E12_mel

Global Summary

%DE = 0.22

genes with fdr < 0.2 = 2767 (1649 + / 1118 −)

genes with fdr < 0.1 = 2283 (1374 + / 909 −)

genes with fdr < 0.05 = 1919 (1160 + / 759 −)

genes with fdr < 0.01 = 1160 (713 + / 447 −)

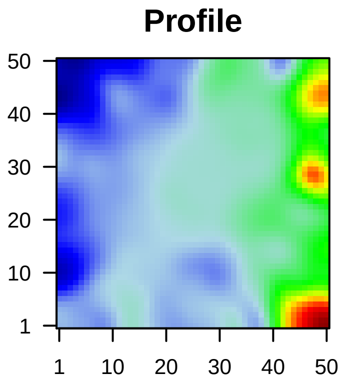
genes in genesets = 14839

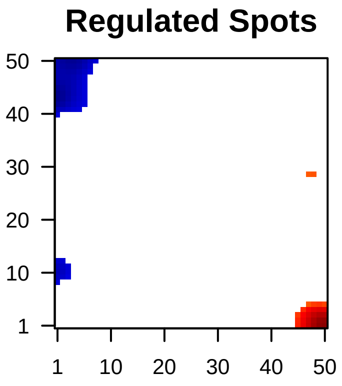
<FC> = 0

<shrinkage−t> = −0.03

<p−value> = 0.07

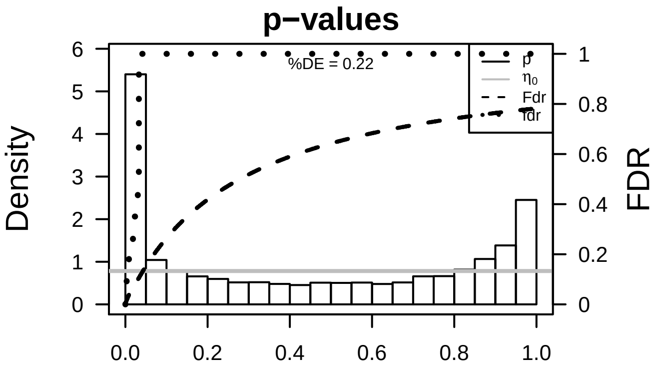
<fdr> = 0.78





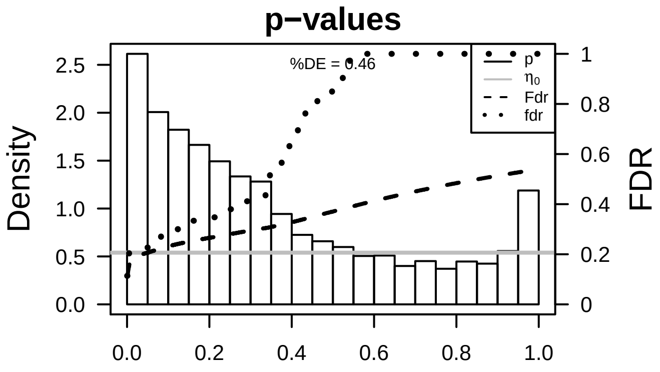
Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	ABCB5	−1.5	2e−16	9e−14	1 x 43	ATP−binding cassette, sub−family B (MDR/TAP), member 5 [S
2	ARPC1A	−1.44	2e−16	9e−14	6 x 34	actin related protein 2/3 complex, subunit 1A, 41kDa [Source:
3	ATP6V0A1	−1.64	2e−16	9e−14	1 x 10	ATPase, H+ transporting, lysosomal V0 subunit a1 [Source:H
4	BACE2	−1.78	2e−16	9e−14	1 x 42	beta−site APP−cleaving enzyme 2 [Source:HGNC Symbol;Ac
5	C14orf119	−1.65	2e−16	9e−14	40 x 50	chromosome 14 open reading frame 119 [Source:HGNC Sym
6	CAPN3	−2.09	2e−16	9e−14	1 x 43	calpain 3, (p94) [Source:HGNC Symbol;Acc:HGNC:1480]
7	CDK2	−2.1	2e−16	9e−14	1 x 43	cyclin−dependent kinase 2 [Source:HGNC Symbol;Acc:HGN
8	CDKN3	−1.65	2e−16	9e−14	6 x 50	cyclin−dependent kinase inhibitor 3 [Source:HGNC Symbol;A
9	CHCHD6	−1.57	2e−16	9e−14	1 x 43	coiled−coil−helix−coiled−coil−helix domain containing 6 [Sour
10	CITED1	−1.54	2e−16	9e−14	1 x 41	Cbp/p300−interacting transactivator, with Glu/Asp−rich carbo
11	CMTM6	−1.65	2e−16	9e−14	7 x 43	CKLF−like MARVEL transmembrane domain containing 6 [Sc
12	CNOT1	−1.55	2e−16	9e−14	15 x 50	CCR4−NOT transcription complex, subunit 1 [Source:HGNC
13	COMMD4	−1.59	2e−16	9e−14	11 x 50	COMM domain containing 4 [Source:HGNC Symbol;Acc:HGN
14	CRYAB	1.33	2e−16	9e−14	50 x 1	crystallin, alpha B [Source:HGNC Symbol;Acc:HGNC:2389]
15	DDX39A	−1.8	2e−16	9e−14	5 x 46	DEAD (Asp−Glu−Ala−Asp) box polypeptide 39A [Source:HGN
16	DKK1	2.22	2e−16	9e−14	50 x 1	dickkopf WNT signaling pathway inhibitor 1 [Source:HGNC Sy
17	ERGIC2	−1.79	2e−16	9e−14	6 x 44	ERGIC and golgi 2 [Source:HGNC Symbol;Acc:HGNC:30208
18	EXOC3	−0.83	2e−16	9e−14	1 x 42	exocyst complex component 3 [Source:HGNC Symbol;Acc:H
19	FN1	2.23	2e−16	9e−14	50 x 1	fibronectin 1 [Source:HGNC Symbol;Acc:HGNC:3778]
20	HSD17B4	−1.63	2e−16	9e−14	11 x 50	hydroxysteroid (17−beta) dehydrogenase 4 [Source:HGNC Sy



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	8.49	5e−04	385	GSEA C2	REN_ALVEOLAR_RHABDOMYOSARCOMA_DN
2	6.53	1e−03	302	GSEA C2	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_DN
3	6.48	1e−03	400	GSEA C2	HELLER_HDAC_TARGETS_SILENCED_BY_METHYLATION_UP
4	6.35	2e−03	131	Colon Cancer	Marisa_CRC−cluster−a
5	6.17	2e−03	63	GSEA C2	RAGHAVACHARI_PLATELET_SPECIFIC_GENES
6	6.03	2e−03	472	GSEA C2	DUTERTRE_ESTRADIOL_RESPONSE_24HR_DN
7	5.7	2e−03	283	GSEA C2	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
8	5.52	3e−03	54	GSEA C2	VERRECCHIA_EARLY_RESPONSE_TO_TGFB1
9	5.18	3e−03	166	GSEA C2	RODWELL_AGING_KIDNEY_NO_BLOOD_UP
10	5.14	3e−03	361	GSEA C2	BERENJENO_TRANSFORMED_BY_RHOA_DN
11	5.1	3e−03	36	GSEA C2	LIANG_SILENCED_BY_METHYLATION_2
12	5.06	3e−03	168	HM	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
13	4.9	4e−03	594	GSEA C2	WONG_ADULT_TISSUE_STEM_MODULE
14	4.79	4e−03	14	BP	nucleotide metabolic process
15	4.77	4e−03	56	GSEA C2	AMIT_EGF_RESPONSE_240_HELA
16	4.75	4e−03	616	GSEA C2	NABA_MATRISOME
17	4.75	4e−03	164	GSEA C2	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_HSC_UP
18	4.74	4e−03	32	Glio	Colman_survival_associated
19	4.61	5e−03	68	GSEA C2	FRIDMAN_SENESCENCE_UP
20	4.58	5e−03	3132	CC	extracellular region
Underexpressed					
1	−10.49	2e−04	1192	GSEA C2	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
2	−10.38	2e−04	142	Glio	WILLSCHER_GBM_Verhaak−CL_up (C)
3	−9.85	3e−04	550	GSEA C2	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
4	−9.83	3e−04	50	GSEA C2	ISHIDA_E2F_TARGETS
5	−9.79	1e−01	16	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
6	−9.79	3e−04	139	GSEA C2	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
7	−9.77	3e−04	81	GSEA C2	GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
8	−9.74	3e−04	305	GSEA C2	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
9	−9.49	3e−04	327	GSEA C2	BLUM_RESPONSE_TO_SALIRASIB_DN
10	−9.47	3e−04	267	GSEA C2	ZHANG_TLX_TARGETS_60HR_DN
11	−9.13	4e−04	197	HM	HALLMARK_E2F_TARGETS
12	−9.12	4e−04	242	GSEA C2	KOBAYASHI_EGFR_SIGNALING_24HR_DN
13	−8.88	4e−04	18	BP	melanocyte differentiation
14	−8.69	5e−04	1251	GSEA C2	DODD_NASOPHARYNGEAL_CARCINOMA_DN
15	−8.69	5e−04	110	GSEA C2	WHITEFORD_PEDIATRIC_CANCER_MARKERS
16	−8.58	5e−04	390	GSEA C2	PUJANA_BRCA2_PCC_NETWORK
17	−8.54	5e−04	162	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP
18	−8.4	5e−04	145	GSEA C2	CHANG_CYCLING_GENES
19	−8.36	5e−04	54	GSEA C2	KANG_DOXORUBICIN_RESISTANCE_UP
20	−8.29	6e−04	96	GSEA C2	CROONQUIST_IL6_DEPRIVATION_DN



E12_mel

Local Summary

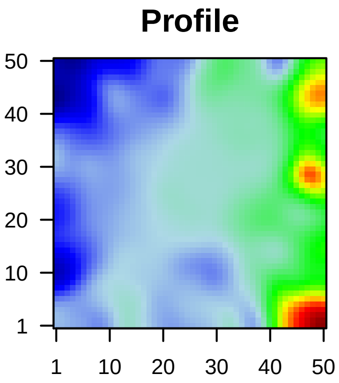
%DE = 0.89
metagenes = 27
genes = 387
genes in genesets = 387

genes with fdr < 0.1 = 296 (282 + / 14 −)
genes with fdr < 0.05 = 271 (264 + / 7 −)
genes with fdr < 0.01 = 230 (226 + / 4 −)

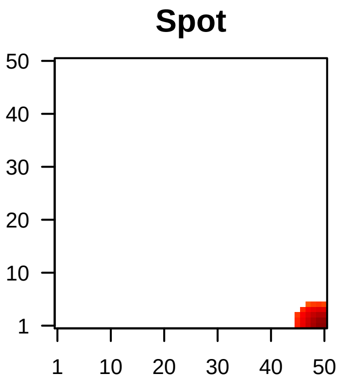
<r> metagenes = 0.96
<r> genes = 0.18

<FC> = 0.71
<shrinkage−t> = 11.32
<p−value> = 0
<fdr> = 0.33

Profile



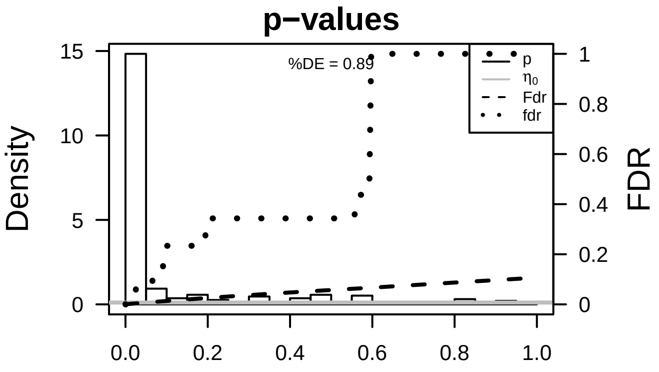
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	CRYAB	1.33	2e−16	2e−15	50 x 1	crystallin, alpha B [Source:HGNC Symbol;Acc:HGNC:2389]
2	DKK1	2.22	2e−16	2e−15	50 x 1	dickkopf WNT signaling pathway inhibitor 1 [Source:HGNC S
3	FN1	2.23	2e−16	2e−15	50 x 1	fibronectin 1 [Source:HGNC Symbol;Acc:HGNC:3778]
4	MYL12A	0.82	2e−16	2e−15	48 x 3	myosin, light chain 12A, regulatory, non−sarcomeric [Source:
5	MYL12B	0.9	2e−16	2e−15	48 x 4	myosin, light chain 12B, regulatory [Source:HGNC Symbol;A
6	S100A10	1.95	4e−15	8e−13	50 x 4	S100 calcium binding protein A10 [Source:HGNC Symbol;Ac
7	RGS2	1.88	4e−14	8e−13	49 x 1	regulator of G−protein signaling 2 [Source:HGNC Symbol;Ac
8	RND3	1.87	4e−14	1e−12	50 x 1	Rho family GTPase 3 [Source:HGNC Symbol;Acc:HGNC:671
9	HIST1H3D	1.85	9e−14	1e−12	50 x 1	histone cluster 1, H3d [Source:HGNC Symbol;Acc:HGNC:47
10	S100A4	1.85	9e−14	2e−11	50 x 1	S100 calcium binding protein A4 [Source:HGNC Symbol;Acc:
11	VTN	1.78	8e−13	2e−11	50 x 1	vitronectin [Source:HGNC Symbol;Acc:HGNC:12724]
12	TFPI	1.78	8e−13	3e−11	50 x 1	tissue factor pathway inhibitor (lipoprotein−associated coagul
13	MATN2	1.73	3e−12	3e−11	50 x 1	matrilin 2 [Source:HGNC Symbol;Acc:HGNC:6908]
14	HIST1H2AC	1.73	3e−12	3e−11	50 x 1	histone cluster 1, H2ac [Source:HGNC Symbol;Acc:HGNC:47
15	TXNRD1	0.71	4e−12	3e−11	48 x 4	thioredoxin reductase 1 [Source:HGNC Symbol;Acc:HGNC:1
16	NT5E	1.72	4e−12	3e−11	50 x 1	5'−nucleotidase, ecto (CD73) [Source:HGNC Symbol;Acc:HG
17	SPARC	0.86	4e−12	3e−11	50 x 2	secreted protein, acidic, cysteine−rich (osteonectin) [Source:
18	S100A16	1.72	5e−12	8e−11	50 x 3	S100 calcium binding protein A16 [Source:HGNC Symbol;Ac
19	PRKG1	1.7	7e−12	3e−10	47 x 4	protein kinase, cGMP−dependent, type I [Source:HGNC Sym
20	HIST1H2BF	1.66	2e−11	3e−10	46 x 4	histone cluster 1, H2bf [Source:HGNC Symbol;Acc:HGNC:47

p−values



E12_mel

Local Summary

%DE = 0.98

metagenes = 2

genes = 50

genes in genesets = 50

genes with fdr < 0.1 = 48 (48 + / 0 −)

genes with fdr < 0.05 = 48 (48 + / 0 −)

genes with fdr < 0.01 = 48 (48 + / 0 −)

<r> metagenes = 1

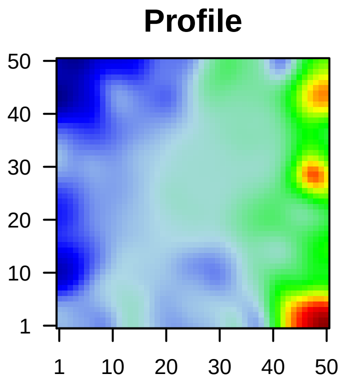
<r> genes = 0.39

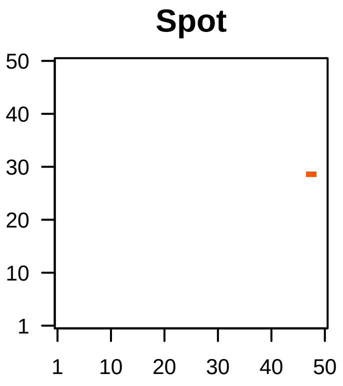
<FC> = 1.14

<shrinkage−t> = 17.35

<p−value> = 0

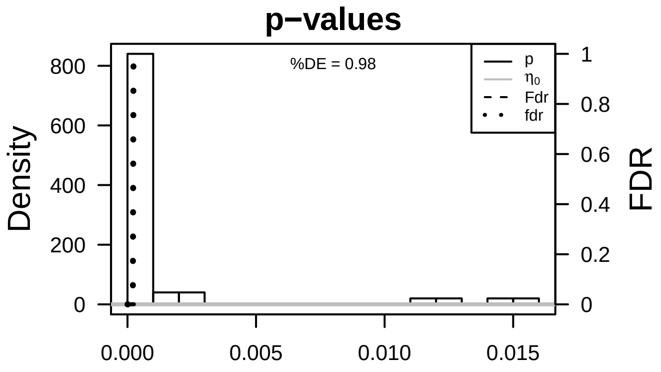
<fdr> = 0.02


Profile


Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	DES	1.82	2e−13	1e−11	47 x 29	desmin [Source:HGNC Symbol;Acc:HGNC:2770]
2	CYP2J2	1.68	1e−11	1e−11	47 x 29	cytochrome P450, family 2, subfamily J, polypeptide 2 [Sourc
3	PLAT	1.66	2e−11	2e−10	47 x 29	plasminogen activator, tissue [Source:HGNC Symbol;Acc:HG
4	FGGY	1.58	2e−10	2e−10	47 x 29	FGGY carbohydrate kinase domain containing [Source:HGN
5	ZNF540	1.55	4e−10	2e−10	48 x 29	zinc finger protein 540 [Source:HGNC Symbol;Acc:HGNC:25
6	CCNI2	1.54	5e−10	2e−09	47 x 29	cyclin I family, member 2 [Source:HGNC Symbol;Acc:HGNC:
7	SLC7A7	1.48	3e−09	2e−09	47 x 29	solute carrier family 7 (amino acid transporter light chain, y+L
8	FAM20C	1.45	5e−09	4e−09	47 x 29	family with sequence similarity 20, member C [Source:HGNC
9	GLYAT	1.43	9e−09	9e−09	47 x 29	glycine−N−acyltransferase [Source:HGNC Symbol;Acc:HGN
10	CD160	1.4	2e−08	2e−08	48 x 29	CD160 molecule [Source:HGNC Symbol;Acc:HGNC:17013]
11	FAM65C	1.37	4e−08	4e−08	47 x 29	family with sequence similarity 65, member C [Source:HGNC
12	DUSP19	1.33	8e−08	4e−08	48 x 29	dual specificity phosphatase 19 [Source:HGNC Symbol;Acc:
13	MAGEC2	1.32	1e−07	4e−08	47 x 29	melanoma antigen family C2 [Source:HGNC Symbol;Acc:HG
14	FAM71F1	1.3	1e−07	5e−08	47 x 29	family with sequence similarity 71, member F1 [Source:HGN
15	DNAH5	1.29	2e−07	7e−08	47 x 29	dynein, axonemal, heavy chain 5 [Source:HGNC Symbol;Acc
16	C19orf73	1.28	3e−07	7e−08	47 x 29	chromosome 19 open reading frame 73 [Source:HGNC Sym
17	TSPYL2	1.26	4e−07	7e−08	47 x 29	TSPY−like 2 [Source:HGNC Symbol;Acc:HGNC:24358]
18	JAM2	1.26	4e−07	1e−07	48 x 29	junctional adhesion molecule 2 [Source:HGNC Symbol;Acc:H
19	DFFB	1.24	6e−07	1e−07	47 x 29	DNA fragmentation factor, 40kDa, beta polypeptide (caspase
20	XAGE3	1.22	9e−07	1e−07	47 x 29	X antigen family, member 3 [Source:HGNC Symbol;Acc:HGN


p−values

E12_mel

Local Summary

%DE = 0.86

metagenes = 12

genes = 198

genes in genesets = 197

genes with fdr < 0.1 = 134 (17 + / 117 −)

genes with fdr < 0.05 = 102 (13 + / 89 −)

genes with fdr < 0.01 = 70 (8 + / 62 −)

<r> metagenes = 0.97

<r> genes = 0.15

<FC> = −0.43

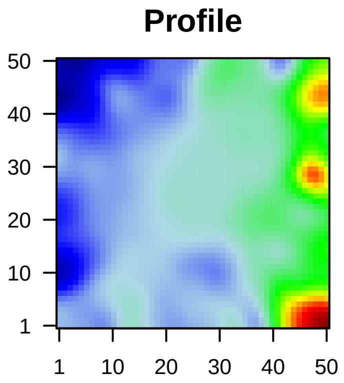
<shrinkage−t> = −7.37

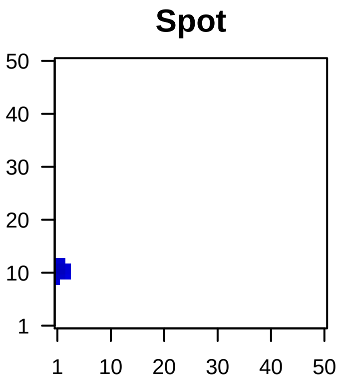
<p−value> = 0

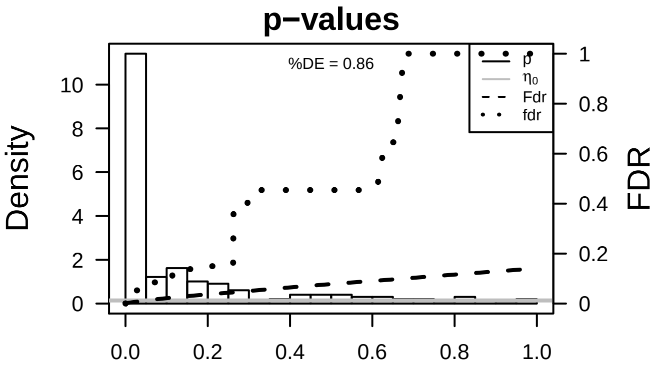
<fdr> = 0.53

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	ATP6V0A1	−1.64	2e−16	2e−15	1 x 10	ATPase, H+ transporting, lysosomal V0 subunit a1 [Source:H
2	ID2	−1.4	2e−16	2e−15	1 x 13	inhibitor of DNA binding 2, dominant negative helix−loop−heli
3	MYO5A	−1.51	2e−16	2e−15	1 x 13	myosin VA (heavy chain 12, myoxin) [Source:HGNC Symbol;
4	NAV2	−1.58	7e−16	1e−12	1 x 12	neuron navigator 2 [Source:HGNC Symbol;Acc:HGNC:15997
5	OCA2	−1.47	8e−14	1e−12	1 x 12	oculocutaneous albinism II [Source:HGNC Symbol;Acc:HGN
6	RAB27A	−1.52	8e−14	1e−12	1 x 11	RAB27A, member RAS oncogene family [Source:HGNC Sym
7	AZI2	−1.49	1e−13	1e−11	1 x 13	5−azacytidine induced 2 [Source:HGNC Symbol;Acc:HGNC:
8	HMGCR	−1.36	5e−13	7e−11	2 x 11	3−hydroxy−3−methylglutaryl−CoA reductase [Source:HGNC
9	EDNRB	−1.37	3e−12	7e−11	1 x 11	endothelin receptor type B [Source:HGNC Symbol;Acc:HGN
10	PIK3CB	−1.46	6e−12	8e−11	1 x 11	phosphatidylinositol−4,5−bisphosphate 3−kinase, catalytic su
11	OSBPL2	−1.45	9e−12	3e−10	2 x 13	oxysterol binding protein−like 2 [Source:HGNC Symbol;Acc:H
12	SEMA6A	−0.87	2e−11	1e−08	1 x 11	sema domain, transmembrane domain (TM), and cytoplasmi
13	CHMP2B	−1.07	1e−09	1e−08	3 x 10	charged multivesicular body protein 2B [Source:HGNC Symb
14	PPARGC1A	−1.35	1e−09	1e−07	1 x 10	peroxisome proliferator−activated receptor gamma, coactivat
15	SNAI2	−1.31	7e−09	1e−07	1 x 11	snail family zinc finger 2 [Source:HGNC Symbol;Acc:HGNC:1
16	KLHL24	−1.3	1e−08	1e−06	1 x 11	kelch−like family member 24 [Source:HGNC Symbol;Acc:HG
17	WDR48	−1.25	5e−08	6e−05	1 x 9	WD repeat domain 48 [Source:HGNC Symbol;Acc:HGNC:30
18	ATP6V1D	−0.57	2e−06	1e−04	1 x 11	ATPase, H+ transporting, lysosomal 34kDa, V1 subunit D [So
19	GPRC5B	−1.04	8e−06	1e−04	1 x 12	G protein−coupled receptor, class C, group 5, member B [Sou
20	SERINC5	−1.06	2e−05	1e−04	1 x 11	serine incorporator 5 [Source:HGNC Symbol;Acc:HGNC:188







E12_mel

Local Summary

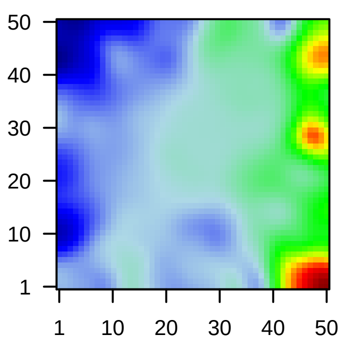
%DE = 0.77
metagenes = 64
genes = 837
genes in genesets = 833

genes with fdr < 0.1 = 453 (76 + / 377 −)
genes with fdr < 0.05 = 385 (53 + / 332 −)
genes with fdr < 0.01 = 255 (24 + / 231 −)

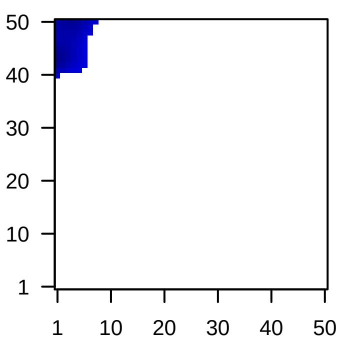
<r> metagenes = 0.77
<r> genes = 0.15

<FC> = −0.35
<shrinkage−t> = −6.28
<p−value> = 0
<fdr> = 0.55

Profile



Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	ABCB5	−1.5	2e−16	3e−15	1 x 43	ATP−binding cassette, sub−family B (MDR/TAP), member 5 [
2	BACE2	−1.78	2e−16	3e−15	1 x 42	beta−site APP−cleaving enzyme 2 [Source:HGNC Symbol;A
3	CAPN3	−2.09	2e−16	3e−15	1 x 43	calpain 3, (p94) [Source:HGNC Symbol;Acc:HGNC:1480]
4	CDK2	−2.1	2e−16	3e−15	1 x 43	cyclin−dependent kinase 2 [Source:HGNC Symbol;Acc:HGN
5	CDKN3	−1.65	2e−16	3e−15	6 x 50	cyclin−dependent kinase inhibitor 3 [Source:HGNC Symbol;A
6	CHCHD6	−1.57	2e−16	3e−15	1 x 43	coiled−coil−helix−coiled−coil−helix domain containing 6 [Sou
7	CITED1	−1.54	2e−16	3e−15	1 x 41	Cbp/p300−interacting transactivator, with Glu/Asp−rich carbo
8	DDX39A	−1.8	2e−16	3e−15	5 x 46	DEAD (Asp−Glu−Ala−Asp) box polypeptide 39A [Source:HG
9	ERGIC2	−1.79	2e−16	3e−15	6 x 44	ERGIC and golgi 2 [Source:HGNC Symbol;Acc:HGNC:30208
10	EXOC3	−0.83	2e−16	3e−15	1 x 42	exocyst complex component 3 [Source:HGNC Symbol;Acc:H
11	MBP	−0.9	2e−16	3e−15	1 x 42	myelin basic protein [Source:HGNC Symbol;Acc:HGNC:6925
12	MITF	−1.67	2e−16	3e−15	1 x 41	microphthalmia−associated transcription factor [Source:HGN
13	MLIP	−1.7	2e−16	3e−15	3 x 44	muscular LMNA−interacting protein [Source:HGNC Symbol;A
14	TRPM1	−1.63	2e−16	3e−15	1 x 42	transient receptor potential cation channel, subfamily M, mem
15	NARS2	−0.78	5e−15	5e−13	1 x 42	asparaginyl−tRNA synthetase 2, mitochondrial (putative) [Sou
16	PGM3	−1.29	6e−15	4e−12	5 x 45	phosphoglucomutase 3 [Source:HGNC Symbol;Acc:HGNC:8
17	UCP2	−1.43	3e−14	6e−12	2 x 46	uncoupling protein 2 (mitochondrial, proton carrier) [Source:H
18	ARHGAP8	−1.26	6e−14	2e−10	1 x 43	Rho GTPase activating protein 8 [Source:HGNC Symbol;Acc
19	RNF14	−1.3	8e−13	2e−10	1 x 43	ring finger protein 14 [Source:HGNC Symbol;Acc:HGNC:100
20	TK1	−1.4	2e−12	3e−10	4 x 50	thymidine kinase 1, soluble [Source:HGNC Symbol;Acc:HGN

p−values