GW_094

Global Summary

%DE = 0.12

genes with fdr < 0.2 = 1308 (871 + / 437 −)

genes with fdr < 0.1 = 1010 (704 + / 306 −)

genes with fdr < 0.05 = 837 (619 + / 218 −)

genes with fdr < 0.01 = 587 (460 + / 127 −)

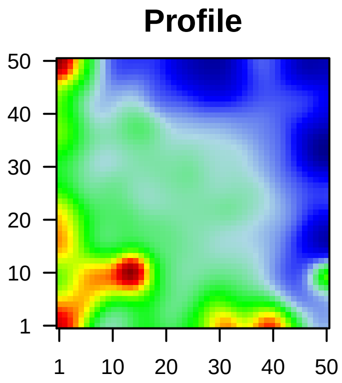
genes in genesets = 16332

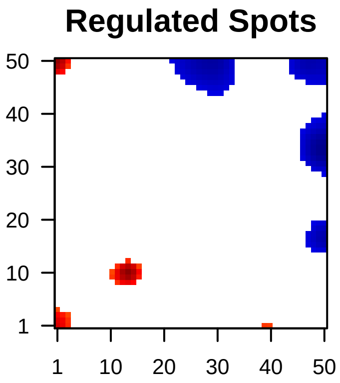
<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.13

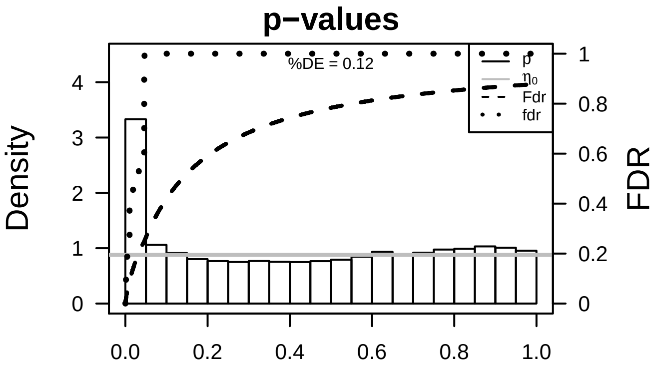
<fdr> = 0.88





Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	57016	−1.38	2e−16	3e−14	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
2	366	1.6	2e−16	3e−14	1 x 1	aquaporin 9 [Source:HGNC Symbol;Acc:643]
3	387695	−1.45	2e−16	3e−14	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Symb
4	92747	2.99	2e−16	3e−14	50 x 10	BPI fold containing family B, member 1 [Source:HGNC Symb
5	29113	1.43	2e−16	3e−14	2 x 47	chromosome 6 open reading frame 15 [Source:HGNC Symbo
6	375791	1.57	2e−16	3e−14	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Symb
7	57124	1.55	2e−16	3e−14	3 x 1	CD248 molecule, endosialin [Source:HGNC Symbol;Acc:182
8	629	1.55	2e−16	3e−14	32 x 1	complement factor B [Source:HGNC Symbol;Acc:1037]
9	84518	1.58	2e−16	3e−14	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
10	49860	1.93	2e−16	3e−14	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
11	10202	2.33	2e−16	3e−14	1 x 15	dehydrogenase/reductase (SDR family) member 2 [Source:H
12	8857	2.34	2e−16	3e−14	50 x 13	Fc fragment of IgG binding protein [Source:HGNC Symbol;Ac
13	10468	1.72	2e−16	3e−14	1 x 5	follistatin [Source:HGNC Symbol;Acc:3971]
14	729428	3.3	2e−16	3e−14	14 x 11	G antigen 12C [Source:HGNC Symbol;Acc:28402]
15	729422	3.7	2e−16	3e−14	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
16	100132399	1.43	2e−16	3e−14	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
17	100008586	3.01	2e−16	3e−14	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
18	645073	2.99	2e−16	3e−14	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
19	729442	3.42	2e−16	3e−14	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
20	26748	3.12	2e−16	3e−14	14 x 11	G antigen 12I [Source:HGNC Symbol;Acc:4105]



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	12.51	NULL	1182	CC	extracellular region
2	11.76	NULL	572	Disease	GUDJ_psoriasis up
3	10.53	NULL	21	CC	cornified envelope
4	10.21	NULL	42	BP	keratinization
5	9.46	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_D
6	9.29	NULL	683	CC	extracellular space
7	9.02	NULL	135	H.Tiss	WIRTH_Mucosa
8	8.5	NULL	1135	Chr	Chr 19
9	8.47	NULL	51	BP	type I interferon signaling pathway
10	8.39	NULL	16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
11	8.37	NULL	717	Chr	Chr 16
12	8.36	NULL	4	MMML CGS	MACIEJ_MMML 23
13	8.17	NULL	16	GSEA C2	MOSERLE_IFNA_RESPONSE
14	8.11	NULL	13	GSEA C2	WONG_ENDMETRIUM_CANCER_UP
15	7.9	NULL	553	Cancer	Lembcke_Colonic Inflammation
16	7.52	NULL	265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
17	7.52	NULL	265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
18	7.52	NULL	265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
19	7.52	NULL	265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
20	7.4	NULL	16	GSEA C2	MAHADEVAN_RESPONSE_TO_MP470_UP
Underexpressed					
1	−7.77	NULL	280	Chr	Chr 13
2	−7.49	NULL	262	miRNA target−starBase	hsa−miR−548l
3	−7.32	NULL	318	miRNA target−starBase	hsa−miR−590−3p
4	−7.22	NULL	436	miRNA target−starBase	hsa−miR−548n
5	−7.19	NULL	633	Chr	Chr 9
6	−7.07	NULL	463	miRNA target−starBase	hsa−miR−301a
7	−6.69	NULL	368	miRNA target−starBase	hsa−miR−144
8	−6.68	NULL	293	miRNA target−starBase	hsa−miR−186
9	−6.68	NULL	699	Chr	Chr 5
10	−6.5	NULL	545	miRNA target−starBase	hsa−miR−93
11	−6.3	NULL	495	miRNA target−starBase	hsa−miR−103
12	−6.28	NULL	232	Chr	Chr 18
13	−6.26	NULL	914	Chr	Chr 3
14	−6.22	NULL	4640	CC	nucleus
15	−6.19	NULL	315	miRNA target−starBase	hsa−miR−30e
16	−6.12	NULL	280	miRNA target−starBase	hsa−miR−320a
17	−6.01	NULL	300	miRNA target−starBase	hsa−miR−548c−3p
18	−5.94	NULL	603	miRNA target−starBase	hsa−miR−20a
19	−5.86	NULL	215	miRNA target−starBase	hsa−miR−199a−3p
20	−5.85	NULL	565	miRNA target−starBase	hsa−miR−20b

GW_094

Local Summary

%DE = 0.62

metagenes = 10

genes = 169

genes in genesets = 169

genes with fdr < 0.1 = 78 (71 + / 7 −)

genes with fdr < 0.05 = 72 (66 + / 6 −)

genes with fdr < 0.01 = 55 (51 + / 4 −)

<r> metagenes = 0.98

<r> genes = 0.42

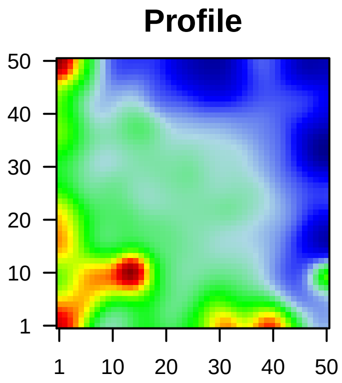
<FC> = 0.37

<shrinkage−t> = 12.86

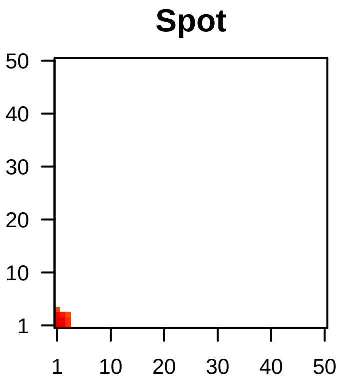
<p−value> = 0

<fdr> = 0.55

Profile



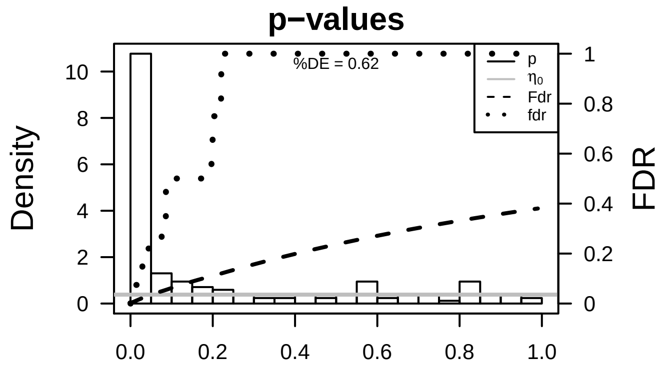
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	366	1.6	2e−16	1e−15	1 x 1	aquaporin 9 [Source:HGNC Symbol;Acc:643]
2	57124	1.55	2e−16	1e−15	3 x 1	CD248 molecule, endosialin [Source:HGNC Symbol;Acc:182
3	3553	1.75	2e−16	1e−15	1 x 1	interleukin 1, beta [Source:HGNC Symbol;Acc:5992]
4	3576	1.51	2e−16	1e−15	1 x 1	interleukin 8 [Source:HGNC Symbol;Acc:6025]
5	4312	−2.17	2e−16	1e−15	1 x 1	matrix metallopeptidase 1 (interstitial collagenase) [Source:H
6	4319	1.93	2e−16	1e−15	1 x 3	matrix metallopeptidase 10 (stromelysin 2) [Source:HGNC Sy
7	4318	2.36	2e−16	1e−15	1 x 1	matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 9
8	5008	1.73	2e−16	1e−15	1 x 1	oncostatin M [Source:HGNC Symbol;Acc:8506]
9	60675	1.85	2e−16	1e−15	1 x 1	prokineticin 2 [Source:HGNC Symbol;Acc:18455]
10	12	2.13	2e−16	1e−15	1 x 1	
11	6515	1.67	2e−16	1e−15	3 x 1	solute carrier family 2 (facilitated glucose transporter), membe
12	7045	1.3	2e−16	1e−15	1 x 2	transforming growth factor, beta−induced, 68kDa [Source:HG
13	4973	1.34	2e−15	2e−11	1 x 1	oxidized low density lipoprotein (lectin−like) receptor 1 [Sourc
14	4502	1.21	6e−13	2e−11	1 x 3	metallothionein 2A [Source:HGNC Symbol;Acc:7406]
15	414062	1.19	1e−12	2e−11	1 x 1	chemokine (C−C motif) ligand 3−like 3 [Source:HGNC Symbo
16	10381	1.19	1e−12	2e−11	1 x 4	tubulin, beta 3 class III [Source:HGNC Symbol;Acc:20772]
17	6695	1.19	2e−12	3e−10	1 x 2	sparc/osteonectin, cwcv and kazal−like domains proteoglycar
18	3678	1.15	7e−12	2e−08	1 x 1	integrin, alpha 5 (fibronectin receptor, alpha polypeptide) [Sou
19	8988	1.05	4e−10	2e−08	1 x 4	heat shock 27kDa protein 3 [Source:HGNC Symbol;Acc:5248
20	5054	1.04	6e−10	5e−08	1 x 2	serpin peptidase inhibitor, clade E (nexin, plasminogen activa

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	26.58	NULL	3 / 6	GSEA C2	AGARWAL_AKT_PATHWAY_TARGETS
2	26.29	NULL	2 / 6	Glio	Martinez_Glio_hypometh
3	25.78	NULL	10 / 15	GSEA C2	CROMER_TUMORIGENESIS_UP
4	22.16	NULL	2 / 6	GSEA C2	SEIKE_LUNG_CANCER_POOR_SURVIVAL
5	20.59	NULL	7 / 19	MF	extracellular matrix binding
6	19.84	NULL	4 / 12	GSEA C2	LY_AGING_MIDDLE_UP
7	16.52	NULL	5 / 16	GSEA C2	URS_ADIPOCYTE_DIFFERENTIATION_DN
8	16.37	NULL	11 / 35	Glio	Colman_survival_associated
9	15.62	NULL	1 / 3	GSEA C2	REN_MIF_TARGETS_DN
10	15.58	NULL	5 / 49	Glio	Christensen_hypomethylated_in_primary_glioblastoma
11	15.17	NULL	1 / 4	GSEA C2	BUDHU_LIVER_CANCER_METASTASIS_DN
12	15.1	NULL	5 / 37	Glio	Christensen_hypomethylated_in_ependymoma
13	14.45	NULL	47 / 242	BP	extracellular matrix organization
14	14.09	NULL	7 / 36	BP	embryo implantation
15	13.56	NULL	6 / 13	GSEA C2	TSAI_RESPONSE_TO_RADIATION_THERAPY
16	13.48	NULL	2 / 11	GSEA C2	YAMANAKA_GLIOBLASTOMA_SURVIVAL_UP
17	13.28	NULL	8 / 15	GSEA C2	ONDER_CDH1_SIGNALING_VIA_CTNNB1
18	13.12	NULL	4 / 11	GSEA C2	ITO_PTTG1_TARGETS_UP
19	13.01	NULL	2 / 14	GSEA C2	DAZARD_UV_RESPONSE_CLUSTER_G4
20	12.92	NULL	3 / 14	GSEA C2	WANG_ESOPHAGUS_CANCER_VS_NORMAL_UP
21	12.63	NULL	2 / 13	BP	positive regulation of vascular endothelial growth factor receptor sig
22	12.61	NULL	2 / 16	GSEA C2	GRAHAM_CML_QUIESCENT_VS_CML_DIVIDING_UP
23	12.41	NULL	61 / 683	CC	extracellular space
24	12.41	NULL	2 / 13	BP	positive regulation of smooth muscle contraction
25	12.4	NULL	3 / 8	GSEA C2	SASAKI_TARGETS_OF_TP73_AND_TP63
26	12.39	NULL	45 / 553	Cancer	Lembcke_Colonic Inflammation
27	12.32	NULL	5 / 16	GSEA C2	CHEN_LVAD_SUPPORT_OF_FAILING_HEART_UP
28	12.16	NULL	4 / 7	GSEA C2	WANG_ESOPHAGUS_CANCER_PROGRESSION_UP
29	12.1	NULL	52 / 250	Lymphoma	LENZ_Stromal signature 1
30	12.09	NULL	2 / 9	GSEA C2	HEDVAT_ELF4_TARGETS_UP
31	11.87	NULL	4 / 15	GSEA C2	MISHRA_CARCINOMA_ASSOCIATED_FIBROBLAST_UP
32	11.86	NULL	2 / 7	GSEA C2	FREDERICK_PRKCI_TARGETS
33	11.77	NULL	4 / 10	GSEA C2	JEON_SMAD6_TARGETS_UP
34	11.75	NULL	5 / 16	GSEA C2	AMIT_EGF_RESPONSE_60_HELA
35	11.69	NULL	7 / 11	MF	platelet−derived growth factor binding
36	11.67	NULL	4 / 15	BP	positive regulation vascular endothelial growth factor production
37	11.61	NULL	2 / 6	GSEA C2	BIOCARTA_IL5_PATHWAY
38	11.38	NULL	6 / 15	GSEA C2	DASU_IL6_SIGNALING_SCAR_DN
39	11.34	NULL	1 / 5	GSEA C2	DEBOSSCHER_NFKB_TARGETS_REPRESSED_BY_GLUCOCO
40	11.34	NULL	2 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN

GW_094

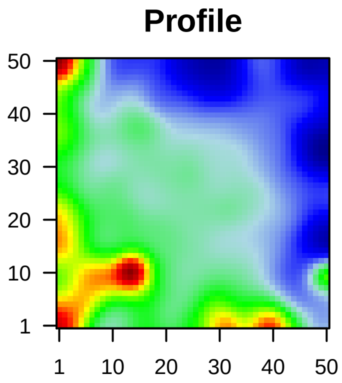
Local Summary

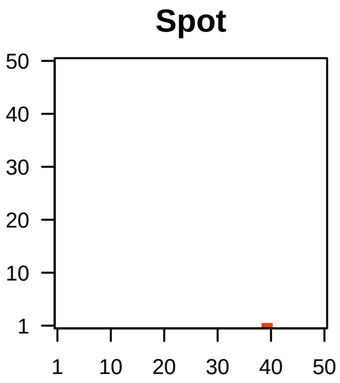
%DE = 0.95
metagenes = 2
genes = 106
genes in genesets = 86

genes with fdr < 0.1 = 94 (93 + / 1 −)
genes with fdr < 0.05 = 83 (83 + / 0 −)
genes with fdr < 0.01 = 79 (79 + / 0 −)

<r> metagenes = 1
<r> genes = 0.66

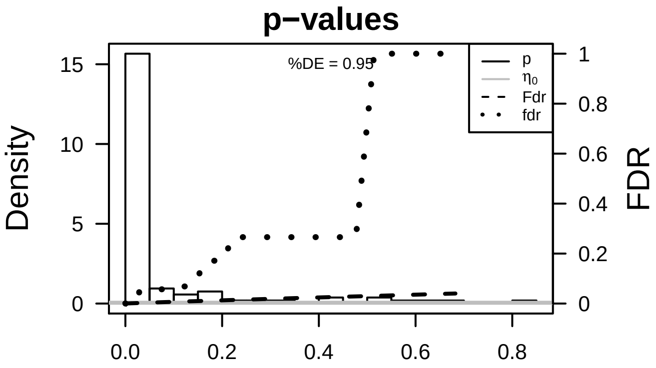
<FC> = 0.47
<shrinkage−t> = 16.59
<p−value> = 0
<fdr> = 0.33





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	618	0.97	7e−09	3e−06	39 x 1	brain cytoplasmic RNA 1 [Source:HGNC Symbol;Acc:1022]
2	55142	0.83	7e−07	3e−06	40 x 1	HAUS augmin−like complex, subunit 2 [Source:HGNC Symbo
3	84061	0.82	1e−06	9e−06	39 x 1	magnesium transporter 1 [Source:HGNC Symbol;Acc:28880]
4	440275	0.78	3e−06	9e−06	40 x 1	eukaryotic translation initiation factor 2 alpha kinase 4 [Sourc
5	26279	0.75	7e−06	9e−06	40 x 1	phospholipase A2, group IID [Source:HGNC Symbol;Acc:903
6	57835	0.75	8e−06	9e−06	40 x 1	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:E7
7	113277	0.74	1e−05	9e−06	40 x 1	transmembrane protein 106A [Source:HGNC Symbol;Acc:28
8	255031	0.74	1e−05	9e−06	40 x 1	long intergenic non−protein coding RNA 957 [Source:HGNC
9	136051	0.74	1e−05	2e−05	40 x 1	zinc finger protein 786 [Source:HGNC Symbol;Acc:21806]
10	401494	0.72	2e−05	2e−05	40 x 1	protein tyrosine phosphatase−like A domain containing 2 [So
11	90639	0.71	2e−05	2e−05	40 x 1	cytochrome c oxidase assembly homolog 19 (S. cerevisiae) [
12	29797	0.71	3e−05	2e−05	40 x 1	
13	641737	0.66	3e−05	2e−05	40 x 1	
14	1762	0.7	3e−05	2e−05	40 x 1	dystrophia myotonica, WD repeat containing [Source:HGNC
15	126205	0.69	4e−05	2e−05	40 x 1	NLR family, pyrin domain containing 8 [Source:HGNC Symbo
16	57464	0.69	4e−05	2e−05	40 x 1	striatin interacting protein 2 [Source:HGNC Symbol;Acc:2220
17	22834	0.69	4e−05	2e−05	40 x 1	zinc finger protein 652 [Source:HGNC Symbol;Acc:29147]
18	25862	0.69	4e−05	2e−05	40 x 1	ubiquitin specific peptidase 49 [Source:HGNC Symbol;Acc:2
19	7813	0.68	5e−05	2e−05	40 x 1	ecotropic viral integration site 5 [Source:HGNC Symbol;Acc:3
20	56127	0.68	5e−05	2e−05	40 x 1	protocadherin beta 10 [Source:HGNC Symbol;Acc:8681]



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	17.46	NULL	2 / 4	GSEA C2	BIOCARTA_CYTOKINE_PATHWAY
2	13.49	NULL	3 / 14	MMML CGS	MACIEJ_MMML 8
3	12.9	NULL	3 / 13	GSEA C2	SPIRA_SMOKERS_LUNG_CANCER_DN
4	8.91	NULL	1 / 5	GSEA C2	BIOCARTA_INFLAM_PATHWAY
5	8.67	NULL	3 / 16	GSEA C2	HAMAI_APOPTOSIS_VIA_TRAIL_UP
6	7.94	NULL	1 / 6	GSEA C2	BUDHU_LIVER_CANCER_METASTASIS_UP
7	7.94	NULL	1 / 6	GSEA C2	SEIKE_LUNG_CANCER_POOR_SURVIVAL
8	7.78	NULL	2 / 15	Glio	Donson−chemokines/cytokines−associated with LTS in HGA
9	7.75	NULL	2 / 14	BP	cellular response to estradiol stimulus
10	7.7	NULL	1 / 14	Cancer	LIU_COMMON_CANCER_GENES
11	7.58	NULL	1 / 10	CC	oligosaccharyltransferase complex
12	7.18	NULL	2 / 24	BP	negative regulation of T cell proliferation
13	7.07	NULL	2 / 14	BP	mitochondrion morphogenesis
14	7	NULL	1 / 4	MMML CGS	MACIEJ_MMML 44
15	6.8	NULL	1 / 11	GSEA C2	BIOCARTA_EIF2_PATHWAY
16	6.63	NULL	1 / 8	GSEA C2	BIOCARTA_ASBCELL_PATHWAY
17	6.61	NULL	1 / 7	GSEA C2	KEGG_STEROID_HORMONE_BIOSYNTHESIS
18	6.47	NULL	1 / 13	MF	magnesium ion transmembrane transporter activity
19	6.41	NULL	1 / 9	GSEA C2	SA_MMP_CYTOKINE_CONNECTION
20	6.28	NULL	1 / 14	Cancer	LIU_COMMON_CANCER_GENES
21	6.21	NULL	1 / 12	BP	phosphatidylinositol acyl−chain remodeling
22	6.18	NULL	1 / 14	BP	magnesium ion transport
23	6.15	NULL	1 / 9	GSEA C2	BROWNE_HCMV_INFECTION_1HR_DN
24	6.01	NULL	1 / 10	BP	negative thymic T cell selection
25	5.92	NULL	1 / 13	BP	phosphatidylserine acyl−chain remodeling
26	5.89	NULL	1 / 13	MF	dynein binding
27	5.78	NULL	1 / 10	BP	negative regulation of nitric oxide biosynthetic process
28	5.78	NULL	1 / 10	GSEA C2	BIOCARTA_IL10_PATHWAY
29	5.7	NULL	1 / 16	BP	cognition
30	5.65	NULL	1 / 14	BP	phosphatidylglycerol acyl−chain remodeling
31	5.62	NULL	1 / 12	GSEA C2	YAGI_AML_WITH_T_9_11_TRANSLOCATION
32	5.62	NULL	1 / 12	GSEA C2	HEDENFALK_BREAST_CANCER_BRACX_DN
33	5.45	NULL	1 / 11	BP	negative regulation of interleukin−12 production
34	5.45	NULL	1 / 11	GSEA C2	SU_PANCREAS
35	5.42	NULL	1 / 15	MF	phospholipase A2 activity
36	5.37	NULL	1 / 12	BP	negative regulation of T cell activation
37	5.35	NULL	1 / 13	GSEA C2	WANG_RESPONSE_TO_ANDROGEN_UP
38	5.29	NULL	1 / 10	GSEA C2	REACTOME_TRANSFORMATION_OF_LANOSTEROL_TO_CHO
39	5.17	NULL	1 / 12	BP	negative regulation of growth of symbiont in host
40	5.15	NULL	1 / 12	BP	retina layer formation

GW_094

Local Summary

%DE = 0.67

metagenes = 22

genes = 104

genes in genesets = 79

genes with fdr < 0.1 = 47 (43 + / 4 −)

genes with fdr < 0.05 = 47 (43 + / 4 −)

genes with fdr < 0.01 = 39 (39 + / 0 −)

<r> metagenes = 0.95

<r> genes = 0.28

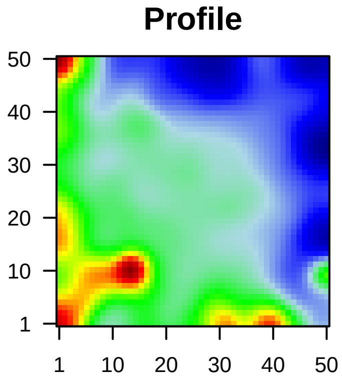
<FC> = 0.67

<shrinkage−t> = 23.4

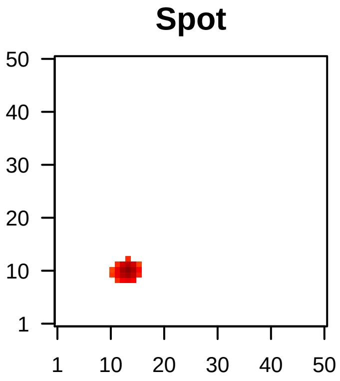
<p−value> = 0

<fdr> = 0.54

Profile



Spot



Local Genelist

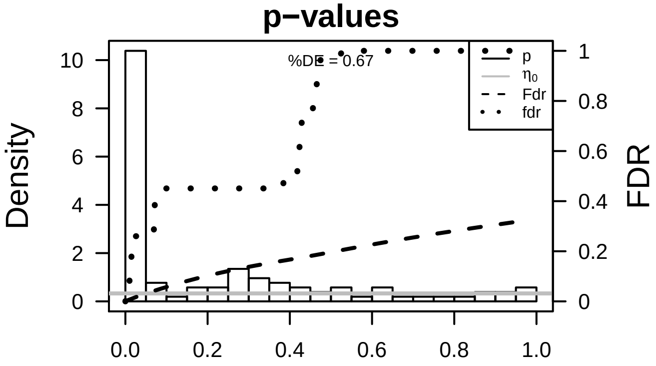
Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	729428	3.3	2e−16	3e−16	14 x 11	G antigen 12C [Source:HGNC Symbol;Acc:28402]
2	729422	3.7	2e−16	3e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
3	100132399	1.43	2e−16	3e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
4	100008586	3.01	2e−16	3e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
5	645073	2.99	2e−16	3e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
6	729442	3.42	2e−16	3e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
7	26748	3.12	2e−16	3e−16	14 x 11	G antigen 12I [Source:HGNC Symbol;Acc:4105]
8	729396	2.43	2e−16	3e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
9	729447	2.62	2e−16	3e−16	14 x 11	G antigen 2A [Source:HGNC Symbol;Acc:4099]
10	645037	3.67	2e−16	3e−16	14 x 11	G antigen 2C [Source:HGNC Symbol;Acc:31958]
11	26749	2.68	2e−16	3e−16	14 x 11	G antigen 2E [Source:HGNC Symbol;Acc:31960]
12	2576	3.24	2e−16	3e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
13	2577	3.2	2e−16	3e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
14	2578	1.88	2e−16	3e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
15	2579	2.14	2e−16	3e−16	14 x 11	G antigen 12I [Source:HGNC Symbol;Acc:4105]
16	100101629	2.07	2e−16	3e−16	14 x 11	G antigen 2E [Source:HGNC Symbol;Acc:31960]
17	121355	1.45	2e−16	3e−16	14 x 11	gametocyte specific factor 1 [Source:HGNC Symbol;Acc:265
18	4100	1.39	2e−16	3e−16	14 x 11	melanoma antigen family A, 1 (directs expression of antigen
19	4109	1.62	2e−16	3e−16	14 x 11	melanoma antigen family A, 10 [Source:HGNC Symbol;Acc:6
20	30014	1.41	2e−16	3e−16	16 x 11	sperm protein associated with the nucleus, X−linked, family

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	19.44	NULL	3 / 14	GSEA C2	MAHADEVAN_IMATINIB_RESISTANCE_UP
2	17.21	NULL	30 / 630	Chr	Chr X
3	14.42	NULL	1 / 12	GSEA C2	RAY_TARGETS_OF_P210_BCR_ABL_FUSION_UP
4	9.32	NULL	1 / 11	GSEA C2	SU_PLACENTA
5	8.29	NULL	3 / 15	GSEA C2	MATTIOLI_MULTIPLE_MYELOMA_SUBGROUPS
6	8.03	NULL	1 / 14	GSEA C2	NIELSEN_GIST
7	7.7	NULL	1 / 15	GSEA C2	BROWNE_HCMV_INFECTION_8HR_DN
8	7.34	NULL	1 / 15	GSEA C2	MASRI_RESISTANCE_TO_TAMOXIFEN_AND_AROMATASE_INH
9	6.51	NULL	1 / 10	GSEA C2	XU_RESPONSE_TO_TRETINOIN_DN
10	6.11	NULL	9 / 120	H.Tiss	WIRTH_Testis
11	5.62	NULL	1 / 10	GSEA C2	NAKAMURA_TUMOR_ZONE_PERIPHERAL_VS_CENTRAL_DN
12	5.42	NULL	1 / 5	GSEA C2	CHOI_ATL_ACUTE_STAGE
13	5.37	NULL	1 / 21	BP	negative regulation of Notch signaling pathway
14	5.29	NULL	1 / 11	GSEA C2	NIKOLSKY_BREAST_CANCER_7Q21_Q22_AMPLICON
15	5	NULL	1 / 12	GSEA C2	HSIAO_LIVER_SPECIFIC_GENES
16	4.79	NULL	10 / 549	MF	molecular_function
17	4.76	NULL	1 / 13	GSEA C2	HOSHIDA_LIVER_CANCER_SURVIVAL_DN
18	4.4	NULL	10 / 481	BP	biological_process
19	4.35	NULL	1 / 15	GSEA C2	WHITEFORD_PEDIATRIC_CANCER_MARKERS
20	4.35	NULL	1 / 15	GSEA C2	AGUIRRE_PANCREATIC_CANCER_COPY_NUMBER_UP
21	4.35	NULL	1 / 15	GSEA C2	SHEDDEN_LUNG_CANCER_GOOD_SURVIVAL_A4
22	4.35	NULL	1 / 15	GSEA C2	HOSHIDA_LIVER_CANCER_SUBCLASS_S3
23	4.18	NULL	1 / 16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_A
24	4.18	NULL	1 / 16	GSEA C2	JI_METASTASIS_REPRESSED_BY_STK11
25	3.99	NULL	1 / 11	Glio	willscher_GBM_Verhaak−CL_expression_M_down
26	3.99	NULL	1 / 11	Glio	willscher_GBM_Verhaak−MES_expression_M_down
27	3.99	NULL	1 / 11	Glio	willscher_GBM_Verhaak−PNmut_expression_M_up
28	3.83	NULL	1 / 19	BP	oogenesis
29	3.61	NULL	1 / 26	MF	cyclin−dependent protein serine/threonine kinase activity
30	3.48	NULL	8 / 419	CC	cellular_component
31	3.41	NULL	1 / 4	GSEA C2	WEBER_METHYLATED_ICP_IN_SPERM_DN
32	3.38	NULL	1 / 10	GSEA C2	TSUNODA_CISPLATIN_RESISTANCE_DN
33	3.13	NULL	1 / 15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
34	3	NULL	1 / 12	Glio	willscher_GBM_LTSmut_proteomics−B_UP
35	3	NULL	1 / 12	Glio	willscher_GBM_STSwt_proteomics−B_DOWN
36	3	NULL	1 / 12	GSEA C2	YOSHIOKA_LIVER_CANCER_EARLY_RECURRENCE_UP
37	2.98	NULL	2 / 68	MF	histone deacetylase binding
38	2.72	NULL	1 / 11	GSEA C2	GARCIA_TARGETS_OF_FLI1_AND_DAX1_UP
39	2.6	NULL	1 / 15	GSEA C2	LOPEZ_MBD_TARGETS_IMPRINTED_AND_X_LINKED
40	2.6	NULL	1 / 15	GSEA C2	ALONSO_METASTASIS_NEURAL_UP

p−values



GW_094

Local Summary

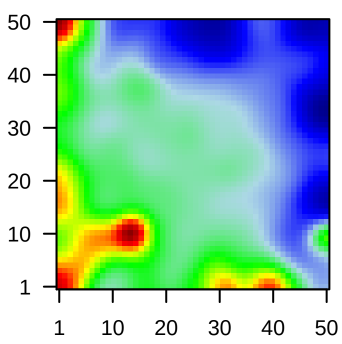
%DE = 0.9
metagenes = 8
genes = 137
genes in genesets = 134

genes with fdr < 0.1 = 105 (87 + / 18 −)
genes with fdr < 0.05 = 95 (80 + / 15 −)
genes with fdr < 0.01 = 90 (76 + / 14 −)

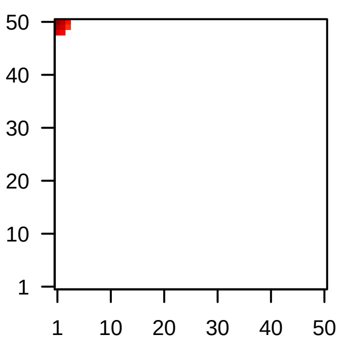
<r> metagenes = 0.99
<r> genes = 0.52

<FC> = 0.57
<shrinkage−t> = 20.12
<p−value> = 0
<fdr> = 0.32

Profile

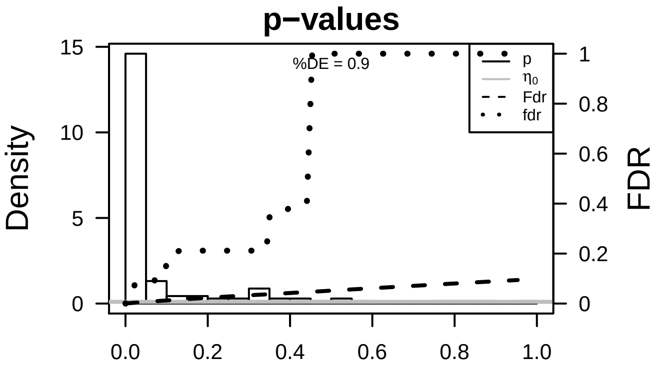


Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	57016	−1.38	2e−16	1e−16	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
2	387695	−1.45	2e−16	1e−16	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Symb
3	375791	1.57	2e−16	1e−16	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Symb
4	84518	1.58	2e−16	1e−16	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
5	49860	1.93	2e−16	1e−16	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
6	26525	1.61	2e−16	1e−16	1 x 49	interleukin 36 receptor antagonist [Source:HGNC Symbol;Acc
7	43849	1.67	2e−16	1e−16	1 x 50	kallikrein−related peptidase 12 [Source:HGNC Symbol;Acc:6
8	26085	1.67	2e−16	1e−16	1 x 50	kallikrein−related peptidase 13 [Source:HGNC Symbol;Acc:6
9	5653	2.24	2e−16	1e−16	1 x 50	kallikrein−related peptidase 6 [Source:HGNC Symbol;Acc:63
10	192666	2.54	2e−16	1e−16	1 x 50	keratin 24 [Source:HGNC Symbol;Acc:18527]
11	196374	1.85	2e−16	1e−16	1 x 50	keratin 78 [Source:HGNC Symbol;Acc:28926]
12	3934	1.37	2e−16	1e−16	1 x 50	lipocalin 2 [Source:HGNC Symbol;Acc:6526]
13	643479	1.49	2e−16	1e−16	1 x 49	
14	80740	1.47	2e−16	1e−16	2 x 48	lymphocyte antigen 6 complex, locus G6C [Source:HGNC Sy
15	137797	1.58	2e−16	1e−16	1 x 50	LY6/PLAUR domain containing 2 [Source:HGNC Symbol;Acc
16	4118	1.96	2e−16	1e−16	1 x 50	mal, T−cell differentiation protein [Source:HGNC Symbol;Acc
17	342897	1.46	2e−16	1e−16	1 x 50	non−specific cytotoxic cell receptor protein 1 homolog (zebraf
18	83886	1.96	2e−16	1e−16	1 x 50	protease, serine 27 [Source:HGNC Symbol;Acc:15475]
19	84659	1.46	2e−16	1e−16	1 x 48	ribonuclease, RNase A family, 7 [Source:HGNC Symbol;Acc:
20	6286	1.68	2e−16	1e−16	1 x 50	S100 calcium binding protein P [Source:HGNC Symbol;Acc:1



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	33.91	NULL	14 / 21	CC	cornified envelope
2	31.13	NULL	16 / 42	BP	keratinization
3	29.83	NULL	63 / 135	H.Tiss	WIRTH_Mucosa
4	22.51	NULL	19 / 53	BP	keratinocyte differentiation
5	19.21	NULL	6 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
6	18.47	NULL	16 / 76	BP	epidermis development
7	17.71	NULL	5 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
8	17.3	NULL	6 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
9	17.15	NULL	65 / 572	Disease	GUDJ_psoriasis up
10	16.72	NULL	8 / 19	BP	peptide cross−linking
11	12.78	NULL	4 / 10	MF	RAGE receptor binding
12	12.18	NULL	6 / 15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
13	11.32	NULL	5 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
14	10.53	NULL	10 / 122	MF	serine−type endopeptidase activity
15	10.24	NULL	2 / 11	GSEA C2	ROME_INSULIN_TARGETS_IN_MUSCLE_DN
16	9.91	NULL	2 / 16	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_LUNG_UP
17	9.66	NULL	2 / 17	Disease	BCHETNIA_EBM up
18	9.29	NULL	3 / 15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
19	8.81	NULL	3 / 15	GSEA C2	CHANG_IMMORTALIZED_BY_HPV31_DN
20	8.58	NULL	2 / 15	GSEA C2	ALONSO_METASTASIS_NEURAL_UP
21	8.43	NULL	3 / 16	GSEA C2	CHEOK_RESPONSE_TO_MERCAPTOPURINE_AND_LD_MTX_
22	8.1	NULL	3 / 13	GSEA C2	HAN_SATB1_TARGETS_DN
23	8.09	NULL	2 / 15	GSEA C2	LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
24	7.86	NULL	2 / 38	BP	myelination
25	7.86	NULL	3 / 16	GSEA C2	AMIT_SERUM_RESPONSE_480_MCF10A
26	7.84	NULL	2 / 8	GSEA C2	MCLACHLAN_DENTAL_CARIES_UP
27	7.77	NULL	6 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
28	7.74	NULL	4 / 27	BP	response to bacterium
29	7.4	NULL	1 / 11	Glio	VERHAAK_Brain
30	7.35	NULL	1 / 14	BP	tissue regeneration
31	7.29	NULL	2 / 9	GSEA C2	MCLACHLAN_DENTAL_CARIES_DN
32	7.05	NULL	1 / 15	BP	hormone metabolic process
33	7.03	NULL	6 / 83	CC	anchored to membrane
34	7.02	NULL	1 / 12	MF	channel activity
35	7.01	NULL	1 / 6	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_LIVER_UP
36	6.98	NULL	41 / 1182	CC	extracellular region
37	6.87	NULL	1 / 12	GSEA C2	ODONNELL_METASTASIS_DN
38	6.87	NULL	1 / 12	GSEA C2	SYED_ESTRADIOL_RESPONSE
39	6.84	NULL	2 / 10	GSEA C2	NIKOLSKY_BREAST_CANCER_20Q12_Q13_AMPLICON
40	6.69	NULL	1 / 13	GSEA C2	HASLINGER_B_CLL_WITH_MUTATED_VH_GENES

GW_094

Local Summary

%DE = 0.62

metagenes = 21

genes = 233

genes in genesets = 230

genes with fdr < 0.1 = 62 (3 + / 59 −)

genes with fdr < 0.05 = 50 (2 + / 48 −)

genes with fdr < 0.01 = 10 (0 + / 10 −)

<r> metagenes = 0.97

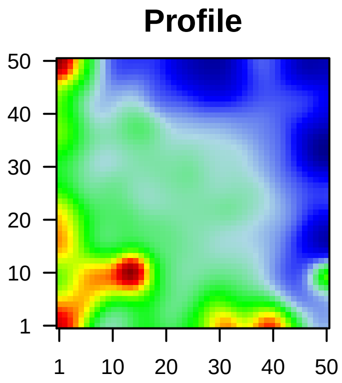
<r> genes = 0.33

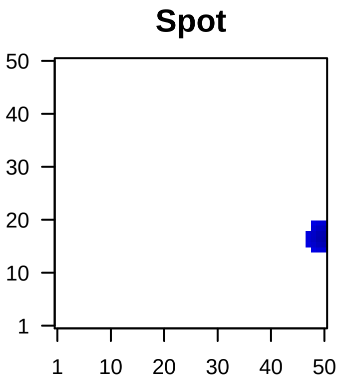
<FC> = −0.23

<shrinkage−t> = −8.03

<p−value> = 0.06

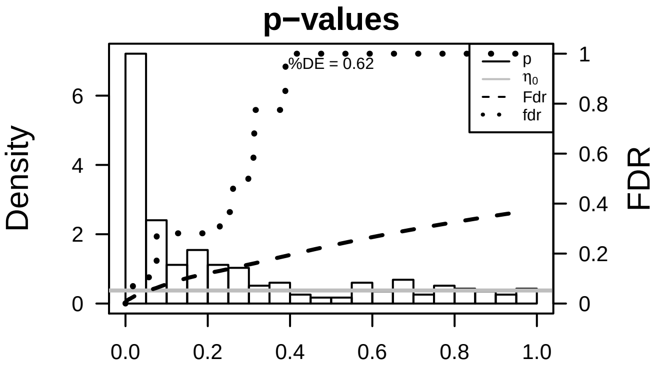
<fdr> = 0.75





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	217	−1.03	8e−10	2e−05	50 x 15	aldehyde dehydrogenase 2 family (mitochondrial) [Source:HG
2	1959	−0.88	2e−07	8e−04	50 x 19	early growth response 2 [Source:HGNC Symbol;Acc:3239]
3	26002	−0.75	9e−06	1e−03	50 x 16	monooxygenase, DBH−like 1 [Source:HGNC Symbol;Acc:21
4	10439	−0.71	2e−05	2e−03	50 x 17	olfactomedin 1 [Source:HGNC Symbol;Acc:17187]
5	728715	−0.68	5e−05	4e−03	50 x 18	
6	909	−0.65	1e−04	4e−03	50 x 16	CD1a molecule [Source:HGNC Symbol;Acc:1634]
7	494470	−0.64	1e−04	5e−03	50 x 17	ring finger protein 165 [Source:HGNC Symbol;Acc:31696]
8	22882	−0.61	3e−04	5e−03	50 x 18	zinc fingers and homeoboxes 2 [Source:HGNC Symbol;Acc:1
9	84188	−0.6	3e−04	5e−03	48 x 15	fatty acyl CoA reductase 1 [Source:HGNC Symbol;Acc:2622
10	155066	−0.6	4e−04	5e−03	50 x 15	ATPase, H+ transporting V0 subunit e2 [Source:HGNC Symb
11	9847	−0.6	4e−04	1e−02	50 x 16	C2 calcium−dependent domain containing 5 [Source:HGNC
12	28951	0.57	6e−04	1e−02	50 x 17	tribbles pseudokinase 2 [Source:HGNC Symbol;Acc:30809]
13	23506	−0.56	9e−04	1e−02	48 x 16	GLTSCR1−like [Source:HGNC Symbol;Acc:21111]
14	79899	−0.55	1e−03	1e−02	50 x 19	proline rich 5 like [Source:HGNC Symbol;Acc:25878]
15	6263	−0.55	1e−03	1e−02	50 x 18	ryanodine receptor 3 [Source:HGNC Symbol;Acc:10485]
16	694	−0.5	1e−03	1e−02	50 x 18	B−cell translocation gene 1, anti−proliferative [Source:HGNC
17	57189	−0.55	1e−03	1e−02	50 x 15	KIAA1147 [Source:HGNC Symbol;Acc:29472]
18	56997	−0.54	1e−03	1e−02	50 x 16	aarF domain containing kinase 3 [Source:HGNC Symbol;Acc
19	221061	−0.54	1e−03	2e−02	50 x 16	family with sequence similarity 171, member A1 [Source:HGN
20	5757	−0.53	2e−03	2e−02	50 x 19	prothymosin, alpha [Source:HGNC Symbol;Acc:9623]



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−14.38	NULL	5 / 16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_A
2	−11.23	NULL	2 / 9	GSEA C2	REACTOME_ETHANOL_OXIDATION
3	−10.17	NULL	1 / 5	GSEA C2	STAEGE_EWING_FAMILY_TUMOR
4	−10.02	NULL	1 / 7	GSEA C2	LOPEZ_MESOTELIOMA_SURVIVAL_TIME_DN
5	−9.29	NULL	3 / 15	GSEA C2	MASSARWEH_RESPONSE_TO_ESTRADIOL
6	−8.31	NULL	1 / 3	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_30
7	−8.27	NULL	1 / 10	GSEA C2	KEGG_ASCORBATE_AND_ALDARATE_METABOLISM
8	−8.27	NULL	1 / 10	GSEA C2	KEGG_LIMONENE_AND_PINENE_DEGRADATION
9	−8.17	NULL	2 / 10	Cancer	LIU_BREAST_CANCER
10	−8.05	NULL	1 / 2	TF	MYC_Cell cycle DOWN
11	−7.85	NULL	1 / 11	BP	neurotransmitter biosynthetic process
12	−7.43	NULL	2 / 10	BP	positive regulation of histone H3−K4 methylation
13	−7.41	NULL	1 / 9	GSEA C2	ABE_VEGFA_TARGETS_30MIN
14	−7.3	NULL	3 / 16	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_UP
15	−7.06	NULL	10 / 81	miRNA target starBase	hsa−miR−188−5p
16	−6.99	NULL	1 / 10	BP	cellular response to gonadotropin stimulus
17	−6.99	NULL	1 / 10	BP	regulation of ossification
18	−6.99	NULL	1 / 10	GSEA C2	CHASSOT_SKIN_WOUND
19	−6.99	NULL	1 / 10	GSEA C2	ABE_VEGFA_TARGETS
20	−6.9	NULL	2 / 5	Lymphoma	MASCQUE_mBL UP
21	−6.82	NULL	2 / 13	GSEA C2	BROWNE_HCMV_INFECTION_48HR_DN
22	−6.76	NULL	2 / 11	miRNA target starBase	hsa−miR−1180
23	−6.62	NULL	1 / 15	Cancer	LIU_PROSTATE_CANCER_DN
24	−6.62	NULL	1 / 15	GSEA C2	KEGG_BETA_ALANINE_METABOLISM
25	−6.61	NULL	2 / 13	BP	mRNA catabolic process
26	−6.55	NULL	3 / 10	CC	nBAF complex
27	−6.44	NULL	2 / 26	BP	protein sumoylation
28	−6.38	NULL	1 / 16	GSEA C2	ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_UP
29	−6.33	NULL	6 / 64	miRNA target starBase	hsa−miR−324−5p
30	−6.32	NULL	1 / 12	GSEA C2	BIOCARTA_VIP_PATHWAY
31	−6.27	NULL	1 / 9	GSEA C2	RODWELL_AGING_KIDNEY_UP
32	−6.21	NULL	3 / 11	CC	npBAF complex
33	−6.14	NULL	3 / 13	BP	histone H4−K16 acetylation
34	−6.04	NULL	4 / 42	BP	B cell differentiation
35	−5.97	NULL	2 / 12	GSEA C2	PROVENZANI_METASTASIS_UP
36	−5.96	NULL	3 / 16	GSEA C2	BILBAN_B_CLL_LPL_DN
37	−5.92	NULL	3 / 12	CC	SWI/SNF complex
38	−5.91	NULL	1 / 10	GSEA C2	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_
39	−5.84	NULL	4 / 15	GSEA C2	GOLUB_ALL_VS_AML_UP
40	−5.83	NULL	1 / 4	GSEA C2	IGARASHI_ATF4_TARGETS_UP

GW_094

Local Summary

%DE = 0.55

metagenes = 46

genes = 507

genes in genesets = 504

genes with fdr < 0.1 = 71 (1 + / 70 −)

genes with fdr < 0.05 = 20 (1 + / 19 −)

genes with fdr < 0.01 = 7 (0 + / 7 −)

<r> metagenes = 0.92

<r> genes = 0.24

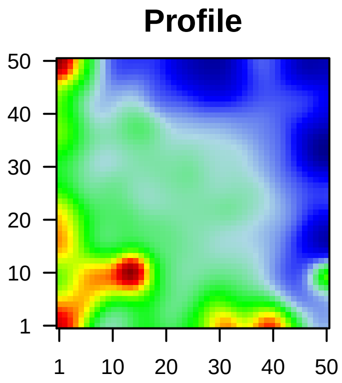
<FC> = −0.21

<shrinkage−t> = −7.45

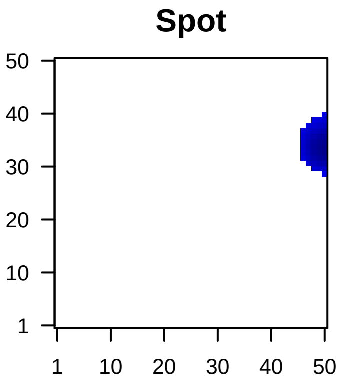
<p−value> = 0.13

<fdr> = 0.86

Profile



Spot



Local Genelist

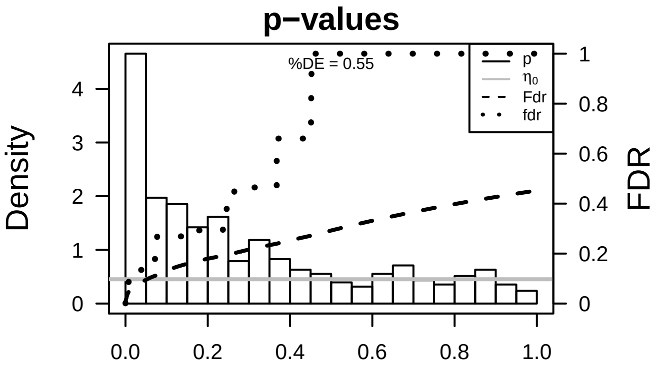
Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	85460	−0.89	1e−07	7e−04	50 x 39	zinc finger protein 518B [Source:HGNC Symbol;Acc:29365]
2	58527	−0.78	3e−06	1e−02	50 x 33	ABRA C−terminal like [Source:HGNC Symbol;Acc:21230]
3	3187	−0.68	5e−05	1e−02	50 x 35	heterogeneous nuclear ribonucleoprotein H1 (H) [Source:HG
4	22889	−0.64	1e−04	1e−02	50 x 37	KIAA0907 [Source:HGNC Symbol;Acc:29145]
5	201965	−0.62	2e−04	1e−02	50 x 32	RWD domain containing 4 [Source:HGNC Symbol;Acc:23750
6	55556	−0.62	2e−04	1e−02	50 x 37	enolase superfamily member 1 [Source:HGNC Symbol;Acc:3
7	961	−0.62	3e−04	1e−02	48 x 32	CD47 molecule [Source:HGNC Symbol;Acc:1682]
8	7743	−0.62	3e−04	2e−02	50 x 31	zinc finger protein 189 [Source:HGNC Symbol;Acc:12980]
9	23731	−0.59	4e−04	2e−02	47 x 35	transmembrane protein 245 [Source:HGNC Symbol;Acc:136
10	58486	−0.59	4e−04	2e−02	50 x 34	zinc finger, BED−type containing 5 [Source:HGNC Symbol;A
11	27075	0.58	5e−04	2e−02	50 x 38	tetraspanin 13 [Source:HGNC Symbol;Acc:21643]
12	9879	−0.58	5e−04	3e−02	49 x 32	DEAD (Asp−Glu−Ala−Asp) box polypeptide 46 [Source:HGN
13	10314	−0.56	9e−04	3e−02	50 x 35	LanC lantibiotic synthetase component C−like 1 (bacterial) [S
14	10923	−0.55	1e−03	3e−02	50 x 32	SUB1 homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:1
15	728026	−0.55	1e−03	3e−02	50 x 35	prothymosin, alpha [Source:HGNC Symbol;Acc:9623]
16	6146	−0.54	1e−03	3e−02	50 x 34	ribosomal protein L22 [Source:HGNC Symbol;Acc:10315]
17	25941	−0.54	1e−03	3e−02	50 x 36	tubulin polyglutamylase complex subunit 2 [Source:HGNC Sy
18	27031	−0.54	1e−03	3e−02	50 x 38	nephronophthisis 3 (adolescent) [Source:HGNC Symbol;Acc:
19	9474	−0.53	2e−03	3e−02	49 x 30	autophagy related 5 [Source:HGNC Symbol;Acc:589]
20	10420	−0.53	2e−03	5e−02	46 x 34	testis−specific kinase 2 [Source:HGNC Symbol;Acc:11732]

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset
1	−9.3	NULL	26 / 153	miRNA target starBase hsa−miR−450b−5p
2	−8.59	NULL	10 / 45	miRNA target starBase hsa−miR−411
3	−8.13	NULL	37 / 318	miRNA target starBase hsa−miR−590−3p
4	−8.13	NULL	15 / 85	miRNA target starBase hsa−miR−557
5	−8.06	NULL	26 / 284	miRNA target starBase hsa−miR−503
6	−7.9	NULL	21 / 113	miRNA target starBase hsa−miR−507
7	−7.83	NULL	18 / 151	miRNA target starBase hsa−miR−518a−5p
8	−7.69	NULL	18 / 155	miRNA target starBase hsa−miR−527
9	−7.66	NULL	22 / 232	Chr Chr 18
10	−7.66	NULL	23 / 172	miRNA target starBase hsa−miR−607
11	−7.59	NULL	54 / 595	MF RNA binding
12	−7.53	NULL	21 / 150	miRNA target starBase hsa−miR−633
13	−7.5	NULL	16 / 100	miRNA target starBase hsa−miR−544
14	−7.41	NULL	50 / 699	Chr Chr 5
15	−7.36	NULL	18 / 101	miRNA target starBase hsa−miR−410
16	−7.28	NULL	6 / 33	miRNA target starBase hsa−miR−892b
17	−7.2	NULL	3 / 9	GSEA C2 PUJANA_BREAST_CANCER_WITH_BRCA1_MUTATED_DN
18	−7.12	NULL	13 / 89	miRNA target starBase hsa−miR−505
19	−7.08	NULL	34 / 336	miRNA target starBase hsa−miR−548b−5p
20	−7.05	NULL	22 / 121	miRNA target starBase hsa−miR−543
21	−6.91	NULL	24 / 189	miRNA target starBase hsa−miR−1283
22	−6.86	NULL	22 / 171	miRNA target starBase hsa−miR−369−3p
23	−6.83	NULL	49 / 603	miRNA target starBase hsa−miR−20a
24	−6.82	NULL	21 / 189	miRNA target starBase hsa−miR−573
25	−6.79	NULL	24 / 229	BP RNA splicing
26	−6.63	NULL	22 / 163	BP mRNA splicing, via spliceosome
27	−6.63	NULL	18 / 122	miRNA target starBase hsa−miR−380
28	−6.57	NULL	18 / 93	miRNA target starBase hsa−miR−10b
29	−6.55	NULL	24 / 229	miRNA target starBase hsa−miR−520g
30	−6.49	NULL	30 / 303	miRNA target starBase hsa−miR−302b
31	−6.48	NULL	13 / 90	miRNA target starBase hsa−miR−362−5p
32	−6.38	NULL	43 / 421	miRNA target starBase hsa−let−7b
33	−6.37	NULL	9 / 49	miRNA 3UTR GTTT−154−−487
34	−6.3	NULL	9 / 58	miRNA target starBase hsa−miR−455−5p
35	−6.29	NULL	10 / 52	miRNA target starBase hsa−miR−487a
36	−6.28	NULL	30 / 264	miRNA target starBase hsa−miR−449a
37	−6.25	NULL	19 / 181	miRNA target starBase hsa−miR−381
38	−6.23	NULL	16 / 121	miRNA target starBase hsa−miR−493
39	−6.18	NULL	14 / 122	miRNA target starBase hsa−miR−105
40	−6.16	NULL	30 / 280	miRNA target starBase hsa−miR−320a

p−values



GW_094

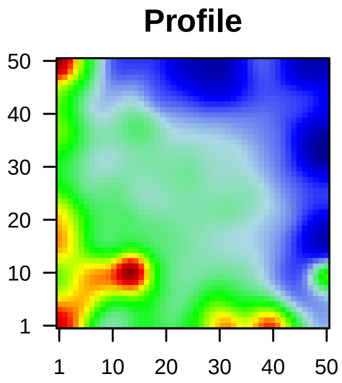
Local Summary

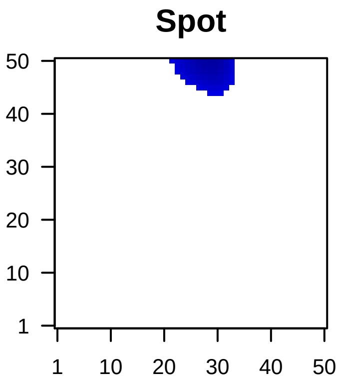
%DE = 0.45
metagenes = 62
genes = 735
genes in genesets = 725

genes with fdr < 0.1 = 48 (3 + / 45 −)
genes with fdr < 0.05 = 30 (3 + / 27 −)
genes with fdr < 0.01 = 9 (1 + / 8 −)

<r> metagenes = 0.85
<r> genes = 0.21

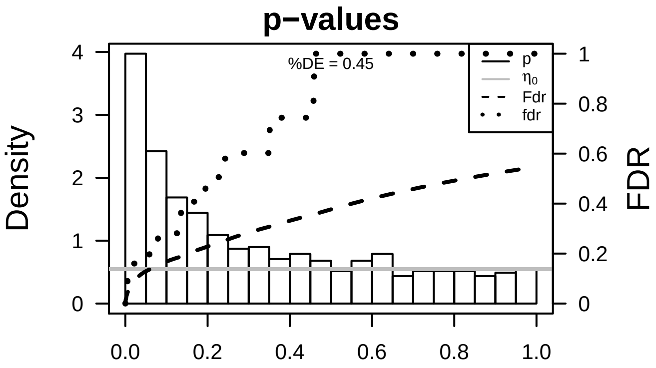
<FC> = −0.2
<shrinkage−t> = −6.87
<p−value> = 0.13
<fdr> = 0.87





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	2354	−1.21	4e−13	1e−05	22 x 50	FBJ murine osteosarcoma viral oncogene homolog B [Source
2	8560	−0.94	3e−08	3e−04	27 x 50	delta(4)−desaturase, sphingolipid 1 [Source:HGNC Symbol;A
3	3459	−0.83	8e−07	9e−04	22 x 50	interferon gamma receptor 1 [Source:HGNC Symbol;Acc:543
4	100008589	−0.77	4e−06	9e−04	23 x 50	RNA, 28S ribosomal 5 [Source:HGNC Symbol;Acc:37659]
5	91612	−0.76	5e−06	9e−04	24 x 48	churchill domain containing 1 [Source:HGNC Symbol;Acc:20
6	1843	−0.69	8e−06	1e−03	22 x 50	dual specificity phosphatase 1 [Source:HGNC Symbol;Acc:3
7	23645	0.74	1e−05	3e−03	22 x 50	protein phosphatase 1, regulatory subunit 15A [Source:HGN
8	3094	−0.66	2e−05	3e−03	32 x 50	histidine triad nucleotide binding protein 1 [Source:HGNC Sy
9	114908	−0.71	2e−05	4e−03	26 x 50	transmembrane protein 123 [Source:HGNC Symbol;Acc:301
10	3725	−0.7	3e−05	1e−02	22 x 50	jun proto−oncogene [Source:HGNC Symbol;Acc:6204]
11	7538	0.67	6e−05	1e−02	22 x 50	ZFP36 ring finger protein [Source:HGNC Symbol;Acc:12862]
12	58487	−0.66	9e−05	3e−02	26 x 48	CREB/ATF bZIP transcription factor [Source:HGNC Symbol;A
13	10150	−0.63	2e−04	3e−02	27 x 46	muscleblind−like splicing regulator 2 [Source:HGNC Symbol;
14	10950	−0.61	3e−04	3e−02	28 x 50	BTG family, member 3 [Source:HGNC Symbol;Acc:1132]
15	6622	0.6	4e−04	3e−02	27 x 50	synuclein, alpha (non A4 component of amyloid precursor) [S
16	5887	−0.6	4e−04	3e−02	23 x 50	RAD23 homolog B (S. cerevisiae) [Source:HGNC Symbol;Ac
17	6130	−0.58	6e−04	3e−02	32 x 47	ribosomal protein L7a [Source:HGNC Symbol;Acc:10364]
18	84833	−0.57	6e−04	3e−02	33 x 50	up−regulated during skeletal muscle growth 5 homolog (mous
19	221960	−0.56	8e−04	3e−02	26 x 47	CCZ1 vacuolar protein trafficking and biogenesis associated
20	8065	−0.56	8e−04	3e−02	30 x 48	cullin 5 [Source:HGNC Symbol;Acc:2556]



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−16.16	NULL	5 / 10	GSEA C2	CHASSOT_SKIN_WOUND
2	−11.52	NULL	8 / 11	MMML CGS	MACIEJ_MMML 49
3	−11.13	NULL	2 / 9	GSEA C2	GUTIERREZ_WALDENSTROEMS_MACROGLOBULINEMIA_1_D
4	−10.33	NULL	7 / 16	GSEA C2	AMIT_SERUM_RESPONSE_40_MCF10A
5	−9.78	NULL	44 / 269	miRNA target starBase	hsa−miR−1244
6	−9.68	NULL	7 / 39	BP	response to cAMP
7	−9.55	NULL	6 / 16	TF Tissue	VAQUERIZAS_Pancreas
8	−8.81	NULL	66 / 436	miRNA target starBase	hsa−miR−548n
9	−8.59	NULL	2 / 3	miRNA target	miR−373
10	−8.57	NULL	8 / 16	GSEA C2	NAGASHIMA_EGF_SIGNALING_UP
11	−8.44	NULL	4 / 16	GSEA C2	PODAR_RESPONSE_TO_ADAPHOSTIN_UP
12	−8.43	NULL	3 / 12	GSEA C2	SESTO_RESPONSE_TO_UV_C3
13	−8.3	NULL	50 / 310	miRNA target starBase	hsa−miR−340
14	−8.29	NULL	18 / 83	BP	respiratory electron transport chain
15	−8.25	NULL	13 / 61	miRNA target starBase	hsa−miR−659
16	−8.21	NULL	41 / 280	miRNA target starBase	hsa−miR−320a
17	−8.18	NULL	3 / 15	BP	response to corticosterone
18	−8.14	NULL	5 / 24	TF Tissue	VAQUERIZAS_Trachea
19	−7.95	NULL	26 / 166	miRNA target starBase	hsa−miR−320b
20	−7.93	NULL	19 / 119	miRNA target starBase	hsa−miR−515−5p
21	−7.84	NULL	42 / 262	miRNA target starBase	hsa−miR−548l
22	−7.82	NULL	4 / 30	BP	cellular response to hormone stimulus
23	−7.8	NULL	3 / 16	GSEA C2	AMIT_EGF_RESPONSE_60_HELA
24	−7.67	NULL	27 / 172	miRNA target starBase	hsa−miR−607
25	−7.65	NULL	4 / 30	BP	cellular response to calcium ion
26	−7.61	NULL	23 / 142	miRNA target starBase	hsa−miR−320c
27	−7.6	NULL	21 / 128	miRNA target starBase	hsa−miR−320d
28	−7.51	NULL	27 / 150	miRNA target starBase	hsa−miR−200c
29	−7.5	NULL	2 / 5	miRNA target	miR−372
30	−7.41	NULL	6 / 19	CC	mitochondrial proton−transporting ATP synthase complex
31	−7.3	NULL	24 / 152	BP	cellular metabolic process
32	−7.3	NULL	77 / 957	Chr	Chr 11
33	−7.26	NULL	6 / 15	MMML CGS	MACIEJ_MMML 22
34	−7.2	NULL	3 / 16	GSEA C2	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_T
35	−7.19	NULL	32 / 189	miRNA target starBase	hsa−miR−513a−3p
36	−7.15	NULL	47 / 300	miRNA target starBase	hsa−miR−561
37	−7	NULL	28 / 187	miRNA target starBase	hsa−miR−520d−5p
38	−6.97	NULL	2 / 13	GSEA C2	CHIANG_LIVER_CANCER_SUBCLASS_UNANNOTATED_UP
39	−6.97	NULL	3 / 16	GSEA C2	WATTEL_AUTONOMOUS_THYROID_ADENOMA_DN
40	−6.96	NULL	30 / 206	miRNA target starBase	hsa−miR−148b

GW_094

Local Summary

%DE = 0.56

metagenes = 31

genes = 409

genes in genesets = 405

genes with fdr < 0.1 = 110 (18 + / 92 −)

genes with fdr < 0.05 = 105 (18 + / 87 −)

genes with fdr < 0.01 = 56 (12 + / 44 −)

<r> metagenes = 0.89

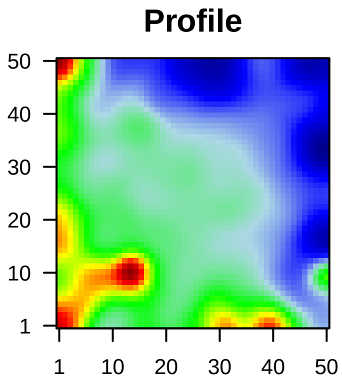
<r> genes = 0.27

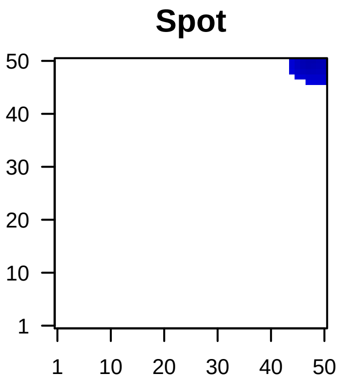
<FC> = −0.2

<shrinkage−t> = −7.08

<p−value> = 0.02

<fdr> = 0.69





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	3866	−1.81	2e−16	1e−14	50 x 50	keratin 15 [Source:HGNC Symbol;Acc:6421]
2	4922	1.42	2e−16	1e−14	50 x 50	neurotensin [Source:HGNC Symbol;Acc:8038]
3	139728	2.4	2e−16	1e−14	49 x 49	pregnancy up−regulated nonubiquitous CaM kinase [Source:
4	83888	1.34	2e−15	1e−08	50 x 50	fibroblast growth factor binding protein 2 [Source:HGNC Sym
5	2719	1.1	7e−11	1e−08	50 x 50	glypican 3 [Source:HGNC Symbol;Acc:4451]
6	94234	−1.08	1e−10	8e−08	50 x 50	forkhead box Q1 [Source:HGNC Symbol;Acc:20951]
7	440	1.04	6e−10	2e−07	50 x 46	asparagine synthetase (glutamine−hydrolyzing) [Source:HGN
8	200634	1.01	2e−09	4e−07	50 x 49	keratinocyte associated protein 3 [Source:HGNC Symbol;Acc
9	3880	0.98	5e−09	4e−07	50 x 49	keratin 19 [Source:HGNC Symbol;Acc:6436]
10	84707	−0.98	6e−09	9e−07	50 x 48	brain expressed X−linked 2 [Source:HGNC Symbol;Acc:3093
11	291	−0.96	1e−08	1e−06	50 x 46	solute carrier family 25 (mitochondrial carrier; adenine nucleo
12	1056	−0.94	2e−08	1e−06	50 x 50	carboxyl ester lipase [Source:HGNC Symbol;Acc:1848]
13	1974	−0.86	3e−08	1e−06	49 x 47	eukaryotic translation initiation factor 4A2 [Source:HGNC Sy
14	655	−0.93	4e−08	3e−05	50 x 50	bone morphogenetic protein 7 [Source:HGNC Symbol;Acc:1
15	4690	−0.87	2e−07	3e−05	49 x 50	NCK adaptor protein 1 [Source:HGNC Symbol;Acc:7664]
16	55872	−0.84	6e−07	3e−05	45 x 49	PDZ binding kinase [Source:HGNC Symbol;Acc:18282]
17	59342	−0.84	6e−07	3e−05	50 x 47	serine carboxypeptidase 1 [Source:HGNC Symbol;Acc:29507
18	56963	−0.83	7e−07	4e−05	50 x 50	repulsive guidance molecule family member a [Source:HGNC
19	10057	−0.82	1e−06	4e−05	50 x 50	ATP−binding cassette, sub−family C (CFTR/MRP), member 5
20	26047	−0.82	1e−06	6e−05	50 x 50	contactin associated protein−like 2 [Source:HGNC Symbol;A

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−20.05	NULL	70 / 142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
2	−20.05	NULL	70 / 142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
3	−12.36	NULL	12 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_2
4	−12.34	NULL	9 / 14	GSEA C2	ZHAN_MULTIPLE_MYELOMA_PR_UP
5	−10.63	NULL	7 / 15	GSEA C2	WU_APOPTOSIS_BY_CDKN1A_VIA_TP53
6	−10.36	NULL	8 / 15	GSEA C2	LEE_EARLY_T_LYMPHOCYTE_UP
7	−9.96	NULL	6 / 13	GSEA C2	PUJANA_XPRSS_INT_NETWORK
8	−9.79	NULL	6 / 10	GSEA C2	MONTERO_THYROID_CANCER_POOR_SURVIVAL_UP
9	−9.54	NULL	6 / 16	GSEA C2	MEINHOLD_OVARIAN_CANCER_LOW_GRADE_DN
10	−9.52	NULL	7 / 14	GSEA C2	PUJANA_BRCA_CENTERED_NETWORK
11	−9.19	NULL	75 / 914	Chr	Chr 3
12	−9.05	NULL	22 / 57	Glio	developing astrocytes
13	−8.88	NULL	12 / 16	GSEA C2	FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
14	−8.73	NULL	8 / 16	GSEA C2	KANG_DOXORUBICIN_RESISTANCE_UP
15	−8.62	NULL	8 / 14	GSEA C2	AMUNDSON_GAMMA_RADIATION_RESPONSE
16	−8.46	NULL	7 / 11	GSEA C2	KALMA_E2F1_TARGETS
17	−8.42	NULL	6 / 12	BP	mitotic chromosome condensation
18	−8.37	NULL	4 / 8	GSEA C2	REACTOME_E2F_TRANSCRIPTIONAL_TARGETS_AT_G1_S
19	−8.1	NULL	11 / 15	GSEA C2	FINETTI_BREAST_CANCER_KINOME_RED
20	−7.97	NULL	7 / 16	GSEA C2	SONG_TARGETS_OF_IE86_CMV_PROTEIN
21	−7.82	NULL	8 / 15	GSEA C2	ODONNELL_TARGETS_OF_MYC_AND_TFRC_DN
22	−7.77	NULL	5 / 15	GSEA C2	KAUFFMANN_MELANOMA_RELAPSE_UP
23	−7.68	NULL	66 / 370	BP	mitotic cell cycle
24	−7.63	NULL	6 / 15	GSEA C2	KEGG_CELL_CYCLE
25	−7.38	NULL	8 / 15	GSEA C2	BOYAULT_LIVER_CANCER_SUBCLASS_G23_UP
26	−7.22	NULL	7 / 31	CC	nuclear chromosome
27	−7.07	NULL	4 / 15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
28	−7.05	NULL	4 / 16	GSEA C2	RODWELL_AGING_KIDNEY_DN
29	−7.02	NULL	4 / 11	GSEA C2	REACTOME_E2F_MEDIATED_REGULATION_OF_DNA_REPLIC
30	−7.01	NULL	1 / 15	H.Tiss	WIRTH_Cerebellum
31	−7	NULL	8 / 16	GSEA C2	PUJANA_BREAST_CANCER_WITH_BRCA1_MUTATED_UP
32	−6.76	NULL	1 / 16	GSEA C2	ROY_WOUND_BLOOD_VESSEL_DN
33	−6.68	NULL	7 / 15	GSEA C2	CHANG_CYCLING_GENES
34	−6.68	NULL	2 / 13	GSEA C2	BROWNE_HCMV_INFECTION_6HR_DN
35	−6.67	NULL	3 / 13	GSEA C2	JAERVINEN_AMPLIFIED_IN_LARYNGEAL_CANCER
36	−6.6	NULL	5 / 14	GSEA C2	PUJANA_BRCA2_PCC_NETWORK
37	−6.58	NULL	68 / 530	Cancer	Lembcke_Normal vs Adenoma
38	−6.52	NULL	4 / 16	GSEA C2	DAZARD_RESPONSE_TO_UV_NHEK_DN
39	−6.49	NULL	2 / 14	CC	membrane−bounded vesicle
40	−6.42	NULL	6 / 15	GSEA C2	FOURNIER_ACINAR_DEVELOPMENT_LATE_DN