GW_044

Global Summary

%DE = 0.13

genes with fdr < 0.2 = 1640 (956 + / 684 −)

genes with fdr < 0.1 = 1148 (710 + / 438 −)

genes with fdr < 0.05 = 1003 (629 + / 374 −)

genes with fdr < 0.01 = 681 (448 + / 233 −)

genes in genesets = 16332

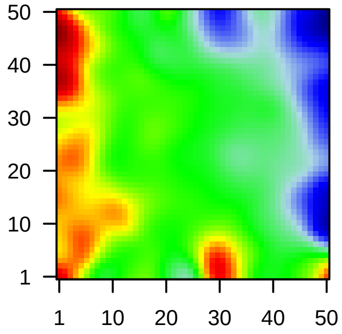
<FC> = 0

<shrinkage−t> = 0

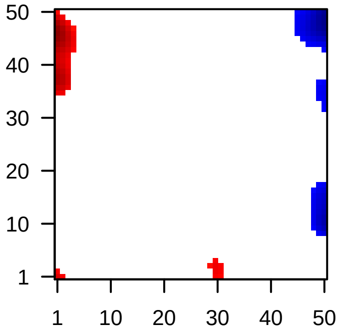
<p−value> = 0.13

<fdr> = 0.87

Profile



Regulated Spots



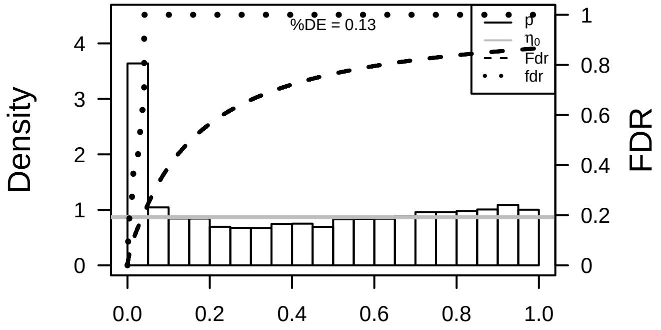
Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	131	−2.09	2e−16	5e−14	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	216	−1.47	2e−16	5e−14	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGNC
3	218	−2.73	2e−16	5e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
4	241	1.41	2e−16	5e−14	50 x 1	arachidonate 5−lipoxygenase−activating protein [Source:HGN
5	341	2.07	2e−16	5e−14	50 x 1	apolipoprotein C−I [Source:HGNC Symbol;Acc:607]
6	348	2.1	2e−16	5e−14	50 x 1	apolipoprotein E [Source:HGNC Symbol;Acc:613]
7	366	1.81	2e−16	5e−14	1 x 1	aquaporin 9 [Source:HGNC Symbol;Acc:643]
8	10974	−1.86	2e−16	5e−14	5 x 50	adipogenesis regulatory factor [Source:HGNC Symbol;Acc:2
9	199675	1.4	2e−16	5e−14	5 x 4	chromosome 19 open reading frame 59 [Source:HGNC Sym
10	713	2.38	2e−16	5e−14	50 x 1	complement component 1, q subcomponent, B chain [Source
11	714	2.03	2e−16	5e−14	50 x 1	complement component 1, q subcomponent, C chain [Source
12	6362	1.39	2e−16	5e−14	48 x 5	chemokine (C−C motif) ligand 18 (pulmonary and activation−
13	6348	1.41	2e−16	5e−14	4 x 4	chemokine (C−C motif) ligand 3 [Source:HGNC Symbol;Acc:
14	414062	2	2e−16	5e−14	1 x 1	chemokine (C−C motif) ligand 3−like 3 [Source:HGNC Symb
15	929	1.45	2e−16	5e−14	50 x 3	CD14 molecule [Source:HGNC Symbol;Acc:1628]
16	9332	1.6	2e−16	5e−14	50 x 4	CD163 molecule [Source:HGNC Symbol;Acc:1631]
17	81037	1.42	2e−16	5e−14	1 x 14	CLPTM1−like [Source:HGNC Symbol;Acc:24308]
18	1436	1.46	2e−16	5e−14	50 x 1	colony stimulating factor 1 receptor [Source:HGNC Symbol;A
19	1441	1.51	2e−16	5e−14	5 x 4	colony stimulating factor 3 receptor (granulocyte) [Source:HG
20	441520	1.63	2e−16	5e−14	14 x 11	cancer/testis antigen family 45, member A2 [Source:HGNC S

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	16.12	NULL	572	Disease	GUDJ_psoriasis up
2	14.45	NULL	265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
3	14.45	NULL	265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
4	14.45	NULL	265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
5	14.45	NULL	265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
6	12.96	NULL	135	H.Tiss	WIRTH_Mucosa
7	11.09	NULL	269	BP	inflammatory response
8	9.59	NULL	717	Chr	Chr 16
9	9.39	NULL	312	BP	immune response
10	9.23	NULL	4	GSEA C2	REACTOME_CLASSICAL_ANTIBODY_MEDIATED_COMPLEMEN
11	9.15	NULL	553	Cancer	Lembcke_Colonic Inflammation
12	9.09	NULL	111	BP	chemotaxis
13	8.82	NULL	36	BP	neutrophil chemotaxis
14	8.67	NULL	1135	Chr	Chr 19
15	8.44	NULL	10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
16	8.32	NULL	11	GSEA C2	APPEL_IMATINIB_RESPONSE
17	8.16	NULL	6	Glio	Martinez_Glio_hypometh
18	8.12	NULL	13	MMML CGS	MACIEJ_MMML 6
19	8.04	NULL	2659	CC	plasma membrane
20	8.03	NULL	7	GSEA C2	BIOCARTA_COMP_PATHWAY
Underexpressed					
1	−8.65	NULL	633	Chr	Chr 9
2	−7.62	NULL	519	Chr	Chr 14
3	−7.38	NULL	370	BP	mitotic cell cycle
4	−6.63	NULL	618	Chr	Chr 4
5	−6.24	NULL	949	CC	nucleoplasm
6	−6.12	NULL	714	Chr	Chr 6
7	−6.01	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_D
8	−5.95	NULL	9	GSEA C2	NIKOLSKY_BREAST_CANCER_17P11_AMPLICON
9	−5.66	NULL	375	Disease	GUDJ_psoriasis down
10	−5.53	NULL	940	MF	nucleic acid binding
11	−5.53	NULL	386	Chr	Chr 22
12	−5.25	NULL	271	miRNA target−starBase	hsa−miR−101
13	−5.21	NULL	9	GSEA C2	REACTOME_ETHANOL_OXIDATION
14	−5	NULL	148	BP	G1/S transition of mitotic cell cycle
15	−4.93	NULL	229	BP	RNA splicing
16	−4.89	NULL	649	BP	gene expression
17	−4.86	NULL	310	miRNA target−starBase	hsa−miR−340
18	−4.85	NULL	6	GSEA C2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_B_DN
19	−4.83	NULL	269	miRNA target−starBase	hsa−miR−1244
20	−4.81	NULL	318	miRNA target−starBase	hsa−miR−590−3p

p−values



GW_044

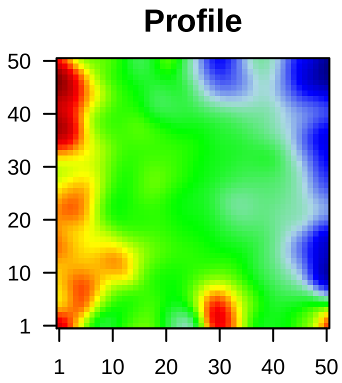
Local Summary

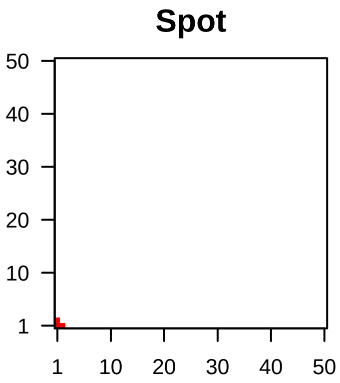
%DE = 0.6
metagenes = 3
genes = 75
genes in genesets = 75

genes with fdr < 0.1 = 34 (29 + / 5 −)
genes with fdr < 0.05 = 30 (26 + / 4 −)
genes with fdr < 0.01 = 27 (24 + / 3 −)

<r> metagenes = 1
<r> genes = 0.46

<FC> = 0.4
<shrinkage−t> = 14.11
<p−value> = 0
<fdr> = 0.55





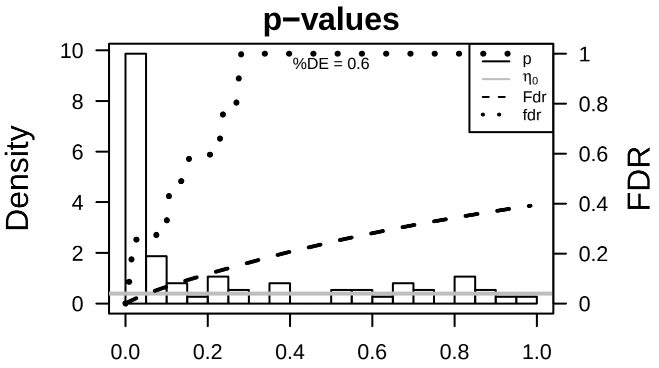
Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	366	1.81	2e−16	8e−16	1 x 1	aquaporin 9 [Source:HGNC Symbol;Acc:643]
2	414062	2	2e−16	8e−16	1 x 1	chemokine (C−C motif) ligand 3−like 3 [Source:HGNC Symbo
3	6372	2.39	2e−16	8e−16	1 x 1	chemokine (C−X−C motif) ligand 6 [Source:HGNC Symbol;Ac
4	3553	2.09	2e−16	8e−16	1 x 1	interleukin 1, beta [Source:HGNC Symbol;Acc:5992]
5	3576	1.53	2e−16	8e−16	1 x 1	interleukin 8 [Source:HGNC Symbol;Acc:6025]
6	4973	1.71	2e−16	8e−16	1 x 1	oxidized low density lipoprotein (lectin−like) receptor 1 [Sourc
7	5008	1.42	2e−16	8e−16	1 x 1	oncostatin M [Source:HGNC Symbol;Acc:8506]
8	6696	1.38	2e−16	8e−16	2 x 1	secreted phosphoprotein 1 [Source:HGNC Symbol;Acc:1125
9	6374	1.26	9e−14	2e−11	1 x 1	chemokine (C−X−C motif) ligand 5 [Source:HGNC Symbol;Ac
10	2919	1.21	8e−13	3e−11	1 x 1	chemokine (C−X−C motif) ligand 1 (melanoma growth stimula
11	4311	1.18	2e−12	3e−11	2 x 1	membrane metallo−endopeptidase [Source:HGNC Symbol;A
12	12	1.18	3e−12	3e−09	1 x 1	
13	60675	1.09	1e−10	1e−07	1 x 1	prokineticin 2 [Source:HGNC Symbol;Acc:18455]
14	5054	0.99	4e−09	1e−06	1 x 2	serpin peptidase inhibitor, clade E (nexin, plasminogen activa
15	2920	0.92	5e−08	8e−06	1 x 1	chemokine (C−X−C motif) ligand 2 [Source:HGNC Symbol;Ac
16	10409	0.85	5e−07	8e−06	1 x 2	brain abundant, membrane attached signal protein 1 [Source:
17	1514	0.84	6e−07	9e−06	1 x 2	cathepsin L [Source:HGNC Symbol;Acc:2537]
18	6999	0.83	9e−07	1e−05	1 x 2	tryptophan 2,3−dioxygenase [Source:HGNC Symbol;Acc:117
19	4318	0.81	1e−06	3e−05	1 x 1	matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 9
20	7130	0.8	2e−06	3e−04	1 x 1	tumor necrosis factor, alpha−induced protein 6 [Source:HGN

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	37.06	NULL	2 / 6	GSEA C2	SEIKE_LUNG_CANCER_POOR_SURVIVAL
2	28.4	NULL	1 / 4	GSEA C2	BUDHU_LIVER_CANCER_METASTASIS_DN
3	27.97	NULL	6 / 43	MF	chemokine activity
4	26.01	NULL	1 / 3	GSEA C2	REN_MIF_TARGETS_DN
5	25.02	NULL	2 / 6	GSEA C2	BIOCARTA_IL5_PATHWAY
6	23.94	NULL	2 / 6	Glio	Martinez_Glio_hypometh
7	23.78	NULL	3 / 16	GSEA C2	MAHADEVAN_RESPONSE_TO_MP470_UP
8	20.14	NULL	2 / 16	GSEA C2	GRAHAM_CML_QUIESCENT_VS_CML_DIVIDING_UP
9	19.7	NULL	1 / 5	GSEA C2	SMIRNOV_CIRCULATING_ENDOTHELIOCYTES_IN_CANCER_
10	19.36	NULL	3 / 14	GSEA C2	WANG_ESOPHAGUS_CANCER_VS_NORMAL_UP
11	19.29	NULL	8 / 111	BP	chemotaxis
12	19.25	NULL	2 / 9	GSEA C2	HEDVAT_ELF4_TARGETS_UP
13	18.29	NULL	2 / 13	Glio	Christensen_hypomethylated_in_grade2_oligodendroglioma
14	18.11	NULL	2 / 10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
15	17.68	NULL	1 / 5	GSEA C2	DEBOSSCHER_NFKB_TARGETS_REPRESSED_BY_GLUCOC
16	17.54	NULL	3 / 36	BP	neutrophil chemotaxis
17	16.69	NULL	3 / 6	GSEA C2	AGARWAL_AKT_PATHWAY_TARGETS
18	16.54	NULL	8 / 15	GSEA C2	CROMER_TUMORIGENESIS_UP
19	16.37	NULL	2 / 8	GSEA C2	OSAWA_TNF_TARGETS
20	16.36	NULL	15 / 269	BP	inflammatory response
21	15.89	NULL	6 / 11	MF	platelet−derived growth factor binding
22	15.81	NULL	2 / 13	BP	positive regulation of vascular endothelial growth factor receptor si
23	15.64	NULL	12 / 312	BP	immune response
24	15.6	NULL	1 / 6	GSEA C2	MIZUKAMI_HYPOXIA_DN
25	15.6	NULL	1 / 6	GSEA C2	BUDHU_LIVER_CANCER_METASTASIS_UP
26	15.02	NULL	2 / 20	BP	positive regulation of interleukin−8 production
27	14.81	NULL	2 / 9	GSEA C2	ZERBINI_RESPONSE_TO_SULINDAC_UP
28	14.49	NULL	1 / 11	BP	negative regulation of lipid catabolic process
29	14.49	NULL	1 / 11	GSEA C2	LEI_MYB_TARGETS
30	14.08	NULL	1 / 7	GSEA C2	BIOCARTA_FREE_PATHWAY
31	13.91	NULL	4 / 49	Glio	Christensen_hypomethylated_in_primary_glioblastoma
32	13.86	NULL	29 / 553	Cancer	Lembcke_Colonic Inflammation
33	13.74	NULL	1 / 12	BP	positive regulation of histone acetylation
34	13.74	NULL	1 / 12	BP	positive regulation of membrane protein ectodomain proteolysis
35	13.42	NULL	1 / 4	GSEA C2	DACOSTA_LOW_DOSE_UV_RESPONSE_VIA_ERCC3_XPCS_
36	13.29	NULL	1 / 10	GSEA C2	THEILGAARD_NEUTROPHIL_AT_SKIN_WOUND_UP
37	13.14	NULL	5 / 36	BP	embryo implantation
38	13.09	NULL	1 / 13	BP	positive regulation of interleukin−2 biosynthetic process
39	13.09	NULL	1 / 13	BP	positive regulation of protein export from nucleus
40	13.07	NULL	2 / 11	GSEA C2	BIOCARTA_STEM_PATHWAY



GW_044

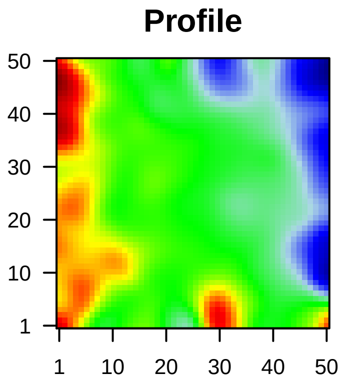
Local Summary

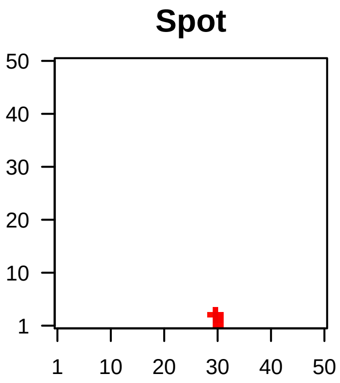
%DE = 0.78
metagenes = 8
genes = 36
genes in genesets = 36

genes with fdr < 0.1 = 24 (22 + / 2 −)
genes with fdr < 0.05 = 23 (21 + / 2 −)
genes with fdr < 0.01 = 17 (17 + / 0 −)

<r> metagenes = 0.97
<r> genes = 0.31

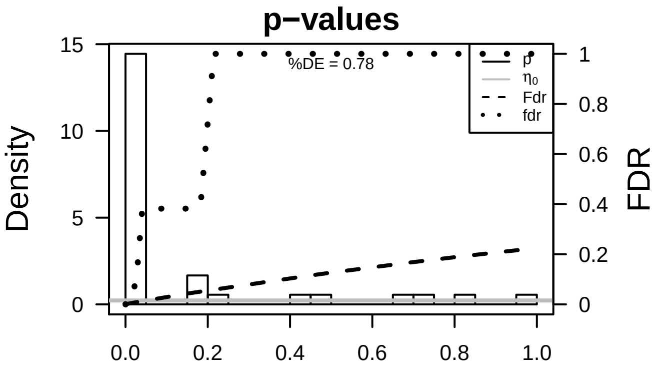
<FC> = 0.45
<shrinkage−t> = 15.73
<p−value> = 0
<fdr> = 0.37





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	79931	1.43	2e−16	2e−15	31 x 3	TNFAIP3 interacting protein 3 [Source:HGNC Symbol;Acc:19
2	712	1.13	2e−11	2e−08	30 x 2	complement component 1, q subcomponent, A chain [Source
3	6288	1.01	2e−09	2e−08	31 x 1	serum amyloid A1 [Source:HGNC Symbol;Acc:10513]
4	30817	0.98	5e−09	1e−06	30 x 4	egf−like module containing, mucin−like, hormone receptor−lik
5	6507	0.88	2e−07	3e−06	30 x 4	solute carrier family 1 (glial high affinity glutamate transporter
6	50856	0.84	6e−07	1e−05	30 x 4	C−type lectin domain family 4, member A [Source:HGNC Syn
7	10288	0.8	2e−06	1e−04	30 x 4	leukocyte immunoglobulin−like receptor, subfamily B (with TM
8	3566	0.68	6e−05	1e−04	30 x 3	interleukin 4 receptor [Source:HGNC Symbol;Acc:6015]
9	341405	0.66	8e−05	1e−04	30 x 1	ankyrin repeat domain 33 [Source:HGNC Symbol;Acc:13788]
10	91107	0.66	8e−05	1e−04	31 x 3	tripartite motif containing 47 [Source:HGNC Symbol;Acc:190
11	53	0.66	9e−05	1e−04	30 x 2	acid phosphatase 2, lysosomal [Source:HGNC Symbol;Acc:1
12	822	0.65	1e−04	1e−04	30 x 2	capping protein (actin filament), gelsolin−like [Source:HGNC
13	10261	0.65	1e−04	1e−04	30 x 4	immunoglobulin superfamily, member 6 [Source:HGNC Symb
14	27166	0.65	1e−04	1e−03	29 x 3	PRELI domain containing 1 [Source:HGNC Symbol;Acc:3025
15	717	0.61	3e−04	1e−03	30 x 2	complement component 2 [Source:HGNC Symbol;Acc:1248]
16	968	0.59	4e−04	1e−03	29 x 3	CD68 molecule [Source:HGNC Symbol;Acc:1693]
17	57817	0.59	5e−04	2e−03	30 x 4	hepcidin antimicrobial peptide [Source:HGNC Symbol;Acc:15
18	10318	0.57	7e−04	1e−02	30 x 3	TNFAIP3 interacting protein 1 [Source:HGNC Symbol;Acc:16
19	51246	0.5	3e−03	1e−02	30 x 1	shisa family member 5 [Source:HGNC Symbol;Acc:30376]
20	5872	0.48	4e−03	2e−02	29 x 3	RAB13, member RAS oncogene family [Source:HGNC Symb



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	32.43	NULL	1 / 4	GSEA C2	REACTOME_CLASSICAL_ANTIBODY_MEDIATED_COMPLEMEN
2	31.65	NULL	2 / 7	GSEA C2	BIOCARTA_COMP_PATHWAY
3	28.74	NULL	2 / 8	GSEA C2	BIOCARTA_CLASSIC_PATHWAY
4	28.74	NULL	2 / 8	GSEA C2	REACTOME_COMPLEMENT_CASCADE
5	28.74	NULL	2 / 8	GSEA C2	REACTOME_INITIAL_TRIGGERING_OF_COMPLEMENT
6	17.62	NULL	1 / 4	MMML CGS	MACIEJ_MMML 2
7	16.89	NULL	3 / 22	BP	complement activation, classical pathway
8	15.82	NULL	2 / 20	BP	complement activation
9	15.23	NULL	3 / 30	BP	negative regulation of I−kappaB kinase/NF−kappaB signaling
10	14.82	NULL	2 / 10	MF	acid phosphatase activity
11	14.49	NULL	1 / 8	GSEA C2	MCCABE_HOXC6_TARGETS_UP
12	13.73	NULL	1 / 6	GSEA C2	ST_INTERLEUKIN_13_PATHWAY
13	13.73	NULL	1 / 6	GSEA C2	ST_IL_13_PATHWAY
14	13.36	NULL	4 / 49	Glio	Donson−innate immunity−associated with LTS in HGA
15	12.6	NULL	1 / 12	BP	macrophage chemotaxis
16	12.52	NULL	2 / 15	GSEA C2	VALK_AML_CLUSTER_4
17	12.4	NULL	1 / 10	MF	L−glutamate transmembrane transporter activity
18	12.27	NULL	1 / 22	MF	polyubiquitin binding
19	11.76	NULL	1 / 7	Glio	willscher_GBM_LTSmut_proteomics−P_DOWN
20	11.63	NULL	1 / 11	BP	positive regulation of synaptic transmission
21	11.39	NULL	1 / 14	CC	endocytic vesicle lumen
22	11.08	NULL	1 / 7	GSEA C2	BIOCARTA_LECTIN_PATHWAY
23	11.08	NULL	1 / 8	GSEA C2	SASAKI_TARGETS_OF_TP73_AND_TP63
24	10.98	NULL	1 / 12	BP	glutamate metabolic process
25	10.98	NULL	1 / 12	BP	L−glutamate transport
26	10.98	NULL	1 / 12	Glio	astrocytes_glio
27	10.9	NULL	1 / 15	CC	high−density lipoprotein particle
28	10.67	NULL	1 / 8	GSEA C2	HASLINGER_B_CLL_WITH_6Q21_DELETION
29	10.54	NULL	1 / 11	BP	negative regulation of calcium ion transport
30	10.21	NULL	1 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
31	10.19	NULL	1 / 9	GSEA C2	BALLIF_DEVELOPMENTAL_DISABILITY_P16_P12_DELETION
32	10.19	NULL	1 / 9	GSEA C2	GUTIERREZ_WALDENSTROEMS_MACROGLOBULINEMIA_1_U
33	10.19	NULL	1 / 9	GSEA C2	BIOCARTA_IL4_PATHWAY
34	10.18	NULL	1 / 20	Lymphoma	DAVE_Immune response 2
35	10.05	NULL	1 / 8	GSEA C2	KEGG_COMPLEMENT_AND_COAGULATION_CASCADES
36	9.94	NULL	1 / 12	MF	MHC class I protein binding
37	9.93	NULL	1 / 14	BP	response to light stimulus
38	9.48	NULL	1 / 10	GSEA C2	LEE_EARLY_T_LYMPHOCYTE_DN
39	9.28	NULL	3 / 73	BP	cellular response to lipopolysaccharide
40	9.25	NULL	1 / 9	GSEA C2	ABE_VEGFA_TARGETS_30MIN

GW_044

Local Summary

%DE = 0.64

metagenes = 49

genes = 598

genes in genesets = 585

genes with fdr < 0.1 = 287 (223 + / 64 −)

genes with fdr < 0.05 = 272 (211 + / 61 −)

genes with fdr < 0.01 = 204 (161 + / 43 −)

<r> metagenes = 0.85

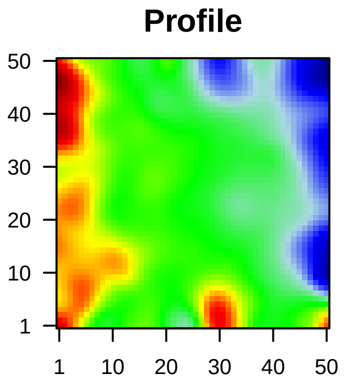
<r> genes = 0.29

<FC> = 0.25

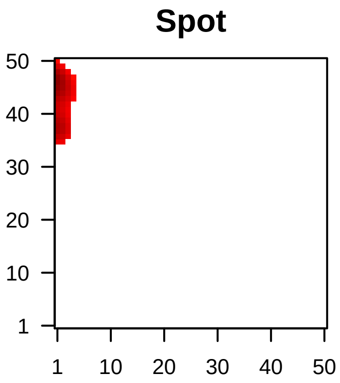
<shrinkage−t> = 8.73

<p−value> = 0

<fdr> = 0.53



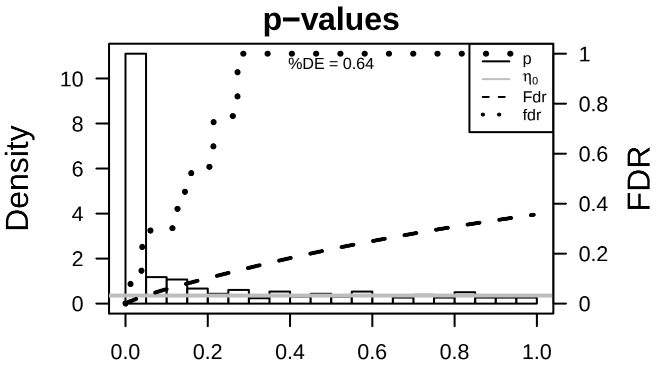
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	131	−2.09	2e−16	2e−15	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	218	−2.73	2e−16	2e−15	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
3	1672	1.48	2e−16	2e−15	1 x 50	defensin, beta 1 [Source:HGNC Symbol;Acc:2766]
4	1673	2.54	2e−16	2e−15	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
5	2731	1.43	2e−16	2e−15	1 x 38	glycine dehydrogenase (decarboxylating) [Source:HGNC Syn
6	3552	1.51	2e−16	2e−15	1 x 43	interleukin 1, alpha [Source:HGNC Symbol;Acc:5991]
7	26085	2.06	2e−16	2e−15	1 x 50	kallikrein−related peptidase 13 [Source:HGNC Symbol;Acc:6
8	3868	1.38	2e−16	2e−15	1 x 46	keratin 16 [Source:HGNC Symbol;Acc:6423]
9	192666	−1.49	2e−16	2e−15	1 x 50	keratin 24 [Source:HGNC Symbol;Acc:18527]
10	286887	1.44	2e−16	2e−15	1 x 47	keratin 6C [Source:HGNC Symbol;Acc:20406]
11	9119	1.63	2e−16	2e−15	1 x 44	keratin 75 [Source:HGNC Symbol;Acc:24431]
12	56901	1.56	2e−16	2e−15	1 x 44	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4−li
13	10158	1.84	2e−16	2e−15	1 x 47	PDZK1 interacting protein 1 [Source:HGNC Symbol;Acc:168
14	5266	1.36	2e−16	2e−15	1 x 49	peptidase inhibitor 3, skin−derived [Source:HGNC Symbol;Ac
15	170680	1.67	2e−16	2e−15	1 x 35	psoriasis susceptibility 1 candidate 2 [Source:HGNC Symbol;
16	6278	1.98	2e−16	2e−15	1 x 49	S100 calcium binding protein A7 [Source:HGNC Symbol;Acc:
17	338324	2.88	2e−16	2e−15	1 x 48	S100 calcium binding protein A7A [Source:HGNC Symbol;Ac
18	6286	1.39	2e−16	2e−15	1 x 50	S100 calcium binding protein P [Source:HGNC Symbol;Acc:1
19	374897	1.43	2e−16	2e−15	1 x 49	suprabasin [Source:HGNC Symbol;Acc:24950]
20	6317	1.61	2e−16	2e−15	1 x 49	serpin peptidase inhibitor, clade B (ovalbumin), member 3 [Sc



p−values

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	25.99	NULL	89 / 135	H.Tiss	WIRTH_Mucosa
2	23.48	NULL	149 / 572	Disease	GUDJ_psoriasis up
3	14.66	NULL	3 / 15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
4	13.45	NULL	34 / 76	BP	epidermis development
5	13.09	NULL	8 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
6	10.88	NULL	5 / 10	MF	RAGE receptor binding
7	10.54	NULL	6 / 15	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_3
8	10.22	NULL	10 / 52	BP	negative regulation of endopeptidase activity
9	10.17	NULL	6 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_4
10	10.14	NULL	5 / 16	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_DN
11	10.09	NULL	4 / 11	GSEA C2	LEI_MYB_TARGETS
12	9.78	NULL	7 / 29	BP	regulation of proteolysis
13	9.5	NULL	18 / 21	CC	cornified envelope
14	9.18	NULL	8 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
15	9.01	NULL	8 / 15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL
16	8.94	NULL	3 / 10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
17	8.91	NULL	5 / 13	BP	negative regulation of peptidase activity
18	8.67	NULL	7 / 15	GSEA C2	AIGNER_ZEB1_TARGETS
19	8.65	NULL	3 / 13	GSEA C2	FARMER_BREAST_CANCER_APOCRINE VS LUMINAL
20	8.08	NULL	11 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
21	8.05	NULL	6 / 16	GSEA C2	LEE_LIVER_CANCER_MYC_TGFA_UP
22	7.77	NULL	7 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
23	7.58	NULL	6 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
24	7.15	NULL	1 / 2	MMML CGS	MACIEJ_MMML 43
25	7.08	NULL	2 / 8	GSEA C2	MCLACHLAN_DENTAL_CARIES_UP
26	7.08	NULL	7 / 16	GSEA C2	COLDREN_GEFITINIB_RESISTANCE_DN
27	6.98	NULL	5 / 15	GSEA C2	LEE_LIVER_CANCER_DENA_UP
28	6.84	NULL	3 / 10	GSEA C2	SMID_BREAST_CANCER_ERBB2_UP
29	6.84	NULL	2 / 16	BP	response to reactive oxygen species
30	6.84	NULL	4 / 15	GSEA C2	LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
31	6.81	NULL	5 / 16	GSEA C2	LEE_LIVER_CANCER_ACOX1_UP
32	6.77	NULL	15 / 79	MF	serine−type endopeptidase inhibitor activity
33	6.73	NULL	1 / 4	GSEA C2	BUDHU_LIVER_CANCER_METASTASIS_DN
34	6.63	NULL	2 / 9	GSEA C2	MCLACHLAN_DENTAL_CARIES_DN
35	6.59	NULL	6 / 16	GSEA C2	JAEGER_METASTASIS_DN
36	6.45	NULL	4 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_DN
37	6.38	NULL	3 / 11	GSEA C2	STEIN_ESRRA_TARGETS_DN
38	6.34	NULL	3 / 15	GSEA C2	LIANG_SILENCED_BY_METHYLATION_2
39	6.33	NULL	5 / 25	BP	response to zinc ion
40	6.29	NULL	6 / 14	GSEA C2	CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U

GW_044

Local Summary

%DE = 0.65

metagenes = 28

genes = 338

genes in genesets = 334

genes with fdr < 0.1 = 139 (19 + / 120 −)

genes with fdr < 0.05 = 119 (15 + / 104 −)

genes with fdr < 0.01 = 73 (11 + / 62 −)

<r> metagenes = 0.87

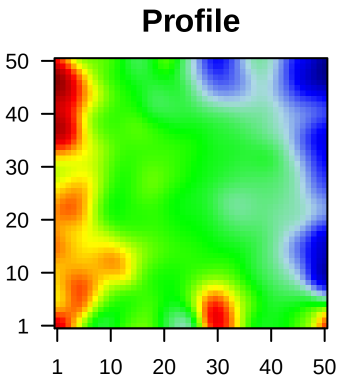
<r> genes = 0.24

<FC> = −0.25

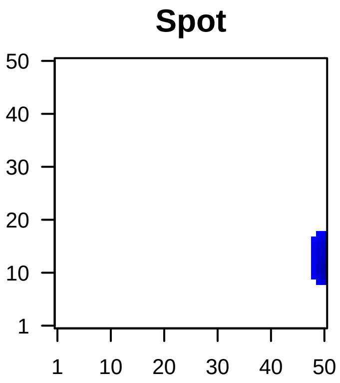
<shrinkage−t> = −8.74

<p−value> = 0.01

<fdr> = 0.63



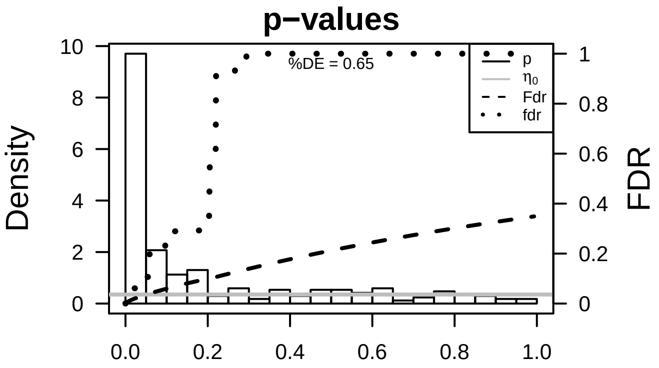
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	7033	−1.43	2e−16	3e−14	50 x 10	trefoil factor 3 (intestinal) [Source:HGNC Symbol;Acc:11757]
2	260293	1.34	2e−15	2e−10	50 x 14	cytochrome P450, family 4, subfamily X, polypeptide 1 [Sourc
3	92747	−1.18	2e−12	2e−10	50 x 10	BPI fold containing family B, member 1 [Source:HGNC Symb
4	7018	−1.17	3e−12	6e−09	50 x 10	transferrin [Source:HGNC Symbol;Acc:11740]
5	1776	−1.1	6e−11	2e−08	48 x 12	deoxyribonuclease I−like 3 [Source:HGNC Symbol;Acc:2959]
6	79191	1.06	3e−10	2e−08	50 x 15	iroquois homeobox 3 [Source:HGNC Symbol;Acc:14360]
7	83988	−1.05	5e−10	2e−08	50 x 17	neurocalcin delta [Source:HGNC Symbol;Acc:7655]
8	54102	−1.05	6e−10	1e−07	50 x 10	chloride intracellular channel 6 [Source:HGNC Symbol;Acc:2
9	83699	−1.01	2e−09	1e−07	50 x 11	SH3 domain binding glutamic acid−rich protein like 2 [Source
10	10439	−1.01	2e−09	1e−06	50 x 17	olfactomedin 1 [Source:HGNC Symbol;Acc:17187]
11	8842	−0.95	2e−08	1e−06	50 x 10	prominin 1 [Source:HGNC Symbol;Acc:9454]
12	3248	−0.94	2e−08	1e−06	50 x 13	hydroxyprostaglandin dehydrogenase 15−(NAD) [Source:HG
13	55930	−0.93	4e−08	1e−06	50 x 13	myosin VC [Source:HGNC Symbol;Acc:7604]
14	66002	−0.93	4e−08	3e−06	50 x 13	cytochrome P450, family 4, subfamily F, polypeptide 12 [Sour
15	2139	0.9	8e−08	3e−06	50 x 13	eyes absent homolog 2 (Drosophila) [Source:HGNC Symbol;
16	92304	−0.9	1e−07	3e−06	50 x 10	secretoglobin, family 3A, member 1 [Source:HGNC Symbol;A
17	55638	−0.9	1e−07	2e−05	50 x 11	syntabulin (syntaxin−interacting) [Source:HGNC Symbol;Acc:
18	26002	−0.86	3e−07	2e−05	50 x 16	monooxygenase, DBH−like 1 [Source:HGNC Symbol;Acc:21
19	148170	0.85	4e−07	2e−05	50 x 9	CDC42 effector protein (Rho GTPase binding) 5 [Source:HG
20	11272	−0.84	6e−07	3e−05	50 x 10	proline rich 4 (lacrimal) [Source:HGNC Symbol;Acc:18020]



p−values

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset
1	−24.73	NULL	11 / 16	GSEA C2 RICKMAN_HEAD_AND_NECK_CANCER_D
2	−13.47	NULL	6 / 15	GSEA C2 POOLA_INVASIVE_BREAST_CANCER_DN
3	−11.12	NULL	3 / 13	GSEA C2 WONG_ENDMETRIUM_CANCER_UP
4	−10.61	NULL	1 / 5	GSEA C2 FERRARI_RESPONSE_TO_FENRETINIDE_DN
5	−9.54	NULL	3 / 13	GSEA C2 BOYAULT_LIVER_CANCER_SUBCLASS_G3_DN
6	−9.4	NULL	3 / 12	GSEA C2 CHIANG_LIVER_CANCER_SUBCLASS_INTERFERON_UP
7	−9.29	NULL	4 / 9	GSEA C2 REACTOME_ETHANOL_OXIDATION
8	−9.01	NULL	2 / 13	GSEA C2 CERVERA_SDHB_TARGETS_2
9	−8.73	NULL	2 / 10	GSEA C2 LUI_THYROID_CANCER_CLUSTER_5
10	−8.37	NULL	33 / 375	Disease GUDJ_psoriasis down
11	−7.83	NULL	2 / 10	BP negative regulation of blood coagulation
12	−7.64	NULL	1 / 9	GSEA C2 GOUYER_TATI_TARGETS_UP
13	−7.62	NULL	4 / 14	GSEA C2 SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_
14	−7.36	NULL	1 / 3	miRNA target miR−148a
15	−7.27	NULL	2 / 13	GSEA C2 YANG_BREAST_CANCER_ESR1_UP
16	−7.22	NULL	4 / 16	GSEA C2 CHANDRAN_METASTASIS_DN
17	−7.21	NULL	5 / 16	GSEA C2 RICKMAN_HEAD_AND_NECK_CANCER_A
18	−6.98	NULL	3 / 14	GSEA C2 LIEN_BREAST_CARCINOMA_METAPLASTIC_VS_DUCTAL_DN
19	−6.87	NULL	4 / 21	BP drug metabolic process
20	−6.86	NULL	3 / 15	GSEA C2 MASSARWEH_RESPONSE_TO_ESTRADIOL
21	−6.84	NULL	2 / 12	MF NAD+ binding
22	−6.81	NULL	4 / 37	BP digestion
23	−6.69	NULL	1 / 2	TF MYC_Cell cycle DOWN
24	−6.68	NULL	3 / 16	GSEA C2 YANG_BREAST_CANCER_ESR1_BULK_UP
25	−6.63	NULL	2 / 9	GSEA C2 RODWELL_AGING_KIDNEY_UP
26	−6.29	NULL	2 / 17	BP iron ion transport
27	−6.16	NULL	2 / 14	GSEA C2 PEREZ_TP53_AND_TP63_TARGETS
28	−5.94	NULL	1 / 8	GSEA C2 REACTOME_IONOTROPIC_ACTIVITY_OF_KAINATE_RECEPTO
29	−5.86	NULL	1 / 9	GSEA C2 LEE_LIVER_CANCER
30	−5.86	NULL	1 / 9	GSEA C2 LEE_LIVER_CANCER_TOP50
31	−5.83	NULL	2 / 10	BP lipoxygenase pathway
32	−5.81	NULL	2 / 14	GSEA C2 VANTVEER_BREAST_CANCER_ESR1_UP
33	−5.8	NULL	3 / 9	GSEA C2 GOZGIT_ESR1_TARGETS_DN
34	−5.8	NULL	1 / 7	GSEA C2 GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
35	−5.76	NULL	2 / 6	GSEA C2 RIZKI_TUMOR_INVASIVENESS_3D_UP
36	−5.72	NULL	3 / 4	miRNA target miR−204
37	−5.72	NULL	2 / 15	GSEA C2 COLIN_PILOCYTIC_ASTROCYTOMA_VS_GLIOBLASTOMA_UP
38	−5.69	NULL	2 / 11	GSEA C2 RIGGI_EWING_SARCOMA_PROGENITOR_DN
39	−5.65	NULL	1 / 7	GSEA C2 GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_DN
40	−5.64	NULL	6 / 16	GSEA C2 CROMER_TUMORIGENESIS_DN

GW_044

Local Summary

%DE = 0.48

metagenes = 10

genes = 215

genes in genesets = 215

genes with fdr < 0.1 = 57 (4 + / 53 −)

genes with fdr < 0.05 = 32 (2 + / 30 −)

genes with fdr < 0.01 = 16 (2 + / 14 −)

<r> metagenes = 0.97

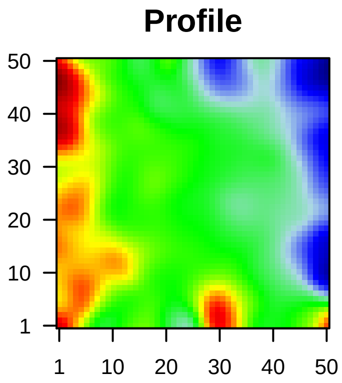
<r> genes = 0.31

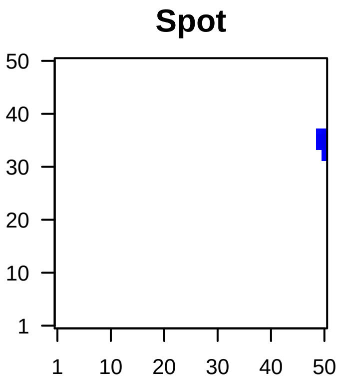
<FC> = −0.2

<shrinkage−t> = −7.17

<p−value> = 0.07

<fdr> = 0.77





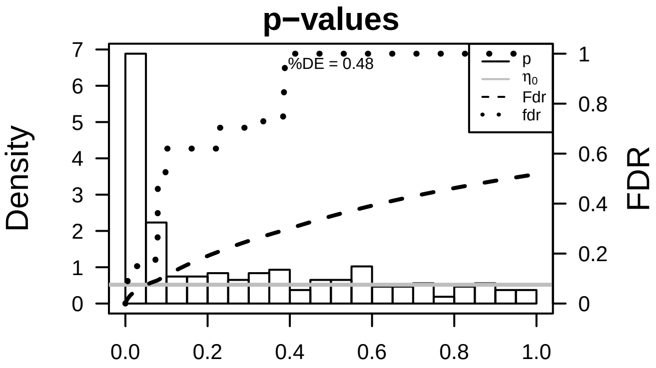
Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	9908	−0.99	5e−09	3e−06	50 x 36	GTPase activating protein (SH3 domain) binding protein 2 [Sc
2	7520	−0.93	3e−08	3e−04	50 x 35	X−ray repair complementing defective repair in Chinese hams
3	55170	−0.79	3e−06	3e−04	50 x 37	protein arginine methyltransferase 6 [Source:HGNC Symbol;A
4	1429	0.76	6e−06	2e−03	50 x 34	crystallin, zeta (quinone reductase) [Source:HGNC Symbol;A
5	57088	−0.71	3e−05	2e−03	50 x 36	phospholipid scramblase 4 [Source:HGNC Symbol;Acc:1649
6	23530	−0.7	4e−05	2e−03	50 x 36	nicotinamide nucleotide transhydrogenase [Source:HGNC Sy
7	57092	−0.68	5e−05	3e−03	50 x 35	PEST proteolytic signal containing nuclear protein [Source:HG
8	64747	0.67	8e−05	5e−03	50 x 34	major facilitator superfamily domain containing 1 [Source:HGI
9	283489	−0.64	1e−04	5e−03	50 x 32	chromosome alignment maintaining phosphoprotein 1 [Sourc
10	23588	−0.64	2e−04	7e−03	50 x 33	kelch domain containing 2 [Source:HGNC Symbol;Acc:20231
11	51663	−0.6	3e−04	7e−03	50 x 37	zinc finger RNA binding protein [Source:HGNC Symbol;Acc:1
12	10914	−0.59	5e−04	7e−03	50 x 33	poly(A) polymerase alpha [Source:HGNC Symbol;Acc:14981]
13	22878	−0.59	5e−04	7e−03	50 x 34	trafficking protein particle complex 8 [Source:HGNC Symbol;A
14	54664	−0.58	5e−04	7e−03	50 x 37	transmembrane protein 106B [Source:HGNC Symbol;Acc:224
15	54495	−0.58	5e−04	7e−03	50 x 34	thioredoxin−related transmembrane protein 3 [Source:HGNC
16	10250	−0.58	6e−04	7e−03	50 x 35	serine/arginine repetitive matrix 1 [Source:HGNC Symbol;Acc
17	728026	−0.58	6e−04	2e−02	50 x 35	prothymosin, alpha [Source:HGNC Symbol;Acc:9623]
18	4254	−0.56	8e−04	3e−02	50 x 36	KIT ligand [Source:HGNC Symbol;Acc:6343]
19	6429	−0.55	1e−03	3e−02	49 x 37	serine/arginine−rich splicing factor 4 [Source:HGNC Symbol;A
20	120534	−0.54	1e−03	3e−02	50 x 33	ADP−ribosylation factor−like 14 effector protein [Source:HGN

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−9.56	NULL	2 / 11	GSEA C2	ROZANOV_MMP14_CORRELATED
2	−8.73	NULL	5 / 41	BP	mRNA 3'−end processing
3	−8.39	NULL	5 / 44	BP	termination of RNA polymerase II transcription
4	−8.14	NULL	3 / 14	GSEA C2	REACTOME_MRNA_3_END_PROCESSING
5	−8.14	NULL	2 / 13	BP	double−strand break repair via nonhomologous end joining
6	−8.03	NULL	1 / 2	MMML CGS	MACIEJ_MMML 38
7	−7.98	NULL	6 / 45	miRNA target starBase	hsa−miR−411
8	−7.74	NULL	1 / 6	GSEA C2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_B_DN
9	−7.57	NULL	7 / 118	miRNA target starBase	hsa−miR−519e
10	−7.49	NULL	13 / 189	miRNA target starBase	hsa−miR−1283
11	−7.4	NULL	1 / 11	BP	cellular response to fatty acid
12	−7.4	NULL	1 / 11	MF	telomeric DNA binding
13	−7.4	NULL	1 / 11	GSEA C2	KEGG_NON_HOMOLOGOUS_END_JOINING
14	−7.34	NULL	5 / 46	miRNA target starBase	hsa−miR−581
15	−7.32	NULL	16 / 314	miRNA target starBase	hsa−miR−520c−3p
16	−7.06	NULL	1 / 12	GSEA C2	REACTOME_EARLY_PHASE_OF_HIV_LIFE_CYCLE
17	−7	NULL	9 / 155	miRNA target starBase	hsa−miR−298
18	−6.91	NULL	6 / 95	miRNA 3UTR	CTGGC−365
19	−6.81	NULL	14 / 271	miRNA target starBase	hsa−miR−520b
20	−6.8	NULL	8 / 178	miRNA target starBase	hsa−miR−520f
21	−6.78	NULL	1 / 2	miRNA target	miR−98
22	−6.73	NULL	17 / 325	miRNA target starBase	hsa−miR−302d
23	−6.71	NULL	8 / 159	CC	nuclear speck
24	−6.69	NULL	2 / 14	GSEA C2	ZHAN_MULTIPLE_MYELOMA_CD1_AND_CD2_UP
25	−6.63	NULL	10 / 163	BP	mRNA splicing, via spliceosome
26	−6.63	NULL	1 / 15	MF	receptor signaling complex scaffold activity
27	−6.63	NULL	1 / 15	GSEA C2	SUNG_METASTASIS_STROMA_DN
28	−6.61	NULL	11 / 171	miRNA target starBase	hsa−miR−369−3p
29	−6.55	NULL	97 / 4640	CC	nucleus
30	−6.54	NULL	14 / 229	miRNA target starBase	hsa−miR−520g
31	−6.51	NULL	3 / 59	miRNA target starBase	hsa−miR−526b*
32	−6.47	NULL	27 / 595	MF	RNA binding
33	−6.46	NULL	11 / 229	BP	RNA splicing
34	−6.39	NULL	5 / 38	miRNA target starBase	hsa−miR−1277
35	−6.37	NULL	8 / 93	CC	spliceosomal complex
36	−6.36	NULL	17 / 303	miRNA target starBase	hsa−miR−302b
37	−6.35	NULL	17 / 271	miRNA target starBase	hsa−miR−101
38	−6.33	NULL	22 / 538	miRNA target starBase	hsa−miR−17
39	−6.21	NULL	1 / 11	MF	histone methyltransferase activity
40	−6.11	NULL	2 / 14	GSEA C2	BIOCARTA_TEL_PATHWAY



GW_044

Local Summary

%DE = 0.64

metagenes = 40

genes = 472

genes in genesets = 468

genes with fdr < 0.1 = 178 (32 + / 146 −)

genes with fdr < 0.05 = 140 (28 + / 112 −)

genes with fdr < 0.01 = 105 (19 + / 86 −)

<r> metagenes = 0.9

<r> genes = 0.24

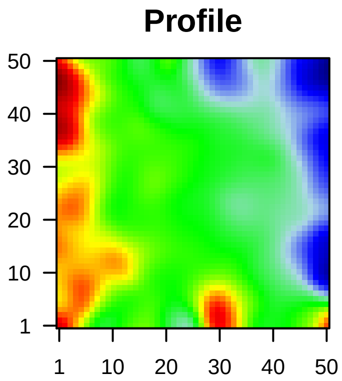
<FC> = −0.22

<shrinkage−t> = −7.8

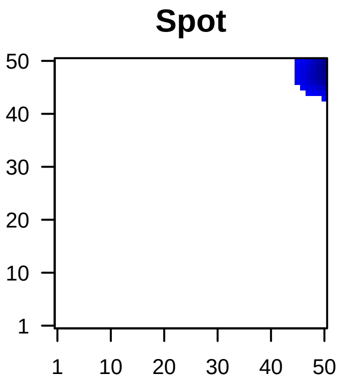
<p−value> = 0.01

<fdr> = 0.65

Profile



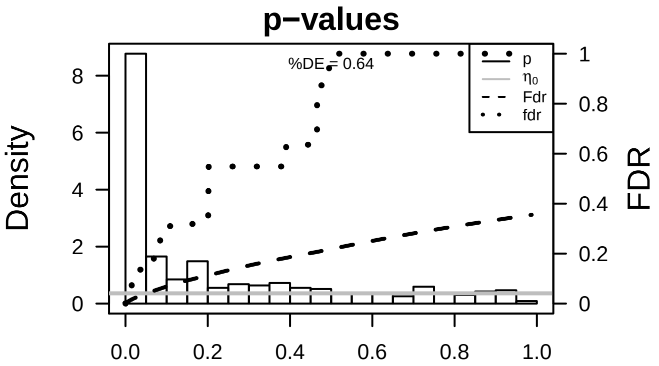
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	216	−1.47	2e−16	8e−15	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGNC
2	3856	−2	2e−16	8e−15	50 x 48	keratin 8 pseudogene 3 [Source:HGNC Symbol;Acc:31056]
3	4953	−1.8	2e−16	8e−15	50 x 50	ornithine decarboxylase 1 [Source:HGNC Symbol;Acc:8109]
4	26227	−1.41	2e−16	8e−15	50 x 46	phosphoglycerate dehydrogenase [Source:HGNC Symbol;Ac
5	11166	−1.76	2e−16	8e−15	50 x 50	SRY (sex determining region Y)−box 21 [Source:HGNC Symb
6	6657	−1.33	4e−15	2e−12	50 x 50	SRY (sex determining region Y)−box 2 [Source:HGNC Symbo
7	445	−1.3	1e−14	8e−12	50 x 47	argininosuccinate synthase 1 [Source:HGNC Symbol;Acc:75
8	7037	1.16	6e−14	3e−11	47 x 50	transferrin receptor [Source:HGNC Symbol;Acc:11763]
9	200634	1.22	5e−13	3e−11	50 x 49	keratinocyte associated protein 3 [Source:HGNC Symbol;Acc
10	4922	−1.21	6e−13	3e−11	50 x 50	neurotensin [Source:HGNC Symbol;Acc:8038]
11	1780	1.21	6e−13	1e−10	50 x 50	dynein, cytoplasmic 1, intermediate chain 1 [Source:HGNC S
12	4915	−1.19	1e−12	3e−10	50 x 50	neurotrophic tyrosine kinase, receptor, type 2 [Source:HGNC
13	655	−1.17	3e−12	7e−10	50 x 50	bone morphogenetic protein 7 [Source:HGNC Symbol;Acc:1
14	256764	1.15	7e−12	3e−08	50 x 50	WD repeat domain 72 [Source:HGNC Symbol;Acc:26790]
15	339512	−1.07	2e−10	3e−08	50 x 50	chromosome 1 open reading frame 110 [Source:HGNC Symb
16	604	1.06	3e−10	3e−08	50 x 50	B−cell CLL/lymphoma 6 [Source:HGNC Symbol;Acc:1001]
17	25975	1.05	5e−10	2e−07	48 x 50	EGF−like−domain, multiple 6 [Source:HGNC Symbol;Acc:32
18	84171	−1.01	2e−09	2e−07	50 x 49	lysyl oxidase−like 4 [Source:HGNC Symbol;Acc:17171]
19	7358	−1	3e−09	4e−07	50 x 50	UDP−glucose 6−dehydrogenase [Source:HGNC Symbol;Acc
20	51804	−0.98	7e−09	4e−07	50 x 46	SIX homeobox 4 [Source:HGNC Symbol;Acc:10890]

p−values



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset
1	−15.05	NULL	5 / 15	GSEA C2 KEGG_GLUTATHIONE_METABOLISM
2	−13.01	NULL	3 / 9	GSEA C2 REACTOME_METABOLISM_OF_AMINO_ACIDS
3	−12.55	NULL	2 / 7	GSEA C2 MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
4	−10.87	NULL	4 / 13	GSEA C2 LEE_LIVER_CANCER_SURVIVAL_DN
5	−10.53	NULL	7 / 11	GSEA C2 KALMA_E2F1_TARGETS
6	−10.39	NULL	3 / 7	GSEA C2 REACTOME_G1_S_TRANSITION
7	−10.33	NULL	4 / 8	GSEA C2 REACTOME_E2F_TRANSCRIPTIONAL_TARGETS_AT_G1_S
8	−10.19	NULL	2 / 12	GSEA C2 MOROSETTI_FACIOSCAPULOHUMERAL_MUSCULAR_DISTRO
9	−9.92	NULL	12 / 30	BP DNA strand elongation involved in DNA replication
10	−9.69	NULL	3 / 11	MF glutathione binding
11	−9.69	NULL	3 / 11	GSEA C2 KEGG_DRUG_METABOLISM_CYTOCHROME_P450
12	−9.66	NULL	10 / 16	GSEA C2 EGUCHI_CELL_CYCLE_RB1_TARGETS
13	−9.64	NULL	4 / 13	GSEA C2 KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_
14	−9.51	NULL	3 / 12	GSEA C2 CASORELLI_ACUTE_PROMYELOCYTIC_LEUKEMIA_DN
15	−9.51	NULL	6 / 11	GSEA C2 REACTOME_UNWINDING_OF_DNA
16	−9.3	NULL	4 / 16	GSEA C2 KAN_RESPONSE_TO_ARSENIC_TRIOXIDE
17	−9.08	NULL	4 / 16	GSEA C2 FUJII_YBX1_TARGETS_DN
18	−8.97	NULL	4 / 15	GSEA C2 WHITEFORD_PEDIATRIC_CANCER_MARKERS
19	−8.89	NULL	2 / 6	GSEA C2 GAUSSMANN_MLL_AF4_FUSION_TARGETS_D_DN
20	−8.84	NULL	1 / 7	GSEA C2 REACTOME_REGULATION_OF_ORNITHINE_DECARBOXYLAS
21	−8.83	NULL	5 / 20	MF glutathione transferase activity
22	−8.82	NULL	7 / 16	GSEA C2 SONG_TARGETS_OF_IE86_CMV_PROTEIN
23	−8.82	NULL	6 / 16	GSEA C2 PUJANA_BREAST_CANCER_WITH_BRCA1_MUTATED_UP
24	−8.81	NULL	4 / 14	GSEA C2 FOURNIER_ACINAR_DEVELOPMENT_LATE_2
25	−8.75	NULL	4 / 16	GSEA C2 KOBAYASHI_EGFR_SIGNALING_24HR_DN
26	−8.74	NULL	3 / 14	GSEA C2 RUIZ_TNC_TARGETS_DN
27	−8.67	NULL	6 / 25	BP glutathione derivative biosynthetic process
28	−8.66	NULL	4 / 11	GSEA C2 REACTOME_E2F_MEDIATED_REGULATION_OF_DNA_REPLIC
29	−8.63	NULL	4 / 13	BP regulation of blood vessel size
30	−8.62	NULL	5 / 19	BP cellular amino acid biosynthetic process
31	−8.53	NULL	3 / 19	BP anatomical structure formation involved in morphogenesis
32	−8.44	NULL	5 / 16	GSEA C2 CAIRO_HEPATOBLASTOMA_CLASSES_UP
33	−8.42	NULL	3 / 16	GSEA C2 BOYAULT_LIVER_CANCER_SUBCLASS_G1_DN
34	−8.33	NULL	3 / 12	GSEA C2 SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_DN
35	−8.23	NULL	4 / 16	GSEA C2 HORIUCHI_WTAP_TARGETS_DN
36	−8.21	NULL	2 / 12	BP cellular aldehyde metabolic process
37	−8.21	NULL	1 / 8	GSEA C2 PUJANA_CHEK2_PCC_NETWORK
38	−8.09	NULL	5 / 14	GSEA C2 SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_UP
39	−7.98	NULL	2 / 10	GSEA C2 CONRAD_STEM_CELL
40	−7.95	NULL	2 / 23	BP stem cell differentiation