E11_mel

Global Summary

%DE = 0.23

genes with fdr < 0.2 = 2890 (1661 + / 1229 −)

genes with fdr < 0.1 = 2524 (1454 + / 1070 −)

genes with fdr < 0.05 = 2086 (1222 + / 864 −)

genes with fdr < 0.01 = 1371 (814 + / 557 −)

genes in genesets = 14839

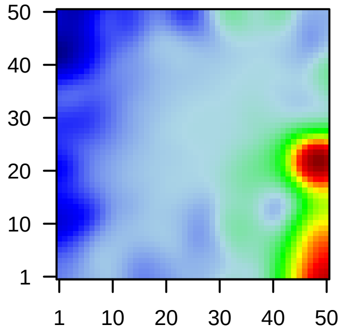
<FC> = 0

<shrinkage−t> = −0.15

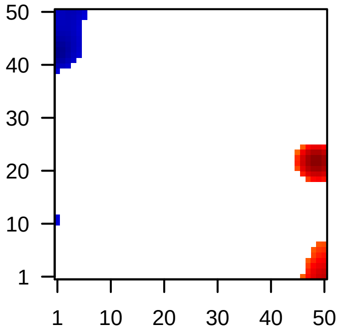
<p−value> = 0.06

<fdr> = 0.77

Profile



Regulated Spots



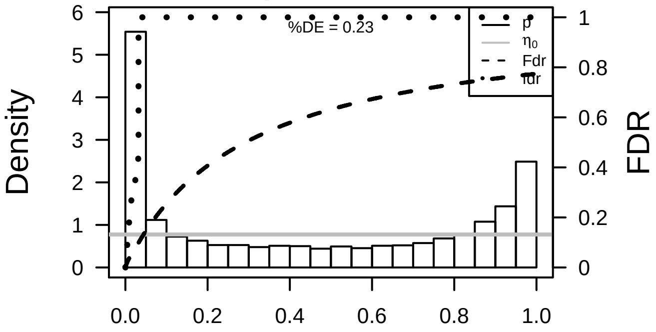
Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	ACTL6A	−1.88	2e−16	3e−14	4 x 50	actin−like 6A [Source:HGNC Symbol;Acc:HGNC:24124]
2	ANXA1	2.44	2e−16	3e−14	50 x 1	annexin A1 [Source:HGNC Symbol;Acc:HGNC:533]
3	ATP1A1	−1.65	2e−16	3e−14	1 x 42	ATPase, Na+/K+ transporting, alpha 1 polypeptide [Source:H
4	ATP1B3	−2.05	2e−16	3e−14	1 x 21	ATPase, Na+/K+ transporting, beta 3 polypeptide [Source:HG
5	ATP6V0A1	−1.64	2e−16	3e−14	1 x 10	ATPase, H+ transporting, lysosomal V0 subunit a1 [Source:H
6	ATP6V1H	−1.84	2e−16	3e−14	5 x 44	ATPase, H+ transporting, lysosomal 50/57kDa, V1 subunit H
7	AVPI1	−1.61	2e−16	3e−14	49 x 50	arginine vasopressin−induced 1 [Source:HGNC Symbol;Acc:
8	C6orf1	−1.63	2e−16	3e−14	1 x 39	chromosome 6 open reading frame 1 [Source:HGNC Symbol
9	CALD1	1.71	2e−16	3e−14	50 x 1	caldesmon 1 [Source:HGNC Symbol;Acc:HGNC:1441]
10	CAPN3	−1.86	2e−16	3e−14	1 x 43	calpain 3, (p94) [Source:HGNC Symbol;Acc:HGNC:1480]
11	CDK2	−1.65	2e−16	3e−14	1 x 43	cyclin−dependent kinase 2 [Source:HGNC Symbol;Acc:HGN
12	CDK4	−0.93	2e−16	3e−14	3 x 44	cyclin−dependent kinase 4 [Source:HGNC Symbol;Acc:HGN
13	CKS2	−1.66	2e−16	3e−14	5 x 50	CDC28 protein kinase regulatory subunit 2 [Source:HGNC S
14	CNN3	0.94	2e−16	3e−14	47 x 1	calponin 3, acidic [Source:HGNC Symbol;Acc:HGNC:2157]
15	COPZ1	−1.68	2e−16	3e−14	46 x 45	coatomer protein complex, subunit zeta 1 [Source:HGNC Syn
16	DCT	−1.25	2e−16	3e−14	1 x 11	dopachrome tautomerase [Source:HGNC Symbol;Acc:HGNC
17	DKC1	−1.67	2e−16	3e−14	7 x 43	dyskeratosis congenita 1, dyskerin [Source:HGNC Symbol;Ac
18	DKK1	2.85	2e−16	3e−14	50 x 1	dickkopf WNT signaling pathway inhibitor 1 [Source:HGNC S
19	ELP5	−1.64	2e−16	3e−14	3 x 44	elongator acetyltransferase complex subunit 5 [Source:HGNC
20	ERAL1	−1.53	2e−16	3e−14	46 x 44	Era−like 12S mitochondrial rRNA chaperone 1 [Source:HGN

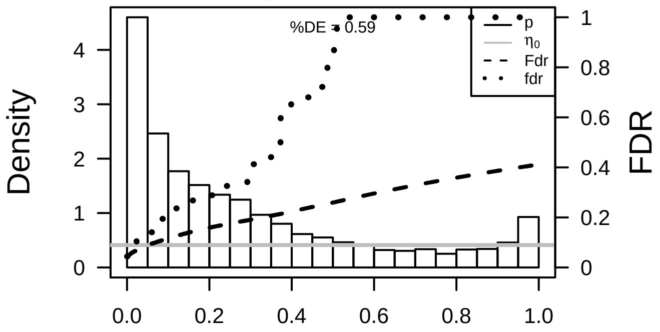
Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	10.89	2e−04	472	GSEA C2	DUTERTRE_ESTRADIOL_RESPONSE_24HR_DN
2	10.75	2e−04	286	GSEA C2	PASINI_SUZ12_TARGETS_DN
3	9.47	3e−04	594	GSEA C2	WONG_ADULT_TISSUE_STEM_MODULE
4	8.44	5e−04	302	GSEA C2	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_DN
5	8.42	5e−04	168	HM	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
6	8.4	5e−04	195	GSEA C2	SENESE_HDAC1_AND_HDAC2_TARGETS_DN
7	8.02	6e−04	410	GSEA C2	LIM_MAMMARY_STEM_CELL_UP
8	7.81	7e−04	55	GSEA C2	AMIT_SERUM_RESPONSE_60_MCF10A
9	7.76	7e−04	212	Lymphoma	LENZ_Stromal signature 1
10	7.45	8e−04	3897	Colon Cancer	Quies1_Colon
11	7.44	8e−04	2188	Lymphoma	HOPP_Poised_promoter
12	7.39	8e−04	749	GSEA C2	CUI_TCF21_TARGETS_2_DN
13	7.35	9e−04	71	GSEA C2	RODRIGUES_THYROID_CARCINOMA_DN
14	7.34	9e−04	385	GSEA C2	REN_ALVEOLAR_RHABDOMYOSARCOMA_DN
15	7.34	9e−04	3396	Lymphoma	HOPP_Repressed
16	7.32	9e−04	161	GSEA C2	ELVIDGE_HYPOXIA_UP
17	7.31	9e−04	283	GSEA C2	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
18	7.17	1e−03	618	GSEA C2	GOZGIT_ESR1_TARGETS_DN
19	7.1	1e−03	401	GSEA C2	CHARAFE_BREAST_CANCER_LUMINAL_VS_BASAL_DN
20	6.98	1e−03	833	GSEA C2	DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
Underexpressed					
1	−11.99	1e−04	1192	GSEA C2	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
2	−11.98	1e−04	305	GSEA C2	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
3	−11.87	1e−04	756	GSEA C2	WEI_MYCN_TARGETS_WITH_E_BOX
4	−11.27	2e−04	142	Glio	WILLSCHER_GBM_Verhaak−CL_up (C)
5	−11.22	2e−04	197	HM	HALLMARK_E2F_TARGETS
6	−11.12	2e−04	562	GSEA C2	CAIRO_HEPATOBLASTOMA_CLASSES_UP
7	−10.96	2e−04	13	BP	melanin biosynthetic process
8	−10.77	2e−04	1460	GSEA C2	PUJANA_BRCA1_PCC_NETWORK
9	−10.68	2e−04	242	GSEA C2	KOBAYASHI_EGFR_SIGNALING_24HR_DN
10	−10.56	2e−04	124	GSEA C2	ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_24HR
11	−10.55	2e−04	50	GSEA C2	ISHIDA_E2F_TARGETS
12	−10.47	1e−02	16	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
13	−10.46	2e−04	724	GSEA C2	PUJANA_CHEK2_PCC_NETWORK
14	−10.43	2e−04	278	GSEA C2	MANALO_HYPOXIA_DN
15	−10.39	2e−04	139	GSEA C2	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
16	−10.06	3e−04	436	GSEA C2	SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
17	−9.61	3e−04	81	GSEA C2	GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
18	−9.4	3e−04	550	GSEA C2	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
19	−9.19	4e−04	405	GSEA C2	MOOTHA_HUMAN_MITODB_6_2002
20	−9.04	4e−04	84	GSEA C2	ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_6HR

p−values



p−values



E11_mel

Local Summary

%DE = 0.91

metagenes = 25

genes = 389

genes in genesets = 388

genes with fdr < 0.1 = 328 (314 + / 14 −)

genes with fdr < 0.05 = 309 (297 + / 12 −)

genes with fdr < 0.01 = 263 (258 + / 5 −)

<r> metagenes = 0.96

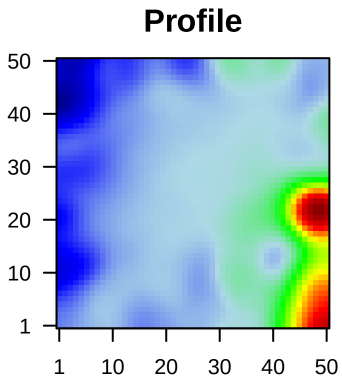
<r> genes = 0.17

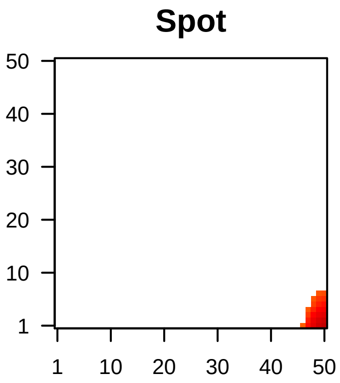
<FC> = 0.89

<shrinkage−t> = 14.3

<p−value> = 0

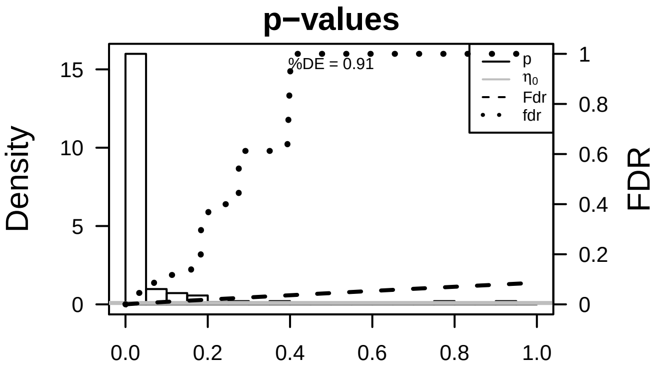
<fdr> = 0.27





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	ANXA1	2.44	2e−16	6e−16	50 x 1	annexin A1 [Source:HGNC Symbol;Acc:HGNC:533]
2	CALD1	1.71	2e−16	6e−16	50 x 1	caldesmon 1 [Source:HGNC Symbol;Acc:HGNC:1441]
3	CNN3	0.94	2e−16	6e−16	47 x 1	calponin 3, acidic [Source:HGNC Symbol;Acc:HGNC:2157]
4	DKK1	2.85	2e−16	6e−16	50 x 1	dickkopf WNT signaling pathway inhibitor 1 [Source:HGNC S
5	HBEGF	2.46	2e−16	6e−16	48 x 1	heparin−binding EGF−like growth factor [Source:HGNC Sym
6	HIST1H3D	2.25	2e−16	6e−16	50 x 1	histone cluster 1, H3d [Source:HGNC Symbol;Acc:HGNC:47
7	LMCD1	2.2	2e−16	6e−16	47 x 1	LIM and cysteine−rich domains 1 [Source:HGNC Symbol;Acc
8	LUM	2.14	2e−16	6e−16	49 x 7	lumican [Source:HGNC Symbol;Acc:HGNC:6724]
9	MYL12A	1.18	2e−16	6e−16	48 x 3	myosin, light chain 12A, regulatory, non−sarcomeric [Source:
10	MYL12B	1.09	2e−16	6e−16	48 x 4	myosin, light chain 12B, regulatory [Source:HGNC Symbol;A
11	NAV3	2.3	2e−16	6e−16	50 x 1	neuron navigator 3 [Source:HGNC Symbol;Acc:HGNC:15998
12	PTPRZ1	2.31	2e−16	6e−16	50 x 1	protein tyrosine phosphatase, receptor−type, Z polypeptide 1
13	CRYAB	1.37	1e−15	2e−14	50 x 1	crystallin, alpha B [Source:HGNC Symbol;Acc:HGNC:2389]
14	CAV1	2.08	2e−15	2e−14	50 x 3	caveolin 1, caveolae protein, 22kDa [Source:HGNC Symbol;
15	MAP2	2.07	2e−15	1e−13	50 x 2	microtubule−associated protein 2 [Source:HGNC Symbol;Acc
16	RAB3IP	2.01	2e−14	1e−13	50 x 3	RAB3A interacting protein [Source:HGNC Symbol;Acc:HGNC
17	S100A16	2.01	2e−14	1e−13	50 x 3	S100 calcium binding protein A16 [Source:HGNC Symbol;Ac
18	CTGF	2.01	2e−14	1e−13	50 x 1	connective tissue growth factor [Source:HGNC Symbol;Acc:H
19	PALLD	2.01	2e−14	1e−12	50 x 4	palladin, cytoskeletal associated protein [Source:HGNC Sym
20	SLIT2	1.96	7e−14	1e−12	50 x 1	slit homolog 2 (Drosophila) [Source:HGNC Symbol;Acc:HGN



E11_mel

Local Summary

%DE = 0.99

metagenes = 38

genes = 335

genes in genesets = 333

genes with fdr < 0.1 = 330 (330 + / 0 −)

genes with fdr < 0.05 = 330 (330 + / 0 −)

genes with fdr < 0.01 = 328 (328 + / 0 −)

<r> metagenes = 0.94

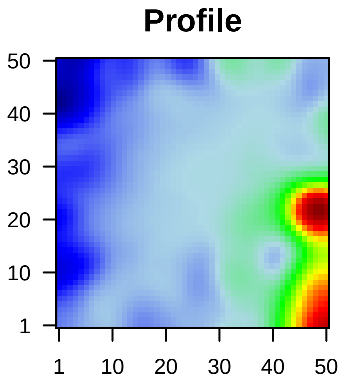
<r> genes = 0.19

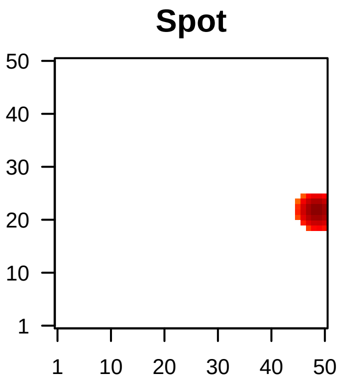
<FC> = 1.17

<shrinkage−t> = 17.82

<p−value> = 0

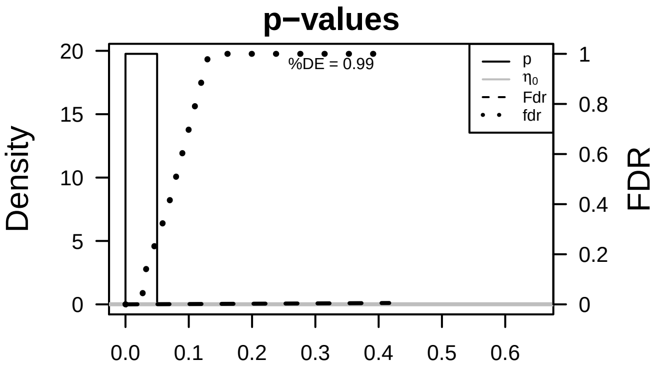
<fdr> = 0.04





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	VCAN	2.39	2e−16	6e−16	49 x 23	versican [Source:HGNC Symbol;Acc:HGNC:2464]
2	SCN2A	1.98	4e−14	7e−14	49 x 23	sodium channel, voltage gated, type II alpha subunit [Source:
3	CLHC1	1.96	8e−14	7e−14	49 x 23	clathrin heavy chain linker domain containing 1 [Source:HGN
4	CEMIP	1.96	8e−14	2e−13	49 x 22	cell migration inducing protein, hyaluronan binding [Source:H
5	OXTR	1.94	1e−13	2e−13	48 x 22	oxytocin receptor [Source:HGNC Symbol;Acc:HGNC:8529]
6	MYL4	1.93	2e−13	2e−13	48 x 23	myosin, light chain 4, alkali; atrial, embryonic [Source:HGNC
7	PHLDB2	1.91	3e−13	7e−13	49 x 23	pleckstrin homology−like domain, family B, member 2 [Source
8	CHL1	1.89	5e−13	8e−13	48 x 23	cell adhesion molecule L1−like [Source:HGNC Symbol;Acc:H
9	CCDC81	1.88	8e−13	2e−12	48 x 23	coiled−coil domain containing 81 [Source:HGNC Symbol;Acc
10	SDC2	1.85	2e−12	2e−12	49 x 23	syndecan 2 [Source:HGNC Symbol;Acc:HGNC:10659]
11	GAD1	1.84	2e−12	1e−11	48 x 22	glutamate decarboxylase 1 (brain, 67kDa) [Source:HGNC Sy
12	NEGR1	1.79	8e−12	1e−11	48 x 23	neuronal growth regulator 1 [Source:HGNC Symbol;Acc:HGN
13	TPCN1	1.78	1e−11	1e−11	48 x 23	two pore segment channel 1 [Source:HGNC Symbol;Acc:HG
14	NFKBIZ	1.76	2e−11	1e−11	49 x 24	nuclear factor of kappa light polypeptide gene enhancer in B−
15	HIST1H2BH	1.76	2e−11	1e−11	49 x 22	histone cluster 1, H2bh [Source:HGNC Symbol;Acc:HGNC:47
16	PLXNB1	1.76	2e−11	1e−11	49 x 21	plexin B1 [Source:HGNC Symbol;Acc:HGNC:9103]
17	KLF7	1.75	2e−11	2e−11	47 x 22	Kruppel−like factor 7 (ubiquitous) [Source:HGNC Symbol;Acc
18	MORC2	1.73	4e−11	2e−11	49 x 24	MORC family CW−type zinc finger 2 [Source:HGNC Symbol;
19	SPRY1	1.73	4e−11	2e−11	48 x 23	sprouty homolog 1, antagonist of FGF signaling (Drosophila)
20	CCNYL1	1.71	6e−11	2e−11	47 x 23	cyclin Y−like 1 [Source:HGNC Symbol;Acc:HGNC:26868]



E11_mel

Local Summary

%DE = 0.88

metagenes = 2

genes = 87

genes in genesets = 86

genes with fdr < 0.1 = 61 (5 + / 56 −)

genes with fdr < 0.05 = 61 (5 + / 56 −)

genes with fdr < 0.01 = 47 (5 + / 42 −)

<r> metagenes = 1

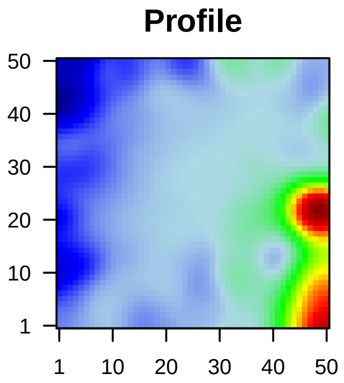
<r> genes = 0.21

<FC> = −0.51

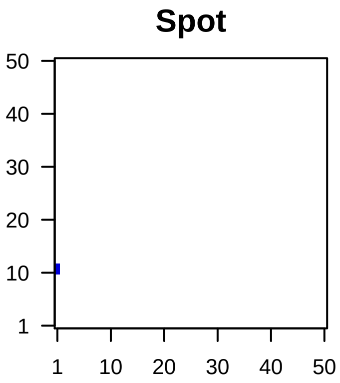
<shrinkage−t> = −8.84

<p−value> = 0

<fdr> = 0.45



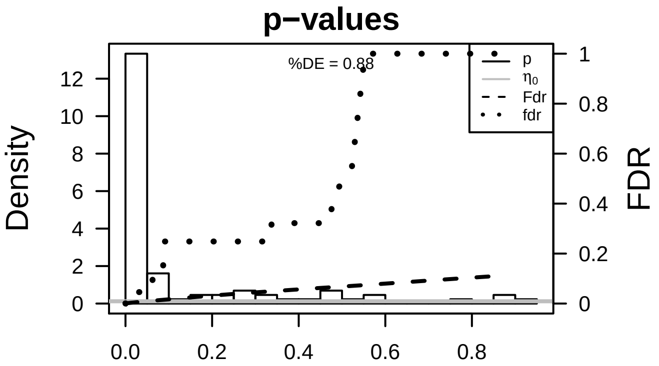
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	DCT	−1.25	2e−16	1e−15	1 x 11	dopachrome tautomerase [Source:HGNC Symbol;Acc:HGNC
2	GPR143	−1.46	2e−16	1e−15	1 x 11	G protein−coupled receptor 143 [Source:HGNC Symbol;Acc:
3	SEMA6A	−1.05	2e−14	6e−11	1 x 11	sema domain, transmembrane domain (TM), and cytoplasmi
4	OCA2	−1.43	6e−12	2e−10	1 x 12	oculocutaneous albinism II [Source:HGNC Symbol;Acc:HGN
5	RAB27A	−1.43	3e−11	4e−09	1 x 11	RAB27A, member RAS oncogene family [Source:HGNC Sym
6	CCDC171	−1.3	4e−10	4e−09	1 x 11	coiled−coil domain containing 171 [Source:HGNC Symbol;Ac
7	SAT1	−0.65	8e−10	8e−08	1 x 11	spermidine/spermine N1−acetyltransferase 1 [Source:HGNC
8	HSPB8	−1.35	8e−09	2e−07	1 x 11	heat shock 22kDa protein 8 [Source:HGNC Symbol;Acc:HGN
9	FAM96A	−0.76	2e−08	2e−07	1 x 11	family with sequence similarity 96, member A [Source:HGNC
10	SNAI2	−1.31	4e−08	2e−05	1 x 11	snail family zinc finger 2 [Source:HGNC Symbol;Acc:HGNC:1
11	RASGRP3	1.25	2e−06	5e−05	1 x 12	RAS guanyl releasing protein 3 (calcium and DAG−regulated)
12	BAIAP2	−1.15	6e−06	1e−04	1 x 12	BAI1−associated protein 2 [Source:HGNC Symbol;Acc:HGN
13	VEPH1	−1.11	2e−05	1e−04	1 x 11	ventricular zone expressed PH domain−containing 1 [Source:
14	TMEM101	−1.09	3e−05	5e−04	1 x 11	transmembrane protein 101 [Source:HGNC Symbol;Acc:HGN
15	C10orf90	−1	1e−04	5e−04	1 x 11	chromosome 10 open reading frame 90 [Source:HGNC Sym
16	SEMA6D	−1	1e−04	5e−04	1 x 11	sema domain, transmembrane domain (TM), and cytoplasmi
17	SOCS6	−0.9	2e−04	9e−04	1 x 11	suppressor of cytokine signaling 6 [Source:HGNC Symbol;Ac
18	SERINC5	−0.93	4e−04	9e−04	1 x 11	serine incorporator 5 [Source:HGNC Symbol;Acc:HGNC:188
19	SORD	−0.93	4e−04	9e−04	1 x 11	sorbitol dehydrogenase [Source:HGNC Symbol;Acc:HGNC:1
20	LONRF1	−0.9	6e−04	9e−04	1 x 12	LON peptidase N−terminal domain and ring finger 1 [Source:



p−values

E11_mel

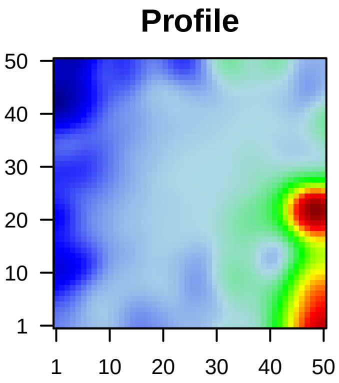
Local Summary

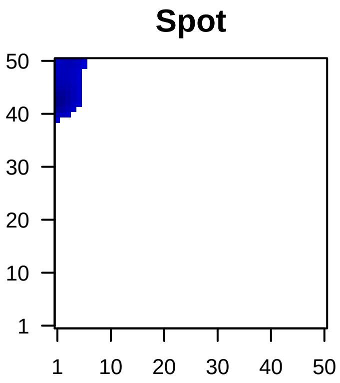
%DE = 0.81
metagenes = 55
genes = 764
genes in genesets = 761

genes with fdr < 0.1 = 509 (64 + / 445 −)
genes with fdr < 0.05 = 436 (53 + / 383 −)
genes with fdr < 0.01 = 309 (31 + / 278 −)

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

<FC> = −0.49
<shrinkage−t> = −9.1
<p−value> = 0
<fdr> = 0.45





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	ACTL6A	−1.88	2e−16	1e−15	4 x 50	actin−like 6A [Source:HGNC Symbol;Acc:HGNC:24124]
2	ATP1A1	−1.65	2e−16	1e−15	1 x 42	ATPase, Na+/K+ transporting, alpha 1 polypeptide [Source:H
3	ATP6V1H	−1.84	2e−16	1e−15	5 x 44	ATPase, H+ transporting, lysosomal 50/57kDa, V1 subunit H
4	C6orf1	−1.63	2e−16	1e−15	1 x 39	chromosome 6 open reading frame 1 [Source:HGNC Symbol
5	CAPN3	−1.86	2e−16	1e−15	1 x 43	calpain 3, (p94) [Source:HGNC Symbol;Acc:HGNC:1480]
6	CDK2	−1.65	2e−16	1e−15	1 x 43	cyclin−dependent kinase 2 [Source:HGNC Symbol;Acc:HGN
7	CDK4	−0.93	2e−16	1e−15	3 x 44	cyclin−dependent kinase 4 [Source:HGNC Symbol;Acc:HGN
8	CKS2	−1.66	2e−16	1e−15	5 x 50	CDC28 protein kinase regulatory subunit 2 [Source:HGNC S
9	ELP5	−1.64	2e−16	1e−15	3 x 44	elongator acetyltransferase complex subunit 5 [Source:HGNC
10	GLRX3	−1.72	2e−16	1e−15	4 x 42	glutaredoxin 3 [Source:HGNC Symbol;Acc:HGNC:15987]
11	GNPDA1	−1.77	2e−16	1e−15	1 x 42	glucosamine−6−phosphate deaminase 1 [Source:HGNC Sy
12	GOT1	−1.63	2e−16	1e−15	1 x 39	glutamic−oxaloacetic transaminase 1, soluble [Source:HGNC
13	HBS1L	−1.89	2e−16	1e−15	3 x 44	HBS1−like translational GTPase [Source:HGNC Symbol;Acc:
14	IDH3A	−2.08	2e−16	1e−15	1 x 42	isocitrate dehydrogenase 3 (NAD+) alpha [Source:HGNC Sy
15	IFRD2	−1.76	2e−16	1e−15	1 x 44	interferon−related developmental regulator 2 [Source:HGNC
16	MLIP	−1.54	2e−16	1e−15	3 x 44	muscular LMNA−interacting protein [Source:HGNC Symbol;
17	MTCH2	−1.29	2e−16	1e−15	2 x 42	mitochondrial carrier 2 [Source:HGNC Symbol;Acc:HGNC:17
18	MTX2	−1.52	2e−16	1e−15	1 x 42	metaxin 2 [Source:HGNC Symbol;Acc:HGNC:7506]
19	NT5DC3	−1.62	2e−16	1e−15	1 x 41	5'−nucleotidase domain containing 3 [Source:HGNC Symbol;
20	PLP1	−1.93	2e−16	1e−15	1 x 42	proteolipid protein 1 [Source:HGNC Symbol;Acc:HGNC:9086