F5_mel

Global Summary

%DE = 0.2

genes with fdr < 0.2 = 2591 (1507 + / 1084 −)

genes with fdr < 0.1 = 1970 (1158 + / 812 −)

genes with fdr < 0.05 = 1615 (950 + / 665 −)

genes with fdr < 0.01 = 1007 (570 + / 437 −)

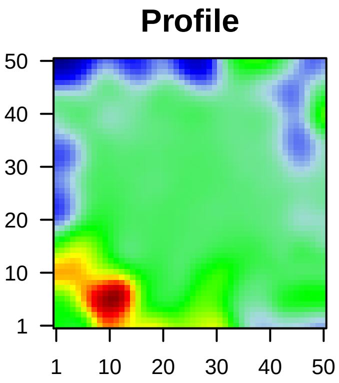
genes in genesets = 14839

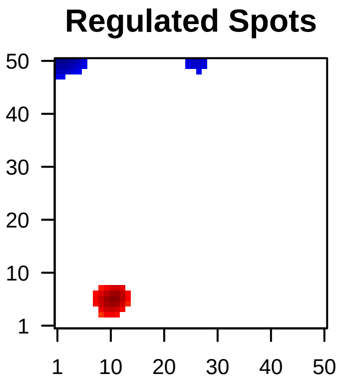
<FC> = 0

<shrinkage−t> = −0.03

<p−value> = 0.09

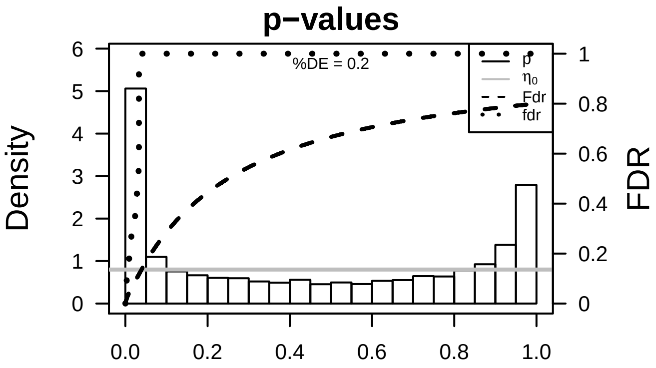
<fdr> = 0.8





Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	ANKRD10	−1.5	2e−16	1e−13	1 x 24	ankyrin repeat domain 10 [Source:HGNC Symbol;Acc:HGNC
2	APOO	−1.63	2e−16	1e−13	2 x 46	apolipoprotein O [Source:HGNC Symbol;Acc:HGNC:28727]
3	ATRX	−1.95	2e−16	1e−13	43 x 7	alpha thalassemia/mental retardation syndrome X−linked [So
4	CD59	−1.28	2e−16	1e−13	49 x 12	CD59 molecule, complement regulatory protein [Source:HGN
5	CERS2	−1.86	2e−16	1e−13	3 x 34	ceramide synthase 2 [Source:HGNC Symbol;Acc:HGNC:140
6	CKS2	−1.65	2e−16	1e−13	5 x 50	CDC28 protein kinase regulatory subunit 2 [Source:HGNC Sy
7	DKC1	−1.67	2e−16	1e−13	7 x 43	dyskeratosis congenita 1, dyskerin [Source:HGNC Symbol;Ac
8	EIF3G	−1.69	2e−16	1e−13	47 x 39	eukaryotic translation initiation factor 3, subunit G [Source:HG
9	G6PC3	−1.64	2e−16	1e−13	48 x 49	glucose 6 phosphatase, catalytic, 3 [Source:HGNC Symbol;A
10	HSPA8	−1.06	2e−16	1e−13	49 x 50	heat shock 70kDa protein 8 [Source:HGNC Symbol;Acc:HGN
11	MAGED2	−2.04	2e−16	1e−13	28 x 50	melanoma antigen family D2 [Source:HGNC Symbol;Acc:HG
12	MARS	−1.72	2e−16	1e−13	43 x 47	methionyl−tRNA synthetase [Source:HGNC Symbol;Acc:HGN
13	MDM2	−1.23	2e−16	1e−13	46 x 37	MDM2 proto−oncogene, E3 ubiquitin protein ligase [Source:H
14	PDHA1	−1.33	2e−16	1e−13	16 x 50	pyruvate dehydrogenase (lipoamide) alpha 1 [Source:HGNC
15	PGK1	−1.14	2e−16	1e−13	29 x 46	phosphoglycerate kinase 1 [Source:HGNC Symbol;Acc:HGN
16	PSMD13	−1.41	2e−16	1e−13	29 x 50	proteasome (prosome, macropain) 26S subunit, non−ATPase
17	RHOC	−1.27	2e−16	1e−13	47 x 50	ras homolog family member C [Source:HGNC Symbol;Acc:H
18	S100A11	−2.25	2e−16	1e−13	46 x 37	S100 calcium binding protein A11 [Source:HGNC Symbol;Ac
19	SAT1	−1.85	2e−16	1e−13	1 x 11	spermidine/spermine N1−acetyltransferase 1 [Source:HGNC
20	SDF2	−1.67	2e−16	1e−13	48 x 50	stromal cell−derived factor 2 [Source:HGNC Symbol;Acc:HG



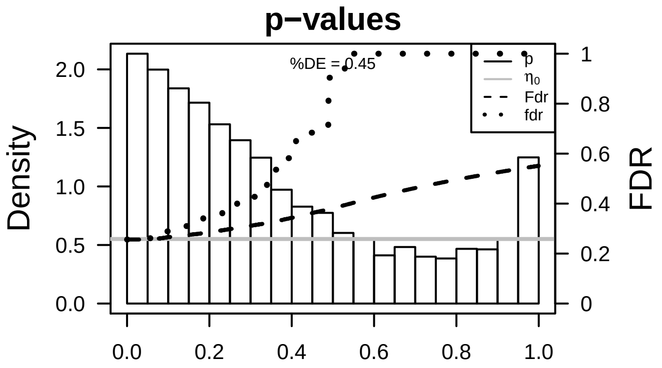
Global Geneset Analysis

Overexpressed

Rank	GSZ	p−value	#all	Geneset	
1	5.3	0.003	2563	Lymphoma	HOPP_Heterochrom
2	4.87	0.004	730	GSEA C2	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIA
3	4.54	0.005	993	Chr	Chr 2
4	4.33	0.006	31	BP	muscle cell differentiation
5	4.2	0.006	2188	Lymphoma	HOPP_Poised_promoter
6	4.13	0.007	3383	Colon Cancer	EnhWk2_Colon
7	4.06	0.007	3897	Colon Cancer	Quies1_Colon
8	4.05	0.007	3396	Lymphoma	HOPP_Repressed
9	4.01	0.007	995	GSEA C2	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_DN
10	3.87	0.008	5693	Lymphoma	HOPP_Weak_enhancer
11	3.72	0.009	59	BP	smoothened signaling pathway
12	3.61	0.010	9020	Brain	Overlap_fetal_midbrain_ReprPCWk
13	3.6	0.011	14	BP	RNA phosphodiester bond hydrolysis
14	3.59	0.011	21	BP	positive regulation of muscle cell differentiation
15	3.58	0.011	310	GSEA C2	MOREAUX_MULTIPLE_MYELOMA_BY_TACI_UP
16	3.54	0.011	2210	BP	anatomical structure development
17	3.52	0.011	10	MF	gamma−catenin binding
18	3.49	0.012	786	Brain	Fetal_EnhG
19	3.44	0.012	10	CC	cell−cell contact zone
20	3.41	0.012	473	GSEA C2	DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN

Underexpressed

Rank	GSZ	p−value	#all	Geneset	
1	−13.41	8e−05	551	Chr	Chr X
2	−8.17	6e−04	700	GSEA C2	MARSON_BOUND_BY_E2F4_UNSTIMULATED
3	−7.48	8e−04	1037	Chr	Chr 19
4	−7.44	8e−04	412	BP	mitotic cell cycle
5	−7.32	9e−04	1115	Toxic	LU_BPDE 1h DN
6	−7.09	1e−03	1192	GSEA C2	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
7	−6.82	1e−03	305	GSEA C2	DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP
8	−6.77	1e−03	1110	BP	cell cycle
9	−6.72	1e−03	25	GSEA C2	REACTOME_REGULATION_OF_GLUCOKINASE_BY_GLUCOKI
10	−6.65	1e−03	388	GSEA C2	REACTOME_CELL_CYCLE
11	−6.64	1e−03	550	GSEA C2	GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
12	−6.6	1e−03	32	GSEA C2	REACTOME_INTERACTIONS_OF_VPR_WITH_HOST_CELLULA
13	−6.59	1e−03	145	GSEA C2	CHANG_CYCLING_GENES
14	−6.58	1e−03	27	GSEA C2	REACTOME_TRANSPORT_OF_RIBONUCLEOPROTEINS_INTO
15	−6.49	1e−03	113	GSEA C2	REACTOME_HOST_INTERACTIONS_OF_HIV_FACTORS
16	−6.46	1e−03	181	GSEA C2	REACTOME_DNA_REPLICATION
17	−6.46	1e−03	33	GSEA C2	REACTOME_TRANSPORT_OF_MATURE_MRNA_DERIVED_FR
18	−6.45	1e−03	142	Glio	WILLSCHER_GBM_Verhaak−CL_up (C)
19	−6.41	1e−03	27	GSEA C2	REACTOME_NEP_NS2_INTERACTS_WITH_THE_CELLULAR_E
20	−6.35	2e−03	301	GSEA C2	REACTOME_CELL_CYCLE_MITOTIC



F5_mel

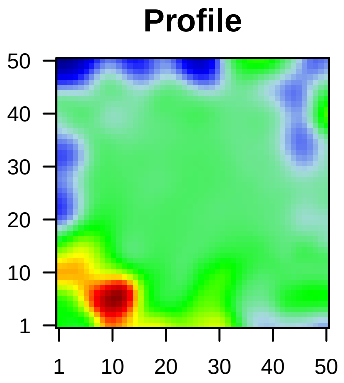
Local Summary

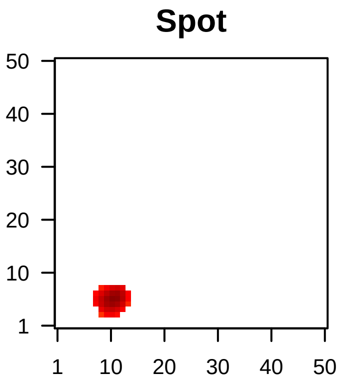
%DE = 0.7
metagenes = 35
genes = 239
genes in genesets = 237

genes with fdr < 0.1 = 145 (145 + / 0 −)
genes with fdr < 0.05 = 132 (132 + / 0 −)
genes with fdr < 0.01 = 110 (110 + / 0 −)

<r> metagenes = 0.82
<r> genes = 0.14

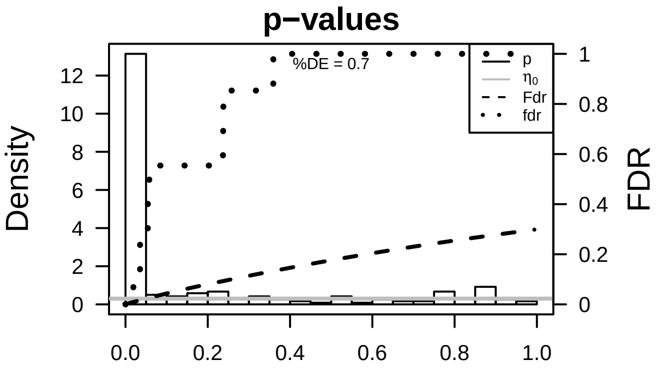
<FC> = 0.66
<shrinkage−t> = 10.27
<p−value> = 0
<fdr> = 0.42





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	TRAF2	1.82	5e−12	2e−10	12 x 6	TNF receptor−associated factor 2 [Source:HGNC Symbol;Ac
2	TBC1D32	1.81	6e−12	2e−10	12 x 6	TBC1 domain family, member 32 [Source:HGNC Symbol;Acc
3	GPR171	1.8	8e−12	3e−09	9 x 8	G protein−coupled receptor 171 [Source:HGNC Symbol;Acc:
4	KDM7A	1.73	5e−11	5e−09	12 x 7	lysine (K)−specific demethylase 7A [Source:HGNC Symbol;A
5	HKDC1	1.69	1e−10	8e−09	12 x 7	hexokinase domain containing 1 [Source:HGNC Symbol;Acc:
6	PSG4	1.67	2e−10	1e−08	12 x 6	pregnancy specific beta−1−glycoprotein 4 [Source:HGNC Sy
7	PYGL	1.64	4e−10	3e−08	10 x 6	phosphorylase, glycogen, liver [Source:HGNC Symbol;Acc:H
8	ZNF627	1.6	1e−09	3e−08	11 x 6	zinc finger protein 627 [Source:HGNC Symbol;Acc:HGNC:30
9	JRK	1.6	1e−09	5e−08	10 x 6	Jrk homolog (mouse) [Source:HGNC Symbol;Acc:HGNC:619
10	DQX1	1.58	2e−09	2e−07	12 x 7	DEAQ box RNA−dependent ATPase 1 [Source:HGNC Symb
11	SYN3	1.52	7e−09	2e−07	12 x 7	synapsin III [Source:HGNC Symbol;Acc:HGNC:11496]
12	NEURL2	1.52	8e−09	2e−07	12 x 6	neuralized E3 ubiquitin protein ligase 2 [Source:HGNC Symb
13	LRRN3	1.51	1e−08	1e−06	10 x 7	leucine rich repeat neuronal 3 [Source:HGNC Symbol;Acc:H
14	FAM178B	1.46	3e−08	7e−06	9 x 8	family with sequence similarity 178, member B [Source:HGN
15	AZGP1	1.37	2e−07	7e−06	13 x 7	alpha−2−glycoprotein 1, zinc−binding [Source:HGNC Symbol
16	PNMA1	1.35	3e−07	7e−06	8 x 6	paraneoplastic Ma antigen 1 [Source:HGNC Symbol;Acc:HG
17	C2CD2L	1.33	5e−07	7e−06	13 x 7	C2CD2−like [Source:HGNC Symbol;Acc:HGNC:29000]
18	DHRS3	1.32	5e−07	7e−06	12 x 7	dehydrogenase/reductase (SDR family) member 3 [Source:H
19	AGO3	1.32	5e−07	1e−05	10 x 5	argonaute RISC catalytic component 3 [Source:HGNC Symb
20	VWCE	1.29	8e−07	1e−05	12 x 6	von Willebrand factor C and EGF domains [Source:HGNC Sy



F5_mel

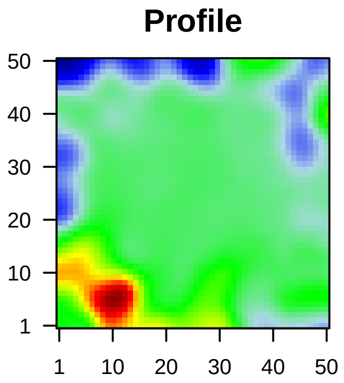
Local Summary

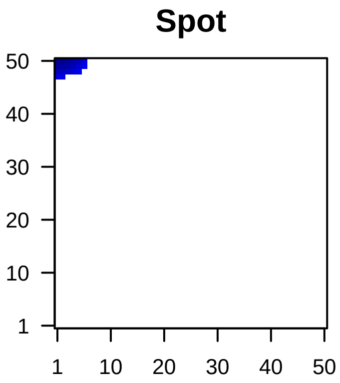
%DE = 0.83
metagenes = 19
genes = 324
genes in genesets = 323

genes with fdr < 0.1 = 195 (37 + / 158 −)
genes with fdr < 0.05 = 165 (31 + / 134 −)
genes with fdr < 0.01 = 89 (18 + / 71 −)

<r> metagenes = 0.94
<r> genes = 0.29

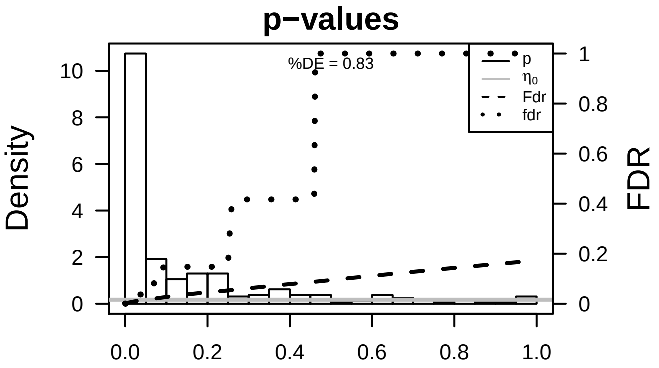
<FC> = −0.33
<shrinkage−t> = −5.15
<p−value> = 0.01
<fdr> = 0.59





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	CKS2	−1.65	2e−16	1e−14	5 x 50	CDC28 protein kinase regulatory subunit 2 [Source:HGNC S
2	NUP85	−1.56	1e−13	3e−11	1 x 50	nucleoporin 85kDa [Source:HGNC Symbol;Acc:HGNC:8734]
3	SMC1A	−1.38	7e−13	7e−09	3 x 48	structural maintenance of chromosomes 1A [Source:HGNC
4	GMNN	−1.45	1e−10	4e−08	2 x 50	geminin, DNA replication inhibitor [Source:HGNC Symbol;Ac
5	NUP54	−1.41	8e−10	4e−07	1 x 50	nucleoporin 54kDa [Source:HGNC Symbol;Acc:HGNC:17359
6	SAAL1	−1.35	1e−08	4e−07	1 x 47	serum amyloid A−like 1 [Source:HGNC Symbol;Acc:HGNC:2
7	FEN1	−1.34	2e−08	4e−07	1 x 50	flap structure−specific endonuclease 1 [Source:HGNC Symb
8	SMCHD1	−1.33	2e−08	8e−07	1 x 48	structural maintenance of chromosomes flexible hinge domai
9	MCM7	−1.29	7e−08	8e−07	2 x 50	minichromosome maintenance complex component 7 [Sourc
10	EXOSC9	−1.29	8e−08	8e−07	1 x 50	exosome component 9 [Source:HGNC Symbol;Acc:HGNC:91
11	HMGB2	−1.28	9e−08	8e−07	5 x 50	high mobility group box 2 [Source:HGNC Symbol;Acc:HGNC
12	PLEKHJ1	−1.28	1e−07	8e−07	1 x 47	pleckstrin homology domain containing, family J member 1 [
13	DNMT1	−0.94	1e−07	8e−07	2 x 48	DNA (cytosine−5−)−methyltransferase 1 [Source:HGNC Sym
14	PRPS2	−1.28	1e−07	8e−07	2 x 48	phosphoribosyl pyrophosphate synthetase 2 [Source:HGNC
15	TIMM9	−1.27	1e−07	7e−06	1 x 47	translocase of inner mitochondrial membrane 9 homolog (yea
16	RRM1	−1.08	3e−07	8e−06	2 x 50	ribonucleotide reductase M1 [Source:HGNC Symbol;Acc:HG
17	HELLS	−1.23	5e−07	8e−06	1 x 50	helicase, lymphoid−specific [Source:HGNC Symbol;Acc:HGN
18	STMN1	0.53	7e−07	8e−06	5 x 50	stathmin 1 [Source:HGNC Symbol;Acc:HGNC:6510]
19	CENPK	−1.22	8e−07	8e−06	3 x 50	centromere protein K [Source:HGNC Symbol;Acc:HGNC:294
20	FTSJ2	−1.21	1e−06	8e−06	1 x 48	FtsJ RNA methyltransferase homolog 2 (E. coli) [Source:HG



F5_mel

Local Summary

%DE = 0.69

metagenes = 9

genes = 115

genes in genesets = 115

genes with fdr < 0.1 = 41 (5 + / 36 −)

genes with fdr < 0.05 = 41 (5 + / 36 −)

genes with fdr < 0.01 = 34 (3 + / 31 −)

<r> metagenes = 0.96

<r> genes = 0.1

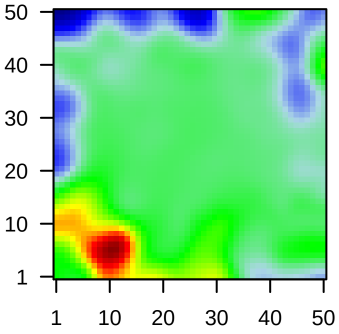
<FC> = −0.38

<shrinkage−t> = −6.33

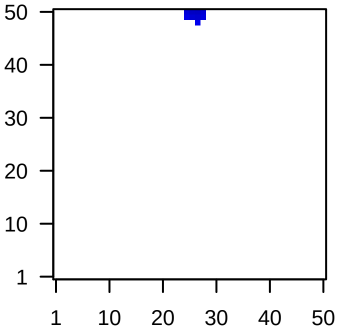
<p−value> = 0.01

<fdr> = 0.61

Profile



Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	MAGED2	−2.04	2e−16	8e−15	28 x 50	melanoma antigen family D2 [Source:HGNC Symbol;Acc:HG
2	DDX49	−1.58	2e−14	3e−10	27 x 50	DEAD (Asp−Glu−Ala−Asp) box polypeptide 49 [Source:HGN
3	DHPS	−1.49	1e−11	3e−09	27 x 50	deoxyhypusine synthase [Source:HGNC Symbol;Acc:HGNC:
4	TCEAL8	−1.46	8e−11	8e−08	26 x 50	transcription elongation factor A (SII)−like 8 [Source:HGNC S
5	SNX17	−1.39	2e−09	1e−06	26 x 50	sorting nexin 17 [Source:HGNC Symbol;Acc:HGNC:14979]
6	AP3D1	−1.28	4e−08	1e−06	27 x 50	adaptor−related protein complex 3, delta 1 subunit [Source:H
7	MFSD12	−1.3	6e−08	8e−06	27 x 50	major facilitator superfamily domain containing 12 [Source:H
8	NAA50	−0.98	3e−07	4e−05	28 x 50	N(alpha)−acetyltransferase 50, NatE catalytic subunit [Source
9	PUS7L	1.27	1e−06	1e−04	26 x 50	pseudouridylate synthase 7 homolog (S. cerevisiae)−like [So
10	PWP1	−0.65	5e−06	2e−04	25 x 50	PWP1 homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:H
11	TRUB2	−1.13	1e−05	2e−04	25 x 50	TruB pseudouridine (psi) synthase family member 2 [Source:
12	KRTCAP2	−0.76	2e−05	2e−04	26 x 50	keratinocyte associated protein 2 [Source:HGNC Symbol;Acc
13	CMAS	−1.11	2e−05	2e−04	26 x 50	cytidine monophosphate N−acetylneuraminic acid synthetase
14	SLC35A1	−1.1	2e−05	2e−04	26 x 50	solute carrier family 35 (CMP−sialic acid transporter), membe
15	CAPNS1	−1.08	3e−05	3e−04	25 x 50	calpain, small subunit 1 [Source:HGNC Symbol;Acc:HGNC:1
16	CALM3	−1.06	5e−05	3e−04	28 x 50	calmodulin 3 (phosphorylase kinase, delta) [Source:HGNC S
17	CCDC12	−1.06	5e−05	7e−04	28 x 50	coiled−coil domain containing 12 [Source:HGNC Symbol;Acc
18	CARS	−1.03	7e−05	7e−04	28 x 50	cysteinyl−tRNA synthetase [Source:HGNC Symbol;Acc:HGN
19	PROSC	−1.03	9e−05	7e−04	26 x 50	proline synthetase co−transcribed homolog (bacterial) [Sourc
20	SSNA1	−1.02	1e−04	2e−03	25 x 50	Sjogren syndrome nuclear autoantigen 1 [Source:HGNC Sym

p−values