C5_mel

Global Summary

%DE = 0.22

genes with fdr < 0.2 = 3026 (1782 + / 1244 −)

genes with fdr < 0.1 = 2367 (1418 + / 949 −)

genes with fdr < 0.05 = 2095 (1266 + / 829 −)

genes with fdr < 0.01 = 1415 (882 + / 533 −)

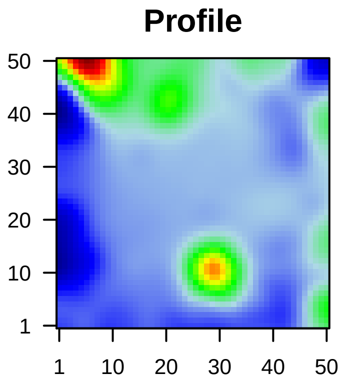
genes in genesets = 14839

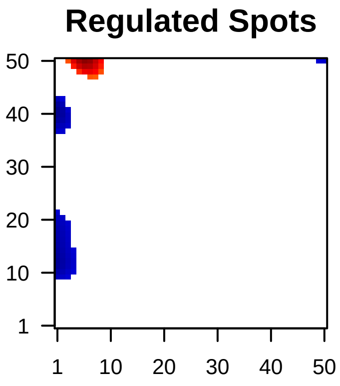
<FC> = 0

<shrinkage−t> = −0.06

<p−value> = 0.06

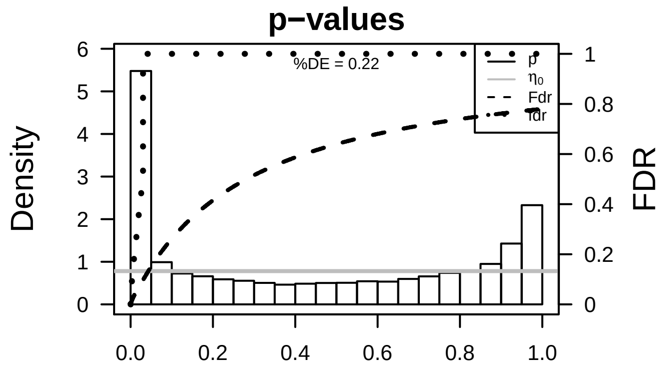
<fdr> = 0.78





Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	AHSA1	−1.92	2e−16	5e−14	46 x 35	AHA1, activator of heat shock 90kDa protein ATPase homolog
2	ALG3	−1.73	2e−16	5e−14	48 x 50	ALG3, alpha−1,3− mannosyltransferase [Source:HGNC Symb
3	ANP32E	1.06	2e−16	5e−14	8 x 50	acidic (leucine−rich) nuclear phosphoprotein 32 family, memb
4	ARHGAP8	−1.76	2e−16	5e−14	1 x 43	Rho GTPase activating protein 8 [Source:HGNC Symbol;Acc:
5	AURKB	2.03	2e−16	5e−14	6 x 50	aurora kinase B [Source:HGNC Symbol;Acc:HGNC:11390]
6	BACE2	−1.37	2e−16	5e−14	1 x 42	beta−site APP−cleaving enzyme 2 [Source:HGNC Symbol;Ac
7	CCDC171	−1.53	2e−16	5e−14	1 x 11	coiled−coil domain containing 171 [Source:HGNC Symbol;Ac
8	CDK1	2.16	2e−16	5e−14	5 x 50	cyclin−dependent kinase 1 [Source:HGNC Symbol;Acc:HGN
9	CDKN3	1.65	2e−16	5e−14	6 x 50	cyclin−dependent kinase inhibitor 3 [Source:HGNC Symbol;A
10	CFL2	−1.69	2e−16	5e−14	50 x 7	cofilin 2 (muscle) [Source:HGNC Symbol;Acc:HGNC:1875]
11	COX5A	−1.53	2e−16	5e−14	1 x 21	cytochrome c oxidase subunit Va [Source:HGNC Symbol;Acc
12	CTSD	−1.59	2e−16	5e−14	1 x 37	cathepsin D [Source:HGNC Symbol;Acc:HGNC:2529]
13	ECHDC1	−1.38	2e−16	5e−14	42 x 46	ethylmalonyl−CoA decarboxylase 1 [Source:HGNC Symbol;A
14	EXOC3	−1.61	2e−16	5e−14	1 x 42	exocyst complex component 3 [Source:HGNC Symbol;Acc:H
15	FAHD1	−1.65	2e−16	5e−14	1 x 40	fumarylacetoacetate hydrolase domain containing 1 [Source:
16	FDFT1	−1.79	2e−16	5e−14	1 x 38	farnesyl−diphosphate farnesyltransferase 1 [Source:HGNC S
17	GPR161	−2.02	2e−16	5e−14	3 x 16	G protein−coupled receptor 161 [Source:HGNC Symbol;Acc:
18	HDAC2	−1.38	2e−16	5e−14	1 x 45	histone deacetylase 2 [Source:HGNC Symbol;Acc:HGNC:48
19	HIST1H4C	1.04	2e−16	5e−14	5 x 49	histone cluster 1, H4c [Source:HGNC Symbol;Acc:HGNC:47
20	HSPA5	−1.21	2e−16	5e−14	11 x 1	heat shock 70kDa protein 5 (glucose−regulated protein, 78kD



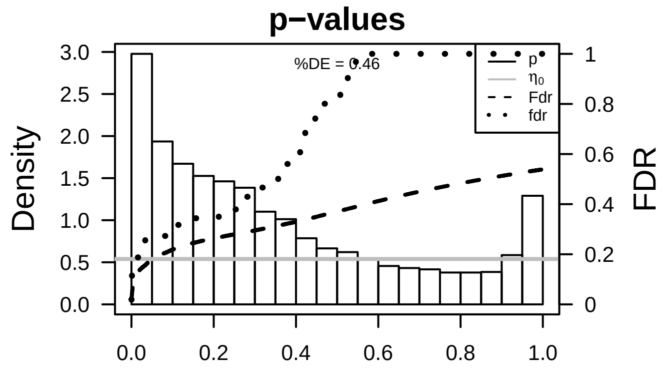
Global Geneset Analysis

Overexpressed

Rank	GSZ	p−value	#all	Geneset	
1	18.82	2e−05	142	Glio	WILLSCHER_GBM_Verhaak−CL_up (C)
2	17.89	2e−05	550	GSEA C2	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
3	17.25	3e−05	139	GSEA C2	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
4	15.01	1e−03	16	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
5	14.74	6e−05	99	GSEA C2	LEE_EARLY_T_LYMPHOCYTE_UP
6	14.38	6e−05	145	GSEA C2	CHANG_CYCLING_GENES
7	14.1	7e−05	197	HM	HALLMARK_E2F_TARGETS
8	14.09	7e−05	96	GSEA C2	CROONQUIST_IL6_DEPRIVATION_DN
9	13.96	7e−05	93	GSEA C2	KONG_E2F3_TARGETS
10	13.7	7e−05	155	GSEA C2	HOFFMANN_LARGE_TO_SMALL_PRE_BII_LYMPHOCYTE_UP
11	13.43	8e−05	54	GSEA C2	KANG_DOXORUBICIN_RESISTANCE_UP
12	13.33	8e−05	700	GSEA C2	MARSON_BOUND_BY_E2F4_UNSTIMULATED
13	13.3	8e−05	124	GSEA C2	ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_24HR
14	13.22	8e−05	390	GSEA C2	PUJANA_BRCA2_PCC_NETWORK
15	13.16	9e−05	291	GSEA C2	HORIUCHI_WTAP_TARGETS_DN
16	13.13	9e−05	110	GSEA C2	WHITEFORD_PEDIATRIC_CANCER_MARKERS
17	13.09	9e−05	242	GSEA C2	KOBAYASHI_EGFR_SIGNALING_24HR_DN
18	12.99	9e−05	305	GSEA C2	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
19	12.99	9e−05	183	GSEA C2	ZHANG_TLX_TARGETS_36HR_DN
20	12.98	9e−05	160	GSEA C2	PUJANA_XPRSS_INT_NETWORK

Underexpressed

Rank	GSZ	p−value	#all	Geneset	
1	−9.35	3e−04	576	Chr	Chr 9
2	−8.7	5e−04	2798	Colon Cancer	TxEnhG1_Colon
3	−8.49	5e−04	3081	Brain	Mid_Frontal_Lobe_ZNF
4	−7.96	6e−04	233	GSEA C2	PENG_RAPAMYCIN_RESPONSE_DN
5	−7.91	7e−04	925	GSEA C2	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
6	−7.59	8e−04	325	GSEA C2	PENG_GLUTAMINE_DEPRIVATION_DN
7	−7.55	8e−04	94	CC	melanosome
8	−7.04	1e−03	13	BP	melanin biosynthetic process
9	−6.86	1e−03	1468	CC	mitochondrion
10	−6.83	1e−03	181	GSEA C2	PENG_LEUCINE_DEPRIVATION_DN
11	−6.8	1e−03	135	CC	myelin sheath
12	−6.69	1e−03	2984	CC	integral component of membrane
13	−6.46	1e−03	831	GSEA C2	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
14	−5.87	2e−03	11	GSEA C2	BIOCARTA_PARKIN_PATHWAY
15	−5.82	2e−03	745	CC	cytoplasmic membrane−bounded vesicle
16	−5.68	2e−03	465	Chr	Chr 15
17	−5.63	2e−03	17	BP	synaptic vesicle endocytosis
18	−5.62	2e−03	1201	CC	endoplasmic reticulum
19	−5.6	2e−03	37	GSEA C2	KAAB_FAILED_HEART_VENTRICLE_DN
20	−5.59	2e−03	9653	Colon Cancer	Enh_Colon



C5_mel

Local Summary

%DE = 0.88

metagenes = 20

genes = 240

genes in genesets = 240

genes with fdr < 0.1 = 195 (193 + / 2 −)

genes with fdr < 0.05 = 192 (190 + / 2 −)

genes with fdr < 0.01 = 180 (180 + / 0 −)

<r> metagenes = 0.97

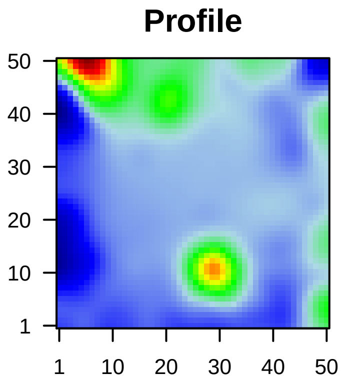
<r> genes = 0.36

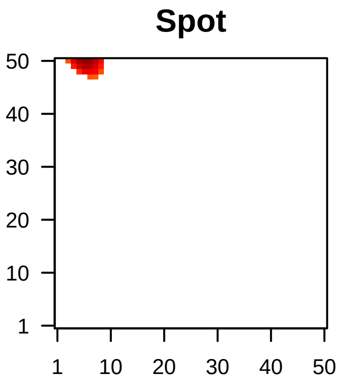
<FC> = 0.93

<shrinkage−t> = 15.05

<p−value> = 0

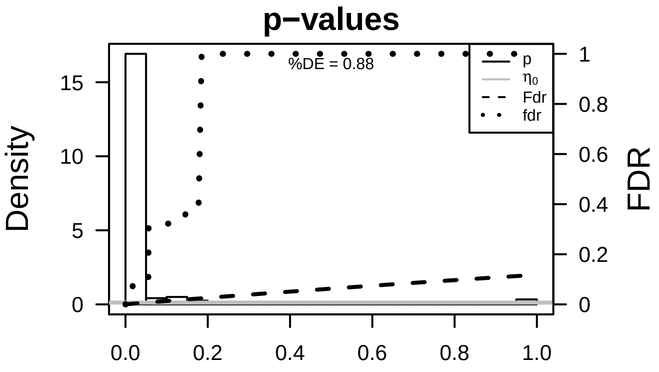
<fdr> = 0.19


Profile


Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	ANP32E	1.06	2e−16	9e−16	8 x 50	acidic (leucine−rich) nuclear phosphoprotein 32 family, memb
2	AURKB	2.03	2e−16	9e−16	6 x 50	aurora kinase B [Source:HGNC Symbol;Acc:HGNC:11390]
3	CDK1	2.16	2e−16	9e−16	5 x 50	cyclin−dependent kinase 1 [Source:HGNC Symbol;Acc:HGN
4	CDKN3	1.65	2e−16	9e−16	6 x 50	cyclin−dependent kinase inhibitor 3 [Source:HGNC Symbol;A
5	HIST1H4C	1.04	2e−16	9e−16	5 x 49	histone cluster 1, H4c [Source:HGNC Symbol;Acc:HGNC:47
6	NUF2	2.2	2e−16	9e−16	6 x 50	NUF2, NDC80 kinetochore complex component [Source:HGN
7	STMN1	1.43	2e−16	9e−16	5 x 50	stathmin 1 [Source:HGNC Symbol;Acc:HGNC:6510]
8	SGOL1	1.91	4e−16	2e−14	5 x 50	shugoshin−like 1 (S. pombe) [Source:HGNC Symbol;Acc:HG
9	UBE2C	1.87	1e−15	1e−13	6 x 50	ubiquitin−conjugating enzyme E2C [Source:HGNC Symbol;A
10	C5orf34	1.84	5e−15	2e−13	6 x 50	chromosome 5 open reading frame 34 [Source:HGNC Symb
11	ACTL6A	1.08	1e−14	2e−13	4 x 50	actin−like 6A [Source:HGNC Symbol;Acc:HGNC:24124]
12	HMMR	1.79	2e−14	5e−13	7 x 50	hyaluronan−mediated motility receptor (RHAMM) [Source:HG
13	KPNA2	0.74	4e−14	4e−12	7 x 50	karyopherin alpha 2 (RAG cohort 1, importin alpha 1) [Sourc
14	KIF20A	1.72	2e−13	7e−12	7 x 50	kinesin family member 20A [Source:HGNC Symbol;Acc:HGN
15	SYCP2	1.7	4e−13	1e−11	7 x 47	synaptonemal complex protein 2 [Source:HGNC Symbol;Acc:
16	PLP2	1.67	1e−12	1e−11	9 x 50	proteolipid protein 2 (colonic epithelium−enriched) [Source:H
17	CKAP2L	1.67	1e−12	2e−11	6 x 50	cytoskeleton associated protein 2−like [Source:HGNC Symb
18	INCENP	1.65	2e−12	2e−11	8 x 50	inner centromere protein antigens 135/155kDa [Source:HGN
19	ECT2	1.64	2e−12	8e−11	6 x 50	epithelial cell transforming 2 [Source:HGNC Symbol;Acc:HG
20	ASPM	1.61	6e−12	8e−11	6 x 50	asp (abnormal spindle) homolog, microcephaly associated (D


p−values

C5_mel

Local Summary

%DE = 0.75

metagenes = 41

genes = 553

genes in genesets = 551

genes with fdr < 0.1 = 285 (38 + / 247 −)

genes with fdr < 0.05 = 219 (24 + / 195 −)

genes with fdr < 0.01 = 146 (13 + / 133 −)

<r> metagenes = 0.64

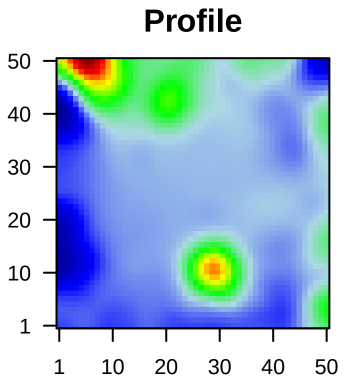
<r> genes = 0.07

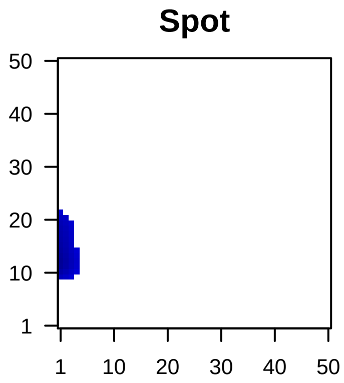
<FC> = −0.35

<shrinkage−t> = −6.02

<p−value> = 0

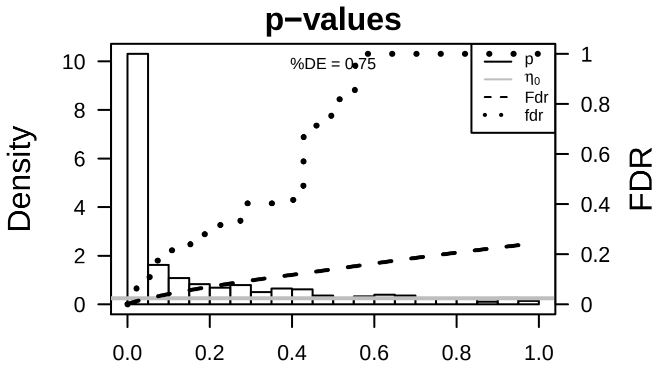
<fdr> = 0.59





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	CCDC171	−1.53	2e−16	4e−15	1 x 11	coiled−coil domain containing 171 [Source:HGNC Symbol;Ac
2	COX5A	−1.53	2e−16	4e−15	1 x 21	cytochrome c oxidase subunit Va [Source:HGNC Symbol;Acc
3	GPR161	−2.02	2e−16	4e−15	3 x 16	G protein−coupled receptor 161 [Source:HGNC Symbol;Acc:
4	OSTM1	−1.3	2e−16	4e−15	1 x 17	osteopetrosis associated transmembrane protein 1 [Source:H
5	SCD	−1.94	2e−16	4e−15	1 x 14	stearoyl−CoA desaturase (delta−9−desaturase) [Source:HGN
6	SEMA6A	−1.04	2e−16	4e−15	1 x 11	sema domain, transmembrane domain (TM), and cytoplasmic
7	UGCG	−1.51	2e−16	4e−15	1 x 11	UDP−glucose ceramide glucosyltransferase [Source:HGNC
8	VAT1	−0.98	2e−16	4e−15	1 x 17	vesicle amine transport 1 [Source:HGNC Symbol;Acc:HGNC:
9	GTF3A	−1.24	4e−15	2e−13	1 x 20	general transcription factor IIIA [Source:HGNC Symbol;Acc:H
10	MPZL1	−1.52	4e−15	2e−13	1 x 19	myelin protein zero−like 1 [Source:HGNC Symbol;Acc:HGNC
11	RAB27A	−1.51	4e−15	8e−13	1 x 11	RAB27A, member RAS oncogene family [Source:HGNC Sym
12	MYO5A	−1.29	1e−14	6e−11	1 x 13	myosin VA (heavy chain 12, myoxin) [Source:HGNC Symbol;
13	TXNDC16	1.69	6e−13	6e−11	3 x 11	thioredoxin domain containing 16 [Source:HGNC Symbol;Acc
14	PIK3CB	−1.42	1e−12	6e−11	1 x 11	phosphatidylinositol−4,5−bisphosphate 3−kinase, catalytic su
15	SURF4	−1.44	1e−12	7e−11	1 x 21	surfeit 4 [Source:HGNC Symbol;Acc:HGNC:11476]
16	TTYH3	−1.38	2e−12	7e−11	1 x 12	tweety family member 3 [Source:HGNC Symbol;Acc:HGNC:2
17	SCARB1	−1.35	2e−12	2e−10	2 x 20	scavenger receptor class B, member 1 [Source:HGNC Symb
18	SYNGR2	−1.42	4e−12	6e−10	1 x 21	synaptogyrin 2 [Source:HGNC Symbol;Acc:HGNC:11499]
19	BLVRA	−1.38	8e−12	8e−10	2 x 14	biliverdin reductase A [Source:HGNC Symbol;Acc:HGNC:10
20	RAB32	−0.75	2e−11	8e−10	1 x 20	RAB32, member RAS oncogene family [Source:HGNC Symb



C5_mel

Local Summary

%DE = 0.71

metagenes = 18

genes = 276

genes in genesets = 275

genes with fdr < 0.1 = 145 (15 + / 130 −)

genes with fdr < 0.05 = 145 (15 + / 130 −)

genes with fdr < 0.01 = 113 (7 + / 106 −)

<r> metagenes = 0.96

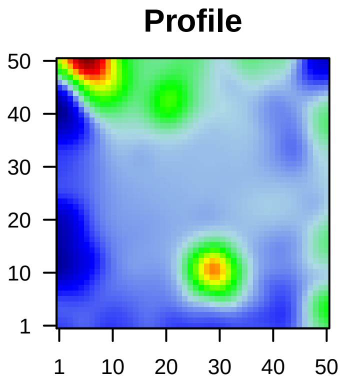
<r> genes = 0.16

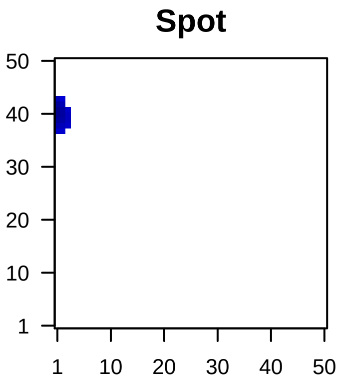
<FC> = −0.44

<shrinkage−t> = −9.17

<p−value> = 0

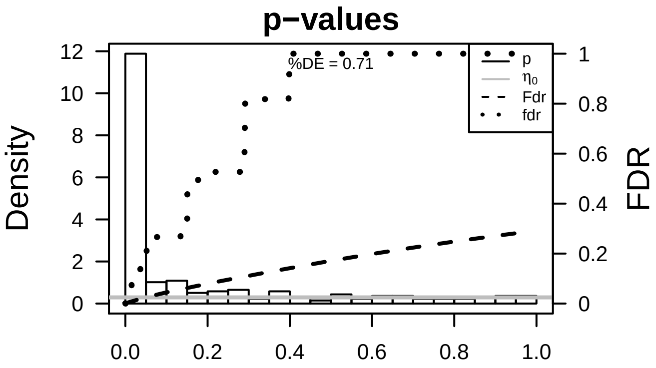
<fdr> = 0.48





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	ARHGAP8	−1.76	2e−16	1e−15	1 x 43	Rho GTPase activating protein 8 [Source:HGNC Symbol;Acc
2	BACE2	−1.37	2e−16	1e−15	1 x 42	beta−site APP−cleaving enzyme 2 [Source:HGNC Symbol;Ac
3	CTSD	−1.59	2e−16	1e−15	1 x 37	cathepsin D [Source:HGNC Symbol;Acc:HGNC:2529]
4	EXOC3	−1.61	2e−16	1e−15	1 x 42	exocyst complex component 3 [Source:HGNC Symbol;Acc:H
5	FAHD1	−1.65	2e−16	1e−15	1 x 40	fumarylacetoacetate hydrolase domain containing 1 [Source:
6	FDFT1	−1.79	2e−16	1e−15	1 x 38	farnesyl−diphosphate farnesyltransferase 1 [Source:HGNC S
7	MBP	−2.21	2e−16	1e−15	1 x 42	myelin basic protein [Source:HGNC Symbol;Acc:HGNC:6925
8	MTCH2	−1.95	2e−16	1e−15	2 x 42	mitochondrial carrier 2 [Source:HGNC Symbol;Acc:HGNC:17
9	NARS2	−1.28	2e−16	1e−15	1 x 42	asparaginyl−tRNA synthetase 2, mitochondrial (putative) [Sou
10	PDE4DIP	−1.9	2e−16	1e−15	1 x 43	phosphodiesterase 4D interacting protein [Source:HGNC Syn
11	SLC18B1	−1.61	2e−16	1e−15	1 x 42	solute carrier family 18, subfamily B, member 1 [Source:HGN
12	SLC45A2	−1.95	2e−16	1e−15	1 x 42	solute carrier family 45, member 2 [Source:HGNC Symbol;Ac
13	SNCA	−2.49	2e−16	1e−15	1 x 40	synuclein, alpha (non A4 component of amyloid precursor) [S
14	TRPM1	−2.08	2e−16	1e−15	1 x 42	transient receptor potential cation channel, subfamily M, mem
15	TYR	−1.25	2e−16	1e−15	1 x 42	tyrosinase [Source:HGNC Symbol;Acc:HGNC:12442]
16	CNDP2	−1.14	7e−16	5e−13	3 x 40	CNDP dipeptidase 2 (metallopeptidase M20 family) [Source:
17	GOT2	−1.51	7e−15	2e−12	1 x 40	glutamic−oxaloacetic transaminase 2, mitochondrial [Source:
18	CTSL	−0.77	4e−14	3e−12	2 x 40	cathepsin L [Source:HGNC Symbol;Acc:HGNC:2537]
19	SQLE	−1.27	7e−14	1e−11	1 x 38	squalene epoxidase [Source:HGNC Symbol;Acc:HGNC:1127
20	CTSC	−0.96	2e−13	1e−11	1 x 42	cathepsin C [Source:HGNC Symbol;Acc:HGNC:2528]



C5_mel

Local Summary

%DE = 0.83

metagenes = 2

genes = 80

genes in genesets = 80

genes with fdr < 0.1 = 53 (10 + / 43 −)

genes with fdr < 0.05 = 53 (10 + / 43 −)

genes with fdr < 0.01 = 33 (5 + / 28 −)

<r> metagenes = 1

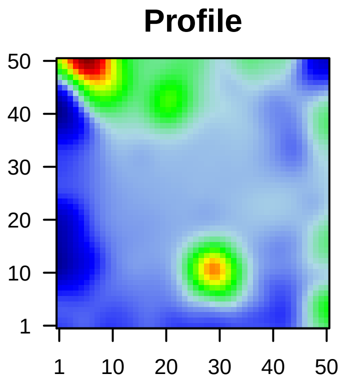
<r> genes = 0.11

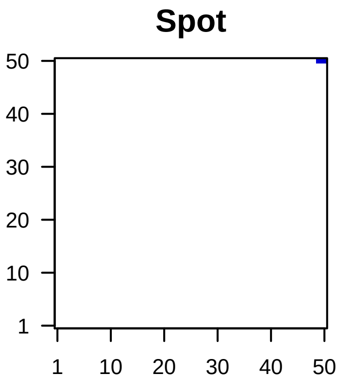
<FC> = −0.39

<shrinkage−t> = −6.63

<p−value> = 0

<fdr> = 0.48





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	NQO2	−1.68	2e−16	1e−15	50 x 50	NAD(P)H dehydrogenase, quinone 2 [Source:HGNC Symbol;
2	PLEKHA5	−1.53	2e−16	1e−15	50 x 50	pleckstrin homology domain containing, family A member 5 [
3	NIP7	−1.46	2e−13	1e−11	50 x 50	NIP7, nucleolar pre−rRNA processing protein [Source:HGNC
4	PIGP	−1.37	1e−12	4e−10	50 x 50	phosphatidylinositol glycan anchor biosynthesis, class P [Sou
5	AVPI1	−1.02	3e−11	8e−10	49 x 50	arginine vasopressin−induced 1 [Source:HGNC Symbol;Acc:
6	FRYL	−1.34	1e−10	1e−08	50 x 50	FRY−like [Source:HGNC Symbol;Acc:HGNC:29127]
7	WDR26	−1.29	1e−09	5e−08	50 x 50	WD repeat domain 26 [Source:HGNC Symbol;Acc:HGNC:21
8	CMC1	0.81	5e−09	5e−08	50 x 50	C−x(9)−C motif containing 1 [Source:HGNC Symbol;Acc:HG
9	ITIH3	1.35	9e−09	7e−08	50 x 50	inter−alpha−trypsin inhibitor heavy chain 3 [Source:HGNC Sy
10	CIRH1A	−1.24	1e−08	1e−07	49 x 50	cirrhosis, autosomal recessive 1A (cirhin) [Source:HGNC Syn
11	LGMN	−1.23	2e−08	2e−07	50 x 50	legumain [Source:HGNC Symbol;Acc:HGNC:9472]
12	NSMCE1	−1.22	4e−08	2e−07	50 x 50	non−SMC element 1 homolog (S. cerevisiae) [Source:HGNC
13	COQ4	−1.2	5e−08	3e−06	50 x 50	coenzyme Q4 [Source:HGNC Symbol;Acc:HGNC:19693]
14	EIF2B2	−1.17	3e−07	6e−05	49 x 50	eukaryotic translation initiation factor 2B, subunit 2 beta, 39k
15	MRPL49	−1.03	7e−06	6e−05	50 x 50	mitochondrial ribosomal protein L49 [Source:HGNC Symbol;
16	EHMT1	−1.01	2e−05	6e−05	50 x 50	euchromatic histone−lysine N−methyltransferase 1 [Source:H
17	MIF4GD	−1.01	2e−05	6e−05	50 x 50	MIF4G domain containing [Source:HGNC Symbol;Acc:HGNC
18	ENTPD6	−0.91	2e−05	6e−05	50 x 50	ectonucleoside triphosphate diphosphohydrolase 6 (putative)
19	KLHL28	−0.99	2e−05	4e−04	50 x 50	kelch−like family member 28 [Source:HGNC Symbol;Acc:HG
20	SMUG1	−0.93	8e−05	4e−04	49 x 50	single−strand−selective monofunctional uracil−DNA glycosyl