targets
22	3e-04	13 / 94	GSE/ KIM_GASTRIC_CANCER_CHEMOSENSITIVITY
23	3e-04	179 / 3210	CC plasma membrane
24	3e-04	51 / 697	GSE/ BENPORATH_SUZ12_TARGETS
25	3e-04	35 / 423	Gliom Down_a
26	3e-04	31 / 361	BP intracellular signal transduction
27	4e-04	12 / 85	BP glucose homeostasis
28	4e-04	15 / 125	MF transcriptional activator activity, RNA polymerase II transcription regulatory
29	4e-04	20 / 195	BP chemical synaptic transmission
30	5e-04	10 / 65	BP excitatory postsynaptic potential
31	6e-04	9 / 54	Lymp Hopp_Lymphoma_Epi1_no_zentr_1_B.cell_DN
32	6e-04	57 / 826	GSE/ ZWANG_TRANSIENTLY_UP_BY_2ND_EGF_PULSE_ONLY
33	7e-04	74 / 1148	TF HEBENSTREIT_low expression TF
34	8e-04	29 / 346	MF receptor binding
35	1e-03	9 / 58	BP sodium ion transmembrane transport
36	1e-03	4 / 11	MF platelet-derived growth factor binding
37	1e-03	50 / 722	MF RNA polymerase II transcription factor activity, sequence-specific DNA bin
38	1e-03	37 / 492	Color LaPointe_mucosa-position_kmeans_C_cecum_colon_ascending_colon_tra
39	1e-03	8 / 49	GSE/ EBAUER_MYOGENIC_TARGETS_OF_PAX3_FOXO1_FUSION
40	1e-03	40 / 548	Chr Chr 16

Overview Map

Spot



p-values



Rank	p-value	#in/all	Geneset
1	0.02	10 / 107	HORVATH_aging_genes_meth_UP
2	0.22	6 / 92	HORVATH_aging_genes_meth_DOWN
3	0.62	2 / 47	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	

Rank	p-value	#in/all	Geneset
1	3e-04	179 / 3210	plasma membrane
2	2e-03	71 / 1128	integral component of plasma membrane
3	2e-03	175 / 3270	integral component of membrane
4	3e-03	12 / 109	dendritic spine
5	3e-03	29 / 382	synapse
6	4e-03	7 / 47	postsynapse
7	6e-03	22 / 277	neuron projection
8	6e-03	7 / 50	terminal bouton
9	7e-03	266 / 5339	membrane
10	9e-03	3 / 10	synaptic cleft
11	1e-02	7 / 55	presynapse
12	1e-02	4 / 21	non-motile cilium
13	1e-02	7 / 57	acrosomal vesicle
14	2e-02	5 / 134	cortical actin cytoskeleton
15	2e-02	8 / 74	secretory granule

Rank	p-value	#in/all	Geneset
1	5e-18	384 / 6368	LaPointe_mucosa-position_kmeans_F_cecum_colon_transverse_colon_UP_
2	3e-09	52 / 483	Lembcke_TCGA-expr_kmeans_H_CIMP_H_UP_Cluster3_DN
3	1e-03	37 / 492	LaPointe_mucosa-position_kmeans_C_cecum_colon_ascending_colon_trans_
4	7e-03	53 / 848	LaPointe_mucosa-position_kmeans_O_transverse_colon_UP
5	8e-03	36 / 532	LaPointe_mucosa-position_kmeans_B_ascending_colon_transverse_colon_UI
6	2e-02	19 / 255	Kosinski_top_crypt-long-list
7	4e-02	23 / 349	Lembcke_TCGA_meth_kmeans_F_CIMP_H_UP_
8	8e-02	31 / 539	Lembcke_TCGA_meth_kmeans_L_CIMP_H_DN
9	1e-01	18 / 290	Lembcke_TCGA_meth_kmeans_O_CIMP_H_DN
10	1e-01	26 / 448	Lembcke_TCGA_meth_kmeans_J_CIMP_H_DN
11	1e-01	11 / 164	Lembcke_TCGA_meth_kmeans_B_Cluster4_DN
12	1e-01	14 / 221	Lembcke_TCGA_meth_kmeans_A_Cluster4_DN
13	1e-01	60 / 1166	LaPointe_mucosa-position_kmeans_K_transverse_colon_UP_cecum_colon_a
14	2e-01	2 / 16	Budinska_B_Lower_crypt-like_UP
15	2e-01	18 / 318	Lembcke_TCGA_meth_kmeans_E_CIMP_H_UP_

Rank	p-value	#in/all	Geneset
1	0.01	16 / 194	HALLMARK_MYOGENESIS
2	0.03	15 / 194	HALLMARK_ESTROGEN_RESPONSE_EARLY
3	0.03	15 / 195	HALLMARK_KRAS_SIGNALING_DN
4	0.05	13 / 174	HALLMARK_APICAL_JUNCTION
5	0.06	4 / 34	HALLMARK_APICAL_SURFACE
6	0.09	9 / 122	HALLMARK_SPERMATOGENESIS
7	0.15	11 / 174	HALLMARK_ADIPOGENESIS
8	0.17	9 / 139	HALLMARK_FATTY_ACID_METABOLISM
9	0.19	4 / 51	HALLMARK_TGF_BETA_SIGNALING
10	0.35	10 / 193	HALLMARK_ESTROGEN_RESPONSE_LATE
11	0.41	7 / 141	HALLMARK_UV_RESPONSE_DN
12	0.49	3 / 59	HALLMARK_CHOLESTEROL_HOMEOSTASIS
13	0.49	7 / 149	HALLMARK_UV_RESPONSE_UP
14	0.51	2 / 38	HALLMARK_WNT_BETA_CATENIN_SIGNALING
15	0.52	6 / 130	HALLMARK_COAGULATION

Rank	p-value	#in/all	Geneset
1	7e-08	131 / 1894	HOPP_Poised_promoter
2	8e-08	196 / 3168	HOPP_Repressed
3	6e-04	3	Hopp_Lymphoma_Epi1_no_zentr_1_B.cell_DN
4	2e-03	11 / 87	Hopp_Lymphoma_Epi1_w/ht_zentr_v_B.cell_DN
5	1e-02	6 / 45	Subero_INT_hypo_meth
6	3e-02	6 / 53	LENZ_Stromal_signature_2
7	3e-02	11 / 132	Subero_DLBCL_hyper_meth
8	3e-02	5 / 32	ROSLOWOWSKI_blue_DOWN
9	8e-02	8 / 102	ROSLOWOWSKI_blue_total
10	1e-01	5 / 56	Subero_mBL_hyper_meth
11	1e-01	2 / 14	Subero_B-ALL_hypo_meth
12	1e-01	4 / 46	Subero_DLBCL_hypo_meth
13	2e-01	3 / 33	Subero_T-PILL_hypo_meth
14	2e-01	5 / 70	Subero_FL_hyper_meth
15	2e-01	3 / 35	Subero_MM_hyper_meth

Rank	p-value	#in/all	Geneset
1	0.03	2 / 6	hsa-miR-886-5p
2	0.03	4 / 28	hsa-miR-296-5p
3	0.04	5 / 43	hsa-miR-328
4	0.05	3 / 19	hsa-miR-636
5	0.05	4 / 32	hsa-miR-615-5p
6	0.06	3 / 21	hsa-miR-483-3p
7	0.07	4 / 36	hsa-miR-146b-3p
8	0.08	6 / 68	hsa-miR-608
9	0.08	2 / 11	hsa-miR-1249
10	0.09	4 / 38	hsa-miR-769-3p
11	0.10	2 / 12	hsa-miR-191*
12	0.10	6 / 72	hsa-miR-339-5p
13	0.11	3 / 26	hsa-miR-558
14	0.11	3 / 26	hsa-miR-555
15	0.11	5 / 58	hsa-miR-331-3p

Rank	p-value	#in/all	Geneset
1	0.7	1 / 27	Nabeta1n_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	

Rank	p-value	#in/all	Geneset
1	1e-05	8 / 34	regulation of synaptic plasticity
2	2e-04	8 / 34	regulatory gaseous exchange
3	2e-04	5 / 13	lens fiber cell differentiation
4	3e-04	31 / 361	intracellular signal transduction
5	4e-04	12 / 85	glucose homeostasis
6	4e-04	20 / 195	chemical synaptic transmission
7	1e-03	10 / 65	excitatory postsynaptic potential
8	1e-03	9 / 58	sodium ion transmembrane transport
9	1e-03	4 / 12	urogenital system development
10	2e-03	9 / 63	regulation of insulin secretion
11	2e-03	55 / 833	multicellular organism development
12	3e-03	6 / 33	cell death
13	4e-03	56 / 885	positive regulation of transcription from RNA polymerase II promoter
14	5e-03	12 / 114	calcium ion transport
15	5e-03	5 / 26	associative learning

Rank	p-value	#in/all	Geneset
1	0.001	40 / 548	Chr 16
2	0.007	25 / 333	Chr 22
3	0.012	33 / 492	Chr 9
4	0.012	48 / 776	Chr 17
5	0.018	46 / 756	Chr 11
6	0.045	11 / 139	Chr 21
7	0.053	47 / 833	Chr 19
8	0.273	4 / 27	Chr Y
9	0.445	37 / 585	Chr 7
10	0.458	32 / 700	Chr 12
11	0.473	17 / 369	Chr 20
12	0.571	19 / 437	Chr 8
13	0.580	24 / 353	Chr 5
14	0.581	29 / 689	Chr 6
15	0.916	5 / 184	Chr 18

Rank	p-value	#in/all	Geneset
1	1e-04	104 / 1652	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
2	3e-04	35 / 423	Down_a
3	1e-03	11 / 86	Sturm_GBM_Meth_overexpression_B_adult_UP
4	3e-03	3 / 9	M34T5_GBM_Meth_overexpression_C_G34T5_UP
5	5e-03	4 / 16	VERHAAR_C1_subtype
6	7e-03	9 / 78	Hopp_Sturm_GBM_Epi3_A1_Mesenchymal_UP
7	1e-02	9 / 81	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
8	1e-02	29 / 421	Down_b
9	3e-02	11 / 132	Christensen_hypermethylated_in_grade3_oligoastrocytoma
10	4e-02	10 / 41	Hopp_Sturm_GBM_Epi3_C1_IDH_up_fetus_DN
11	4e-02	2 / 7	oligodendrocytes_glio
12	5e-02	4 / 32	WIRTH_PN_subtype
13	6e-02	11 / 144	Christensen_hypermethylated_in_grade2_oligodendroglioma
14	6e-02	4 / 33	Sturm_GBM_Meth_overexpression_F_IDH_UP
15	6e-02	6 / 64	Weller_LGG_gradell-vs-III_UP

Rank	p-value	#in/all	Geneset
1	0.005	4 / 16	Angelova Immune-metagenes-Th17
2	0.097	2 / 12	Angelova Immune-metagenes-NK56_dim
3	0.203	1 / 5	Angelova Immune-metagenes-NK56_bright
4	0.239	1 / 6	Immunity Immune-checkpoint-inhibitors
5	0.305	1 / 8	Angelova Immune-metagenes-mDC
6	0.325	2 / 25	Angelova Immune-metagenes-DC
7	0.365	7 / 10	Angelova Immune-metagenes-TFH
8	0.365	1 / 10	Angelova_CRC Immunoinhibitors
9	0.371	2 / 29	Angelova Immune-metagenes-Th1
10	0.471	1 / 14	Angelova Immune-metagenes-eosinophil
11	0.538	1 / 17	Angelova Immune-metagenes-central_memory_CD8
12	0.578	1 / 19	Angelova Immune-metagenes-IDC
13	0.600	2 / 45	Angelova Immune-metagenes-MDSC
14	0.648	1 / 23	Angelova Immune-metagenes-Th2
15	0.648	1 / 23	Angelova Immune-metagenes-Treg

Rank	p-value	#in/all	Geneset
1	0.005	6 / 37	Hugo_melanoma-all-MET_DN
2	0.008	3 / 10	Joensuu_Melanoma_Normal_like_subtype
3	0.038	15 / 204	Landsberg_dedifferentiation_down
4	0.083	4	Tirosh_genes_shared_by_CD8_T_cells_and_malign_cells_in_Mel179-melanoma
5	0.087	1 / 2	Melanoma_Epi-Enzyme_Cluster 1
6	0.127	1 / 3	Melanoma_Epi-Enzyme_Cluster 4
7	0.190	4 / 51	Tirosh_genes_from_CD8_T_cells_in_Mel179-melanoma
8	0.249	3 / 39	Tirosh_CD80_correlated_genes_PC4
9	0.249	3 / 39	Tirosh_melanoma_specific_genes
10	0.265	5 / 78	Tirosh_CAF-cell_specific_genes
11	0.266	4 / 59	TCGA_melanoma_keratin_high
12	0.314	13 / 249	Gerber_w/wt_melanoma-cells-SpotE
13	0.481	8 / 171	Landsberg_dedifferentiation_up
14	0.508	2 / 38	Hugo_melanoma-BRAFmut-MET_UP
15	0.545	3 / 64	Harbst_melanoma_lowgrade_up

Rank	p-value	#in/all	Geneset
1	0.4	3 / 54	Burnham_timecourse
2	0.5	3 / 57	Burnham_day1_vs_5_UP
3	0.6	1 / 18	Scicluna_UP
4	0.6	2 / 71	Burnham_cap_fp_vs_con_UP
5	0.8	2 / 68	Burnham_sep_vs_con_UP
6	0.8	1 / 37	Sweeney_viral_up
7	0.8	1 / 41	Scicluna_DN
8	0.9	1 / 48	Burnham_viral_DN
9	0.9	3 / 129	Terre_MS_influenza_meta_signature
10	0.9	1 / 56	Burnham_sep_vs_con_DN
11	0.9	1 / 57	Burnham_viral_UP
12	1.0	3 / 179	Terre_MS_multiple_respiratory_viruses_dn
13	1.0	1 / 135	Terre_MS_multiple_respiratory_viruses_up
14	1.0	0 / 48	Burnham_cap_fp_vs_con_DN
15	1.0	0 / 52	Burnham_day1_vs_5_DN

Rank	p-value	#in/all	Geneset
1	1e-05	143 / 2321	ICGC_Rad21_targets
2	2e-04	39 / 485	ICGC_NrsfPcr2_targets
3	7e-04	74 / 1148	HEBENSTREIT_low expression TF
4	5e-02	101 / 1941	ICGC_Bcl3_targets
5	5e-02	170 / 3435	ICGC_Ebits137065_targets
6	6e-02	201 / 4131	ICGC_Tcf3_targets
7	7e-02	233 / 4851	ICGC_Runx3_targets
8	8e-02	55 / 1025	ICGC_NrsfPcr1_targets
9	9e-02	220 / 4602	ICGC_Elf1_targets
10	1e-01	152 / 3121	ICGC_Egr1_targets
11	1e-01	182 / 3804	ICGC_Stat5_targets
12	2e-01	198 / 4278	ICGC_Yy1_targets
13	3e-01	188 / 4072	ICGC_Mta3_targets
14	4e-01	165 / 3630	ICGC_Sp1_targets
15	4e-01	167 / 3703	ICGC_Foxm1_targets

Rank	p-value	#in/all	Geneset
1	0.06	2 / 9	WANG_ER_DN
2	0.10	2 / 12	LIU_BREAST_CANCER
3	0.13	2 / 14	LIU_COMMON_CANCER_GENES
4	0.13	2 / 14	BENTINK_ras.6
5	0.13	12 / 187	PanCan_Pi3K_geneset_nanostring
6	0.13	7 / 96	PanCan_TXmisReg_geneset_nanostring
7	0.19	2 / 18	PanCan_Notch_geneset_nanostring
8	0.24	8 / 134	PanCan_RAS_geneset_nanostring
9	0.32	1 / 16	LIU_LIVER_CANCER
10	0.35	3 / 47	PanCan_TGF-B_geneset_nanostring
11	0.36	7 / 130	PanCan_CC+Apop_geneset_nanostring
12	0.39	6 / 113	PanCan_Driver_Gene_geneset_nanostring
13	0.42	10 / 12	GENTLES_modul12
14	0.45	1 / 13	GENTLES_modul18
15	0.47	1 / 14	LIU_PROSTATE_CANCER_DN

Rank	p-value	#in/all	Geneset
1	2e-21	166 / 1813	8_EnhP_Fibroblasts
2	4e-20	127 / 1239	EnhP_Color
3	5e-19	147 / 1634	8_EnhP_Melanocytes
4	9e-17	257 / 3724	Tcells_peripheral_blood_12_EnhBiv
5	3e-16	148 / 1729	8_EnhP_Skeletal_Muscle
6	1e-14	180 / 2375	10_ReprPC_Fibroblasts
7	2e-14	172 / 2245	1_Tssp_Fibroblasts
8	6e-13	165 / 2015	8_ReprC_Color
9	2e-12	193 / 2747	Bcells_peripheral_blood_12_EnhBiv
10	2e-12	243 / 3734	Tcells_peripheral_blood_13_ReprPC
11	2e-12	215 / 3184	monocytes_peripheral_blood_12_EnhBiv
12	3e-12	149 / 1943	Tssp_Color
13	4e-12	160 / 2146	10_ReprPC_Skeletal_Muscle
14	4e-12	179 / 2507	Mid_Frontal_Lobe_ReprPC
15	4e-12	184 / 2602	natural killer cells_peripheral_blood_12_EnhBiv

Rank	p-value	#in/all	Geneset
1	9e-30	74 / 358	MOREAU_MULTIPLE_MYELOMA_BY_TACI_UP
2	3e-13	22 / 72	MOREAU_B_LYMPHOCYTE_MATURATION_BY_TACI_UP
3	1e-08	38 / 311	SHEN_SMARCA2_TARGETS_DN
4	4e-07	48 / 501	MARTINS_TRETIININ_RESPONSE_UP
5	6e-07	62 / 730	BENPORATH_ES_WITH_H3K2

Correlation Cluster

Spot Summary: A1

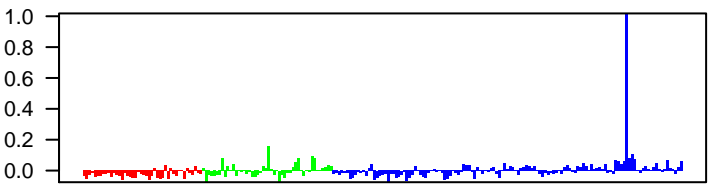
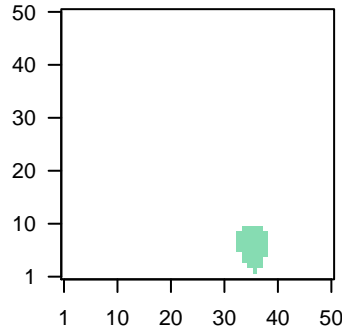
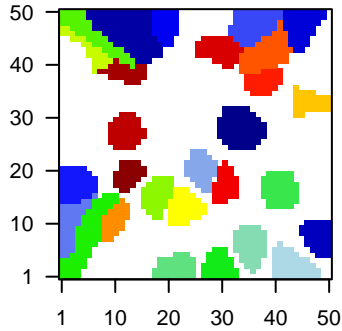
metagenes = 41
genes = 419

<r> metagenes = 0.95
<r> genes = 0.1
beta: r2= 0.7 / log p= -Inf

samples with spot = 2 (0.9 %)
intermediate : 1 (2.1 %)
non-mBL : 1 (0.8 %)

Overview Map

Spot

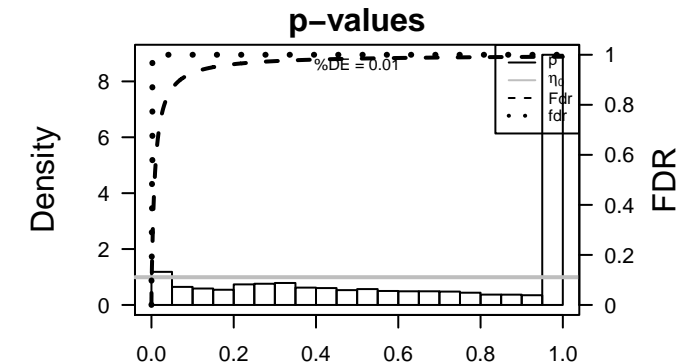


Spot Genelist

Rank	ID	max e	r	min e	Description
					Symbol
1	202768_at	2.75	-0.96	0.35	FOSB FosB proto-oncogene, AP-1 transcription factor subunit [Sou
2	218332_at	2.62	-0.7	0.29	BEX1 brain expressed X-linked 1 [Source:HGNC Symbol;Acc:HGNC
3	205767_at	2.62	-0.51	0.57	EREG epiregulin [Source:HGNC Symbol;Acc:HGNC:3443]
4	216248_s_at	2.32	-0.9	0.35	NR4A2 nuclear receptor subfamily 4 group A member 2 [Source:HGNC
5	204622_x_at	2.28	-0.78	0.35	NR4A2 nuclear receptor subfamily 4 group A member 2 [Source:HGNC
6	205051_s_at	2.19	-0.76	0.25	KIT KIT proto-oncogene receptor tyrosine kinase [Source:HGNC
7	205752_s_at	2.08	-0.69	0.31	GSTM5 glutathione S-transferase mu 5 [Source:HGNC Symbol;Acc:HGNC
8	203949_at	2.03	-0.73	0.32	MPO myeloperoxidase [Source:HGNC Symbol;Acc:HGNC:7218]
9	210426_x_at	2.01	-0.68	0.32	RORA RAR related orphan receptor A [Source:HGNC Symbol;Acc:HGNC
10	201465_s_at	1.99	-0.91	0.17	JUN Jun proto-oncogene, AP-1 transcription factor subunit [Source
11	207857_at	1.99	-0.76	0.19	LILRA2 leukocyte immunoglobulin like receptor A2 [Source:HGNC Sy
12	210254_at	1.98	-0.67	0.51	MS4A3 membrane spanning 4-domains A3 [Source:HGNC Symbol;Acc:HGNC
13	60084_at	1.96	-0.57	0.5	CYLD CYLD lysine 63 deubiquitinase [Source:HGNC Symbol;Acc:HGNC
14	214651_s_at	1.95	-0.58	0.23	HOXA9 homeobox A9 [Source:HGNC Symbol;Acc:HGNC:5109]
15	222309_at	1.95	-0.89	0.26	
16	207723_s_at	1.94	-0.77	0.19	KLRC3 killer cell lectin like receptor C3 [Source:HGNC Symbol;Acc:HGNC
17	216015_s_at	1.9	-0.45	0.51	NLRP3 NLR family pyrin domain containing 3 [Source:HGNC Symbol
18	210123_s_at	1.88	-0.81	0.41	CHRFAM7A chr7orf77 (exons 5-10) and FAM7A (exons A-E) fusion [Sour
19	209369_at	1.87	-0.57	0.38	ANXA3 annexin A3 [Source:HGNC Symbol;Acc:HGNC:541]
20	205239_at	1.86	-0.59	0.37	AREG amphiregulin [Source:HGNC Symbol;Acc:HGNC:651]

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	2e-11	26 / 218	Refer WIRTH_pre+post GC B-cells
2	2e-09	17 / 112	GSE# PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_DN
3	2e-08	205 / 6368	Colon LaPointe_mucosa-position_kmeans_F_cecum_colon_transverse_colon_UP
4	5e-08	14 / 93	Refer Chaussabel_1,4_Replication
5	2e-06	23 / 311	GSE# SHEN_SMARCA2_TARGETS_DN
6	3e-06	18 / 204	Refer Chaussabel_3,2_Inflammation I
7	8e-06	10 / 71	Pneui Burnham_cap_fp_vs_con_UP
8	9e-06	5 / 13	Refer WIRTH_Bone marrow
9	2e-05	11 / 94	GSE# GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_BLUE_UP
10	2e-05	22 / 329	MF RNA polymerase II proximal promoter sequence-specific DNA binding
11	4e-05	9 / 68	Pneui Burnham_sep_vs_con_UP
12	5e-05	8 / 54	GSE# NAGASHIMA_EGF_SIGNALING_UP
13	6e-05	6 / 29	HM HALLMARK_NOTCH_SIGNALING
14	6e-05	24 / 407	GSE# MITSIADES_RESPONSE_TO_APLIDIN_UP
15	7e-05	22 / 358	GSE# MOREAUX_MULTIPLE_MYELOMA_BY_TACI_UP
16	9e-05	9 / 75	GSE# O'DONNELL_METASTASIS_UP
17	1e-04	5 / 20	BP sodium-independent organic anion transport
18	1e-04	5 / 21	GSE# ST_GA12_PATHWAY
19	2e-04	106 / 3168	Lymph HOPP_Repressed
20	2e-04	6 / 36	Refer VAQUERIZAS_Prostate_TF
21	3e-04	3 / 6	GSE# TESAR_JAK_TARGETS_MOUSE_ES_D3_UP
22	3e-04	7 / 54	miRN hsa-miR-1184
23	3e-04	15 / 220	GSE# OSWALD_HEMATOPOIETIC_STEM_CELL_IN_COLLAGEN_GEL_UP
24	4e-04	6 / 40	BP intracellular receptor signaling pathway
25	4e-04	11 / 132	Lymph Subero_DLBCL_hyper_meth
26	4e-04	11 / 132	Gliom Christensen_hypermethylated_in_grade3_oligoastrocytoma
27	4e-04	10 / 112	Gliom Christensen_hypermethylated_in_grade3_astrocytoma
28	5e-04	35 / 788	GSE# BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP
29	5e-04	10 / 114	Gliom Christensen_hypermethylated_in_grade2_oligoastrocytoma
30	5e-04	38 / 885	BP positive regulation of transcription from RNA polymerase II promoter
31	5e-04	4 / 16	MF sodium-independent organic anion transmembrane transporter activity
32	5e-04	6 / 42	GSE# AMIT_EGF_RESPONSE_60_HELA
33	6e-04	12 / 160	GSE# CASORELLI_ACUTE_PROMYELOCYTIC_LEUKEMIA_UP
34	6e-04	8 / 77	CC specific granule membrane
35	6e-04	8 / 77	GSE# KEGG_HEMATOPOIETIC_CELL_LINEAGE
36	6e-04	7 / 60	CC tertiary granule membrane
37	6e-04	12 / 162	GSE# TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_8D_DN
38	7e-04	6 / 44	GSE# REACTOME_NUCLEAR_RECEPTOR_TRANSCRIPTION_PATHWAY
39	7e-04	6 / 44	GSE# PARENT_MTOR_SIGNALING_DN
40	7e-04	42 / 1029	GSE# DODD_NASOPHARYNGEAL_CARCINOMA_UP



Rank	p-value	#in/all	Geneset
1	0.07	5/ 92	HORVATH_aging_genes_meth_DOWN
2	0.33	1/ 107	HORVATH_aging_genes_meth_UP
3	1.00	0/ 47	TSCHEUNDORFF_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-04	5/ 20	sodium-independent organic anion transport
2	4e-04	6/ 40	intracellular receptor signaling pathway
3	5e-04	38/ 885	positive regulation of transcription from RNA polymerase II promoter
4	9e-04	21/ 403	neutrophil degranulation
5	2e-03	3/ 10	peripheral nervous system neuron development
6	2e-03	5/ 37	neurotransmitter transport
7	2e-03	3/ 11	mast cell degranulation
8	2e-03	3/ 11	positive regulation of calcium ion-dependent exocytosis
9	2e-03	6/ 56	steroid hormone mediated signaling pathway
10	3e-03	4/ 26	glutamate secretion
11	3e-03	5/ 42	response to cAMP
12	3e-03	3/ 13	calcium ion regulated exocytosis
13	3e-03	3/ 13	plasma membrane organization
14	5e-03	4/ 29	cAMP-mediated signaling
15	8e-03	3/ 17	positive regulation of excitatory postsynaptic potential

Cancer Rank	p-value	#in/all	Geneset
1	0.009	3/ 18	PanCan_Notch_geneset_nanostring
2	0.021	7/ 113	PanCan_Driver_Geneset_geneset_nanostring
3	0.024	4/ 45	KUIPER_MM_poor_survival
4	0.046	7/ 134	PanCan_RAS_geneset_nanostring
5	0.057	2/ 16	SOTTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
6	0.069	7/ 147	PanCan_MAPK_geneset_nanostring
7	0.086	5/ 93	PanCan_Tkmtreg_geneset_nanostring
8	0.132	4/ 80	PanCan_JAK-ST_geneset_nanostring
9	0.175	7/ 187	PanCan_PI3K_geneset_nanostring
10	0.200	1/ 9	WANG_ER_DN
11	0.213	5/ 130	PanCan_CC+Apop_geneset_nanostring
12	0.219	12/ 10	BENTINK_ras
13	0.257	1/ 12	LIU_BREAST_CANCER
14	0.275	1/ 13	GENTLES_modul17
15	0.275	1/ 13	GENTLES_modul18

CC Rank	p-value	#in/all	Geneset
1	6e-04	8/ 77	specific granule membrane
2	6e-04	7/ 60	tertiary granule membrane
3	2e-03	102/ 3210	plasma membrane
4	2e-03	4/ 23	voltage-gated calcium channel complex
5	4e-03	42/ 1128	integral component of plasma membrane
6	1e-02	3/ 19	Flemming body
7	1e-02	3/ 19	mast cell granule
8	1e-02	9/ 153	basolateral plasma membrane
9	2e-02	7/ 113	receptor complex
10	2e-02	2/ 10	intrinsic component of the cytoplasmic side of the plasma membrane
11	2e-02	9/ 171	nuclear chromatin
12	3e-02	4/ 47	synaptic vesicle membrane
13	3e-02	3/ 74	secretory granule
14	4e-02	50/ 1611	extracellular region
15	5e-02	5/ 81	synaptic vesicle

Chr Rank	p-value	#in/all	Geneset
1	0.02	22/ 548	Chr 16
2	0.03	28/ 776	Chr 17
3	0.22	12/ 333	Chr 2
4	0.14	9/ 242	Chr 13
5	0.15	13/ 382	Chr 15
6	0.17	38/ 1325	Chr 1
7	0.25	5/ 139	Chr 21
8	0.27	2/ 16	Chr 7
9	0.33	19/ 689	Chr 3
10	0.40	11/ 403	Chr 14
11	0.42	10/ 369	Chr 20
12	0.45	18/ 700	Chr 12
13	0.48	21/ 453	Chr 19
14	0.49	19/ 756	Chr 11
15	0.66	4/ 184	Chr 18

Chromatin states Rank	p-value	#in/all	Geneset
1	2e-06	61/ 1352	11_K9K27me3_Melanocytes
2	3e-06	91/ 2375	10_ReprPC_Fibroblasts
3	9e-06	78/ 1984	10_ReprPC_Melanocytes
4	2e-05	72/ 1813	8_EnhP_Fibroblasts
5	2e-05	68/ 1700	Bcells_peripheral_blood_11_BivFlnk
6	4e-05	87/ 2374	9_ReprPCwk_Fibroblasts
7	5e-05	124/ 3734	Tcells_peripheral_blood_13_ReprPC
8	7e-05	87/ 2417	10_ReprPCwk_Melanocytes
9	8e-05	64/ 1634	8_EnhP_Melanocytes
10	8e-05	96/ 2747	Bcells_peripheral_blood_12_EnhBiv
11	9e-05	84/ 2327	14_ReprPCwk_ESC_Mesoderm
12	2e-04	42/ 967	11_K9K27me3_MSC_Adipocyte
13	2e-04	90/ 2602	natural killer cells_peripheral_blood_12_EnhBiv
14	3e-04	120/ 3724	Tcells_peripheral_blood_12_EnhBiv
15	4e-04	22/ 401	11_K9K27me3_Skeletal_Muscle

Colon Cancer Rank	p-value	#in/all	Geneset
1	2e-08	205/ 6368	LaPointe_mucosa-position_kmeans_F_cecum_colon_transverse_colon_UP_
2	6e-08	6/ 72	Ang_CRC-CIMPH-vs-L_hyپر
3	1e-02	6/ 77	Ang_CRC_Hypermethylated
4	2e-02	20/ 492	LaPointe_mucosa-position_kmeans_C_cecum_colon_ascending_colon_trans
5	2e-02	3/ 24	Pentrack_CRC_TCGA_corr_H_mss_UP_msi-h_DN
6	3e-02	31/ 883	LaPointe_mucosa-position_kmeans_L_transverse_colon_cecum_colon_DN
7	3e-02	22/ 589	Lembcke_TCGA-expr_kmeans_E_CIMPH_UP_Cluster4_DN
8	3e-02	2/ 12	Juehling_CN2CC-mutated-in-4
9	4e-02	2/ 14	TCGA_Mutated-in-CRC_non-hypermethylated
10	6e-02	3/ 36	Ang_CRC_Hypermethylated
11	6e-02	2/ 16	Vilar_mutated-in-CRC-Camp
12	6e-02	2/ 16	Vilar_non-hypermethylated-in-CRC
13	7e-02	28/ 854	LaPointe_mucosa-position_kmeans_A_ascending_colon_UP_
14	1e-01	1/ 5	Hewish_dMMR-secondary-mutations_Apoptosis
15	1e-01	2/ 25	Ang_CRC-CIMPH-vs-L_hyپر

Glioma Rank	p-value	#in/all	Geneset
1	4e-04	11/ 132	Christensen_hypermethylated_in_grade3_oligoastrocytoma
2	4e-04	10/ 112	Christensen_hypermethylated_in_grade3_astrocytoma
3	5e-04	10/ 114	Christensen_hypermethylated_in_grade2_oligoastrocytoma
4	1e-03	8/ 87	Christensen_hypermethylated_in_secondary_glioblastoma
5	3e-03	10/ 144	Christensen_hypermethylated_in_grade2_oligodendroglioma
6	5e-03	6/ 66	Christensen_hypermethylated_in_grade2_astrocytoma
7	6e-03	14/ 268	Scov_0_05_Sturm_M2_Mesenchymal_RTK1_PDGFR_A_DN
8	7e-03	11/ 191	Scov_0_5_Sturm_CN2_RTK1_PDGFR_A_DN
9	2e-02	6/ 82	laffaire_hypermeth_LGG_vs_control
10	2e-02	3/ 22	Martini_hypermeth
11	2e-02	53/ 1652	Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
12	2e-02	2/ 10	WILLSCHER_GBM_LTSwt_proteomics-G_UP
13	2e-02	4/ 45	OL_vs_MOG-OL
14	2e-02	5/ 67	Sturm_GBM_Meth_overexpression_L_RTK1_PDGFR_A_UP
15	3e-02	4/ 50	Christensen_hypomethylated_in_primary_glioblastoma

GSEA C2 Rank	p-value	#in/all	Geneset
1	2e-09	17/ 112	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_DN
2	2e-06	23/ 311	SHEN_SMARCA2_TARGETS_DN
3	2e-05	11/ 94	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_BLUE_UP
4	5e-05	8/ 54	NASHIMA_EGF_SIGNALING_UP
5	6e-05	24/ 407	MITSUDA'S_RESPONSE_TO_APLINDIN_UP
6	7e-05	22/ 358	MOOREAU_MULTIPLE_MYELOMA_BY_TACI_UP
7	9e-05	9/ 75	ORDONNELL_METASTASIS_UP
8	1e-04	5/ 21	ST_GA12_PATHWAY
9	3e-04	3/ 6	TERRAR_JAK_TARGETS_MOUSE_ES_D3_UP
10	3e-04	11/ 220	OSWALD_HEMATOPOIETIC STEM CELL_IN_COLLAGEN_GEL_UP
11	5e-04	35/ 788	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP
12	5e-04	6/ 42	AMIT_EGF_RESPONSE_60_HELA
13	6e-04	12/ 160	CASORELLI_ACUTE_PROMYELOCYTIC_LEUKEMIA_UP
14	6e-04	8/ 77	KEGG_HEMATOPOIETIC_CELL_LINEAGE
15	6e-04	12/ 162	TAKEEDA_TARGETS_OF_NUP98_HOXA9_FUSION_8D_DN

LM Rank	p-value	#in/all	Geneset
1	6e-05	6/ 29	HALLMARK_NOTCH_SIGNALING
2	7e-03	11/ 190	HALLMARK_TNFA_SIGNALING_VIA_NFKB
3	2e-02	10/ 187	HALLMARK_INFLAMMATORY_RESPONSE
4	2e-02	10/ 193	HALLMARK_HEME_METABOLISM
5	2e-02	10/ 195	HALLMARK_KRAS_SIGNALING_DN
6	2e-01	11/ 176	HALLMARK_IL6_JAK_STAT3_SIGNALING
7	2e-01	7/ 194	HALLMARK_ESTROGEN_RESPONSE_EARLY
8	2e-01	7/ 194	HALLMARK_MYOGENESIS
9	2e-01	4/ 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING
10	2e-01	2/ 39	HALLMARK_PANCREAS_BETA_CELLS
11	3e-01	6/ 178	HALLMARK_ALLOGRAFT_REJECTION
12	3e-01	6/ 178	HALLMARK_COMPLEMENT
13	3e-01	5/ 149	HALLMARK_UV_RESPONSE_UP
14	3e-01	5/ 150	HALLMARK_APOPTOSIS
15	5e-01	5/ 181	HALLMARK_XENOBIOTIC_METABOLISM

Immunome Rank	p-value	#in/all	Geneset
1	0.01	4/ 38	Angelova Immune-metagenes-central_cells
2	0.09	2/ 21	Angelova Immune-metagenes-mememory_CD4
3	0.12	1/ 5	Angelova Immune-metagenes-NKT
4	0.22	1/ 10	Angelova Immune-metagenes-neutrophils
5	0.26	1/ 12	Angelova Immune-metagenes-memory_B_cells
6	0.28	1/ 25	Angelova Immune-metagenes-NK56_dim
7	0.28	1/ 13	Angelova Immune-metagenes-activated_B_cells
8	0.31	1/ 15	Angelova Immune-metagenes-NK
9	0.33	1/ 16	Angelova Immune-metagenes-Th17
10	0.43	1/ 23	Angelova Immune-metagenes-Th2
11	0.55	1/ 32	Angelova Immune-metagenes-effector_memory_CD8
12	0.65	1/ 42	Angelova Immune-metagenes-TGD
13	0.67	1/ 45	Angelova Immune-metagenes-MDSC
14	0.81	1/ 67	Angelova Immune-metagenes-T_cells
15	1.00	0/ 26	Angelova Immune-metagenes-activated_CD4

Lifestyle Rank	p-value	#in/all	Geneset
1	0.1	1/ 5	DUMEAUX_Estrogen_related_in_smokers_literature_genes_up
2	0.1	8/ 210	Homeu_BMI-associated_genes_DN
3	0.4	1/ 22	DUMEAUX_High bmi enriched genes
4	0.5	2/ 62	DUMEAUX_Smoking enriched genes
5	0.5	4/ 150	Homeu_BMI-associated_genes_UP
6	1.0	3/ 10	DUMEAUX_Smoking literature genes up
7	1.0	0/ 4	DUMEAUX_Exercise non smoker literature enriched genes
8	1.0	0/ 7	DUMEAUX_Estrogen_related_in_non_smokers_literature_genes_up
9	1.0	0/ 7	DUMEAUX_Hormon therapy in non smokers literature genes up
10	1.0	0/ 9	DUMEAUX_Monocytes in smokers literature genes up
11	1.0	0/ 9	DUMEAUX_Red blood cells in non smokers literature genes up
12	1.0	0/ 12	DUMEAUX_Women normal BMI literature genes up
13	1.0	0/ 22	DUMEAUX_Fasting enriched genes
14	1.0	0/ 14	Huan_blood-pressure_SBP-signature
15	1.0	0/ 13	Huan_blood-pressure_DBP-signature

Lymphoma Rank	p-value	#in/all	Geneset
1	2e-04	106/ 3168	HOPP_Repressed
2	4e-04	11/ 132	Subero_DLBCL_hyper_meth
3	1e-03	8/ 87	Hopp_Lymphoma_Epi1_with_zentr_v_B_cell_DN
4	2e-03	9/ 118	Subero_INT_hyper_meth
5	7e-03	7/ 91	Subero_T-ALL_hyper_meth
6	1e-02	4/ 35	Subero_MM_hyper_meth
7	2e-02	60/ 1894	HOPP_Poised_promoter
8	2e-02	46/ 178	TARTE_Mature plasma cell signature
9	3e-02	5/ 70	Hopp_Lymphoma_Epi1_no_zentr_3_B_cell_DN
10	3e-02	4/ 49	LEE_Developmental_regulators
11	5e-02	4/ 56	Subero_mBL_hyper_meth
12	6e-02	10/ 234	Hopp_Lymphoma_Epi1_no_zentr_6_MCL_DN
13	6e-02	34/ 2206	HOPP_Heterochromatin
14	1e-01	3/ 45	Subero_INT_hypo_meth
15	1e-01	3/ 46	Subero_DLBCL_hypo_meth

Melanoma Rank	p-value	#in/all	Geneset
1	0.03	2/ 11	Tirosh_genes shared by CD8 T-cells and malign cells in Mel79-melanoma
2	0.05	6/ 107	Tirosh_Exitus program in Mel75
3	0.06	1/ 2	Melanoma_EpEnzyme Cluster 2
4	0.06	9/ 204	Landsberg_dedifferentiation_down
5	0.08	3/ 41	Tirosh_top50 correlated genes PC3
6	0.08	8/ 185	Tirosh_genes from malignant cells in Mel79-melanoma
7	0.13	7/ 171	Landsberg_dedifferentiation_up
8	0.19	3/ 59	TCGA_melanoma_high
9	0.20	1/ 9	Joensuu_Melanoma Pigmentation subtype
10	0.21	3/ 64	Harbst_melanoma_lowgrade_up
11	0.23	2/ 37	Hugo_melanoma-all-MET_DN
12	0.28	3/ 75	Tirosh_Endothelial-cell specific genes-melanoma
13	0.31	3/ 32	Tirosh_Genes shared by CD8 T-cells and malign cells in Mel79-melanoma
14	0.33	7/ 230	Gerber_wt/wt_melanoma-cells-SpotC
15	0.36	2/ 51	Tirosh_genes from CD8 T-cells in Mel79-melanoma

MF Rank	p-value	#in/all	Geneset
1	2e-05	22/ 329	RNA polymerase II proximal promoter sequence-specific DNA binding
2	5e-04	4/ 16	sodium-independent organic anion transmembrane transporter activity
3	8e-04	32/ 722	RNA polymerase II transcription factor activity, sequence-specific DNA binding
4	6e-02	6/ 52	steroid hormone receptor activity
5	2e-03	5/ 39	nuclear receptor activity
6	3e-03	6/ 57	thiol-dependent ubiquitin-specific protease activity
7	3e-03	3/ 13	protein tyrosine kinase binding
8	4e-03	21/ 450	sequence-specific DNA binding
9	4e-03	3/ 14	antigen antiporter activity
10	5e-03	6/ 65	thiol-dependent ubiquitinyl hydrolase activity
11	5e-03	3/ 15	inorganic anion exchanger activity
12	5e-03	3/ 15	transcription coactivator binding
13	7e-03	11/ 191	transmembrane signaling receptor activity
14	1e-02	12/ 234	transcriptional activator activity, RNA polymerase II proximal promoter sequer
15	1e-02	4/ 38	signal transducer activity, downstream of receptor

mikRNA target Rank	p-value	#in/all	Geneset
1	3e-04	7/ 54	hsa-miR-1184
2	7e-04	5/ 30	hsa-miR-1258
3	6e-03	4/ 33	hsa-miR-588
4	9e-04	5/ 32	hsa-miR-514
5	2e-02	4/ 41	hsa-miR-346
6	2e-02	10/ 189	hsa-miR-27a
7	2e-02	4/ 44	hsa-miR-629
8	3e-02	5/ 71	hsa-miR-134
9	4e-02	4/ 50	hsa-miR-1251
10	4e-02	4/ 51	hsa-miR-455-3p
11	6e-02	11/ 260	hsa-let-7e
12	6e-02	4/ 59	hsa-miR-361-3p
13	7e-02	3/ 39	hsa-miR-362-3p
14	7e-02	5/ 20	hsa-miR-22
15	7e-02	4/ 64	hsa-miR-365

Pneumonia Rank	p-value	#in/all	Geneset
1	8e-06	10/ 71	Burnham_cap_fp_vs_con_UP
2	4e-05	9/ 68	Burnham_sep_vs_con_UP
3	3e-03	6/ 57	Burnham_day1_vs_5_UP
4	3e-03	3/ 48	Burnham_cap_vs_con_DN
5	1e-01	3/ 48	Burnham_viral_DN
6	2e-01	3/ 56	Burnham_sep_vs_con_DN
7	3e-01	6/ 179	Terre_MSV_multiple_respiratory_viruses_dn
8	4e-01	2/ 52	Burnham_day1_vs_5_DN
9	4e-01	2/ 54	Burnham_course
10	6e-01	1/ 33	Sweeney_viral_dn
11	6e-01		

Correlation Cluster

Spot Summary: B1

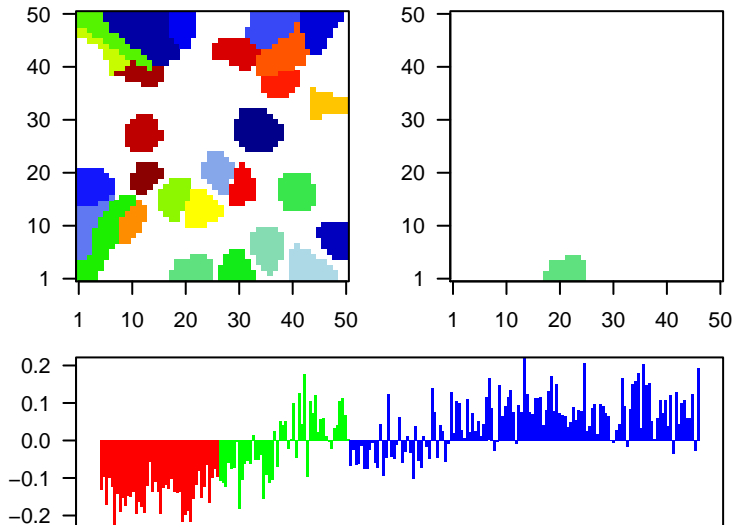
metagenes = 33
genes = 255

<r> metagenes = 0.95
<r> genes = 0.2
beta: r2= 1.78 / log p= -Inf

samples with spot = 15 (6.8 %)
intermediate : 1 (2.1 %)
non-mBL : 14 (10.9 %)

Overview Map

Spot



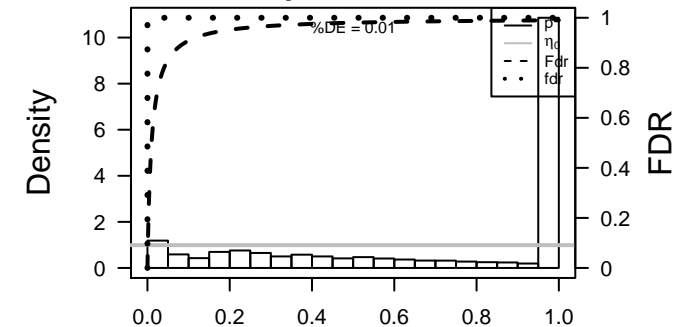
Spot Genelist

Rank	ID	max e	r	min e	Description
1	211583_x_at	3.03	-1.02	0	NCR3 natural cytotoxicity triggering receptor 3 [Source:HGNC Synt
2	204540_at	2.25	-0.76	0.29	EEF1A2 eukaryotic translation elongation factor 1 alpha 2 [Source:HG
3	207914_x_at	1.85	-1.12	0.32	EVX1 even-skipped homeobox 1 [Source:HGNC Symbol;Acc:HGNC
4	205268_s_at	1.67	-0.66	0.25	ADD2 adducin 2 [Source:HGNC Symbol;Acc:HGNC:244]
5	205612_at	1.59	-0.91	0.27	MMRN1 multimerin 1 [Source:HGNC Symbol;Acc:HGNC:7178]
6	219699_at	1.55	-0.93	0.41	LGI2 leucine rich repeat LGI family member 2 [Source:HGNC Syml
7	201203_s_at	1.49	-1.22	0.54	RRBP1 ribosome binding protein 1 [Source:HGNC Symbol;Acc:HGNC
8	203591_s_at	1.47	-0.96	0.48	CSF3R colony stimulating factor 3 receptor [Source:HGNC Symbol;A
9	205766_at	1.37	-0.83	0.51	TCAP titin-cap [Source:HGNC Symbol;Acc:HGNC:11610]
10	204443_at	1.34	-0.89	0.65	ARSA arylsulfatase A [Source:HGNC Symbol;Acc:HGNC:713]
11	202426_s_at	1.33	-0.66	0.49	RXRA retinoid X receptor alpha [Source:HGNC Symbol;Acc:HGNC:
12	221799_at	1.29	-1.42	0.45	CHPF2 chondroitin polymerizing factor 2 [Source:HGNC Symbol;Acc:
13	214428_x_at	1.29	-0.91	0.53	C4A complement C4A (Rodgers blood group) [Source:HGNC Sym
14	209506_s_at	1.29	-0.74	0.46	NR2F1 nuclear receptor subfamily 2 group F member 1 [Source:HGN
15	201206_s_at	1.27	-1.44	0.46	RRBP1 ribosome binding protein 1 [Source:HGNC Symbol;Acc:HGNC
16	215079_at	1.25	-0.66	0.35	
17	202997_s_at	1.23	-0.8	0.39	LOXL2 lysyl oxidase like 2 [Source:HGNC Symbol;Acc:HGNC:6666]
18	207765_s_at	1.23	-1.12	0.71	FAM214B family with sequence similarity 214 member B [Source:HGNC
19	221432_s_at	1.21	-1.26	0.32	SLC25A28 solute carrier family 25 member 28 [Source:HGNC Symbol;A
20	205779_at	1.2	-0.69	0.36	RAMP2 receptor activity modifying protein 2 [Source:HGNC Symbol;A

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	7e-09	46 / 1083	Colon LaPointe_mucosa-position_kmeans_J_cecum colon_ascending colon_tran
2	4e-08	23 / 353	GSE/ JOHNSTONE_PARVB_TARGETS_3_UP
3	2e-07	131 / 5404	Lymph HOPP_Strong_enhancer
4	5e-07	44 / 1166	Colon LaPointe_mucosa-position_kmeans_K_transverse colon_UP_cecum colon
5	2e-06	53 / 1602	GSE/ BLALOCK_ALZHEIMERS_DISEASE_UP
6	2e-06	21 / 376	GSE/ GARY_CD5_TARGETS_UP
7	5e-06	125 / 5339	CC membrane
8	5e-06	17 / 275	GSE/ DEBIASI_APOPTOSIS_BY_REOVIRUS_INFECTION_DN
9	1e-05	104 / 4261	Lymph HOPP_Txn_transition
10	1e-05	5 / 19	BP clathrin-dependent endocytosis
11	2e-05	49 / 1578	TF ICGC_GabpPcr2_targets
12	3e-05	34 / 938	CC Golgi apparatus
13	3e-05	15 / 251	GSE/ KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_DN
14	3e-05	23 / 518	GSE/ MILL_PSEUDOPODIA_HAPTOTAXIS_DN
15	3e-05	8 / 72	miRN hsa-miR-339-5p
16	3e-05	17 / 317	Canci SPANG_BCL6-index2
17	4e-05	125 / 5529	Lymph HOPP_Txn_elongation
18	4e-05	4 / 12	CC uropod
19	6e-05	51 / 1729	Colon LaPointe_mucosa-position_kmeans_G_cecum colon_ascending colon_UP
20	7e-05	27 / 700	GSE/ KIM_ALL_DISORDERS_OLIGODENDROCYTE_NUMBER_CORR_UP
21	7e-05	8 / 81	Gliom GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
22	8e-05	13 / 213	GSE/ THEILGAARD_NEUTROPHIL_AT_SKIN_WOUND_DN
23	8e-05	35 / 1035	CC endoplasmic reticulum
24	9e-05	6 / 43	BP cellular response to hormone stimulus
25	9e-05	130 / 5908	Lymph HOPP_Active_promoter
26	1e-04	87 / 3564	TF ICGC_Taf1_targets
27	1e-04	22 / 537	CC perinuclear region of cytoplasm
28	2e-04	8 / 90	GSE/ KAYO_CALORIE_RESTRICTION_MUSCLE_UP
29	2e-04	97 / 4131	TF ICGC_Tcf3_targets
30	2e-04	6 / 51	CC clathrin-coated vesicle
31	3e-04	90 / 3804	TF ICGC_Stat5_targets
32	3e-04	4 / 19	MF ligand-dependent nuclear receptor binding
33	3e-04	5 / 35	GSE/ CHANDRAN_METASTASIS_TOP50_DN
34	3e-04	16 / 346	GSE/ YAGI_AML_WITH_T_8_21_TRANSLOCATION
35	3e-04	11 / 183	GSE/ ZHANG_TLX_TARGETS_36HR_UP
36	3e-04	13 / 246	GSE/ DOUGLAS_BM11_TARGETS_DN
37	3e-04	10 / 155	miRN hsa-miR-586
38	4e-04	17 / 386	GSE/ MULLIGHAN_MLL_SIGNATURE_2_UP
39	4e-04	104 / 4602	TF ICGC_Elf1_targets
40	4e-04	6 / 56	GSE/ MARSON_FOXP3_TARGETS_UP

p-values



Rank	p-value	#in/all	Geneset
1	0.2	3 / 92	HORVATH_aging_genes_meth_DOWN
2	0.3	1 / 107	HORVATH_aging_genes_meth_UP
3	1.0	0 / 47	TSCHEENDORFF_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	5 / 13	clathrin-dependent endocytosis
2	9e-04	6 / 43	cellular response to hormone stimulus
3	7e-04	3 / 11	protein maturation
4	2e-03	7 / 102	macromolecular complex assembly
5	2e-03	3 / 16	actin filament-based movement
6	3e-03	3 / 17	negative regulation of stress fiber assembly
7	4e-03	4 / 38	lactation
8	5e-03	6 / 93	response to estradiol
9	7e-03	5 / 71	response to endoplasmic reticulum stress
10	9e-03	3 / 25	carbohydrate transport
11	9e-03	3 / 25	protein monoubiquitination
12	1e-02	4 / 50	endosomal transport
13	1e-02	2 / 10	positive regulation of nuclear-transcribed mRNA poly(A) tail shortening
14	1e-02	2 / 10	response to pH
15	1e-02	16 / 502	protein transport

Cancer Rank	p-value	#in/all	Geneset
1	3e-05	17 / 317	SPANG_BCL6-index2
2	2e-01	1 / 10	BENTINK_ras.4
3	2e-01	1 / 11	LIU_PROSTATE_CANCER_UP
4	2e-01	1 / 12	GENTLES_modul12
5	2e-01	1 / 12	BENTINK_ras.1
6	2e-01	1 / 13	GENTLES_modul1
7	2e-01	1 / 13	BENTINK_ras.2
8	2e-01	1 / 14	BENTINK_src.2
9	2e-01	1 / 16	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
10	2e-01	1 / 15	BEN-PORATH_UP
11	2e-01	1 / 16	GENTLES_modul16
12	3e-01	9 / 409	Lembcke_Normal_vs_Adenoma
13	4e-01	1 / 32	KUIPER_MM_good_survival
14	5e-01	1 / 36	ZHANG_MM_UP
15	5e-01	3 / 147	PanCan_MAPK_geneset_nanostring

CC Rank	p-value	#in/all	Geneset
1	5e-06	125 / 5339	membrane
2	3e-05	34 / 938	Golgi apparatus
3	4e-05	4 / 12	uropod
4	8e-05	35 / 1035	endoplasmic reticulum
5	1e-04	22 / 537	perinuclear region of cytoplasm
6	2e-04	6 / 51	clathrin-coated vesicle
7	6e-04	19 / 479	Golgi membrane
8	7e-04	24 / 663	endoplasmic reticulum membrane
9	1e-03	11 / 219	lysosomal membrane
10	2e-03	7 / 104	trans-Golgi network
11	2e-03	5 / 55	brush border
12	2e-03	5 / 55	phagocytic vesicle
13	5e-03	16 / 201	early endosome
14	5e-03	12 / 292	microtubule organizing center
15	6e-03	6 / 96	Melanosome

Chr Rank	p-value	#in/all	Geneset
1	0.003	19 / 556	Chr X
2	0.004	24 / 776	Chr 17
3	0.017	20 / 813	Chr 19
4	0.027	16 / 548	Chr 16
5	0.029	11 / 333	Chr 22
6	0.186	9 / 369	Chr 20
7	0.229	16 / 756	Chr 11
8	0.319	14 / 500	Chr 12
9	0.681	9 / 585	Chr 7
10	0.687	21 / 1325	Chr 1
11	0.720	10 / 669	Chr 6
12	0.845	7 / 554	Chr 5
13	0.898	4 / 133	Chr 15
14	0.911	8 / 689	Chr 3
15	0.913	10 / 832	Chr 2

Chromatin states Rank	p-value	#in/all	Geneset
1	6e-31	125 / 2704	4_TxTrans_Fibroblasts
2	8e-25	108 / 2380	TXEHG1_Colon
3	1e-24	139 / 3803	6_EnhG_Fibroblasts
4	5e-24	146 / 4208	Cells_peripheral_blood_6_EnhG
5	5e-23	199 / 7635	monocytes_peripheral_blood_1_TssA
6	4e-21	121 / 3223	monocytes_peripheral_blood_6_EnhG
7	5e-21	166 / 5620	TssF_Colon
8	5e-21	800 / 7957	Cells_peripheral_blood_2_TssAFlnk
9	2e-20	147 / 4635	6_EnhG_Melanocytes
10	4e-20	202 / 8200	monocytes_peripheral_blood_2_TssAFlnk
11	5e-20	204 / 8370	natural_killer_cells_peripheral_blood_2_TssAFlnk
12	3e-19	196 / 7833	Bcells_peripheral_blood_1_TssA
13	5e-19	205 / 8322	T_CD8+naive_cells_peripheral_blood_1_TssA
14	8e-19	128 / 3767	Bcells_peripheral_blood_6_EnhG
15	2e-18	198 / 8068	Thelper_cells_peripheral_blood_1_TssA

Colon Cancer Rank	p-value	#in/all	Geneset
1	7e-09	46 / 1083	LaPointe_mucosa-position_kmeans_J_cecum_colon_ascending_colon_transv
2	5e-07	44 / 1166	LaPointe_mucosa-position_kmeans_K_transverse_colon_UP_cecum_colon_transv
3	6e-05	51 / 1729	LaPointe_mucosa-position_kmeans_G_cecum_colon_ascending_colon_UP_t
4	3e-03	27 / 883	LaPointe_mucosa-position_kmeans_L_transverse_colon_cecum_colon_DN
5	6e-03	2 / 12	TCGA_CRC_aggressive-disease-markers
6	3e-02	10 / 288	Pentrack_CRC_TCGA_corr_J_msi-h_UP_mss_DN
7	4e-02	32 / 1354	LaPointe_mucosa-position_kmeans_N_cecum_colon_ascending_colon_UP_a
8	1e-01	8 / 297	Pentrack_CRC_TCGA_group_over_B_msi-h_UP
9	2e-01	1 / 10	KIM_CRC_MSI-regulated_DN
10	2e-01	16 / 738	Lembcke_TCGA_expr_kmeans_N_CIMP_H_DN
11	4e-01	9 / 448	Lembcke_TCGA_meth_kmeans_J_CIMP_H_DN
12	4e-01	22 / 1174	LaPointe_mucosa-position_kmeans_E_transverse_colon_UP_transverse_colo
13	4e-01	16 / 854	LaPointe_mucosa-position_kmeans_A_ascending_colon_UP
14	4e-01	5 / 255	Kosinski_top_crypt-long-list
15	5e-01	9 / 483	Lembcke_TCGA_expr_kmeans_H_CIMP_H_UP_Cluster3_DN

Glioma Rank	p-value	#in/all	Geneset
1	7e-05	8 / 81	GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
2	5e-04	5 / 38	WILLSCHER_GBM_Verhaak-PNwt_up
3	5e-02	4 / 78	Hopp_Sturm_GBM_Epi3_A1_Mesenchymal_UP
4	6e-02	12 / 423	Down_a
5	1e-01	1 / 75	KIM_epithelial-mesenchymal-transition_related_genes_decreased_expression
6	1e-01	4 / 109	Hopp_Sturm_GBM_Epi3_D_adult_fetus_IDH_UP
7	2e-01	1 / 10	WILLSCHER_GBM_LTSmut_proteomics-B_UP
8	2e-01	2 / 43	Patel_stemness_signatures
9	2e-01	1 / 11	Sturm_GBM_Meth_overexpression_G_IDH_UP
10	3e-01	1 / 10	WILLSCHER_GBM_STSwt_proteomics-O_UP
11	2e-01	8 / 330	Up
12	2e-01	1 / 15	Mukasa_UP_in_GBM
13	3e-01	2 / 62	GIEZELT_GBM_STS_down_VS_LTS
14	3e-01	9 / 421	Down_b
15	3e-01	1 / 21	Barbus_GBM_STS_vs_-LTS

GSEA C2 Rank	p-value	#in/all	Geneset
1	4e-08	23 / 353	JOHNSTONE_PARVB_TARGETS_3_UP
2	2e-06	53 / 1062	BLALOCK_ALZHEIMERS_DISEASE_UP
3	2e-06	21 / 376	GARY_CD5_TARGETS_UP
4	5e-06	17 / 275	DBIASI_APOPTOSIS_BY_REOVIRUS_INFECTION_DN
5	3e-05	15 / 251	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_DN
6	3e-05	23 / 518	MILI_PSEUDOPODIA_HAPTOTAXIS_DN
7	7e-05	27 / 700	KIM_ALL_DISORDERS_OLIGODENDROCYTE_NUMBER_CORR_UP
8	8e-05	13 / 213	THEILGAARD_NEUTROPHIL_AT_SKIN_WOUND_DN
9	2e-04	8 / 90	KAYO_CALORIE_RESTRICTION_MUSCLE_UP
10	3e-04	5 / 35	CHANDRAN_METASTASIS_TOP50_DN
11	3e-04	16 / 346	YAGI_AML_WITH_T_8_21_TRANSLOCATION
12	3e-04	11 / 183	ZHANG_TLX_TARGETS_36HR_UP
13	3e-04	13 / 246	DOUGLAS_BMI1_TARGETS_DN
14	4e-04	17 / 386	MULLIGHAN_MLL_SIGNATURE_2_UP
15	4e-04	6 / 56	MARSON_FOXP3_TARGETS_UP

BM Rank	p-value	#in/all	Geneset
1	0.02	3 / 35	HALLMARK_HEDGEHOG_SIGNALING
2	0.02	7 / 166	HALLMARK_INTERFERON_GAMMA_RESPONSE
3	0.04	4 / 76	HALLMARK_INTERFERON_ALPHA_RESPONSE
4	0.05	7 / 192	HALLMARK_MTORC1_SIGNALING
5	0.05	7 / 193	HALLMARK_HEME_METABOLISM
6	0.06	6 / 194	HALLMARK_MYOGENESIS
7	0.08	6 / 173	HALLMARK_MITOTIC_SPINDLE
8	0.11	4 / 106	HALLMARK_UNFOLDED_PROTEIN_RESPONSE
9	0.11	6 / 191	HALLMARK_P53_PATHWAY
10	0.14	2 / 38	HALLMARK_WNT_BETA_CATENIN_SIGNALING
11	0.14	2 / 39	HALLMARK_PANCREAS_BETA_CELLS
12	0.20	4 / 133	HALLMARK_DNA_REPAIR
13	0.22	2 / 51	HALLMARK_TGF_BETA_SIGNALING
14	0.23	5 / 190	HALLMARK_TNFA_SIGNALING_VIA_NFKB
15	0.23	3 / 97	HALLMARK_PI3K_AKT_MTOR_SIGNALING

Immunome Rank	p-value	#in/all	Geneset
1	0.003	3 / 18	Angelova Immune-metagenes-pDC
2	0.174	1 / 11	Angelova Immune-metagenes-macrophages
3	0.188	1 / 12	Angelova Immune-metagenes-memory_B-cells
4	0.188	1 / 12	Angelova Immune-metagenes-NK56_dim
5	0.242	1 / 16	Angelova Immune-metagenes-Th17
6	0.352	1 / 35	Angelova Immune-metagenes-DC
7	0.483	1 / 38	Angelova Immune-metagenes-mast-cells
8	1.000	0 / 13	Angelova Immune-metagenes-activated_B-cells
9	1.000	0 / 26	Angelova Immune-metagenes-activated_CD4
10	1.000	0 / 19	Angelova Immune-metagenes-activated_CD8
11	1.000	0 / 21	Angelova Immune-metagenes-central_memory_CD4
12	1.000	0 / 17	Angelova Immune-metagenes-central_memory_CD8
13	1.000	0 / 7	Angelova Immune-metagenes-cytotoxic_cells
14	1.000	0 / 12	Angelova Immune-metagenes-effector_memory_CD4
15	1.000	0 / 32	Angelova Immune-metagenes-effector_memory_CD8

Lifestyle Rank	p-value	#in/all	Geneset
1	0.01	9 / 210	Horuth_BMI-associated_genes_DN
2	0.02	2 / 14	Huan_blood-pressure_SBP-signature
3	0.19	1 / 12	DUMEAUX_Women_normal_BMI_literature_genes_up
4	0.32	1 / 22	DUMEAUX_Fasting_enriched_genes
5	0.43	1 / 32	Marjolein_aging_genes_DN
6	0.43	3 / 150	stomach_BMI-associated_genes_UP
7	1.00	0 / 62	DUMEAUX_Hormone_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 / 7	DUMEAUX_Hormontherapy_in_non_smokers_literature_genes_up
13	1.00	0 / 9	DUMEAUX_Monocytes_in_smokers_literature_genes_up
14	1.00	0 / 16	DUMEAUX_Red_blood_cells_in_non_smokers_literature_genes_up
15	1.00	0 / 22	DUMEAUX_High_bmi_enriched_genes

Lymphoma Rank	p-value	#in/all	Geneset
1	2e-07	131 / 5404	HOPP_Strong_enhancer
2	1e-05	104 / 4261	HOPP_Txn_transition
3	4e-05	28 / 5529	HOPP_Txn_elongation
4	9e-05	130 / 5908	HOPP_Active_promoter
5	1e-02	115 / 5682	HOPP_Weak_promoter
6	6e-02	22 / 906	SPANG_BCR_DN
7	9e-02	7 / 213	SPANG_IL21_DN
8	2e-01	1 / 14	DAVE_IL_DN
9	2e-01	1 / 14	YAMANE_AICDA_targets_recruited
10	2e-01	1 / 14	Subero_B-ALL_hypo_meth
11	2e-01	3 / 96	SPANG_LPS_6hrs_UP
12	3e-01	1 / 18	DAVE_Immune_response_2
13	4e-01	1 / 26	DAVE_Immune_response_1
14	4e-01	18 / 955	SPANG_BCR_UP
15	4e-01	1 / 33	Subero_T-PLL_hypo_meth

Melanoma Rank	p-value	#in/all	Geneset
1	0.02	9 / 236	Gerber_wt/wt_group3-specific
2	0.04	8 / 222	Gerber_wt/wt_melanoma-cells-SpotF
3	0.11	6 / 189	Tirosh_genes_preferentially_expressed_by_Tregs
4	0.16	3 / 81	Tirosh_Genes_in_the_MITF_program
5	0.17	1 / 11	Tirosh_genes_shared_by_CD8_T-cells_and_malignant_cells_in_Mel79-melanoma
6	0.21	5 / 185	Tirosh_genes_from_malignant_cells_in_Mel79-melanoma
7	0.34	4 / 171	Landsberg_dedifferentiation_up
8	0.37	2 / 85	Tirosh_endothelial-cell_specific_genes-melanoma
9	0.43	2 / 85	Tirosh_AXL-signature
10	0.49	9 / 497	Gerber_wt/wt_melanoma-cells-SpotD
11	0.49	1 / 39	Tirosh_top50_correlated_genes_PC4
12	0.51	1 / 41	Tirosh_top50_correlated_genes_PC3
13	0.51	1 / 46	Tirosh_top50_correlated_genes_PC5
14	0.59	1 / 51	Tirosh_genes_from_CD8_T-cells_in_Mel79-melanoma
15	0.67	1 / 64	Harbst_melanoma_lowgrade_up

MF Rank	p-value	#in/all	Geneset
1	3e-04	4 / 19	ligand-dependent_nuclear_receptor_binding
2	2e-03	13 / 291	actin_binding
3	2e-03	12 / 256	cadherin_binding
4	2e-03	11 / 225	transcription_coactivator_activity
5	2e-03	5 / 54	peptide_binding
6	3e-03	4 / 34	histone_acetyltransferase_activity
7	6e-03	154 / 7864	protein_binding
8	1e-02	2 / 11	small_GTPase_binding
9	2e-02	3 / 32	Hsp70_protein_binding
10	2e-02	2 / 12	actin-dependent_ATPase_activity
11	2e-02	2 / 12	misfolded_protein_binding
12	2e-02	2 / 12	ubiquitin-ubiquitin_ligase_activity
13	2e-02	2 / 13	sulfate_ester_hydrolase_activity
14	2e-02	2 / 13	vitamin_D_receptor_binding
15	2e-02	3 / 35	beta-tubulin_binding

mikRNA target Rank	p-value	#in/all	Geneset
1	3e-05	8 / 72	hsa-miR-339-5p
2	3e-04	10 / 155	hsa-miR-586
3	7e-04	6 / 63	hsa-miR-877
4	1e-03	3 / 155	hsa-miR-125-5p
5	3e-03	3 / 17	hsa-miR-323-5p
6	3e-03	4 / 36	hsa-miR-146b-3p
7	4e-03	5 / 61	hsa-miR-939
8	5e-03	5 / 64	hsa-miR-890
9	6e-03	9 / 157	hsa-miR-34b
10	8e-03	7 / 134	hsa-miR-31
11	9e-03	8 / 169	hsa-miR-148a
12	1e-02	10 / 244	hsa-miR-34c-5p
13	1e-02	3 / 26	hsa-miR-631
14	1e-02	6 / 107	hsa-miR-198
15			