

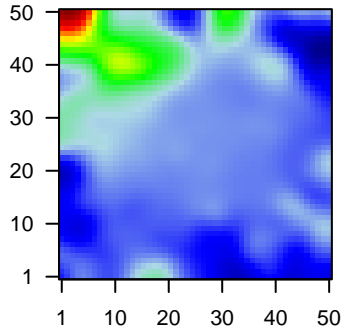
C12_mel

Global Summary

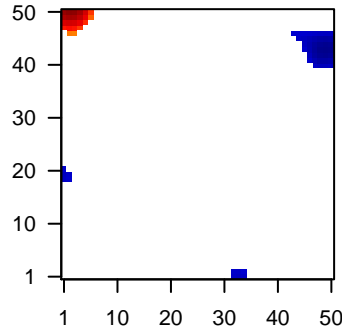
%DE = 0.21
 # genes with fdr < 0.2 = 2695 (1634 + / 1061 -)
 # genes with fdr < 0.1 = 2155 (1336 + / 819 -)
 # genes with fdr < 0.05 = 1763 (1104 + / 659 -)
 # genes with fdr < 0.01 = 1117 (721 + / 396 -)
 # genes in genesets = 14839

<FC> = 0
 <shrinkage-t> = 0.03
 <p-value> = 0.08
 <fdr> = 0.79

Profile



Regulated Spots



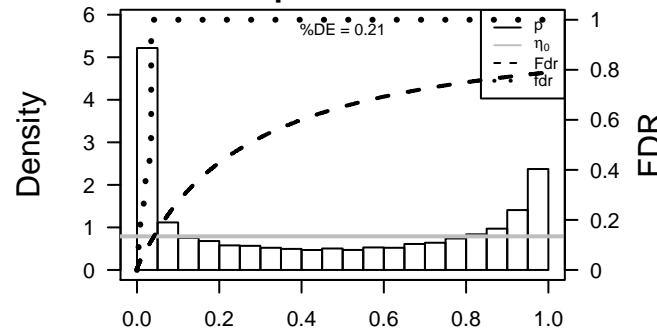
Global Genelist

Rank	ID	log(FC)	fdr	Description	
		p-value		Metagene	
1	AAMDC	-0.98	2e-16	2e-13	41 x 46 adipogenesis associated, Mth938 domain containing [Source:HGNC Symbol;Acc:HGNC:545]
2	ANXA7	-1.38	2e-16	2e-13	25 x 48 annexin A7 [Source:HGNC Symbol;Acc:HGNC:545]
3	BCAP29	-1.62	2e-16	2e-13	41 x 47 B-cell receptor-associated protein 29 [Source:HGNC Symbol;Acc:HGNC:545]
4	CCT7	-1.3	2e-16	2e-13	1 x 17 chaperonin containing TCP1, subunit 7 (eta) [Source:HGNC Symbol;Acc:HGNC:545]
5	DCAF13	-1.42	2e-16	2e-13	1 x 1 DDB1 and CUL4 associated factor 13 [Source:HGNC Symbol;Acc:HGNC:545]
6	GLUL	-1.56	2e-16	2e-13	36 x 1 glutamate-ammonia ligase [Source:HGNC Symbol;Acc:HGNC:545]
7	HN1	-1.67	2e-16	2e-13	47 x 39 hematological and neurological expressed 1 [Source:HGNC Symbol;Acc:HGNC:545]
8	HSPH1	-1.53	2e-16	2e-13	27 x 11 heat shock 105kDa/110kDa protein 1 [Source:HGNC Symbol;Acc:HGNC:545]
9	LLPH	-1.51	2e-16	2e-13	19 x 8 LLP homolog, long-term synaptic facilitation (Aplysia) [Source:HGNC Symbol;Acc:HGNC:545]
10	MSC	-1.62	2e-16	2e-13	32 x 1 musculin [Source:HGNC Symbol;Acc:HGNC:7321]
11	OPHN1	2.15	2e-16	2e-13	36 x 28 oligophrenin 1 [Source:HGNC Symbol;Acc:HGNC:8148]
12	PPIP5K2	-1.49	2e-16	2e-13	27 x 12 diphosphoinositol pentakisphosphate kinase 2 [Source:HGNC Symbol;Acc:HGNC:8148]
13	SBDS	-1.42	2e-16	2e-13	44 x 45 Shwachman-Bodian-Diamond syndrome [Source:HGNC Symbol;Acc:HGNC:8148]
14	SCP2	-1.54	2e-16	2e-13	50 x 40 sterol carrier protein 2 [Source:HGNC Symbol;Acc:HGNC:10148]
15	SLC6A15	-1.84	2e-16	2e-13	48 x 45 solute carrier family 6 (neutral amino acid transporter), memb
16	VPS2	-1.47	2e-16	2e-13	50 x 43 vacuolar protein sorting 72 homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:HGNC:10148]
17	WBSR22	-1.75	2e-16	2e-13	45 x 48 Williams Beuren syndrome chromosome region 22 [Source:HGNC Symbol;Acc:HGNC:10148]
18	KLHL32	1.89	4e-16	5e-12	16 x 40 kelch-like family member 32 [Source:HGNC Symbol;Acc:HGNC:10148]
19	PYURF	-1.52	4e-16	5e-12	1 x 19 PIGY upstream reading frame [Source:HGNC Symbol;Acc:HGNC:10148]
20	STOM	-1.46	4e-16	5e-12	50 x 14 stomatin [Source:HGNC Symbol;Acc:HGNC:3383]

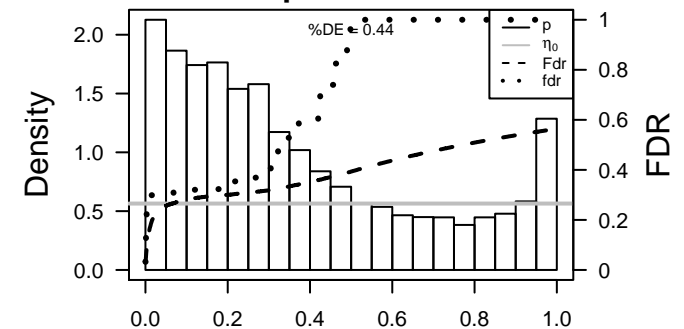
Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	18.25	2e-05	305	GSEA C2DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
2	15.38	5e-05	242	GSEA C2KOBAYASHI_EGFR_SIGNALING_24HR_DN
3	15.05	5e-05	197	HM HALLMARK_E2F_TARGETS
4	14.98	5e-05	550	GSEA C2GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
5	14.37	6e-05	267	GSEA C2ZHANG_TLX_TARGETS_60HR_DN
6	14.04	7e-05	142	Glio WILLSCHER_GBM_Verhaak-CL_up (C)
7	12.96	9e-05	390	GSEA C2PUJANA_BRCA2_PCC_NETWORK
8	12.94	9e-05	436	GSEA C2SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
9	12.35	1e-04	700	GSEA C2MARSON_BOUND_BY_E2F4_UNSTIMULATED
10	12.27	1e-04	81	GSEA C2GRAHAM_NORMAL QUIESCENT_VS_NORMAL_DIVIDING_DN
11	12.23	1e-04	1192	GSEA C2KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
12	11.94	1e-04	171	GSEA C2SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_UP
13	11.83	1e-04	327	GSEA C2BLUM_RESPONSE_TO_SALIRASIB_DN
14	11.72	1e-04	99	GSEA C2BURTON_ADIPOGENESIS_3
15	11.69	1e-04	145	GSEA C2CHANG_CYCLING_GENES
16	11.69	1e-04	139	GSEA C2ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
17	11.28	2e-04	160	GSEA C2PUJANA_XPRSS_INT_NETWORK
18	11.11	2e-04	68	GSEA C2VERNELL_RETINOBLASTOMA_PATHWAY_UP
19	11.08	2e-04	162	GSEA C2GRAHAM_CML_DIVIDING_VS_NORMAL QUIESCENT_UP
20	11.05	2e-04	724	GSEA C2PUJANA_CHEK2_PCC_NETWORK
<i>Underexpressed</i>				
1	-5.31	0.003	930	GSEA C2NUYTEN_EZH2_TARGETS_UP
2	-4.13	0.007	85	GSEA C2KEEN_RESPONSE_TO_ROSIGLITAZONE_DN
3	-3.85	0.008	245	GSEA C2WANG_SMARCE1_TARGETS_UP
4	-3.78	0.009	315	Glio WILLSCHER_GBM_Verhaak-PNwt & CL_up
5	-3.71	0.010	18	BP membrane protein ectodomain proteolysis
6	-3.68	0.010	10	GSEA C2REACTOME_SIGNALING_BY_NOTCH2
7	-3.66	0.010	298	Cancer SPANG_BCL6-index2
8	-3.57	0.011	44	miRNA target-miR-640
9	-3.56	0.011	39	CC autophagic vacuole
10	-3.55	0.011	594	GSEA C2WONG_ADULT_TISSUE_STEM_MODULE
11	-3.52	0.011	104	MF iron ion binding
12	-3.51	0.011	19	BP Notch receptor processing
13	-3.48	0.012	314	GSEA C2RICKMAN_METASTASIS_UP
14	-3.48	0.012	80	miRNA target-miR-584
15	-3.43	0.012	15	MF L-ascorbic acid binding
16	-3.42	0.012	10	GSEA C2REACTOME_SIGNALING_BY_NOTCH3
17	-3.41	0.012	164	GSEA C2TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_HSC_UP
18	-3.4	0.013	20	GSEA C2DAVIES_MULTIPLE_MYELOMA_VS_MGUS_DN
19	-3.39	0.013	24	miRNA target-miR-602
20	-3.35	0.013	385	GSEA C2REN_ALVEOLAR_RHABDOMYOSARCOMA_DN

p-values



p-values



C12_mel

Local Summary

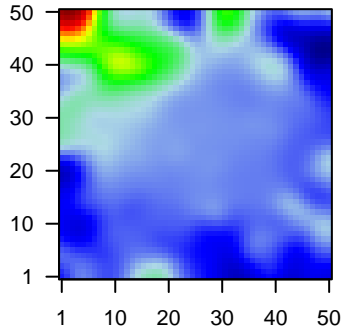
%DE = 0.89
 # metagenes = 23
 # genes = 349
 # genes in genesets = 348

 # genes with $fdr < 0.1$ = 282 (250 + / 32 -)
 # genes with $fdr < 0.05$ = 282 (250 + / 32 -)
 # genes with $fdr < 0.01$ = 202 (188 + / 14 -)

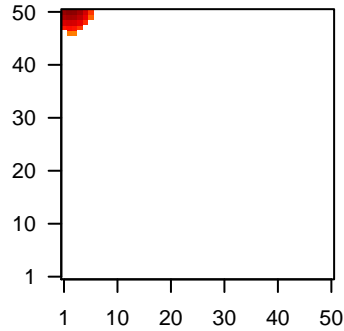
$\langle r \rangle$ metagenes = 0.93
 $\langle r \rangle$ genes = 0.28

 $\langle FC \rangle$ = 0.56
 $\langle \text{shrinkage-t} \rangle$ = 8.94
 $\langle p\text{-value} \rangle$ = 0
 $\langle fdr \rangle$ = 0.32

Profile



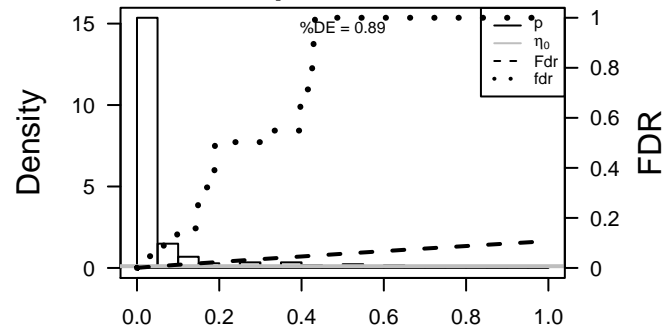
Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	ACTL6A	1.08	5e-15	2e-11	4 x 50 actin-like 6A [Source:HGNC Symbol;Acc:HGNC:24124]
2	NCAPH2	1.68	5e-13	2e-11	1 x 50 non-SMC condensin II complex, subunit H2 [Source:HGNC S
3	DTL	1.66	9e-13	9e-10	1 x 50 denticleless E3 ubiquitin protein ligase homolog (Drosophila)
4	ANLN	1.55	3e-11	9e-10	5 x 50 anillin, actin binding protein [Source:HGNC Symbol;Acc:HGN
5	POLA2	1.53	5e-11	3e-09	1 x 48 polymerase (DNA directed), alpha 2, accessory subunit [Sour
6	ZGRF1	1.49	1e-10	7e-09	1 x 50 zinc finger, GRF-type containing 1 [Source:HGNC Symbol;Ac
7	ORC1	1.45	5e-10	7e-09	1 x 49 origin recognition complex, subunit 1 [Source:HGNC Symbol;
8	CHEK2	1.44	5e-10	7e-09	3 x 50 checkpoint kinase 2 [Source:HGNC Symbol;Acc:HGNC:1662
9	MCM5	1.43	8e-10	7e-09	1 x 49 minichromosome maintenance complex component 5 [Source
10	EXO1	1.43	8e-10	9e-09	1 x 50 exonuclease 1 [Source:HGNC Symbol;Acc:HGNC:3511]
11	KIF2C	1.42	1e-09	2e-08	6 x 50 kinesin family member 2C [Source:HGNC Symbol;Acc:HGNC
12	CDC45	1.4	2e-09	2e-08	1 x 50 cell division cycle 45 [Source:HGNC Symbol;Acc:HGNC:1736
13	TK1	1.11	2e-09	2e-08	4 x 50 thymidine kinase 1, soluble [Source:HGNC Symbol;Acc:HGN
14	LIG1	1.37	4e-09	2e-08	2 x 50 ligase I, DNA, ATP-dependent [Source:HGNC Symbol;Acc:H
15	HJURP	1.36	5e-09	2e-08	6 x 50 Holliday junction recognition protein [Source:HGNC Symbol;A
16	HMGB2	1.24	5e-09	2e-08	5 x 50 high mobility group box 2 [Source:HGNC Symbol;Acc:HGNC:
17	CDK1	1.34	5e-09	2e-08	5 x 50 cyclin-dependent kinase 1 [Source:HGNC Symbol;Acc:HGN(
18	FBXO5	1.35	7e-09	2e-08	4 x 50 F-box protein 5 [Source:HGNC Symbol;Acc:HGNC:13584]
19	TIFA	1.35	7e-09	2e-08	3 x 47 TRAF-interacting protein with forkhead-associated domain [
20	EZH2	1.35	7e-09	2e-08	2 x 50 enhancer of zeste 2 polycomb repressive complex 2 subunit [

p-values



C12_mel

Local Summary

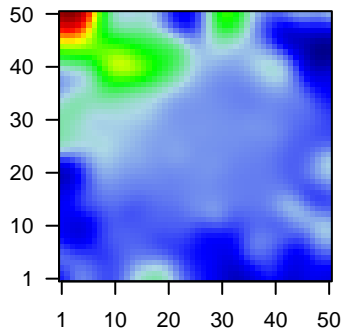
%DE = 0.47
 # metagenes = 6
 # genes = 80
 # genes in genesets = 78

 # genes with $fdr < 0.1 = 8$ (1 + / 7 -)
 # genes with $fdr < 0.05 = 6$ (0 + / 6 -)
 # genes with $fdr < 0.01 = 3$ (0 + / 3 -)

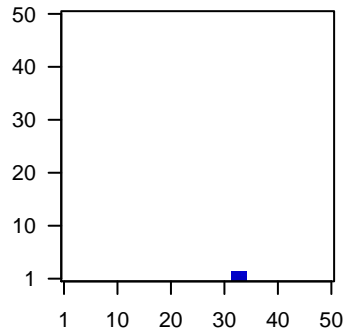
$\langle r \rangle$ metagenes = 0.98
 $\langle r \rangle$ genes = 0.15

 $\langle FC \rangle = -0.26$
 $\langle \text{shrinkage-t} \rangle = -3.98$
 $\langle p\text{-value} \rangle = 0.09$
 $\langle fdr \rangle = 0.84$

Profile



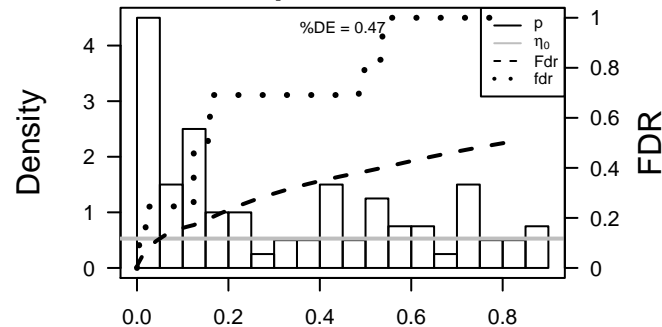
Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	MSC	-1.62	2e-16	9e-15	32 x 1 musculin [Source:HGNC Symbol;Acc:HGNC:7321]
2	FASTKD5	-0.91	9e-05	4e-03	32 x 1 FAST kinase domains 5 [Source:HGNC Symbol;Acc:HGNC:2
3	SPAG9	-0.77	2e-04	5e-03	32 x 1 sperm associated antigen 9 [Source:HGNC Symbol;Acc:HGNC
4	SLC12A2	-0.84	3e-04	1e-02	33 x 1 solute carrier family 12 (sodium/potassium/chloride transport
5	SCARB2	-0.8	6e-04	5e-02	34 x 1 scavenger receptor class B, member 2 [Source:HGNC Symb
6	LZTFL1	-0.72	2e-03	5e-02	34 x 1 leucine zipper transcription factor-like 1 [Source:HGNC Synt
7	TRIM16L	0.68	3e-03	5e-02	33 x 1 tripartite motif containing 16-like [Source:HGNC Symbol;Acc:
8	EXD2	-0.65	5e-03	5e-02	33 x 1 exonuclease 3'-5' domain containing 2 [Source:HGNC Symb
9	LPP	-0.65	5e-03	1e-01	32 x 1 LIM domain containing preferred translocation partner in lipor
10	ARFGAP2	-0.57	1e-02	1e-01	34 x 1 ADP-ribosylation factor GTPase activating protein 2 [Source:
11	ALDH16A1	-0.57	1e-02	1e-01	33 x 1 aldehyde dehydrogenase 16 family, member A1 [Source:HGNC
12	PIGB	-0.55	2e-02	1e-01	33 x 1 phosphatidylinositol glycan anchor biosynthesis, class B [Sou
13	ABHD14A	-0.54	2e-02	1e-01	34 x 1 abhydrolase domain containing 14A [Source:HGNC Symbol;#
14	TMEM98	0.49	2e-02	2e-01	32 x 1 transmembrane protein 98 [Source:HGNC Symbol;Acc:HGNC
15	ZNF28	-0.51	3e-02	2e-01	32 x 1 zinc finger protein 28 [Source:HGNC Symbol;Acc:HGNC:130
16	ARHGEF3	-0.5	3e-02	2e-01	32 x 1 Rho guanine nucleotide exchange factor (GEF) 3 [Source:HG
17	GATC	-0.47	4e-02	2e-01	32 x 1 glutamyl-tRNA(Gln) amidotransferase, subunit C [Source:HG
18	ACTR8	-0.46	5e-02	2e-01	33 x 1 ARP8 actin-related protein 8 homolog (yeast) [Source:HGNC
19	PXN	-0.43	7e-02	2e-01	34 x 1 paxillin [Source:HGNC Symbol;Acc:HGNC:9718]
20	FOXRED2	-0.42	7e-02	2e-01	34 x 2 FAD-dependent oxidoreductase domain containing 2 [Source

p-values



C12_mel

Local Summary

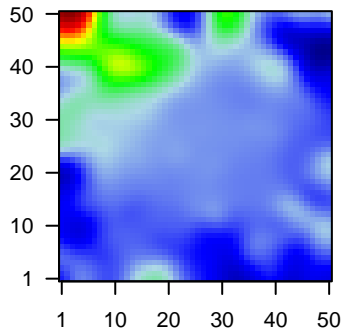
%DE = 0.6
 # metagenes = 5
 # genes = 164
 # genes in genesets = 164

 # genes with $fdr < 0.1$ = 66 (11 + / 55 -)
 # genes with $fdr < 0.05$ = 54 (7 + / 47 -)
 # genes with $fdr < 0.01$ = 37 (5 + / 32 -)

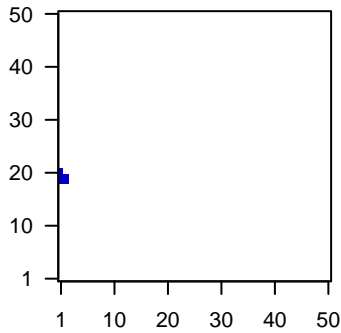
$\langle r \rangle$ metagenes = 0.99
 $\langle r \rangle$ genes = 0.19

 $\langle FC \rangle = -0.27$
 $\langle \text{shrinkage-t} \rangle = -4.7$
 $\langle p\text{-value} \rangle = 0.01$
 $\langle fdr \rangle = 0.6$

Profile



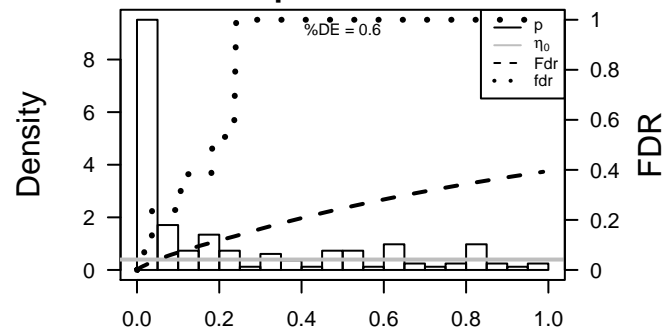
Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	PYURF	-1.52	4e-16	6e-08	1 x 19 PIGY upstream reading frame [Source:HGNC Symbol;Acc:HK
2	SQSTM1	-0.65	1e-09	8e-07	1 x 21 sequestosome 1 [Source:HGNC Symbol;Acc:HGNC:11280]
3	APOE	-1.23	1e-08	3e-06	1 x 20 apolipoprotein E [Source:HGNC Symbol;Acc:HGNC:613]
4	UBQLN1	-1.14	8e-08	3e-06	1 x 21 ubiquilin 1 [Source:HGNC Symbol;Acc:HGNC:12508]
5	GUK1	-0.59	1e-07	4e-06	1 x 21 guanylate kinase 1 [Source:HGNC Symbol;Acc:HGNC:4693]
6	SLC9A3R1	-1.18	2e-07	4e-06	1 x 21 solute carrier family 9, subfamily A (NHE3, cation proton anti
7	TXNL4A	-1.1	2e-07	1e-05	1 x 19 thioredoxin-like 4A [Source:HGNC Symbol;Acc:HGNC:30551]
8	PIGY	-0.54	4e-07	3e-05	1 x 20 phosphatidylinositol glycan anchor biosynthesis, class Y [Sou
9	FBXO7	-0.82	1e-06	3e-05	1 x 20 F-box protein 7 [Source:HGNC Symbol;Acc:HGNC:13586]
10	SERPINE2	-1.1	2e-06	3e-05	1 x 20 serpin peptidase inhibitor, clade E (nexin, plasminogen activa
11	SCAND1	-1.03	3e-06	3e-05	1 x 21 SCAN domain containing 1 [Source:HGNC Symbol;Acc:HGNC
12	TMEM134	-1.08	3e-06	9e-05	1 x 19 transmembrane protein 134 [Source:HGNC Symbol;Acc:HGNC
13	HMG20B	-0.85	4e-06	1e-04	1 x 20 high mobility group 20B [Source:HGNC Symbol;Acc:HGNC:5
14	MAP1LC3B2	-0.96	1e-05	1e-04	1 x 21 microtubule-associated protein 1 light chain 3 beta 2 [Source
15	EI24	-1.02	1e-05	1e-04	1 x 20 etoposide induced 2.4 [Source:HGNC Symbol;Acc:HGNC:13
16	DPAGT1	1.02	1e-05	1e-04	1 x 21 dolichyl-phosphate (UDP-N-acetylglucosamine) N-acetylgl
17	FBXO7	-0.41	1e-05	4e-04	1 x 21 ferritin, heavy polypeptide 1 [Source:HGNC Symbol;Acc:HGNC
18	C18orf8	-0.98	2e-05	4e-04	1 x 19 chromosome 18 open reading frame 8 [Source:HGNC Symbc
19	RIOK2	-0.98	2e-05	5e-04	1 x 20 RIO kinase 2 [Source:HGNC Symbol;Acc:HGNC:18999]
20	CDKN2A	-0.96	4e-05	5e-04	1 x 21 cyclin-dependent kinase inhibitor 2A [Source:HGNC Symbol;

p-values



C12_mel

Local Summary

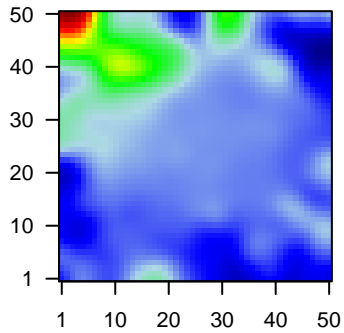
%DE = 0.75
 # metagenes = 41
 # genes = 356
 # genes in genesets = 354

 # genes with $fdr < 0.1$ = 161 (40 + / 121 -)
 # genes with $fdr < 0.05$ = 134 (33 + / 101 -)
 # genes with $fdr < 0.01$ = 82 (18 + / 64 -)

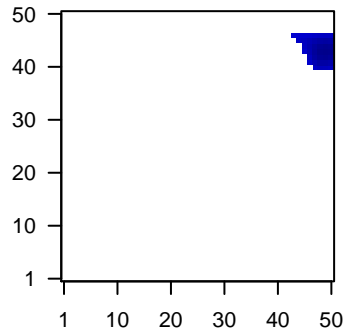
$\langle r \rangle$ metagenes = 0.82
 $\langle r \rangle$ genes = 0.07

 $\langle FC \rangle$ = -0.23
 $\langle \text{shrinkage-t} \rangle$ = -3.78
 $\langle p\text{-value} \rangle$ = 0.01
 $\langle fdr \rangle$ = 0.6

Profile



Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	SBDS	-1.42	2e-16	5e-15	44 x 45 Shwachman-Bodian-Diamond syndrome [Source:HGNC Sy]
2	SCP2	-1.54	2e-16	5e-15	50 x 40 sterol carrier protein 2 [Source:HGNC Symbol;Acc:HGNC:10]
3	SLC6A15	-1.84	2e-16	5e-15	48 x 45 solute carrier family 6 (neutral amino acid transporter), memb
4	VPS72	-1.47	2e-16	5e-15	50 x 43 vacuolar protein sorting 72 homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:HGNC:10]
5	CSRP1	-1.39	1e-11	6e-08	50 x 46 cysteine and glycine-rich protein 1 [Source:HGNC Symbol;Acc:HGNC:10]
6	TRIB2	-1.27	7e-10	6e-08	44 x 46 tribbles pseudokinase 2 [Source:HGNC Symbol;Acc:HGNC:3]
7	RARS	-1.09	2e-09	6e-08	50 x 43 arginyl-tRNA synthetase [Source:HGNC Symbol;Acc:HGNC:3]
8	PXYLP1	1.4	2e-09	1e-07	46 x 44 2-phosphoxylose phosphatase 1 [Source:HGNC Symbol;Acc:HGNC:3]
9	MRPS22	-1.26	3e-09	1e-07	47 x 43 mitochondrial ribosomal protein S22 [Source:HGNC Symbol;Acc:HGNC:3]
10	SEC14L1	-1.2	5e-09	5e-07	50 x 40 SEC14-like 1 (S. cerevisiae) [Source:HGNC Symbol;Acc:HGNC:3]
11	UNC50	-1.24	1e-08	5e-07	50 x 45 unc-50 homolog (C. elegans) [Source:HGNC Symbol;Acc:HGNC:3]
12	SLC38A6	-1.23	2e-08	2e-06	48 x 42 solute carrier family 38, member 6 [Source:HGNC Symbol;Acc:HGNC:3]
13	STYXL1	1.28	3e-08	2e-06	49 x 43 serine/threonine/tyrosine interacting-like 1 [Source:HGNC Sy]
14	MOSPD1	-1.16	5e-08	6e-06	50 x 43 motile sperm domain containing 1 [Source:HGNC Symbol;Acc:HGNC:3]
15	WDR74	-1.16	2e-07	6e-06	50 x 45 WD repeat domain 74 [Source:HGNC Symbol;Acc:HGNC:25]
16	AAR2	-1.14	2e-07	6e-06	43 x 46 AAR2 splicing factor homolog (S. cerevisiae) [Source:HGNC:25]
17	EIF4H	-1.11	3e-07	1e-05	46 x 46 eukaryotic translation initiation factor 4H [Source:HGNC Syml]
18	ABCD4	-1.15	4e-07	1e-05	50 x 45 ATP-binding cassette, sub-family D (ALD), member 4 [Sourc]
19	PRPF3	-1.09	6e-07	1e-05	50 x 42 pre-mRNA processing factor 3 [Source:HGNC Symbol;Acc:H]
20	PRMT7	1.15	7e-07	1e-05	50 x 45 protein arginine methyltransferase 7 [Source:HGNC Symbol;A]

p-values

