

F1_mel

Global Summary

%DE = 0.21
 # genes with fdr < 0.2 = 2513 (1578 + / 935 -)
 # genes with fdr < 0.1 = 2039 (1327 + / 712 -)
 # genes with fdr < 0.05 = 1571 (1044 + / 527 -)
 # genes with fdr < 0.01 = 1019 (702 + / 317 -)
 # genes in genesets = 14839

<FC> = 0
 <shrinkage-t> = 0.08
 <p-value> = 0.09
 <fdr> = 0.79

Global Genelist

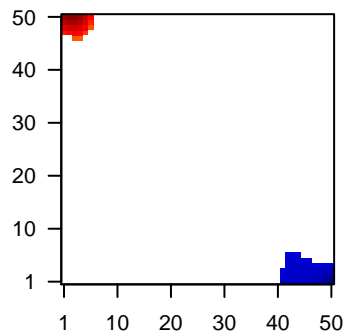
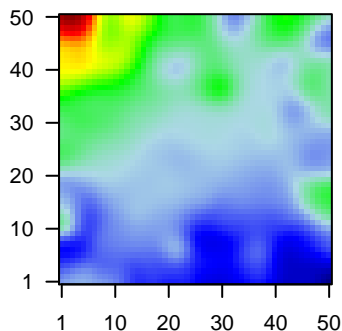
Rank	ID	log(FC)	fdr	Description
		p-value		Metagene
1	ATP6V1D	-0.98	2e-16	3e-13 1 x 11 ATPase, H+ transporting, lysosomal 34kDa, V1 subunit D [So
2	BBX	-1.53	2e-16	3e-13 50 x 7 bobby sox homolog (Drosophila) [Source:HGNC Symbol;Acc:
3	CRYAB	-1.82	2e-16	3e-13 50 x 1 crystallin, alpha B [Source:HGNC Symbol;Acc:HGNC:2389]
4	EXOSC7	-1.65	2e-16	3e-13 22 x 1 exosome component 7 [Source:HGNC Symbol;Acc:HGNC:2E
5	HSD17B4	-1.63	2e-16	3e-13 11 x 50 hydroxysteroid (17-beta) dehydrogenase 4 [Source:HGNC S
6	PHYHIPL	1.83	2e-16	3e-13 13 x 46 phytanoyl-CoA 2-hydroxylase interacting protein-like [Source
7	RABGGTB	-1.5	2e-16	3e-13 28 x 50 Rab geranylgeranyltransferase, beta subunit [Source:HGNC
8	TMEM208	-1.63	2e-16	3e-13 48 x 46 transmembrane protein 208 [Source:HGNC Symbol;Acc:HGNC
9	UQCC1	-1.5	2e-16	3e-13 48 x 15 ubiquinol-cytochrome c reductase complex assembly factor 1
10	MSC	-1.35	2e-15	9e-12 32 x 1 musculin [Source:HGNC Symbol;Acc:HGNC:7321]
11	ZNF638	-1.05	3e-15	9e-12 26 x 9 zinc finger protein 638 [Source:HGNC Symbol;Acc:HGNC:17:
12	STAMPB	-1.47	3e-15	9e-12 9 x 2 STAM binding protein [Source:HGNC Symbol;Acc:HGNC:16E
13	C5orf15	-1.44	4e-15	9e-12 48 x 5 chromosome 5 open reading frame 15 [Source:HGNC Symbc
14	ITM2B	-1.25	4e-15	1e-11 50 x 10 integral membrane protein 2B [Source:HGNC Symbol;Acc:HC
15	UCP2	-1.31	5e-15	1e-10 2 x 46 uncoupling protein 2 (mitochondrial, proton carrier) [Source:H
16	VAMP7	-1.44	2e-14	1e-10 42 x 37 vesicle-associated membrane protein 7 [Source:HGNC Symb
17	HNRNP2	-1.37	2e-14	1e-10 29 x 12 heterogeneous nuclear ribonucleoprotein H2 (H') [Source:HG
18	DNAJA4	1.67	4e-14	1e-10 11 x 6 DnaJ (Hsp40) homolog, subfamily A, member 4 [Source:HGNC
19	RAB33A	1.67	4e-14	1e-10 27 x 16 RAB33A, member RAS oncogene family [Source:HGNC Sym
20	SHMT2	-1.32	5e-14	1e-10 31 x 50 serine hydroxymethyltransferase 2 (mitochondrial) [Source:HC

Global Geneset Analysis

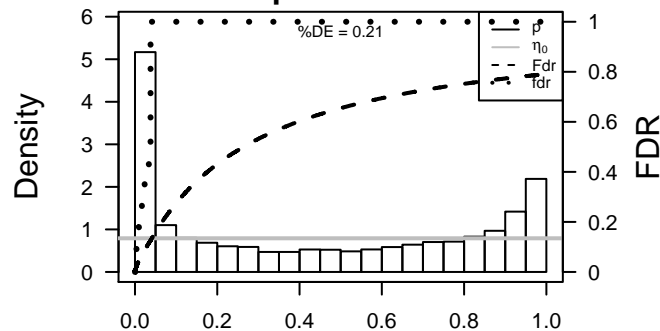
Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	15.32	5e-05	242	GSEA C2KOBAYASHI_EGFR_SIGNALING_24HR_DN
2	13.96	7e-05	305	GSEA C2DUTERTRE ESTRADIOL_RESPONSE_24HR_UP
3	12.81	1e-04	1192	GSEA C2KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
4	12.79	1e-04	550	GSEA C2BOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
5	12.47	1e-04	197	HM HALLMARK_E2F_TARGETS
6	12.29	1e-04	267	GSEA C2ZHANG_TLX_TARGETS_60HR_DN
7	12.18	1e-04	142	Glio WILLSCHER_GBM_Verhaak-CL_up (C)
8	10.8	2e-04	436	GSEA C2SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
9	10.68	2e-04	373	GSEA C2ECCHI_GASTRIC_CANCER_EARLY_UP
10	10.64	2e-04	84	GSEA C2ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_6HR
11	10.64	2e-04	700	GSEA C2MARSON_BOUND_BY_E2F4_UNSTIMULATED
12	10.64	2e-04	1251	GSEA C2DODD_NASOPHARYNGEAL_CARCINOMA_DN
13	10.43	2e-04	139	GSEA C2ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
14	10.43	2e-04	834	GSEA C2LEE_BMP2_TARGETS_DN
15	10.37	1e-01	16	Cancer SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
16	10.29	2e-04	110	GSEA C2WHITEFORD_PEDIATRIC_CANCER_MARKERS
17	10.2	2e-04	81	GSEA C2GRAHAM_NORMAL QUIESCENT_VS_NORMAL_DIVIDING_DN
18	10.16	2e-04	58	GSEA C2SONG_TARGETS_OF_IE86_CMV_PROTEIN
19	10.1	3e-04	278	GSEA C2MANALO_HYPOXIA_DN
20	9.79	3e-04	116	GSEA C2MISSIAGLIA_REGULATED_BY_METHYLATION_DN
<i>Underexpressed</i>				
1	-3.88	0.008	683	GSEA C2KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP
2	-3.85	0.008	435	GSEA C2GARY_CD5_TARGETS_UP
3	-3.77	0.009	196	GSEA C2CHANG_CORE_SERUM_RESPONSE_DN
4	-3.71	0.010	15	GSEA C2NIELSEN_SYNOVIAL_SARCOMA_DN
5	-3.67	0.010	280	LymphomaPANG_CD40_6hrs_UP
6	-3.59	0.011	25	GSEA C2BIOCARTA_GSK3_PATHWAY
7	-3.55	0.011	20	GSEA C2VERNELL_RETINOBLASTOMA_PATHWAY_DN
8	-3.52	0.011	27	GSEA C2DARWICHE_PAPILLOMA_RISK_HIGH_VS_LOW_DN
9	-3.5	0.011	4	GSEA C2Y_AGING_OLD_UP
10	-3.43	0.012	40	BP ER-associated ubiquitin-dependent protein catabolic process
11	-3.42	0.012	12	GSEA C2REACTOME_AKT_PHOSPHORYLATES_TARGETS_IN_THE_CY
12	-3.4	0.012	1394	GSEA C2ZWANG_TRANSIENTLY_UP_BY_1ST_EGF_PULSE_ONLY
13	-3.4	0.013	35	GSEA C2KEGG_SNARE_INTERACTIONS_IN_VESICULAR_TRANSPORT
14	-3.4	0.013	3081	Brain Mid_Frontal_Lobe_ZNF
15	-3.35	0.013	19	BP positive regulation of dendrite morphogenesis
16	-3.29	0.014	21	GSEA C2BIOCARTA_P53HYPOXIA_PATHWAY
17	-3.24	0.015	68	GSEA C2FRIDMAN_SENESCENCE_UP
18	-3.21	0.015	13	CC contractile fiber
19	-3.19	0.015	11	BP alpha-linolenic acid metabolic process
20	-3.19	0.015	11	BP unsaturated fatty acid metabolic process

Profile

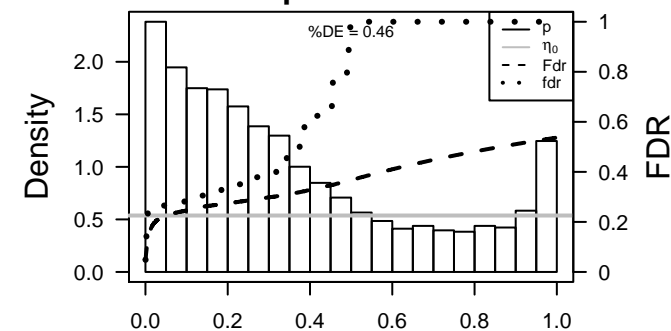
Regulated Spots



p-values



p-values



F1_mel

Local Summary

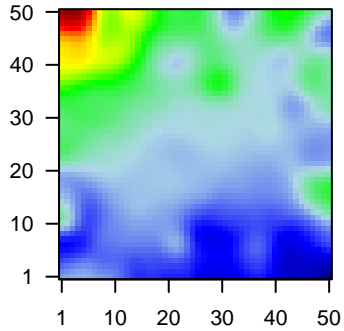
%DE = 0.8
 # metagenes = 25
 # genes = 366
 # genes in genesets = 365

 # genes with $fdr < 0.1$ = 249 (222 + / 27 -)
 # genes with $fdr < 0.05$ = 240 (215 + / 25 -)
 # genes with $fdr < 0.01$ = 168 (159 + / 9 -)

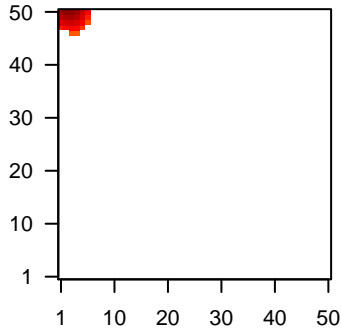
$\langle r \rangle$ metagenes = 0.94
 $\langle r \rangle$ genes = 0.27

 $\langle FC \rangle$ = 0.43
 $\langle \text{shrinkage-t} \rangle$ = 7.01
 $\langle p\text{-value} \rangle$ = 0
 $\langle fdr \rangle$ = 0.4

Profile



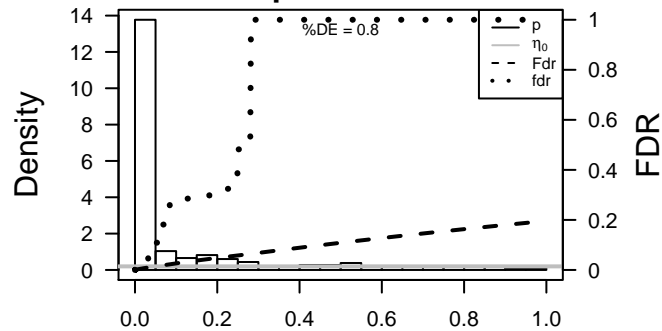
Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	HIST1H1A	1.64	1e-13	3e-10	5 x 49 histone cluster 1, H1a [Source:HGNC Symbol;Acc:HGNC:47
2	HIST1H4C	0.62	5e-12	2e-09	5 x 49 histone cluster 1, H4c [Source:HGNC Symbol;Acc:HGNC:47
3	EXO1	1.46	4e-11	2e-09	1 x 50 exonuclease 1 [Source:HGNC Symbol;Acc:HGNC:3511]
4	AURKB	1.45	6e-11	3e-08	6 x 50 aurora kinase B [Source:HGNC Symbol;Acc:HGNC:11390]
5	ACTL6A	0.81	9e-10	3e-08	4 x 50 actin-like 6A [Source:HGNC Symbol;Acc:HGNC:24124]
6	STIL	1.35	1e-09	4e-08	5 x 47 SCL/TAL1 interrupting locus [Source:HGNC Symbol;Acc:HGNC:24124]
7	CENPU	1.34	1e-09	6e-08	2 x 50 centromere protein U [Source:HGNC Symbol;Acc:HGNC:213
8	PRC1	1.26	2e-09	4e-07	5 x 50 protein regulator of cytokinesis 1 [Source:HGNC Symbol;Acc:HGNC:213
9	C5orf34	1.23	3e-08	4e-07	6 x 50 chromosome 5 open reading frame 34 [Source:HGNC Symbol;Acc:HGNC:213
10	HIST1H3C	1.22	3e-08	4e-07	6 x 48 histone cluster 1, H3c [Source:HGNC Symbol;Acc:HGNC:47
11	CDK1	1.21	3e-08	4e-07	5 x 50 cyclin-dependent kinase 1 [Source:HGNC Symbol;Acc:HGNC:213
12	RFC2	1.19	3e-08	4e-07	1 x 50 replication factor C (activator 1) 2, 40kDa [Source:HGNC Symbol;Acc:HGNC:213
13	GGH	0.89	4e-08	4e-07	4 x 47 gamma-glutamyl hydrolase (conjugase, folypolygamma
14	CKAP2L	1.22	4e-08	4e-07	6 x 50 cytoskeleton associated protein 2-like [Source:HGNC Symbol;Acc:HGNC:213
15	ATAD2	1.21	5e-08	4e-07	2 x 50 ATPase family, AAA domain containing 2 [Source:HGNC Symbol;Acc:HGNC:213
16	HMGB2	1.1	5e-08	4e-07	5 x 50 high mobility group box 2 [Source:HGNC Symbol;Acc:HGNC:213
17	CLSPN	1.2	6e-08	4e-07	1 x 50 claspin [Source:HGNC Symbol;Acc:HGNC:19715]
18	PHF5A	1.2	6e-08	4e-07	1 x 47 PHD finger protein 5A [Source:HGNC Symbol;Acc:HGNC:18
19	TRAF1	1.19	7e-08	5e-07	5 x 50 TRAF interacting protein [Source:HGNC Symbol;Acc:HGNC:213
20	HAUS8	1.19	7e-08	9e-07	3 x 50 HAUS augmin-like complex, subunit 8 [Source:HGNC Symbol;Acc:HGNC:213

p-values



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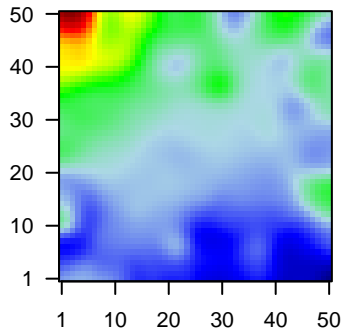
%DE = 0.82
 # metagenes = 47
 # genes = 550
 # genes in genesets = 550

 # genes with $fdr < 0.1$ = 260 (68 + / 192 -)
 # genes with $fdr < 0.05$ = 183 (47 + / 136 -)
 # genes with $fdr < 0.01$ = 116 (34 + / 82 -)

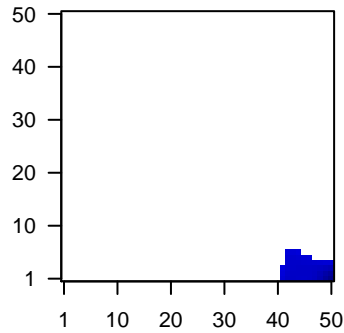
$\langle r \rangle$ metagenes = 0.89
 $\langle r \rangle$ genes = 0.15

 $\langle FC \rangle = -0.2$
 $\langle \text{shrinkage-t} \rangle = -3.11$
 $\langle p\text{-value} \rangle = 0.03$
 $\langle fdr \rangle = 0.68$

Profile



Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description	
1	CRYAB	-1.82	2e-16	2e-14	50 x 1	crystallin, alpha B [Source:HGNC Symbol;Acc:HGNC:2389]
2	SHOC2	-1.25	7e-12	2e-08	42 x 6	soc-2 suppressor of clear homolog (C. elegans) [Source:HGI]
3	ABL2	-1.26	5e-10	2e-08	46 x 1	ABL, proto-oncogene 2, non-receptor tyrosine kinase [Source:HGNC Symbol;Acc:HGNC:2389]
4	MCAM	1.38	5e-10	2e-08	46 x 1	melanoma cell adhesion molecule [Source:HGNC Symbol;Acc:HGNC:2389]
5	ARMC9	-1.21	5e-10	4e-08	50 x 3	armadillo repeat containing 9 [Source:HGNC Symbol;Acc:HGNC:2389]
6	DST	-0.92	1e-09	4e-08	46 x 1	dystonin [Source:HGNC Symbol;Acc:HGNC:1090]
7	CTSF	1.34	1e-09	3e-07	41 x 2	cathepsin F [Source:HGNC Symbol;Acc:HGNC:2531]
8	PALLD	1.3	4e-09	3e-06	50 x 4	palladin, cytoskeletal associated protein [Source:HGNC Synt
9	PDLIM1	1.21	4e-08	3e-06	50 x 1	PDZ and LIM domain 1 [Source:HGNC Symbol;Acc:HGNC:21
10	ABHD4	1.19	7e-08	3e-06	49 x 1	abhydrolase domain containing 4 [Source:HGNC Symbol;Acc
11	GBE1	-1.07	1e-07	3e-06	50 x 3	glucan (1,4-alpha-), branching enzyme 1 [Source:HGNC Syr
12	GALNT2	1.17	1e-07	4e-06	44 x 1	polypeptide N-acetylgalactosaminyltransferase 2 [Source:HG
13	CWC27	-1.12	2e-07	4e-06	43 x 1	CWC27 spliceosome-associated protein homolog (S. cerevis
14	ACTR1A	-1.13	2e-07	4e-06	42 x 1	ARP1 actin-related protein 1 homolog A, centractin alpha (ye
15	YPEL5	-1.12	3e-07	7e-06	50 x 1	yippee-like 5 (Drosophila) [Source:HGNC Symbol;Acc:HGNC
16	EDIL3	-1.11	3e-07	9e-06	50 x 1	EGF-like repeats and discoidin I-like domains 3 [Source:HGI
17	KITLG	1.12	4e-07	8e-05	48 x 1	KIT ligand [Source:HGNC Symbol;Acc:HGNC:6343]
18	PTPRM	-1.03	3e-06	8e-05	50 x 1	protein tyrosine phosphatase, receptor type, M [Source:HGNC
19	CTNNA1	-0.42	3e-06	8e-05	46 x 4	catenin (cadherin-associated protein), alpha 1, 102kDa [Sou
20	XPC	-1.03	3e-06	2e-04	43 x 6	xeroderma pigmentosum, complementation group C [Source:

p-values

