

H11_mel

Global Summary

%DE = 0.23
 # genes with fdr < 0.2 = 3094 (1810 + / 1284 -)
 # genes with fdr < 0.1 = 2517 (1522 + / 995 -)
 # genes with fdr < 0.05 = 2205 (1337 + / 868 -)
 # genes with fdr < 0.01 = 1515 (930 + / 585 -)
 # genes in genesets = 14839

<FC> = 0
 <shrinkage-t> = -0.06
 <p-value> = 0.05
 <fdr> = 0.77

Global Genelist

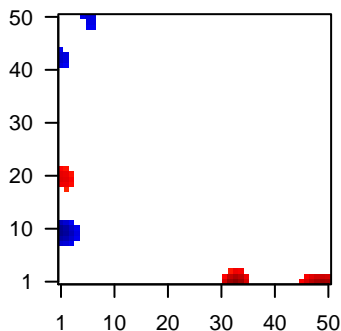
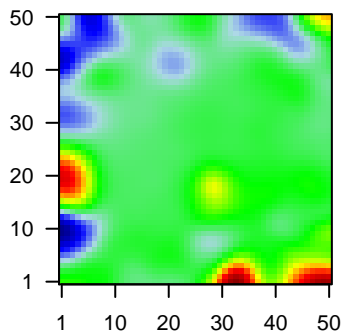
Rank	ID	log(FC)	p-value	fdr	Description
1	ABCB5	-1.61	2e-16	6e-14	1 x 43 ATP-binding cassette, sub-family B (MDR/TAP), member 5 [
2	ALDH9A1	-1.22	2e-16	6e-14	12 x 50 aldehyde dehydrogenase 9 family, member A1 [Source:HGNC
3	ALG8	-0.95	2e-16	6e-14	5 x 43 ALG8, alpha-1,3-glucosyltransferase [Source:HGNC Symb
4	ANXA1	2.13	2e-16	6e-14	50 x 1 annexin A1 [Source:HGNC Symbol;Acc:HGNC:533]
5	APEH	-1.61	2e-16	6e-14	1 x 42 acylaminoacyl-peptidase [Source:HGNC Symbol;Acc
6	APOO	-1.69	2e-16	6e-14	2 x 46 apolipoprotein O [Source:HGNC Symbol;Acc:HGNC:28727]
7	ATP5G3	-0.87	2e-16	6e-14	1 x 41 ATP synthase, H+ transporting, mitochondrial Fo complex, su
8	AUP1	-1.54	2e-16	6e-14	46 x 47 ancient ubiquitous protein 1 [Source:HGNC Symbol;Acc:HGNC
9	C5orf22	-1.56	2e-16	6e-14	2 x 12 chromosome 5 open reading frame 22 [Source:HGNC Symb
10	CAPN3	-1.12	2e-16	6e-14	1 x 43 calpain 3, (p94) [Source:HGNC Symbol;Acc:HGNC:1480]
11	CCNG1	-1.12	2e-16	6e-14	12 x 48 cyclin G1 [Source:HGNC Symbol;Acc:HGNC:1592]
12	CDC42BPA	-1.44	2e-16	6e-14	50 x 38 CDC42 binding protein kinase alpha (DMPK-like) [Source:HC
13	CDKN3	-1.65	2e-16	6e-14	6 x 50 cyclin-dependent kinase inhibitor 3 [Source:HGNC Symbol;A
14	CRYZL1	-1.72	2e-16	6e-14	44 x 50 crystallin, zeta (quinone reductase)-like 1 [Source:HGNC Syr
15	DDX39A	-1.34	2e-16	6e-14	5 x 46 DEAD (Asp-Glu-Ala-Asp) box polypeptide 39A [Source:HG
16	DGKD	1.97	2e-16	6e-14	24 x 9 diacylglycerol kinase, delta 130kDa [Source:HGNC Symbol;A
17	DHRS7	-1.56	2e-16	6e-14	41 x 49 dehydrogenase/reductase (SDR family) member 7 [Source:Hi
18	ERGIC2	-1.87	2e-16	6e-14	6 x 44 ERGIC and golgi 2 [Source:HGNC Symbol;Acc:HGNC:30208
19	ETFA	-1.37	2e-16	6e-14	3 x 33 electron-transfer-flavoprotein, alpha polypeptide [Source:HG
20	GPR143	-1.4	2e-16	6e-14	1 x 11 G protein-coupled receptor 143 [Source:HGNC Symbol;Acc:cl

Global Geneset Analysis

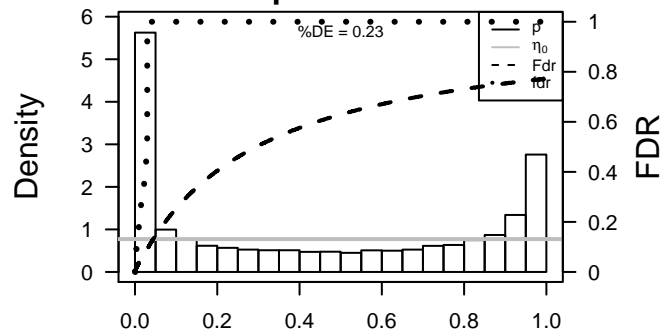
Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	5.31	0.003	925	GSEA C2KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
2	5.28	0.003	385	GSEA C2REN_ALVEOLAR_RHABDOMYOSARCOMA_DN
3	4.73	0.004	168	HM HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
4	4.71	0.004	831	GSEA C2KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
5	4.68	0.004	286	GSEA C2PASINI_SUZ12_TARGETS_DN
6	4.17	0.007	530	MF calcium ion binding
7	4.1	0.007	94	Glio WILLSCHER_GBM_proteomics_wtOnly_SpotB
8	4.07	0.007	263	Colon CaRectrack_CRC_TCGA_corr_J_msi-h_UP_mss_DN
9	4.05	0.007	85	GSEA C2BURTON_ADIPOGENESIS_9
10	4.05	0.007	212	LymphomaL1ENZ_Stromal signature 1
11	3.99	0.008	157	GSEA C2YAMAZAKI_TCEB3_TARGETS_UP
12	3.98	0.008	70	GSEA C2ONDER_CDH1_SIGNALING_VIA_CTNNB1
13	3.82	0.009	14	MF ferrous iron binding
14	3.75	0.009	281	Colon CaRectrack_CRC_TCGA_group.over_B_msi-h_UP
15	3.72	0.009	18	BP positive regulation of cell-matrix adhesion
16	3.7	0.010	9	miRNA target-miR-720
17	3.69	0.010	145	CC endoplasmic reticulum lumen
18	3.69	0.010	14	GSEA C2BIOCARTA_CDMAC_PATHWAY
19	3.68	0.010	7	TF Tissue/AQUERIZAS_Appendix
20	3.68	0.010	35	BP positive regulation of cysteine-type endopeptidase activity involve
<i>Underexpressed</i>				
1	-6.13	0.073	16	Cancer SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
2	-6.09	0.002	139	GSEA C2ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
3	-5.95	0.002	291	GSEA C2HORIUCHI_WTAP_TARGETS_DN
4	-5.85	0.002	162	GSEA C2GRAHAM_CML_DIVIDING_VS_NORMAL QUIESCENT_UP
5	-5.45	0.003	99	GSEA C2LEE_EARLY_T_LYMPHOCYTE_UP
6	-5.44	0.003	165	GSEA C2CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_UP
7	-5.39	0.003	142	Glio WILLSCHER_GBM_Verhaak-CL_up (C
8	-5.33	0.003	10	GSEA C2KUMAMOTO_RESPONSE_TO_NUTLIN_3A_DN
9	-5.33	0.003	81	GSEA C2GRAHAM_NORMAL QUIESCENT_VS_NORMAL_DIVIDING_DN
10	-5.21	0.003	436	GSEA C2SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
11	-5.2	0.003	50	GSEA C2SHIDA_E2F_TARGETS
12	-5.15	0.003	198	HM HALLMARK_OXIDATIVE_PHOSPHORYLATION
13	-5.13	0.003	54	GSEA C2KANG_DOXORUBICIN_RESISTANCE_UP
14	-5.12	0.003	245	GSEA C2MITSIADES_RESPONSE_TO_APLIDIN_DN
15	-5.09	0.003	312	BP mitotic nuclear division
16	-4.99	0.004	40	GSEA C2AMUNDSON_GAMMA_RADIATION_RESPONSE
17	-4.97	0.004	114	GSEA C2REACTOME_TCA_CYCLE_AND_RESPIRATORY_ELECTRON_T
18	-4.97	0.004	435	Disease GUDJ_poriasis up
19	-4.92	0.004	93	GSEA C2KONG_E2F3_TARGETS
20	-4.89	0.004	45	GSEA C2ZHAN_MULTIPLE_MYELOMA_PR_UP

Profile

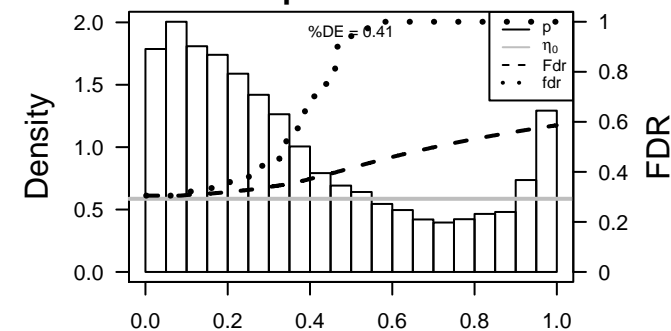
Regulated Spots



p-values



p-values



H11_mel

Local Summary

%DE = 0.76
 # metagenes = 13
 # genes = 136
 # genes in genesets = 134

 # genes with $fdr < 0.1$ = 80 (80 + / 0 -)
 # genes with $fdr < 0.05$ = 73 (73 + / 0 -)
 # genes with $fdr < 0.01$ = 63 (63 + / 0 -)

<r> metagenes = 0.95

<r> genes = 0.12

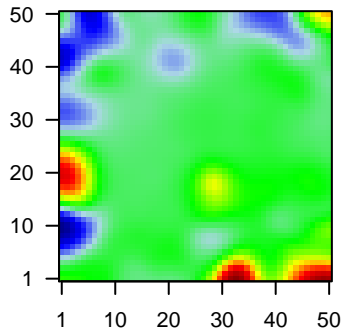
<FC> = 0.66

<shrinkage-t> = 10.06

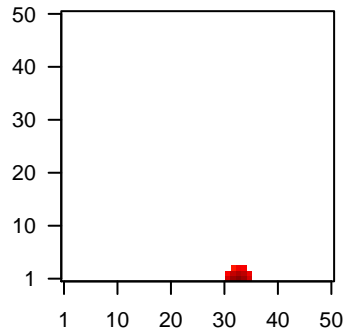
<p-value> = 0

<fdr> = 0.46

Profile



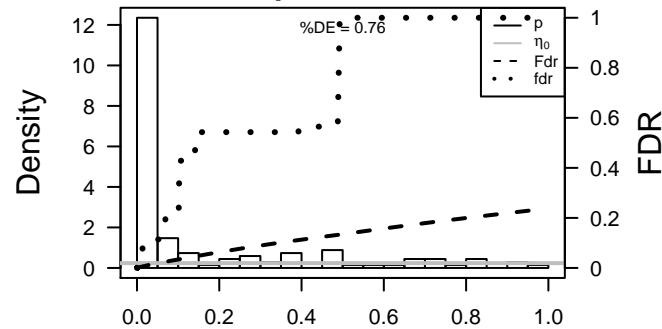
Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	AKAP7	1.92	7e-16	2e-13	33 x 1 A kinase (PRKA) anchor protein 7 [Source:HGNC Symbol;Acc:HGNC:1
2	CAPNS2	1.85	6e-15	2e-10	33 x 1 calpain, small subunit 2 [Source:HGNC Symbol;Acc:HGNC:1
3	AKR1C2	1.64	5e-12	3e-10	31 x 1 aldo-keto reductase family 1, member C2 [Source:HGNC Syr
4	APOBEC3H	1.6	1e-11	1e-09	34 x 1 apolipoprotein B mRNA editing enzyme, catalytic polypeptide
5	GBX2	1.56	4e-11	3e-09	33 x 1 gastrulation brain homeobox 2 [Source:HGNC Symbol;Acc:Hi
6	SEPT4	1.52	1e-10	2e-08	32 x 1 septin 4 [Source:HGNC Symbol;Acc:HGNC:9165]
7	ZNF701	1.46	8e-10	2e-08	33 x 1 zinc finger protein 701 [Source:HGNC Symbol;Acc:HGNC:25
8	AK8	1.44	1e-09	3e-08	32 x 1 adenylate kinase 8 [Source:HGNC Symbol;Acc:HGNC:26526
9	ADM5	1.41	3e-09	3e-08	32 x 1 adrenomedullin 5 (putative) [Source:HGNC Symbol;Acc:HGNC
10	ARID3B	1.4	4e-09	3e-08	32 x 1 AT rich interactive domain 3B (BRIGHT-like) [Source:HGNC :
11	ZNF507	1.39	5e-09	3e-08	31 x 1 zinc finger protein 507 [Source:HGNC Symbol;Acc:HGNC:23
12	NMNAT3	1.39	5e-09	3e-08	33 x 2 nicotinamide nucleotide adenylyltransferase 3 [Source:HGNC
13	BCL9	1.38	6e-09	7e-08	33 x 1 B-cell CLL/lymphoma 9 [Source:HGNC Symbol;Acc:HGNC:1
14	COL4A1	1.37	8e-09	1e-07	34 x 1 collagen, type IV, alpha 1 [Source:HGNC Symbol;Acc:HGNC:
15	AFAP1L2	1.35	1e-08	1e-07	34 x 1 actin filament associated protein 1-like 2 [Source:HGNC Syrr
16	STXBP5	1.33	2e-08	1e-07	31 x 1 syntaxin binding protein 5 (tomosyn) [Source:HGNC Symbol;
17	ARIH2OS	1.32	2e-08	1e-07	31 x 1 ariadne homolog 2 opposite strand [Source:HGNC Symbol;A
18	BTN3A3	1.32	2e-08	1e-07	35 x 1 butyrophilin, subfamily 3, member A3 [Source:HGNC Symbol
19	KLHDC8B	1.32	2e-08	1e-07	35 x 1 kelch domain containing 8B [Source:HGNC Symbol;Acc:HGNC
20	ZNF138	1.31	3e-08	1e-07	34 x 1 zinc finger protein 138 [Source:HGNC Symbol;Acc:HGNC:12

p-values



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Local Summary

%DE = 0.85
 # metagenes = 11
 # genes = 236
 # genes in genesets = 236

 # genes with $fdr < 0.1$ = 175 (155 + / 20 -)
 # genes with $fdr < 0.05$ = 140 (130 + / 10 -)
 # genes with $fdr < 0.01$ = 116 (109 + / 7 -)

<r> metagenes = 0.98

<r> genes = 0.21

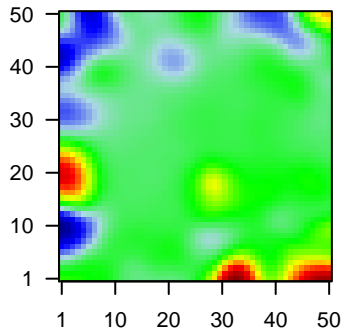
<FC> = 0.53

<shrinkage-t> = 8.44

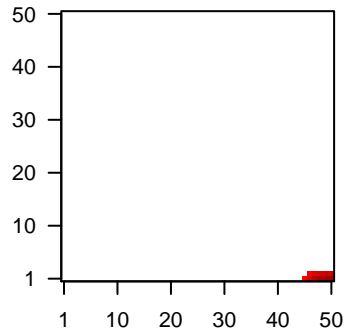
<p-value> = 0

<fdr> = 0.42

Profile



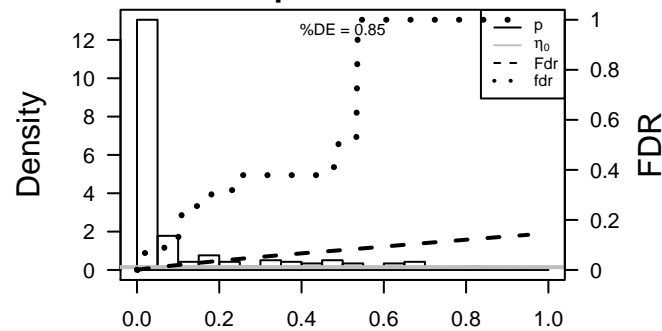
Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	ANXA1	2.13	2e-16	8e-15	50 x 1 annexin A1 [Source:HGNC Symbol;Acc:HGNC:533]
2	F2R	1.86	4e-15	8e-14	50 x 1 coagulation factor II (thrombin) receptor [Source:HGNC Synt
3	SORBS2	1.86	5e-15	4e-12	50 x 1 sorbin and SH3 domain containing 2 [Source:HGNC Symbol;
4	PLK2	1.31	1e-13	8e-11	50 x 1 polo-like kinase 2 [Source:HGNC Symbol;Acc:HGNC:19699]
5	C10orf10	1.65	3e-12	8e-11	49 x 1 chromosome 10 open reading frame 10 [Source:HGNC Synt
6	RAPH1	1.64	5e-12	8e-11	46 x 1 Ras association (RalGDS/AF-6) and pleckstrin homology dor
7	PALMD	1.63	7e-12	1e-09	50 x 1 palmdelphin [Source:HGNC Symbol;Acc:HGNC:15846]
8	THBS1	1.57	4e-11	1e-09	50 x 1 thrombospondin 1 [Source:HGNC Symbol;Acc:HGNC:11785]
9	CTHRC1	1.54	9e-11	1e-09	49 x 1 collagen triple helix repeat containing 1 [Source:HGNC Symb
10	ACTA2	1.53	1e-10	2e-09	50 x 1 actin, alpha 2, smooth muscle, aorta [Source:HGNC Symbol;
11	CNN3	0.61	2e-10	2e-09	47 x 1 calponin 3, acidic [Source:HGNC Symbol;Acc:HGNC:2157]
12	GJC1	1.5	3e-10	7e-09	46 x 1 gap junction protein, gamma 1, 45kDa [Source:HGNC Symbc
13	TNFRSF12A	1.47	6e-10	7e-09	50 x 1 tumor necrosis factor receptor superfamily, member 12A [Sou
14	VTN	1.46	8e-10	7e-09	50 x 1 vitronectin [Source:HGNC Symbol;Acc:HGNC:12724]
15	SPOCK1	1.46	8e-10	1e-08	50 x 1 sparc/osteonectin, cwcv and kazal-like domains proteoglycar
16	RGS2	1.44	1e-09	1e-08	49 x 1 regulator of G-protein signaling 2 [Source:HGNC Symbol;Acc
17	HDAC9	1.43	1e-09	1e-08	50 x 1 histone deacetylase 9 [Source:HGNC Symbol;Acc:HGNC:146
18	HSPB2-C110	1.43	2e-09	1e-08	50 x 1 HSPB2-C11orf52 readthrough (NMD candidate) [Source:HG
19	SATB1	1.4	3e-09	1e-08	50 x 1 SATB homeobox 1 [Source:HGNC Symbol;Acc:HGNC:10541]
20	LMCD1	1.4	3e-09	1e-08	47 x 1 LIM and cysteine-rich domains 1 [Source:HGNC Symbol;Acc

p-values



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Local Summary

%DE = 0.73
 # metagenes = 12
 # genes = 206
 # genes in genesets = 205

 # genes with $fdr < 0.1$ = 108 (97 + / 11 -)
 # genes with $fdr < 0.05$ = 105 (95 + / 10 -)
 # genes with $fdr < 0.01$ = 86 (79 + / 7 -)

<r> metagenes = 0.98

<r> genes = 0.17

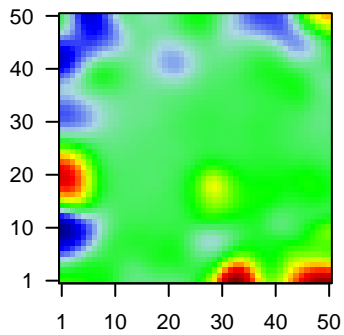
<FC> = 0.4

<shrinkage-t> = 6.73

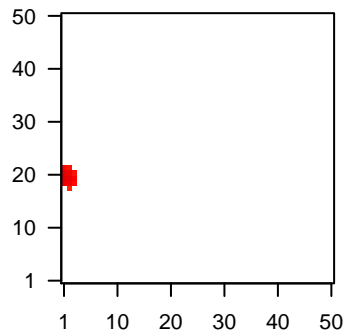
<p-value> = 0

<fdr> = 0.49

Profile



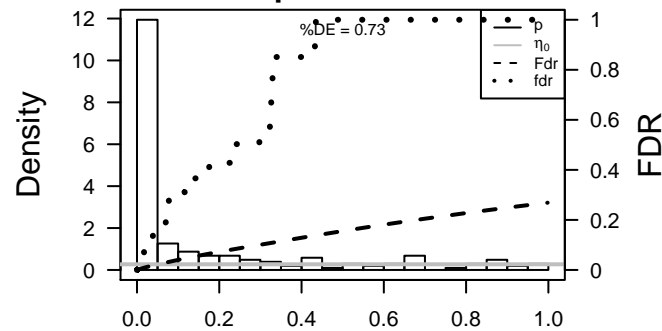
Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	DBNDD2	1.77	8e-14	2e-09	1 x 22 dysbindin (dystrobrein binding protein 1) domain containing :
2	SLC35A3	1.58	3e-11	2e-08	1 x 22 solute carrier family 35 (UDP-N-acetylglucosamine (UDP-G
3	PEX10	1.49	3e-10	2e-08	1 x 20 peroxisomal biogenesis factor 10 [Source:HGNC Symbol;Acc
4	IFNAR2	1.45	1e-09	2e-08	1 x 20 interferon (alpha, beta and omega) receptor 2 [Source:HGNC
5	MOK	-1.31	1e-09	2e-08	1 x 21 MOK protein kinase [Source:HGNC Symbol;Acc:HGNC:9833
6	TP53I13	1.43	1e-09	3e-07	1 x 20 tumor protein p53 inducible protein 13 [Source:HGNC Symb
7	P4HB	0.55	9e-09	3e-07	1 x 20 prolyl 4-hydroxylase, beta polypeptide [Source:HGNC Symb
8	CRELD2	1.35	1e-08	2e-06	1 x 20 cysteine-rich with EGF-like domains 2 [Source:HGNC Symb
9	PUSL1	1.29	5e-08	2e-06	2 x 22 pseudouridylyl synthase-like 1 [Source:HGNC Symbol;Acc:
10	NR2C2AP	1.27	9e-08	2e-06	1 x 21 nuclear receptor 2C2-associated protein [Source:HGNC Syrr
11	HEXB	1.08	1e-07	2e-06	1 x 21 hexosaminidase B (beta polypeptide) [Source:HGNC Symbol
12	RAB32	0.59	1e-07	8e-06	1 x 20 RAB32, member RAS oncogene family [Source:HGNC Symb
13	SDF2L1	1.2	4e-07	8e-06	1 x 20 stromal cell-derived factor 2-like 1 [Source:HGNC Symbol;A
14	C17orf89	1.19	5e-07	8e-06	1 x 21 chromosome 17 open reading frame 89 [Source:HGNC Synt
15	GTF3A	0.8	6e-07	1e-05	1 x 20 general transcription factor IIIA [Source:HGNC Symbol;Acc:H
16	RIOK2	1.17	8e-07	1e-05	1 x 20 RIO kinase 2 [Source:HGNC Symbol;Acc:HGNC:18999]
17	RNF135	1.16	9e-07	3e-05	2 x 19 ring finger protein 135 [Source:HGNC Symbol;Acc:HGNC:21
18	RRP7A	1.14	1e-06	4e-05	1 x 22 ribosomal RNA processing 7 homolog A (S. cerevisiae) [Sou
19	TMEM134	1.1	3e-06	4e-05	1 x 19 transmembrane protein 134 [Source:HGNC Symbol;Acc:HGNC
20	CRTAP	0.97	3e-06	5e-05	1 x 19 cartilage associated protein [Source:HGNC Symbol;Acc:HGNC

p-values



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Local Summary

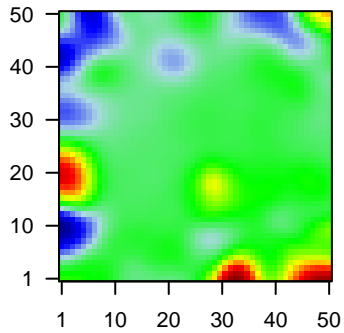
%DE = 0.84
 # metagenes = 18
 # genes = 239
 # genes in genesets = 237

 # genes with $fdr < 0.1$ = 137 (20 + / 117 -)
 # genes with $fdr < 0.05$ = 119 (15 + / 104 -)
 # genes with $fdr < 0.01$ = 90 (11 + / 79 -)

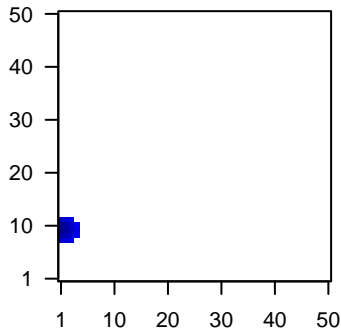
<r> metagenes = 0.95
 <r> genes = 0.13

 <FC> = -0.4
 <shrinkage-t> = -6.9
 <p-value> = 0
 <fdr> = 0.52

Profile



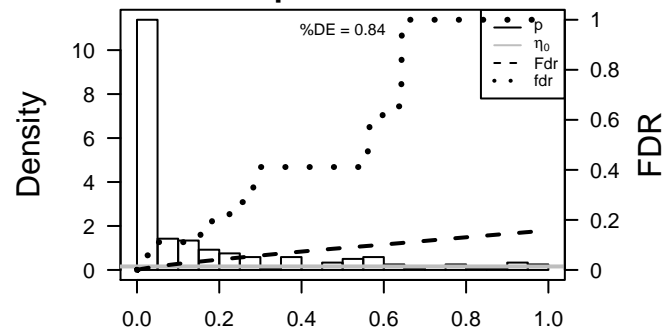
Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	C5orf22	-1.56	2e-16	2e-15	2 x 12 chromosome 5 open reading frame 22 [Source:HGNC Symbol;Acc:NC_000005.7]
2	GPR143	-1.4	2e-16	2e-15	1 x 11 G protein-coupled receptor 143 [Source:HGNC Symbol;Acc:NC_000005.7]
3	MSMO1	-1.48	2e-16	2e-15	1 x 8 methylsterol monooxygenase 1 [Source:HGNC Symbol;Acc:NC_000005.7]
4	SDCBP	-1.5	2e-16	2e-15	3 x 11 syndecan binding protein (syntenin) [Source:HGNC Symbol;Acc:NC_000005.7]
5	UGCG	-1.64	2e-16	2e-15	1 x 11 UDP-glucose ceramide glucosyltransferase [Source:HGNC Symbol;Acc:NC_000005.7]
6	RAB27A	-1.52	5e-15	9e-12	1 x 11 RAB27A, member RAS oncogene family [Source:HGNC Symbol;Acc:NC_000005.7]
7	FMN1	-1.46	3e-13	9e-12	2 x 10 formin 1 [Source:HGNC Symbol;Acc:HGNC:3768]
8	SEMA6A	-0.9	5e-13	9e-12	1 x 11 sema domain, transmembrane domain (TM), and cytoplasmic tail domain containing protein 6A [Source:HGNC Symbol;Acc:NC_000005.7]
9	DCT	-0.99	7e-13	1e-11	1 x 11 dopachrome tautomerase [Source:HGNC Symbol;Acc:HGNC:10000]
10	EDNRB	-1.34	1e-12	5e-10	1 x 11 endothelin receptor type B [Source:HGNC Symbol;Acc:HGNC:10000]
11	WDFY1	-1.4	3e-11	5e-10	1 x 12 WD repeat and FYVE domain containing 1 [Source:HGNC Symbol;Acc:NC_000005.7]
12	CHMP2B	-1.12	3e-11	3e-09	3 x 10 charged multivesicular body protein 2B [Source:HGNC Symbol;Acc:NC_000005.7]
13	TRAK2	-0.97	2e-10	3e-09	1 x 12 trafficking protein, kinesin binding 2 [Source:HGNC Symbol;Acc:NC_000005.7]
14	HSPB8	-1.35	2e-10	4e-08	1 x 11 heat shock 22kDa protein 8 [Source:HGNC Symbol;Acc:HGNC:10000]
15	SNAI2	-1.31	1e-09	5e-08	1 x 11 snail family zinc finger 2 [Source:HGNC Symbol;Acc:HGNC:10000]
16	HMGCR	-1.07	3e-09	1e-07	2 x 11 3-hydroxy-3-methylglutaryl-CoA reductase [Source:HGNC Symbol;Acc:NC_000005.7]
17	SAT1	-0.56	6e-09	8e-07	1 x 11 spermidine/spermine N1-acetyltransferase 1 [Source:HGNC Symbol;Acc:NC_000005.7]
18	GPRC5B	-1.21	5e-08	8e-07	1 x 12 G protein-coupled receptor, class C, group 5, member B [Source:HGNC Symbol;Acc:NC_000005.7]
19	PAIP1	-1.02	6e-08	8e-07	1 x 9 poly(A) binding protein interacting protein 1 [Source:HGNC Symbol;Acc:NC_000005.7]
20	PPARGC1A	-1.14	7e-08	1e-05	1 x 10 peroxisome proliferator-activated receptor gamma, coactivator 1A [Source:HGNC Symbol;Acc:NC_000005.7]

p-values



H11_mel

Local Summary

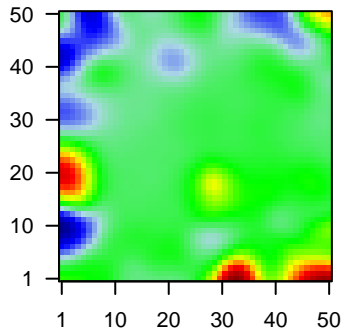
%DE = 0.82
 # metagenes = 7
 # genes = 146
 # genes in genesets = 146

 # genes with $fdr < 0.1$ = 97 (16 + / 81 -)
 # genes with $fdr < 0.05$ = 94 (16 + / 78 -)
 # genes with $fdr < 0.01$ = 78 (12 + / 66 -)

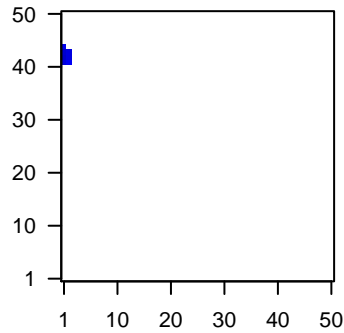
$\langle r \rangle$ metagenes = 0.98
 $\langle r \rangle$ genes = 0.23

 $\langle FC \rangle$ = -0.45
 $\langle \text{shrinkage-t} \rangle$ = -9.73
 $\langle p\text{-value} \rangle$ = 0
 $\langle fdr \rangle$ = 0.38

Profile



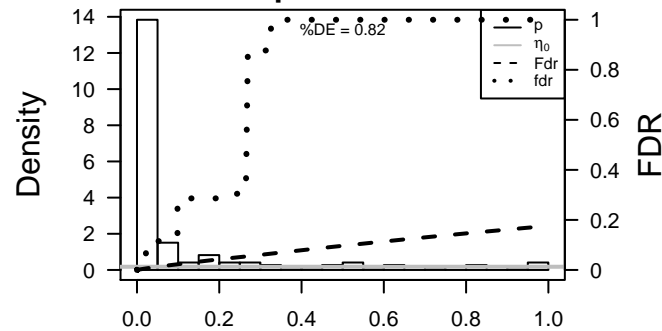
Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	ABCB5	-1.61	2e-16	4e-16	1 x 43 ATP-binding cassette, sub-family B (MDR/TAP), member 5 [
2	APEH	-1.61	2e-16	4e-16	1 x 42 acylaminoacyl-peptide hydrolase [Source:HGNC Symbol;Acc
3	ATP5G3	-0.87	2e-16	4e-16	1 x 41 ATP synthase, H+ transporting, mitochondrial Fo complex, su
4	CAPN3	-1.12	2e-16	4e-16	1 x 43 calpain 3, (p94) [Source:HGNC Symbol;Acc:HGNC:1480]
5	IDH3A	-1.04	2e-16	4e-16	1 x 42 isocitrate dehydrogenase 3 (NAD+) alpha [Source:HGNC Syr
6	MLANA	-1.83	2e-16	4e-16	1 x 43 melan-A [Source:HGNC Symbol;Acc:HGNC:7124]
7	MYH10	-1.33	2e-16	4e-16	1 x 44 myosin, heavy chain 10, non-muscle [Source:HGNC Symbol.
8	NARS2	-1.08	2e-16	4e-16	1 x 42 asparaginyl-tRNA synthetase 2, mitochondrial (putative) [So
9	PDE4DIP	-1.55	2e-16	4e-16	1 x 43 phosphodiesterase 4D interacting protein [Source:HGNC Syn
10	RNF14	-1.45	2e-16	4e-16	1 x 43 ring finger protein 14 [Source:HGNC Symbol;Acc:HGNC:100:
11	SLC24A5	-1.48	2e-16	4e-16	1 x 43 solute carrier family 24 (sodium/potassium/calcium exchange
12	ST6GALNAC1	-1.6	2e-16	4e-16	1 x 44 ST6 (alpha-N-acetyl-neuraminy-2,3-beta-galactosyl-1,3)-
13	TRPM1	-1.43	2e-16	4e-16	1 x 42 transient receptor potential cation channel, subfamily M, merr
14	TYR	-1.5	2e-16	4e-16	1 x 42 tyrosinase [Source:HGNC Symbol;Acc:HGNC:12442]
15	MBP	-0.77	7e-16	9e-14	1 x 42 myelin basic protein [Source:HGNC Symbol;Acc:HGNC:6925
16	FAM213A	-1.39	4e-15	4e-13	1 x 41 family with sequence similarity 213, member A [Source:HGNC
17	NT5DC3	-1.21	2e-14	6e-13	1 x 41 5'-nucleotidase domain containing 3 [Source:HGNC Symbol;
18	SLC18B1	-1.34	4e-14	8e-13	1 x 42 solute carrier family 18, subfamily B, member 1 [Source:HGNC
19	MLPH	-1.48	7e-14	6e-11	1 x 43 melanophilin [Source:HGNC Symbol;Acc:HGNC:29643]
20	CHCHD6	-0.88	3e-12	6e-11	1 x 43 coiled-coil-helix-coiled-coil-helix domain containing 6 [Sour

p-values



H11_mel

Local Summary

%DE = 0.85
 # metagenes = 7
 # genes = 126
 # genes in genesets = 126

 # genes with $fdr < 0.1$ = 91 (10 + / 81 -)
 # genes with $fdr < 0.05$ = 79 (10 + / 69 -)
 # genes with $fdr < 0.01$ = 45 (8 + / 37 -)

<r> metagenes = 0.99

<r> genes = 0.48

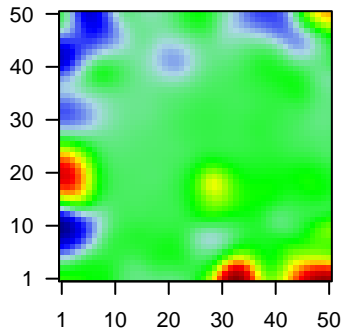
<FC> = -0.39

<shrinkage-t> = -6.26

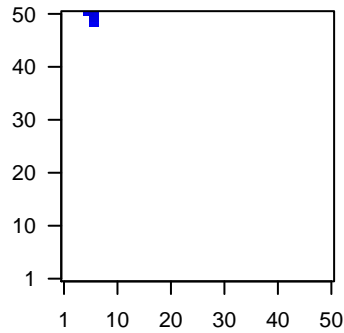
<p-value> = 0.01

<fdr> = 0.53

Profile



Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	CDKN3	-1.65	2e-16	4e-15	6 x 50 cyclin-dependent kinase inhibitor 3 [Source:HGNC Symbol;A
2	CKS2	-1.22	4e-12	3e-09	5 x 50 CDC28 protein kinase regulatory subunit 2 [Source:HGNC Sy
3	MAD2L1	-1.35	2e-10	1e-07	5 x 50 MAD2 mitotic arrest deficient-like 1 (yeast) [Source:HGNC S
4	DEPDC1B	1.37	7e-09	7e-07	7 x 50 DEP domain containing 1B [Source:HGNC Symbol;Acc:HGN
5	PLK4	1.3	4e-08	7e-07	5 x 50 polo-like kinase 4 [Source:HGNC Symbol;Acc:HGNC:11397]
6	C5orf34	1.26	1e-07	7e-07	6 x 50 chromosome 5 open reading frame 34 [Source:HGNC Symbc
7	PRC1	-1.2	1e-07	4e-06	5 x 50 protein regulator of cytokinesis 1 [Source:HGNC Symbol;Acc:
8	MPHOSPH9	-1.17	4e-07	4e-06	7 x 49 M-phase phosphoprotein 9 [Source:HGNC Symbol;Acc:HGN
9	FAM64A	1.19	5e-07	1e-05	7 x 50 family with sequence similarity 64, member A [Source:HGNC
10	ZWINT	-1.13	1e-06	1e-05	5 x 50 ZW10 interacting kinetochore protein [Source:HGNC Symbol;
11	CENPF	-1.07	2e-06	2e-05	6 x 50 centromere protein F, 350/400kDa [Source:HGNC Symbol;Ac
12	CDK1	-1.11	2e-06	3e-05	5 x 50 cyclin-dependent kinase 1 [Source:HGNC Symbol;Acc:HGN
13	CENPW	-1.08	4e-06	6e-05	6 x 50 centromere protein W [Source:HGNC Symbol;Acc:HGNC:214
14	UBE2C	-1.05	8e-06	6e-05	6 x 50 ubiquitin-conjugating enzyme E2C [Source:HGNC Symbol;A
15	HMGB2	-0.95	1e-05	5e-04	5 x 50 high mobility group box 2 [Source:HGNC Symbol;Acc:HGNC:
16	CCNB2	-0.94	7e-05	5e-04	6 x 50 cyclin B2 [Source:HGNC Symbol;Acc:HGNC:1580]
17	RHNO1	-0.93	9e-05	5e-04	5 x 50 RAD9-HUS1-RAD1 interacting nuclear orphan 1 [Source:HC
18	SPAG5	-0.93	9e-05	5e-04	6 x 50 sperm associated antigen 5 [Source:HGNC Symbol;Acc:HGN
19	TPX2	-0.92	1e-04	7e-04	6 x 50 TPX2, microtubule-associated [Source:HGNC Symbol;Acc:H
20	MIS18BP1	-0.9	1e-04	1e-03	6 x 50 MIS18 binding protein 1 [Source:HGNC Symbol;Acc:HGNC:2

p-values

