

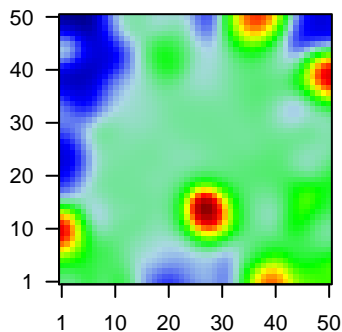
F10_mel

Global Summary

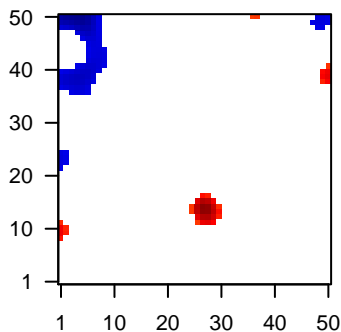
%DE = 0.22
 # genes with fdr < 0.2 = 2986 (1784 + / 1202 -)
 # genes with fdr < 0.1 = 2345 (1437 + / 908 -)
 # genes with fdr < 0.05 = 1991 (1226 + / 765 -)
 # genes with fdr < 0.01 = 1236 (782 + / 454 -)
 # genes in genesets = 14839

<FC> = 0
 <shrinkage-t> = -0.03
 <p-value> = 0.07
 <fdr> = 0.78

Profile



Regulated Spots



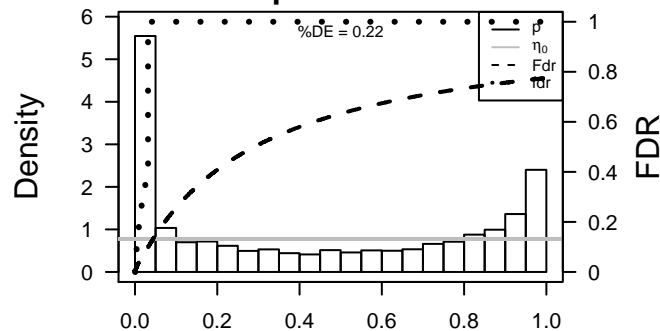
Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	ADSL	-1.6	2e-16	9e-14	28 x 50 adenylosuccinate lyase [Source:HGNC Symbol;Acc:HGNC:21
2	ALG3	-1.41	2e-16	9e-14	48 x 50 ALG3, alpha-1,3- mannosyltransferase [Source:HGNC Syml
3	AVP11	-1.82	2e-16	9e-14	49 x 50 arginine vasopressin-induced 1 [Source:HGNC Symbol;Acc:1
4	BRX1	-1.83	2e-16	9e-14	6 x 43 BRX1, biogenesis of ribosomes [Source:HGNC Symbol;Acc:t
5	CDKN3	-1.65	2e-16	9e-14	6 x 50 cyclin-dependent kinase inhibitor 3 [Source:HGNC Symbol;A
6	CERS2	-1.87	2e-16	9e-14	3 x 34 ceramide synthase 2 [Source:HGNC Symbol;Acc:HGNC:140
7	CMC2	-1.34	2e-16	9e-14	5 x 44 C-x(9)-C motif containing 2 [Source:HGNC Symbol;Acc:HGt
8	DDX39A	-1.47	2e-16	9e-14	5 x 46 DEAD (Asp-Glu-Ala-Asp) box polypeptide 39A [Source:HGt
9	DDX49	-1.58	2e-16	9e-14	27 x 50 DEAD (Asp-Glu-Ala-Asp) box polypeptide 49 [Source:HGNC
10	EIF4E	-1.42	2e-16	9e-14	9 x 41 eukaryotic translation initiation factor 4E [Source:HGNC Syml
11	EXOSC7	-1.64	2e-16	9e-14	22 x 1 exosome component 7 [Source:HGNC Symbol;Acc:HGNC:2E
12	ID3	-1.73	2e-16	9e-14	11 x 50 inhibitor of DNA binding 3, dominant negative helix-loop-heli
13	LSM8	-1.59	2e-16	9e-14	12 x 44 LSM8 homolog, U6 small nuclear RNA associated (S. cerevis
14	NAA50	-1.51	2e-16	9e-14	28 x 50 N(alpha)-acetyltransferase 50, NatE catalytic subunit [Source
15	NOP56	-0.96	2e-16	9e-14	11 x 42 NOP56 ribonucleoprotein [Source:HGNC Symbol;Acc:HGNC
16	PABPC4	-1.64	2e-16	9e-14	50 x 7 poly(A) binding protein, cytoplasmic 4 (inducible form) [Sourc
17	PGK1	-1.29	2e-16	9e-14	29 x 46 phosphoglycerate kinase 1 [Source:HGNC Symbol;Acc:HGNC
18	PLP1	0.81	2e-16	9e-14	1 x 42 proteolipid protein 1 [Source:HGNC Symbol;Acc:HGNC:9086
19	PMP22	1.35	2e-16	9e-14	48 x 1 peripheral myelin protein 22 [Source:HGNC Symbol;Acc:HGNC
20	PPF1A1	-1.69	2e-16	9e-14	11 x 45 protein tyrosine phosphatase, receptor type, f polypeptide (P1

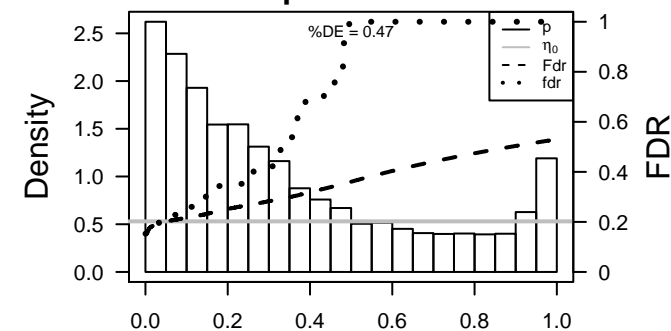
Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	5.42	0.003	42	GSEA C2KEGG_VALINE_LEUCINE_AND_ISOLEUCINE_DEGRADATION
2	5.32	0.003	3396	LymphomaOPP_Repressed
3	5.15	0.003	164	GSEA C2TINKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_HSC_UP
4	5.07	0.003	3897	Colon Cancer1_Colon
5	4.75	0.004	13	BP melanin biosynthetic process
6	4.74	0.004	730	GSEA C2RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIA
7	4.68	0.004	16	GSEA C2REACTOME_BRANCHED_CHAIN_AMINO_ACID_CATABOLISM
8	4.54	0.005	2563	LymphomaOPP_Heterochrom
9	4.49	0.005	256	GSEA C2PASQUALUCCI_LYMPHOMA_BY_GC_STAGE_UP
10	4.42	0.005	231	GSEA C2DURAND_STROMA_S_UP
11	4.4	0.005	16	BP branched-chain amino acid catabolic process
12	4.3	0.006	594	GSEA C2WONG_ADULT_TISSUE_STEM_MODULE
13	4.27	0.006	94	CC melanosome
14	4.23	0.006	302	GSEA C2KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_DN
15	4.23	0.006	57	GSEA C2GARCIA_TARGETS_OF_FL11_AND_DAX1_UP
16	4.14	0.007	62	GSEA C2BOSCO_INTERFERON_INDUCED_ANTIVIRAL_MODULE
17	4.13	0.007	361	GSEA C2BERENJENO_TRANSFORMED_BY_RHOA_DN
18	4.01	0.007	2188	LymphomaOPP_Poised_promoter
19	3.98	0.008	3088	CC plasma membrane
20	3.98	0.008	622	GSEA C2LEE_BMP2_TARGETS_UP
<i>Underexpressed</i>				
1	-12.33	1e-04	1192	GSEA C2KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
2	-11.52	2e-04	242	GSEA C2KOBAYASHI_EGFR_SIGNALING_24HR_DN
3	-11.21	2e-04	724	GSEA C2PUJANA_CHEK2_PCC_NETWORK
4	-10.81	2e-04	197	HM HALLMARK_E2F_TARGETS
5	-10.54	2e-04	1460	GSEA C2PUJANA_BRCA1_PCC_NETWORK
6	-9.9	3e-04	834	GSEA C2LEE_BMP2_TARGETS_DN
7	-9.6	3e-04	390	GSEA C2PUJANA_BRCA2_PCC_NETWORK
8	-9.53	3e-04	1251	GSEA C2DODD_NASOPHARYNGEAL_CARCINOMA_DN
9	-9.18	4e-04	312	GSEA C2WONG_EMBRYONIC_STEM_CELL_CORE
10	-9.12	4e-04	550	GSEA C2GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
11	-9.1	4e-04	436	GSEA C2SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
12	-9.03	2e-02	16	Cancer SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
13	-8.67	5e-04	113	GSEA C2PUJANA_BRCA_CENTERED_NETWORK
14	-8.66	5e-04	160	GSEA C2PUJANA_XPRSS_INT_NETWORK
15	-8.32	5e-04	142	Glio WILLSCHEER_GBM_Verhaak-CL_up (C)
16	-8.28	6e-04	305	GSEA C2DUTERTRE ESTRADIOL_RESPONSE_24HR_UP
17	-8.09	6e-04	562	GSEA C2CAIRO_HEPATOBLASTOMA_CLASSES_UP
18	-7.95	6e-04	268	GSEA C2FOURNIER_ACINAR_DEVELOPMENT_LATE_2
19	-7.8	7e-04	505	GSEA C2BERENJENO_TRANSFORMED_BY_RHOA_UP
20	-7.78	7e-04	700	GSEA C2MARSON_BOUND_BY_E2F4_UNSTIMULATED

p-values



p-values



F10_mel

Local Summary

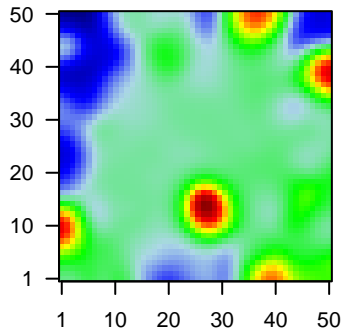
%DE = 0.79
 # metagenes = 6
 # genes = 154
 # genes in genesets = 153

 # genes with $fdr < 0.1$ = 98 (89 + / 9 -)
 # genes with $fdr < 0.05$ = 93 (86 + / 7 -)
 # genes with $fdr < 0.01$ = 66 (61 + / 5 -)

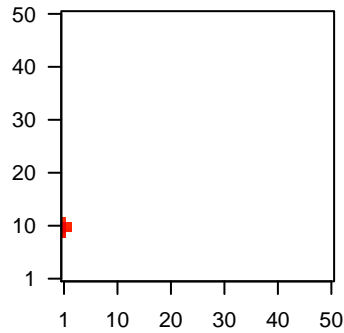
 $\langle r \rangle$ metagenes = 0.98
 $\langle r \rangle$ genes = 0.17

 $\langle FC \rangle$ = 0.47
 $\langle \text{shrinkage-t} \rangle$ = 7.67
 $\langle p\text{-value} \rangle$ = 0
 $\langle fdr \rangle$ = 0.42

Profile



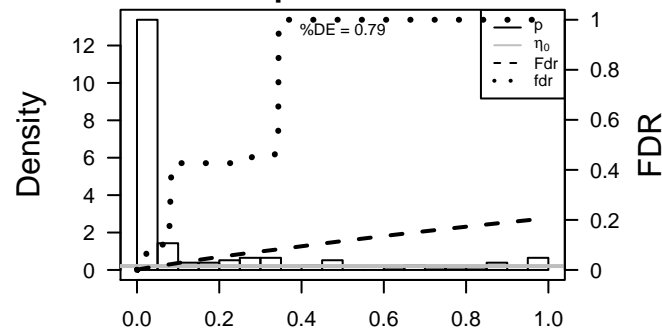
Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	SAT1	0.66	2e-11	1e-08	1 x 11 spermidine/spermine N1-acetyltransferase 1 [Source:HGNC
2	SCIN	1.52	5e-10	7e-08	1 x 12 scinderin [Source:HGNC Symbol;Acc:HGNC:21695]
3	DCT	0.84	3e-09	8e-08	1 x 11 dopachrome tautomerase [Source:HGNC Symbol;Acc:HGNC
4	PLA1A	1.41	8e-09	8e-08	1 x 10 phospholipase A1 member A [Source:HGNC Symbol;Acc:HG
5	GAS8	1.41	8e-09	3e-07	1 x 10 growth arrest-specific 8 [Source:HGNC Symbol;Acc:HGNC:4
6	SNAI2	1.24	3e-08	3e-07	1 x 11 snail family zinc finger 2 [Source:HGNC Symbol;Acc:HGNC:1
7	DGKI	1.36	3e-08	1e-06	1 x 11 diacylglycerol kinase, iota [Source:HGNC Symbol;Acc:HGNC
8	ROPN1B	1.31	8e-08	1e-06	1 x 10 rhophilin associated tail protein 1B [Source:HGNC Symbol;Ac
9	IRF4	1.3	1e-07	7e-06	1 x 11 interferon regulatory factor 4 [Source:HGNC Symbol;Acc:HGI
10	VEPH1	1.23	3e-07	1e-05	1 x 11 ventricular zone expressed PH domain-containing 1 [Source:
11	TIAM1	1.21	8e-07	1e-05	1 x 10 T-cell lymphoma invasion and metastasis 1 [Source:HGNC S
12	GPR143	0.66	2e-06	1e-05	1 x 11 G protein-coupled receptor 143 [Source:HGNC Symbol;Acc:I
13	MARK1	1.16	2e-06	1e-05	1 x 9 MAP/microtubule affinity-regulating kinase 1 [Source:HGNC
14	ARAP1	1.16	2e-06	1e-05	1 x 11 ArfGAP with RhoGAP domain, ankyrin repeat and PH domain
15	ESRP1	1.15	2e-06	1e-05	1 x 12 epithelial splicing regulatory protein 1 [Source:HGNC Symbol
16	BHLHE41	-1.13	3e-06	3e-05	1 x 12 basic helix-loop-helix family, member e41 [Source:HGNC Sy
17	PRKCH	1.13	4e-06	6e-05	1 x 12 protein kinase C, eta [Source:HGNC Symbol;Acc:HGNC:940:
18	BIN1	1.07	1e-05	6e-05	1 x 10 bridging integrator 1 [Source:HGNC Symbol;Acc:HGNC:1052
19	RGS12	1.07	1e-05	6e-05	1 x 9 regulator of G-protein signaling 12 [Source:HGNC Symbol;Ar
20	METTL16	1.07	1e-05	6e-05	1 x 10 methyltransferase like 16 [Source:HGNC Symbol;Acc:HGNC:

p-values



F10_mel

Local Summary

%DE = 0.75
 # metagenes = 27
 # genes = 163
 # genes in genesets = 161

 # genes with $fdr < 0.1$ = 115 (115 + / 0 -)
 # genes with $fdr < 0.05$ = 106 (106 + / 0 -)
 # genes with $fdr < 0.01$ = 87 (87 + / 0 -)

<r> metagenes = 0.9

<r> genes = 0.16

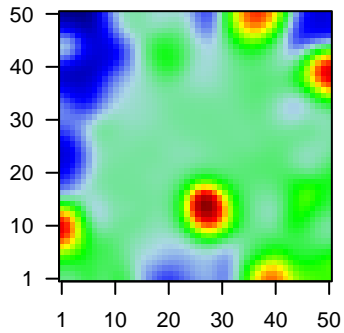
<FC> = 0.75

<shrinkage-t> = 11.52

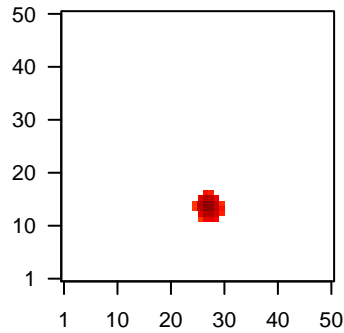
<p-value> = 0

<fdr> = 0.31

Profile



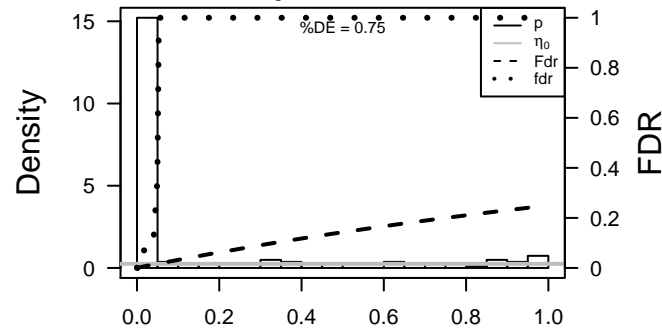
Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	GDA	1.99	4e-16	2e-13	27 x 15 guanine deaminase [Source:HGNC Symbol;Acc:HGNC:4212]
2	DOCK10	1.91	5e-15	8e-13	29 x 13 dedicator of cytokinesis 10 [Source:HGNC Symbol;Acc:HGNC:4212]
3	OR52H1	1.86	3e-14	8e-12	27 x 15 olfactory receptor, family 52, subfamily H, member 1 [Source:HGNC Symbol;Acc:HGNC:4212]
4	HOMER2	1.79	2e-13	1e-10	27 x 16 homer scaffolding protein 2 [Source:HGNC Symbol;Acc:HGNC:4212]
5	KIAA0408	1.71	3e-12	5e-10	27 x 16 KIAA0408 [Source:HGNC Symbol;Acc:HGNC:21636]
6	DZIP1L	1.65	2e-11	5e-09	30 x 13 DAZ interacting zinc finger protein 1-like [Source:HGNC Symbol;Acc:HGNC:4212]
7	FGF13	1.57	1e-10	9e-09	26 x 14 fibroblast growth factor 13 [Source:HGNC Symbol;Acc:HGNC:4212]
8	TMEM135	1.54	3e-10	2e-08	27 x 14 transmembrane protein 135 [Source:HGNC Symbol;Acc:HGNC:4212]
9	FAM212A	1.5	9e-10	2e-08	27 x 15 family with sequence similarity 212, member A [Source:HGNC Symbol;Acc:HGNC:4212]
10	TTC12	1.49	1e-09	2e-08	27 x 16 tetratricopeptide repeat domain 12 [Source:HGNC Symbol;Acc:HGNC:4212]
11	NID2	1.47	2e-09	6e-08	27 x 15 nidogen 2 (osteonidogen) [Source:HGNC Symbol;Acc:HGNC:4212]
12	ITGB7	1.45	3e-09	1e-07	27 x 16 integrin, beta 7 [Source:HGNC Symbol;Acc:HGNC:6162]
13	PPP5D1	1.41	8e-09	1e-07	27 x 16 PPP5 tetratricopeptide repeat domain containing 1 [Source:HGNC Symbol;Acc:HGNC:4212]
14	EML2	1.41	9e-09	1e-07	28 x 14 echinoderm microtubule associated protein like 2 [Source:HGNC Symbol;Acc:HGNC:4212]
15	CDON	1.39	1e-08	1e-07	28 x 14 cell adhesion associated, oncogene regulated [Source:HGNC Symbol;Acc:HGNC:4212]
16	THBS4	1.38	2e-08	1e-07	27 x 16 thrombospondin 4 [Source:HGNC Symbol;Acc:HGNC:11788]
17	CDRT4	1.38	2e-08	2e-07	27 x 14 CMT1A duplicated region transcript 4 [Source:HGNC Symbol;Acc:HGNC:4212]
18	GPHA2	1.37	2e-08	3e-07	27 x 16 glycoprotein hormone alpha 2 [Source:HGNC Symbol;Acc:HGNC:4212]
19	RBM38	1.36	3e-08	5e-07	27 x 16 RNA binding motif protein 38 [Source:HGNC Symbol;Acc:HGNC:4212]
20	SHROOM2	1.34	4e-08	6e-07	26 x 15 shroom family member 2 [Source:HGNC Symbol;Acc:HGNC:4212]

p-values



F10_mel

Local Summary

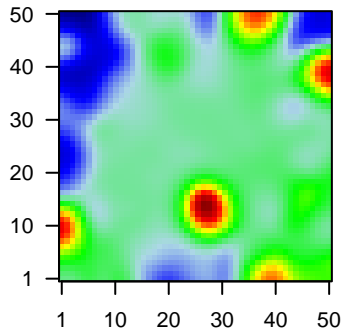
%DE = 0.72
 # metagenes = 7
 # genes = 118
 # genes in genesets = 117

 # genes with $fdr < 0.1$ = 74 (66 + / 8 -)
 # genes with $fdr < 0.05$ = 62 (56 + / 6 -)
 # genes with $fdr < 0.01$ = 55 (49 + / 6 -)

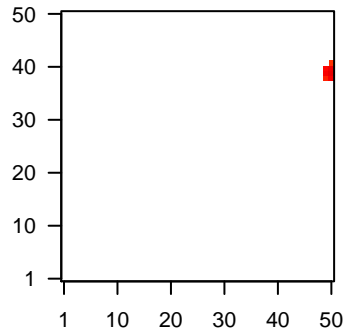
$\langle r \rangle$ metagenes = 0.98
 $\langle r \rangle$ genes = 0.1

 $\langle FC \rangle$ = 0.44
 $\langle \text{shrinkage-t} \rangle$ = 7.24
 $\langle p\text{-value} \rangle$ = 0
 $\langle fdr \rangle$ = 0.45

Profile



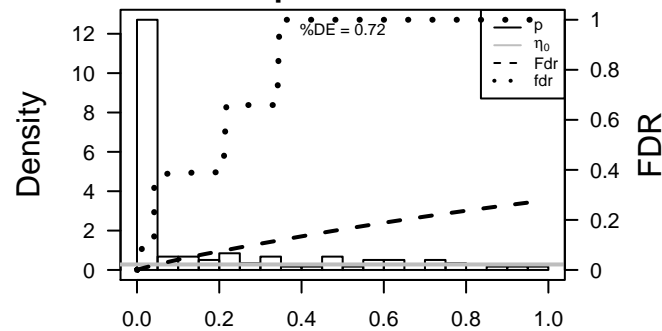
Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	SMOX	1.56	2e-10	3e-08	49 x 40 spermine oxidase [Source:HGNC Symbol;Acc:HGNC:15862]
2	ZNF133	1.49	1e-09	2e-07	50 x 39 zinc finger protein 133 [Source:HGNC Symbol;Acc:HGNC:12
3	DEPDC5	1.41	7e-09	1e-06	50 x 41 DEP domain containing 5 [Source:HGNC Symbol;Acc:HGNC
4	PDK3	1.35	4e-08	2e-06	50 x 38 pyruvate dehydrogenase kinase, isozyme 3 [Source:HGNC S
5	MARCH7	-0.87	1e-07	2e-06	50 x 41 membrane-associated ring finger (C3HC4) 7, E3 ubiquitin pr
6	RNF217	1.29	1e-07	6e-06	50 x 39 ring finger protein 217 [Source:HGNC Symbol;Acc:HGNC:21
7	ZNF75A	1.25	3e-07	6e-06	50 x 38 zinc finger protein 75a [Source:HGNC Symbol;Acc:HGNC:13
8	DPH3	-1.12	6e-07	6e-06	49 x 39 diphthamide biosynthesis 3 [Source:HGNC Symbol;Acc:HGNC
9	FAM229B	1.21	7e-07	9e-06	50 x 40 family with sequence similarity 229, member B [Source:HGNC
10	RGS3	1.2	1e-06	5e-05	50 x 40 regulator of G-protein signaling 3 [Source:HGNC Symbol;Acc
11	PARN	1.14	3e-06	5e-05	50 x 39 poly(A)-specific ribonuclease [Source:HGNC Symbol;Acc:HC
12	TRAPP6A	1.13	4e-06	1e-04	50 x 41 trafficking protein particle complex 6A [Source:HGNC Symbol
13	P2RX7	1.07	1e-05	1e-04	50 x 38 purinergic receptor P2X, ligand gated ion channel, 7 [Source:
14	TFAP2A	0.71	1e-05	1e-04	50 x 40 transcription factor AP-2 alpha (activating enhancer binding f
15	HDAC6	1.04	2e-05	1e-04	50 x 39 histone deacetylase 6 [Source:HGNC Symbol;Acc:HGNC:14
16	USP11	1.02	2e-05	1e-04	49 x 40 ubiquitin specific peptidase 11 [Source:HGNC Symbol;Acc:HC
17	COPB2	0.65	3e-05	1e-04	50 x 39 coatomer protein complex, subunit beta 2 (beta prime) [Sourc
18	FBXO38	1.02	3e-05	1e-04	50 x 38 F-box protein 38 [Source:HGNC Symbol;Acc:HGNC:28844]
19	VAMP4	1.02	3e-05	1e-04	50 x 40 vesicle-associated membrane protein 4 [Source:HGNC Syml
20	FEZ2	1.02	3e-05	1e-04	49 x 40 fasciculation and elongation protein zeta 2 (zyglin II) [Source:t

p-values



F10_mel

Local Summary

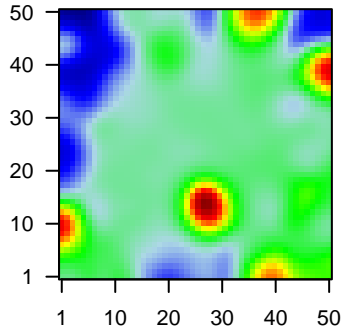
%DE = 0.89
 # metagenes = 2
 # genes = 40
 # genes in genesets = 40

 # genes with $fdr < 0.1$ = 28 (21 + / 7 -)
 # genes with $fdr < 0.05$ = 25 (21 + / 4 -)
 # genes with $fdr < 0.01$ = 19 (17 + / 2 -)

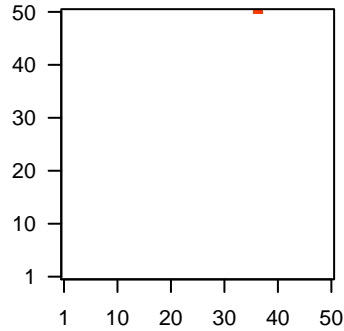
$\langle r \rangle$ metagenes = 0.99
 $\langle r \rangle$ genes = 0.12

 $\langle FC \rangle$ = 0.38
 $\langle \text{shrinkage-t} \rangle$ = 6.13
 $\langle p\text{-value} \rangle$ = 0
 $\langle fdr \rangle$ = 0.39

Profile



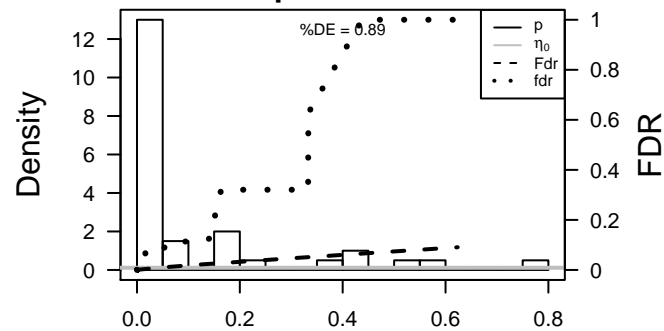
Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	TRAM1L1	1.61	5e-11	6e-10	36 x 50 translocation associated membrane protein 1-like 1 [Source:]
2	GLYCTK	1.56	2e-10	2e-08	37 x 50 glycerate kinase [Source:HGNC Symbol;Acc:HGNC:24247]
3	MRPL18	-1.12	5e-09	2e-08	36 x 50 mitochondrial ribosomal protein L18 [Source:HGNC Symbol;]
4	GMPR2	1.39	9e-09	2e-06	37 x 50 guanosine monophosphate reductase 2 [Source:HGNC Symt
5	ELP2	0.92	6e-07	1e-05	37 x 50 elongator acetyltransferase complex subunit 2 [Source:HGNC
6	ENOX2	1.11	5e-06	1e-05	36 x 50 ecto-NOX disulfide-thiol exchanger 2 [Source:HGNC Symbo
7	PXK	1.1	7e-06	3e-05	36 x 50 PX domain containing serine/threonine kinase [Source:HGNC
8	EDEM2	1.04	2e-05	3e-05	37 x 50 ER degradation enhancer, mannosidase alpha-like 2 [Source
9	TRIM37	1.01	2e-05	3e-05	37 x 50 tripartite motif containing 37 [Source:HGNC Symbol;Acc:HG
10	TRAPPC11	1.03	2e-05	2e-04	36 x 50 trafficking protein particle complex 11 [Source:HGNC Symbol
11	KDM4A	0.98	6e-05	2e-04	36 x 50 lysine (K)-specific demethylase 4A [Source:HGNC Symbol;A
12	DDX59	-0.93	1e-04	2e-04	36 x 50 DEAD (Asp-Glu-Ala-Asp) box polypeptide 59 [Source:HGNC
13	TRPA1	0.91	2e-04	2e-04	36 x 50 transient receptor potential cation channel, subfamily A, mem
14	ERCC6	0.91	2e-04	1e-03	36 x 50 excision repair cross-complementation group 6 [Source:HGNC
15	PIGN	0.84	4e-04	1e-03	36 x 50 phosphatidylinositol glycan anchor biosynthesis, class N [Sou
16	NDUFA10	0.59	6e-04	1e-03	37 x 50 NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 10,
17	NPC2	0.33	8e-04	2e-03	37 x 50 Niemann-Pick disease, type C2 [Source:HGNC Symbol;Acc:
18	PPA1	0.53	1e-03	2e-03	36 x 50 pyrophosphatase (inorganic) 1 [Source:HGNC Symbol;Acc:H
19	ANAPC16	0.68	2e-03	5e-03	36 x 50 anaphase promoting complex subunit 16 [Source:HGNC Sym
20	MECR	-0.74	3e-03	1e-02	37 x 50 mitochondrial trans-2-enoyl-CoA reductase [Source:HGNC:

p-values



F10_mel

Local Summary

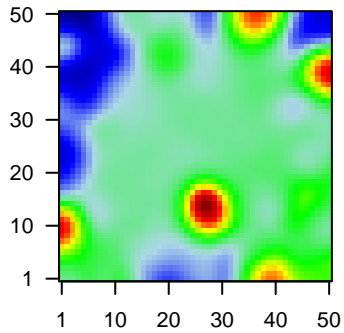
%DE = 0.75
 # metagenes = 7
 # genes = 68
 # genes in genesets = 66

 # genes with $fdr < 0.1$ = 25 (2 + / 23 -)
 # genes with $fdr < 0.05$ = 24 (2 + / 22 -)
 # genes with $fdr < 0.01$ = 19 (1 + / 18 -)

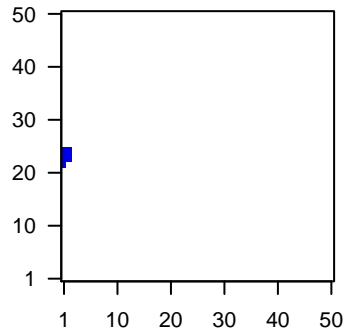
$\langle r \rangle$ metagenes = 0.95
 $\langle r \rangle$ genes = 0.11

 $\langle FC \rangle$ = -0.34
 $\langle \text{shrinkage-t} \rangle$ = -5.58
 $\langle p\text{-value} \rangle$ = 0.02
 $\langle fdr \rangle$ = 0.62

Profile



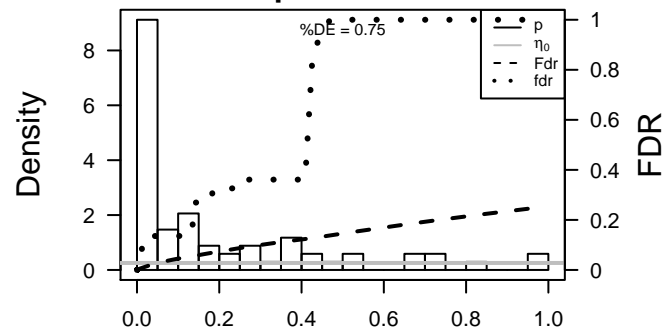
Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	SRSF4	-1.23	9e-08	8e-07	1 x 24 serine/arginine-rich splicing factor 4 [Source:HGNC Symbol;]
2	NOP58	-0.73	1e-07	2e-04	1 x 25 NOP58 ribonucleoprotein [Source:HGNC Symbol;Acc:HGNC
3	ENOPH1	-1.03	2e-05	2e-04	1 x 22 enolase-phosphatase 1 [Source:HGNC Symbol;Acc:HGNC:2
4	SCML1	-1.02	3e-05	2e-04	1 x 25 sex comb on midleg-like 1 (Drosophila) [Source:HGNC Symt
5	NIPA2	-1.02	3e-05	6e-04	1 x 23 non imprinted in Prader-Willi/Angelman syndrome 2 [Source:
6	ME2	-0.96	8e-05	6e-04	1 x 24 malic enzyme 2, NAD(+)-dependent, mitochondrial [Source:t
7	GALNT11	0.95	1e-04	1e-03	1 x 24 polypeptide N-acetylgalactosaminyltransferase 11 [Source:H
8	BTG3	-0.53	2e-04	1e-03	1 x 23 BTG family, member 3 [Source:HGNC Symbol;Acc:HGNC:11
9	RCN1	-0.44	2e-04	2e-03	1 x 23 reticulocalbin 1, EF-hand calcium binding domain [Source:HK
10	OMA1	-0.86	4e-04	2e-03	1 x 25 OMA1 zinc metallopeptidase [Source:HGNC Symbol;Acc:HG
11	STK25	-0.86	4e-04	3e-03	1 x 22 serine/threonine kinase 25 [Source:HGNC Symbol;Acc:HGNC
12	SETD4	-0.83	7e-04	3e-03	1 x 22 SET domain containing 4 [Source:HGNC Symbol;Acc:HGNC:
13	CSNK2A3	-0.79	1e-03	3e-03	1 x 24 casein kinase 2, alpha 3 polypeptide [Source:HGNC Symbol;]
14	RRP7A	-0.79	1e-03	3e-03	1 x 22 ribosomal RNA processing 7 homolog A (S. cerevisiae) [Sour
15	ATR	-0.79	1e-03	3e-03	1 x 22 ATR serine/threonine kinase [Source:HGNC Symbol;Acc:HGI
16	TSEN54	-0.79	1e-03	3e-03	1 x 22 TSEN54 tRNA splicing endonuclease subunit [Source:HGNC
17	USP14	-0.62	1e-03	8e-03	1 x 22 ubiquitin specific peptidase 14 (tRNA-guanine transglycosyla
18	NFYA	-0.75	2e-03	8e-03	1 x 25 nuclear transcription factor Y, alpha [Source:HGNC Symbol;A
19	SRP54	-0.61	3e-03	8e-03	1 x 22 signal recognition particle 54kDa [Source:HGNC Symbol;Acc
20	SNRNP200	-0.65	3e-03	1e-02	1 x 25 small nuclear ribonucleoprotein 200kDa (U5) [Source:HGNC

p-values



F10_mel

Local Summary

%DE = 0.72
 # metagenes = 86
 # genes = 836
 # genes in genesets = 833

 # genes with $fdr < 0.1$ = 426 (95 + / 331 -)
 # genes with $fdr < 0.05$ = 312 (71 + / 241 -)
 # genes with $fdr < 0.01$ = 220 (43 + / 177 -)

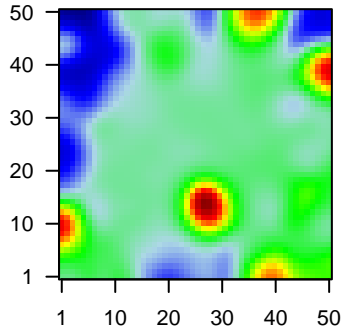
 $\langle r \rangle$ metagenes = 0.7
 $\langle r \rangle$ genes = 0.12

 $\langle FC \rangle$ = -0.27
 $\langle \text{shrinkage-t} \rangle$ = -4.57
 $\langle p\text{-value} \rangle$ = 0.01
 $\langle fdr \rangle$ = 0.58

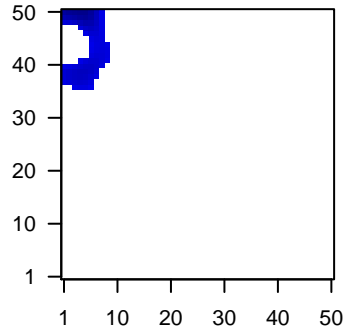
Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	BRX1	-1.83	2e-16	1e-14	6 x 43 BRX1, biogenesis of ribosomes [Source:HGNC Symbol;Acc:HGNC:10000]
2	CDKN3	-1.65	2e-16	1e-14	6 x 50 cyclin-dependent kinase inhibitor 3 [Source:HGNC Symbol;Acc:HGNC:10000]
3	DDX39A	-1.47	2e-16	1e-14	5 x 46 DEAD (Asp-Glu-Ala-Asp) box polypeptide 39A [Source:HGNC Symbol;Acc:HGNC:10000]
4	EIF4E	-1.42	2e-16	1e-14	9 x 41 eukaryotic translation initiation factor 4E [Source:HGNC Symbol;Acc:HGNC:10000]
5	SMC3	-1.46	2e-16	1e-14	7 x 47 structural maintenance of chromosomes 3 [Source:HGNC Symbol;Acc:HGNC:10000]
6	ACN9	-1.55	9e-16	1e-12	1 x 40
7	HAT1	-1.48	7e-15	1e-12	1 x 50 histone acetyltransferase 1 [Source:HGNC Symbol;Acc:HGNC:10000]
8	RAE1	-1.41	1e-14	5e-11	7 x 46 ribonucleic acid export 1 [Source:HGNC Symbol;Acc:HGNC:10000]
9	AP1S2	-0.83	2e-13	2e-10	4 x 41 adaptor-related protein complex 1, sigma 2 subunit [Source:HGNC Symbol;Acc:HGNC:10000]
10	SMC4	-1.45	1e-12	2e-10	5 x 50 structural maintenance of chromosomes 4 [Source:HGNC Symbol;Acc:HGNC:10000]
11	ZNF30	1.71	3e-12	2e-10	4 x 37 zinc finger protein 30 [Source:HGNC Symbol;Acc:HGNC:13000]
12	HNRNPDL	-0.76	3e-12	2e-10	6 x 40 heterogeneous nuclear ribonucleoprotein D-like [Source:HGNC Symbol;Acc:HGNC:10000]
13	MCM3	-1.37	4e-12	1e-09	1 x 50 minichromosome maintenance complex component 3 [Source:HGNC Symbol;Acc:HGNC:10000]
14	EXOSC8	-1.19	8e-12	4e-09	1 x 50 exosome component 8 [Source:HGNC Symbol;Acc:HGNC:17000]
15	COQ9	-1.35	2e-11	2e-08	1 x 38 coenzyme Q9 [Source:HGNC Symbol;Acc:HGNC:25302]
16	PSMG3	-1.3	1e-10	2e-08	6 x 40 proteasome (prosome, macropain) assembly chaperone 3 [Source:HGNC Symbol;Acc:HGNC:10000]
17	MRPL27	-0.85	2e-10	3e-08	4 x 38 mitochondrial ribosomal protein L27 [Source:HGNC Symbol;Acc:HGNC:10000]
18	UTP11L	-1.16	3e-10	2e-07	5 x 41 UTP11-like, U3 small nucleolar ribonucleoprotein (yeast) [Source:HGNC Symbol;Acc:HGNC:10000]
19	POLR2D	-1.32	2e-09	2e-07	7 x 40 polymerase (RNA) II (DNA directed) polypeptide D [Source:HGNC Symbol;Acc:HGNC:10000]
20	UTP18	-1.26	3e-09	2e-07	1 x 39 UTP18 small subunit (SSU) processome component homolog 1 [Source:HGNC Symbol;Acc:HGNC:10000]

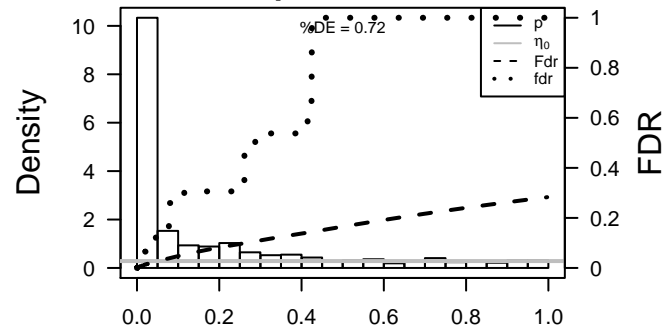
Profile



Spot



p-values



F10_mel

Local Summary

%DE = 0.74
 # metagenes = 9
 # genes = 156
 # genes in genesets = 156

 # genes with $fdr < 0.1$ = 92 (32 + / 60 -)
 # genes with $fdr < 0.05$ = 64 (19 + / 45 -)
 # genes with $fdr < 0.01$ = 39 (9 + / 30 -)

 $\langle r \rangle$ metagenes = 0.97
 $\langle r \rangle$ genes = 0.1

 $\langle FC \rangle$ = -0.18
 $\langle \text{shrinkage-t} \rangle$ = -3.28
 $\langle p\text{-value} \rangle$ = 0
 $\langle fdr \rangle$ = 0.61

Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	ALG3	-1.41	2e-16	5e-15	48 x 50 ALG3, alpha-1,3- mannosyltransferase [Source:HGNC Syml
2	AVPH1	-1.82	2e-16	5e-15	49 x 50 arginine vasopressin-induced 1 [Source:HGNC Symbol;Acc:1
3	SEH1L	-1.56	1e-15	4e-12	49 x 48 SEH1-like (S. cerevisiae) [Source:HGNC Symbol;Acc:HGNC
4	BLOC1S2	-1.5	9e-14	5e-12	48 x 50 biogenesis of lysosomal organelles complex-1, subunit 2 [So
5	ARPC1B	-1.49	2e-13	1e-11	49 x 50 actin related protein 2/3 complex, subunit 1B, 41kDa [Source:
6	MTFR1L	-1.47	8e-13	1e-11	50 x 50 mitochondrial fission regulator 1-like [Source:HGNC Symbol;
7	HSPA8	-0.71	8e-13	3e-10	49 x 50 heat shock 70kDa protein 8 [Source:HGNC Symbol;Acc:HGN
8	DDIT3	-1.44	8e-12	3e-09	50 x 50 DNA-damage-inducible transcript 3 [Source:HGNC Symbol;
9	NIP7	-1.34	9e-11	4e-08	50 x 50 NIP7, nucleolar pre-rRNA processing protein [Source:HGNC
10	FAF2	-1.29	1e-09	4e-08	50 x 50 Fas associated factor family member 2 [Source:HGNC Symb
11	SDHAF2	-1.33	2e-09	1e-05	49 x 48 succinate dehydrogenase complex assembly factor 2 [Source
12	UGP2	0.88	4e-07	1e-05	50 x 50 UDP-glucose pyrophosphorylase 2 [Source:HGNC Symbol;A
13	LAMTOR1	-0.5	5e-07	1e-05	48 x 48 late endosomal/lysosomal adaptor, MAPK and MTOR activat
14	TRPT1	-1.17	8e-07	2e-05	50 x 49 tRNA phosphotransferase 1 [Source:HGNC Symbol;Acc:HGN
15	PCID2	-1.16	1e-06	5e-05	48 x 50 PCI domain containing 2 [Source:HGNC Symbol;Acc:HGNC::
16	UPP1	-1.14	2e-06	3e-04	50 x 50 uridine phosphorylase 1 [Source:HGNC Symbol;Acc:HGNC:1
17	WDR26	0.94	2e-05	3e-04	50 x 50 WD repeat domain 26 [Source:HGNC Symbol;Acc:HGNC:21:
18	ZBTB21	-1.03	2e-05	3e-04	50 x 50 zinc finger and BTB domain containing 21 [Source:HGNC Sy
19	EIF2B2	-1	3e-05	3e-04	49 x 50 eukaryotic translation initiation factor 2B, subunit 2 beta, 39kE
20	UFSP2	1.01	4e-05	3e-04	48 x 48 UFM1-specific peptidase 2 [Source:HGNC Symbol;Acc:HGN

Profile

Spot

