G3_mel

Global Summary

%DE = 0.22

genes with fdr < 0.2 = 2848 (1678 + / 1170 −)

genes with fdr < 0.1 = 2338 (1402 + / 936 −)

genes with fdr < 0.05 = 1876 (1116 + / 760 −)

genes with fdr < 0.01 = 1202 (744 + / 458 −)

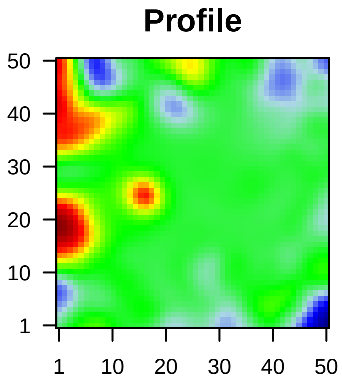
genes in genesets = 14839

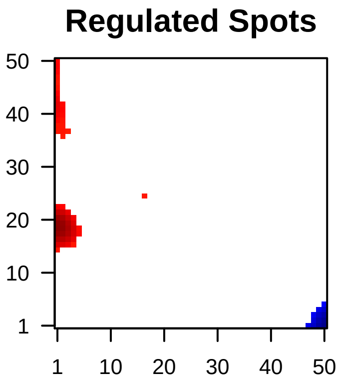
<FC> = 0

<shrinkage−t> = 0.02

<p−value> = 0.07

<fdr> = 0.78



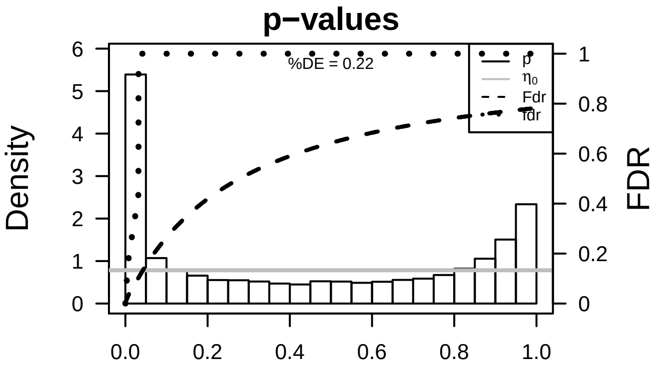


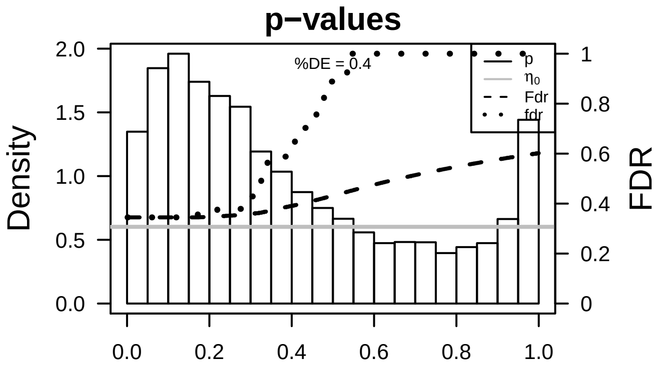
Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	ACTL6A	−1.88	2e−16	1e−13	4 x 50	actin−like 6A [Source:HGNC Symbol;Acc:HGNC:24124]
2	ATPIF1	−1.14	2e−16	1e−13	50 x 47	ATPase inhibitory factor 1 [Source:HGNC Symbol;Acc:HGNC
3	CCNDBP1	−1.68	2e−16	1e−13	1 x 21	cyclin D−type binding−protein 1 [Source:HGNC Symbol;Acc:
4	CDKN3	−1.65	2e−16	1e−13	6 x 50	cyclin−dependent kinase inhibitor 3 [Source:HGNC Symbol;A
5	CRYAB	−1.82	2e−16	1e−13	50 x 1	crystallin, alpha B [Source:HGNC Symbol;Acc:HGNC:2389]
6	DCXR	0.79	2e−16	1e−13	5 x 37	dicarbonyl/L−xylulose reductase [Source:HGNC Symbol;Acc:
7	DTYMK	−1.55	2e−16	1e−13	7 x 47	deoxythymidylate kinase (thymidylate kinase) [Source:HGNC
8	EIF1B	−1.68	2e−16	1e−13	4 x 43	eukaryotic translation initiation factor 1B [Source:HGNC Sym
9	EIF2A	−1.8	2e−16	1e−13	50 x 12	eukaryotic translation initiation factor 2A, 65kDa [Source:HG
10	ENY2	−1.86	2e−16	1e−13	12 x 47	enhancer of yellow 2 homolog (Drosophila) [Source:HGNC S
11	EXOC3	0.82	2e−16	1e−13	1 x 42	exocyst complex component 3 [Source:HGNC Symbol;Acc:H
12	GARNL3	2.01	2e−16	1e−13	1 x 4	GTPase activating Rap/RanGAP domain−like 3 [Source:HGN
13	MARS	−1.44	2e−16	1e−13	43 x 47	methionyl−tRNA synthetase [Source:HGNC Symbol;Acc:HG
14	MRPL22	−1.71	2e−16	1e−13	40 x 47	mitochondrial ribosomal protein L22 [Source:HGNC Symbol;
15	MRPS12	−1.6	2e−16	1e−13	48 x 50	mitochondrial ribosomal protein S12 [Source:HGNC Symbol;
16	NUP85	−1.56	2e−16	1e−13	1 x 50	nucleoporin 85kDa [Source:HGNC Symbol;Acc:HGNC:8734]
17	PAK1IP1	−1.65	2e−16	1e−13	7 x 44	PAK1 interacting protein 1 [Source:HGNC Symbol;Acc:HGNC
18	PNRC2	−1.62	2e−16	1e−13	9 x 46	proline−rich nuclear receptor coactivator 2 [Source:HGNC Sy
19	POP4	−1.63	2e−16	1e−13	15 x 50	processing of precursor 4, ribonuclease P/MRP subunit (S. c
20	PPT1	−1.19	2e−16	1e−13	34 x 46	palmitoyl−protein thioesterase 1 [Source:HGNC Symbol;Acc:

Global Geneset Analysis

Rank	GSZ	p−value	#all		Geneset
Overexpressed					
1	6.59	0.001	925	GSEA C2	KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
2	5.66	0.002	834	GSEA C2	LEE_BMP2_TARGETS_DN
3	5.62	0.002	831	GSEA C2	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
4	4.63	0.005	278	GSEA C2	MANALO_HYPOXIA_DN
5	4.34	0.006	78	GSEA C2	SCHUHMACHER_MYC_TARGETS_UP
6	4.33	0.006	335	GSEA C2	WANG_RESPONSE_TO_GSK3_INHIBITOR_SB216763_DN
7	4.22	0.006	43	GSEA C2	ZHAN_MULTIPLE_MYELOMA_CD2_DN
8	4.14	0.007	325	GSEA C2	PENG_GLUTAMINE_DEPRIVATION_DN
9	4.11	0.007	212	GSEA C2	DUTERTRE_ESTRADIOL_RESPONSE_6HR_UP
10	3.97	0.008	83	GSEA C2	LI_DCP2_BOUND_MRNA
11	3.91	0.008	15	GSEA C2	REACTOME_DESTABILIZATION_OF_MRNA_BY_KSRP
12	3.9	0.008	476	GSEA C2	IVANOVA_HEMATOPOIESIS_LATE_PROGENITOR
13	3.89	0.008	338	GSEA C2	DAIRKEE_TERT_TARGETS_UP
14	3.86	0.008	14	CC	exocyst
15	3.83	0.009	756	GSEA C2	WEI_MYCN_TARGETS_WITH_E_BOX
16	3.83	0.009	57	HM	HALLMARK_MYC_TARGETS_V2
17	3.81	0.009	39	miRNA target	hsa−miR−518f*
18	3.74	0.009	562	GSEA C2	CAIRO_HEPATOBLASTOMA_CLASSES_UP
19	3.73	0.009	79	GSEA C2	ACOSTA_PROLIFERATION_INDEPENDENT_MYC_TARGETS_U
20	3.73	0.009	68	GSEA C2	CHEBOTAEV_GR_TARGETS_UP
Underexpressed					
1	−4.62	0.005	22	BP	negative regulation of endothelial cell proliferation
2	−3.94	0.008	1394	GSEA C2	ZWANG_TRANSIENTLY_UP_BY_1ST_EGF_PULSE_ONLY
3	−3.92	0.008	16	MF	extracellular matrix binding
4	−3.79	0.009	104	GSEA C2	LAIHO_COLORECTAL_CANCER_SERRATED_UP
5	−3.76	0.009	285	BP	organelle organization
6	−3.71	0.010	9	Colon Cancer	Budinska_D_Mesenchymal_UP
7	−3.67	0.010	96	BP	mitochondrial translation
8	−3.63	0.010	45	GSEA C2	BOYAULT_LIVER_CANCER_SUBCLASS_G123_UP
9	−3.61	0.010	212	Lymphoma	LENZ_Stromal signature 1
10	−3.58	0.011	83	BP	mitochondrial translational elongation
11	−3.58	0.011	14	GSEA C2	MARIADASON_RESPONSE_TO_BUTYRATE_CURCUMIN_SULI
12	−3.56	0.011	503	GSEA C2	MARTINEZ_RB1_AND_TP53_TARGETS_UP
13	−3.5	0.011	83	BP	muscle contraction
14	−3.48	0.012	40	GSEA C2	DORN_ADENOVIRUS_INFECTION_24HR_DN
15	−3.48	0.012	38	GSEA C2	DELPUECH_FOXO3_TARGETS_DN
16	−3.46	0.012	5	Colon Cancer	Budinska_C_CIMP−H−like_UP
17	−3.44	0.012	155	GSEA C2	SMIRNOV_RESPONSE_TO_IR_6HR_UP
18	−3.42	0.012	138	CC	microtubule cytoskeleton
19	−3.42	0.012	51	GSEA C2	HU_GENOTOXIN_ACTION_DIRECT_VS_INDIRECT_24HR
20	−3.38	0.013	39	GSEA C2	PID_AURORA_B_PATHWAY





G3_mel

Local Summary

%DE = 0.73

metagenes = 32

genes = 358

genes in genesets = 356

genes with fdr < 0.1 = 177 (150 + / 27 −)

genes with fdr < 0.05 = 171 (145 + / 26 −)

genes with fdr < 0.01 = 107 (92 + / 15 −)

<r> metagenes = 0.86

<r> genes = 0.11

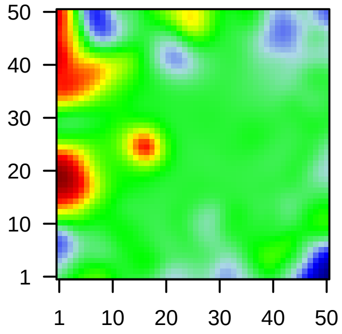
<FC> = 0.29

<shrinkage−t> = 4.97

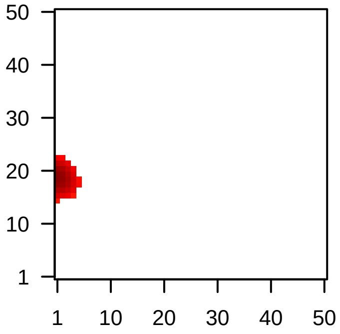
<p−value> = 0.01

<fdr> = 0.54

Profile



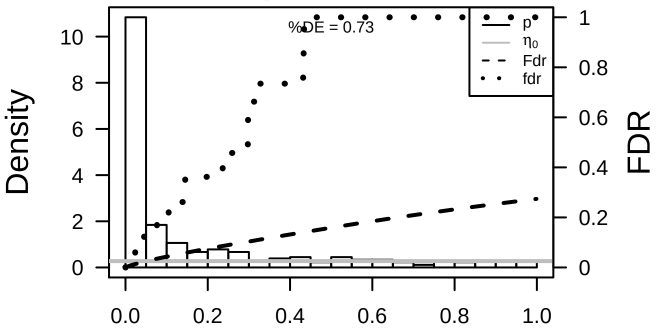
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	CCNDBP1	−1.68	2e−16	2e−14	1 x 21	cyclin D−type binding−protein 1 [Source:HGNC Symbol;Acc:H
2	PIGY	0.68	2e−10	1e−08	1 x 20	phosphatidylinositol glycan anchor biosynthesis, class Y [Sou
3	RCN1	0.73	2e−10	2e−08	1 x 23	reticulocalbin 1, EF−hand calcium binding domain [Source:H
4	ANKRD13A	1.45	4e−10	5e−07	1 x 16	ankyrin repeat domain 13A [Source:HGNC Symbol;Acc:HGN
5	TACO1	1.34	7e−09	5e−07	2 x 19	translational activator of mitochondrially encoded cytochrome
6	OSTM1	0.56	1e−08	7e−07	1 x 17	osteopetrosis associated transmembrane protein 1 [Source:H
7	PTGES2	1.3	2e−08	2e−06	1 x 17	prostaglandin E synthase 2 [Source:HGNC Symbol;Acc:HGN
8	ZNF511	1.27	5e−08	2e−06	1 x 21	zinc finger protein 511 [Source:HGNC Symbol;Acc:HGNC:28
9	PMF1−BGLAI	1.26	6e−08	3e−06	3 x 16	PMF1−BGLAP readthrough [Source:HGNC Symbol;Acc:HGN
10	PTDSS2	1.24	1e−07	3e−06	1 x 19	phosphatidylserine synthase 2 [Source:HGNC Symbol;Acc:H
11	LMLN	1.23	1e−07	7e−06	1 x 20	leishmanolysin−like (metallopeptidase M8 family) [Source:HG
12	AGPAT2	1.18	4e−07	7e−06	1 x 21	1−acylglycerol−3−phosphate O−acyltransferase 2 [Source:H
13	SIRT3	1.18	4e−07	7e−06	4 x 16	sirtuin 3 [Source:HGNC Symbol;Acc:HGNC:14931]
14	STARD3	1.18	4e−07	7e−06	1 x 15	StAR−related lipid transfer (START) domain containing 3 [Sou
15	CUL4A	1.18	4e−07	1e−05	1 x 23	cullin 4A [Source:HGNC Symbol;Acc:HGNC:2554]
16	EGLN2	1.15	7e−07	1e−05	1 x 23	egl−9 family hypoxia−inducible factor 2 [Source:HGNC Symb
17	NCALD	−1.13	8e−07	1e−05	1 x 15	neurocalcin delta [Source:HGNC Symbol;Acc:HGNC:7655]
18	EVA1A	1.14	9e−07	1e−05	2 x 17	eva−1 homolog A (C. elegans) [Source:HGNC Symbol;Acc:H
19	DCAKD	1.14	9e−07	3e−05	3 x 19	dephospho−CoA kinase domain containing [Source:HGNC S
20	MDH1B	1.12	1e−06	3e−05	4 x 19	malate dehydrogenase 1B, NAD (soluble) [Source:HGNC Sy

p−values



G3_mel

Local Summary

%DE = 0.95

metagenes = 1

genes = 25

genes in genesets = 24

genes with fdr < 0.1 = 22 (22 + / 0 −)

genes with fdr < 0.05 = 22 (22 + / 0 −)

genes with fdr < 0.01 = 20 (20 + / 0 −)

<r> metagenes = NA

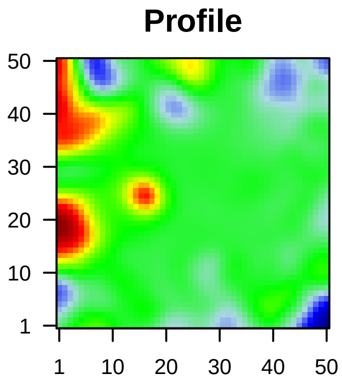
<r> genes = 0.57

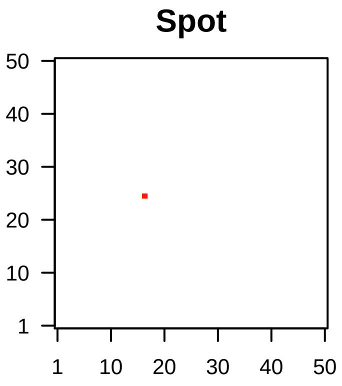
<FC> = 1.01

<shrinkage−t> = 15.29

<p−value> = 0

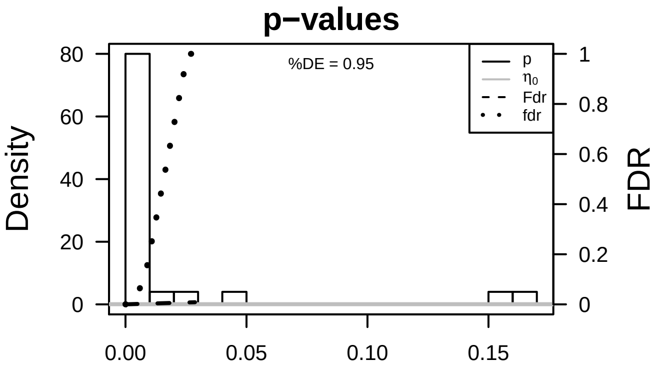
<fdr> = 0.16





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	ZNF688	1.75	4e−14	5e−13	17 x 25	zinc finger protein 688 [Source:HGNC Symbol;Acc:HGNC:30
2	CTSS	1.68	5e−13	2e−12	17 x 25	cathepsin S [Source:HGNC Symbol;Acc:HGNC:2545]
3	CD101	1.63	2e−12	6e−12	17 x 25	CD101 molecule [Source:HGNC Symbol;Acc:HGNC:5949]
4	KCTD14	1.59	7e−12	1e−10	17 x 25	potassium channel tetramerization domain containing 14 [Sou
5	DHDH	1.5	1e−10	3e−09	17 x 25	dihydrodiol dehydrogenase (dimeric) [Source:HGNC Symbol;
6	HOXD13	1.38	3e−09	4e−08	17 x 25	homeobox D13 [Source:HGNC Symbol;Acc:HGNC:5136]
7	CLDN2	1.26	6e−08	4e−08	17 x 25	claudin 2 [Source:HGNC Symbol;Acc:HGNC:2041]
8	TESC	1.25	7e−08	8e−08	17 x 25	tescalcin [Source:HGNC Symbol;Acc:HGNC:26065]
9	CECR2	1.22	1e−07	2e−07	17 x 25	cat eye syndrome chromosome region, candidate 2 [Source:
10	ERF	1.18	4e−07	2e−07	17 x 25	Ets2 repressor factor [Source:HGNC Symbol;Acc:HGNC:344
11	HOXC10	1.17	5e−07	1e−05	17 x 25	homeobox C10 [Source:HGNC Symbol;Acc:HGNC:5122]
12	GNB1L	1.03	9e−06	1e−05	17 x 25	guanine nucleotide binding protein (G protein), beta polypepti
13	HIST2H2AB	0.99	2e−05	9e−05	17 x 25	histone cluster 2, H2ab [Source:HGNC Symbol;Acc:HGNC:2
14	LRRN4CL	0.91	9e−05	1e−04	17 x 25	LRRN4 C−terminal like [Source:HGNC Symbol;Acc:HGNC:3
15	EMR2	0.86	2e−04	1e−04	17 x 25	
16	IL1R2	0.84	3e−04	9e−04	17 x 25	interleukin 1 receptor, type II [Source:HGNC Symbol;Acc:HG
17	KCTD11	0.74	1e−03	9e−04	17 x 25	potassium channel tetramerization domain containing 11 [Sou
18	LRRC3	0.72	2e−03	2e−03	17 x 25	leucine rich repeat containing 3 [Source:HGNC Symbol;Acc:
19	SSC4D	0.67	4e−03	4e−03	17 x 25	scavenger receptor cysteine rich family, 4 domains [Source:H
20	CNTD2	0.61	9e−03	4e−03	17 x 25	cyclin N−terminal domain containing 2 [Source:HGNC Symb



G3_mel

Local Summary

%DE = 0.77

metagenes = 22

genes = 471

genes in genesets = 468

genes with fdr < 0.1 = 283 (219 + / 64 −)

genes with fdr < 0.05 = 233 (182 + / 51 −)

genes with fdr < 0.01 = 177 (136 + / 41 −)

<r> metagenes = 0.82

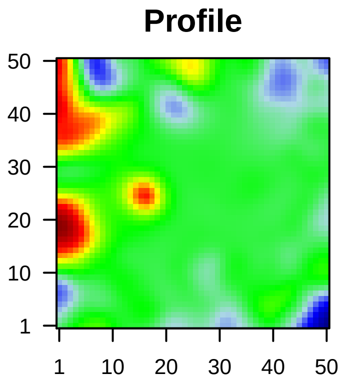
<r> genes = 0.14

<FC> = 0.26

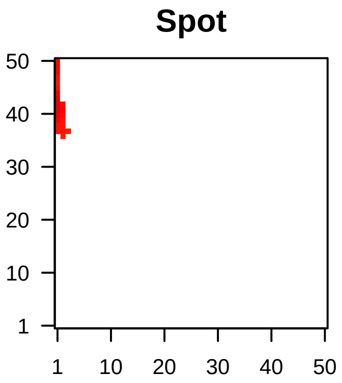
<shrinkage−t> = 4.53

<p−value> = 0

<fdr> = 0.48



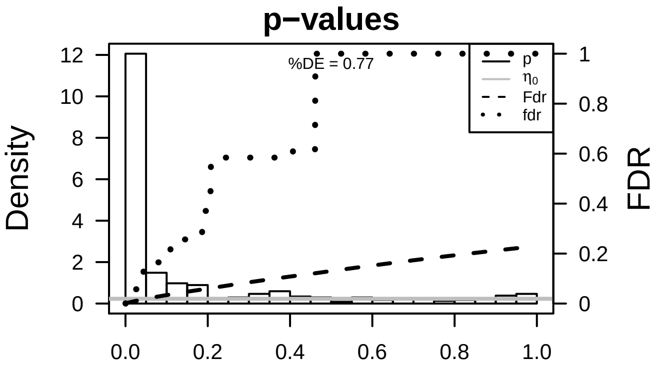
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	EXOC3	0.82	2e−16	1e−14	1 x 42	exocyst complex component 3 [Source:HGNC Symbol;Acc:H
2	NUP85	−1.56	2e−16	1e−14	1 x 50	nucleoporin 85kDa [Source:HGNC Symbol;Acc:HGNC:8734]
3	GOT1	−1.36	6e−15	1e−12	1 x 39	glutamic−oxaloacetic transaminase 1, soluble [Source:HGNC
4	MYH10	−0.88	2e−14	1e−10	1 x 44	myosin, heavy chain 10, non−muscle [Source:HGNC Symbol
5	RNASEH2B	1.65	1e−12	4e−10	1 x 50	ribonuclease H2, subunit B [Source:HGNC Symbol;Acc:HGN
6	KNTC1	1.58	5e−12	1e−09	1 x 50	kinetochore associated 1 [Source:HGNC Symbol;Acc:HGNC:
7	PAFAH1B3	−1.38	2e−11	2e−08	1 x 43	platelet−activating factor acetylhydrolase 1b, catalytic subunit
8	DDX55	1.45	5e−10	2e−08	1 x 44	DEAD (Asp−Glu−Ala−Asp) box polypeptide 55 [Source:HGN
9	CTSL	0.63	5e−10	2e−08	2 x 40	cathepsin L [Source:HGNC Symbol;Acc:HGNC:2537]
10	MBP	0.58	7e−10	2e−08	1 x 42	myelin basic protein [Source:HGNC Symbol;Acc:HGNC:6925
11	PDE6D	−1.3	8e−10	3e−08	1 x 44	phosphodiesterase 6D, cGMP−specific, rod, delta [Source:H
12	LGALS3	1.25	1e−09	2e−07	1 x 43	lectin, galactoside−binding, soluble, 3 [Source:HGNC Symbol
13	METTL9	0.86	4e−09	2e−07	1 x 43	methyltransferase like 9 [Source:HGNC Symbol;Acc:HGNC:2
14	SEPSECS	1.36	4e−09	2e−07	1 x 37	Sep (O−phosphoserine) tRNA:Sec (selenocysteine) tRNA sy
15	CA14	−1.08	8e−09	2e−07	1 x 46	carbonic anhydrase XIV [Source:HGNC Symbol;Acc:HGNC:1
16	ANO2	1.33	9e−09	4e−07	1 x 42	anoctamin 2, calcium activated chloride channel [Source:HG
17	ST3GAL1	1.31	2e−08	4e−07	1 x 40	ST3 beta−galactoside alpha−2,3−sialyltransferase 1 [Source:
18	MUC7	1.31	2e−08	4e−07	1 x 46	mucin 7, secreted [Source:HGNC Symbol;Acc:HGNC:7518]
19	TRMT1	1.3	2e−08	4e−07	1 x 40	tRNA methyltransferase 1 homolog (S. cerevisiae) [Source:H
20	CDCA7	1.3	2e−08	6e−07	1 x 49	cell division cycle associated 7 [Source:HGNC Symbol;Acc:H



p−values

G3_mel

Local Summary

%DE = 0.72

metagenes = 13

genes = 256

genes in genesets = 256

genes with fdr < 0.1 = 107 (18 + / 89 −)

genes with fdr < 0.05 = 95 (17 + / 78 −)

genes with fdr < 0.01 = 44 (8 + / 36 −)

<r> metagenes = 0.98

<r> genes = 0.2

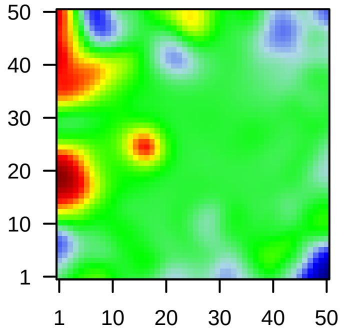
<FC> = −0.27

<shrinkage−t> = −4.45

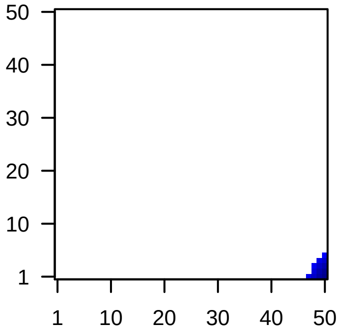
<p−value> = 0.02

<fdr> = 0.63

Profile



Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	CRYAB	−1.82	2e−16	8e−15	50 x 1	crystallin, alpha B [Source:HGNC Symbol;Acc:HGNC:2389]
2	SPARC	−1.27	2e−16	8e−15	50 x 2	secreted protein, acidic, cysteine−rich (osteonectin) [Source:
3	PLK2	−1.32	2e−14	2e−11	50 x 1	polo−like kinase 2 [Source:HGNC Symbol;Acc:HGNC:19699]
4	SATB1	1.68	5e−13	2e−11	50 x 1	SATB homeobox 1 [Source:HGNC Symbol;Acc:HGNC:10541
5	FABP3	−1.44	5e−13	4e−11	50 x 1	fatty acid binding protein 3, muscle and heart [Source:HGNC
6	SNAP23	−1.31	1e−12	1e−05	50 x 1	synaptosomal−associated protein, 23kDa [Source:HGNC Sy
7	PCYOX1	−1.16	3e−07	1e−05	49 x 4	prenylcysteine oxidase 1 [Source:HGNC Symbol;Acc:HGNC:
8	FAM98A	−1.16	3e−07	3e−05	49 x 1	family with sequence similarity 98, member A [Source:HGNC
9	LMCD1	1.14	9e−07	3e−05	47 x 1	LIM and cysteine−rich domains 1 [Source:HGNC Symbol;Acc
10	RAB31	−1.09	2e−06	3e−05	50 x 3	RAB31, member RAS oncogene family [Source:HGNC Symb
11	CTHRC1	1.1	2e−06	3e−05	49 x 1	collagen triple helix repeat containing 1 [Source:HGNC Symb
12	PLSCR4	1.09	2e−06	3e−05	49 x 1	phospholipid scramblase 4 [Source:HGNC Symbol;Acc:HGN
13	PTPRM	−1.08	3e−06	1e−04	50 x 1	protein tyrosine phosphatase, receptor type, M [Source:HGN
14	MT2A	−1.06	4e−06	4e−04	50 x 3	metallothionein 2A [Source:HGNC Symbol;Acc:HGNC:7406]
15	FAM46A	−1.02	1e−05	4e−04	47 x 1	family with sequence similarity 46, member A [Source:HGNC
16	MAP4K4	−1	2e−05	8e−04	50 x 5	mitogen−activated protein kinase kinase kinase kinase 4 [So
17	STAM	−0.87	3e−05	8e−04	50 x 3	signal transducing adaptor molecule (SH3 domain and ITAM
18	TM7SF3	−0.95	4e−05	8e−04	50 x 5	transmembrane 7 superfamily member 3 [Source:HGNC Sym
19	TMEM67	0.94	5e−05	2e−03	50 x 1	transmembrane protein 67 [Source:HGNC Symbol;Acc:HGN
20	FSTL1	−0.92	7e−05	2e−03	50 x 1	follistatin−like 1 [Source:HGNC Symbol;Acc:HGNC:3972]

p−values