

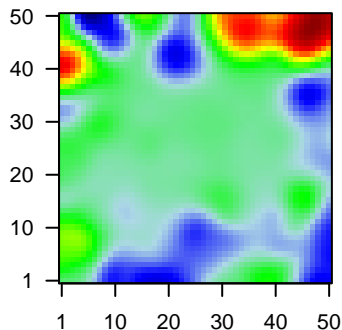
F11_mel

Global Summary

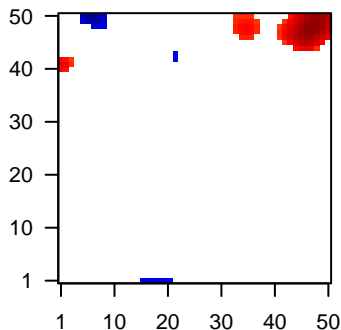
%DE = 0.21
 # genes with $fdr < 0.2$ = 2727 (1667 + / 1060 -)
 # genes with $fdr < 0.1$ = 2053 (1283 + / 770 -)
 # genes with $fdr < 0.05$ = 1668 (1069 + / 599 -)
 # genes with $fdr < 0.01$ = 1043 (680 + / 363 -)
 # genes in genesets = 14839

<FC> = 0
 <shrinkage-t> = 0.06
 <p-value> = 0.08
 <fdr> = 0.79

Profile



Regulated Spots

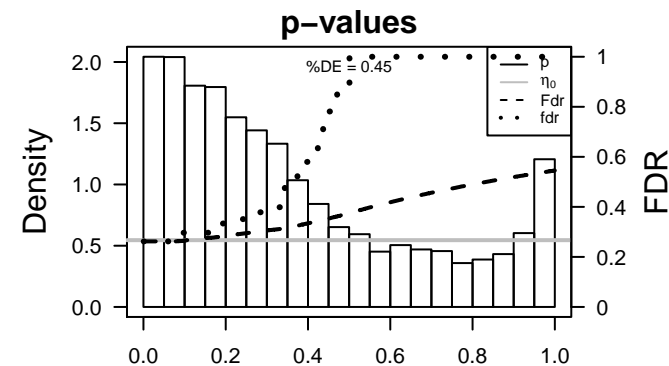
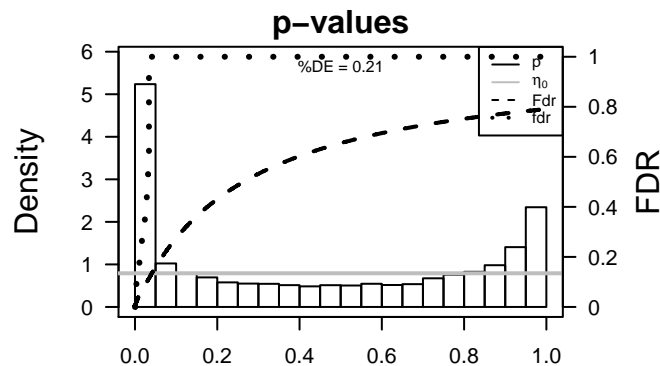


Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	ACTL6A	-1.91	2e-16	2e-13	4 x 50 actin-like 6A [Source:HGNC Symbol;Acc:HGNC:24124]
2	AHSA1	-1.91	2e-16	2e-13	46 x 35 AHA1, activator of heat shock 90kDa protein ATPase homolog
3	ALDH9A1	-1.68	2e-16	2e-13	12 x 50 aldehyde dehydrogenase 9 family, member A1 [Source:HGNC]
4	ANKRD28	-1.69	2e-16	2e-13	50 x 5 ankyrin repeat domain 28 [Source:HGNC Symbol;Acc:HGNC]
5	CHD4	-1.36	2e-16	2e-13	21 x 43 chromodomain helicase DNA binding protein 4 [Source:HGNC]
6	KIT	-1.57	2e-16	2e-13	16 x 2 v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog
7	NAE1	-1.31	2e-16	2e-13	10 x 45 NEDD8 activating enzyme E1 subunit 1 [Source:HGNC Symbol]
8	NUP85	-1.56	2e-16	2e-13	1 x 50 nucleoporin 85kDa [Source:HGNC Symbol;Acc:HGNC:8734]
9	PTP4A2	-1.2	2e-16	2e-13	10 x 45 protein tyrosine phosphatase type IVA, member 2 [Source:HGNC]
10	RBM34	-1.57	2e-16	2e-13	50 x 16 RNA binding motif protein 34 [Source:HGNC Symbol;Acc:HGNC]
11	RBM5	-1.73	2e-16	2e-13	19 x 1 RNA binding motif protein 5 [Source:HGNC Symbol;Acc:HGNC]
12	SYNE1	-1.48	2e-16	2e-13	49 x 1 spectrin repeat containing, nuclear envelope 1 [Source:HGNC]
13	D2HGDH	1.83	2e-15	7e-12	30 x 23 D-2-hydroxyglutarate dehydrogenase [Source:HGNC Symbol]
14	DNTTIP2	-1.22	2e-15	7e-12	12 x 47 deoxynucleotidyltransferase, terminal, interacting protein 2 [Source:HGNC]
15	STMN1	-0.73	2e-15	9e-12	5 x 50 stathmin 1 [Source:HGNC Symbol;Acc:HGNC:6510]
16	MRPL24	-1.16	3e-15	9e-12	6 x 18 mitochondrial ribosomal protein L24 [Source:HGNC Symbol;Acc:HGNC:10000]
17	PLRG1	-1.49	4e-15	9e-12	12 x 49 pleiotropic regulator 1 [Source:HGNC Symbol;Acc:HGNC:9080]
18	LLPH	-1.43	4e-15	5e-11	19 x 8 LLP homolog, long-term synaptic facilitation (Aplysia) [Source:HGNC]
19	PLN	1.77	1e-14	5e-11	43 x 44 phospholamban [Source:HGNC Symbol;Acc:HGNC:9080]
20	EIF4A2	-0.83	1e-14	5e-11	50 x 11 eukaryotic translation initiation factor 4A2 [Source:HGNC Symbol]

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	7.15	0.001	198	HM HALLMARK_OXIDATIVE_PHOSPHORYLATION
2	6.5	0.001	401	CC mitochondrial inner membrane
3	6.21	0.002	368	GSEA C2STEIN_ESRRA_TARGETS_UP
4	6.14	0.002	213	GSEA C2WONG_MITOCHONDRIA_GENE_MODULE
5	5.9	0.002	421	GSEA C2MOOTHA_MITOCHONDRIA
6	5.87	0.002	405	GSEA C2MOOTHA_HUMAN_MITODB_6_2002
7	5.74	0.002	311	BP generation of precursor metabolites and energy
8	5.41	0.003	2984	CC integral component of membrane
9	5.29	0.003	135	BP cellular metabolic process
10	5.24	0.003	85	GSEA C2MOOTHA_VOXPPOS
11	5.21	0.003	2755	BP transport
12	5.15	0.003	13	BP melanin biosynthetic process
13	5.14	0.003	114	GSEA C2REACTOME_TCA_CYCLE_AND_RESPIRATORY_ELECTRON_TRANSPORT
14	5.11	0.003	1468	CC mitochondrion
15	5.09	0.003	500	GSEA C2STEIN_ESRRA_TARGETS
16	5.04	0.003	94	BP respiratory electron transport chain
17	5.02	0.003	94	CC melanosome
18	5	0.004	1201	CC endoplasmic reticulum
19	4.99	0.004	398	GSEA C2MOOTHA_PGC
20	4.91	0.004	1730	BP small molecule metabolic process
<i>Underexpressed</i>				
1	-7.91	7e-04	39	GSEA C2BURTON_ADIPOGENESIS_PEAK_AT_24HR
2	-6.96	1e-03	142	Glio WILLSCHER_GBM_Verhaak-CL_up (C)
3	-6.32	2e-03	72	GSEA C2CROONQUIST_NRAS_SIGNALING_DN
4	-6.21	2e-03	50	GSEA C2SHIDA_E2F_TARGETS
5	-5.89	2e-03	2037	MF DNA binding
6	-5.86	2e-03	52	GSEA C2TANG_SENESCENCE_TP53_TARGETS_DN
7	-5.81	2e-03	663	CC chromosome
8	-5.78	2e-03	139	GSEA C2ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
9	-5.77	2e-03	11	GSEA C2MONTERO_THYROID_CANCER_POOR_SURVIVAL_UP
10	-5.75	2e-03	116	GSEA C2MISSIAGLIA_REGULATED_BY_METHYLATION_DN
11	-5.68	2e-03	550	GSEA C2SOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
12	-5.62	2e-03	165	GSEA C2CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_UP
13	-5.61	2e-03	118	GSEA C2ODONNELL_TFRC_TARGETS_DN
14	-5.56	2e-03	721	BP chromosome organization
15	-5.46	3e-03	162	GSEA C2GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP
16	-5.43	3e-03	45	GSEA C2ZHAN_MULTIPLE_MYELOMA_PR_UP
17	-5.42	3e-03	1394	GSEA C2ZWANG_TRANSIENTLY_UP_BY_1ST_EGF_PULSE_ONLY
18	-5.4	3e-03	40	GSEA C2AMUNDSON_GAMMA_RADIATION_RESPONSE
19	-5.32	3e-03	16	GSEA C2YAGING_MIDDLE_DN
20	-5.31	3e-03	196	HM HALLMARK_G2M_CHECKPOINT



F11_mel

Local Summary

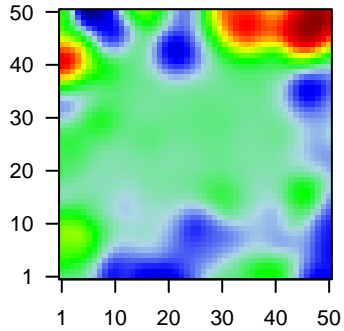
%DE = 0.8
 # metagenes = 8
 # genes = 126
 # genes in genesets = 125

 # genes with $fdr < 0.1$ = 87 (75 + / 12 -)
 # genes with $fdr < 0.05$ = 75 (66 + / 9 -)
 # genes with $fdr < 0.01$ = 42 (40 + / 2 -)

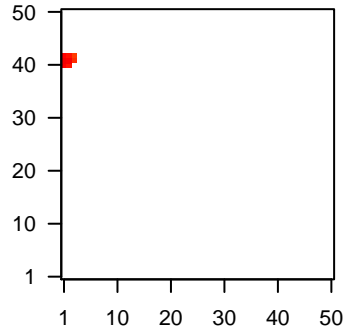
$\langle r \rangle$ metagenes = 0.99
 $\langle r \rangle$ genes = 0.22

 $\langle FC \rangle$ = 0.34
 $\langle \text{shrinkage-t} \rangle$ = 6.47
 $\langle p\text{-value} \rangle$ = 0.01
 $\langle fdr \rangle$ = 0.47

Profile



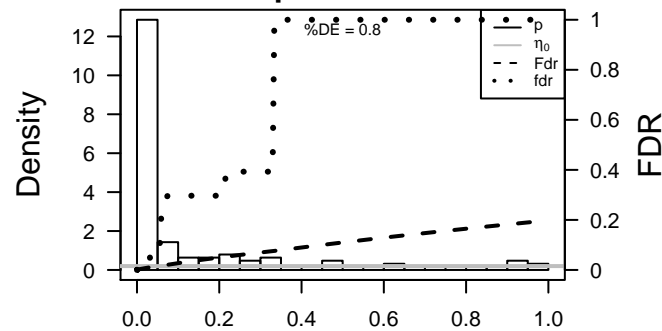
Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	MAPK10	1.57	8e-12	4e-09	1 x 41 mitogen-activated protein kinase 10 [Source:HGNC Symbol;]
2	CITED1	0.83	2e-10	4e-07	1 x 41 Cbp/p300-interacting transactivator, with Glu/Asp-rich carbo:
3	IFI35	1.3	2e-08	1e-06	3 x 41 interferon-induced protein 35 [Source:HGNC Symbol;Acc:HC
4	ANO2	1.24	6e-08	5e-06	1 x 42 anoctamin 2, calcium activated chloride channel [Source:HG
5	RGS20	1.17	3e-07	1e-05	1 x 41 regulator of G-protein signaling 20 [Source:HGNC Symbol;Ar
6	PEPD	0.57	8e-07	1e-05	2 x 42 peptidase D [Source:HGNC Symbol;Acc:HGNC:8840]
7	CCNB1IP1	-1.08	2e-06	1e-05	1 x 41 cyclin B1 interacting protein 1, E3 ubiquitin protein ligase [Sou
8	TUBB4A	0.94	2e-06	1e-05	1 x 42 tubulin, beta 4A class IVa [Source:HGNC Symbol;Acc:HGNC:
9	TRMT1	1.09	2e-06	5e-05	1 x 40 tRNA methyltransferase 1 homolog (S. cerevisiae) [Source:Hi
10	SLC45A2	0.6	4e-06	7e-05	1 x 42 solute carrier family 45, member 2 [Source:HGNC Symbol;Ac
11	PLGRKT	1.02	8e-06	7e-05	1 x 41 plasminogen receptor, C-terminal lysine transmembrane prot
12	GABRB3	1.01	1e-05	9e-05	1 x 41 gamma-aminobutyric acid (GABA) A receptor, beta 3 [Source
13	EGR1	0.9	2e-05	9e-05	1 x 40 early growth response 1 [Source:HGNC Symbol;Acc:HGNC:3
14	ZNF749	0.97	2e-05	9e-05	1 x 42 zinc finger protein 749 [Source:HGNC Symbol;Acc:HGNC:32
15	SNX8	0.96	3e-05	9e-05	1 x 42 sorting nexin 8 [Source:HGNC Symbol;Acc:HGNC:14972]
16	APEH	0.71	3e-05	9e-05	1 x 42 acylaminoacyl-peptide hydrolase [Source:HGNC Symbol;Acc
17	EXOC3	0.39	3e-05	9e-05	1 x 42 exocyst complex component 3 [Source:HGNC Symbol;Acc:Hi
18	AIFM1	0.85	3e-05	9e-05	1 x 42 apoptosis-inducing factor, mitochondrion-associated, 1 [Sou
19	CRYL1	0.95	3e-05	4e-04	1 x 41 crystallin, lambda 1 [Source:HGNC Symbol;Acc:HGNC:1824
20	ATP1A1	0.62	5e-05	4e-04	1 x 42 ATPase, Na+/K+ transporting, alpha 1 polypeptide [Source:Hi

p-values



F11_mel

Local Summary

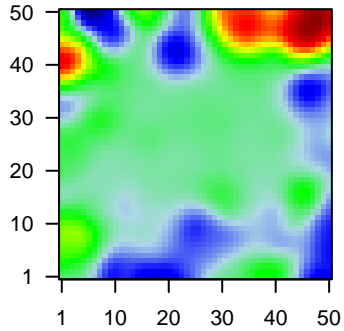
%DE = 0.81
 # metagenes = 60
 # genes = 591
 # genes in genesets = 589

 # genes with $fdr < 0.1$ = 341 (285 + / 56 -)
 # genes with $fdr < 0.05$ = 284 (241 + / 43 -)
 # genes with $fdr < 0.01$ = 201 (174 + / 27 -)

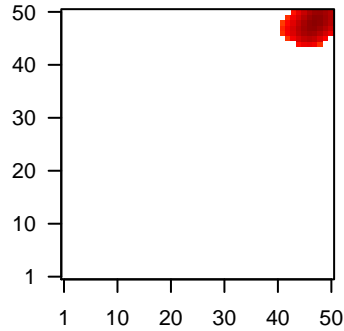
 $\langle r \rangle$ metagenes = 0.78
 $\langle r \rangle$ genes = 0.06

 $\langle FC \rangle$ = 0.29
 $\langle \text{shrinkage-t} \rangle$ = 4.92
 $\langle p\text{-value} \rangle$ = 0.01
 $\langle fdr \rangle$ = 0.53

Profile



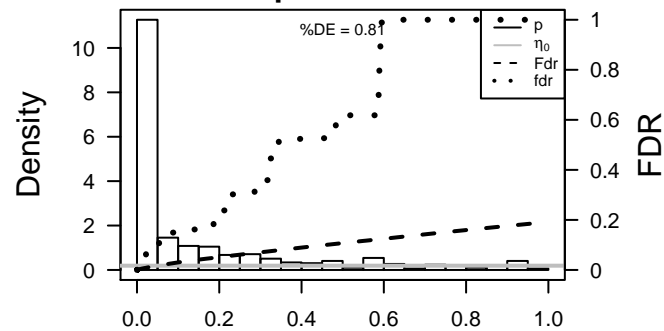
Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	CYP19A1	1.62	2e-12	2e-10	49 x 48 cytochrome P450, family 19, subfamily A, polypeptide 1 [Sou
2	C1S	1.6	3e-12	2e-09	49 x 45 complement component 1, s subcomponent [Source:HGNC S
3	MNAT1	-1.35	4e-11	2e-09	43 x 50 MNAT CDK-activating kinase assembly factor 1 [Source:HGNC
4	KRTCAP3	1.49	7e-11	2e-09	44 x 46 keratinocyte associated protein 3 [Source:HGNC Symbol;Acc
5	OAS1	1.49	8e-11	2e-09	48 x 47 2'-5'-oligoadenylate synthetase 1, 40/46kDa [Source:HGNC
6	AP4M1	1.49	9e-11	1e-07	44 x 50 adaptor-related protein complex 4, mu 1 subunit [Source:HGI
7	PACRGL	1.37	2e-09	1e-07	47 x 44 PARK2 co-regulated-like [Source:HGNC Symbol;Acc:HGNC
8	DENND2D	1.37	2e-09	2e-07	46 x 45 DENN/MADD domain containing 2D [Source:HGNC Symbol;A
9	AAAS	1.34	5e-09	2e-07	50 x 47 achalasia, adrenocortical insufficiency, alacrimia [Source:HGI
10	ANKRA2	1.33	6e-09	2e-07	50 x 49 ankyrin repeat, family A (RFXANK-like), 2 [Source:HGNC Sy
11	RABGGTA	1.33	7e-09	2e-07	48 x 50 Rab geranylgeranyltransferase, alpha subunit [Source:HGNC
12	TMEM63A	1.32	8e-09	2e-07	50 x 50 transmembrane protein 63A [Source:HGNC Symbol;Acc:HGNC
13	LRRC39	1.31	1e-08	3e-07	47 x 45 leucine rich repeat containing 39 [Source:HGNC Symbol;Acc
14	CC2D2A	1.3	1e-08	3e-07	50 x 46 coiled-coil and C2 domain containing 2A [Source:HGNC Syrr
15	PIGV	1.29	2e-08	3e-07	48 x 48 phosphatidylinositol glycan anchor biosynthesis, class V [Sou
16	CPVL	1.29	2e-08	6e-07	44 x 45 carboxypeptidase, vitellogenic-like [Source:HGNC Symbol;A
17	IL18R1	1.28	3e-08	6e-07	46 x 44 interleukin 18 receptor 1 [Source:HGNC Symbol;Acc:HGNC:f
18	ZDHHC9	1.27	3e-08	4e-06	48 x 47 zinc finger, DHHC-type containing 9 [Source:HGNC Symbol;A
19	ZNF649	1.2	2e-07	4e-06	45 x 49 zinc finger protein 649 [Source:HGNC Symbol;Acc:HGNC:25
20	GRB10	1.19	2e-07	4e-06	44 x 45 growth factor receptor-bound protein 10 [Source:HGNC Sym

p-values



F11_mel

Local Summary

%DE = 0.86
 # metagenes = 22
 # genes = 162
 # genes in genesets = 161

 # genes with $fdr < 0.1$ = 104 (81 + / 23 -)
 # genes with $fdr < 0.05$ = 96 (76 + / 20 -)
 # genes with $fdr < 0.01$ = 60 (49 + / 11 -)

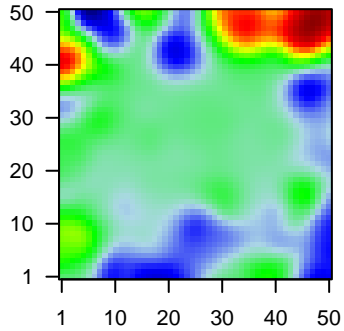
$\langle r \rangle$ metagenes = 0.93
 $\langle r \rangle$ genes = 0.08

 $\langle FC \rangle$ = 0.26
 $\langle \text{shrinkage-t} \rangle$ = 4.43
 $\langle p\text{-value} \rangle$ = 0.01
 $\langle fdr \rangle$ = 0.53

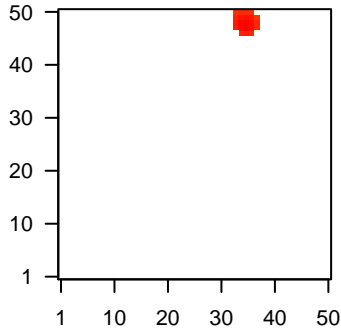
Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	KIAA1211	1.4	9e-10	1e-07	33 x 47 KIAA1211 [Source:HGNC Symbol;Acc:HGNC:29219]
2	ZNF708	1.33	7e-09	3e-07	33 x 47 zinc finger protein 708 [Source:HGNC Symbol;Acc:HGNC:12
3	PRMT5	-1.08	2e-08	3e-07	34 x 50 protein arginine methyltransferase 5 [Source:HGNC Symbol;f
4	COA7	1.26	4e-08	3e-07	37 x 48 cytochrome c oxidase assembly factor 7 (putative) [Source:H
5	TRAM1L1	1.25	5e-08	3e-07	36 x 50 translocation associated membrane protein 1-like 1 [Source:l
6	IL7	1.25	5e-08	8e-07	35 x 47 interleukin 7 [Source:HGNC Symbol;Acc:HGNC:6023]
7	JMJD7-PLA2	1.21	1e-07	8e-07	34 x 47 JMJD7-PLA2G4B readthrough [Source:HGNC Symbol;Acc:t
8	UBXN8	1.2	1e-07	8e-07	33 x 50 UBX domain protein 8 [Source:HGNC Symbol;Acc:HGNC:30
9	ALG12	1.2	2e-07	8e-07	33 x 50 ALG12, alpha-1,6-mannosyltransferase [Source:HGNC Sym
10	LTA4H	-1.16	2e-07	2e-06	35 x 50 leukotriene A4 hydrolase [Source:HGNC Symbol;Acc:HGNC:
11	MRPL52	-0.88	3e-07	2e-06	35 x 50 mitochondrial ribosomal protein L52 [Source:HGNC Symbol;f
12	DMAP1	1.17	3e-07	2e-06	36 x 50 DNA methyltransferase 1 associated protein 1 [Source:HGNC
13	PCGF1	1.16	4e-07	2e-06	33 x 50 polycomb group ring finger 1 [Source:HGNC Symbol;Acc:HG
14	FKBP15	1.15	5e-07	2e-06	34 x 50 FK506 binding protein 15, 133kDa [Source:HGNC Symbol;Ac
15	PIGN	1.11	6e-07	2e-06	36 x 50 phosphatidylinositol glycan anchor biosynthesis, class N [Sou
16	CDK10	1.14	7e-07	2e-06	37 x 49 cyclin-dependent kinase 10 [Source:HGNC Symbol;Acc:HG
17	SLC27A3	1.13	8e-07	2e-06	36 x 47 solute carrier family 27 (fatty acid transporter), member 3 [So
18	METTL18	1.13	8e-07	7e-06	36 x 50 methyltransferase like 18 [Source:HGNC Symbol;Acc:HGNC:
19	HSBP1	0.45	1e-06	7e-06	35 x 47 heat shock factor binding protein 1 [Source:HGNC Symbol;Ac
20	CNIH3	1.11	1e-06	1e-05	35 x 49 cornichon family AMPA receptor auxiliary protein 3 [Source:H

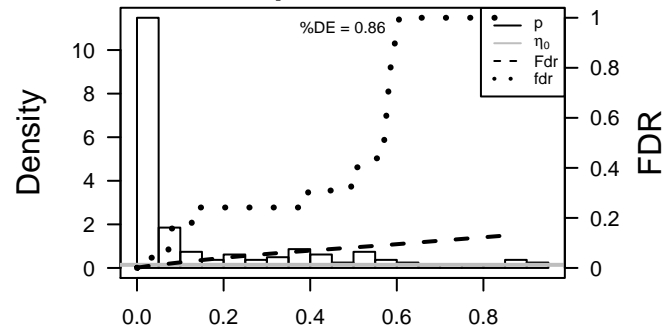
Profile



Spot



p-values



F11_mel

Local Summary

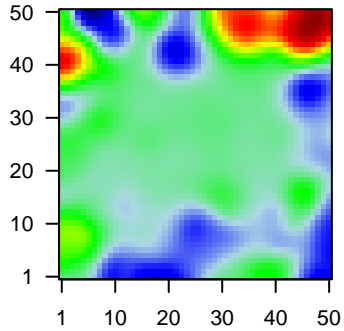
%DE = 0.72
 # metagenes = 6
 # genes = 120
 # genes in genesets = 118

 # genes with $fdr < 0.1$ = 39 (8 + / 31 -)
 # genes with $fdr < 0.05$ = 25 (3 + / 22 -)
 # genes with $fdr < 0.01$ = 15 (2 + / 13 -)

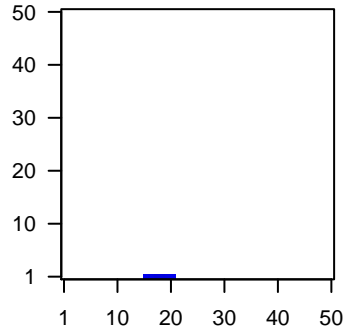
<r> metagenes = 0.91
 <r> genes = 0.12

 <FC> = -0.23
 <shrinkage-t> = -3.57
 <p-value> = 0.04
 <fdr> = 0.71

Profile



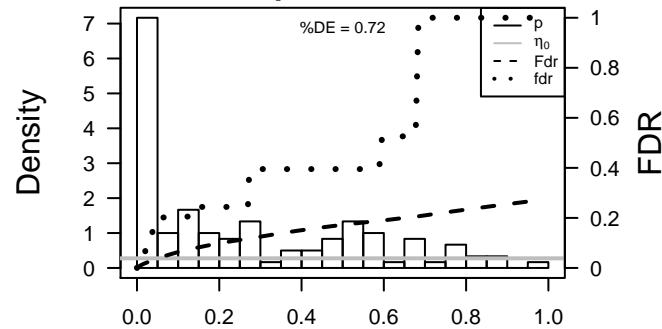
Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	RBM5	-1.73	2e-16	7e-15	19 x 1 RNA binding motif protein 5 [Source:HGNC Symbol;Acc:HGN
2	PPID	-1.26	2e-09	6e-06	18 x 1 peptidylprolyl isomerase D [Source:HGNC Symbol;Acc:HGN
3	PTPN9	1.2	2e-07	1e-04	21 x 1 protein tyrosine phosphatase, non-receptor type 9 [Source:H
4	CNOT4	-1.05	4e-06	2e-04	21 x 1 CCR4-NOT transcription complex, subunit 4 [Source:HGNC :
5	ARMC1	-1.01	9e-06	3e-04	16 x 1 armadillo repeat containing 1 [Source:HGNC Symbol;Acc:HG
6	YAE1D1	-0.98	2e-05	4e-04	19 x 1 Yae1 domain containing 1 [Source:HGNC Symbol;Acc:HGNC
7	IFT22	-0.93	5e-05	4e-04	21 x 1 intraflagellar transport 22 [Source:HGNC Symbol;Acc:HGNC:
8	ZBTB43	-0.91	6e-05	4e-04	20 x 1 zinc finger and BTB domain containing 43 [Source:HGNC Sym
9	HDAC8	-0.92	6e-05	1e-03	21 x 1 histone deacetylase 8 [Source:HGNC Symbol;Acc:HGNC:13
10	RRP8	-0.89	9e-05	4e-03	18 x 1 ribosomal RNA processing 8, methyltransferase, homolog (ye
11	NR1D2	-0.85	2e-04	6e-03	19 x 1 nuclear receptor subfamily 1, group D, member 2 [Source:HG
12	C17orf58	-0.81	4e-04	6e-03	21 x 1 chromosome 17 open reading frame 58 [Source:HGNC Synt
13	CHMP1B	0.75	7e-04	6e-03	21 x 1 charged multivesicular body protein 1B [Source:HGNC Symb
14	SYNC	-0.77	8e-04	6e-03	16 x 1 syncollin, intermediate filament protein [Source:HGNC Symb
15	DAG1	-0.74	1e-03	6e-03	18 x 1 dystroglycan 1 (dystrophin-associated glycoprotein 1) [Sour
16	WWP1	-0.74	1e-03	1e-02	21 x 1 WW domain containing E3 ubiquitin protein ligase 1 [Source:l
17	AREL1	-0.71	2e-03	1e-02	19 x 1 apoptosis resistant E3 ubiquitin protein ligase 1 [Source:HGN
18	PSMD1	-0.39	2e-03	1e-02	16 x 1 proteasome (prosome, macropain) 26S subunit, non-ATPase
19	GDAP2	-0.69	2e-03	1e-02	18 x 1 ganglioside induced differentiation associated protein 2 [Sour
20	TET2	-0.68	3e-03	1e-02	18 x 1 tet methylcytosine dioxygenase 2 [Source:HGNC Symbol;Acc

p-values



F11_mel

Local Summary

%DE = 0.7
 # metagenes = 2
 # genes = 16
 # genes in genesets = 16

 # genes with $fdr < 0.1 = 5$ (1 + / 4 -)
 # genes with $fdr < 0.05 = 4$ (1 + / 3 -)
 # genes with $fdr < 0.01 = 0$ (0 + / 0 -)

<r> metagenes = 1

<r> genes = 0.17

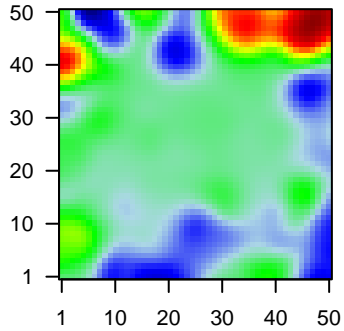
<FC> = -0.26

<shrinkage-t> = -4.22

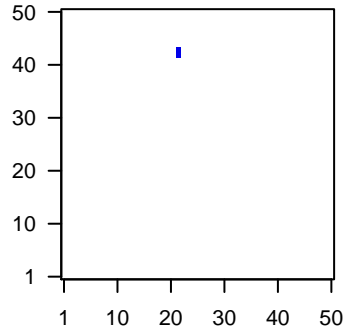
<p-value> = 0.07

<fdr> = 0.82

Profile



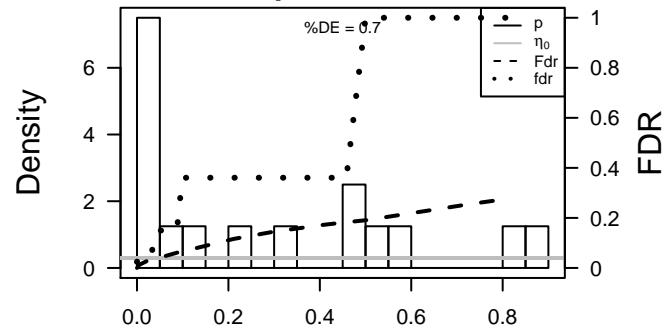
Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	GTF2F1	-1.09	1e-06	0.02	22 x 42 general transcription factor IIF, polypeptide 1, 74kDa [Source:
2	AP3M2	-0.64	5e-03	0.05	22 x 43 adaptor-related protein complex 3, mu 2 subunit [Source:HGI
3	GOPC	0.5	3e-02	0.05	22 x 43 golgi-associated PDZ and coiled-coil motif containing [Sourc
4	ZNF394	-0.49	3e-02	0.05	22 x 42 zinc finger protein 394 [Source:HGNC Symbol;Acc:HGNC:18
5	RARS2	-0.4	4e-02	0.06	22 x 42 arginyl-tRNA synthetase 2, mitochondrial [Source:HGNC Syr
6	ACP1	-0.26	5e-02	0.15	22 x 43 acid phosphatase 1, soluble [Source:HGNC Symbol;Acc:HGNC
7	CCDC101	-0.38	1e-01	0.15	22 x 43 coiled-coil domain containing 101 [Source:HGNC Symbol;Ac
8	C11orf74	-0.37	1e-01	0.36	22 x 43 chromosome 11 open reading frame 74 [Source:HGNC Synt
9	NUDT12	-0.27	2e-01	0.36	22 x 43 nudix (nucleoside diphosphate linked moiety X)-type motif 12
10	ABHD3	-0.22	3e-01	0.36	22 x 43 abhydrolase domain containing 3 [Source:HGNC Symbol;Acc
11	DISP1	-0.17	5e-01	0.36	22 x 42 dispatched homolog 1 (Drosophila) [Source:HGNC Symbol;A
12	LRIG1	-0.17	5e-01	0.36	22 x 43 leucine-rich repeats and immunoglobulin-like domains 1 [So
13	CCDC176	-0.15	5e-01	0.36	22 x 43 coiled-coil domain containing 176 [Source:HGNC Symbol;Ac
14	SGMS2	-0.13	6e-01	1.00	22 x 43 sphingomyelin synthase 2 [Source:HGNC Symbol;Acc:HGNC
15	PHF20	0.03	8e-01	1.00	22 x 43 PHD finger protein 20 [Source:HGNC Symbol;Acc:HGNC:16
16	IDH3B	0.02	9e-01	1.00	22 x 43 isocitrate dehydrogenase 3 (NAD+) beta [Source:HGNC Sym

p-values



F11_mel

Local Summary

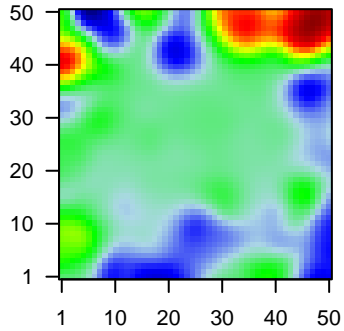
%DE = 0.88
 # metagenes = 13
 # genes = 184
 # genes in genesets = 184

 # genes with $fdr < 0.1$ = 129 (24 + / 105 -)
 # genes with $fdr < 0.05$ = 123 (24 + / 99 -)
 # genes with $fdr < 0.01$ = 84 (16 + / 68 -)

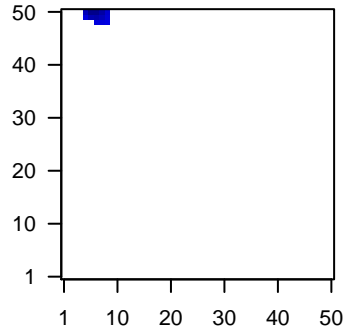
$\langle r \rangle$ metagenes = 0.99
 $\langle r \rangle$ genes = 0.39

 $\langle FC \rangle$ = -0.33
 $\langle \text{shrinkage-t} \rangle$ = -5.32
 $\langle p\text{-value} \rangle$ = 0.01
 $\langle fdr \rangle$ = 0.52

Profile



Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	STMN1	-0.73	2e-15	6e-09	5 x 50 stathmin 1 [Source:HGNC Symbol;Acc:HGNC:6510]
2	HMG2	-0.72	3e-10	2e-07	8 x 50 high mobility group nucleosomal binding domain 2 [Source:HGNC Symbol;Acc:HGNC:6511]
3	MAD2L1	-1.18	8e-09	3e-07	5 x 50 MAD2 mitotic arrest deficient-like 1 (yeast) [Source:HGNC Symbol;Acc:HGNC:6512]
4	TRIP13	-1.2	2e-08	3e-07	5 x 50 thyroid hormone receptor interactor 13 [Source:HGNC Symbol;Acc:HGNC:6513]
5	PRC1	-1.2	4e-08	3e-07	5 x 50 protein regulator of cytokinesis 1 [Source:HGNC Symbol;Acc:HGNC:6514]
6	NDC1	1.25	5e-08	6e-07	7 x 48 NDC1 transmembrane nucleoporin [Source:HGNC Symbol;Acc:HGNC:6515]
7	H2AFZ	-0.5	7e-08	8e-07	7 x 48 H2A histone family, member Z [Source:HGNC Symbol;Acc:HGNC:6516]
8	HMGB2	-1.11	1e-07	2e-06	5 x 50 high mobility group box 2 [Source:HGNC Symbol;Acc:HGNC:6517]
9	SMC2	-1.1	2e-07	1e-05	5 x 50 structural maintenance of chromosomes 2 [Source:HGNC Symbol;Acc:HGNC:6518]
10	KANSL2	-1.11	1e-06	1e-05	9 x 50 KAT8 regulatory NSL complex subunit 2 [Source:HGNC Symbol;Acc:HGNC:6519]
11	PCNX4	-1.09	2e-06	1e-05	9 x 48 pecanex-like 4 (Drosophila) [Source:HGNC Symbol;Acc:HGNC:6520]
12	CCNB1	-1.08	2e-06	1e-05	7 x 50 cyclin B1 [Source:HGNC Symbol;Acc:HGNC:1579]
13	KNSTRN	-1.07	2e-06	1e-05	8 x 50 kinetochore-localized astrin/SPAG5 binding protein [Source:HGNC Symbol;Acc:HGNC:6521]
14	G2E3	1.07	3e-06	2e-05	8 x 50 G2/M-phase specific E3 ubiquitin protein ligase [Source:HGNC Symbol;Acc:HGNC:6522]
15	UBE2C	-1.05	4e-06	3e-05	6 x 50 ubiquitin-conjugating enzyme E2C [Source:HGNC Symbol;Acc:HGNC:6523]
16	NUSAP1	-1.02	5e-06	3e-05	6 x 50 nucleolar and spindle associated protein 1 [Source:HGNC Symbol;Acc:HGNC:6524]
17	CDK1	-1.02	7e-06	7e-05	5 x 50 cyclin-dependent kinase 1 [Source:HGNC Symbol;Acc:HGNC:6525]
18	WDR34	-0.99	1e-05	7e-05	5 x 50 WD repeat domain 34 [Source:HGNC Symbol;Acc:HGNC:2818]
19	PHF19	0.99	2e-05	7e-05	5 x 50 PHD finger protein 19 [Source:HGNC Symbol;Acc:HGNC:2448]
20	CDC48	0.98	2e-05	7e-05	6 x 50 cell division cycle associated 8 [Source:HGNC Symbol;Acc:HGNC:6526]

p-values

