GW_292

Global Summary

%DE = 0.16

genes with fdr < 0.2 = 1991 (1149 + / 842 −)

genes with fdr < 0.1 = 1611 (963 + / 648 −)

genes with fdr < 0.05 = 1265 (789 + / 476 −)

genes with fdr < 0.01 = 893 (592 + / 301 −)

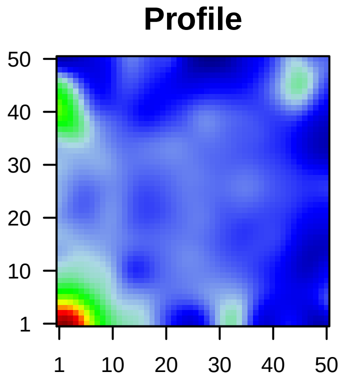
genes in genesets = 16332

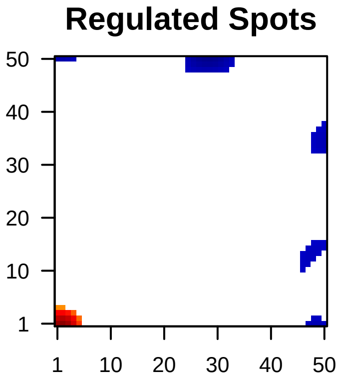
<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.09

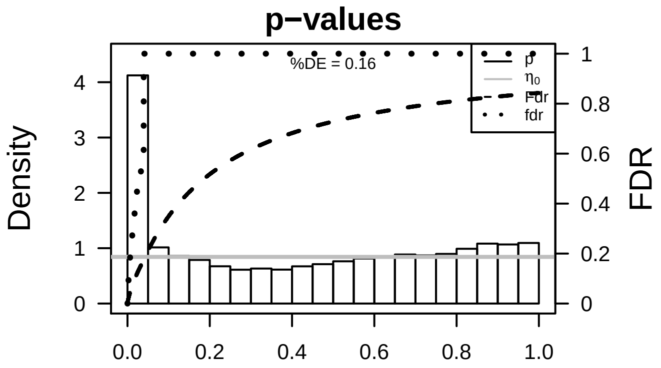
<fdr> = 0.84





Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	59	1.57	2e−16	3e−14	3 x 1	actin, alpha 2, smooth muscle, aorta [Source:HGNC Symbol;
2	124	2.24	2e−16	3e−14	50 x 11	alcohol dehydrogenase 1A (class I), alpha polypeptide [Sourc
3	126	1.93	2e−16	3e−14	50 x 12	alcohol dehydrogenase 1C (class I), gamma polypeptide [Sou
4	57016	−2.05	2e−16	3e−14	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
5	441282	−1.75	2e−16	3e−14	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC S
6	249	1.86	2e−16	3e−14	6 x 1	alkaline phosphatase, liver/bone/kidney [Source:HGNC Symb
7	401138	1.68	2e−16	3e−14	1 x 5	amelotin [Source:HGNC Symbol;Acc:33188]
8	60370	1.58	2e−16	3e−14	1 x 39	arginine vasopressin−induced 1 [Source:HGNC Symbol;Acc:
9	633	1.87	2e−16	3e−14	3 x 1	biglycan [Source:HGNC Symbol;Acc:1044]
10	650	1.79	2e−16	3e−14	1 x 4	bone morphogenetic protein 2 [Source:HGNC Symbol;Acc:1
11	24141	1.47	2e−16	3e−14	7 x 1	lysosomal−associated membrane protein family, member 5 [
12	51806	1.5	2e−16	3e−14	4 x 50	calmodulin−like 5 [Source:HGNC Symbol;Acc:18180]
13	8900	1.71	2e−16	3e−14	1 x 42	cyclin A1 [Source:HGNC Symbol;Acc:1577]
14	1009	1.57	2e−16	3e−14	3 x 1	cadherin 11, type 2, OB−cadherin (osteoblast) [Source:HGN
15	1041	1.79	2e−16	3e−14	1 x 46	corneodesmosin [Source:HGNC Symbol;Acc:1802]
16	1152	1.52	2e−16	3e−14	1 x 17	creatine kinase, brain [Source:HGNC Symbol;Acc:1991]
17	22802	−1.64	2e−16	3e−14	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
18	26047	2.34	2e−16	3e−14	50 x 50	contactin associated protein−like 2 [Source:HGNC Symbol;A
19	1307	1.7	2e−16	3e−14	1 x 2	collagen, type XVI, alpha 1 [Source:HGNC Symbol;Acc:2193]
20	1277	2.2	2e−16	3e−14	2 x 1	collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]



Global Geneset Analysis

Overexpressed

Rank	GSZ	p−value	#all	Geneset	
1	16.18	NULL	250	Lymphoma	LENZ_Stromal signature 1
2	14.93	NULL	190	CC	extracellular matrix
3	13.58	NULL	242	BP	extracellular matrix organization
4	13.24	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
5	13.14	NULL	683	CC	extracellular space
6	12.84	NULL	16	MMML CGS	MACIEJ_MMML 1
7	11.35	NULL	449	Chr	Chr 20
8	10.98	NULL	1182	CC	extracellular region
9	10.53	NULL	57	MF	extracellular matrix structural constituent
10	9.72	NULL	69	BP	extracellular matrix disassembly
11	9.71	NULL	183	CC	proteinaceous extracellular matrix
12	9.7	NULL	37	BP	collagen fibril organization
13	9.37	NULL	16	GSEA C2	AMIT_EGF_RESPONSE_60_MCF10A
14	9.15	NULL	19	MF	extracellular matrix binding
15	8.56	NULL	11	MF	platelet−derived growth factor binding
16	8.31	NULL	13	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
17	8.31	NULL	119	Lymphoma	ROSOLOWSKI_green total
18	8.02	NULL	10	GSEA C2	NIKOLSKY_BREAST_CANCER_20Q12_Q13_AMPLICON
19	7.88	NULL	6	GSEA C2	AGARWAL_AKT_PATHWAY_TARGETS
20	7.71	NULL	13	GSEA C2	FRIDMAN_SENESCENCE_UP

Underexpressed

Rank	GSZ	p−value	#all	Geneset	
1	−10.67	NULL	914	Chr	Chr 3
2	−8.88	NULL	15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
3	−8.34	NULL	699	Chr	Chr 5
4	−7.05	NULL	8	GSEA C2	RUNNE_GENDER_EFFECT_UP
5	−6.82	NULL	7	MMML CGS	MACIEJ_MMML 5
6	−6.44	NULL	10	MF	RAGE receptor binding
7	−6.31	NULL	253	BP	translation
8	−6.31	NULL	417	H.Tiss	WIRTH_Immune system
9	−5.72	NULL	187	Chr	Chr 21
10	−5.34	NULL	128	BP	translational initiation
11	−5.24	NULL	714	Chr	Chr 6
12	−5.1	NULL	9	GSEA C2	REACTOME_PEPTIDE_CHAIN_ELONGATION
13	−5.1	NULL	9	GSEA C2	REACTOME_VIRAL_MRNA_TRANSLATION
14	−5.01	NULL	86	Lymphoma	ROSOLOWSKI_red total
15	−4.96	NULL	9	GSEA C2	KEGG_RIBOSOME
16	−4.92	NULL	20	Lymphoma	ROSOLOWSKI_red UP
17	−4.88	NULL	9	GSEA C2	REACTOME_FORMATION_OF_A_POOL_OF_FREE_40S_SUBU
18	−4.82	NULL	10	GSEA C2	REACTOME_TRANSLATION
19	−4.79	NULL	153	MF	structural constituent of ribosome
20	−4.76	NULL	34	Chr	Chr Y

GW_292

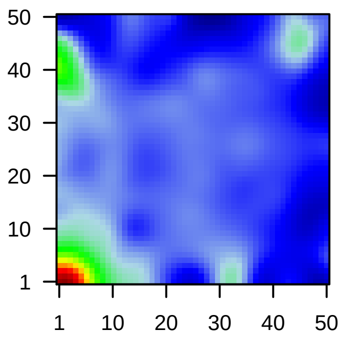
Local Summary

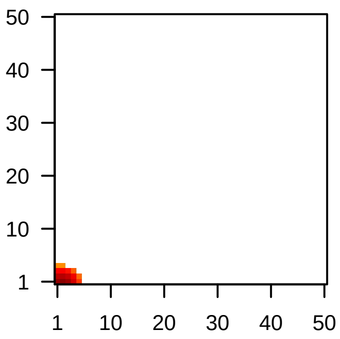
%DE = 0.82
metagenes = 16
genes = 258
genes in genesets = 257

genes with fdr < 0.1 = 172 (153 + / 19 −)
genes with fdr < 0.05 = 162 (147 + / 15 −)
genes with fdr < 0.01 = 154 (141 + / 13 −)

<r> metagenes = 0.96
<r> genes = 0.4

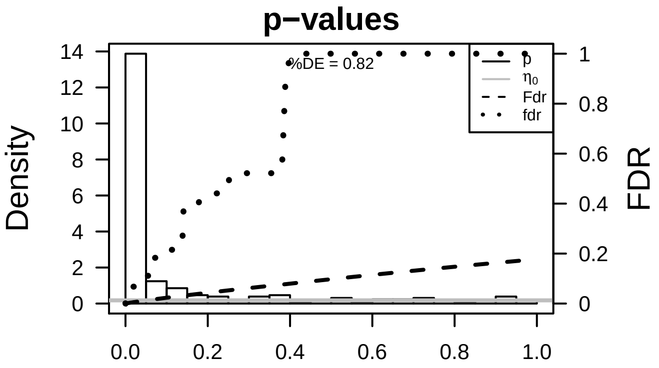
<FC> = 0.59
<shrinkage−t> = 20.87
<p−value> = 0
<fdr> = 0.36


Profile


Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	59	1.57	2e−16	3e−16	3 x 1	actin, alpha 2, smooth muscle, aorta [Source:HGNC Symbol;
2	633	1.87	2e−16	3e−16	3 x 1	biglycan [Source:HGNC Symbol;Acc:1044]
3	650	1.79	2e−16	3e−16	1 x 4	bone morphogenetic protein 2 [Source:HGNC Symbol;Acc:1
4	1009	1.57	2e−16	3e−16	3 x 1	cadherin 11, type 2, OB−cadherin (osteoblast) [Source:HGN
5	1307	1.7	2e−16	3e−16	1 x 2	collagen, type XVI, alpha 1 [Source:HGNC Symbol;Acc:2193]
6	1277	2.2	2e−16	3e−16	2 x 1	collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
7	1278	2.14	2e−16	3e−16	2 x 1	collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198]
8	1281	1.66	2e−16	3e−16	2 x 1	collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]
9	1289	1.84	2e−16	3e−16	2 x 1	collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209]
10	1290	1.66	2e−16	3e−16	2 x 1	collagen, type V, alpha 2 [Source:HGNC Symbol;Acc:2210]
11	1490	2.03	2e−16	3e−16	3 x 1	connective tissue growth factor [Source:HGNC Symbol;Acc:2
12	1513	1.68	2e−16	3e−16	4 x 1	cathepsin K [Source:HGNC Symbol;Acc:2536]
13	2919	1.71	2e−16	3e−16	1 x 1	chemokine (C−X−C motif) ligand 1 (melanoma growth stimula
14	2920	1.81	2e−16	3e−16	1 x 1	chemokine (C−X−C motif) ligand 2 [Source:HGNC Symbol;A
15	6372	1.65	2e−16	3e−16	1 x 1	chemokine (C−X−C motif) ligand 6 [Source:HGNC Symbol;A
16	3491	1.51	2e−16	3e−16	2 x 1	cysteine−rich, angiogenic inducer, 61 [Source:HGNC Symbol
17	84624	2.26	2e−16	3e−16	3 x 1	fibronectin type III domain containing 1 [Source:HGNC Symb
18	8870	1.99	2e−16	3e−16	1 x 3	immediate early response 3 [Source:HGNC Symbol;Acc:539
19	3553	1.52	2e−16	3e−16	1 x 1	interleukin 1, beta [Source:HGNC Symbol;Acc:5992]
20	3569	1.79	2e−16	3e−16	1 x 1	interleukin 6 (interferon, beta 2) [Source:HGNC Symbol;Acc:


p−values

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	39.52	NULL	15 / 16	MMML CGS	MACIEJ_MMML 1
2	36.89	NULL	12 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
3	34.94	NULL	71 / 250	Lymphoma	LENZ_Stromal signature 1
4	31.94	NULL	62 / 190	CC	extracellular matrix
5	28.91	NULL	65 / 242	BP	extracellular matrix organization
6	28.06	NULL	8 / 11	MF	platelet−derived growth factor binding
7	27.11	NULL	4 / 6	GSEA C2	AGARWAL_AKT_PATHWAY_TARGETS
8	25.86	NULL	30 / 69	BP	extracellular matrix disassembly
9	25.1	NULL	11 / 19	MF	extracellular matrix binding
10	24.39	NULL	14 / 37	BP	collagen fibril organization
11	23.61	NULL	27 / 64	BP	collagen catabolic process
12	23.11	NULL	19 / 57	MF	extracellular matrix structural constituent
13	22.39	NULL	8 / 12	miRNA target	miR−29c
14	22.18	NULL	6 / 13	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
15	20.79	NULL	2 / 3	GSEA C2	KONDO_HYPOXIA
16	20.37	NULL	4 / 7	GSEA C2	TSUNODA_CISPLATIN_RESISTANCE_UP
17	20.12	NULL	7 / 16	GSEA C2	CROONQUIST_STROMAL_STIMULATION_UP
18	19.97	NULL	5 / 15	GSEA C2	CHANG_POU5F1_TARGETS_UP
19	19.81	NULL	6 / 16	GSEA C2	AMIT_SERUM_RESPONSE_60_MCF10A
20	19.68	NULL	6 / 16	GSEA C2	AMIT_EGF_RESPONSE_60_MCF10A
21	19.61	NULL	7 / 16	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_
22	18.88	NULL	76 / 683	CC	extracellular space
23	18.46	NULL	17 / 68	CC	collagen
24	18.46	NULL	23 / 119	Lymphoma	ROSOLOWSKI_green total
25	18.12	NULL	4 / 5	GSEA C2	COLLER_MYC_TARGETS_DN
26	17.93	NULL	5 / 16	GSEA C2	LU_TUMOR_VASCULATURE_UP
27	17.93	NULL	5 / 15	GSEA C2	TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_DUCTAL_N
28	17.85	NULL	4 / 13	GSEA C2	CHIBA_RESPONSE_TO_TSA_UP
29	17.61	NULL	102 / 1182	CC	extracellular region
30	17.26	NULL	5 / 16	GSEA C2	FERRARI_RESPONSE_TO_FENRETINIDE_UP
31	17	NULL	6 / 13	GSEA C2	FRIDMAN_SENESCENCE_UP
32	16.92	NULL	5 / 10	GSEA C2	KEGG_ECM_RECEPTOR_INTERACTION
33	16.77	NULL	4 / 12	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C2
34	16.4	NULL	7 / 15	GSEA C2	DASU_IL6_SIGNALING_SCAR_DN
35	16.31	NULL	39 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
36	16.31	NULL	39 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
37	16.31	NULL	39 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
38	16.31	NULL	39 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
39	16.22	NULL	4 / 10	BP	protein heterotrimerization
40	16.02	NULL	2 / 6	Glio	Martinez_Glio_hypometh

GW_292

Local Summary

%DE = 0.72

metagenes = 6

genes = 167

genes in genesets = 165

genes with fdr < 0.1 = 78 (13 + / 65 −)

genes with fdr < 0.05 = 51 (9 + / 42 −)

genes with fdr < 0.01 = 33 (8 + / 25 −)

<r> metagenes = 1

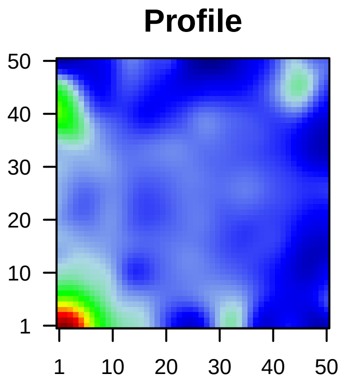
<r> genes = 0.66

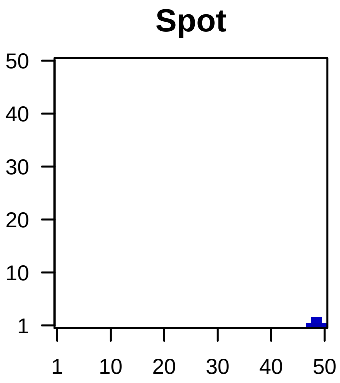
<FC> = −0.21

<shrinkage−t> = −7.24

<p−value> = 0.01

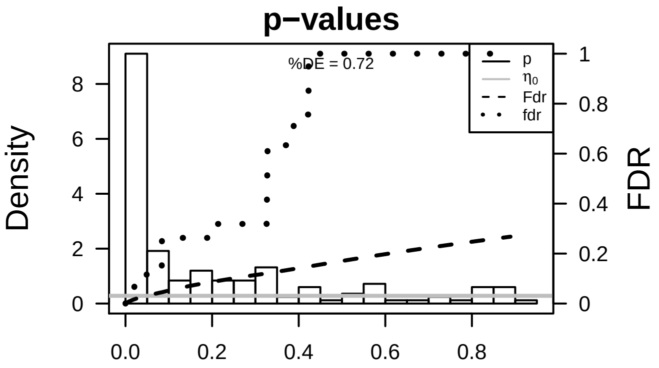
<fdr> = 0.65





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	3120	2.11	2e−16	3e−15	47 x 1	major histocompatibility complex, class II, DQ beta 2 [Source:
2	5920	1.53	2e−16	3e−15	48 x 1	retinoic acid receptor responder (tazarotene induced) 3 [Sour
3	10628	−1.78	2e−16	3e−15	48 x 1	thioredoxin interacting protein [Source:HGNC Symbol;Acc:16
4	3001	1.42	9e−16	2e−12	48 x 1	granzyme A (granzyme 1, cytotoxic T−lymphocyte−associate
5	3512	−1.33	5e−14	5e−10	50 x 1	immunoglobulin J polypeptide, linker protein for immunoglobu
6	1512	1.2	1e−11	3e−08	47 x 1	cathepsin H [Source:HGNC Symbol;Acc:2535]
7	57172	−1.09	7e−10	2e−06	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
8	7412	0.96	5e−08	2e−06	50 x 1	vascular cell adhesion molecule 1 [Source:HGNC Symbol;Ac
9	54855	−0.94	9e−08	2e−06	49 x 1	family with sequence similarity 46, member C [Source:HGNC
10	51755	−0.94	1e−07	2e−06	49 x 1	cyclin−dependent kinase 12 [Source:HGNC Symbol;Acc:242
11	915	−0.93	1e−07	8e−05	49 x 1	CD3d molecule, delta (CD3−TCR complex) [Source:HGNC S
12	939	−0.81	5e−06	8e−05	49 x 1	CD27 molecule [Source:HGNC Symbol;Acc:11922]
13	5730	−0.8	6e−06	8e−05	50 x 1	prostaglandin D2 synthase 21kDa (brain) [Source:HGNC Syn
14	393	0.79	8e−06	8e−05	49 x 1	Rho GTPase activating protein 4 [Source:HGNC Symbol;Acc:
15	5450	−0.79	8e−06	8e−05	48 x 1	POU class 2 associating factor 1 [Source:HGNC Symbol;Acc:
16	3543	−0.72	9e−06	7e−04	49 x 1	immunoglobulin lambda−like polypeptide 1 [Source:HGNC Sy
17	3669	−0.74	2e−05	1e−03	48 x 1	interferon stimulated exonuclease gene 20kDa [Source:HGN
18	91353	−0.7	7e−05	1e−03	48 x 1	
19	10320	−0.7	8e−05	1e−03	49 x 1	IKAROS family zinc finger 1 (Ikaros) [Source:HGNC Symbol;
20	51466	−0.68	1e−04	1e−03	48 x 1	Enah/Vasp−like [Source:HGNC Symbol;Acc:20234]



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−27.88	NULL	3 / 5	GSEA C2	WONG_ENDOMETRIAL_CANCER_LATE
2	−23.81	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
3	−17.32	NULL	72 / 417	H.Tiss	WIRTH_Immune system
4	−17.32	NULL	6 / 11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
5	−14.71	NULL	64 / 553	Cancer	Lembcke_Colonic Inflammation
6	−14.66	NULL	3 / 14	GSEA C2	WINNEPENNINCKX_MELANOMA_METASTASIS_DN
7	−14.65	NULL	2 / 15	GSEA C2	SHIPP_DLBCL_VS_FOLLICULAR_LYMPHOMA_DN
8	−13.91	NULL	5 / 11	GSEA C2	BIOCARTA_THELPER_PATHWAY
9	−13.89	NULL	4 / 10	GSEA C2	LEE_DIFFERENTIATING_T_LYMPHOCYTE
10	−13.71	NULL	5 / 13	Cancer	GENTLES_modul18
11	−13.62	NULL	4 / 10	GSEA C2	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_
12	−13.29	NULL	1 / 2	GSEA C2	GUTIERREZ_MULTIPLE_MYELOMA_UP
13	−12.91	NULL	3 / 13	GSEA C2	HAHTOLA_MYCOSIS_FUNGOIDES_DN
14	−12.55	NULL	2 / 15	GSEA C2	KENNY_CTNNB1_TARGETS_DN
15	−11.41	NULL	1 / 11	GSEA C2	AMIT_EGF_RESPONSE_20_HELA
16	−10.97	NULL	4 / 13	GSEA C2	BIOCARTA_IL17_PATHWAY
17	−10.88	NULL	1 / 12	GSEA C2	TSAI_DNAJB4_TARGETS_UP
18	−10.57	NULL	2 / 8	GSEA C2	REACTOME_IMMUNOREGULATORY_INTERACTIONS_BETWEE
19	−9.63	NULL	1 / 15	GSEA C2	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_
20	−9.63	NULL	1 / 15	GSEA C2	NADERI_BREAST_CANCER_PROGNOSIS_DN
21	−9.63	NULL	1 / 15	GSEA C2	MARKS_HDAC_TARGETS_UP
22	−9.6	NULL	3 / 7	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
23	−9.3	NULL	1 / 16	GSEA C2	GAJATE_RESPONSE_TO_TRABECTEDIN_UP
24	−9.26	NULL	6 / 15	GSEA C2	FINAK_BREAST_CANCER_SDPP_SIGNATURE
25	−9.2	NULL	7 / 45	BP	T cell activation
26	−8.99	NULL	1 / 17	miRNA target−starBase	hsa−miR−551b
27	−8.85	NULL	2 / 16	GSEA C2	CASORELLI_ACUTE_PROMYELOCYTIC_LEUKEMIA_UP
28	−8.74	NULL	2 / 9	GSEA C2	GUTIERREZ_WALDENSTROEMS_MACROGLOBULINEMIA_1_D
29	−8.72	NULL	1 / 18	miRNA target−starBase	hsa−miR−551a
30	−8.61	NULL	2 / 7	Glio	Donson−adaptive−immunity−associated with LTS in HGA
31	−8.5	NULL	5 / 12	GSEA C2	BIOCARTA_CTL_PATHWAY
32	−8.48	NULL	2 / 10	GSEA C2	GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
33	−8.46	NULL	4 / 14	GSEA C2	FINETTI_BREAST_CANCER_KINOME_GREEN
34	−8.31	NULL	1 / 11	GSEA C2	GUTIERREZ_CHRONIC_LYMPHOCYTIC_LEUKEMIA_UP
35	−8.2	NULL	1 / 6	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_8
36	−8.05	NULL	3 / 27	MF	antigen binding
37	−8.03	NULL	19 / 162	CC	external side of plasma membrane
38	−7.93	NULL	5 / 12	BP	immunoglobulin mediated immune response
39	−7.77	NULL	5 / 11	BP	positive regulation of B cell differentiation
40	−7.73	NULL	3 / 28	BP	T cell differentiation

GW_292

Local Summary

%DE = 0.71

metagenes = 17

genes = 161

genes in genesets = 156

genes with fdr < 0.1 = 62 (13 + / 49 −)

genes with fdr < 0.05 = 62 (13 + / 49 −)

genes with fdr < 0.01 = 25 (5 + / 20 −)

<r> metagenes = 0.95

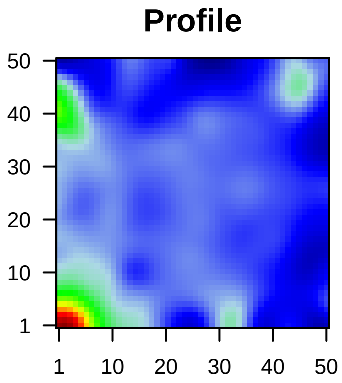
<r> genes = 0.3

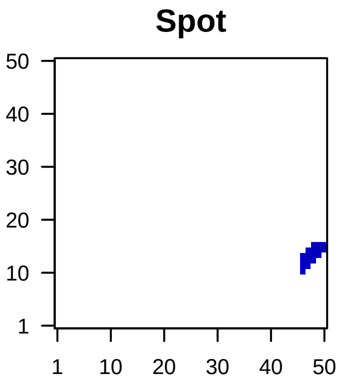
<FC> = −0.19

<shrinkage−t> = −6.81

<p−value> = 0.02

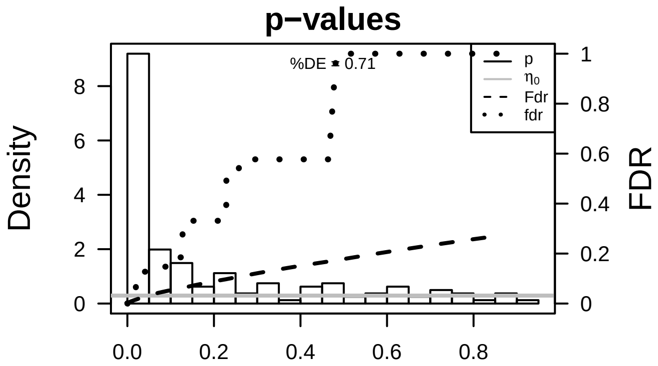
<fdr> = 0.64


Profile


Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	5382	1.34	3e−14	1e−09	48 x 15	postmeiotic segregation increased 2 pseudogene 4 [Source:H
2	909	1.17	3e−11	1e−09	50 x 16	CD1a molecule [Source:HGNC Symbol;Acc:1634]
3	51315	−1.16	5e−11	6e−06	47 x 14	lysine−rich coiled−coil 1 [Source:HGNC Symbol;Acc:28039]
4	55788	−0.93	1e−07	6e−06	46 x 11	LMBR1 domain containing 1 [Source:HGNC Symbol;Acc:230
5	55577	−0.91	3e−07	1e−05	47 x 12	N−acetylglucosamine kinase [Source:HGNC Symbol;Acc:171
6	26002	−0.89	5e−07	1e−05	50 x 16	monooxygenase, DBH−like 1 [Source:HGNC Symbol;Acc:21
7	4602	−0.88	7e−07	1e−04	50 x 16	v−myb avian myeloblastosis viral oncogene homolog [Source
8	285195	−0.82	4e−06	1e−04	49 x 14	solute carrier family 9, subfamily A (NHE9, cation proton anti
9	4255	−0.78	9e−06	1e−04	48 x 15	O−6−methylguanine−DNA methyltransferase [Source:HGNC
10	8799	−0.77	1e−05	1e−04	46 x 12	peroxisomal biogenesis factor 11 beta [Source:HGNC Symbo
11	79762	0.76	2e−05	1e−04	50 x 15	chromosome 1 open reading frame 115 [Source:HGNC Sym
12	84188	−0.75	2e−05	1e−04	48 x 15	fatty acyl CoA reductase 1 [Source:HGNC Symbol;Acc:2622
13	51660	−0.75	2e−05	5e−04	48 x 14	mitochondrial pyruvate carrier 1 [Source:HGNC Symbol;Acc:
14	4214	−0.73	4e−05	5e−04	47 x 13	mitogen−activated protein kinase kinase kinase 1, E3 ubiquiti
15	2051	0.72	5e−05	5e−04	48 x 14	EPH receptor B6 [Source:HGNC Symbol;Acc:3396]
16	9649	−0.72	5e−05	5e−04	50 x 15	Ral GEF with PH domain and SH3 binding motif 1 [Source:H
17	7915	−0.71	6e−05	6e−04	50 x 16	aldehyde dehydrogenase 5 family, member A1 [Source:HGN
18	217	0.7	7e−05	1e−03	50 x 15	aldehyde dehydrogenase 2 family (mitochondrial) [Source:HG
19	6138	−0.69	1e−04	1e−03	48 x 13	ribosomal protein L15 [Source:HGNC Symbol;Acc:10306]
20	6493	−0.67	2e−04	1e−03	49 x 14	single−minded family bHLH transcription factor 2 [Source:HG


p−values

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−10.4	NULL	2 / 16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_A
2	−9.22	NULL	2 / 11	GSEA C2	RIGGI_EWING_SARCOMA_PROGENITOR_DN
3	−8	NULL	2 / 14	GSEA C2	SMID_BREAST_CANCER_LUMINAL_A_UP
4	−7.71	NULL	2 / 15	GSEA C2	POOLA_INVASIVE_BREAST_CANCER_DN
5	−7.52	NULL	2 / 16	GSEA C2	CHANDRAN_METASTASIS_DN
6	−7.48	NULL	1 / 2	TF	MYC_Cell cycle DOWN
7	−7.43	NULL	1 / 8	GSEA C2	ADDYA_ERYTHROID_DIFFERENTIATION_BY_HEMIN
8	−7.09	NULL	2 / 13	BP	N−acetylglucosamine metabolic process
9	−7.07	NULL	1 / 9	GSEA C2	RODWELL_AGING_KIDNEY_UP
10	−6.96	NULL	1 / 9	GSEA C2	BASSO_CD40_SIGNALING_UP
11	−6.96	NULL	1 / 9	GSEA C2	GUTIERREZ_WALDENSTROEMS_MACROGLOBULINEMIA_2
12	−6.67	NULL	1 / 10	GSEA C2	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_
13	−6.61	NULL	1 / 8	GSEA C2	SCHLESINGER_METHYLATED_IN_COLON_CANCER
14	−6.57	NULL	1 / 10	BP	positive regulation of histone H3−K4 methylation
15	−6.33	NULL	1 / 11	GSEA C2	NUYTTEN_EZH2_TARGETS_UP
16	−6.24	NULL	1 / 11	BP	homeostasis of number of cells
17	−6.24	NULL	1 / 11	Pathw Ac	BENTINK_e2f3.2
18	−6.24	NULL	1 / 11	GSEA C2	DOANE_BREAST_CANCER_ESR1_UP
19	−6.24	NULL	1 / 11	GSEA C2	TURJANSKI_MAPK1_AND_MAPK2_TARGETS
20	−6.15	NULL	2 / 10	BP	cellular response to antibiotic
21	−6.04	NULL	1 / 12	GSEA C2	PEREZ_TP53_TARGETS
22	−6.04	NULL	1 / 12	GSEA C2	BOHN_PRIMARY_IMMUNODEFICIENCY_SYNDROM_DN
23	−6.04	NULL	1 / 12	GSEA C2	CHIANG_LIVER_CANCER_SUBCLASS_INTERFERON_UP
24	−5.95	NULL	1 / 12	GSEA C2	DING_LUNG_CANCER_BY_MUTATION_RATE
25	−5.95	NULL	2 / 14	GSEA C2	HEDENFALK_BREAST_CANCER_BRACX_UP
26	−5.85	NULL	1 / 10	GSEA C2	HANN_RESISTANCE_TO_BCL2_INHIBITOR_DN
27	−5.79	NULL	1 / 10	BP	peroxisome fission
28	−5.78	NULL	1 / 9	GSEA C2	BIOCARTA_NFKB_PATHWAY
29	−5.78	NULL	1 / 13	GSEA C2	LINDGREN_BLADDER_CANCER_CLUSTER_2B
30	−5.78	NULL	1 / 13	GSEA C2	BENPORATH_EED_TARGETS
31	−5.78	NULL	1 / 13	GSEA C2	CERVERA_SDHB_TARGETS_2
32	−5.78	NULL	1 / 13	GSEA C2	BROWNE_HCMV_INFECTION_48HR_DN
33	−5.69	NULL	1 / 13	GSEA C2	OSADA_ASCL1_TARGETS_UP
34	−5.69	NULL	1 / 13	GSEA C2	ALONSO_METASTASIS_UP
35	−5.69	NULL	1 / 13	GSEA C2	RAY_TARGETS_OF_P210_BCR_ABL_FUSION_DN
36	−5.59	NULL	1 / 8	GSEA C2	BOQUEST_STEM_CELL_DN
37	−5.54	NULL	1 / 14	GSEA C2	DAVICIONI_RHABDOMYOSARCOMA_PAX_FOXO1_FUSION_DN
38	−5.54	NULL	1 / 14	GSEA C2	VANHARANTA_UTERINE_FIBROID_DN
39	−5.54	NULL	1 / 14	GSEA C2	PEREZ_TP53_AND_TP63_TARGETS
40	−5.54	NULL	1 / 14	GSEA C2	WEST_ADRENOCORTICAL_TUMOR_DN

GW_292

Local Summary

%DE = 0.43

metagenes = 15

genes = 260

genes in genesets = 260

genes with fdr < 0.1 = 41 (9 + / 32 −)

genes with fdr < 0.05 = 37 (8 + / 29 −)

genes with fdr < 0.01 = 14 (5 + / 9 −)

<r> metagenes = 0.97

<r> genes = 0.3

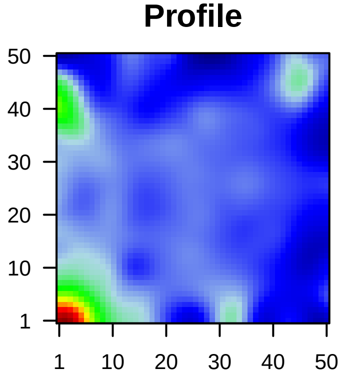
<FC> = −0.15

<shrinkage−t> = −5.32

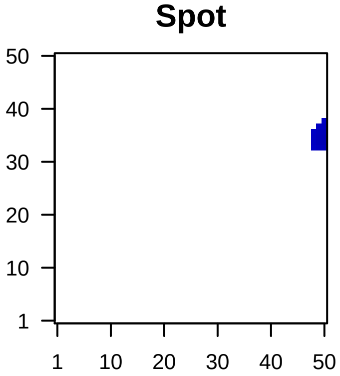
<p−value> = 0.07

<fdr> = 0.77

Profile



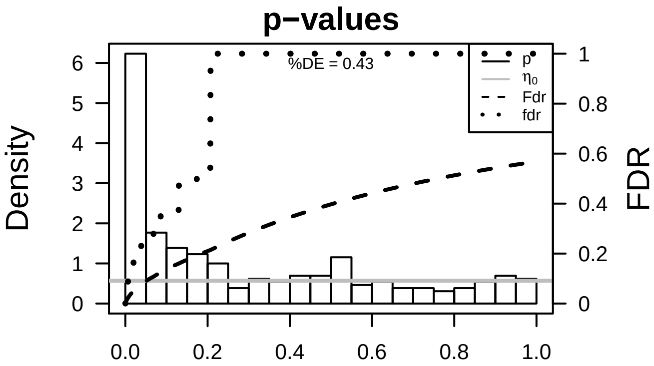
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	25874	−1	1e−08	1e−04	50 x 34	mitochondrial pyruvate carrier 2 [Source:HGNC Symbol;Acc:2
2	51015	−0.86	1e−06	2e−04	50 x 33	isochorismatase domain containing 1 [Source:HGNC Symbol
3	10099	0.82	4e−06	2e−04	50 x 37	tetraspanin 3 [Source:HGNC Symbol;Acc:17752]
4	23215	0.82	4e−06	4e−04	50 x 37	proline−rich coiled−coil 2C [Source:HGNC Symbol;Acc:2490
5	51455	0.8	6e−06	6e−04	50 x 35	REV1, polymerase (DNA directed) [Source:HGNC Symbol;Ac
6	23469	−0.78	1e−05	2e−03	50 x 36	PHD finger protein 3 [Source:HGNC Symbol;Acc:8921]
7	34	−0.73	3e−05	2e−03	50 x 34	acyl−CoA dehydrogenase, C−4 to C−12 straight chain [Sourc
8	8539	−0.72	4e−05	2e−03	50 x 35	apoptosis inhibitor 5 [Source:HGNC Symbol;Acc:594]
9	58486	−0.72	5e−05	2e−03	50 x 34	zinc finger, BED−type containing 5 [Source:HGNC Symbol;Ac
10	9685	−0.71	6e−05	2e−03	50 x 34	clathrin interactor 1 [Source:HGNC Symbol;Acc:23186]
11	10314	−0.69	9e−05	2e−03	50 x 35	LanC lantibiotic synthetase component C−like 1 (bacterial) [S
12	10311	−0.68	1e−04	2e−03	49 x 34	Down syndrome critical region gene 3 [Source:HGNC Symbo
13	25782	0.68	1e−04	2e−03	49 x 34	RAB3 GTPase activating protein subunit 2 (non−catalytic) [Sc
14	9849	0.67	1e−04	4e−03	50 x 35	zinc finger protein 518A [Source:HGNC Symbol;Acc:29009]
15	3150	−0.67	2e−04	1e−02	50 x 35	high mobility group nucleosome binding domain 1 [Source:HC
16	10015	−0.65	3e−04	1e−02	50 x 34	programmed cell death 6 interacting protein [Source:HGNC S
17	22889	−0.64	3e−04	1e−02	50 x 37	KIAA0907 [Source:HGNC Symbol;Acc:29145]
18	9512	−0.62	5e−04	1e−02	50 x 38	peptidase (mitochondrial processing) beta [Source:HGNC Sy
19	167153	−0.61	6e−04	1e−02	50 x 34	PAP associated domain containing 4 [Source:HGNC Symbol;
20	29058	0.6	6e−04	1e−02	50 x 38	transmembrane protein 230 [Source:HGNC Symbol;Acc:1587

p−values



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−8.3	NULL	6 / 70	miRNA target starBase	hsa−miR−622
2	−6.86	NULL	2 / 8	GSEA C2	RUNNE_GENDER_EFFECT_UP
3	−6.58	NULL	2 / 13	GSEA C2	BROWNE_HCMV_INFECTION_6HR_DN
4	−6.56	NULL	2 / 15	GSEA C2	BARRIER_CANCER_RELAPSE_NORMAL_SAMPLE_UP
5	−6.28	NULL	10 / 93	miRNA target starBase	hsa−miR−10b
6	−6.09	NULL	10 / 95	miRNA target starBase	hsa−miR−1259
7	−6.09	NULL	2 / 15	GSEA C2	HADDAD_T_LYMPHOCYTE_AND_NK_PROGENITOR_UP
8	−6.04	NULL	3 / 11	GSEA C2	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_L
9	−5.69	NULL	1 / 8	GSEA C2	YAGI_AML_WITH_T_8_21_TRANSLOCATION
10	−5.66	NULL	18 / 215	miRNA target starBase	hsa−miR−203
11	−5.62	NULL	3 / 16	GSEA C2	YANG_BREAST_CANCER_ESR1_BULK_UP
12	−5.55	NULL	8 / 58	miRNA target starBase	hsa−miR−455−5p
13	−5.55	NULL	10 / 122	miRNA target starBase	hsa−miR−105
14	−5.39	NULL	5 / 102	miRNA target starBase	hsa−miR−600
15	−5.38	NULL	12 / 146	miRNA target starBase	hsa−miR−922
16	−5.26	NULL	1 / 10	GSEA C2	LUI_THYROID_CANCER_CLUSTER_5
17	−5.26	NULL	1 / 10	GSEA C2	REACTOME_MITOCHONDRIAL_FATTY_ACID_BETA_OXIDATION
18	−5.21	NULL	2 / 15	GSEA C2	GENTILE_UV_RESPONSE_CLUSTER_D2
19	−5.17	NULL	7 / 107	miRNA 3'UTR	AACA−409−3P
20	−5.11	NULL	9 / 142	miRNA target starBase	hsa−miR−522
21	−5.11	NULL	2 / 11	GSEA C2	BIOCARTA_EIF2_PATHWAY
22	−5.11	NULL	2 / 23	miRNA target starBase	hsa−miR−943
23	−5.08	NULL	2 / 19	miRNA target starBase	hsa−miR−542−5p
24	−5.03	NULL	2 / 15	GSEA C2	SHEN_SMARCA2_TARGETS_UP
25	−4.92	NULL	2 / 15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
26	−4.9	NULL	16 / 171	miRNA target starBase	hsa−miR−369−3p
27	−4.88	NULL	25 / 479	miRNA target starBase	hsa−miR−15b
28	−4.87	NULL	8 / 93	CC	spliceosomal complex
29	−4.87	NULL	11 / 127	miRNA target starBase	hsa−miR−335
30	−4.8	NULL	9 / 90	miRNA target starBase	hsa−miR−10a
31	−4.8	NULL	9 / 114	miRNA 3'UTR	TGTA−485−3P
32	−4.77	NULL	1 / 12	GSEA C2	KEGG_PPAR_SIGNALING_PATHWAY
33	−4.76	NULL	13 / 180	miRNA target starBase	hsa−miR−374a
34	−4.74	NULL	2 / 34	miRNA target starBase	hsa−miR−555
35	−4.73	NULL	20 / 699	Chr	Chr 5
36	−4.73	NULL	4 / 38	miRNA target starBase	hsa−miR−770−5p
37	−4.7	NULL	1 / 11	MF	glutathione binding
38	−4.69	NULL	6 / 169	Glio	willscher_GBM_proteomics_wtOnly_Differencelist_
39	−4.68	NULL	8 / 99	miRNA target starBase	hsa−miR−1301
40	−4.6	NULL	2 / 14	GSEA C2	PUJANA_BRCA2_PCC_NETWORK

GW_292

Local Summary

%DE = 0.58

metagenes = 26

genes = 396

genes in genesets = 390

genes with fdr < 0.1 = 126 (16 + / 110 −)

genes with fdr < 0.05 = 88 (15 + / 73 −)

genes with fdr < 0.01 = 60 (6 + / 54 −)

<r> metagenes = 0.89

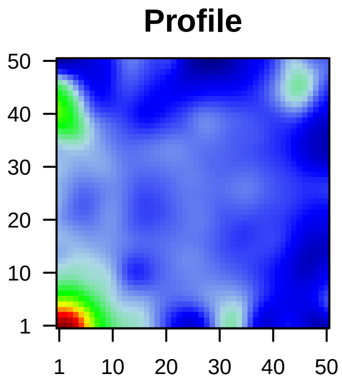
<r> genes = 0.28

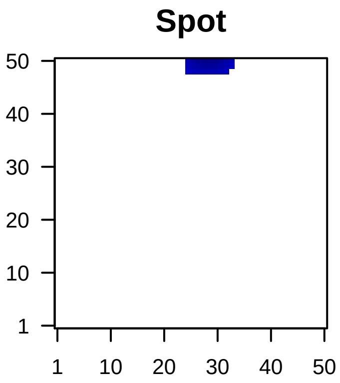
<FC> = −0.2

<shrinkage−t> = −7.11

<p−value> = 0.04

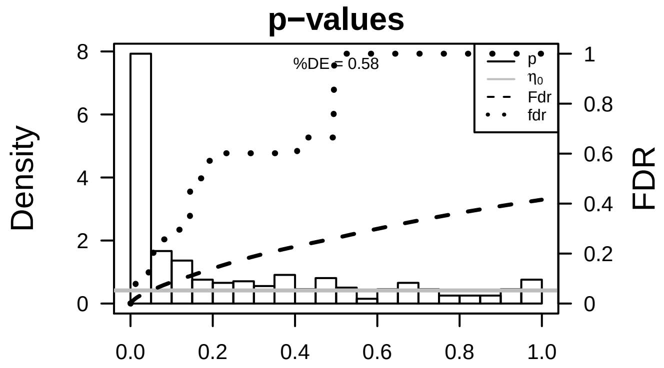
<fdr> = 0.71


Profile


Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	6622	1.38	5e−15	4e−06	27 x 50	synuclein, alpha (non A4 component of amyloid precursor) [S
2	3094	−0.9	3e−08	4e−06	32 x 50	histidine triad nucleotide binding protein 1 [Source:HGNC Syr
3	539	−0.96	5e−08	6e−05	32 x 50	ATP synthase, H+ transporting, mitochondrial F1 complex, O
4	113402	−0.87	7e−07	6e−05	29 x 49	SFT2 domain containing 1 [Source:HGNC Symbol;Acc:21102
5	4724	−0.87	8e−07	1e−04	33 x 50	NADH dehydrogenase (ubiquinone) Fe−S protein 4, 18kDa (N
6	10480	−0.85	1e−06	3e−04	32 x 49	eukaryotic translation initiation factor 3, subunit M [Source:HG
7	26092	0.81	4e−06	3e−04	25 x 49	torsin A interacting protein 1 [Source:HGNC Symbol;Acc:294
8	51074	−0.79	7e−06	3e−04	31 x 49	APAF1 interacting protein [Source:HGNC Symbol;Acc:17581]
9	10412	−0.78	1e−05	3e−04	31 x 49	NSA2 ribosome biogenesis homolog (S. cerevisiae) [Source:I
10	157567	−0.78	1e−05	3e−04	29 x 50	ankyrin repeat domain 46 [Source:HGNC Symbol;Acc:27229]
11	10787	−0.77	1e−05	3e−04	25 x 50	NCK−associated protein 1 [Source:HGNC Symbol;Acc:7666]
12	80255	−0.76	2e−05	3e−04	26 x 50	solute carrier family 35, member F5 [Source:HGNC Symbol;A
13	79627	−0.76	2e−05	3e−04	30 x 50	opioid growth factor receptor−like 1 [Source:HGNC Symbol;A
14	9519	−0.75	2e−05	3e−04	30 x 49	TBP−like 1 [Source:HGNC Symbol;Acc:11589]
15	10694	−0.75	2e−05	3e−04	30 x 48	chaperonin containing TCP1, subunit 8 (theta) [Source:HGNC
16	2992	−0.75	2e−05	4e−04	27 x 48	glycogenin 1 [Source:HGNC Symbol;Acc:4699]
17	7416	−0.72	3e−05	4e−04	27 x 50	voltage−dependent anion channel 1 pseudogene 1 [Source:H
18	10196	−0.74	3e−05	4e−04	29 x 50	protein arginine methyltransferase 3 [Source:HGNC Symbol;A
19	147463	−0.74	3e−05	4e−04	25 x 50	ankyrin repeat domain 29 [Source:HGNC Symbol;Acc:27110]
20	100093630	0.73	3e−05	6e−04	32 x 48	small nucleolar RNA host gene 8 (non−protein coding) [Sourc


p−values

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−10.12	NULL	18 / 83	BP	respiratory electron transport chain
2	−10.04	NULL	5 / 13	GSEA C2	REACTOME_FORMATION_OF_ATP_BY_CHEMIOSMOTIC_COU
3	−9.65	NULL	5 / 14	BP	mitochondrial ATP synthesis coupled proton transport
4	−9.61	NULL	6 / 19	CC	mitochondrial proton−transporting ATP synthase complex
5	−9.3	NULL	5 / 15	BP	ATP synthesis coupled proton transport
6	−9.25	NULL	2 / 3	miRNA target	miR−214
7	−8.22	NULL	4 / 15	MMML CGS	MACIEJ_MMML 22
8	−8.2	NULL	3 / 14	CC	eukaryotic 43S preinitiation complex
9	−7.96	NULL	7 / 35	BP	mitochondrial electron transport, NADH to ubiquinone
10	−7.84	NULL	22 / 152	BP	cellular metabolic process
11	−7.58	NULL	1 / 2	TF	MYC_Signal transduction UP
12	−7.57	NULL	2 / 5	GSEA C2	NAGY_PCAF_COMPONENTS_HUMAN
13	−7.06	NULL	7 / 34	MF	NADH dehydrogenase (ubiquinone) activity
14	−6.84	NULL	7 / 36	CC	mitochondrial respiratory chain complex I
15	−6.79	NULL	5 / 27	BP	DNA−dependent transcription, initiation
16	−6.76	NULL	29 / 699	Chr	Chr 5
17	−6.69	NULL	27 / 304	CC	mitochondrial inner membrane
18	−6.61	NULL	4 / 25	miRNA target−starBase	hsa−miR−1273
19	−6.54	NULL	3 / 13	GSEA C2	SAKAI_TUMOR_INFILTRATING_MONOCYTES_DN
20	−6.22	NULL	3 / 15	CC	eukaryotic translation initiation factor 3 complex
21	−6.17	NULL	3 / 19	BP	ATP biosynthetic process
22	−6.14	NULL	24 / 300	miRNA target−starBase	hsa−miR−561
23	−6.1	NULL	1 / 3	miRNA target	miR−19a
24	−6.01	NULL	19 / 169	Glio	willscher_GBM_proteomics_wtOnly_Differencelist_
25	−5.94	NULL	3 / 13	GSEA C2	NAGY_TFTC_COMPONENTS_HUMAN
26	−5.91	NULL	6 / 45	miRNA target−starBase	hsa−miR−575
27	−5.87	NULL	2 / 8	GSEA C2	NAGY_STAGA_COMPONENTS_HUMAN
28	−5.77	NULL	9 / 75	miRNA target−starBase	hsa−miR−592
29	−5.7	NULL	3 / 14	CC	transcription factor TFTC complex
30	−5.7	NULL	3 / 16	Glio	willscher_GBM_STSwt_proteomics−O_UP
31	−5.57	NULL	6 / 54	MF	translation initiation factor activity
32	−5.54	NULL	14 / 146	miRNA target−starBase	hsa−miR−494
33	−5.49	NULL	2 / 13	CC	eukaryotic 48S preinitiation complex
34	−5.46	NULL	17 / 128	BP	translational initiation
35	−5.37	NULL	12 / 134	miRNA target−starBase	hsa−miR−656
36	−5.31	NULL	4 / 15	GSEA C2	SEIDEN_ONCOGENESIS_BY_MET
37	−5.27	NULL	2 / 14	BP	formation of translation preinitiation complex
38	−5.1	NULL	2 / 19	CC	aggresome
39	−5.07	NULL	19 / 184	miRNA target−starBase	hsa−miR−586
40	−5.04	NULL	2 / 13	GSEA C2	BENPORATH_ES_CORE_NINE_CORRELATED

GW_292

Local Summary

%DE = 0.78

metagenes = 4

genes = 110

genes in genesets = 108

genes with fdr < 0.1 = 73 (15 + / 58 −)

genes with fdr < 0.05 = 63 (13 + / 50 −)

genes with fdr < 0.01 = 59 (12 + / 47 −)

<r> metagenes = 0.99

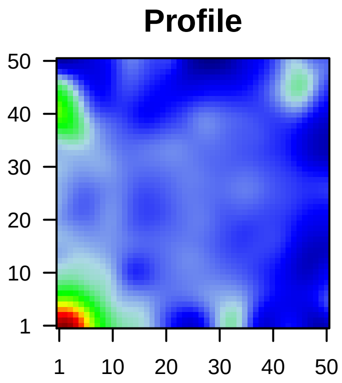
<r> genes = 0.53

<FC> = −0.35

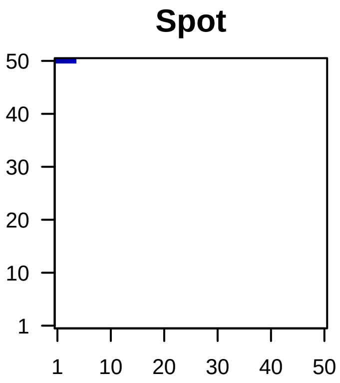
<shrinkage−t> = −12.43

<p−value> = 0

<fdr> = 0.38



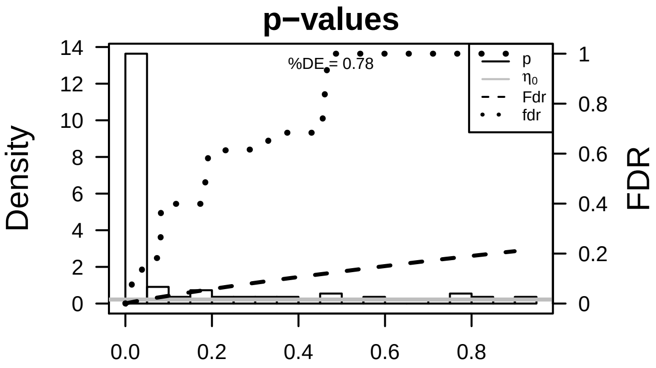
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	57016	−2.05	2e−16	5e−16	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
2	51806	1.5	2e−16	5e−16	4 x 50	calmodulin−like 5 [Source:HGNC Symbol;Acc:18180]
3	22802	−1.64	2e−16	5e−16	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
4	49860	−2.7	2e−16	5e−16	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
5	5653	−1.53	2e−16	5e−16	1 x 50	kallikrein−related peptidase 6 [Source:HGNC Symbol;Acc:63
6	3851	1.46	2e−16	5e−16	1 x 50	keratin 4 [Source:HGNC Symbol;Acc:6441]
7	5055	2.32	2e−16	5e−16	1 x 50	serpin peptidase inhibitor, clade B (ovalbumin), member 2 [S
8	6707	−1.79	2e−16	5e−16	1 x 50	small proline−rich protein 3 [Source:HGNC Symbol;Acc:1126
9	339967	−1.52	2e−16	5e−16	2 x 50	transmembrane protease, serine 11A [Source:HGNC Symbol
10	132724	−1.56	2e−16	5e−16	1 x 50	transmembrane protease, serine 11B [Source:HGNC Symbol
11	3860	−1.3	9e−16	1e−13	1 x 50	keratin 13 [Source:HGNC Symbol;Acc:6415]
12	10874	1.38	6e−15	1e−13	4 x 50	neuromedin U [Source:HGNC Symbol;Acc:7859]
13	6286	1.36	1e−14	1e−13	1 x 50	S100 calcium binding protein P [Source:HGNC Symbol;Acc:1
14	131177	−1.36	2e−14	2e−12	3 x 50	family with sequence similarity 3, member D [Source:HGNC
15	5275	1.31	1e−13	4e−12	1 x 50	serpin peptidase inhibitor, clade B (ovalbumin), member 13 [
16	7739	−1.28	3e−13	4e−12	1 x 50	zinc finger protein 185 (LIM domain) [Source:HGNC Symbol;
17	220963	−1.28	4e−13	2e−10	4 x 50	solute carrier family 16, member 9 [Source:HGNC Symbol;Ac
18	23120	−1.21	8e−12	2e−10	1 x 50	ATPase, class V, type 10B [Source:HGNC Symbol;Acc:13543
19	1992	−1.19	2e−11	1e−09	1 x 50	serpin peptidase inhibitor, clade B (ovalbumin), member 1 [S
20	79755	−1.14	1e−10	1e−09	1 x 50	zinc finger protein 750 [Source:HGNC Symbol;Acc:25843]



p−values

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−23.55	NULL	49 / 135	H.Tiss	WIRTH_Mucosa
2	−18.47	NULL	3 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
3	−16.98	NULL	4 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
4	−14.72	NULL	2 / 10	GSEA C2	SMID_BREAST_CANCER_ERBB2_UP
5	−14.59	NULL	2 / 10	GSEA C2	KEGG_LINOLEIC_ACID_METABOLISM
6	−13.79	NULL	2 / 14	GSEA C2	CHIANG_LIVER_CANCER_SUBCLASS_POLYSOMY7_DN
7	−12.72	NULL	2 / 12	BP	cellular aldehyde metabolic process
8	−11.52	NULL	1 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
9	−11.28	NULL	2 / 15	GSEA C2	LI_AMPLIFIED_IN_LUNG_CANCER
10	−11.28	NULL	1 / 9	GSEA C2	GOUYER_TUMOR_INVASIVENESS
11	−10.93	NULL	2 / 14	GSEA C2	CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U
12	−10.12	NULL	2 / 16	GSEA C2	KOBAYASHI_EGFR_SIGNALING_24HR_UP
13	−10.05	NULL	6 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
14	−9.99	NULL	1 / 6	GSEA C2	SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_DN
15	−9.78	NULL	2 / 15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
16	−9.52	NULL	1 / 5	GSEA C2	NAKAMURA_LUNG_CANCER
17	−9.52	NULL	1 / 5	GSEA C2	NAKAMURA_LUNG_CANCER_MARKERS
18	−9.51	NULL	1 / 12	GSEA C2	ONDER_CDH1_TARGETS_1_UP
19	−9.07	NULL	1 / 13	GSEA C2	BRUECKNER_TARGETS_OF_MIRLET7A3_DN
20	−9.07	NULL	1 / 13	GSEA C2	KEGG_BUTANOATE_METABOLISM
21	−8.8	NULL	3 / 14	GSEA C2	KIM_RESPONSE_TO_TSA_AND_DECITABINE_UP
22	−8.34	NULL	1 / 15	GSEA C2	PUIFFE_INVASION_INHIBITED_BY_ASCITES_UP
23	−8.34	NULL	1 / 15	GSEA C2	LIAO_HAVE_SOX4_BINDING_SITES
24	−8.33	NULL	1 / 6	GSEA C2	CLAUS_PGR_POSITIVE_MENINGIOMA_UP
25	−8.04	NULL	1 / 16	GSEA C2	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_
26	−8.04	NULL	1 / 16	GSEA C2	KAN_RESPONSE_TO_ARSENIC_TRIOXIDE
27	−8.04	NULL	1 / 16	GSEA C2	MAHAJAN_RESPONSE_TO_IL1A_DN
28	−8.04	NULL	1 / 16	GSEA C2	KEGG_FRUCTOSE_AND_MANNOSE_METABOLISM
29	−7.56	NULL	1 / 7	Glio	KIM_epithelial−mesenchymal−transition related genes_decreased
30	−7.5	NULL	2 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
31	−7.3	NULL	1 / 10	GSEA C2	MURAKAMI_UV_RESPONSE_1HR_UP
32	−7.09	NULL	9 / 122	MF	serine−type endopeptidase activity
33	−7.07	NULL	2 / 15	GSEA C2	LUI_THYROID_CANCER_CLUSTER_2
34	−7	NULL	2 / 13	GSEA C2	LUI_THYROID_CANCER_PAX8_PPARG_UP
35	−6.89	NULL	1 / 11	GSEA C2	MURAKAMI_UV_RESPONSE_6HR_DN
36	−6.76	NULL	4 / 13	BP	negative regulation of peptidase activity
37	−6.64	NULL	1 / 8	GSEA C2	LINDGREN_BLADDER_CANCER_CLUSTER_2A_UP
38	−6.46	NULL	11 / 42	BP	keratinization
39	−6.43	NULL	12 / 76	BP	epidermis development
40	−6.42	NULL	1 / 14	BP	tissue regeneration