GW_205

Global Summary

%DE = 0.16

genes with fdr < 0.2 = 2034 (1089 + / 945 −)

genes with fdr < 0.1 = 1643 (875 + / 768 −)

genes with fdr < 0.05 = 1423 (761 + / 662 −)

genes with fdr < 0.01 = 1019 (556 + / 463 −)

genes in genesets = 16332

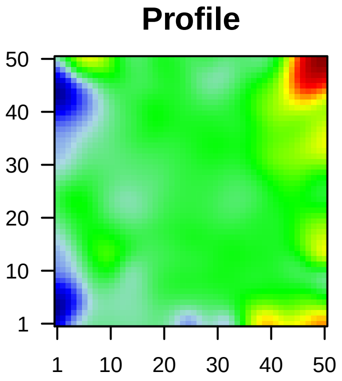
<FC> = 0

<shrinkage−t> = 0

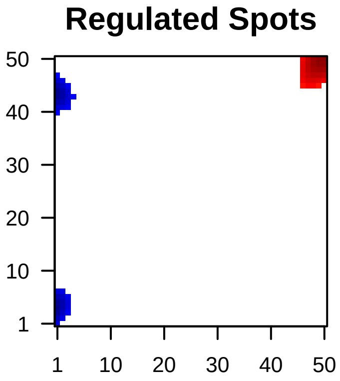
<p−value> = 0.08

<fdr> = 0.84

Profile



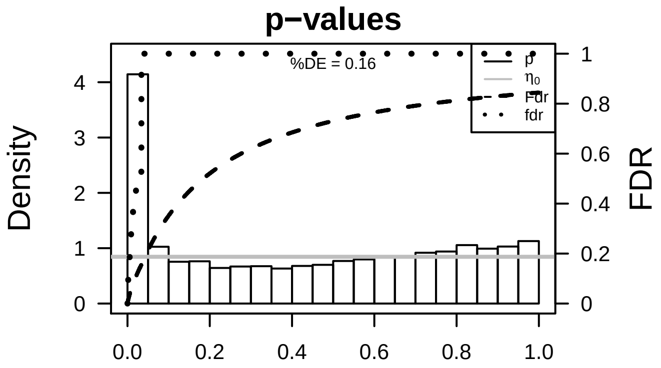
Regulated Spots



Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	154664	1.48	2e−16	3e−14	50 x 50	ATP−binding cassette, sub−family A (ABC1), member 13 [Sou
2	131	1.75	2e−16	3e−14	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
3	113146	−1.36	2e−16	3e−14	1 x 44	AHNAK nucleoprotein 2 [Source:HGNC Symbol;Acc:20125]
4	57016	−1.8	2e−16	3e−14	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
5	441282	−1.68	2e−16	3e−14	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC Sy
6	218	−1.61	2e−16	3e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
7	501	−1.42	2e−16	3e−14	6 x 46	aldehyde dehydrogenase 7 family, member A1 [Source:HGNC
8	249	1.54	2e−16	3e−14	6 x 1	alkaline phosphatase, liver/bone/kidney [Source:HGNC Symb
9	55107	−1.67	2e−16	3e−14	1 x 5	anoctamin 1, calcium activated chloride channel [Source:HGN
10	341	1.73	2e−16	3e−14	50 x 1	apolipoprotein C−I [Source:HGNC Symbol;Acc:607]
11	348	1.56	2e−16	3e−14	50 x 1	apolipoprotein E [Source:HGNC Symbol;Acc:613]
12	8702	1.7	2e−16	3e−14	50 x 50	UDP−Gal:betaGlcNAc beta 1,4− galactosyltransferase, polyp
13	80115	−1.71	2e−16	3e−14	1 x 43	BAI1−associated protein 2−like 2 [Source:HGNC Symbol;Acc
14	121551	−1.57	2e−16	3e−14	1 x 47	BTB (POZ) domain containing 11 [Source:HGNC Symbol;Acc
15	10974	−1.59	2e−16	3e−14	5 x 50	adipogenesis regulatory factor [Source:HGNC Symbol;Acc:24
16	64073	−1.97	2e−16	3e−14	1 x 46	chromosome 19 open reading frame 33 [Source:HGNC Symb
17	339512	2	2e−16	3e−14	50 x 50	chromosome 1 open reading frame 110 [Source:HGNC Symb
18	387103	1.72	2e−16	3e−14	45 x 49	centromere protein W [Source:HGNC Symbol;Acc:21488]
19	760	−1.65	2e−16	3e−14	1 x 44	carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
20	51806	2.01	2e−16	3e−14	4 x 50	calmodulin−like 5 [Source:HGNC Symbol;Acc:18180]

p−values



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	11.68	NULL	914	Chr	Chr 3
2	8.86	NULL	13	GSEA C2	SLEBOS_HEAD_AND_NECK_CANCER_WITH_HPV_UP
3	8.82	NULL	7	GSEA C2	MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
4	7.93	NULL	15	CC	MHC class II protein complex
5	7.14	NULL	15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
6	6.37	NULL	417	H.Tiss	WIRTH_Immune system
7	6.05	NULL	21	CC	clathrin−coated endocytic vesicle membrane
8	5.87	NULL	11	Glio	neurons_glio
9	5.69	NULL	8	GSEA C2	RUNNE_GENDER_EFFECT_UP
10	5.61	NULL	16	Cancer	WOLFER_overlap genes
11	5.47	NULL	12	GSEA C2	ZHAN_MULTIPLE_MYELOMA_DN
12	5.4	NULL	60	BP	T cell costimulation
13	5.35	NULL	6	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_7
14	5.32	NULL	16	GSEA C2	SHEDDEN_LUNG_CANCER_GOOD_SURVIVAL_A5
15	5.24	NULL	7	MMML CGS	MACIEJ_MMML 5
16	5.18	NULL	949	CC	nucleoplasm
17	5.14	NULL	86	Lymphoma	ROSOLOWSKI_red total
18	5.13	NULL	84	BP	T cell receptor signaling pathway
19	4.93	NULL	142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
20	4.93	NULL	142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
Underexpressed					
1	−12.34	NULL	957	Chr	Chr 11
2	−10.56	NULL	12	BP	hemidesmosome assembly
3	−7.36	NULL	4	MMML CGS	MACIEJ_MMML 23
4	−6.85	NULL	7	MMML CGS	MACIEJ_MMML 9
5	−6.83	NULL	51	BP	type I interferon signaling pathway
6	−6.42	NULL	12	GSEA C2	SANCHEZ_MDM2_TARGETS
7	−6.26	NULL	1182	CC	extracellular region
8	−5.89	NULL	16	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_LUNG_UP
9	−5.77	NULL	13	GSEA C2	REACTOME_REGULATION_OF_INSULIN_LIKE_GROWTH_FACT
10	−5.76	NULL	534	Chr	Chr 8
11	−5.74	NULL	35	Glio	Colman_survival_associated
12	−5.69	NULL	14	GSEA C2	DAZARD_UV_RESPONSE_CLUSTER_G4
13	−5.67	NULL	5	GSEA C2	VERNELL_RETINOBLASTOMA_PATHWAY_DN
14	−5.65	NULL	16	GSEA C2	UROSEVIC_RESPONSE_TO_IMIQUIMOD
15	−5.4	NULL	25	BP	response to zinc ion
16	−5.33	NULL	15	GSEA C2	LEE_LIVER_CANCER_HEPATOBLAST
17	−5.29	NULL	14	GSEA C2	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_8D_UP
18	−5.28	NULL	4	GSEA C2	BUDHU_LIVER_CANCER_METASTASIS_DN
19	−5.22	NULL	10	MF	neutral amino acid transmembrane transporter activity
20	−5.22	NULL	83	CC	basement membrane

GW_205

Local Summary

%DE = 0.81

metagenes = 29

genes = 345

genes in genesets = 343

genes with fdr < 0.1 = 243 (218 + / 25 −)

genes with fdr < 0.05 = 220 (202 + / 18 −)

genes with fdr < 0.01 = 197 (181 + / 16 −)

<r> metagenes = 0.92

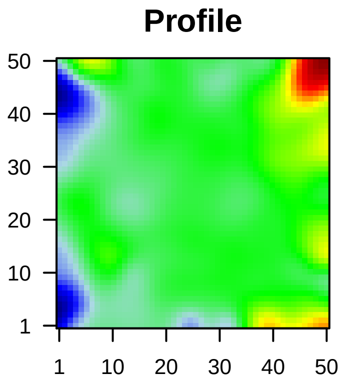
<r> genes = 0.25

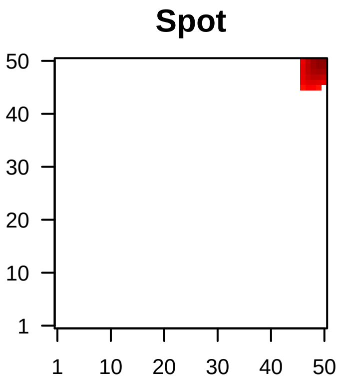
<FC> = 0.48

<shrinkage−t> = 16.88

<p−value> = 0

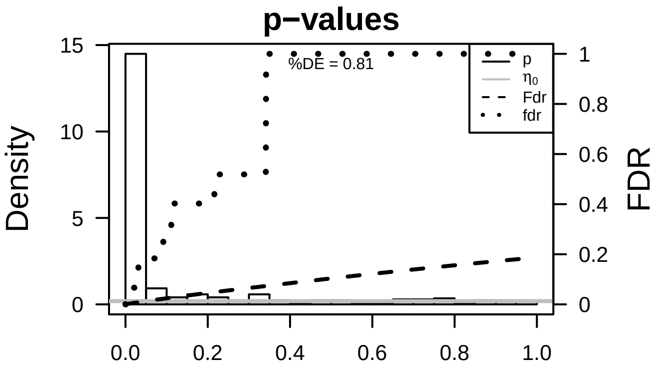
<fdr> = 0.34





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	154664	1.48	2e−16	8e−16	50 x 50	ATP−binding cassette, sub−family A (ABC1), member 13 [Sou
2	8702	1.7	2e−16	8e−16	50 x 50	UDP−Gal:betaGlcNAc beta 1,4− galactosyltransferase, polyp
3	339512	2	2e−16	8e−16	50 x 50	chromosome 1 open reading frame 110 [Source:HGNC Symb
4	9076	1.47	2e−16	8e−16	49 x 50	claudin 1 [Source:HGNC Symbol;Acc:2032]
5	1857	1.34	2e−16	8e−16	49 x 50	dishevelled segment polarity protein 3 [Source:HGNC Symbo
6	2944	1.92	2e−16	8e−16	50 x 50	glutathione S−transferase mu 1 [Source:HGNC Symbol;Acc:4
7	3304	1.26	2e−16	8e−16	49 x 49	heat shock 70kDa protein 1A [Source:HGNC Symbol;Acc:523
8	10643	1.39	2e−16	8e−16	48 x 50	insulin−like growth factor 2 mRNA binding protein 3 [Source:H
9	3787	1.54	2e−16	8e−16	46 x 45	potassium voltage−gated channel, delayed−rectifier, subfamil
10	3866	2.14	2e−16	8e−16	50 x 50	keratin 15 [Source:HGNC Symbol;Acc:6421]
11	3880	2.15	2e−16	8e−16	50 x 49	keratin 19 [Source:HGNC Symbol;Acc:6436]
12	79682	1.46	2e−16	8e−16	46 x 47	centromere protein U [Source:HGNC Symbol;Acc:21348]
13	4922	5.09	2e−16	8e−16	50 x 50	neurotensin [Source:HGNC Symbol;Acc:8038]
14	10388	1.52	2e−16	8e−16	47 x 46	synaptonemal complex protein 2 [Source:HGNC Symbol;Acc:
15	11073	1.45	2e−16	8e−16	47 x 48	topoisomerase (DNA) II binding protein 1 [Source:HGNC Sym
16	79679	1.68	2e−16	8e−16	50 x 50	V−set domain containing T cell activation inhibitor 1 [Source:H
17	84215	1.33	2e−16	8e−16	46 x 45	zinc finger protein 541 [Source:HGNC Symbol;Acc:25294]
18	2946	1.28	7e−16	6e−14	50 x 50	glutathione S−transferase mu 2 (muscle) [Source:HGNC Sym
19	1974	1.16	2e−15	1e−13	49 x 47	eukaryotic translation initiation factor 4A2 [Source:HGNC Syn
20	54800	1.25	3e−15	1e−13	50 x 48	kelch−like family member 24 [Source:HGNC Symbol;Acc:259



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	22.51	NULL	2 / 7	GSEA C2	MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
2	18.09	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
3	17.39	NULL	4 / 13	BP	regulation of blood vessel size
4	15.19	NULL	75 / 914	Chr	Chr 3
5	14.8	NULL	1 / 11	Glio	neurons_glio
6	13.3	NULL	6 / 14	GSEA C2	PUJANA_BRCA_CENTERED_NETWORK
7	13.04	NULL	5 / 13	GSEA C2	PUJANA_XPRSS_INT_NETWORK
8	12.44	NULL	1 / 15	MF	neuropeptide hormone activity
9	11.94	NULL	4 / 13	GSEA C2	SLEBOS_HEAD_AND_NECK_CANCER_WITH_HPV_UP
10	11.04	NULL	3 / 6	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_7
11	11.01	NULL	4 / 13	GSEA C2	KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_
12	10.8	NULL	3 / 9	GSEA C2	BROWNE_HCMV_INFECTION_8HR_UP
13	10.43	NULL	3 / 11	MF	glutathione binding
14	10.43	NULL	3 / 11	GSEA C2	KEGG_DRUG_METABOLISM_CYTOCHROME_P450
15	10.11	NULL	4 / 15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
16	10.07	NULL	4 / 11	GSEA C2	KALMA_E2F1_TARGETS
17	9.49	NULL	3 / 14	GSEA C2	KORKOLA_YOLK_SAC_TUMOR
18	9.22	NULL	1 / 2	GSEA C2	KUROKAWA_LIVER_CANCER_EARLY_RECURRENCE_UP
19	9.21	NULL	4 / 15	GSEA C2	KIM_MYCN_AMPLIFICATION_TARGETS_DN
20	8.95	NULL	5 / 16	GSEA C2	SONG_TARGETS_OF_IE86_CMV_PROTEIN
21	8.87	NULL	4 / 16	GSEA C2	PUJANA_BREAST_CANCER_WITH_BRCA1_MUTATED_UP
22	8.86	NULL	3 / 13	GSEA C2	JAERVINEN_AMPLIFIED_IN_LARYNGEAL_CANCER
23	8.62	NULL	3 / 16	Cancer	WOLFER_overlap genes
24	8.45	NULL	3 / 15	GSEA C2	KAUFFMANN_DNA_REPLICATION_GENES
25	8.43	NULL	3 / 8	GSEA C2	REACTOME_E2F_TRANSCRIPTIONAL_TARGETS_AT_G1_S
26	8.27	NULL	8 / 30	BP	DNA strand elongation involved in DNA replication
27	8.09	NULL	4 / 11	GSEA C2	REACTOME_UNWINDING_OF_DNA
28	8.07	NULL	4 / 16	GSEA C2	RODWELL_AGING_KIDNEY_DN
29	7.67	NULL	2 / 15	GSEA C2	LEE_LIVER_CANCER_MYC_UP
30	7.67	NULL	2 / 15	GSEA C2	LEE_LIVER_CANCER_E2F1_UP
31	7.56	NULL	2 / 14	GSEA C2	AMBROSINI_FLAVOPIRIDOL_TREATMENT_TP53
32	7.52	NULL	5 / 15	GSEA C2	KEGG_GLUTATHIONE_METABOLISM
33	7.46	NULL	1 / 5	GSEA C2	TURASHVILI_BREAST_CARCINOMA_DUCTAL_VS_LOBULAR_
34	7.21	NULL	4 / 11	GSEA C2	LIANG_SILENCED_BY_METHYLATION_DN
35	7.2	NULL	2 / 7	GSEA C2	REACTOME_G1_S_TRANSITION
36	7.09	NULL	4 / 15	GSEA C2	KEGG_CELL_CYCLE
37	7.01	NULL	3 / 11	GSEA C2	REACTOME_E2F_MEDIATED_REGULATION_OF_DNA_REPLIC
38	6.96	NULL	3 / 16	GSEA C2	RODWELL_AGING_KIDNEY_NO_BLOOD_DN
39	6.95	NULL	1 / 41	CC	transport vesicle
40	6.71	NULL	4 / 16	GSEA C2	BILD_E2F3_ONCOGENIC_SIGNATURE

GW_205

Local Summary

%DE = 0.86

metagenes = 17

genes = 247

genes in genesets = 244

genes with fdr < 0.1 = 172 (12 + / 160 −)

genes with fdr < 0.05 = 162 (11 + / 151 −)

genes with fdr < 0.01 = 125 (7 + / 118 −)

<r> metagenes = 0.96

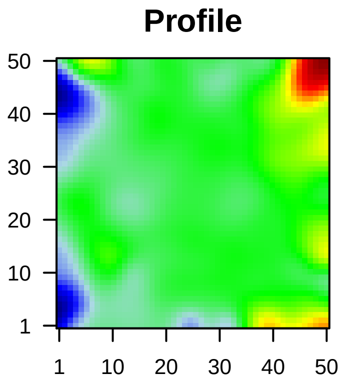
<r> genes = 0.34

<FC> = −0.47

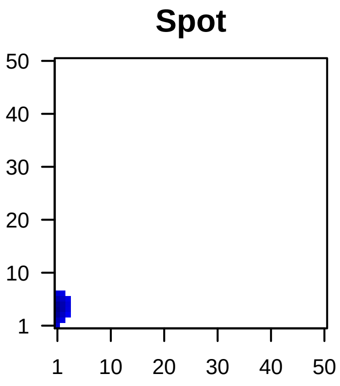
<shrinkage−t> = −16.5

<p−value> = 0

<fdr> = 0.41



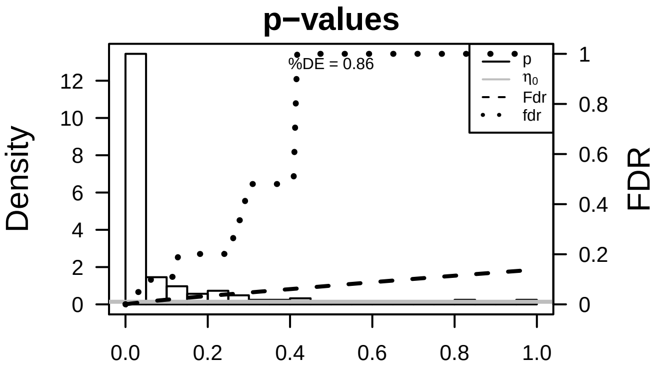
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	55107	−1.67	2e−16	6e−16	1 x 5	anoctamin 1, calcium activated chloride channel [Source:HGN
2	857	−1.5	2e−16	6e−16	1 x 4	caveolin 1, caveolae protein, 22kDa [Source:HGNC Symbol;A
3	595	−1.46	2e−16	6e−16	1 x 6	cyclin D1 [Source:HGNC Symbol;Acc:1582]
4	8727	−1.31	2e−16	6e−16	1 x 5	catenin (cadherin−associated protein), alpha−like 1 [Source:H
5	28514	−1.57	2e−16	6e−16	1 x 5	delta−like 1 (Drosophila) [Source:HGNC Symbol;Acc:2908]
6	3553	−1.68	2e−16	6e−16	1 x 1	interleukin 1, beta [Source:HGNC Symbol;Acc:5992]
7	4319	−1.77	2e−16	6e−16	1 x 3	matrix metallopeptidase 10 (stromelysin 2) [Source:HGNC Sy
8	4502	−1.59	2e−16	6e−16	1 x 3	metallothionein 2A [Source:HGNC Symbol;Acc:7406]
9	10630	−1.44	2e−16	6e−16	1 x 2	podoplanin [Source:HGNC Symbol;Acc:29602]
10	56907	−1.38	2e−16	6e−16	3 x 5	spire−type actin nucleation factor 1 [Source:HGNC Symbol;A
11	7045	−1.3	2e−16	6e−16	1 x 2	transforming growth factor, beta−induced, 68kDa [Source:HG
12	25907	−1.29	2e−16	6e−16	1 x 1	transmembrane protein 158 (gene/pseudogene) [Source:HGN
13	3371	−2.02	2e−16	6e−16	1 x 3	tenascin C [Source:HGNC Symbol;Acc:5318]
14	5270	−1.21	2e−14	1e−12	1 x 3	serpin peptidase inhibitor, clade E (nexin, plasminogen activa
15	55450	−1.19	6e−14	1e−12	1 x 4	calcium/calmodulin−dependent protein kinase II inhibitor 1 [S
16	3909	−1.18	9e−14	7e−12	1 x 5	laminin, alpha 3 [Source:HGNC Symbol;Acc:6483]
17	374378	−1.14	6e−13	7e−12	1 x 6	UDP−N−acetyl−alpha−D−galactosamine:polypeptide N−acety
18	3486	−1.14	7e−13	7e−12	1 x 6	insulin−like growth factor binding protein 3 [Source:HGNC Sy
19	360132	−1.13	7e−13	7e−12	1 x 4	FK506 binding protein 9−like [Source:HGNC Symbol;Acc:235
20	1464	−1.13	9e−13	1e−11	1 x 3	chondroitin sulfate proteoglycan 4 [Source:HGNC Symbol;Ac



p−values

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−21.08	NULL	9 / 35	Glio	Colman_survival_associated
2	−16.91	NULL	1 / 2	miRNA target	miR−16−1
3	−16.03	NULL	6 / 15	GSEA C2	LEE_LIVER_CANCER_HEPATOBLAST
4	−15.05	NULL	2 / 6	GSEA C2	BIOCARTA_IL5_PATHWAY
5	−14.96	NULL	2 / 4	miRNA target	miR−195
6	−14.8	NULL	3 / 10	BP	cellular response to zinc ion
7	−14.8	NULL	37 / 242	BP	extracellular matrix organization
8	−14.75	NULL	2 / 5	GSEA C2	VERNELL_RETINOBLASTOMA_PATHWAY_DN
9	−13.9	NULL	4 / 14	GSEA C2	LOPEZ_MESOTHELIOMA_SURVIVAL_OVERALL_DN
10	−13.3	NULL	40 / 403	BP	cell adhesion
11	−13.19	NULL	5 / 12	BP	hemidesmosome assembly
12	−13.13	NULL	1 / 3	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_11
13	−13.09	NULL	4 / 13	GSEA C2	CHIN_BREAST_CANCER_COPY_NUMBER_UP
14	−13.07	NULL	4 / 14	GSEA C2	SIMBULAN_UV_RESPONSE_IMMORTALIZED_DN
15	−13.04	NULL	4 / 16	GSEA C2	BEGUM_TARGETS_OF_PAX3_FOXO1_FUSION_DN
16	−13.02	NULL	8 / 15	GSEA C2	CROMER_TUMORIGENESIS_UP
17	−12.87	NULL	49 / 683	CC	extracellular space
18	−12.43	NULL	4 / 9	GSEA C2	WEINMANN_ADAPTATION_TO_HYPOXIA_DN
19	−12.42	NULL	2 / 7	MMML CGS	MACIEJ_MMML 13
20	−12.32	NULL	7 / 16	MF	fibronectin binding
21	−12.18	NULL	2 / 7	GSEA C2	FREDERICK_PRKCI_TARGETS
22	−12.09	NULL	4 / 16	GSEA C2	LI_PROSTATE_CANCER_EPIGENETIC
23	−12.06	NULL	4 / 16	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C1
24	−12.03	NULL	5 / 13	GSEA C2	MAHADEVAN_GIST_MORPHOLOGICAL_SWITCH
25	−12.02	NULL	74 / 1182	CC	extracellular region
26	−11.96	NULL	4 / 16	GSEA C2	KERLEY_RESPONSE_TO_CISPLATIN_UP
27	−11.89	NULL	1 / 4	GSEA C2	BUDHU_LIVER_CANCER_METASTASIS_DN
28	−11.79	NULL	2 / 6	miRNA target	let−7b
29	−11.77	NULL	3 / 15	BP	negative regulation of growth
30	−11.62	NULL	5 / 16	GSEA C2	FERRARI_RESPONSE_TO_FENRETINIDE_UP
31	−11.39	NULL	2 / 9	GSEA C2	MARKS_HDAC_TARGETS_DN
32	−11.38	NULL	2 / 12	BP	regulation of G1/S transition of mitotic cell cycle
33	−11.04	NULL	1 / 4	miRNA target	miR−20a
34	−11.01	NULL	3 / 15	GSEA C2	SNIJDERS_AMPLIFIED_IN_HEAD_AND_NECK_TUMORS
35	−10.87	NULL	4 / 10	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C4
36	−10.71	NULL	4 / 15	BP	negative regulation of anoikis
37	−10.54	NULL	10 / 83	CC	basement membrane
38	−10.47	NULL	4 / 17	BP	negative regulation of signal transduction
39	−10.43	NULL	4 / 16	GSEA C2	ABRAHAM_ALPC_VS_MULTIPLE_MYELOMA_UP
40	−10.14	NULL	10 / 68	Glio	cultured astroglia vs. in vivo astrocytes

GW_205

Local Summary

%DE = 0.81

metagenes = 20

genes = 269

genes in genesets = 263

genes with fdr < 0.1 = 174 (24 + / 150 −)

genes with fdr < 0.05 = 165 (22 + / 143 −)

genes with fdr < 0.01 = 156 (21 + / 135 −)

<r> metagenes = 0.95

<r> genes = 0.36

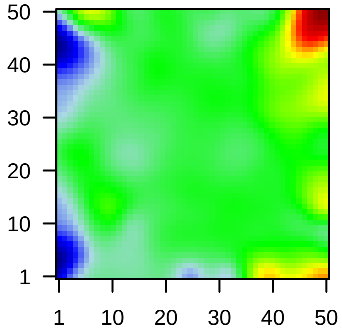
<FC> = −0.42

<shrinkage−t> = −14.74

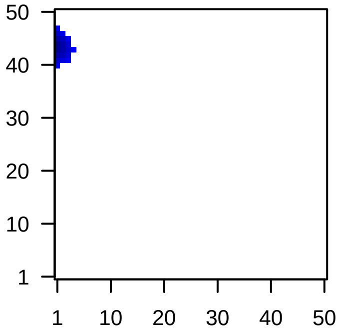
<p−value> = 0

<fdr> = 0.38

Profile



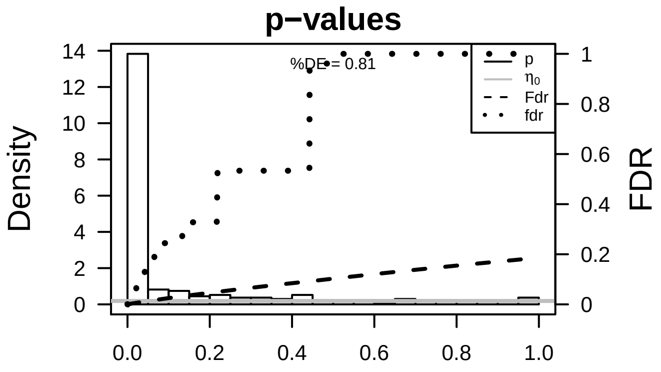
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	113146	−1.36	2e−16	5e−16	1 x 44	AHNAK nucleoprotein 2 [Source:HGNC Symbol;Acc:20125]
2	80115	−1.71	2e−16	5e−16	1 x 43	BAI1−associated protein 2−like 2 [Source:HGNC Symbol;Acc
3	121551	−1.57	2e−16	5e−16	1 x 47	BTB (POZ) domain containing 11 [Source:HGNC Symbol;Acc
4	64073	−1.97	2e−16	5e−16	1 x 46	chromosome 19 open reading frame 33 [Source:HGNC Symb
5	760	−1.65	2e−16	5e−16	1 x 44	carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
6	1001	−1.52	2e−16	5e−16	1 x 43	cadherin 3, type 1, P−cadherin (placental) [Source:HGNC Sy
7	1308	−2.64	2e−16	5e−16	1 x 43	collagen, type XVII, alpha 1 [Source:HGNC Symbol;Acc:2194
8	1515	−1.62	2e−16	5e−16	1 x 44	cathepsin V [Source:HGNC Symbol;Acc:2538]
9	9547	−1.93	2e−16	5e−16	1 x 46	chemokine (C−X−C motif) ligand 14 [Source:HGNC Symbol;
10	2167	−1.57	2e−16	5e−16	1 x 44	fatty acid binding protein 4, adipocyte [Source:HGNC Symbol
11	3489	−1.66	2e−16	5e−16	1 x 44	insulin−like growth factor binding protein 6 [Source:HGNC Sy
12	3552	−1.33	2e−16	5e−16	1 x 43	interleukin 1, alpha [Source:HGNC Symbol;Acc:5991]
13	53833	1.4	2e−16	5e−16	1 x 46	interleukin 20 receptor beta [Source:HGNC Symbol;Acc:6004
14	3848	−1.44	2e−16	5e−16	1 x 47	keratin 1 [Source:HGNC Symbol;Acc:6412]
15	3861	−3.44	2e−16	5e−16	1 x 45	keratin 14 [Source:HGNC Symbol;Acc:6416]
16	3868	−1.51	2e−16	5e−16	1 x 46	keratin 16 [Source:HGNC Symbol;Acc:6423]
17	348938	−1.37	2e−16	5e−16	1 x 46	NIPA−like domain containing 4 [Source:HGNC Symbol;Acc:2
18	5744	−1.89	2e−16	5e−16	1 x 43	parathyroid hormone−like hormone [Source:HGNC Symbol;A
19	8140	−2.06	2e−16	5e−16	1 x 43	solute carrier family 7 (amino acid transporter light chain, L sy
20	55076	1.33	2e−16	5e−16	1 x 46	transmembrane protein 45A [Source:HGNC Symbol;Acc:254

p−values



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−24.53	NULL	5 / 12	BP	hemidesmosome assembly
2	−22.63	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
3	−18.06	NULL	4 / 13	BP	intermediate filament cytoskeleton organization
4	−17.07	NULL	15 / 76	BP	epidermis development
5	−15.37	NULL	3 / 6	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_UP
6	−15	NULL	9 / 44	CC	keratin filament
7	−14.81	NULL	3 / 25	BP	response to zinc ion
8	−14.14	NULL	2 / 8	GSEA C2	DORN_ADENOVIRUS_INFECTION_24HR_UP
9	−13.97	NULL	18 / 82	CC	intermediate filament
10	−12.7	NULL	4 / 38	BP	epithelial cell differentiation
11	−11.76	NULL	11 / 82	MF	structural constituent of cytoskeleton
12	−11.06	NULL	3 / 35	CC	cell periphery
13	−10.62	NULL	6 / 70	BP	cell junction assembly
14	−10.55	NULL	2 / 10	MF	neutral amino acid transmembrane transporter activity
15	−10.4	NULL	2 / 16	GSEA C2	ROY_WOUND_BLOOD_VESSEL_DN
16	−10.12	NULL	2 / 15	GSEA C2	SMID_BREAST_CANCER_LUMINAL_A_DN
17	−9.92	NULL	17 / 186	MF	structural molecule activity
18	−9.55	NULL	2 / 16	GSEA C2	DORN_ADENOVIRUS_INFECTION_12HR_UP
19	−9.54	NULL	1 / 6	miRNA target starBase	hsa−miR−126
20	−9.51	NULL	2 / 12	BP	neutral amino acid transport
21	−8.52	NULL	1 / 5	GSEA C2	BUSA_SAM68_TARGETS_UP
22	−8.34	NULL	3 / 15	GSEA C2	FRIDMAN_IMMORTALIZATION_DN
23	−8.33	NULL	2 / 15	GSEA C2	KANG_CISPLATIN_RESISTANCE_UP
24	−8.25	NULL	4 / 16	GSEA C2	COLDREN_GEFITINIB_RESISTANCE_DN
25	−8.24	NULL	2 / 8	GSEA C2	MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_UP
26	−8.14	NULL	2 / 44	BP	response to ionizing radiation
27	−8.07	NULL	2 / 16	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_LUNG_UP
28	−8.07	NULL	2 / 16	GSEA C2	PACHER_TARGETS_OF_IGF1_AND_IGF2_UP
29	−7.98	NULL	1 / 7	GSEA C2	BEGUM_TARGETS_OF_PAX3_FOXO1_FUSION_AND_PAX3
30	−7.78	NULL	1 / 4	GSEA C2	BUDHU_LIVER_CANCER_METASTASIS_DN
31	−7.41	NULL	2 / 13	BP	response to copper ion
32	−7.33	NULL	4 / 21	BP	filopodium assembly
33	−7.25	NULL	4 / 25	BP	brown fat cell differentiation
34	−7.12	NULL	3 / 15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_DN
35	−7.09	NULL	1 / 10	GSEA C2	YOKOE_CANCER_TESTIS_ANTIGENS
36	−7.01	NULL	3 / 13	GSEA C2	WANG_METHYLATED_IN_BREAST_CANCER
37	−6.99	NULL	2 / 6	GSEA C2	WALLACE_PROSTATE_CANCER_DN
38	−6.97	NULL	1 / 16	GSEA C2	WATTEL_AUTONOMOUS_THYROID_ADENOMA_UP
39	−6.85	NULL	2 / 17	MF	amino acid transmembrane transporter activity
40	−6.75	NULL	1 / 4	GSEA C2	DACOSTA_LOW_DOSE_UV_RESPONSE_VIA_ERCC3_XPCS_D