F3_mel

Global Summary

%DE = 0.24

genes with fdr < 0.2 = 3085 (1874 + / 1211 −)

genes with fdr < 0.1 = 2542 (1590 + / 952 −)

genes with fdr < 0.05 = 2018 (1289 + / 729 −)

genes with fdr < 0.01 = 1345 (864 + / 481 −)

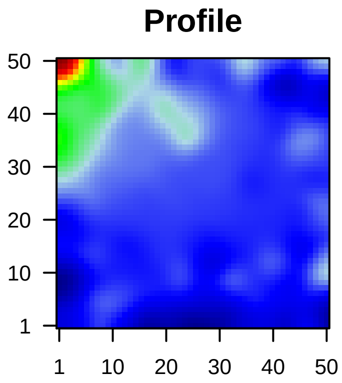
genes in genesets = 14839

<FC> = 0

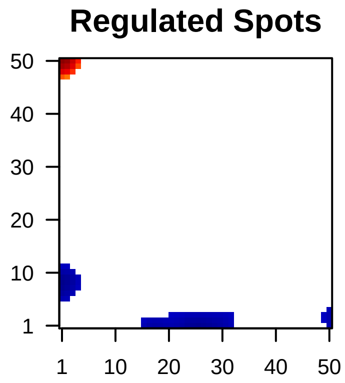
<shrinkage−t> = 0.07

<p−value> = 0.06

<fdr> = 0.76



Profile



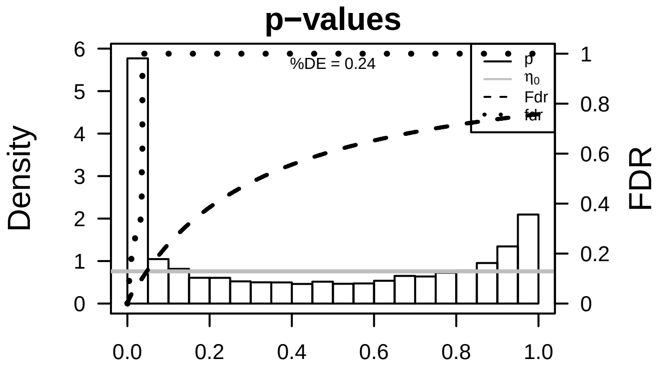
Regulated Spots

Global Genelist

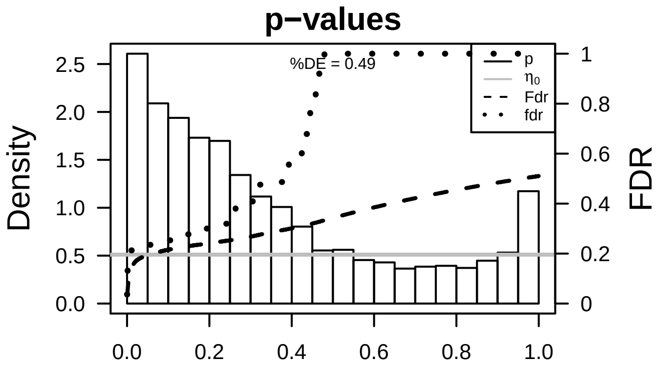
Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	AARSD1	−1.44	2e−16	9e−14	44 x 50	alanyl−tRNA synthetase domain containing 1 [Source:HGNC
2	AHSA1	−1.54	2e−16	9e−14	46 x 35	AHA1, activator of heat shock 90kDa protein ATPase homolo
3	COMMD9	−1.46	2e−16	9e−14	31 x 1	COMM domain containing 9 [Source:HGNC Symbol;Acc:HGN
4	COPB2	−1.64	2e−16	9e−14	50 x 39	coatomer protein complex, subunit beta 2 (beta prime) [Sourc
5	CRYAB	−1.82	2e−16	9e−14	50 x 1	crystallin, alpha B [Source:HGNC Symbol;Acc:HGNC:2389]
6	CUEDC2	−1.39	2e−16	9e−14	1 x 38	CUE domain containing 2 [Source:HGNC Symbol;Acc:HGNC
7	DHRS7B	−1.55	2e−16	9e−14	45 x 50	dehydrogenase/reductase (SDR family) member 7B [Source:
8	FAXC	1.75	2e−16	9e−14	21 x 43	failed axon connections homolog (Drosophila) [Source:HGNC
9	GSTM4	−1.45	2e−16	9e−14	1 x 41	glutathione S−transferase mu 4 [Source:HGNC Symbol;Acc:
10	IAH1	−1.68	2e−16	9e−14	35 x 14	isoamyl acetate−hydrolyzing esterase 1 homolog (S. cerevisia
11	ICT1	−1.47	2e−16	9e−14	1 x 26	immature colon carcinoma transcript 1 [Source:HGNC Symbo
12	KITLG	1.97	2e−16	9e−14	48 x 1	KIT ligand [Source:HGNC Symbol;Acc:HGNC:6343]
13	LGALS1	−1.49	2e−16	9e−14	50 x 1	lectin, galactoside−binding, soluble, 1 [Source:HGNC Symbol
14	NGDN	−1.44	2e−16	9e−14	22 x 45	neuroguidin, EIF4E binding protein [Source:HGNC Symbol;A
15	PDCD10	−1.2	2e−16	9e−14	13 x 50	programmed cell death 10 [Source:HGNC Symbol;Acc:HGNC
16	PDCD11	2.19	2e−16	9e−14	8 x 1	programmed cell death 11 [Source:HGNC Symbol;Acc:HGNC
17	PMP22	−1.14	2e−16	9e−14	48 x 1	peripheral myelin protein 22 [Source:HGNC Symbol;Acc:HGN
18	PPCS	−1.46	2e−16	9e−14	29 x 50	phosphopantothenoylcysteine synthetase [Source:HGNC Sy
19	RNASEH2B	1.84	2e−16	9e−14	1 x 50	ribonuclease H2, subunit B [Source:HGNC Symbol;Acc:HGN
20	RNF10	−1.54	2e−16	9e−14	37 x 48	ring finger protein 10 [Source:HGNC Symbol;Acc:HGNC:100

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	15.94	4e−05	242	GSEA C2	KOBAYASHI_EGFR_SIGNALING_24HR_DN
2	14.26	6e−05	1192	GSEA C2	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
3	13.94	7e−05	305	GSEA C2	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
4	13.89	7e−05	267	GSEA C2	ZHANG_TLX_TARGETS_60HR_DN
5	13.54	8e−05	197	HM	HALLMARK_E2F_TARGETS
6	12.31	1e−04	834	GSEA C2	LEE_BMP2_TARGETS_DN
7	11.65	1e−04	1251	GSEA C2	DODD_NASOPHARYNGEAL_CARCINOMA_DN
8	11.64	1e−04	436	GSEA C2	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
9	11.19	2e−04	550	GSEA C2	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
10	10.95	2e−04	505	GSEA C2	BERENJENO_TRANSFORMED_BY_RHOA_UP
11	10.89	2e−04	412	BP	mitotic cell cycle
12	10.82	2e−04	390	GSEA C2	PUJANA_BRCA2_PCC_NETWORK
13	10.59	2e−04	145	GSEA C2	CHANG_CYCLING_GENES
14	10.44	2e−04	139	GSEA C2	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
15	10.3	2e−04	312	GSEA C2	WONG_EMBRYONIC_STEM_CELL_CORE
16	10.28	2e−04	756	GSEA C2	WEI_MYCN_TARGETS_WITH_E_BOX
17	10.25	2e−04	609	GSEA C2	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIA
18	10.21	2e−04	160	GSEA C2	PUJANA_XPRSS_INT_NETWORK
19	10.2	2e−04	278	GSEA C2	MANALO_HYPOXIA_DN
20	10.17	2e−04	388	GSEA C2	REACTOME_CELL_CYCLE
Underexpressed					
1	−4.58	0.005	730	GSEA C2	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIA
2	−4.33	0.006	57	GSEA C2	GARCIA_TARGETS_OF_FLI1_AND_DAX1_UP
3	−4.21	0.006	8	GSEA C2	STANHILL_HRAS_TRANSFROMATION_UP
4	−4.2	0.006	12	GSEA C2	GERHOLD_RESPONSE_TO_TZD_DN
5	−3.91	0.008	2142	Colon Cancer	ReprPC_Colon
6	−3.89	0.008	3396	Lymphoma	HOPP_Repressed
7	−3.85	0.008	9	GSEA C2	FOURNIER_ACINAR_DEVELOPMENT_LATE_UP
8	−3.8	0.009	1889	Colon Cancer	ReprPCWk_Colon
9	−3.8	0.009	371	GSEA C2	MULLIGHAN_MLL_SIGNATURE_2_UP
10	−3.76	0.009	12	GSEA C2	SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_2FC_UP
11	−3.75	0.009	16	GSEA C2	SA_PTEN_PATHWAY
12	−3.71	0.010	17	CC	protein−DNA complex
13	−3.49	0.012	482	GSEA C2	RODRIGUES_THYROID_CARCINOMA_ANAPLASTIC_DN
14	−3.48	0.012	966	GSEA C2	PEREZ_TP53_TARGETS
15	−3.48	0.012	16	BP	nitrogen compound metabolic process
16	−3.48	0.012	4	GSEA C2	LY_AGING_OLD_UP
17	−3.46	0.012	66	Colon Cancer	Pentrack_CRC_TCGA_corr_N_msi−h_DN
18	−3.45	0.012	9	Colon Cancer	Budinska_D_Mesenchymal_UP
19	−3.42	0.012	10	GSEA C2	REACTOME_COPI_MEDIATED_TRANSPORT
20	−3.39	0.013	2159	Colon Cancer	TcoP_Colon



p−values



p−values

F3_mel

Local Summary

%DE = 0.89

metagenes = 13

genes = 224

genes in genesets = 223

genes with fdr < 0.1 = 185 (172 + / 13 −)

genes with fdr < 0.05 = 167 (158 + / 9 −)

genes with fdr < 0.01 = 147 (141 + / 6 −)

<r> metagenes = 0.97

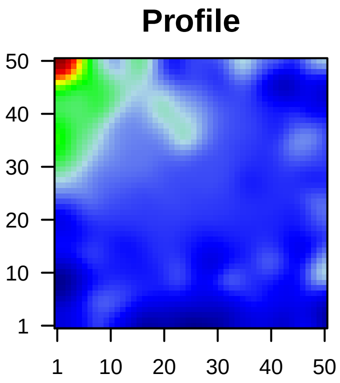
<r> genes = 0.28

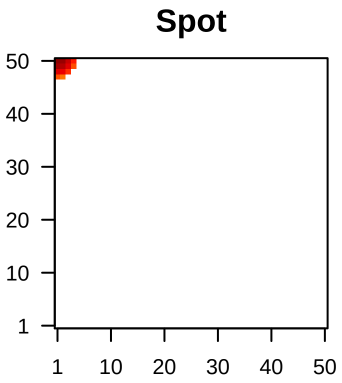
<FC> = 0.6

<shrinkage−t> = 9.56

<p−value> = 0

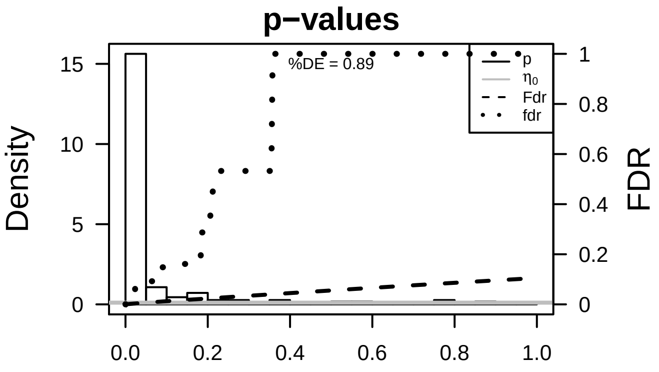
<fdr> = 0.27





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	RNASEH2B	1.84	2e−16	5e−15	1 x 50	ribonuclease H2, subunit B [Source:HGNC Symbol;Acc:HGN
2	CCNE2	1.5	6e−14	9e−11	2 x 50	cyclin E2 [Source:HGNC Symbol;Acc:HGNC:1590]
3	CENPQ	1.36	8e−12	9e−11	2 x 50	centromere protein Q [Source:HGNC Symbol;Acc:HGNC:213
4	RAD54L	1.36	1e−11	9e−11	4 x 50	RAD54−like (S. cerevisiae) [Source:HGNC Symbol;Acc:HGN
5	FBXO5	1.35	2e−11	9e−11	4 x 50	F−box protein 5 [Source:HGNC Symbol;Acc:HGNC:13584]
6	HELLS	1.25	2e−11	9e−11	1 x 50	helicase, lymphoid−specific [Source:HGNC Symbol;Acc:HGN
7	ZNF519	1.34	2e−11	9e−11	3 x 48	zinc finger protein 519 [Source:HGNC Symbol;Acc:HGNC:30
8	ASF1B	1.33	2e−11	2e−10	4 x 50	anti−silencing function 1B histone chaperone [Source:HGNC
9	POLA2	1.32	3e−11	2e−10	1 x 48	polymerase (DNA directed), alpha 2, accessory subunit [Sour
10	CHEK1	1.32	4e−11	3e−10	1 x 50	checkpoint kinase 1 [Source:HGNC Symbol;Acc:HGNC:1925
11	OMD	1.31	5e−11	3e−10	1 x 49	osteomodulin [Source:HGNC Symbol;Acc:HGNC:8134]
12	FANCA	1.3	7e−11	5e−09	1 x 50	Fanconi anemia, complementation group A [Source:HGNC S
13	MCM4	0.99	4e−10	5e−09	1 x 50	minichromosome maintenance complex component 4 [Sourc
14	KNTC1	1.22	6e−10	5e−09	1 x 50	kinetochore associated 1 [Source:HGNC Symbol;Acc:HGNC:
15	RFC4	1.16	1e−09	5e−09	1 x 50	replication factor C (activator 1) 4, 37kDa [Source:HGNC Sy
16	CEP152	1.21	1e−09	5e−09	4 x 50	centrosomal protein 152kDa [Source:HGNC Symbol;Acc:HG
17	CCP110	1.21	2e−09	5e−09	3 x 50	centriolar coiled coil protein 110kDa [Source:HGNC Symbol;
18	IMPA2	1.2	2e−09	5e−09	1 x 48	inositol(myo)−1(or 4)−monophosphatase 2 [Source:HGNC S
19	POLE2	1.2	2e−09	9e−09	1 x 47	polymerase (DNA directed), epsilon 2, accessory subunit [So
20	CDCA7	1.2	2e−09	9e−09	1 x 49	cell division cycle associated 7 [Source:HGNC Symbol;Acc:H



F3_mel

Local Summary

%DE = 0.57

metagenes = 46

genes = 519

genes in genesets = 504

genes with fdr < 0.1 = 96 (23 + / 73 −)

genes with fdr < 0.05 = 70 (18 + / 52 −)

genes with fdr < 0.01 = 43 (11 + / 32 −)

<r> metagenes = 0.79

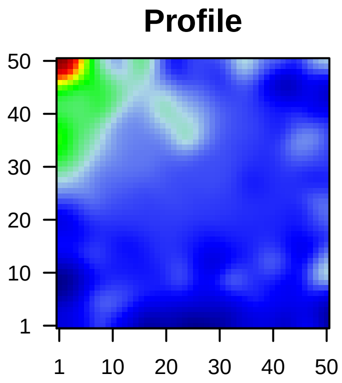
<r> genes = 0.13

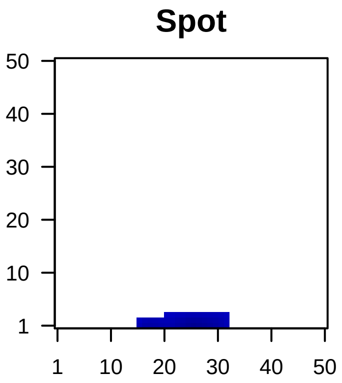
<FC> = −0.17

<shrinkage−t> = −2.55

<p−value> = 0.07

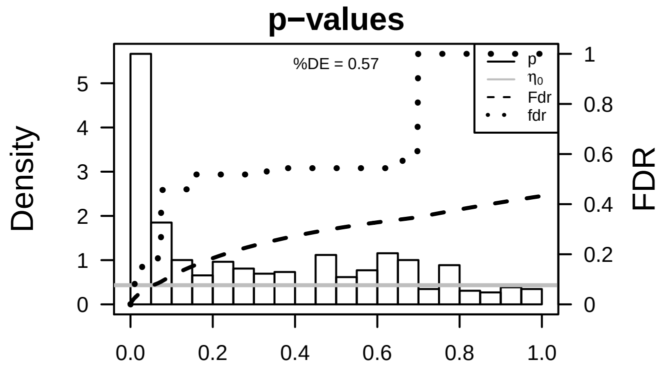
<fdr> = 0.78


Profile


Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	COMMD9	−1.46	2e−16	5e−14	31 x 1	COMM domain containing 9 [Source:HGNC Symbol;Acc:HG
2	AIMP1	−1.09	4e−12	9e−07	31 x 1	aminoacyl tRNA synthetase complex−interacting multifunctio
3	STK4	−1.05	9e−09	9e−07	16 x 1	serine/threonine kinase 4 [Source:HGNC Symbol;Acc:HGNC
4	ATG4A	1.14	1e−08	9e−07	22 x 1	autophagy related 4A, cysteine peptidase [Source:HGNC Sy
5	SLC1A4	−1.12	1e−08	4e−06	32 x 1	solute carrier family 1 (glutamate/neutral amino acid transpor
6	GTF2H2C	−1.08	4e−08	4e−06	17 x 1	GTF2H2 family member C [Source:HGNC Symbol;Acc:HGN
7	ALAS1	−1.07	5e−08	4e−06	24 x 2	5'−aminolevulinate synthase 1 [Source:HGNC Symbol;Acc:H
8	FKBP14	−1.07	7e−08	2e−05	26 x 1	FK506 binding protein 14, 22 kDa [Source:HGNC Symbol;Ac
9	AP2B1	−0.97	2e−07	2e−05	17 x 1	adaptor−related protein complex 2, beta 1 subunit [Source:H
10	QSER1	−1.03	2e−07	1e−04	29 x 1	glutamine and serine rich 1 [Source:HGNC Symbol;Acc:HGN
11	RMDN1	0.88	7e−07	1e−04	19 x 1	regulator of microtubule dynamics 1 [Source:HGNC Symbol;
12	SUGP2	−0.77	1e−06	1e−04	16 x 1	SURP and G patch domain containing 2 [Source:HGNC Sym
13	SYNC	0.95	2e−06	3e−04	16 x 1	syncoilin, intermediate filament protein [Source:HGNC Symb
14	IFT22	−0.93	3e−06	3e−04	21 x 1	intraflagellar transport 22 [Source:HGNC Symbol;Acc:HGNC
15	FASTKD5	−0.91	5e−06	3e−04	32 x 1	FAST kinase domains 5 [Source:HGNC Symbol;Acc:HGNC:2
16	BTG1	−0.9	6e−06	3e−04	25 x 1	B−cell translocation gene 1, anti−proliferative [Source:HGNC
17	GEMIN6	−0.9	7e−06	4e−04	22 x 1	gem (nuclear organelle) associated protein 6 [Source:HGNC
18	CHMP1B	−0.86	1e−05	4e−04	21 x 1	charged multivesicular body protein 1B [Source:HGNC Symb
19	PHF14	−0.87	1e−05	7e−04	16 x 1	PHD finger protein 14 [Source:HGNC Symbol;Acc:HGNC:22
20	SLC30A9	−0.77	2e−05	7e−04	20 x 1	solute carrier family 30 (zinc transporter), member 9 [Source:


p−values

F3_mel

Local Summary

%DE = 0.71

metagenes = 6

genes = 154

genes in genesets = 154

genes with fdr < 0.1 = 77 (28 + / 49 −)

genes with fdr < 0.05 = 59 (20 + / 39 −)

genes with fdr < 0.01 = 53 (19 + / 34 −)

<r> metagenes = 0.99

<r> genes = 0.23

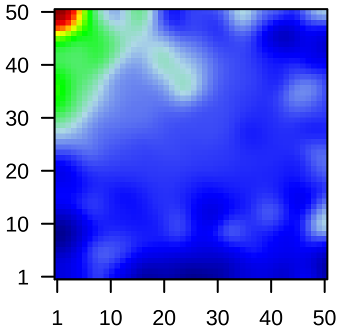
<FC> = −0.19

<shrinkage−t> = −3.18

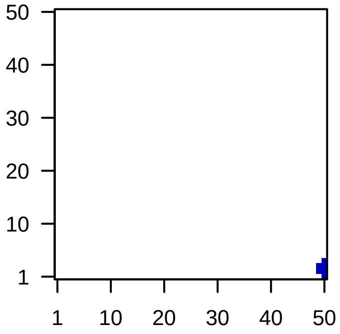
<p−value> = 0

<fdr> = 0.54

Profile



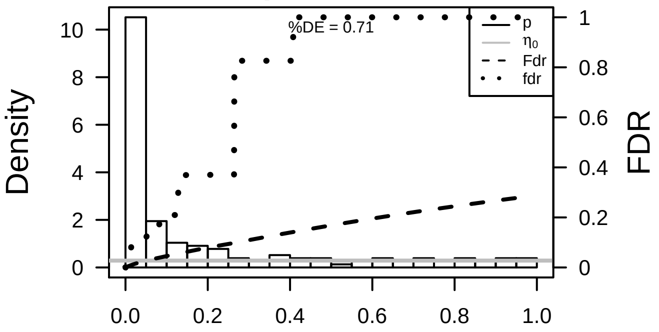
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	CRYAB	−1.82	2e−16	3e−15	50 x 1	crystallin, alpha B [Source:HGNC Symbol;Acc:HGNC:2389]
2	LGALS1	−1.49	2e−16	3e−15	50 x 1	lectin, galactoside−binding, soluble, 1 [Source:HGNC Symbol
3	SNAP23	−1.53	2e−16	3e−15	50 x 1	synaptosomal−associated protein, 23kDa [Source:HGNC Sy
4	ARID5B	−1.34	2e−14	2e−12	50 x 1	AT rich interactive domain 5B (MRF1−like) [Source:HGNC Sy
5	SPARC	−0.75	7e−14	3e−12	50 x 2	secreted protein, acidic, cysteine−rich (osteonectin) [Source:
6	SERPINI1	1.47	2e−13	3e−12	50 x 1	serpin peptidase inhibitor, clade I (neuroserpin), member 1 [S
7	STAM	−1.32	2e−13	1e−11	50 x 3	signal transducing adaptor molecule (SH3 domain and ITAM
8	CALD1	−0.92	5e−13	7e−09	50 x 1	caldesmon 1 [Source:HGNC Symbol;Acc:HGNC:1441]
9	NOV	−1.2	2e−10	1e−08	50 x 1	nephroblastoma overexpressed [Source:HGNC Symbol;Acc:
10	CD55	−1.19	4e−10	4e−06	50 x 1	CD55 molecule, decay accelerating factor for complement (C
11	MT2A	−1.06	1e−07	4e−06	50 x 3	metallothionein 2A [Source:HGNC Symbol;Acc:HGNC:7406]
12	MID1	−1.04	2e−07	5e−06	50 x 3	midline 1 [Source:HGNC Symbol;Acc:HGNC:7095]
13	AASS	−1.02	3e−07	5e−06	50 x 3	aminoadipate−semialdehyde synthase [Source:HGNC Symb
14	PLK2	0.76	4e−07	1e−05	50 x 1	polo−like kinase 2 [Source:HGNC Symbol;Acc:HGNC:19699]
15	GPBP1L1	−0.93	6e−07	3e−05	50 x 4	GC−rich promoter binding protein 1−like 1 [Source:HGNC Sy
16	SYTL2	0.97	1e−06	7e−05	50 x 4	synaptotagmin−like 2 [Source:HGNC Symbol;Acc:HGNC:155
17	ALCAM	−0.92	4e−06	7e−05	50 x 1	activated leukocyte cell adhesion molecule [Source:HGNC S
18	GPR37	0.92	5e−06	1e−04	50 x 1	G protein−coupled receptor 37 (endothelin receptor type B−li
19	TMEM39A	0.87	1e−05	1e−04	50 x 1	transmembrane protein 39A [Source:HGNC Symbol;Acc:HG
20	PITX2	−0.87	1e−05	1e−04	50 x 4	paired−like homeodomain 2 [Source:HGNC Symbol;Acc:HG

p−values



F3_mel

Local Summary

%DE = 0.71

metagenes = 22

genes = 314

genes in genesets = 312

genes with fdr < 0.1 = 150 (50 + / 100 −)

genes with fdr < 0.05 = 126 (43 + / 83 −)

genes with fdr < 0.01 = 76 (31 + / 45 −)

<r> metagenes = 0.9

<r> genes = 0.11

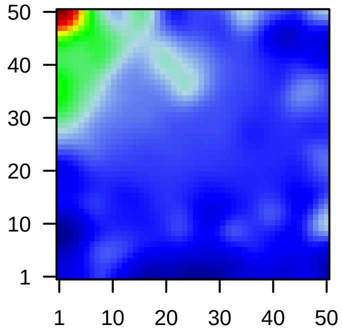
<FC> = −0.14

<shrinkage−t> = −2.1

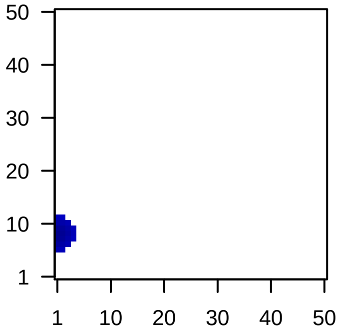
<p−value> = 0.01

<fdr> = 0.58

Profile



Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	SNAI2	−1.31	6e−13	2e−10	1 x 11	snail family zinc finger 2 [Source:HGNC Symbol;Acc:HGNC:1
2	CEACAM1	−1.27	3e−12	2e−08	1 x 10	carcinoembryonic antigen−related cell adhesion molecule 1 (
3	NCOA4	−0.87	2e−10	2e−08	1 x 7	nuclear receptor coactivator 4 [Source:HGNC Symbol;Acc:H
4	WDR48	−1.14	6e−10	2e−08	1 x 9	WD repeat domain 48 [Source:HGNC Symbol;Acc:HGNC:30
5	DCT	−0.72	6e−10	1e−07	1 x 11	dopachrome tautomerase [Source:HGNC Symbol;Acc:HGNC
6	SUOX	1.19	2e−09	1e−07	1 x 12	sulfite oxidase [Source:HGNC Symbol;Acc:HGNC:11460]
7	GALNT3	1.19	3e−09	1e−07	1 x 12	polypeptide N−acetylgalactosaminyltransferase 3 [Source:HG
8	ORC4	1.08	4e−09	1e−06	4 x 10	origin recognition complex, subunit 4 [Source:HGNC Symbol;
9	COPG1	−1.1	2e−08	7e−06	1 x 9	coatomer protein complex, subunit gamma 1 [Source:HGNC
10	BBS5	1.03	2e−07	7e−06	1 x 11	Bardet−Biedl syndrome 5 [Source:HGNC Symbol;Acc:HGNC
11	C4orf45	1.02	3e−07	7e−06	1 x 11	chromosome 4 open reading frame 45 [Source:HGNC Symb
12	SEMA3C	−1.01	3e−07	7e−06	1 x 10	sema domain, immunoglobulin domain (Ig), short basic doma
13	RINT1	−1.02	3e−07	1e−05	2 x 11	RAD50 interactor 1 [Source:HGNC Symbol;Acc:HGNC:2187
14	SULT1C2	−1	6e−07	1e−05	1 x 9	sulfotransferase family, cytosolic, 1C, member 2 [Source:HGN
15	LUZP1	−0.99	8e−07	1e−05	1 x 6	leucine zipper protein 1 [Source:HGNC Symbol;Acc:HGNC:1
16	PIP4K2C	−0.99	8e−07	2e−05	1 x 10	phosphatidylinositol−5−phosphate 4−kinase, type II, gamma [
17	C12orf73	−0.98	1e−06	2e−05	1 x 10	chromosome 12 open reading frame 73 [Source:HGNC Symb
18	RGS12	−0.97	1e−06	3e−05	1 x 9	regulator of G−protein signaling 12 [Source:HGNC Symbol;A
19	SEMA5A	−0.95	2e−06	3e−05	4 x 9	sema domain, seven thrombospondin repeats (type 1 and typ
20	POLR3H	0.95	2e−06	2e−04	1 x 6	polymerase (RNA) III (DNA directed) polypeptide H (22.9kD)

p−values