D6_mel

Global Summary

%DE = 0.22

genes with fdr < 0.2 = 2910 (1728 + / 1182 −)

genes with fdr < 0.1 = 2259 (1372 + / 887 −)

genes with fdr < 0.05 = 1904 (1162 + / 742 −)

genes with fdr < 0.01 = 1188 (747 + / 441 −)

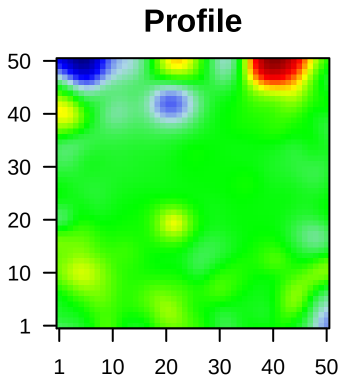
genes in genesets = 14839

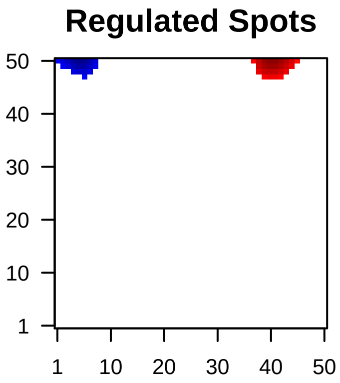
<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.07

<fdr> = 0.78



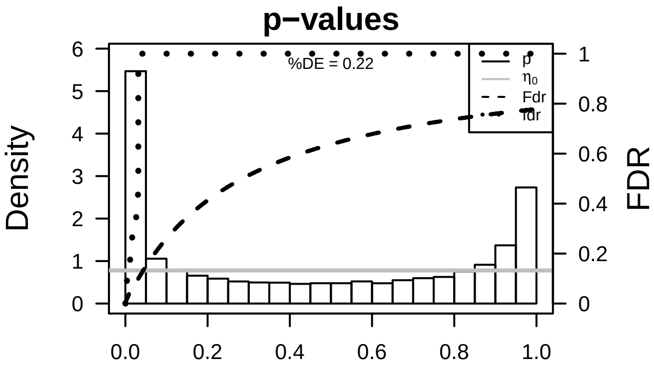


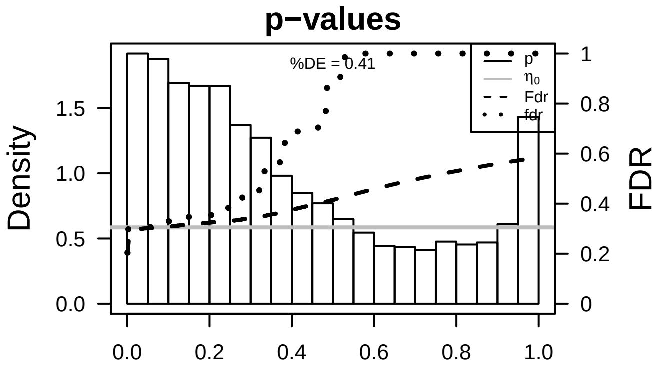
Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	ACTL6A	−1.84	2e−16	1e−13	4 x 50	actin−like 6A [Source:HGNC Symbol;Acc:HGNC:24124]
2	ARHGAP8	−1.54	2e−16	1e−13	1 x 43	Rho GTPase activating protein 8 [Source:HGNC Symbol;Acc:
3	ATP6V1H	−1.39	2e−16	1e−13	5 x 44	ATPase, H+ transporting, lysosomal 50/57kDa, V1 subunit H
4	C1orf198	−1.56	2e−16	1e−13	49 x 1	chromosome 1 open reading frame 198 [Source:HGNC Symb
5	CFL2	−1.64	2e−16	1e−13	50 x 7	cofilin 2 (muscle) [Source:HGNC Symbol;Acc:HGNC:1875]
6	CHD4	−1.47	2e−16	1e−13	21 x 43	chromodomain helicase DNA binding protein 4 [Source:HGN
7	CPNE3	−1.49	2e−16	1e−13	44 x 34	copine III [Source:HGNC Symbol;Acc:HGNC:2316]
8	ECI2	−1.9	2e−16	1e−13	20 x 42	enoyl−CoA delta isomerase 2 [Source:HGNC Symbol;Acc:HG
9	FAM126A	−1.7	2e−16	1e−13	45 x 35	family with sequence similarity 126, member A [Source:HGN
10	GGH	−2.02	2e−16	1e−13	4 x 47	gamma−glutamyl hydrolase (conjugase, folylpolygammagluta
11	ING3	−1.55	2e−16	1e−13	5 x 47	inhibitor of growth family, member 3 [Source:HGNC Symbol;A
12	MSC	−1.62	2e−16	1e−13	32 x 1	musculin [Source:HGNC Symbol;Acc:HGNC:7321]
13	NNT	−1.32	2e−16	1e−13	6 x 47	nicotinamide nucleotide transhydrogenase [Source:HGNC Sy
14	PHF20	−1.33	2e−16	1e−13	22 x 43	PHD finger protein 20 [Source:HGNC Symbol;Acc:HGNC:16
15	PIGY	−1.35	2e−16	1e−13	1 x 20	phosphatidylinositol glycan anchor biosynthesis, class Y [Sou
16	PLK2	−1.65	2e−16	1e−13	50 x 1	polo−like kinase 2 [Source:HGNC Symbol;Acc:HGNC:19699]
17	PLS3	−1.58	2e−16	1e−13	21 x 43	plastin 3 [Source:HGNC Symbol;Acc:HGNC:9091]
18	PMP22	−1.79	2e−16	1e−13	48 x 1	peripheral myelin protein 22 [Source:HGNC Symbol;Acc:HGN
19	POLR2E	−1.41	2e−16	1e−13	5 x 35	polymerase (RNA) II (DNA directed) polypeptide E, 25kDa [S
20	PRDX6	−1.08	2e−16	1e−13	27 x 43	peroxiredoxin 6 [Source:HGNC Symbol;Acc:HGNC:16753]

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	4.7	0.004	15	Cancer	GENTLES_modul1
2	4.41	0.005	17	GSEA C2	KAPOSI_LIVER_CANCER_MET_UP
3	4.31	0.006	235	GSEA C2	BLUM_RESPONSE_TO_SALIRASIB_UP
4	4.29	0.006	739	Colon Cancer	TxEnhG2_Colon
5	4.02	0.007	24	GSEA C2	REACTOME_CYTOSOLIC_TRNA_AMINOACYLATION
6	3.97	0.008	2136	TF	ICGC_GabpPcr2_targets
7	3.78	0.009	16	GSEA C2	TOMIDA_METASTASIS_DN
8	3.77	0.009	784	GSEA C2	BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP
9	3.75	0.009	36	miRNA target	hsa−miR−644
10	3.71	0.009	182	GSEA C2	BILD_MYC_ONCOGENIC_SIGNATURE
11	3.68	0.010	15	CC	RNA polymerase II transcription factor complex
12	3.67	0.010	28	GSEA C2	PID_RAS_PATHWAY
13	3.58	0.011	10	BP	cellular response to antibiotic
14	3.46	0.012	1132	CC	Golgi apparatus
15	3.46	0.012	40	GSEA C2	PENG_GLUCOSE_DEPRIVATION_UP
16	3.45	0.012	44	BP	tRNA aminoacylation for protein translation
17	3.32	0.013	842	GSEA C2	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_UP
18	3.32	0.013	397	MF	transcription factor binding
19	3.32	0.014	179	GSEA C2	SHEPARD_CRUSH_AND_BURN_MUTANT_UP
20	3.29	0.014	60	GSEA C2	PELLICCIOTTA_HDAC_IN_ANTIGEN_PRESENTATION_UP
Underexpressed					
1	−11.07	2e−04	142	Glio	WILLSCHER_GBM_Verhaak−CL_up (C)
2	−10.64	2e−04	550	GSEA C2	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
3	−9.52	3e−04	305	GSEA C2	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
4	−9.2	4e−04	270	GSEA C2	BASAKI_YBX1_TARGETS_UP
5	−8.87	4e−04	139	GSEA C2	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
6	−8.68	5e−04	96	GSEA C2	CROONQUIST_IL6_DEPRIVATION_DN
7	−8.41	5e−04	327	GSEA C2	BLUM_RESPONSE_TO_SALIRASIB_DN
8	−8.39	5e−04	54	GSEA C2	KANG_DOXORUBICIN_RESISTANCE_UP
9	−8.37	5e−04	99	GSEA C2	LEE_EARLY_T_LYMPHOCYTE_UP
10	−8.34	5e−04	72	GSEA C2	CROONQUIST_NRAS_SIGNALING_DN
11	−8.04	6e−04	110	GSEA C2	WHITEFORD_PEDIATRIC_CANCER_MARKERS
12	−7.94	6e−04	390	GSEA C2	PUJANA_BRCA2_PCC_NETWORK
13	−7.78	7e−04	198	GSEA C2	FUJII_YBX1_TARGETS_DN
14	−7.73	7e−04	81	GSEA C2	GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
15	−7.59	5e−02	16	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
16	−7.59	8e−04	84	GSEA C2	MORI_LARGE_PRE_BII_LYMPHOCYTE_UP
17	−7.58	8e−04	162	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP
18	−7.55	8e−04	155	GSEA C2	HOFFMANN_LARGE_TO_SMALL_PRE_BII_LYMPHOCYTE_UP
19	−7.51	8e−04	216	GSEA C2	MARKEY_RB1_ACUTE_LOF_DN
20	−7.37	9e−04	89	GSEA C2	MORI_IMMATURE_B_LYMPHOCYTE_DN





D6_mel

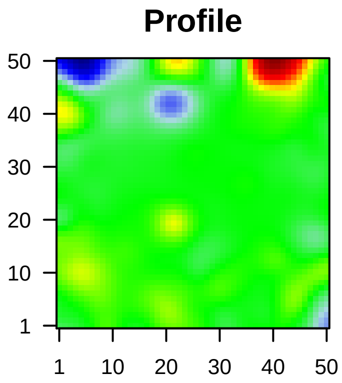
Local Summary

%DE = 0.81
metagenes = 26
genes = 287
genes in genesets = 287

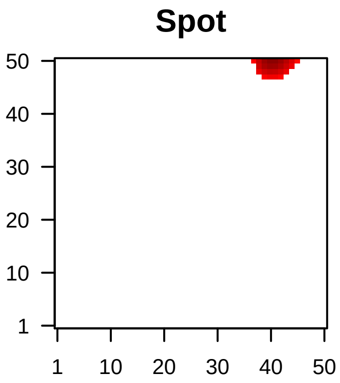
genes with fdr < 0.1 = 186 (165 + / 21 −)
genes with fdr < 0.05 = 177 (157 + / 20 −)
genes with fdr < 0.01 = 128 (120 + / 8 −)

<r> metagenes = 0.88
<r> genes = 0.08

<FC> = 0.45
<shrinkage−t> = 7.32
<p−value> = 0
<fdr> = 0.44



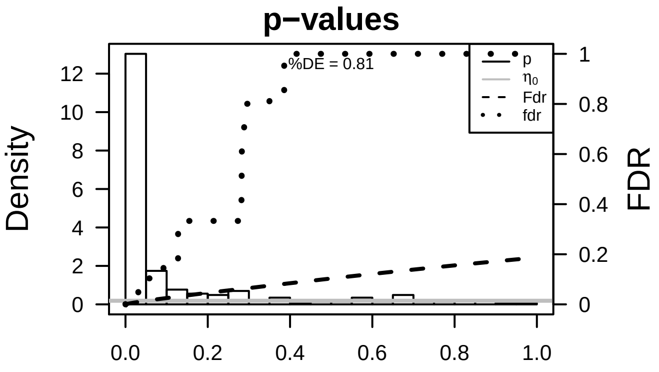
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	GLYCTK	1.67	2e−12	1e−10	37 x 50	glycerate kinase [Source:HGNC Symbol;Acc:HGNC:24247]
2	EML6	1.64	4e−12	6e−10	38 x 50	echinoderm microtubule associated protein like 6 [Source:HG
3	SELL	1.6	1e−11	2e−09	41 x 50	selectin L [Source:HGNC Symbol;Acc:HGNC:10720]
4	PLA2G4A	1.54	7e−11	2e−09	40 x 50	phospholipase A2, group IVA (cytosolic, calcium−dependent)
5	SIL1	1.54	8e−11	5e−08	43 x 50	SIL1 nucleotide exchange factor [Source:HGNC Symbol;Acc:
6	FUCA1	1.45	1e−09	1e−07	41 x 50	fucosidase, alpha−L− 1, tissue [Source:HGNC Symbol;Acc:H
7	PJA1	1.38	5e−09	1e−07	42 x 50	praja ring finger 1, E3 ubiquitin protein ligase [Source:HGNC
8	SBF1	1.37	6e−09	6e−07	38 x 50	SET binding factor 1 [Source:HGNC Symbol;Acc:HGNC:1054
9	BCAP29	0.88	3e−08	6e−07	41 x 47	B−cell receptor−associated protein 29 [Source:HGNC Symbo
10	FAM114A2	1.31	3e−08	3e−06	41 x 50	family with sequence similarity 114, member A2 [Source:HGN
11	ASNS	1.26	8e−08	5e−06	44 x 50	asparagine synthetase (glutamine−hydrolyzing) [Source:HGN
12	CCDC93	1.23	2e−07	5e−06	42 x 50	coiled−coil domain containing 93 [Source:HGNC Symbol;Acc
13	SNX14	0.97	4e−07	5e−06	39 x 50	sorting nexin 14 [Source:HGNC Symbol;Acc:HGNC:14977]
14	SMAP1	1.18	6e−07	5e−06	43 x 50	small ArfGAP 1 [Source:HGNC Symbol;Acc:HGNC:19651]
15	PARP11	1.18	6e−07	5e−06	43 x 50	poly (ADP−ribose) polymerase family, member 11 [Source:HG
16	INSIG2	1.17	7e−07	5e−06	40 x 50	insulin induced gene 2 [Source:HGNC Symbol;Acc:HGNC:20
17	ZP3	1.16	9e−07	5e−06	38 x 50	zona pellucida glycoprotein 3 (sperm receptor) [Source:HGN
18	SNAI1	1.16	9e−07	5e−06	39 x 50	snail family zinc finger 1 [Source:HGNC Symbol;Acc:HGNC:1
19	IFITM2	1.16	9e−07	5e−06	40 x 50	interferon induced transmembrane protein 2 [Source:HGNC S
20	LIPG	1.15	1e−06	5e−06	38 x 50	lipase, endothelial [Source:HGNC Symbol;Acc:HGNC:6623]



p−values

D6_mel

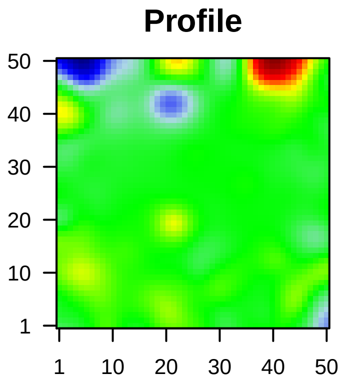
Local Summary

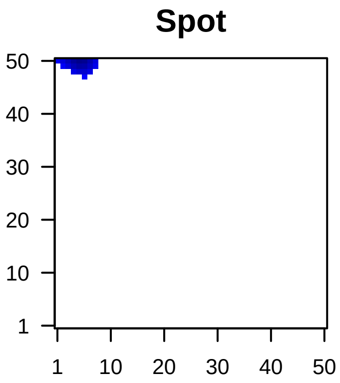
%DE = 0.8
metagenes = 20
genes = 299
genes in genesets = 299

genes with fdr < 0.1 = 185 (22 + / 163 −)
genes with fdr < 0.05 = 154 (16 + / 138 −)
genes with fdr < 0.01 = 110 (12 + / 98 −)

<r> metagenes = 0.94
<r> genes = 0.34

<FC> = −0.41
<shrinkage−t> = −6.56
<p−value> = 0.01
<fdr> = 0.53





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	ACTL6A	−1.84	2e−16	4e−15	4 x 50	actin−like 6A [Source:HGNC Symbol;Acc:HGNC:24124]
2	NNT	−1.32	2e−16	4e−15	6 x 47	nicotinamide nucleotide transhydrogenase [Source:HGNC Sy
3	STMN1	−0.81	2e−16	4e−15	5 x 50	stathmin 1 [Source:HGNC Symbol;Acc:HGNC:6510]
4	SMC4	−1.49	3e−14	5e−10	5 x 50	structural maintenance of chromosomes 4 [Source:HGNC Sy
5	TUBB4B	−1.25	8e−12	2e−08	7 x 50	tubulin, beta 4B class IVb [Source:HGNC Symbol;Acc:HGNC
6	CSE1L	−1.06	3e−10	4e−08	3 x 49	CSE1 chromosome segregation 1−like (yeast) [Source:HGNC
7	BIRC5	−1.31	9e−10	9e−08	6 x 50	baculoviral IAP repeat containing 5 [Source:HGNC Symbol;A
8	H2AFV	−1.19	4e−09	9e−08	8 x 50	H2A histone family, member V [Source:HGNC Symbol;Acc:H
9	TK1	−1.11	5e−09	9e−08	4 x 50	thymidine kinase 1, soluble [Source:HGNC Symbol;Acc:HGN
10	POLD3	−1.27	5e−09	2e−07	2 x 50	polymerase (DNA−directed), delta 3, accessory subunit [Sour
11	SMC2	−1.25	1e−08	2e−07	5 x 50	structural maintenance of chromosomes 2 [Source:HGNC Sy
12	CDKN3	−1	1e−08	9e−07	6 x 50	cyclin−dependent kinase inhibitor 3 [Source:HGNC Symbol;A
13	CENPK	−1.23	3e−08	9e−07	3 x 50	centromere protein K [Source:HGNC Symbol;Acc:HGNC:294
14	CKAP2	−1.22	4e−08	2e−06	6 x 50	cytoskeleton associated protein 2 [Source:HGNC Symbol;Acc
15	PRC1	−1.2	1e−07	2e−06	5 x 50	protein regulator of cytokinesis 1 [Source:HGNC Symbol;Acc
16	RFC4	−1.2	1e−07	2e−06	1 x 50	replication factor C (activator 1) 4, 37kDa [Source:HGNC Syn
17	LRR1	−1.19	1e−07	2e−05	4 x 49	leucine rich repeat protein 1 [Source:HGNC Symbol;Acc:HGN
18	CDCA7L	−1.15	8e−07	2e−05	1 x 50	cell division cycle associated 7−like [Source:HGNC Symbol;A
19	ZWINT	−1.13	1e−06	2e−05	5 x 50	ZW10 interacting kinetochore protein [Source:HGNC Symbol;
20	CENPF	−1.08	1e−06	2e−05	6 x 50	centromere protein F, 350/400kDa [Source:HGNC Symbol;Ac