

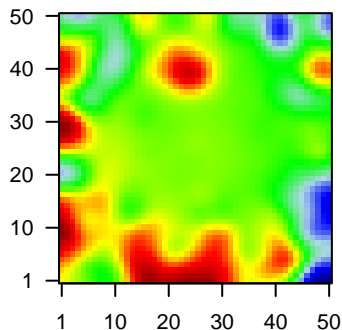
D4_mel

Global Summary

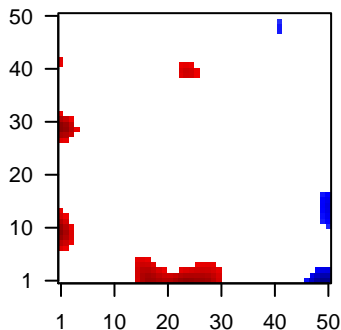
%DE = 0.24
 # genes with $fdr < 0.2$ = 3119 (1809 + / 1310 -)
 # genes with $fdr < 0.1$ = 2521 (1486 + / 1035 -)
 # genes with $fdr < 0.05$ = 2135 (1267 + / 868 -)
 # genes with $fdr < 0.01$ = 1458 (860 + / 598 -)
 # genes in genesets = 14839

<FC> = 0
 <shrinkage-t> = 0
 <p-value> = 0.05
 <fdr> = 0.76

Profile



Regulated Spots



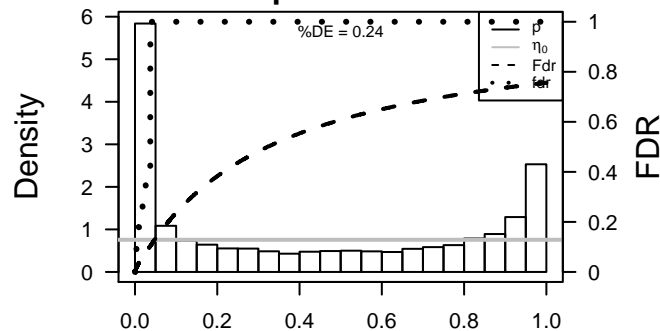
Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	AHSA1	-1.77	2e-16	7e-14	46 x 35 AHA1, activator of heat shock 90kDa protein ATPase homolo
2	ARPC1A	-1.67	2e-16	7e-14	6 x 34 actin related protein 2/3 complex, subunit 1A, 41kDa [Source:
3	ATP1B3	-1.02	2e-16	7e-14	1 x 21 ATPase, Na+/K+ transporting, beta 3 polypeptide [Source:HG
4	BCAP29	-1.5	2e-16	7e-14	41 x 47 B-cell receptor-associated protein 29 [Source:HGNC Symbc
5	CFAP20	-1.62	2e-16	7e-14	40 x 50 cilia and flagella associated protein 20 [Source:HGNC Symbc
6	CPNE3	-1.67	2e-16	7e-14	44 x 34 copine III [Source:HGNC Symbol;Acc:HGNC:2316]
7	DNAJB11	-2.19	2e-16	7e-14	5 x 23 DnaJ (Hsp40) homolog, subfamily B, member 11 [Source:HG
8	EBP	-2.01	2e-16	7e-14	1 x 48 emopamil binding protein (sterol isomerase) [Source:HGNC S
9	EIF4E2	-1.56	2e-16	7e-14	50 x 47 eukaryotic translation initiation factor 4E family member 2 [So
10	FKBP3	-1.77	2e-16	7e-14	41 x 46 FK506 binding protein 3, 25kDa [Source:HGNC Symbol;Acc:l
11	FUBP1	-1.63	2e-16	7e-14	11 x 48 far upstream element (FUSE) binding protein 1 [Source:HGNC
12	HSD17B4	-1.63	2e-16	7e-14	11 x 50 hydroxysteroid (17-beta) dehydrogenase 4 [Source:HGNC S
13	KAT7	-1.54	2e-16	7e-14	12 x 41 K(lysine) acetyltransferase 7 [Source:HGNC Symbol;Acc:HGI
14	KLHL32	1.85	2e-16	7e-14	16 x 40 kelch-like family member 32 [Source:HGNC Symbol;Acc:HGI
15	LAMB2	-1.61	2e-16	7e-14	50 x 6 laminin, beta 2 (laminin S) [Source:HGNC Symbol;Acc:HGNC
16	MRPL22	-1.71	2e-16	7e-14	40 x 47 mitochondrial ribosomal protein L22 [Source:HGNC Symbol;#
17	MRPS6	-1.4	2e-16	7e-14	50 x 3 mitochondrial ribosomal protein S6 [Source:HGNC Symbol;A
18	PABPC4	-1.64	2e-16	7e-14	50 x 7 poly(A) binding protein, cytoplasmic 4 (inducible form) [Sourc
19	PIGB	1.97	2e-16	7e-14	33 x 1 phosphatidylinositol glycan anchor biosynthesis, class B [Sou
20	PLK2	-1.65	2e-16	7e-14	50 x 1 polo-like kinase 2 [Source:HGNC Symbol;Acc:HGNC:19699]

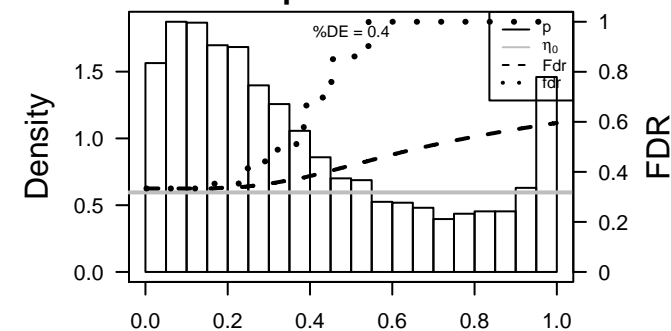
Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	5.63	0.002	35	MF aminoacyl-tRNA ligase activity
2	5.46	0.003	41	GSEA C2KEGG_AMINOACYL_TRNA_BIOSYNTHESIS
3	4.89	0.004	42	GSEA C2REACTOME_TRNA_AMINOACYLATION
4	4.82	0.004	36	MF tRNA binding
5	4.67	0.005	44	BP tRNA aminoacylation for protein translation
6	4.47	0.005	114	GSEA C2REACTOME_TCA_CYCLE_AND_RESPIRATORY_ELECTRON_T
7	4.28	0.006	24	GSEA C2REACTOME_CYTOSOLIC_TRNA_AMINOACYLATION
8	4.26	0.006	47	BP protein targeting to mitochondrion
9	4.16	0.007	135	BP cellular metabolic process
10	4.13	0.007	147	BP tRNA metabolic process
11	4.13	0.007	398	GSEA C2MOOTHA_PGC
12	4.08	0.007	101	BP RNA processing
13	3.82	0.009	405	GSEA C2MOOTHA_HUMAN_MITODB_6_2002
14	3.74	0.009	94	BP respiratory electron transport chain
15	3.73	0.009	157	GSEA C2SCHLOSSER_MYC_TARGETS_REPRESSED_BY_SERUM
16	3.72	0.009	48	GSEA C2REACTOME_MITOCHONDRIAL_PROTEIN_IMPORT
17	3.71	0.009	16	BP tRNA methylation
18	3.69	0.010	198	HM HALLMARK_OXIDATIVE_PHOSPHORYLATION
19	3.62	0.010	1730	BP small molecule metabolic process
20	3.6	0.010	18	BP response to copper ion
<i>Underexpressed</i>				
1	-5.36	0.003	30	GSEA C2CAFFAREL_RESPONSE_TO_THC_DN
2	-5.26	0.003	93	GSEA C2KONG_E2F3_TARGETS
3	-4.78	0.004	49	miRNA target-miR-302b*
4	-4.61	0.005	26	BP regulation of alternative mRNA splicing, via spliceosome
5	-4.49	0.005	13	MF ATPase activator activity
6	-4.39	0.006	99	GSEA C2BURTON_ADIPOGENESIS_3
7	-4.38	0.006	44	GSEA C2WHITFIELD_CELL_CYCLE_LITERATURE
8	-4.16	0.007	139	GSEA C2ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
9	-4.06	0.007	70	miRNA target-miR-502-5p
10	-3.99	0.008	100	GSEA C2SENESE_HDAC2_TARGETS_UP
11	-3.99	0.008	550	GSEA C2SOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
12	-3.95	0.008	700	GSEA C2MARSON_BOUND_BY_E2F4_UNSTIMULATED
13	-3.91	0.008	20	GSEA C2DELLA_RESPONSE_TO_TSA_AND_BUTYRATE
14	-3.9	0.008	272	GSEA C2DEURIG_T_CELL_PROLYMPHOCTIC_LEUKEMIA_DN
15	-3.85	0.008	32	GSEA C2REACTOME_IL_2_SIGNALING
16	-3.83	0.009	13	GSEA C2BIOCARTA_TOB1_PATHWAY
17	-3.83	0.009	63	GSEA C2RAGHAVACHARI_PLATELET_SPECIFIC_GENES
18	-3.73	0.009	616	GSEA C2BENPORATH_CYCLING_GENES
19	-3.72	0.009	145	GSEA C2CHANG_CYCLING_GENES
20	-3.7	0.010	309	GSEA C2GOLDRATH_ANTIGEN_RESPONSE

p-values



p-values



D4_mel

Local Summary

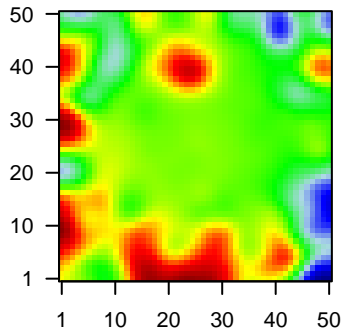
%DE = 0.29
 # metagenes = 57
 # genes = 666
 # genes in genesets = 638

 # genes with $fdr < 0.1 = 107$ (95 + / 12 -)
 # genes with $fdr < 0.05 = 95$ (83 + / 12 -)
 # genes with $fdr < 0.01 = 80$ (71 + / 9 -)

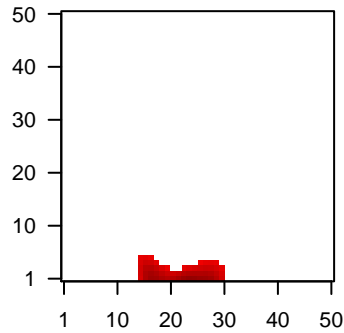
$\langle r \rangle$ metagenes = 0.74
 $\langle r \rangle$ genes = 0.14

 $\langle FC \rangle = 0.16$
 $\langle \text{shrinkage-t} \rangle = 2.52$
 $\langle p\text{-value} \rangle = 0.05$
 $\langle fdr \rangle = 0.77$

Profile



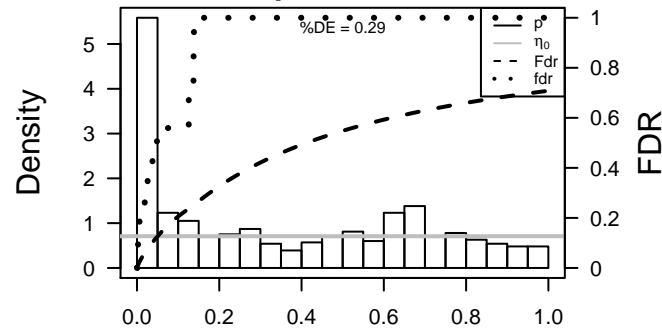
Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	EML1	1.69	4e-14	2e-09	15 x 1 echinoderm microtubule associated protein like 1 [Source:HGNC
2	CA11	1.54	5e-12	5e-09	17 x 5 carbonic anhydrase XI [Source:HGNC Symbol;Acc:HGNC:13
3	ANKAR	1.51	2e-11	1e-08	16 x 3 ankyrin and armadillo repeat containing [Source:HGNC Synt
4	RBM12B	1.47	4e-11	3e-08	16 x 1 RNA binding motif protein 12B [Source:HGNC Symbol;Acc:H
5	ARHGAP22	1.44	1e-10	9e-08	28 x 2 Rho GTPase activating protein 22 [Source:HGNC Symbol;Ac
6	PELP1	1.41	3e-10	9e-08	25 x 1 proline, glutamate and leucine rich protein 1 [Source:HGNC S
7	TAF10	1.38	7e-10	9e-08	21 x 1 TAF10 RNA polymerase II, TATA box binding protein (TBP)-a
8	PPID	-1.26	7e-10	4e-07	18 x 1 peptidylprolyl isomerase D [Source:HGNC Symbol;Acc:HGNC
9	RIOK1	-1.25	1e-09	1e-06	21 x 2 RIO kinase 1 [Source:HGNC Symbol;Acc:HGNC:18656]
10	WDR7	1.29	7e-09	1e-06	15 x 1 WD repeat domain 7 [Source:HGNC Symbol;Acc:HGNC:134
11	URB1	1.29	8e-09	1e-06	17 x 5 URB1 ribosome biogenesis 1 homolog (S. cerevisiae) [Sourc
12	RCBTB2	1.28	1e-08	1e-06	24 x 1 regulator of chromosome condensation (RCC1) and BTB (PC
13	STAM2	1.28	1e-08	1e-06	24 x 1 signal transducing adaptor molecule (SH3 domain and ITAM)
14	METTL4	1.27	1e-08	2e-05	23 x 1 methyltransferase like 4 [Source:HGNC Symbol;Acc:HGNC:2
15	HDAC8	1.19	1e-07	2e-05	21 x 1 histone deacetylase 8 [Source:HGNC Symbol;Acc:HGNC:13
16	CHMP4B	1.19	1e-07	2e-05	17 x 5 charged multivesicular body protein 4B [Source:HGNC Symb
17	CAB39	1.16	2e-07	2e-05	17 x 2 calcium binding protein 39 [Source:HGNC Symbol;Acc:HGNC
18	PPIP5K1	1.16	2e-07	2e-05	15 x 1 diphosphoinositol pentakisphosphate kinase 1 [Source:HGNC
19	CDK12	1.15	2e-07	2e-05	17 x 1 cyclin-dependent kinase 12 [Source:HGNC Symbol;Acc:HGNC
20	TKT	0.62	3e-07	6e-05	16 x 2 transketolase [Source:HGNC Symbol;Acc:HGNC:11834]

p-values



D4_mel

Local Summary

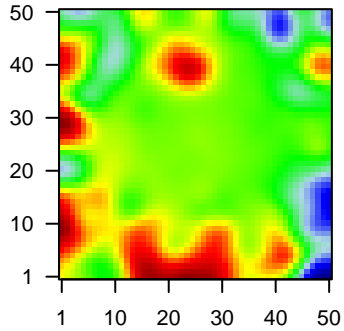
%DE = 0.69
 # metagenes = 19
 # genes = 293
 # genes in genesets = 291

 # genes with $fdr < 0.1$ = 141 (103 + / 38 -)
 # genes with $fdr < 0.05$ = 113 (84 + / 29 -)
 # genes with $fdr < 0.01$ = 80 (59 + / 21 -)

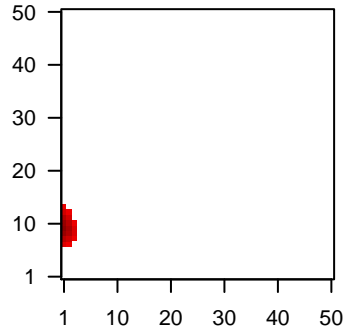
$\langle r \rangle$ metagenes = 0.91
 $\langle r \rangle$ genes = 0.12

 $\langle FC \rangle$ = 0.17
 $\langle \text{shrinkage-t} \rangle$ = 2.85
 $\langle p\text{-value} \rangle$ = 0.01
 $\langle fdr \rangle$ = 0.56

Profile



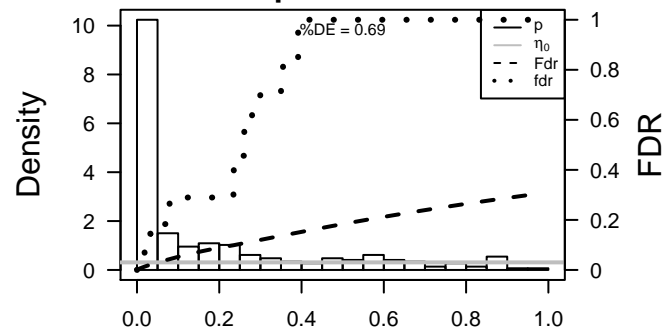
Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	VPS13D	1.65	1e-13	2e-09	1 x 9 vacuolar protein sorting 13 homolog D (S. cerevisiae) [Source:HGNC Symbol;Acc:HGNC:10300]
2	KIF3C	1.5	2e-11	2e-09	1 x 12 kinesin family member 3C [Source:HGNC Symbol;Acc:HGNC:10300]
3	POPDC2	1.47	4e-11	5e-09	1 x 9 popeye domain containing 2 [Source:HGNC Symbol;Acc:HGNC:10300]
4	QRICH1	-0.97	1e-10	5e-09	1 x 8 glutamine-rich 1 [Source:HGNC Symbol;Acc:HGNC:24713]
5	VAV3	1.43	2e-10	1e-08	1 x 14 vav 3 guanine nucleotide exchange factor [Source:HGNC Symbol;Acc:HGNC:10300]
6	DCT	0.82	3e-10	1e-08	1 x 11 dopachrome tautomerase [Source:HGNC Symbol;Acc:HGNC:10300]
7	AGA	1.4	4e-10	5e-08	1 x 7 aspartylglucosaminidase [Source:HGNC Symbol;Acc:HGNC:10300]
8	SAT1	0.55	1e-09	1e-06	1 x 11 spermidine/spermine N1-acetyltransferase 1 [Source:HGNC Symbol;Acc:HGNC:10300]
9	SNX1	-1.2	2e-08	1e-06	1 x 8 sorting nexin 1 [Source:HGNC Symbol;Acc:HGNC:11172]
10	GAS8	1.25	2e-08	3e-06	1 x 10 growth arrest-specific 8 [Source:HGNC Symbol;Acc:HGNC:40000]
11	ADRBK2	1.2	7e-08	3e-06	1 x 10 adrenergic, beta, receptor kinase 2 [Source:HGNC Symbol;Acc:HGNC:10300]
12	BBS5	1.2	8e-08	3e-06	1 x 11 Bardet-Biedl syndrome 5 [Source:HGNC Symbol;Acc:HGNC:10300]
13	CEP104	1.18	1e-07	3e-06	1 x 7 centrosomal protein 104kDa [Source:HGNC Symbol;Acc:HGNC:10300]
14	KCTD21	1.17	1e-07	6e-06	3 x 9 potassium channel tetramerization domain containing 21 [Source:HGNC Symbol;Acc:HGNC:10300]
15	MFSD5	-1.14	2e-07	1e-05	1 x 8 major facilitator superfamily domain containing 5 [Source:HGNC Symbol;Acc:HGNC:10300]
16	OSBPL9	0.93	4e-07	1e-05	1 x 8 oxysterol binding protein-like 9 [Source:HGNC Symbol;Acc:HGNC:10300]
17	C10orf90	1.12	5e-07	1e-05	1 x 11 chromosome 10 open reading frame 90 [Source:HGNC Symbol;Acc:HGNC:10300]
18	SLC5A2	1.12	6e-07	2e-05	1 x 7 solute carrier family 5 (sodium/glucose cotransporter), member 2 [Source:HGNC Symbol;Acc:HGNC:10300]
19	SCUBE3	-1.09	8e-07	2e-05	1 x 12 signal peptide, CUB domain, EGF-like 3 [Source:HGNC Symbol;Acc:HGNC:10300]
20	TNFRSF14	-1	1e-06	2e-05	1 x 11 tumor necrosis factor receptor superfamily, member 14 [Source:HGNC Symbol;Acc:HGNC:10300]

p-values



D4_mel

Local Summary

%DE = 0.64
 # metagenes = 16
 # genes = 94
 # genes in genesets = 93

 # genes with $fdr < 0.1$ = 51 (44 + / 7 -)
 # genes with $fdr < 0.05$ = 47 (40 + / 7 -)
 # genes with $fdr < 0.01$ = 34 (28 + / 6 -)

<r> metagenes = 0.91

<r> genes = 0.09

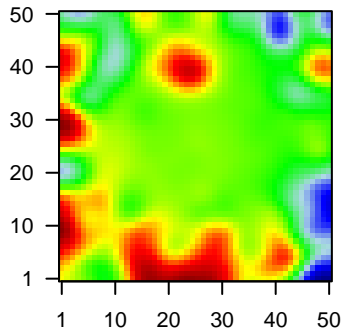
<FC> = 0.34

<shrinkage-t> = 5.42

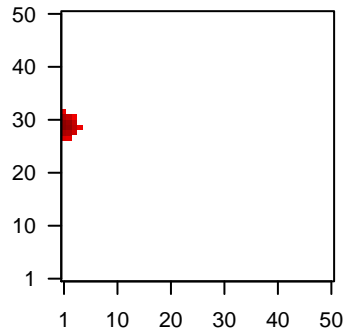
<p-value> = 0

<fdr> = 0.47

Profile



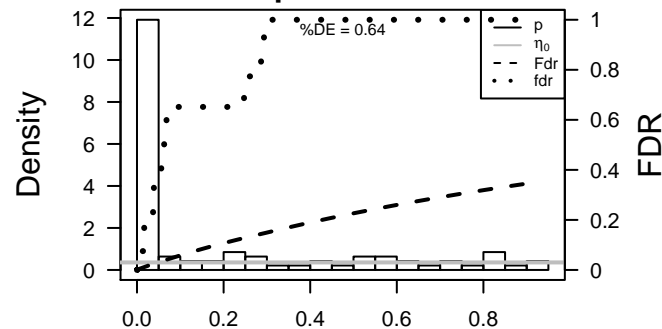
Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	TBCK	1.7	3e-14	7e-10	1 x 29 TBC1 domain containing kinase [Source:HGNC Symbol;Acc:HGNC:10000]
2	PCTP	1.48	4e-11	7e-10	1 x 27 phosphatidylcholine transfer protein [Source:HGNC Symbol;Acc:HGNC:10000]
3	GPR116	1.46	7e-11	7e-10	1 x 27
4	SETD9	1.45	8e-11	7e-10	3 x 31 SET domain containing 9 [Source:HGNC Symbol;Acc:HGNC:10000]
5	DOCK6	1.45	1e-10	7e-10	1 x 29 dedicator of cytokinesis 6 [Source:HGNC Symbol;Acc:HGNC:10000]
6	PDE9A	1.44	1e-10	6e-09	3 x 29 phosphodiesterase 9A [Source:HGNC Symbol;Acc:HGNC:87]
7	CYB5RL	1.4	4e-10	6e-09	1 x 30 cytochrome b5 reductase-like [Source:HGNC Symbol;Acc:HGNC:10000]
8	WLS	1.39	4e-10	5e-08	1 x 30 wntless Wnt ligand secretion mediator [Source:HGNC Symbol;Acc:HGNC:10000]
9	ZNF473	1.34	2e-09	2e-07	3 x 31 zinc finger protein 473 [Source:HGNC Symbol;Acc:HGNC:23]
10	GNB2	1.28	1e-08	2e-07	1 x 31 guanine nucleotide binding protein (G protein), beta polypeptide 2 [Source:HGNC Symbol;Acc:HGNC:10000]
11	POLR3C	-1.2	1e-08	5e-06	1 x 32 polymerase (RNA) III (DNA directed) polypeptide C (62kDa) [Source:HGNC Symbol;Acc:HGNC:10000]
12	CHD1	-0.81	2e-07	5e-06	1 x 31 chromodomain helicase DNA binding protein 1 [Source:HGNC Symbol;Acc:HGNC:10000]
13	LRBA	1.14	3e-07	4e-04	1 x 27 LPS-responsive vesicle trafficking, beach and anchor containing protein 1 [Source:HGNC Symbol;Acc:HGNC:10000]
14	DLEU1	0.97	1e-05	4e-04	1 x 32 deleted in lymphocytic leukemia 1 (non-protein coding) [Source:HGNC Symbol;Acc:HGNC:10000]
15	DDX54	0.95	2e-05	5e-04	2 x 31 DEAD (Asp-Glu-Ala-Asp) box polypeptide 54 [Source:HGNC Symbol;Acc:HGNC:10000]
16	TSHZ1	0.92	4e-05	6e-04	1 x 30 teashirt zinc finger homeobox 1 [Source:HGNC Symbol;Acc:HGNC:10000]
17	POLR1E	0.89	7e-05	6e-04	3 x 31 polymerase (RNA) I polypeptide E, 53kDa [Source:HGNC Symbol;Acc:HGNC:10000]
18	ECM2	0.89	7e-05	6e-04	1 x 28 extracellular matrix protein 2, female organ and adipocyte specific [Source:HGNC Symbol;Acc:HGNC:10000]
19	TBC1D1	-0.87	9e-05	7e-04	1 x 27 TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1 [Source:HGNC Symbol;Acc:HGNC:10000]
20	PRKAR1B	0.86	1e-04	1e-03	2 x 29 protein kinase, cAMP-dependent, regulatory, type I, beta [Source:HGNC Symbol;Acc:HGNC:10000]

p-values



D4_mel

Local Summary

%DE = 0.59
 # metagenes = 11
 # genes = 35
 # genes in genesets = 35

 # genes with $fdr < 0.1$ = 18 (17 + / 1 -)
 # genes with $fdr < 0.05$ = 18 (17 + / 1 -)
 # genes with $fdr < 0.01$ = 17 (16 + / 1 -)

<r> metagenes = 0.94

<r> genes = 0.15

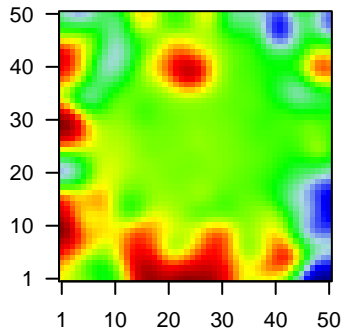
<FC> = 0.56

<shrinkage-t> = 8.9

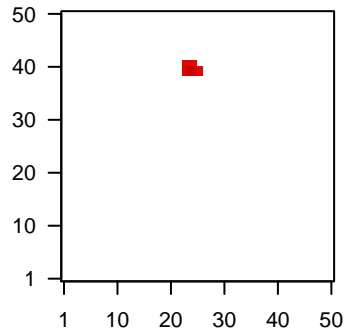
<p-value> = 0

<fdr> = 0.42

Profile



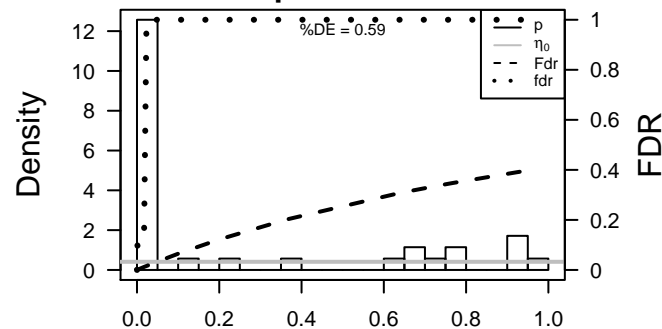
Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	DISP2	1.71	2e-14	1e-08	25 x 39 dispatched homolog 2 (Drosophila) [Source:HGNC Symbol;A
2	PNPLA8	1.38	7e-10	3e-08	24 x 41 patatin-like phospholipase domain containing 8 [Source:HGNC
3	IDI2	1.32	3e-09	3e-08	26 x 39 isopentenyl-diphosphate delta isomerase 2 [Source:HGNC S
4	DTX2	1.31	5e-09	6e-08	23 x 40 deltex 2, E3 ubiquitin ligase [Source:HGNC Symbol;Acc:HGNC
5	FAM72D	1.28	9e-09	6e-08	26 x 39 family with sequence similarity 72, member D [Source:HGNC
6	RSPRY1	1.27	1e-08	2e-07	25 x 40 ring finger and SPRY domain containing 1 [Source:HGNC Sy
7	SLC25A21	1.23	3e-08	2e-07	25 x 39 solute carrier family 25 (mitochondrial oxoadipate carrier), me
8	APOPT1	1.22	4e-08	8e-07	25 x 40 apoptogenic 1, mitochondrial [Source:HGNC Symbol;Acc:HGNC
9	GFER	1.19	9e-08	7e-06	25 x 39 growth factor, augmenter of liver regeneration [Source:HGNC
10	FAM72B	1.08	1e-06	7e-06	26 x 39 family with sequence similarity 72, member B [Source:HGNC
11	FAM72C	1.08	1e-06	7e-06	26 x 39 family with sequence similarity 72, member C [Source:HGNC
12	SPTLC2	1.07	2e-06	8e-05	24 x 41 serine palmitoyltransferase, long chain base subunit 2 [Source:HGNC
13	LMF2	1	7e-06	2e-04	25 x 39 lipase maturation factor 2 [Source:HGNC Symbol;Acc:HGNC
14	STK24	0.95	2e-05	3e-04	23 x 39 serine/threonine kinase 24 [Source:HGNC Symbol;Acc:HGNC
15	PSMD2	0.43	6e-05	3e-04	23 x 39 proteasome (prosome, macropain) 26S subunit, non-ATPase
16	FAM212B	0.89	6e-05	2e-03	26 x 40 family with sequence similarity 212, member B [Source:HGNC
17	USP40	-0.83	2e-04	7e-03	24 x 41 ubiquitin specific peptidase 40 [Source:HGNC Symbol;Acc:HGNC
18	USP13	0.76	7e-04	1e-02	25 x 40 ubiquitin specific peptidase 13 (isopeptidase T-3) [Source:HGNC
19	TAF8	0.7	1e-03	2e-01	23 x 41 TAF8 RNA polymerase II, TATA box binding protein (TBP)-as
20	XRCC6	0.27	2e-02	2e-01	23 x 40 X-ray repair complementing defective repair in Chinese hamst

p-values



D4_mel

Local Summary

%DE = 0.79
 # metagenes = 2
 # genes = 72
 # genes in genesets = 72

 # genes with $fdr < 0.1$ = 37 (28 + / 9 -)
 # genes with $fdr < 0.05$ = 37 (28 + / 9 -)
 # genes with $fdr < 0.01$ = 24 (17 + / 7 -)

<r> metagenes = 1

<r> genes = 0.26

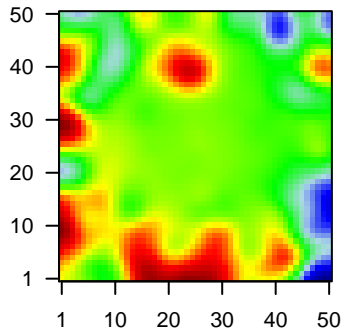
<FC> = 0.16

<shrinkage-t> = 3.69

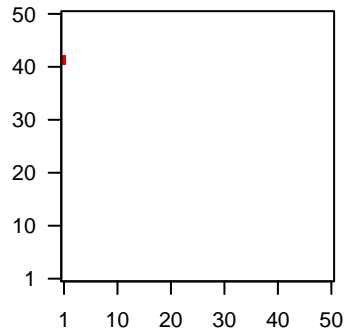
<p-value> = 0

<fdr> = 0.5

Profile



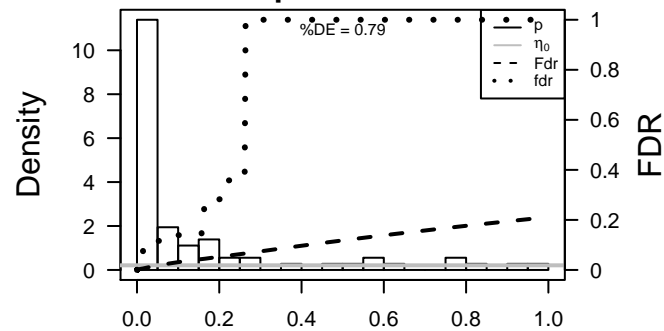
Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	PFKM	-1.42	3e-13	4e-12	1 x 41 phosphofructokinase, muscle [Source:HGNC Symbol;Acc:HG
2	ANO2	1.61	6e-13	3e-09	1 x 42 anoctamin 2, calcium activated chloride channel [Source:HG
3	SFXN4	-1.3	2e-10	1e-08	1 x 41 sideroflexin 4 [Source:HGNC Symbol;Acc:HGNC:16088]
4	MITF	0.62	9e-10	5e-07	1 x 41 microphthalmia-associated transcription factor [Source:HGNC
5	IDH3A	0.55	4e-08	4e-06	1 x 42 isocitrate dehydrogenase 3 (NAD+) alpha [Source:HGNC Syr
6	RGS20	-1.11	5e-07	4e-06	1 x 41 regulator of G-protein signaling 20 [Source:HGNC Symbol;Ar
7	MAPK10	1.12	5e-07	2e-05	1 x 41 mitogen-activated protein kinase 10 [Source:HGNC Symbol;v
8	MLST8	-1.06	2e-06	1e-04	1 x 41 MTOR associated protein, LST8 homolog (S. cerevisiae) [So
9	FAM174B	-0.97	1e-05	1e-04	1 x 42 family with sequence similarity 174, member B [Source:HGNC
10	FRMD3	0.95	2e-05	1e-04	1 x 41 FERM domain containing 3 [Source:HGNC Symbol;Acc:HGN
11	PSMB10	0.82	2e-05	2e-04	1 x 42 proteasome (prosome, macropain) subunit, beta type, 10 [So
12	GSTM4	0.78	5e-05	2e-04	1 x 41 glutathione S-transferase mu 4 [Source:HGNC Symbol;Acc:f
13	HDAC3	0.89	5e-05	6e-04	1 x 41 histone deacetylase 3 [Source:HGNC Symbol;Acc:HGNC:48f
14	PIR	0.47	1e-04	6e-04	1 x 42 pirin (iron-binding nuclear protein) [Source:HGNC Symbol;Ac
15	HES6	-0.85	1e-04	9e-04	1 x 41 hes family bHLH transcription factor 6 [Source:HGNC Symbol
16	NENF	-0.83	2e-04	2e-03	1 x 42 neudesin neurotrophic factor [Source:HGNC Symbol;Acc:HGI
17	QDPR	0.78	5e-04	2e-03	1 x 41 quinoid dihydropteridine reductase [Source:HGNC Symbol;Ac
18	SNRPA	0.68	6e-04	2e-03	1 x 42 small nuclear ribonucleoprotein polypeptide A [Source:HGNC
19	TYR	0.39	6e-04	3e-03	1 x 42 tyrosinase [Source:HGNC Symbol;Acc:HGNC:12442]
20	MICAL1	0.75	8e-04	8e-03	1 x 41 microtubule associated monooxygenase, calponin and LIM do

p-values



D4_mel

Local Summary

%DE = 0.88
 # metagenes = 12
 # genes = 230
 # genes in genesets = 230

 # genes with $fdr < 0.1$ = 140 (30 + / 110 -)
 # genes with $fdr < 0.05$ = 110 (22 + / 88 -)
 # genes with $fdr < 0.01$ = 64 (14 + / 50 -)

<r> metagenes = 0.98

<r> genes = 0.22

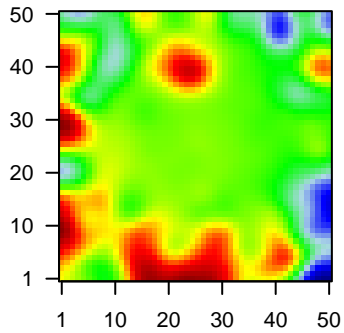
<FC> = -0.28

<shrinkage-t> = -4.74

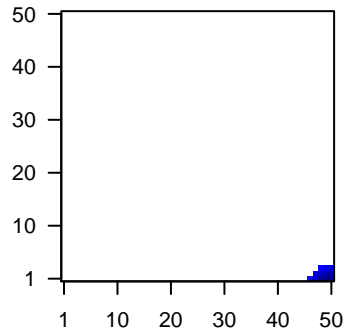
<p-value> = 0.01

<fdr> = 0.56

Profile



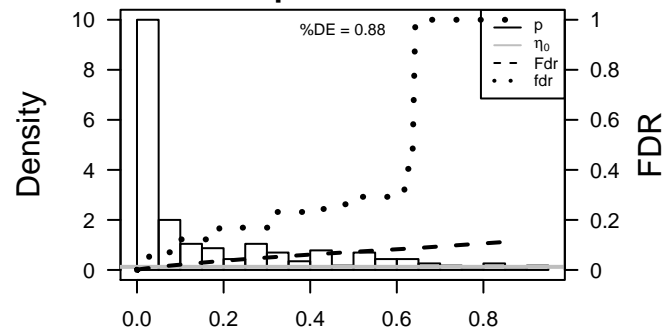
Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	MRPS6	-1.4	2e-16	2e-15	50 x 3 mitochondrial ribosomal protein S6 [Source:HGNC Symbol;Acc:HGNC:19699]
2	PLK2	-1.65	2e-16	2e-15	50 x 1 polo-like kinase 2 [Source:HGNC Symbol;Acc:HGNC:19699]
3	SPARC	-1.42	2e-16	2e-15	50 x 2 secreted protein, acidic, cysteine-rich (osteonectin) [Source:HGNC Symbol;Acc:HGNC:19699]
4	SNAP23	-1.35	2e-14	1e-12	50 x 1 synaptosomal-associated protein, 23kDa [Source:HGNC Symbol;Acc:HGNC:19699]
5	FABP3	-1.44	7e-14	1e-10	50 x 1 fatty acid binding protein 3, muscle and heart [Source:HGNC Symbol;Acc:HGNC:19699]
6	CNN3	-0.62	4e-12	1e-10	47 x 1 calponin 3, acidic [Source:HGNC Symbol;Acc:HGNC:2157]
7	PLOD2	-1.36	9e-12	1e-10	49 x 3 procollagen-lysine, 2-oxoglutarate 5-dioxygenase 2 [Source:HGNC Symbol;Acc:HGNC:2157]
8	DYNC1LI1	-1.35	1e-11	4e-10	47 x 1 dynein, cytoplasmic 1, light intermediate chain 1 [Source:HGNC Symbol;Acc:HGNC:2157]
9	SYNE1	-0.99	3e-11	1e-09	49 x 1 spectrin repeat containing, nuclear envelope 1 [Source:HGNC Symbol;Acc:HGNC:2157]
10	RAB31	1.44	7e-11	5e-08	50 x 3 RAB31, member RAS oncogene family [Source:HGNC Symbol;Acc:HGNC:2157]
11	TMEM45A	1.34	2e-09	9e-08	50 x 1 transmembrane protein 45A [Source:HGNC Symbol;Acc:HGNC:2157]
12	DST	-0.89	5e-09	3e-07	46 x 1 dystonin [Source:HGNC Symbol;Acc:HGNC:1090]
13	SRPX	-1.2	2e-08	1e-06	50 x 1 sushi-repeat containing protein, X-linked [Source:HGNC Symbol;Acc:HGNC:1090]
14	FMN2	-1.16	1e-07	1e-06	48 x 1 formin 2 [Source:HGNC Symbol;Acc:HGNC:14074]
15	YPEL5	-1.15	2e-07	1e-06	50 x 1 yippee-like 5 (Drosophila) [Source:HGNC Symbol;Acc:HGNC:14074]
16	ABL2	-1.07	2e-07	4e-06	46 x 1 ABL proto-oncogene 2, non-receptor tyrosine kinase [Source:HGNC Symbol;Acc:HGNC:14074]
17	ACOT9	-1.06	4e-07	4e-06	47 x 1 acyl-CoA thioesterase 9 [Source:HGNC Symbol;Acc:HGNC:14074]
18	EDIL3	-1.11	5e-07	6e-05	50 x 1 EGF-like repeats and discoidin I-like domains 3 [Source:HGNC Symbol;Acc:HGNC:14074]
19	FAM46A	-1.02	5e-06	6e-05	47 x 1 family with sequence similarity 46, member A [Source:HGNC Symbol;Acc:HGNC:14074]
20	CDKN1A	-1.01	6e-06	6e-05	50 x 1 cyclin-dependent kinase inhibitor 1A (p21, Cip1) [Source:HGNC Symbol;Acc:HGNC:14074]

p-values



D4_mel

Local Summary

%DE = 0.88
 # metagenes = 13
 # genes = 156
 # genes in genesets = 156

 # genes with $fdr < 0.1$ = 104 (27 + / 77 -)
 # genes with $fdr < 0.05$ = 86 (24 + / 62 -)
 # genes with $fdr < 0.01$ = 55 (15 + / 40 -)

<r> metagenes = 0.9

<r> genes = 0.08

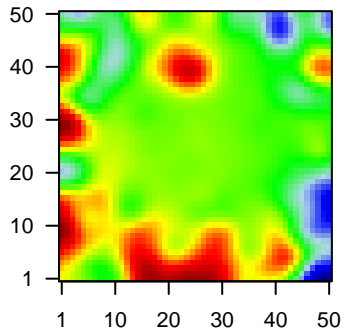
<FC> = -0.24

<shrinkage-t> = -4.17

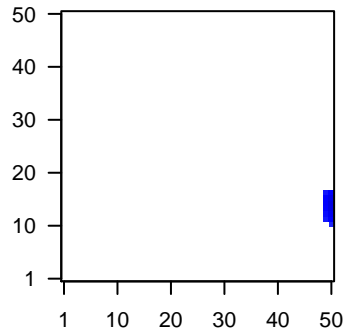
<p-value> = 0.01

<fdr> = 0.54

Profile



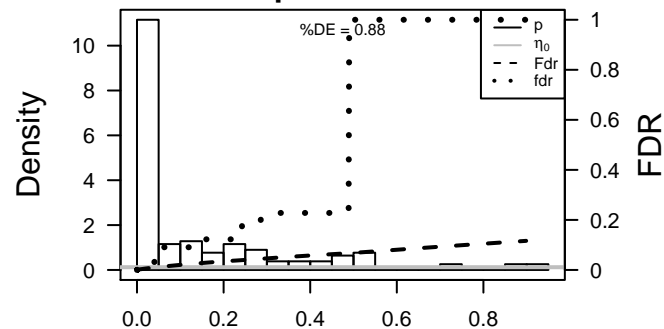
Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	PSMD9	-1.64	2e-16	2e-15	50 x 14 proteasome (prosome, macropain) 26S subunit, non-ATPase
2	SAP18	-2.14	2e-16	2e-15	50 x 16 Sin3A-associated protein, 18kDa [Source:HGNC Symbol;Acc:HGNC:10118]
3	DYNC2H1	-0.99	3e-12	6e-11	50 x 14 dynein, cytoplasmic 2, heavy chain 1 [Source:HGNC Symbol;Acc:HGNC:10118]
4	SGCB	-1.36	7e-12	6e-11	50 x 13 sarcoglycan, beta (43kDa dystrophin-associated glycoprotein)
5	COMT	-1.35	9e-12	2e-09	50 x 15 catechol-O-methyltransferase [Source:HGNC Symbol;Acc:HGNC:10118]
6	FAM200B	-1.3	2e-10	2e-09	50 x 11 family with sequence similarity 200, member B [Source:HGNC Symbol;Acc:HGNC:10118]
7	RBM34	-1.13	2e-10	7e-07	50 x 16 RNA binding motif protein 34 [Source:HGNC Symbol;Acc:HGNC:10118]
8	CCDC57	-1.16	6e-08	7e-07	50 x 11 coiled-coil domain containing 57 [Source:HGNC Symbol;Acc:HGNC:10118]
9	N4BP2L2	-0.71	7e-08	2e-06	50 x 15 NEDD4 binding protein 2-like 2 [Source:HGNC Symbol;Acc:HGNC:10118]
10	WDR18	-1.15	2e-07	2e-06	50 x 12 WD repeat domain 18 [Source:HGNC Symbol;Acc:HGNC:10118]
11	ZNF529	1.15	3e-07	5e-06	50 x 15 zinc finger protein 529 [Source:HGNC Symbol;Acc:HGNC:10118]
12	TMED5	-1.11	6e-07	7e-05	50 x 12 transmembrane emp24 protein transport domain containing 5
13	ERO1L	-0.93	6e-06	7e-05	50 x 16 ERO1-like (S. cerevisiae) [Source:HGNC Symbol;Acc:HGNC:10118]
14	LEMD3	1	8e-06	1e-04	50 x 13 LEM domain containing 3 [Source:HGNC Symbol;Acc:HGNC:10118]
15	GALK1	0.96	2e-05	1e-04	49 x 16 galactokinase 1 [Source:HGNC Symbol;Acc:HGNC:4118]
16	RNF123	0.93	3e-05	1e-04	50 x 17 ring finger protein 123 [Source:HGNC Symbol;Acc:HGNC:21118]
17	CEP350	-0.82	3e-05	1e-04	50 x 14 centrosomal protein 350kDa [Source:HGNC Symbol;Acc:HGNC:10118]
18	ATF6	-0.93	3e-05	1e-04	50 x 15 activating transcription factor 6 [Source:HGNC Symbol;Acc:HGNC:10118]
19	VRK3	-0.92	4e-05	3e-04	49 x 17 vaccinia related kinase 3 [Source:HGNC Symbol;Acc:HGNC:10118]
20	CDK11A	-0.9	6e-05	3e-04	50 x 15 cyclin-dependent kinase 11A [Source:HGNC Symbol;Acc:HGNC:10118]

p-values



D4_mel

Local Summary

%DE = 0.87
 # metagenes = 3
 # genes = 15
 # genes in genesets = 15
 # genes with $fdr < 0.1 = 10$ (1 + / 9 -)
 # genes with $fdr < 0.05 = 8$ (0 + / 8 -)
 # genes with $fdr < 0.01 = 7$ (0 + / 7 -)

<r> metagenes = 0.99

<r> genes = 0.17

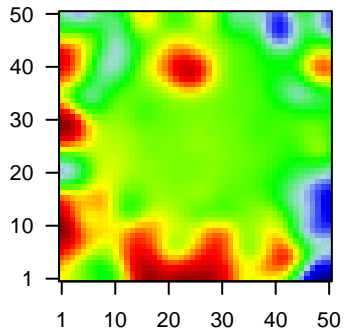
<FC> = -0.58

<shrinkage-t> = -9.91

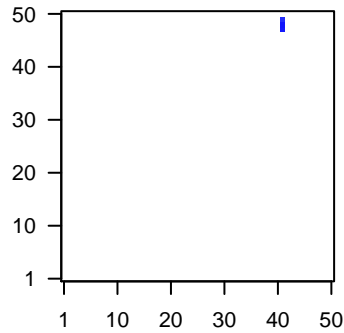
<p-value> = 0

<fdr> = 0.41

Profile



Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	BCAP29	-1.5	2e-16	4e-16	41 x 47 B-cell receptor-associated protein 29 [Source:HGNC Symbol]
2	ATP6V1B2	-1.21	3e-09	6e-08	41 x 47 ATPase, H+ transporting, lysosomal 56/58kDa, V1 subunit B2
3	ORC5	-1.19	3e-08	7e-06	41 x 48 origin recognition complex, subunit 5 [Source:HGNC Symbol]
4	DNAJA1	-0.8	4e-06	9e-05	41 x 47 DnaJ (Hsp40) homolog, subfamily A, member 1 [Source:HGNC Symbol]
5	DDX19A	-0.91	5e-05	2e-04	41 x 47 DEAD (Asp-Glu-Ala-Asp) box polypeptide 19A [Source:HGNC Symbol]
6	IMMT	-0.68	1e-04	8e-04	41 x 48 inner membrane protein, mitochondrial [Source:HGNC Symbol]
7	ABHD10	-0.74	9e-04	8e-04	41 x 48 abhydrolase domain containing 10 [Source:HGNC Symbol;Acc:HGNC:100000]
8	LAS1L	-0.74	9e-04	1e-02	41 x 48 LAS1-like (S. cerevisiae) [Source:HGNC Symbol;Acc:HGNC:100000]
9	LYSMD3	-0.61	6e-03	6e-02	41 x 48 LysM, putative peptidoglycan-binding, domain containing 3 [Source:HGNC Symbol]
10	DHRS7	0.36	4e-02	6e-02	41 x 49 dehydrogenase/reductase (SDR family) member 7 [Source:HGNC Symbol]
11	SNAPC2	-0.41	6e-02	1e-01	41 x 48 small nuclear RNA activating complex, polypeptide 2, 45kDa [Source:HGNC Symbol]
12	GEMIN7	-0.35	1e-01	4e-01	41 x 47 gem (nuclear organelle) associated protein 7 [Source:HGNC Symbol]
13	ANKRD12	0.16	4e-01	4e-01	41 x 47 ankyrin repeat domain 12 [Source:HGNC Symbol;Acc:HGNC:100000]
14	PEX6	-0.16	5e-01	1e+00	41 x 47 peroxisomal biogenesis factor 6 [Source:HGNC Symbol;Acc:HGNC:100000]
15	SLC25A4	0.1	5e-01	1e+00	41 x 47 solute carrier family 25 (mitochondrial carrier; adenine nucleotide carrier) member 4 [Source:HGNC Symbol]

p-values

