

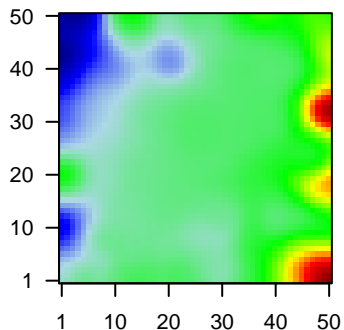
G2_mel

Global Summary

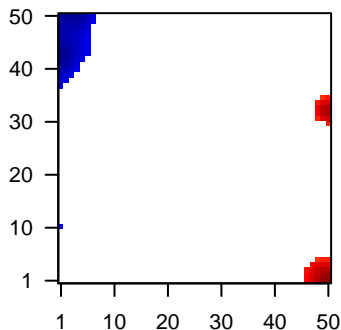
%DE = 0.22
 # genes with $fdr < 0.2 = 2796$ (1635 + / 1161 -)
 # genes with $fdr < 0.1 = 2230$ (1305 + / 925 -)
 # genes with $fdr < 0.05 = 1882$ (1114 + / 768 -)
 # genes with $fdr < 0.01 = 1171$ (669 + / 502 -)
 # genes in genesets = 14839

<FC> = 0
 <shrinkage-t> = -0.07
 <p-value> = 0.07
 <fdr> = 0.78

Profile



Regulated Spots

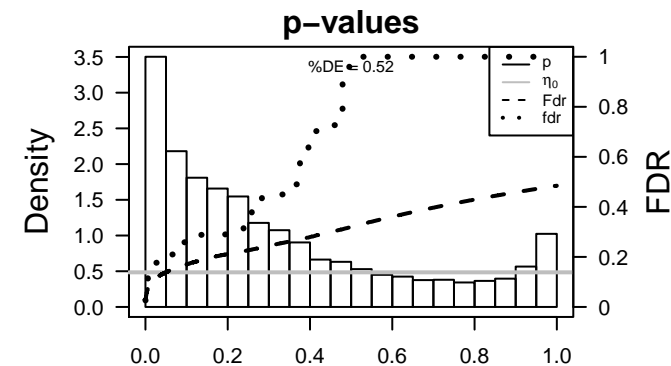
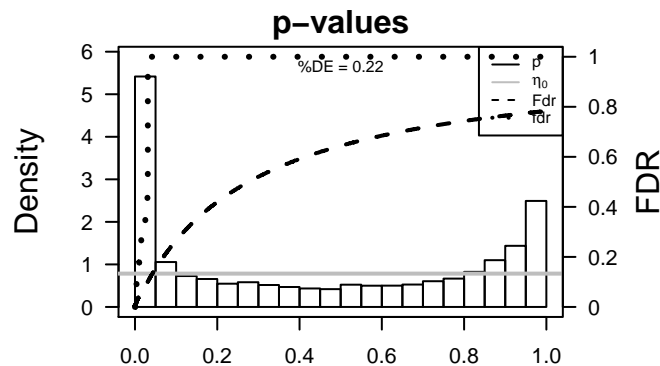


Global Genelist

Rank	ID	log(FC)	fdr p-value	Description Metagene
1	AP1S2	-0.98	2e-16 5e-14	4 x 41 adaptor-related protein complex 1, sigma 2 subunit [Source:HGNC Symbol;Acc:HGNC:10000]
2	ARRDC3	2.09	2e-16 5e-14	50 x 1 arrestin domain containing 3 [Source:HGNC Symbol;Acc:HGNC:10000]
3	BACE2	-1.22	2e-16 5e-14	1 x 42 beta-site APP-cleaving enzyme 2 [Source:HGNC Symbol;Acc:HGNC:10000]
4	BRX1	-1.93	2e-16 5e-14	6 x 43 BRX1, biogenesis of ribosomes [Source:HGNC Symbol;Acc:HGNC:10000]
5	C12orf57	-1.74	2e-16 5e-14	21 x 42 chromosome 12 open reading frame 57 [Source:HGNC Synt
6	CACYBP	-1.54	2e-16 5e-14	8 x 44 calycylin binding protein [Source:HGNC Symbol;Acc:HGNC:3
7	CAPN3	-1.76	2e-16 5e-14	1 x 43 calpain 3, (p94) [Source:HGNC Symbol;Acc:HGNC:1480]
8	CDK2	-2.09	2e-16 5e-14	1 x 43 cyclin-dependent kinase 2 [Source:HGNC Symbol;Acc:HGNC:10000]
9	CDK4	-1.52	2e-16 5e-14	3 x 44 cyclin-dependent kinase 4 [Source:HGNC Symbol;Acc:HGNC:10000]
10	CDKN3	-1.65	2e-16 5e-14	6 x 50 cyclin-dependent kinase inhibitor 3 [Source:HGNC Symbol;A
11	CITED1	-1.99	2e-16 5e-14	1 x 41 Cbp/p300-interacting transactivator, with Glu/Asp-rich carbo
12	CRYAB	1.55	2e-16 5e-14	50 x 1 crystallin, alpha B [Source:HGNC Symbol;Acc:HGNC:2389]
13	CTSC	-1.46	2e-16 5e-14	1 x 42 cathepsin C [Source:HGNC Symbol;Acc:HGNC:2528]
14	DCT	-1.62	2e-16 5e-14	1 x 11 dopachrome tautomerase [Source:HGNC Symbol;Acc:HGNC
15	DERA	-1.79	2e-16 5e-14	1 x 43 deoxyribose-phosphate aldolase (putative) [Source:HGNC S
16	DKC1	-1.67	2e-16 5e-14	7 x 43 dyskeratosis congenita 1, dyskerin [Source:HGNC Symbol;Ac
17	DLD	-1.66	2e-16 5e-14	1 x 7 dihydrolipoamide dehydrogenase [Source:HGNC Symbol;Acc
18	EMC3	-1.62	2e-16 5e-14	5 x 43 ER membrane protein complex subunit 3 [Source:HGNC Syrr
19	EXOSC8	-1.71	2e-16 5e-14	1 x 50 exosome component 8 [Source:HGNC Symbol;Acc:HGNC:17
20	GPR161	-1.23	2e-16 5e-14	3 x 16 G protein-coupled receptor 161 [Source:HGNC Symbol;Acc:l

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	9.01	4e-04	385	GSEA C2REN_ALVEOLAR_RHABDOMYOSARCOMA_DN
2	7.35	9e-04	472	GSEA C2DUTERTRE ESTRADIOL_RESPONSE_24HR_DN
3	6.69	1e-03	594	GSEA C2WONG_ADULT_TISSUE_STEM_MODULE
4	6.53	1e-03	683	GSEA C2KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP
5	6.5	1e-03	256	GSEA C2PASQUALUCCI_LYMPHOMA_BY_GC_STAGE_UP
6	6.28	2e-03	749	GSEA C2CUL_TCF21_TARGETS_2_DN
7	6.23	2e-03	930	GSEA C2NUYTEN_EZH2_TARGETS_UP
8	6.21	2e-03	302	GSEA C2KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_DN
9	6.13	2e-03	176	HM HALLMARK_HYPOXIA
10	5.84	2e-03	3132	CC extracellular region
11	5.74	2e-03	897	BP vesicle-mediated transport
12	5.63	2e-03	212	LymphontREN_Stromal signature 1
13	5.63	2e-03	148	GSEA C2BERTUCCI_MEDULLARY_VS_DUCTAL_BREAST_CANCER_DN
14	5.61	2e-03	1201	CC endoplasmic reticulum
15	5.56	2e-03	157	GSEA C2YAMAZAKI_TCEB3_TARGETS_UP
16	5.56	2e-03	424	GSEA C2MILI_PSEUDOPODIA_CHEMOTAXIS_DN
17	5.5	3e-03	22	GSEA C2REACTOME_SMOOTH_MUSCLE_CONTRACTION
18	5.42	3e-03	50	GSEA C2SSAEVA_MLL2_TARGETS
19	5.28	3e-03	145	CC endoplasmic reticulum lumen
20	5.24	3e-03	66	GSEA C2TARTE_PLASMA_CELL_VS_B_LYMPHOCYTE_UP
<i>Underexpressed</i>				
1	-15.9	4e-05	1192	GSEA C2KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
2	-15.27	5e-05	242	GSEA C2KOBAYASHI_EGFR_SIGNALING_24HR_DN
3	-15.02	5e-05	197	HM HALLMARK_E2F_TARGETS
4	-14.75	3e-03	16	Cancer SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
5	-13.88	7e-05	50	GSEA C2SHIDA_E2F_TARGETS
6	-13.85	7e-05	305	GSEA C2DUTERTRE ESTRADIOL_RESPONSE_24HR_UP
7	-13.53	8e-05	1251	GSEA C2DODD_NASOPHARYNGEAL_CARCINOMA_DN
8	-13.41	8e-05	724	GSEA C2PUJANA_CHEK2_PCC_NETWORK
9	-13.34	8e-05	139	GSEA C2ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
10	-13.23	8e-05	1460	GSEA C2PUJANA_BRCA1_PCC_NETWORK
11	-13.21	9e-05	124	GSEA C2ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_24HR
12	-13.12	9e-05	110	GSEA C2WHITEFORD_PEDIATRIC_CANCER_MARKERS
13	-12.61	1e-04	142	Glio WILLSCHER_GBM_Verhaak-CL_up (C)
14	-12.58	1e-04	550	GSEA C2GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
15	-12.52	1e-04	145	GSEA C2CHANG_CYCLING_GENES
16	-11.98	1e-04	436	GSEA C2SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
17	-11.83	1e-04	99	GSEA C2BURTON_ADIPOGENESIS_3
18	-11.64	1e-04	96	GSEA C2CROONQUIST_IL6_DEPRIVATION_DN
19	-11.57	1e-04	188	HM HALLMARK_MYC_TARGETS_V1
20	-11.52	2e-04	267	GSEA C2ZHANG_TLX_TARGETS_60HR_DN



G2_mel

Local Summary

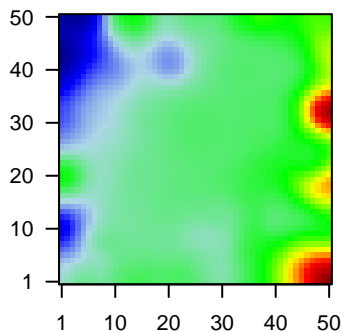
%DE = 0.87
 # metagenes = 22
 # genes = 332
 # genes in genesets = 332

 # genes with $fdr < 0.1$ = 250 (240 + / 10 -)
 # genes with $fdr < 0.05$ = 225 (221 + / 4 -)
 # genes with $fdr < 0.01$ = 195 (193 + / 2 -)

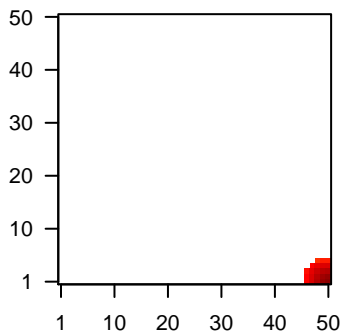
$\langle r \rangle$ metagenes = 0.97
 $\langle r \rangle$ genes = 0.19

$\langle FC \rangle$ = 0.72
 $\langle \text{shrinkage-t} \rangle$ = 11.53
 $\langle p\text{-value} \rangle$ = 0
 $\langle fdr \rangle$ = 0.33

Profile



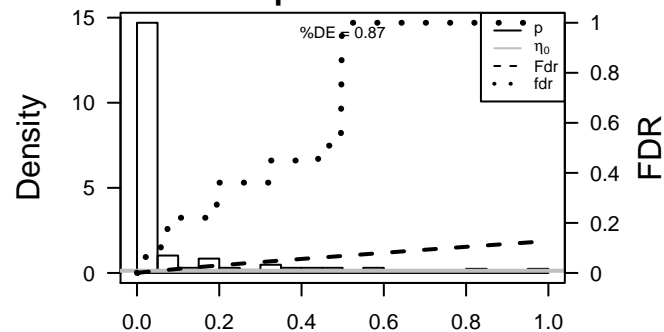
Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	ARRDC3	2.09	2e-16	2e-15	50 x 1 arrestin domain containing 3 [Source:HGNC Symbol;Acc:HGNC:12724]
2	CRYAB	1.55	2e-16	2e-15	50 x 1 crystallin, alpha B [Source:HGNC Symbol;Acc:HGNC:2389]
3	MYL12B	1.02	2e-16	2e-15	48 x 4 myosin, light chain 12B, regulatory [Source:HGNC Symbol;Acc:HGNC:12724]
4	RGS2	2.1	2e-16	2e-15	49 x 1 regulator of G-protein signaling 2 [Source:HGNC Symbol;Acc:HGNC:12724]
5	VTN	2.14	2e-16	2e-15	50 x 1 vitronectin [Source:HGNC Symbol;Acc:HGNC:12724]
6	EFNA1	2.04	2e-15	6e-14	50 x 1 ephrin-A1 [Source:HGNC Symbol;Acc:HGNC:3221]
7	TXNRD1	0.82	3e-15	5e-13	48 x 4 thioredoxin reductase 1 [Source:HGNC Symbol;Acc:HGNC:12724]
8	RAB30	1.96	2e-14	2e-12	50 x 5 RAB30, member RAS oncogene family [Source:HGNC Symbol;Acc:HGNC:12724]
9	MYL12A	0.77	8e-14	2e-12	48 x 3 myosin, light chain 12A, regulatory, non-sarcomeric [Source:HGNC Symbol;Acc:HGNC:12724]
10	DKK1	1.89	1e-13	2e-11	50 x 1 dickkopf WNT signaling pathway inhibitor 1 [Source:HGNC Symbol;Acc:HGNC:12724]
11	TXNIP	1.83	7e-13	2e-11	50 x 1 thioredoxin interacting protein [Source:HGNC Symbol;Acc:HGNC:12724]
12	RDH10	1.82	1e-12	7e-11	48 x 1 retinol dehydrogenase 10 (all-trans) [Source:HGNC Symbol;Acc:HGNC:12724]
13	HIST1H3D	1.77	4e-12	7e-11	50 x 1 histone cluster 1, H3d [Source:HGNC Symbol;Acc:HGNC:476]
14	TCTN1	1.77	5e-12	7e-11	47 x 3 tectonic family member 1 [Source:HGNC Symbol;Acc:HGNC:12724]
15	TNFRSF12A	1.76	6e-12	6e-10	50 x 1 tumor necrosis factor receptor superfamily, member 12A [Source:HGNC Symbol;Acc:HGNC:12724]
16	SERPINI1	1.7	3e-11	6e-10	50 x 1 serpin peptidase inhibitor, clade 1 (neuroserpin), member 1 [Source:HGNC Symbol;Acc:HGNC:12724]
17	TMEM47	1.69	3e-11	1e-09	48 x 4 transmembrane protein 47 [Source:HGNC Symbol;Acc:HGNC:12724]
18	PIEZO2	1.65	9e-11	1e-09	50 x 4 piezo-type mechanosensitive ion channel component 2 [Source:HGNC Symbol;Acc:HGNC:12724]
19	ITGA1	1.65	1e-10	1e-09	50 x 1 integrin, alpha 1 [Source:HGNC Symbol;Acc:HGNC:6134]
20	SRPX	1.55	2e-10	1e-09	50 x 1 sushi-repeat containing protein, X-linked [Source:HGNC Symbol;Acc:HGNC:12724]

p-values



G2_mel

Local Summary

%DE = 0.99
 # metagenes = 15
 # genes = 158
 # genes in genesets = 156

 # genes with $fdr < 0.1$ = 155 (155 + / 0 -)
 # genes with $fdr < 0.05$ = 155 (155 + / 0 -)
 # genes with $fdr < 0.01$ = 152 (152 + / 0 -)

<r> metagenes = 0.93

<r> genes = 0.22

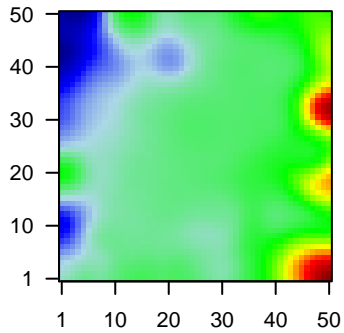
<FC> = 1.04

<shrinkage-t> = 16.29

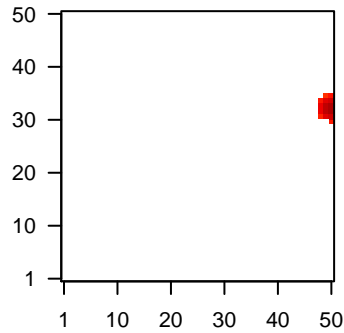
<p-value> = 0

<fdr> = 0.07

Profile



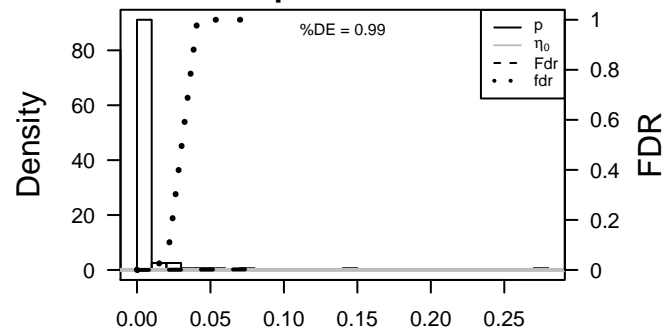
Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	GPX3	2.45	2e-16	3e-16	50 x 33 glutathione peroxidase 3 [Source:HGNC Symbol;Acc:HGNC:10311]
2	RASL11A	1.83	8e-13	8e-13	50 x 32 RAS-like, family 11, member A [Source:HGNC Symbol;Acc:HGNC:10312]
3	CLTCL1	1.81	1e-12	2e-11	50 x 32 clathrin, heavy chain-like 1 [Source:HGNC Symbol;Acc:HGNC:10313]
4	NR2E3	1.72	2e-11	2e-10	50 x 33 nuclear receptor subfamily 2, group E, member 3 [Source:HGNC Symbol;Acc:HGNC:10314]
5	ITGB6	1.62	2e-10	2e-10	50 x 32 integrin, beta 6 [Source:HGNC Symbol;Acc:HGNC:6161]
6	F13A1	1.61	3e-10	2e-10	49 x 31 coagulation factor XIII, A1 polypeptide [Source:HGNC Symbol;Acc:HGNC:10315]
7	STXBP2	1.6	4e-10	2e-10	50 x 33 syntaxin binding protein 2 [Source:HGNC Symbol;Acc:HGNC:10316]
8	MAP1LC3C	1.57	7e-10	2e-10	50 x 32 microtubule-associated protein 1 light chain 3 gamma [Source:HGNC Symbol;Acc:HGNC:10317]
9	AZIN2	1.57	7e-10	2e-10	50 x 33 antizyme inhibitor 2 [Source:HGNC Symbol;Acc:HGNC:2995]
10	FABP4	1.57	8e-10	2e-10	50 x 32 fatty acid binding protein 4, adipocyte [Source:HGNC Symbol;Acc:HGNC:10318]
11	IRAK1	1.56	9e-10	1e-09	48 x 32 interleukin-1 receptor-associated kinase 1 [Source:HGNC Symbol;Acc:HGNC:10319]
12	LIFR	1.52	2e-09	1e-09	50 x 33 leukemia inhibitory factor receptor alpha [Source:HGNC Symbol;Acc:HGNC:10320]
13	N4BP2L1	1.51	3e-09	1e-09	50 x 32 NEDD4 binding protein 2-like 1 [Source:HGNC Symbol;Acc:HGNC:10321]
14	CDH8	1.5	5e-09	1e-09	50 x 32 cadherin 8, type 2 [Source:HGNC Symbol;Acc:HGNC:1767]
15	METTL22	1.49	5e-09	1e-09	50 x 35 methyltransferase like 22 [Source:HGNC Symbol;Acc:HGNC:10322]
16	SUN2	1.48	6e-09	3e-09	50 x 33 Sad1 and UNC84 domain containing 2 [Source:HGNC Symbol;Acc:HGNC:10323]
17	BZW1	0.71	1e-08	3e-09	50 x 30 basic leucine zipper and W2 domains 1 [Source:HGNC Symbol;Acc:HGNC:10324]
18	PPP1R32	1.45	1e-08	3e-09	50 x 32 protein phosphatase 1, regulatory subunit 32 [Source:HGNC Symbol;Acc:HGNC:10325]
19	SUMO4	1.45	1e-08	3e-09	50 x 32 small ubiquitin-like modifier 4 [Source:HGNC Symbol;Acc:HGNC:10326]
20	HYKK	1.45	1e-08	4e-09	49 x 32 hydroxylysine kinase [Source:HGNC Symbol;Acc:HGNC:3441]

p-values



G2_mel

Local Summary

%DE = 0.75
 # metagenes = 1
 # genes = 50
 # genes in genesets = 49

 # genes with fdr < 0.1 = 34 (1 + / 33 -)
 # genes with fdr < 0.05 = 31 (0 + / 31 -)
 # genes with fdr < 0.01 = 21 (0 + / 21 -)

<r> metagenes = NA

<r> genes = 0.23

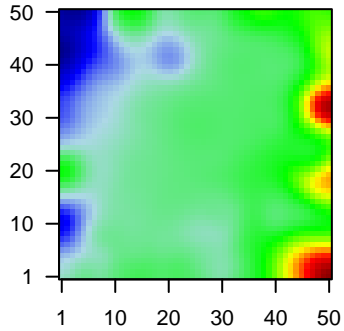
<FC> = -0.58

<shrinkage-t> = -10.89

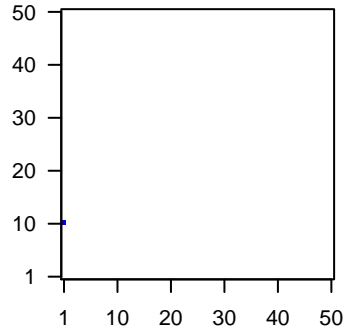
<p-value> = 0

<fdr> = 0.4

Profile



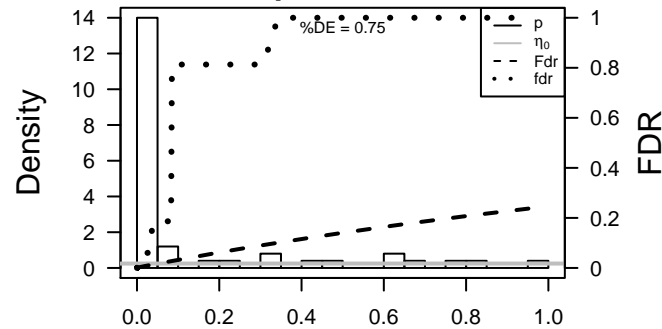
Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	DCT	-1.62	2e-16	1e-15	dopachrome tautomerase [Source:HGNC Symbol;Acc:HGNC
2	SAT1	-1.56	2e-16	1e-15	spermidine/spermine N1-acetyltransferase 1 [Source:HGNC
3	CCDC171	-1.46	6e-13	1e-10	coiled-coil domain containing 171 [Source:HGNC Symbol;Ac
4	GPR143	-0.98	1e-11	4e-08	G protein-coupled receptor 143 [Source:HGNC Symbol;Acc:l
5	HSPB8	-1.35	3e-09	3e-07	heat shock 22kDa protein 8 [Source:HGNC Symbol;Acc:HGN
6	MET	-1.24	3e-08	3e-07	MET proto-oncogene, receptor tyrosine kinase [Source:HGN
7	TNFRSF14	-1.27	5e-08	3e-07	tumor necrosis factor receptor superfamily, member 14 [Sour
8	SOCS6	-1.26	8e-08	6e-05	suppressor of cytokine signaling 6 [Source:HGNC Symbol;Ac
9	SEMA6A	-0.6	6e-06	6e-05	sema domain, transmembrane domain (TM), and cytoplasmic
10	VEPH1	-1.11	1e-05	6e-05	ventricular zone expressed PH domain-containing 1 [Source:
11	TMEM101	-1.09	2e-05	3e-04	transmembrane protein 101 [Source:HGNC Symbol;Acc:HGN
12	FAM96A	-0.52	8e-05	3e-04	family with sequence similarity 96, member A [Source:HGNC
13	C10orf90	-1	9e-05	3e-04	chromosome 10 open reading frame 90 [Source:HGNC Synt
14	SEMA6D	-1	9e-05	3e-03	sema domain, transmembrane domain (TM), and cytoplasmic
15	TRIB1	-0.87	6e-04	3e-03	tribbles pseudokinase 1 [Source:HGNC Symbol;Acc:HGNC:1
16	UGCG	-0.56	8e-04	3e-03	UDP-glucose ceramide glucosyltransferase [Source:HGNC S
17	APH1A	-0.85	8e-04	5e-03	APH1A gamma secretase subunit [Source:HGNC Symbol;Ac
18	SGCD	-0.82	1e-03	5e-03	sarcoglycan, delta (35kDa dystrophin-associated glycoprotei
19	SLC7A6	-0.79	2e-03	5e-03	solute carrier family 7 (amino acid transporter light chain, y+L
20	SNAI2	-0.71	2e-03	5e-03	snail family zinc finger 2 [Source:HGNC Symbol;Acc:HGNC:1

p-values



G2_mel

Local Summary

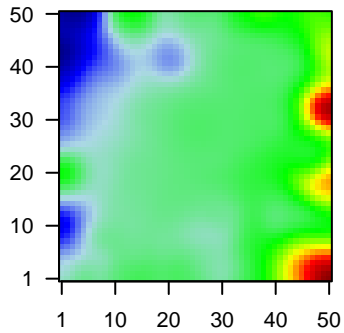
%DE = 0.78
 # metagenes = 69
 # genes = 921
 # genes in genesets = 918

 # genes with $fdr < 0.1$ = 565 (61 + / 504 -)
 # genes with $fdr < 0.05$ = 493 (46 + / 447 -)
 # genes with $fdr < 0.01$ = 334 (24 + / 310 -)

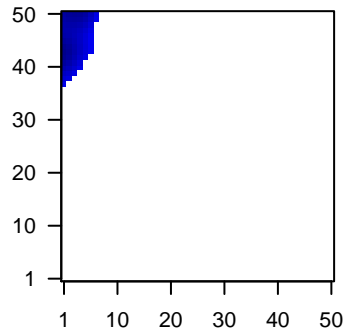
$\langle r \rangle$ metagenes = 0.74
 $\langle r \rangle$ genes = 0.13

 $\langle FC \rangle$ = -0.48
 $\langle \text{shrinkage-t} \rangle$ = -8.78
 $\langle p\text{-value} \rangle$ = 0
 $\langle fdr \rangle$ = 0.49

Profile



Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	AP1S2	-0.98	2e-16	1e-15	4 x 41 adaptor-related protein complex 1, sigma 2 subunit [Source:tr
2	BACE2	-1.22	2e-16	1e-15	1 x 42 beta-site APP-cleaving enzyme 2 [Source:HGNC Symbol;Acc
3	BRX1	-1.93	2e-16	1e-15	6 x 43 BRX1, biogenesis of ribosomes [Source:HGNC Symbol;Acc:†
4	CAPN3	-1.76	2e-16	1e-15	1 x 43 calpain 3, (p94) [Source:HGNC Symbol;Acc:HGNC:1480]
5	CDK2	-2.09	2e-16	1e-15	1 x 43 cyclin-dependent kinase 2 [Source:HGNC Symbol;Acc:HGNC
6	CDK4	-1.52	2e-16	1e-15	3 x 44 cyclin-dependent kinase 4 [Source:HGNC Symbol;Acc:HGNC
7	CDKN3	-1.65	2e-16	1e-15	6 x 50 cyclin-dependent kinase inhibitor 3 [Source:HGNC Symbol;A
8	CITED1	-1.99	2e-16	1e-15	1 x 41 Cbp/p300-interacting transactivator, with Glu/Asp-rich carbo
9	CTSC	-1.46	2e-16	1e-15	1 x 42 cathepsin C [Source:HGNC Symbol;Acc:HGNC:2528]
10	DERA	-1.79	2e-16	1e-15	1 x 43 deoxyribose-phosphate aldolase (putative) [Source:HGNC S
11	EMC3	-1.62	2e-16	1e-15	5 x 43 ER membrane protein complex subunit 3 [Source:HGNC Syrr
12	EXOSC8	-1.71	2e-16	1e-15	1 x 50 exosome component 8 [Source:HGNC Symbol;Acc:HGNC:17
13	HDAC2	-1.81	2e-16	1e-15	1 x 45 histone deacetylase 2 [Source:HGNC Symbol;Acc:HGNC:48†
14	IFRD2	-1.48	2e-16	1e-15	1 x 44 interferon-related developmental regulator 2 [Source:HGNC †
15	IVNS1ABP	-1.64	2e-16	1e-15	4 x 44 influenza virus NS1A binding protein [Source:HGNC Symbol;
16	KPNA2	-2.15	2e-16	1e-15	7 x 50 karyopherin alpha 2 (RAG cohort 1, importin alpha 1) [Source
17	MITF	-0.95	2e-16	1e-15	1 x 41 microphthalmia-associated transcription factor [Source:HGNC
18	MLANA	-2.26	2e-16	1e-15	1 x 43 melan-A [Source:HGNC Symbol;Acc:HGNC:7124]
19	MLIP	-1.89	2e-16	1e-15	3 x 44 muscular LMNA-interacting protein [Source:HGNC Symbol;A
20	NARS2	-1.18	2e-16	1e-15	1 x 42 asparaginyl-tRNA synthetase 2, mitochondrial (putative) [Sou

p-values

