D2_mel

Global Summary

%DE = 0.22

genes with fdr < 0.2 = 2939 (1736 + / 1203 −)

genes with fdr < 0.1 = 2513 (1498 + / 1015 −)

genes with fdr < 0.05 = 2040 (1214 + / 826 −)

genes with fdr < 0.01 = 1385 (829 + / 556 −)

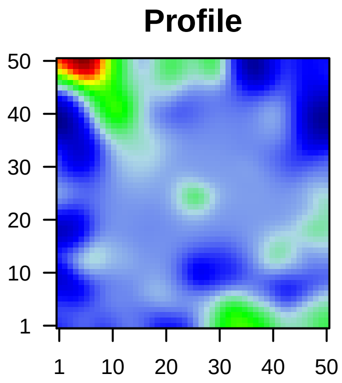
genes in genesets = 14839

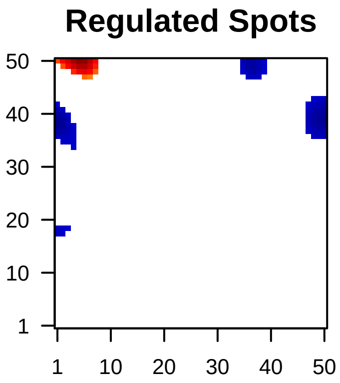
<FC> = 0

<shrinkage−t> = −0.05

<p−value> = 0.06

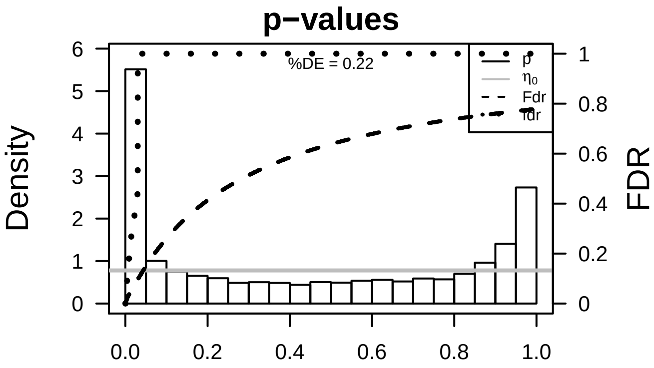
<fdr> = 0.78





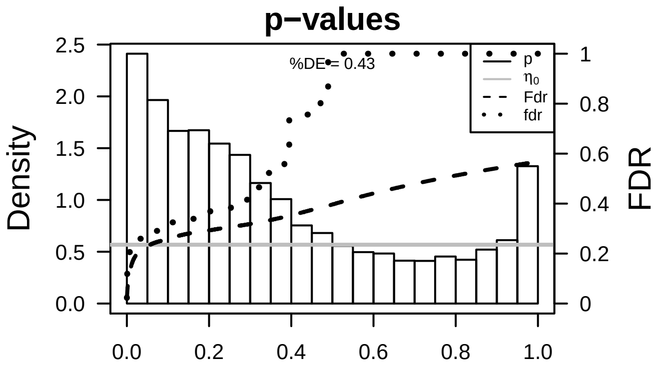
Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	AIMP2	−1.67	2e−16	5e−14	5 x 34	aminoacyl tRNA synthetase complex−interacting multifunctio
2	ARHGAP8	−1.7	2e−16	5e−14	1 x 43	Rho GTPase activating protein 8 [Source:HGNC Symbol;Acc:
3	ATRAID	−1.7	2e−16	5e−14	35 x 50	all−trans retinoic acid−induced differentiation factor [Source:H
4	CCDC47	−1.64	2e−16	5e−14	3 x 18	coiled−coil domain containing 47 [Source:HGNC Symbol;Acc
5	CCNC	−1.67	2e−16	5e−14	43 x 32	cyclin C [Source:HGNC Symbol;Acc:HGNC:1581]
6	CCT7	−0.88	2e−16	5e−14	1 x 17	chaperonin containing TCP1, subunit 7 (eta) [Source:HGNC
7	CERS2	−1.43	2e−16	5e−14	3 x 34	ceramide synthase 2 [Source:HGNC Symbol;Acc:HGNC:140
8	CHD9	−1.59	2e−16	5e−14	31 x 10	chromodomain helicase DNA binding protein 9 [Source:HGN
9	CLK1	−1.69	2e−16	5e−14	50 x 40	CDC−like kinase 1 [Source:HGNC Symbol;Acc:HGNC:2068]
10	COA6	−1.74	2e−16	5e−14	48 x 36	cytochrome c oxidase assembly factor 6 [Source:HGNC Sym
11	COPB2	−1.86	2e−16	5e−14	50 x 39	coatomer protein complex, subunit beta 2 (beta prime) [Sourc
12	CSDE1	−1.47	2e−16	5e−14	36 x 47	cold shock domain containing E1, RNA−binding [Source:HG
13	CUEDC2	−1.63	2e−16	5e−14	1 x 38	CUE domain containing 2 [Source:HGNC Symbol;Acc:HGNC
14	EIF4A2	−0.95	2e−16	5e−14	50 x 11	eukaryotic translation initiation factor 4A2 [Source:HGNC Sy
15	ERAL1	−1.73	2e−16	5e−14	46 x 44	Era−like 12S mitochondrial rRNA chaperone 1 [Source:HGN
16	EXOSC8	−1.71	2e−16	5e−14	1 x 50	exosome component 8 [Source:HGNC Symbol;Acc:HGNC:17
17	FAM127B	−1.46	2e−16	5e−14	47 x 50	family with sequence similarity 127, member B [Source:HGN
18	FDFT1	−1.5	2e−16	5e−14	1 x 38	farnesyl−diphosphate farnesyltransferase 1 [Source:HGNC S
19	FKBP2	−1.74	2e−16	5e−14	36 x 48	FK506 binding protein 2, 13kDa [Source:HGNC Symbol;Acc:
20	G6PC3	−1.64	2e−16	5e−14	48 x 49	glucose 6 phosphatase, catalytic, 3 [Source:HGNC Symbol;A



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	17.17	3e−05	305	GSEA C2	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
2	16.81	3e−05	139	GSEA C2	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
3	16.54	4e−05	142	Glio	WILLSCHER_GBM_Verhaak−CL_up (C)
4	16.28	4e−05	550	GSEA C2	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
5	16.1	4e−05	242	GSEA C2	KOBAYASHI_EGFR_SIGNALING_24HR_DN
6	15.38	4e−03	16	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
7	13.99	7e−05	145	GSEA C2	CHANG_CYCLING_GENES
8	13.92	7e−05	436	GSEA C2	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
9	13.38	8e−05	390	GSEA C2	PUJANA_BRCA2_PCC_NETWORK
10	13.36	8e−05	197	HM	HALLMARK_E2F_TARGETS
11	13.31	8e−05	267	GSEA C2	ZHANG_TLX_TARGETS_60HR_DN
12	13.21	9e−05	96	GSEA C2	CROONQUIST_IL6_DEPRIVATION_DN
13	13.08	9e−05	81	GSEA C2	GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
14	13.06	9e−05	54	GSEA C2	KANG_DOXORUBICIN_RESISTANCE_UP
15	12.97	9e−05	93	GSEA C2	KONG_E2F3_TARGETS
16	12.55	1e−04	155	GSEA C2	HOFFMANN_LARGE_TO_SMALL_PRE_BII_LYMPHOCYTE_UP
17	12.55	1e−04	162	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP
18	12.46	1e−04	110	GSEA C2	WHITEFORD_PEDIATRIC_CANCER_MARKERS
19	12.27	1e−04	327	GSEA C2	BLUM_RESPONSE_TO_SALIRASIB_DN
20	12.26	1e−04	87	GSEA C2	ZHANG_TLX_TARGETS_UP
Underexpressed					
1	−6.11	0.002	1468	CC	mitochondrion
2	−5.8	0.002	198	HM	HALLMARK_OXIDATIVE_PHOSPHORYLATION
3	−5.79	0.002	401	CC	mitochondrial inner membrane
4	−5.21	0.003	368	GSEA C2	STEIN_ESRRA_TARGETS_UP
5	−5.09	0.003	114	GSEA C2	REACTOME_TCA_CYCLE_AND_RESPIRATORY_ELECTRON_T
6	−4.96	0.004	4	GSEA C2	FUNG_IL2_TARGETS_WITH_STAT5_BINDING_SITES
7	−4.71	0.004	135	BP	cellular metabolic process
8	−4.6	0.005	3081	Brain	Mid_Frontal_Lobe_ZNF
9	−4.59	0.005	71	MF	structural constituent of ribosome
10	−4.53	0.005	66	GSEA C2	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTE
11	−4.36	0.006	167	GSEA C2	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTE
12	−4.23	0.006	925	GSEA C2	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
13	−4.22	0.006	2	Glio	WILLSCHER_GBM_LTSmut_proteomics−E_UP
14	−4.14	0.007	838	Chr	Chr 3
15	−4.11	0.007	78	GSEA C2	SCHUHMACHER_MYC_TARGETS_UP
16	−4.07	0.007	94	BP	respiratory electron transport chain
17	−4.06	0.007	322	BP	mitochondrion organization
18	−4.04	0.007	63	Glio	Stuehler_Proteins_up_in_STS
19	−4.03	0.007	83	BP	mitochondrial translational termination
20	−3.9	0.008	831	GSEA C2	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN



D2_mel

Local Summary

%DE = 0.91

metagenes = 22

genes = 317

genes in genesets = 317

genes with fdr < 0.1 = 255 (237 + / 18 −)

genes with fdr < 0.05 = 242 (229 + / 13 −)

genes with fdr < 0.01 = 208 (201 + / 7 −)

<r> metagenes = 0.94

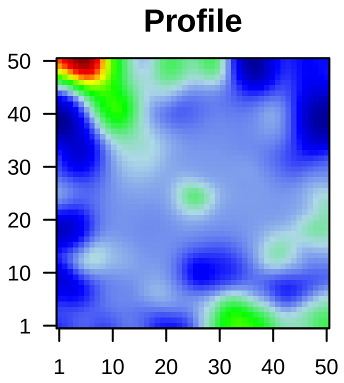
<r> genes = 0.33

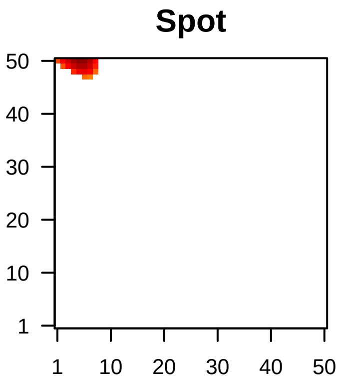
<FC> = 0.69

<shrinkage−t> = 11.08

<p−value> = 0

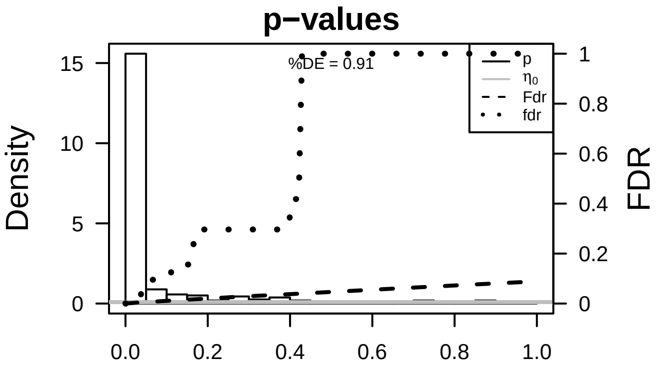
<fdr> = 0.3





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	EXOSC8	−1.71	2e−16	6e−15	1 x 50	exosome component 8 [Source:HGNC Symbol;Acc:HGNC:17
2	NDC80	1.96	7e−16	6e−14	6 x 50	NDC80 kinetochore complex component [Source:HGNC Sym
3	RRM2	1.92	3e−15	6e−12	5 x 50	ribonucleotide reductase M2 [Source:HGNC Symbol;Acc:HG
4	CDK1	1.76	2e−13	8e−12	5 x 50	cyclin−dependent kinase 1 [Source:HGNC Symbol;Acc:HGN
5	TOP2A	1.73	8e−13	8e−12	6 x 50	topoisomerase (DNA) II alpha 170kDa [Source:HGNC Symb
6	CCDC18	1.72	1e−12	8e−12	7 x 48	coiled−coil domain containing 18 [Source:HGNC Symbol;Acc
7	NFYB	1.72	1e−12	8e−12	5 x 50	nuclear transcription factor Y, beta [Source:HGNC Symbol;Ac
8	STMN1	0.69	1e−12	8e−12	5 x 50	stathmin 1 [Source:HGNC Symbol;Acc:HGNC:6510]
9	HIST1H4C	0.69	2e−12	6e−11	5 x 49	histone cluster 1, H4c [Source:HGNC Symbol;Acc:HGNC:47
10	ESCO2	1.68	4e−12	2e−10	4 x 50	establishment of sister chromatid cohesion N−acetyltransfera
11	NCAPG	1.62	2e−11	2e−10	6 x 50	non−SMC condensin I complex, subunit G [Source:HGNC Sy
12	KIF20B	1.62	2e−11	2e−10	6 x 50	kinesin family member 20B [Source:HGNC Symbol;Acc:HGN
13	BLM	1.62	2e−11	2e−10	4 x 50	Bloom syndrome, RecQ helicase−like [Source:HGNC Symbol
14	FBXO5	1.6	4e−11	2e−10	4 x 50	F−box protein 5 [Source:HGNC Symbol;Acc:HGNC:13584]
15	CDKN3	1.19	4e−11	3e−10	6 x 50	cyclin−dependent kinase inhibitor 3 [Source:HGNC Symbol;A
16	CASC5	1.59	5e−11	3e−10	6 x 50	cancer susceptibility candidate 5 [Source:HGNC Symbol;Acc
17	KIF20A	1.59	6e−11	3e−10	7 x 50	kinesin family member 20A [Source:HGNC Symbol;Acc:HGN
18	SPC25	1.58	7e−11	3e−10	6 x 50	SPC25, NDC80 kinetochore complex component [Source:HG
19	PRC1	1.5	8e−11	1e−09	5 x 50	protein regulator of cytokinesis 1 [Source:HGNC Symbol;Acc
20	KIF18A	1.56	1e−10	2e−09	7 x 50	kinesin family member 18A [Source:HGNC Symbol;Acc:HGN



D2_mel

Local Summary

%DE = 0.7

metagenes = 5

genes = 49

genes in genesets = 49

genes with fdr < 0.1 = 28 (2 + / 26 −)

genes with fdr < 0.05 = 17 (2 + / 15 −)

genes with fdr < 0.01 = 15 (2 + / 13 −)

<r> metagenes = 0.99

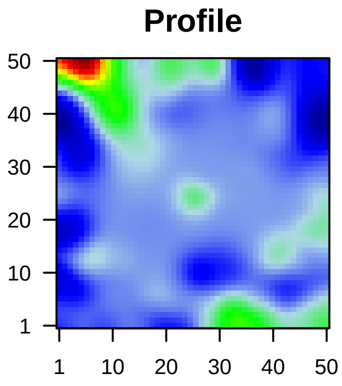
<r> genes = 0.13

<FC> = −0.38

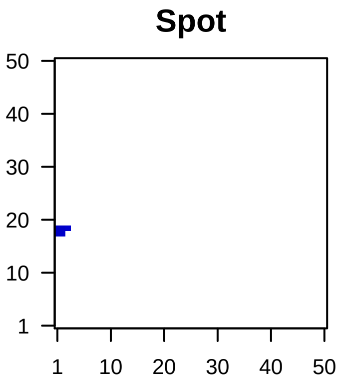
<shrinkage−t> = −6.01

<p−value> = 0.01

<fdr> = 0.6



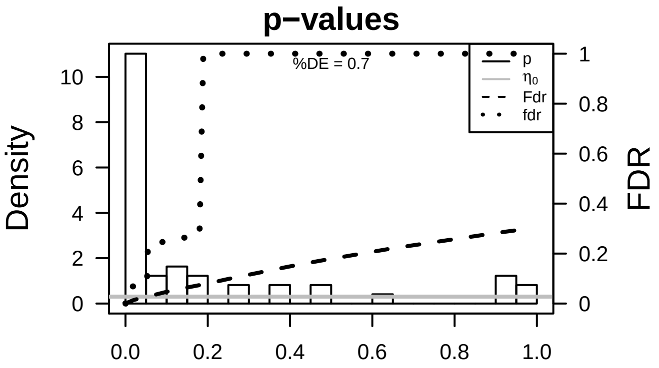
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	PYURF	−1.38	1e−12	9e−08	1 x 19	PIGY upstream reading frame [Source:HGNC Symbol;Acc:H
2	CCSER2	−1.28	6e−09	1e−07	2 x 18	coiled−coil serine−rich protein 2 [Source:HGNC Symbol;Acc:
3	TXNL4A	−1.26	2e−08	5e−05	1 x 19	thioredoxin−like 4A [Source:HGNC Symbol;Acc:HGNC:30551
4	TRAP1	−1.11	4e−06	5e−05	1 x 18	TNF receptor−associated protein 1 [Source:HGNC Symbol;A
5	TMEM134	−1.08	6e−06	3e−04	1 x 19	transmembrane protein 134 [Source:HGNC Symbol;Acc:HG
6	VPS36	−0.94	6e−05	3e−04	1 x 18	vacuolar protein sorting 36 homolog (S. cerevisiae) [Source:
7	NME4	−0.97	7e−05	3e−04	1 x 19	NME/NM23 nucleoside diphosphate kinase 4 [Source:HGNC
8	IDE	−0.95	9e−05	3e−04	1 x 18	insulin−degrading enzyme [Source:HGNC Symbol;Acc:HGN
9	TMEM192	−0.88	9e−05	7e−04	1 x 18	transmembrane protein 192 [Source:HGNC Symbol;Acc:HG
10	DNAJC4	0.92	2e−04	7e−04	1 x 19	DnaJ (Hsp40) homolog, subfamily C, member 4 [Source:HG
11	PUM1	−0.91	2e−04	4e−03	2 x 19	pumilio RNA−binding family member 1 [Source:HGNC Symb
12	RNF130	−0.84	5e−04	4e−03	1 x 18	ring finger protein 130 [Source:HGNC Symbol;Acc:HGNC:18
13	EFR3A	−0.82	7e−04	8e−03	1 x 18	EFR3 homolog A (S. cerevisiae) [Source:HGNC Symbol;Acc:
14	PIK3R4	−0.78	1e−03	8e−03	1 x 18	phosphoinositide−3−kinase, regulatory subunit 4 [Source:HG
15	OVCA2	0.74	2e−03	8e−03	1 x 19	ovarian tumor suppressor candidate 2 [Source:HGNC Symbo
16	KDELR2	−0.59	2e−03	1e−02	1 x 19	KDEL (Lys−Asp−Glu−Leu) endoplasmic reticulum protein ret
17	ACAA1	−0.7	4e−03	1e−02	1 x 18	acetyl−CoA acyltransferase 1 [Source:HGNC Symbol;Acc:HG
18	ATP5D	−0.69	4e−03	7e−02	1 x 18	ATP synthase, H+ transporting, mitochondrial F1 complex, de
19	GID8	−0.57	2e−02	7e−02	1 x 18	GID complex subunit 8 [Source:HGNC Symbol;Acc:HGNC:15
20	FAM195A	−0.57	2e−02	7e−02	1 x 18	family with sequence similarity 195, member A [Source:HGN



p−values

D2_mel

Local Summary

%DE = 0.7

metagenes = 25

genes = 288

genes in genesets = 287

genes with fdr < 0.1 = 139 (25 + / 114 −)

genes with fdr < 0.05 = 107 (15 + / 92 −)

genes with fdr < 0.01 = 85 (10 + / 75 −)

<r> metagenes = 0.92

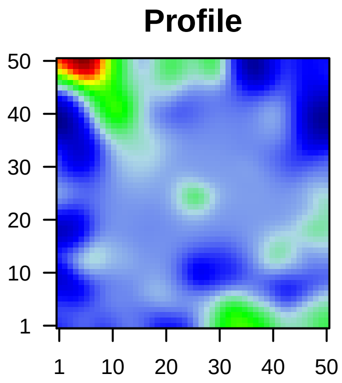
<r> genes = 0.13

<FC> = −0.31

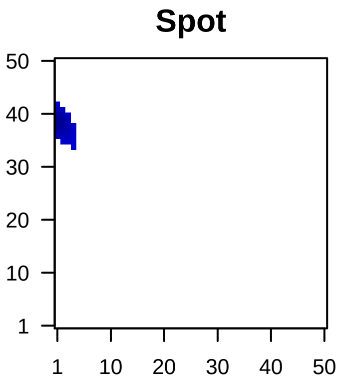
<shrinkage−t> = −5.92

<p−value> = 0

<fdr> = 0.57



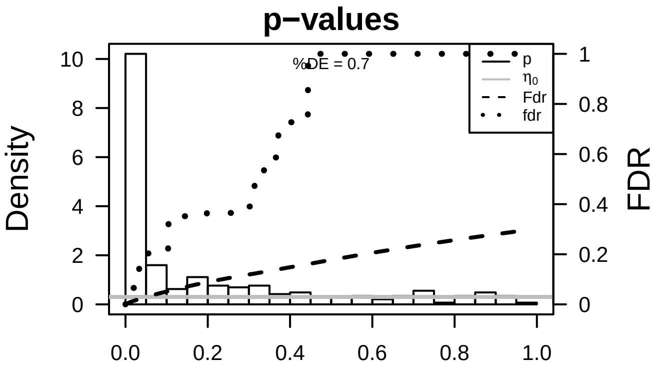
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	CUEDC2	−1.63	2e−16	3e−15	1 x 38	CUE domain containing 2 [Source:HGNC Symbol;Acc:HGNC
2	FDFT1	−1.5	2e−16	3e−15	1 x 38	farnesyl−diphosphate farnesyltransferase 1 [Source:HGNC
3	GOT1	−1.62	2e−16	3e−15	1 x 39	glutamic−oxaloacetic transaminase 1, soluble [Source:HGNC
4	MITF	−1.88	2e−16	3e−15	1 x 41	microphthalmia−associated transcription factor [Source:HGN
5	NOP16	−1.72	2e−16	3e−15	1 x 38	NOP16 nucleolar protein [Source:HGNC Symbol;Acc:HGNC:
6	NTPCR	−1.58	2e−16	3e−15	2 x 35	nucleoside−triphosphatase, cancer−related [Source:HGNC
7	AP3S1	−1.22	3e−15	4e−12	1 x 39	adaptor−related protein complex 3, sigma 1 subunit [Source:
8	CLPP	−1.51	4e−14	4e−11	1 x 38	caseinolytic mitochondrial matrix peptidase proteolytic subuni
9	CITED1	−1	5e−13	5e−11	1 x 41	Cbp/p300−interacting transactivator, with Glu/Asp−rich carbo
10	HADHB	−1.28	1e−12	2e−10	1 x 39	hydroxyacyl−CoA dehydrogenase/3−ketoacyl−CoA thiolase/e
11	GSTM4	−1.44	4e−12	2e−10	1 x 41	glutathione S−transferase mu 4 [Source:HGNC Symbol;Acc:
12	PIR	−0.9	6e−12	2e−10	1 x 42	pirin (iron−binding nuclear protein) [Source:HGNC Symbol;A
13	KIAA1191	−1.44	6e−12	5e−10	1 x 39	KIAA1191 [Source:HGNC Symbol;Acc:HGNC:29209]
14	PFKM	−1.42	2e−11	5e−10	1 x 41	phosphofructokinase, muscle [Source:HGNC Symbol;Acc:H
15	PARL	−1.42	2e−11	6e−10	1 x 39	presenilin associated, rhomboid−like [Source:HGNC Symbol;
16	SUCLA2	−1.41	3e−11	1e−09	2 x 36	succinate−CoA ligase, ADP−forming, beta subunit [Source:H
17	MAP3K13	−1.4	4e−11	2e−09	4 x 34	mitogen−activated protein kinase kinase kinase 13 [Source:H
18	NGLY1	−1.4	6e−11	2e−09	4 x 34	N−glycanase 1 [Source:HGNC Symbol;Acc:HGNC:17646]
19	UROS	−1.39	9e−11	8e−09	3 x 37	uroporphyrinogen III synthase [Source:HGNC Symbol;Acc:H
20	ATG3	−1.22	3e−10	8e−09	1 x 36	autophagy related 3 [Source:HGNC Symbol;Acc:HGNC:2096



p−values

D2_mel

Local Summary

%DE = 0.81

metagenes = 30

genes = 286

genes in genesets = 284

genes with fdr < 0.1 = 149 (37 + / 112 −)

genes with fdr < 0.05 = 110 (24 + / 86 −)

genes with fdr < 0.01 = 77 (16 + / 61 −)

<r> metagenes = 0.89

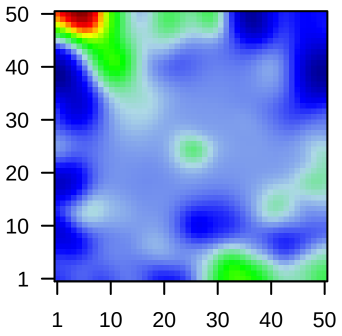
<r> genes = 0.08

<FC> = −0.26

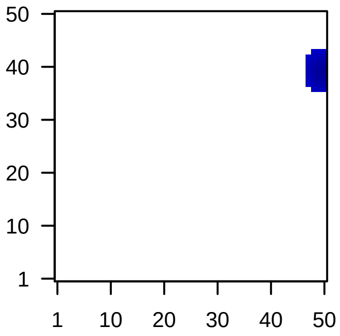
<shrinkage−t> = −4.59

<p−value> = 0.01

<fdr> = 0.6



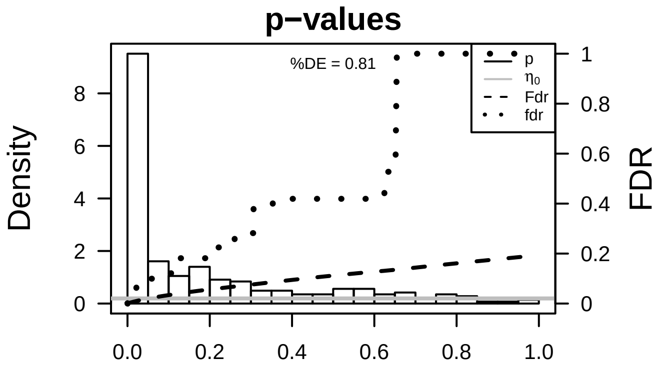
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	CLK1	−1.69	2e−16	2e−15	50 x 40	CDC−like kinase 1 [Source:HGNC Symbol;Acc:HGNC:2068]
2	COA6	−1.74	2e−16	2e−15	48 x 36	cytochrome c oxidase assembly factor 6 [Source:HGNC Sym
3	COPB2	−1.86	2e−16	2e−15	50 x 39	coatomer protein complex, subunit beta 2 (beta prime) [Sourc
4	GNL3	−1.85	2e−16	2e−15	47 x 42	guanine nucleotide binding protein−like 3 (nucleolar) [Source:
5	LAMTOR5	−0.99	2e−16	2e−15	47 x 41	late endosomal/lysosomal adaptor, MAPK and MTOR activat
6	MORN2	−1.79	2e−16	2e−15	47 x 37	MORN repeat containing 2 [Source:HGNC Symbol;Acc:HGN
7	UXT	−1.6	2e−16	2e−15	50 x 38	ubiquitously−expressed, prefoldin−like chaperone [Source:HG
8	TBK1	−1.27	3e−10	1e−08	50 x 37	TANK−binding kinase 1 [Source:HGNC Symbol;Acc:HGNC:1
9	RUFY1	1.52	4e−10	2e−08	50 x 43	RUN and FYVE domain containing 1 [Source:HGNC Symbol;
10	PJA2	−1.34	8e−10	3e−08	49 x 41	praja ring finger 2, E3 ubiquitin protein ligase [Source:HGNC
11	MRPL3	−0.95	1e−09	4e−08	50 x 37	mitochondrial ribosomal protein L3 [Source:HGNC Symbol;A
12	SECISBP2L	−1.32	2e−09	2e−07	47 x 41	SECIS binding protein 2−like [Source:HGNC Symbol;Acc:HG
13	TMEM50B	−1.28	8e−09	2e−07	50 x 43	transmembrane protein 50B [Source:HGNC Symbol;Acc:HG
14	MOSPD1	−1.26	1e−08	2e−07	50 x 43	motile sperm domain containing 1 [Source:HGNC Symbol;Ac
15	LTV1	−1.26	1e−08	1e−06	50 x 36	LTV1 ribosome biogenesis factor [Source:HGNC Symbol;Acc
16	TAF1D	−1.25	3e−08	2e−06	50 x 41	TATA box binding protein (TBP)−associated factor, RNA poly
17	ZNF146	−1.22	8e−08	2e−06	47 x 42	zinc finger protein 146 [Source:HGNC Symbol;Acc:HGNC:12
18	LTN1	−1.21	1e−07	2e−06	50 x 40	listerin E3 ubiquitin protein ligase 1 [Source:HGNC Symbol;A
19	GTF2H3	1.28	1e−07	1e−05	48 x 43	general transcription factor IIH, polypeptide 3, 34kDa [Source
20	ZNHIT1	−1.06	3e−07	2e−05	48 x 40	zinc finger, HIT−type containing 1 [Source:HGNC Symbol;Ac



D2_mel

Local Summary

%DE = 0.61

metagenes = 18

genes = 176

genes in genesets = 176

genes with fdr < 0.1 = 90 (21 + / 69 −)

genes with fdr < 0.05 = 65 (10 + / 55 −)

genes with fdr < 0.01 = 41 (6 + / 35 −)

<r> metagenes = 0.93

<r> genes = 0.09

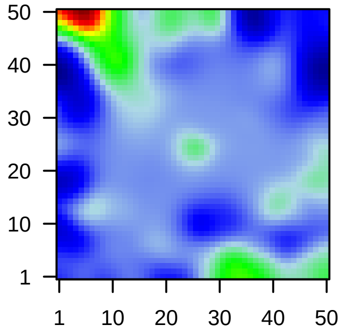
<FC> = −0.33

<shrinkage−t> = −5.64

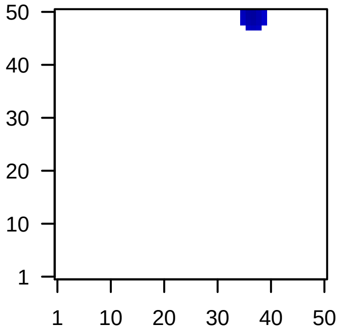
<p−value> = 0

<fdr> = 0.59

Profile



Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	ATRAID	−1.7	2e−16	3e−15	35 x 50	all−trans retinoic acid−induced differentiation factor [Source:H
2	CSDE1	−1.47	2e−16	3e−15	36 x 47	cold shock domain containing E1, RNA−binding [Source:HGN
3	FKBP2	−1.74	2e−16	3e−15	36 x 48	FK506 binding protein 2, 13kDa [Source:HGNC Symbol;Acc:
4	MRPL18	−1.6	2e−16	3e−15	36 x 50	mitochondrial ribosomal protein L18 [Source:HGNC Symbol;
5	MRPS30	−1.58	2e−16	3e−15	38 x 47	mitochondrial ribosomal protein S30 [Source:HGNC Symbol;
6	SETD5	−1.72	2e−16	3e−15	36 x 50	SET domain containing 5 [Source:HGNC Symbol;Acc:HGNC:
7	C8orf59	−1.56	7e−16	2e−13	38 x 48	chromosome 8 open reading frame 59 [Source:HGNC Symbo
8	RNF10	−1.54	4e−15	3e−12	37 x 48	ring finger protein 10 [Source:HGNC Symbol;Acc:HGNC:100
9	POR	−1.51	5e−14	1e−09	36 x 50	P450 (cytochrome) oxidoreductase [Source:HGNC Symbol;A
10	C7orf55	−1.42	1e−11	3e−08	37 x 49	chromosome 7 open reading frame 55 [Source:HGNC Symbo
11	TIPRL	−0.85	5e−10	3e−08	35 x 50	TOR signaling pathway regulator [Source:HGNC Symbol;Acc
12	MRPS27	−1.22	1e−09	3e−08	38 x 47	mitochondrial ribosomal protein S27 [Source:HGNC Symbol;
13	ZMYM6NB	1.47	1e−09	8e−08	38 x 50	ZMYM6 neighbor [Source:HGNC Symbol;Acc:HGNC:40021]
14	RAB4A	−1.32	2e−09	1e−07	35 x 50	RAB4A, member RAS oncogene family [Source:HGNC Symb
15	CUL3	−1.3	4e−09	2e−07	37 x 50	cullin 3 [Source:HGNC Symbol;Acc:HGNC:2553]
16	SPP1	−1.14	8e−09	5e−07	38 x 48	secreted phosphoprotein 1 [Source:HGNC Symbol;Acc:HGN
17	MCFD2	−0.88	2e−08	1e−06	35 x 50	multiple coagulation factor deficiency 2 [Source:HGNC Symb
18	ALG6	−1.22	3e−08	2e−05	35 x 50	ALG6, alpha−1,3−glucosyltransferase [Source:HGNC Symbo
19	IBTK	−1.18	5e−07	2e−05	39 x 50	inhibitor of Bruton agammaglobulinemia tyrosine kinase [Sou
20	TRIM37	−1.18	6e−07	6e−05	37 x 50	tripartite motif containing 37 [Source:HGNC Symbol;Acc:HGN

p−values