

D5_mel

Global Summary

%DE = 0.21
 # genes with $fdr < 0.2$ = 2621 (1634 + / 987 -)
 # genes with $fdr < 0.1$ = 2020 (1301 + / 719 -)
 # genes with $fdr < 0.05$ = 1769 (1157 + / 612 -)
 # genes with $fdr < 0.01$ = 1159 (793 + / 366 -)
 # genes in genesets = 14839

<FC> = 0
 <shrinkage-t> = 0.05
 <p-value> = 0.07
 <fdr> = 0.79

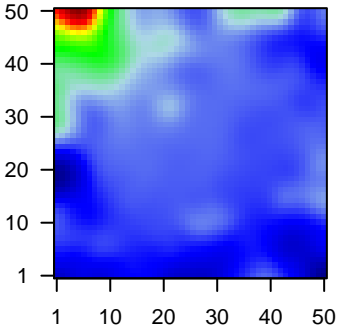
Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	ACTR10	-1.84	2e-16	2e-13	50 x 45 actin-related protein 10 homolog (S. cerevisiae) [Source:HGNC]
2	ATF4	-1.62	2e-16	2e-13	38 x 46 activating transcription factor 4 [Source:HGNC Symbol;Acc:HGNC:10549]
3	ATRX	-1.23	2e-16	2e-13	43 x 7 alpha thalassemia/mental retardation syndrome X-linked (So
4	ATXN10	-1.11	2e-16	2e-13	46 x 17 ataxin 10 [Source:HGNC Symbol;Acc:HGNC:10549]
5	BZW2	-1.72	2e-16	2e-13	2 x 16 basic leucine zipper and W2 domains 2 [Source:HGNC Synt
6	CCNG1	-1.67	2e-16	2e-13	12 x 48 cyclin G1 [Source:HGNC Symbol;Acc:HGNC:1592]
7	CDC123	-1.56	2e-16	2e-13	46 x 50 cell division cycle 123 [Source:HGNC Symbol;Acc:HGNC:166
8	CDK1	1.93	2e-16	2e-13	5 x 50 cyclin-dependent kinase 1 [Source:HGNC Symbol;Acc:HGNC:10549]
9	CDKN3	1.46	2e-16	2e-13	6 x 50 cyclin-dependent kinase inhibitor 3 [Source:HGNC Symbol;A
10	CEP97	1.76	2e-16	2e-13	2 x 47 centrosomal protein 97kDa [Source:HGNC Symbol;Acc:HGNC:10549]
11	GNL3	-1.15	2e-16	2e-13	47 x 42 guanine nucleotide binding protein-like 3 (nucleolar) [Source:
12	HIST1H4C	1.11	2e-16	2e-13	5 x 49 histone cluster 1, H4c [Source:HGNC Symbol;Acc:HGNC:478
13	IARS	-1.79	2e-16	2e-13	16 x 50 isoleucyl-tRNA synthetase [Source:HGNC Symbol;Acc:HGNC:10549]
14	LYRM2	-1.32	2e-16	2e-13	1 x 16 LYR motif containing 2 [Source:HGNC Symbol;Acc:HGNC:25
15	SEMA6A	-1.15	2e-16	2e-13	1 x 11 sema domain, transmembrane domain (TM), and cytoplasmic
16	VPS2	-1.6	2e-16	2e-13	50 x 43 vacuolar protein sorting 72 homolog (S. cerevisiae) [Source:HGNC:10549]
17	AURKB	1.77	4e-16	3e-12	6 x 50 aurora kinase B [Source:HGNC Symbol;Acc:HGNC:11390]
18	DECR1	-1.47	4e-16	3e-12	47 x 50 2,4-dienoyl CoA reductase 1, mitochondrial [Source:HGNC S
19	PRMT5	-1.48	4e-16	3e-12	34 x 50 protein arginine methyltransferase 5 [Source:HGNC Symbol;A
20	STMN1	0.71	4e-16	3e-12	5 x 50 stathmin 1 [Source:HGNC Symbol;Acc:HGNC:6510]

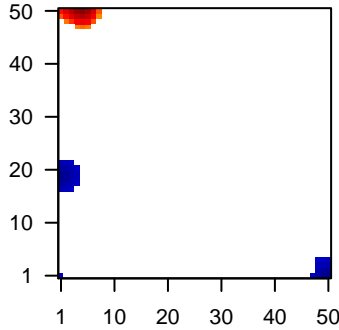
Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	22.41	9e-06	305	GSEA C2DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
2	21.42	1e-05	142	Glio WILLSCHER_GBM_Verhaak-CL_up (C)
3	19.87	1e-05	242	GSEA C2KOBAYASHI_EGFR_SIGNALING_24HR_DN
4	19.72	2e-05	139	GSEA C2ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
5	19.47	2e-05	550	GSEA C2SOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
6	19.08	1e-03	16	Cancer SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
7	17.4	3e-05	700	GSEA C2MARSON_BOUND_BY_E2F4_UNSTIMULATED
8	16.86	3e-05	390	GSEA C2PUJANA_BRCA2_PCC_NETWORK
9	16.45	4e-05	96	GSEA C2CROONQUIST_IL6_DEPRIVATION_DN
10	16.42	4e-05	162	GSEA C2GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP
11	16.32	4e-05	197	HM HALLMARK_E2F_TARGETS
12	16.23	4e-05	155	GSEA C2HOFFMANN_LARGE_TO_SMALL_PRE_BII_LYMPHOCYTE_UP
13	16.11	4e-05	81	GSEA C2GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
14	16.07	4e-05	93	GSEA C2KONG_E2F3_TARGETS
15	15.95	4e-05	267	GSEA C2ZHANG_TLX_TARGETS_60HR_DN
16	15.95	4e-05	50	GSEA C2SHIDA_E2F_TARGETS
17	15.95	4e-05	54	GSEA C2KANG_DOXORUBICIN_RESISTANCE_UP
18	15.9	4e-05	171	GSEA C2SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_UP
19	15.73	4e-05	110	GSEA C2WHITEFORD_PEDIATRIC_CANCER_MARKERS
20	15.64	4e-05	124	GSEA C2ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_24HR
<i>Underexpressed</i>				
1	-4.9	0.004	302	GSEA C2KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_DN
2	-4.6	0.005	594	GSEA C2WONG_ADULT_TISSUE_STEM_MODULE
3	-4.51	0.005	5	GSEA C2JONES_TCOF1_TARGETS
4	-4.4	0.005	37	GSEA C2KERLEY_RESPONSE_TO_CISPLATIN_UP
5	-4.39	0.006	472	GSEA C2DUTERTRE_ESTRADIOL_RESPONSE_24HR_DN
6	-4.28	0.006	28	GSEA C2SIMBULAN_PARP1_TARGETS_UP
7	-4.26	0.006	426	GSEA C2ZWANG_CLASS_1_TRANSIENTLY_INDUCED_BY_EGF
8	-4.14	0.007	2972	Brain Mid_Frontal_Lobe_ReprPC
9	-4.13	0.007	2188	Lymphoid_tOPP_Poised_promoter
10	-4.02	0.007	3396	Lymphoid_tOPP_Repressed
11	-3.93	0.008	32	GSEA C2ONGUSAHA_TP53_TARGETS
12	-3.85	0.008	13	GSEA C2AMUNDSON_DNA_DAMAGE_RESPONSE_TP53
13	-3.84	0.009	33	TF Tissue/AQUERIZAS_Prostate
14	-3.81	0.009	934	Colon Cancer/bckc_TCGA-expr_kmeans_N_CIMP_H_DN
15	-3.77	0.009	2185	Brain Fetal_TssA
16	-3.74	0.009	28	miRNA target-miR-675
17	-3.69	0.010	3081	Brain Mid_Frontal_Lobe_ZNF
18	-3.66	0.010	32	GSEA C2SCHLOSSER_MYC_AND_SERUM_RESPONSE_SYNERGY
19	-3.66	0.010	120	MF sequence-specific DNA binding RNA polymerase II transcription fa
20	-3.66	0.010	26	MF oxidoreductase activity, acting on paired donors, with incorporation

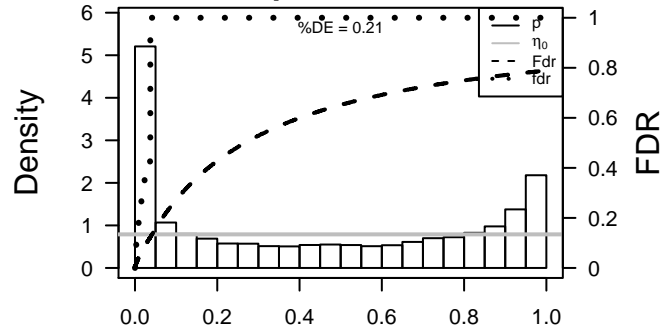
Profile



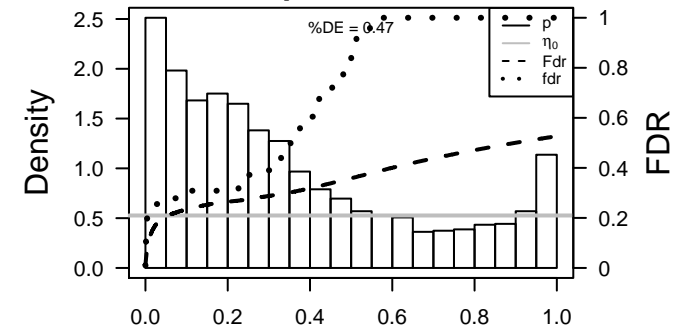
Regulated Spots



p-values



p-values



D5_mel

Local Summary

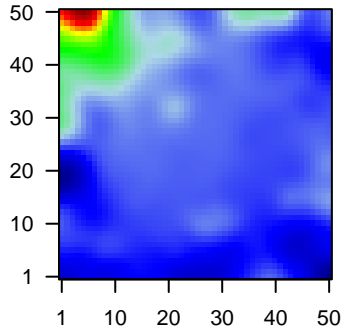
%DE = 0.93
 # metagenes = 25
 # genes = 343
 # genes in genesets = 343

 # genes with $fdr < 0.1$ = 290 (275 + / 15 -)
 # genes with $fdr < 0.05$ = 288 (273 + / 15 -)
 # genes with $fdr < 0.01$ = 249 (243 + / 6 -)

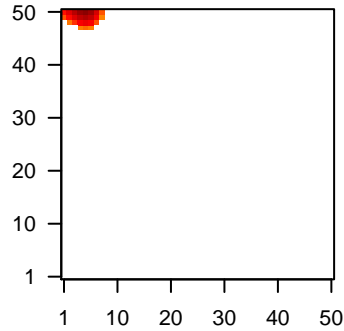
$\langle r \rangle$ metagenes = 0.93
 $\langle r \rangle$ genes = 0.31

 $\langle FC \rangle$ = 0.72
 $\langle \text{shrinkage-t} \rangle$ = 11.58
 $\langle p\text{-value} \rangle$ = 0
 $\langle fdr \rangle$ = 0.22

Profile



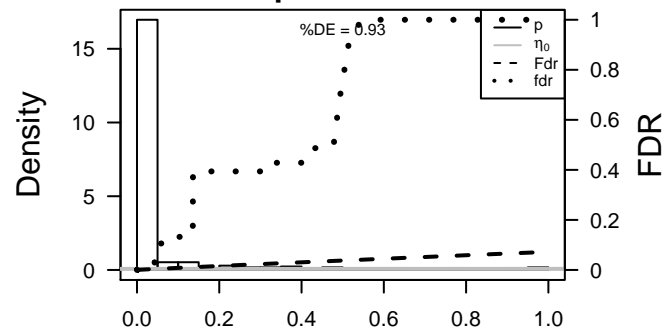
Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	CDK1	1.93	2e-16	2e-15	5 x 50 cyclin-dependent kinase 1 [Source:HGNC Symbol;Acc:HGNC:11390]
2	CDKN3	1.46	2e-16	2e-15	6 x 50 cyclin-dependent kinase inhibitor 3 [Source:HGNC Symbol;Acc:HGNC:11391]
3	HIST1H4C	1.11	2e-16	2e-15	5 x 49 histone cluster 1, H4c [Source:HGNC Symbol;Acc:HGNC:47828]
4	AURKB	1.77	4e-16	3e-14	6 x 50 aurora kinase B [Source:HGNC Symbol;Acc:HGNC:11390]
5	STMN1	0.71	4e-16	3e-14	5 x 50 stathmin 1 [Source:HGNC Symbol;Acc:HGNC:6510]
6	KNTC1	1.7	2e-15	4e-13	1 x 50 kinetochore associated 1 [Source:HGNC Symbol;Acc:HGNC:11392]
7	RRM2	1.66	2e-14	4e-13	5 x 50 ribonucleotide reductase M2 [Source:HGNC Symbol;Acc:HGNC:11393]
8	NCAPG	1.64	4e-14	4e-13	6 x 50 non-SMC condensin I complex, subunit G [Source:HGNC Symbol;Acc:HGNC:11394]
9	HIST1H1A	1.63	5e-14	4e-12	5 x 49 histone cluster 1, H1a [Source:HGNC Symbol;Acc:HGNC:47829]
10	CCNA2	1.58	4e-13	4e-12	6 x 50 cyclin A2 [Source:HGNC Symbol;Acc:HGNC:1578]
11	DNA2	1.58	4e-13	4e-12	2 x 50 DNA replication helicase/nuclease 2 [Source:HGNC Symbol;Acc:HGNC:11395]
12	CKAP2L	1.57	5e-13	7e-12	6 x 50 cytoskeleton associated protein 2-like [Source:HGNC Symbol;Acc:HGNC:11396]
13	PLK4	1.55	8e-13	1e-11	5 x 50 polo-like kinase 4 [Source:HGNC Symbol;Acc:HGNC:11397]
14	CDC42	1.54	1e-12	2e-11	7 x 50 cell division cycle associated 2 [Source:HGNC Symbol;Acc:HGNC:11398]
15	SGOL1	1.53	2e-12	1e-10	5 x 50 shugoshin-like 1 (S. pombe) [Source:HGNC Symbol;Acc:HGNC:11399]
16	ESCO2	1.47	1e-11	1e-10	4 x 50 establishment of sister chromatid cohesion N-acetyltransferase 2 [Source:HGNC Symbol;Acc:HGNC:11400]
17	MELK	1.47	1e-11	1e-10	5 x 50 maternal embryonic leucine zipper kinase [Source:HGNC Symbol;Acc:HGNC:11401]
18	FBXO5	1.46	2e-11	2e-10	4 x 50 F-box protein 5 [Source:HGNC Symbol;Acc:HGNC:13584]
19	NFYB	1.45	3e-11	2e-10	5 x 50 nuclear transcription factor Y, beta [Source:HGNC Symbol;Acc:HGNC:11402]
20	PBK	1.44	3e-11	4e-10	6 x 50 PDZ binding kinase [Source:HGNC Symbol;Acc:HGNC:1828]

p-values



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Local Summary

%DE = 0.74
 # metagenes = 1
 # genes = 62
 # genes in genesets = 62

 # genes with fdr < 0.1 = 32 (5 + / 27 -)
 # genes with fdr < 0.05 = 20 (2 + / 18 -)
 # genes with fdr < 0.01 = 12 (0 + / 12 -)

<r> metagenes = NA

<r> genes = 0.13

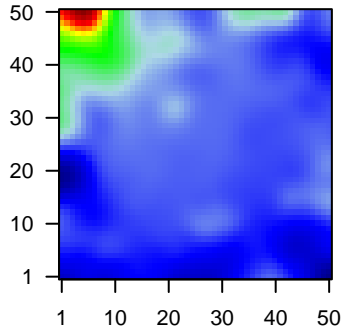
<FC> = -0.31

<shrinkage-t> = -4.74

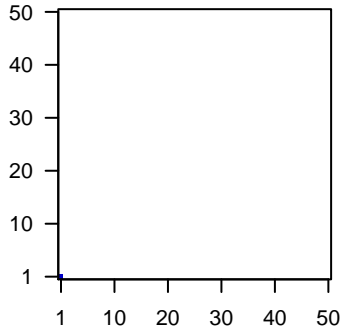
<p-value> = 0.02

<fdr> = 0.62

Profile



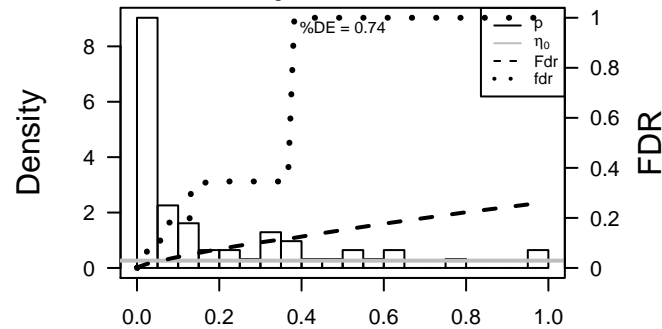
Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	MED28	-1.11	7e-08	7e-07	mediator complex subunit 28 [Source:HGNC Symbol;Acc:HG
2	DHX29	-1.15	8e-08	2e-05	DEAH (Asp-Glu-Ala-His) box polypeptide 29 [Source:HGNC
3	POGLUT1	-1.05	1e-06	2e-04	protein O-glycosyltransferase 1 [Source:HGNC Symbol;Acc:I
4	GUF1	-0.93	2e-05	2e-04	GUF1 GTPase homolog (S. cerevisiae) [Source:HGNC Symb
5	DUSP11	-0.9	4e-05	2e-04	dual specificity phosphatase 11 (RNA/RNP complex 1-intera
6	AASDHPPT	-0.89	4e-05	1e-03	aminoadipate-semialdehyde dehydrogenase-phosphopantet
7	ABCD3	-0.83	1e-04	2e-03	ATP-binding cassette, sub-family D (ALD), member 3 [Sourc
8	RAB24	-0.79	3e-04	2e-03	RAB24, member RAS oncogene family [Source:HGNC Symb
9	MED27	-0.78	3e-04	4e-03	mediator complex subunit 27 [Source:HGNC Symbol;Acc:HG
10	FAM160B1	-0.72	9e-04	4e-03	family with sequence similarity 160, member B1 [Source:HGN
11	ATG10	-0.71	1e-03	4e-03	autophagy related 10 [Source:HGNC Symbol;Acc:HGNC:203
12	FAM208B	-0.71	1e-03	4e-03	family with sequence similarity 208, member B [Source:HGN
13	KAT6A	-0.7	1e-03	2e-02	K(lysine) acetyltransferase 6A [Source:HGNC Symbol;Acc:HK
14	CHD3	-0.62	4e-03	2e-02	chromodomain helicase DNA binding protein 3 [Source:HGN
15	NLN	0.61	5e-03	2e-02	neurolysin (metallopeptidase M3 family) [Source:HGNC Symb
16	ZNF430	-0.6	5e-03	2e-02	zinc finger protein 430 [Source:HGNC Symbol;Acc:HGNC:20
17	PLOD3	0.59	6e-03	2e-02	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3 [Source
18	LYSMD1	-0.58	7e-03	2e-02	LysM, putative peptidoglycan-binding, domain containing 1 [E
19	CCDC126	-0.57	8e-03	2e-02	coiled-coil domain containing 126 [Source:HGNC Symbol;Ac
20	PSMD3	-0.56	9e-03	3e-02	proteasome (prosome, macropain) 26S subunit, non-ATPase

p-values



D5_mel

Local Summary

%DE = 0.85
 # metagenes = 13
 # genes = 234
 # genes in genesets = 234

 # genes with $fdr < 0.1$ = 136 (35 + / 101 -)
 # genes with $fdr < 0.05$ = 111 (29 + / 82 -)
 # genes with $fdr < 0.01$ = 55 (14 + / 41 -)

<r> metagenes = 0.99

<r> genes = 0.21

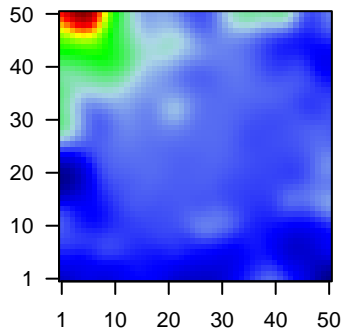
<FC> = -0.23

<shrinkage-t> = -3.62

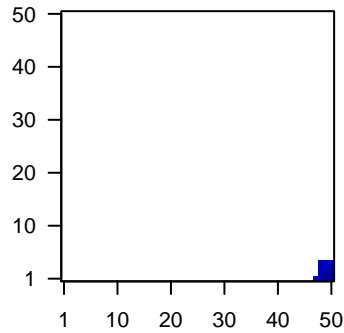
<p-value> = 0.02

<fdr> = 0.61

Profile



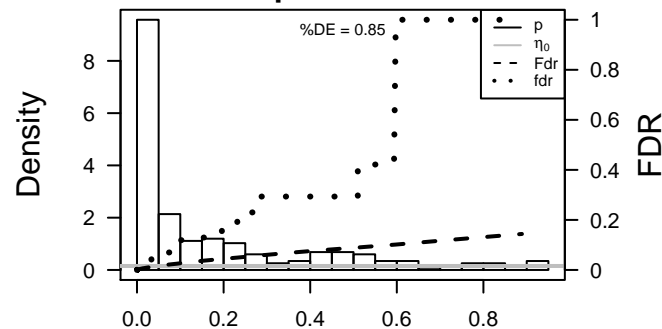
Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	ARMC9	-1.37	7e-13	6e-07	50 x 3 armadillo repeat containing 9 [Source:HGNC Symbol;Acc:HG
2	STAM	-1.1	2e-08	6e-07	50 x 3 signal transducing adaptor molecule (SH3 domain and ITAM r
3	CD55	-1.14	3e-08	1e-06	50 x 1 CD55 molecule, decay accelerating factor for complement (C
4	YPEL5	-1.15	7e-08	3e-06	50 x 1 yippee-like 5 (Drosophila) [Source:HGNC Symbol;Acc:HGNC
5	UBE2E2	-1.12	2e-07	3e-06	50 x 1 ubiquitin-conjugating enzyme E2E 2 [Source:HGNC Symbol;
6	ITFG1	1.05	2e-07	1e-05	50 x 4 integrin alpha FG-GAP repeat containing 1 [Source:HGNC S
7	MBNL2	-1.07	6e-07	1e-05	50 x 1 muscleblind-like splicing regulator 2 [Source:HGNC Symbol;
8	SORBS2	1.05	1e-06	1e-05	50 x 1 sorbin and SH3 domain containing 2 [Source:HGNC Symbol;
9	RAB3IP	1.05	1e-06	3e-05	50 x 3 RAB3A interacting protein [Source:HGNC Symbol;Acc:HGNC
10	CDKN1A	-1.02	2e-06	3e-05	50 x 1 cyclin-dependent kinase inhibitor 1A (p21, Cip1) [Source:HG
11	PDGFA	-1.01	4e-06	3e-05	49 x 1 platelet-derived growth factor alpha polypeptide [Source:HG
12	CDH19	-1	4e-06	3e-05	50 x 1 cadherin 19, type 2 [Source:HGNC Symbol;Acc:HGNC:1758]
13	CTHRC1	0.99	5e-06	6e-05	49 x 1 collagen triple helix repeat containing 1 [Source:HGNC Symb
14	SLC5A3	-0.98	6e-06	1e-04	50 x 2 solute carrier family 5 (sodium/myo-inositol cotransporter), m
15	NOV	-0.89	1e-05	1e-04	50 x 1 nephroblastoma overexpressed [Source:HGNC Symbol;Acc:HGNC:3972]
16	FSTL1	-0.92	2e-05	1e-04	50 x 1 follistatin-like 1 [Source:HGNC Symbol;Acc:HGNC:3972]
17	KITLG	0.92	2e-05	1e-04	48 x 1 KIT ligand [Source:HGNC Symbol;Acc:HGNC:6343]
18	ALCAM	-0.92	2e-05	1e-04	50 x 1 activated leukocyte cell adhesion molecule [Source:HGNC S
19	LAMC1	-0.82	3e-05	2e-04	50 x 3 laminin, gamma 1 (formerly LAMB2) [Source:HGNC Symbol;
20	TNFRSF12A	-0.89	4e-05	2e-04	50 x 1 tumor necrosis factor receptor superfamily, member 12A [Sou

p-values



D5_mel

Local Summary

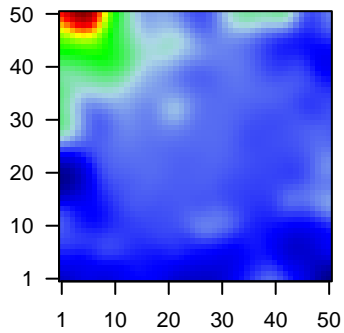
%DE = 0.64
 # metagenes = 22
 # genes = 279
 # genes in genesets = 278

 # genes with $fdr < 0.1$ = 117 (17 + / 100 -)
 # genes with $fdr < 0.05$ = 74 (8 + / 66 -)
 # genes with $fdr < 0.01$ = 57 (6 + / 51 -)

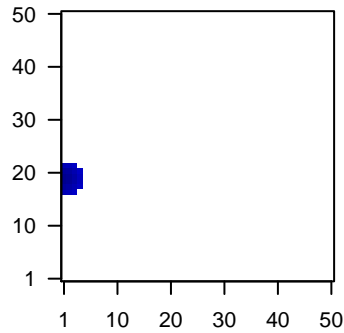
$\langle r \rangle$ metagenes = 0.94
 $\langle r \rangle$ genes = 0.14

 $\langle FC \rangle$ = -0.26
 $\langle \text{shrinkage-t} \rangle$ = -4.27
 $\langle p\text{-value} \rangle$ = 0.01
 $\langle fdr \rangle$ = 0.65

Profile



Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	JTB	-1.15	7e-15	3e-10	1 x 21 jumping translocation breakpoint [Source:HGNC Symbol;Acc:
2	FBXO7	-1.09	3e-12	7e-10	1 x 20 F-box protein 7 [Source:HGNC Symbol;Acc:HGNC:13586]
3	MPZL1	-1.22	1e-11	3e-09	1 x 19 myelin protein zero-like 1 [Source:HGNC Symbol;Acc:HGNC
4	CLTA	-1.02	4e-11	2e-07	1 x 20 clathrin, light chain A [Source:HGNC Symbol;Acc:HGNC:209]
5	PTPN2	-1.14	2e-09	3e-07	1 x 20 protein tyrosine phosphatase, non-receptor type 2 [Source:H
6	TMEM192	-1.17	6e-09	3e-07	1 x 18 transmembrane protein 192 [Source:HGNC Symbol;Acc:HGNC
7	CD47	-1.15	7e-09	1e-06	1 x 22 CD47 molecule [Source:HGNC Symbol;Acc:HGNC:1682]
8	EIF3F	-0.81	2e-08	1e-06	1 x 21 eukaryotic translation initiation factor 3, subunit F [Source:HG
9	FTH1	-0.49	3e-08	1e-06	1 x 21 ferritin, heavy polypeptide 1 [Source:HGNC Symbol;Acc:HGNC
10	MZT2B	-1.05	4e-08	2e-06	1 x 21 mitotic spindle organizing protein 2B [Source:HGNC Symbol;
11	NT5C3B	-1.15	7e-08	2e-06	1 x 20 5'-nucleotidase, cytosolic IIIB [Source:HGNC Symbol;Acc:HC
12	LMNA	-0.76	9e-08	1e-05	2 x 19 lamin A/C [Source:HGNC Symbol;Acc:HGNC:6636]
13	TRAP1	-1.11	3e-07	1e-05	1 x 18 TNF receptor-associated protein 1 [Source:HGNC Symbol;A
14	NXT1	-1.03	4e-07	1e-05	1 x 21 nuclear transport factor 2-like export factor 1 [Source:HGNC
15	DNAJC4	1.09	5e-07	5e-05	1 x 19 DnaJ (Hsp40) homolog, subfamily C, member 4 [Source:HGNC
16	APOE	-0.97	2e-06	5e-05	1 x 20 apolipoprotein E [Source:HGNC Symbol;Acc:HGNC:613]
17	ZDHHC4	-1.03	2e-06	5e-05	1 x 17 zinc finger, DHHC-type containing 4 [Source:HGNC Symbol;
18	VPS36	-0.98	2e-06	5e-05	1 x 18 vacuolar protein sorting 36 homolog (S. cerevisiae) [Source:H
19	RDX	0.9	3e-06	7e-05	1 x 22 radixin [Source:HGNC Symbol;Acc:HGNC:9944]
20	SPIRE1	-1	4e-06	7e-05	1 x 17 spire-type actin nucleation factor 1 [Source:HGNC Symbol;A

p-values

