GW_029

Global Summary

%DE = 0.16

genes with fdr < 0.2 = 2098 (1292 + / 806 −)

genes with fdr < 0.1 = 1605 (1076 + / 529 −)

genes with fdr < 0.05 = 1330 (939 + / 391 −)

genes with fdr < 0.01 = 1019 (780 + / 239 −)

genes in genesets = 16332

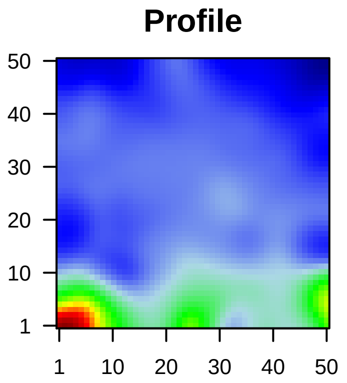
<FC> = 0

<shrinkage−t> = 0

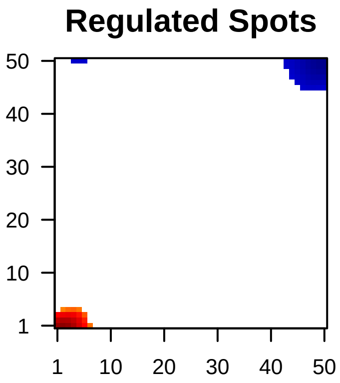
<p−value> = 0.07

<fdr> = 0.84

Profile



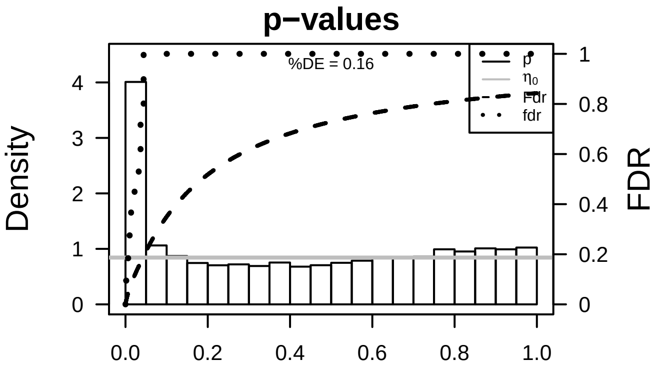
Regulated Spots



Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	2	1.6	2e−16	2e−14	50 x 5	alpha−2−macroglobulin [Source:HGNC Symbol;Acc:7]
2	58	3.49	2e−16	2e−14	25 x 1	actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
3	59	1.89	2e−16	2e−14	3 x 1	actin, alpha 2, smooth muscle, aorta [Source:HGNC Symbol;
4	70	3.69	2e−16	2e−14	25 x 1	actin, alpha, cardiac muscle 1 [Source:HGNC Symbol;Acc:14
5	72	1.66	2e−16	2e−14	4 x 1	actin, gamma 2, smooth muscle, enteric [Source:HGNC Sym
6	9510	1.49	2e−16	2e−14	6 x 1	ADAM metallopeptidase with thrombospondin type 1 motif, 1
7	165	1.48	2e−16	2e−14	3 x 1	AE binding protein 1 [Source:HGNC Symbol;Acc:303]
8	115701	1.58	2e−16	2e−14	50 x 3	alpha−kinase 2 [Source:HGNC Symbol;Acc:20565]
9	249	1.88	2e−16	2e−14	6 x 1	alkaline phosphatase, liver/bone/kidney [Source:HGNC Sym
10	23452	1.9	2e−16	2e−14	3 x 1	angiopoietin−like 2 [Source:HGNC Symbol;Acc:490]
11	27063	1.61	2e−16	2e−14	25 x 1	ankyrin repeat domain 1 (cardiac muscle) [Source:HGNC Sy
12	187	1.71	2e−16	2e−14	5 x 1	apelin receptor [Source:HGNC Symbol;Acc:339]
13	347	1.96	2e−16	2e−14	50 x 7	apolipoprotein D [Source:HGNC Symbol;Acc:612]
14	366	2.7	2e−16	2e−14	1 x 1	aquaporin 9 [Source:HGNC Symbol;Acc:643]
15	64651	1.47	2e−16	2e−14	6 x 2	cysteine−serine−rich nuclear protein 1 [Source:HGNC Symb
16	633	1.57	2e−16	2e−14	3 x 1	biglycan [Source:HGNC Symbol;Acc:1044]
17	199675	1.56	2e−16	2e−14	5 x 4	chromosome 19 open reading frame 59 [Source:HGNC Sym
18	114902	1.58	2e−16	2e−14	4 x 1	C1q and tumor necrosis factor related protein 5 [Source:HGN
19	92747	1.97	2e−16	2e−14	50 x 10	BPI fold containing family B, member 1 [Source:HGNC Symb
20	810	−1.32	2e−16	2e−14	1 x 50	calmodulin−like 3 [Source:HGNC Symbol;Acc:1452]

p−values



Global Geneset Analysis

Overexpressed

Rank	GSZ	p−value	#all	Geneset	
1	27.84	NULL	553	Cancer	Lembcke_Colonic Inflammation
2	26.99	NULL	250	Lymphoma	LENZ_Stromal signature 1
3	25.8	NULL	190	CC	extracellular matrix
4	24.77	NULL	265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
5	24.77	NULL	265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
6	24.77	NULL	265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
7	24.77	NULL	265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
8	20.74	NULL	683	CC	extracellular space
9	20.5	NULL	242	BP	extracellular matrix organization
10	19.88	NULL	1182	CC	extracellular region
11	16.68	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
12	16.26	NULL	69	BP	extracellular matrix disassembly
13	16.17	NULL	183	CC	proteinaceous extracellular matrix
14	15.8	NULL	16	MMML CGS	MACIEJ_MMML 1
15	15.3	NULL	403	BP	cell adhesion
16	15.27	NULL	64	BP	collagen catabolic process
17	14.58	NULL	36	BP	muscle filament sliding
18	13.53	NULL	57	MF	extracellular matrix structural constituent
19	12.91	NULL	11	MF	platelet−derived growth factor binding
20	12.61	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_F

Underexpressed

Rank	GSZ	p−value	#all	Geneset	
1	−8.83	NULL	370	BP	mitotic cell cycle
2	−8.77	NULL	1318	CC	mitochondrion
3	−8.69	NULL	135	H.Tiss	WIRTH_Mucosa
4	−7.63	NULL	1233	TF	KIM_MYC targets
5	−7.3	NULL	4640	CC	nucleus
6	−7.23	NULL	949	CC	nucleoplasm
7	−6.77	NULL	142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
8	−6.77	NULL	142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
9	−6.39	NULL	298	BP	DNA repair
10	−5.89	NULL	304	CC	mitochondrial inner membrane
11	−5.85	NULL	595	MF	RNA binding
12	−5.84	NULL	649	BP	gene expression
13	−5.77	NULL	755	Lymphoma	SPANG_BCR UP
14	−5.65	NULL	83	BP	respiratory electron transport chain
15	−5.47	NULL	152	BP	cellular metabolic process
16	−5.44	NULL	148	BP	G1/S transition of mitotic cell cycle
17	−5.28	NULL	220	CC	mitochondrial matrix
18	−5.26	NULL	1749	MF	DNA binding
19	−5.23	NULL	15	GSEA C2	PODAR_RESPONSE_TO_ADAPHOSTIN_DN
20	−5.22	NULL	940	MF	nucleic acid binding

GW_029

Local Summary

%DE = 0.99

metagenes = 23

genes = 337

genes in genesets = 336

genes with fdr < 0.1 = 328 (325 + / 3 −)

genes with fdr < 0.05 = 328 (325 + / 3 −)

genes with fdr < 0.01 = 320 (318 + / 2 −)

<r> metagenes = 0.95

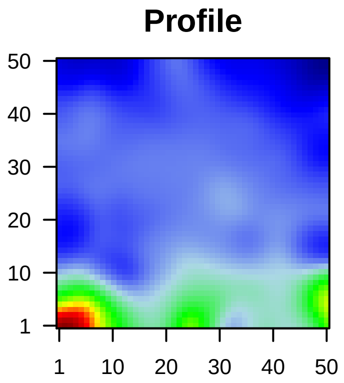
<r> genes = 0.39

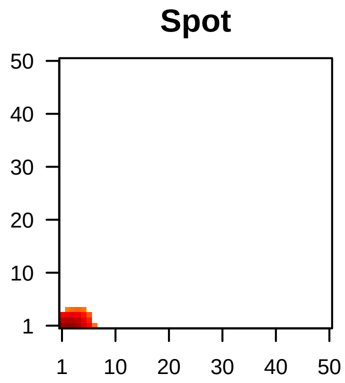
<FC> = 1.19

<shrinkage−t> = 41.65

<p−value> = 0

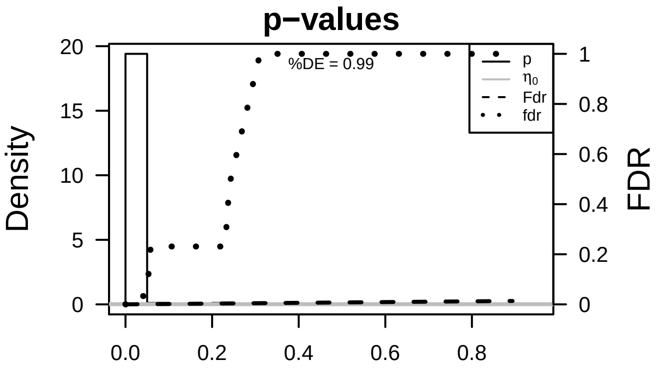
<fdr> = 0.05





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	59	1.89	2e−16	1e−17	3 x 1	actin, alpha 2, smooth muscle, aorta [Source:HGNC Symbol;
2	72	1.66	2e−16	1e−17	4 x 1	actin, gamma 2, smooth muscle, enteric [Source:HGNC Syml
3	9510	1.49	2e−16	1e−17	6 x 1	ADAM metallopeptidase with thrombospondin type 1 motif, 1
4	165	1.48	2e−16	1e−17	3 x 1	AE binding protein 1 [Source:HGNC Symbol;Acc:303]
5	249	1.88	2e−16	1e−17	6 x 1	alkaline phosphatase, liver/bone/kidney [Source:HGNC Symb
6	23452	1.9	2e−16	1e−17	3 x 1	angiopoietin−like 2 [Source:HGNC Symbol;Acc:490]
7	187	1.71	2e−16	1e−17	5 x 1	apelin receptor [Source:HGNC Symbol;Acc:339]
8	366	2.7	2e−16	1e−17	1 x 1	aquaporin 9 [Source:HGNC Symbol;Acc:643]
9	64651	1.47	2e−16	1e−17	6 x 2	cysteine−serine−rich nuclear protein 1 [Source:HGNC Symbo
10	633	1.57	2e−16	1e−17	3 x 1	biglycan [Source:HGNC Symbol;Acc:1044]
11	199675	1.56	2e−16	1e−17	5 x 4	chromosome 19 open reading frame 59 [Source:HGNC Symb
12	114902	1.58	2e−16	1e−17	4 x 1	C1q and tumor necrosis factor related protein 5 [Source:HGN
13	6348	1.59	2e−16	1e−17	4 x 4	chemokine (C−C motif) ligand 3 [Source:HGNC Symbol;Acc:
14	414062	2.2	2e−16	1e−17	1 x 1	chemokine (C−C motif) ligand 3−like 3 [Source:HGNC Symbo
15	57124	1.91	2e−16	1e−17	3 x 1	CD248 molecule, endosialin [Source:HGNC Symbol;Acc:182
16	22918	1.68	2e−16	1e−17	4 x 1	CD93 molecule [Source:HGNC Symbol;Acc:15855]
17	1009	1.42	2e−16	1e−17	3 x 1	cadherin 11, type 2, OB−cadherin (osteoblast) [Source:HGNC
18	1003	1.44	2e−16	1e−17	6 x 1	cadherin 5, type 2 (vascular endothelium) [Source:HGNC Syr
19	51148	1.44	2e−16	1e−17	3 x 3	cerebral endothelial cell adhesion molecule [Source:HGNC S
20	1306	1.52	2e−16	1e−17	4 x 1	collagen, type XV, alpha 1 [Source:HGNC Symbol;Acc:2192]



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	37.27	NULL	70 / 190	CC	extracellular matrix
2	36.58	NULL	85 / 250	Lymphoma	LENZ_Stromal signature 1
3	31.56	NULL	14 / 16	MMML CGS	MACIEJ_MMML 1
4	31.31	NULL	13 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
5	30.8	NULL	33 / 69	BP	extracellular matrix disassembly
6	30	NULL	66 / 242	BP	extracellular matrix organization
7	27.99	NULL	28 / 64	BP	collagen catabolic process
8	25.8	NULL	8 / 11	MF	platelet−derived growth factor binding
9	24.85	NULL	11 / 15	GSEA C2	CROMER_TUMORIGENESIS_UP
10	23.61	NULL	81 / 553	Cancer	Lembcke_Colonic Inflammation
11	22.61	NULL	11 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_UP
12	22.23	NULL	88 / 683	CC	extracellular space
13	22.2	NULL	22 / 57	MF	extracellular matrix structural constituent
14	21.32	NULL	121 / 1182	CC	extracellular region
15	21.22	NULL	42 / 183	CC	proteinaceous extracellular matrix
16	21.17	NULL	8 / 12	miRNA target	miR−29c
17	20.35	NULL	11 / 19	MF	extracellular matrix binding
18	19.36	NULL	46 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
19	19.36	NULL	46 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
20	19.36	NULL	46 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
21	19.36	NULL	46 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
22	18.67	NULL	15 / 37	BP	collagen fibril organization
23	17.14	NULL	7 / 15	GSEA C2	LEE_LIVER_CANCER_HEPATOBLAST
24	16.7	NULL	7 / 12	GSEA C2	LY_AGING_MIDDLE_UP
25	16.56	NULL	7 / 16	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_
26	16.45	NULL	5 / 10	GSEA C2	KEGG_ECM_RECEPTOR_INTERACTION
27	16.07	NULL	6 / 13	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
28	15.97	NULL	7 / 16	GSEA C2	CROONQUIST_STROMAL_STIMULATION_UP
29	15.84	NULL	6 / 10	GSEA C2	JEON_SMAD6_TARGETS_UP
30	15.59	NULL	5 / 10	GSEA C2	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
31	15.29	NULL	17 / 68	CC	collagen
32	15.17	NULL	12 / 35	Glio	Colman_survival_associated
33	15.16	NULL	7 / 11	Glio	Phillips MES up vs Prolif & PN
34	15.04	NULL	22 / 83	CC	basement membrane
35	14.89	NULL	6 / 10	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C4
36	14.86	NULL	5 / 13	GSEA C2	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
37	14.65	NULL	10 / 40	BP	cellular response to amino acid stimulus
38	14.59	NULL	8 / 15	GSEA C2	DASU_IL6_SIGNALING_SCAR_DN
39	14.59	NULL	7 / 16	GSEA C2	ROZANOV_MMP14_TARGETS_SUBSET
40	14.53	NULL	22 / 119	Lymphoma	ROSOLOWSKI_green total

GW_029

Local Summary

%DE = 0.84

metagenes = 41

genes = 513

genes in genesets = 509

genes with fdr < 0.1 = 324 (4 + / 320 −)

genes with fdr < 0.05 = 266 (3 + / 263 −)

genes with fdr < 0.01 = 153 (1 + / 152 −)

<r> metagenes = 0.88

<r> genes = 0.26

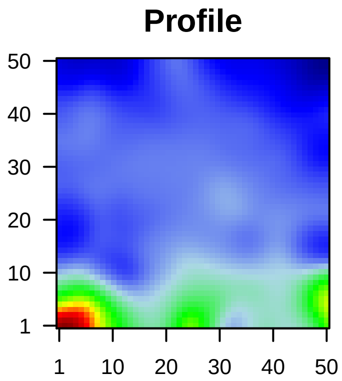
<FC> = −0.39

<shrinkage−t> = −13.79

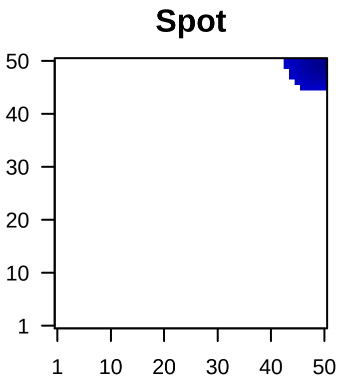
<p−value> = 0.01

<fdr> = 0.58

Profile



Spot



Local Genelist

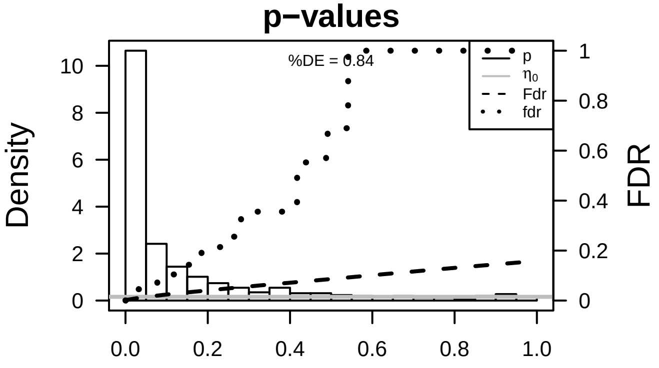
Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	3866	−1.81	2e−16	9e−15	50 x 50	keratin 15 [Source:HGNC Symbol;Acc:6421]
2	11166	−1.61	2e−16	9e−15	50 x 50	SRY (sex determining region Y)−box 21 [Source:HGNC Symb
3	4922	−1.41	4e−16	4e−14	50 x 50	neurotensin [Source:HGNC Symbol;Acc:8038]
4	84223	−1.39	9e−16	4e−11	47 x 46	IQ motif containing G [Source:HGNC Symbol;Acc:25251]
5	139728	−1.25	5e−13	2e−10	49 x 49	pregnancy up−regulated nonubiquitous CaM kinase [Source:
6	8544	−1.2	4e−12	2e−10	50 x 50	pirin (iron−binding nuclear protein) [Source:HGNC Symbol;Ac
7	9076	−1.18	8e−12	2e−10	49 x 50	claudin 1 [Source:HGNC Symbol;Acc:2032]
8	655	−1.18	8e−12	2e−09	50 x 50	bone morphogenetic protein 7 [Source:HGNC Symbol;Acc:10
9	5625	−1.14	3e−11	8e−09	50 x 48	proline dehydrogenase (oxidase) 1 [Source:HGNC Symbol;Ac
10	116028	−1.11	1e−10	1e−08	46 x 47	RecQ mediated genome instability 2 [Source:HGNC Symbol;
11	154664	−1.08	4e−10	1e−08	50 x 50	ATP−binding cassette, sub−family A (ABC1), member 13 [Sou
12	6657	−1.07	5e−10	1e−08	50 x 50	SRY (sex determining region Y)−box 2 [Source:HGNC Symbo
13	3304	−0.97	1e−09	1e−08	49 x 49	heat shock 70kDa protein 1A [Source:HGNC Symbol;Acc:52
14	256764	−1.05	1e−09	1e−08	50 x 50	WD repeat domain 72 [Source:HGNC Symbol;Acc:26790]
15	1056	−1.05	1e−09	1e−08	50 x 50	carboxyl ester lipase [Source:HGNC Symbol;Acc:1848]
16	2304	−1.05	1e−09	1e−08	50 x 50	forkhead box E1 (thyroid transcription factor 2) [Source:HGN
17	875	−1.05	1e−09	1e−08	49 x 47	cystathionine−beta−synthase [Source:HGNC Symbol;Acc:15
18	7546	−1.05	1e−09	1e−08	48 x 50	Zic family member 2 [Source:HGNC Symbol;Acc:12873]
19	200810	−1.05	1e−09	2e−08	49 x 50	ALG1, chitobiosyldiphosphodolichol beta−mannosyltransfera
20	57216	−1.04	2e−09	4e−08	50 x 48	VANGL planar cell polarity protein 2 [Source:HGNC Symbol;

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−22.51	NULL	85 / 142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
2	−22.51	NULL	85 / 142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
3	−16.13	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
4	−13.51	NULL	82 / 370	BP	mitotic cell cycle
5	−13.35	NULL	15 / 16	GSEA C2	EGUCHI_CELL_CYCLE_RB1_TARGETS
6	−13.23	NULL	15 / 30	BP	DNA strand elongation involved in DNA replication
7	−13.02	NULL	93 / 530	Cancer	Lembcke_Normal vs Adenoma
8	−12.48	NULL	13 / 16	GSEA C2	FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
9	−12.37	NULL	37 / 149	BP	DNA replication
10	−11.6	NULL	81 / 914	Chr	Chr 3
11	−11.51	NULL	26 / 57	Glio	developing astrocytes
12	−11.32	NULL	6 / 8	GSEA C2	REACTOME_E2F_TRANSCRIPTIONAL_TARGETS_AT_G1_S
13	−11.3	NULL	12 / 15	GSEA C2	FINETTI_BREAST_CANCER_KINOME_RED
14	−11.13	NULL	2 / 7	GSEA C2	MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
15	−11.04	NULL	9 / 16	GSEA C2	PUJANA_BREAST_CANCER_WITH_BRCA1_MUTATED_UP
16	−10.92	NULL	9 / 16	GSEA C2	REACTOME_DNA_STRAND_ELONGATION
17	−10.88	NULL	8 / 11	GSEA C2	REACTOME_UNWINDING_OF_DNA
18	−10.75	NULL	9 / 16	Cancer	WOLFER_overlap genes
19	−10.18	NULL	4 / 13	BP	regulation of blood vessel size
20	−10.03	NULL	9 / 16	GSEA C2	REACTOME_G2_M_CHECKPOINTS
21	−9.95	NULL	7 / 11	GSEA C2	KALMA_E2F1_TARGETS
22	−9.87	NULL	8 / 14	GSEA C2	PUJANA_BRCA_CENTERED_NETWORK
23	−9.68	NULL	10 / 14	MMML CGS	MACIEJ_MMML 4
24	−9.68	NULL	10 / 22	BP	DNA replication initiation
25	−9.63	NULL	5 / 13	GSEA C2	SLEBOS_HEAD_AND_NECK_CANCER_WITH_HPV_UP
26	−9.59	NULL	9 / 16	GSEA C2	SONG_TARGETS_OF_IE86_CMV_PROTEIN
27	−9.47	NULL	6 / 11	GSEA C2	REACTOME_E2F_MEDIATED_REGULATION_OF_DNA_REPLIC
28	−9.28	NULL	4 / 12	GSEA C2	HELLER_SILENCED_BY_METHYLATION_DN
29	−8.94	NULL	4 / 7	GSEA C2	REACTOME_G1_S_TRANSITION
30	−8.89	NULL	5 / 16	GSEA C2	KAN_RESPONSE_TO_ARSENIC_TRIOXIDE
31	−8.88	NULL	6 / 12	GSEA C2	LI_WILMS_TUMOR_VS_FETAL_KIDNEY_1_DN
32	−8.83	NULL	8 / 15	GSEA C2	WU_APOPTOSIS_BY_CDKN1A_VIA_TP53
33	−8.63	NULL	8 / 16	GSEA C2	REACTOME_ACTIVATION_OF_THE_PRE_REPLICATIVE_COMP
34	−8.56	NULL	38 / 298	BP	DNA repair
35	−8.55	NULL	4 / 13	GSEA C2	KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_
36	−8.51	NULL	8 / 21	BP	telomere maintenance via semi−conservative replication
37	−8.44	NULL	7 / 13	GSEA C2	PUJANA_XPRSS_INT_NETWORK
38	−8.42	NULL	11 / 16	GSEA C2	KANG_DOXORUBICIN_RESISTANCE_UP
39	−8.39	NULL	8 / 14	GSEA C2	AMUNDSON_GAMMA_RADIATION_RESPONSE
40	−8.39	NULL	1 / 2	GSEA C2	KUROKAWA_LIVER_CANCER_EARLY_RECURRENCE_UP

p−values



GW_029

Local Summary

%DE = 0.81

metagenes = 3

genes = 85

genes in genesets = 84

genes with fdr < 0.1 = 49 (3 + / 46 −)

genes with fdr < 0.05 = 42 (1 + / 41 −)

genes with fdr < 0.01 = 38 (1 + / 37 −)

<r> metagenes = 0.99

<r> genes = 0.42

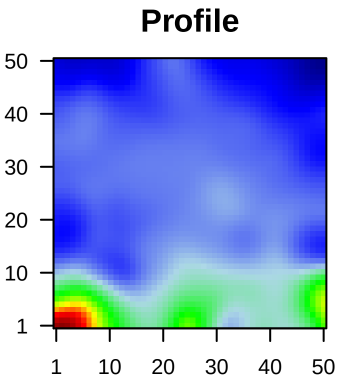
<FC> = −0.41

<shrinkage−t> = −14.45

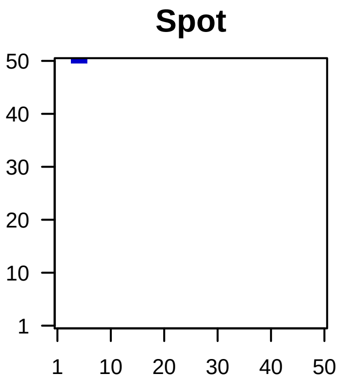
<p−value> = 0

<fdr> = 0.49

Profile



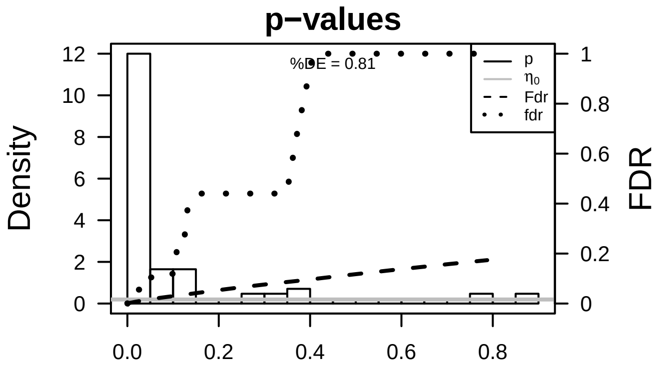
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	51806	−2.44	2e−16	2e−15	4 x 50	calmodulin−like 5 [Source:HGNC Symbol;Acc:18180]
2	100134938	−1.45	2e−16	2e−15	6 x 50	polymerase (RNA) II (DNA directed) polypeptide J3 [Source:H
3	114569	−1.13	6e−11	4e−08	4 x 50	mal, T−cell differentiation protein 2 (gene/pseudogene) [Sour
4	51195	−1.03	3e−09	8e−07	5 x 50	Rap guanine nucleotide exchange factor (GEF)−like 1 [Sourc
5	1577	−0.94	5e−08	2e−06	4 x 50	cytochrome P450, family 3, subfamily A, polypeptide 5 [Sourc
6	1050	−0.9	2e−07	2e−06	6 x 50	CCAAT/enhancer binding protein (C/EBP), alpha [Source:HG
7	1622	−0.89	3e−07	1e−05	6 x 50	diazepam binding inhibitor (GABA receptor modulator, acyl−C
8	1571	−0.84	1e−06	1e−05	5 x 50	cytochrome P450, family 2, subfamily E, polypeptide 1 [Sourc
9	22837	−0.82	2e−06	1e−05	6 x 50	cordon−bleu WH2 repeat protein−like 1 [Source:HGNC Symb
10	200958	−0.82	2e−06	5e−05	6 x 50	mucin 20, cell surface associated [Source:HGNC Symbol;Acc
11	118932	−0.78	6e−06	7e−05	4 x 50	ankyrin repeat domain 22 [Source:HGNC Symbol;Acc:28321]
12	54101	−0.76	1e−05	1e−04	6 x 50	receptor−interacting serine−threonine kinase 4 [Source:HGN
13	7108	−0.74	2e−05	5e−04	4 x 50	transmembrane 7 superfamily member 2 [Source:HGNC Sym
14	54842	−0.69	6e−05	5e−04	6 x 50	major facilitator superfamily domain containing 6 [Source:HG
15	2064	−0.68	9e−05	5e−04	6 x 50	v−erb−b2 avian erythroblastic leukemia viral oncogene homol
16	1999	−0.67	1e−04	5e−04	5 x 50	E74−like factor 3 (ets domain transcription factor, epithelial−s
17	8681	−0.65	2e−04	5e−04	5 x 50	phospholipase A2, group IVB (cytosolic) [Source:HGNC Sym
18	7263	−0.64	2e−04	5e−04	5 x 50	thiosulfate sulfurtransferase (rhodanese) [Source:HGNC Sym
19	5226	−0.64	2e−04	2e−03	6 x 50	phosphogluconate dehydrogenase [Source:HGNC Symbol;A
20	26298	−0.61	4e−04	2e−03	4 x 50	ets homologous factor [Source:HGNC Symbol;Acc:3246]

p−values



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−21.07	NULL	3 / 10	GSEA C2	KEGG_LINOLEIC_ACID_METABOLISM
2	−17.48	NULL	1 / 14	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_B
3	−16.39	NULL	2 / 9	GSEA C2	REACTOME_CYTOCHROME_P450_ARRANGED_BY_SUBSTRA
4	−16.39	NULL	2 / 9	GSEA C2	REACTOME_PHASE_1_FUNCTIONALIZATION_OF_COMPOUND
5	−14.6	NULL	2 / 11	GSEA C2	KEGG_DRUG_METABOLISM_CYTOCHROME_P450
6	−14.6	NULL	2 / 11	GSEA C2	REACTOME_BIOLOGICAL_OXIDATIONS
7	−14.6	NULL	2 / 11	GSEA C2	REACTOME_XENOBIOTICS
8	−13.28	NULL	2 / 13	GSEA C2	KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_
9	−12.01	NULL	2 / 14	GSEA C2	KIM_RESPONSE_TO_TSA_AND_DECITABINE_UP
10	−10.98	NULL	2 / 11	GSEA C2	KEGG_ARACHIDONIC_ACID_METABOLISM
11	−10.5	NULL	3 / 76	BP	epidermis development
12	−10.29	NULL	3 / 15	GSEA C2	LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
13	−9.94	NULL	1 / 7	GSEA C2	KEGG_STEROID_HORMONE_BIOSYNTHESIS
14	−9.27	NULL	2 / 16	GSEA C2	FRASOR_TAMOXIFEN_RESPONSE_UP
15	−9.23	NULL	2 / 12	MF	lysophospholipase activity
16	−9.16	NULL	1 / 11	Glio	neurons_glio
17	−8.97	NULL	2 / 26	MF	oxygen binding
18	−8.7	NULL	1 / 5	GSEA C2	WILLIAMS_ESR1_TARGETS_DN
19	−8.64	NULL	3 / 21	BP	drug metabolic process
20	−8.63	NULL	1 / 8	Lymphoma	MASCQUE_GCB UP
21	−8.57	NULL	1 / 9	GSEA C2	KEGG_RETINOL_METABOLISM
22	−8.2	NULL	1 / 8	GSEA C2	ACEVEDO_LIVER_CANCER_WITH_H3K9ME3_UP
23	−8.05	NULL	1 / 10	GSEA C2	BORCZUK_MALIGNANT_MESOTHELIOMA_DN
24	−7.92	NULL	1 / 9	GSEA C2	KEGG_RNA_POLYMERASE
25	−7.85	NULL	2 / 31	BP	triglyceride metabolic process
26	−7.79	NULL	1 / 6	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_8
27	−7.79	NULL	1 / 6	miRNA target	miR−125a
28	−7.66	NULL	1 / 10	BP	urea cycle
29	−7.66	NULL	1 / 10	BP	white fat cell differentiation
30	−7.65	NULL	1 / 9	GSEA C2	LEE_LIVER_CANCER
31	−7.65	NULL	1 / 9	GSEA C2	LEE_LIVER_CANCER_TOP50
32	−7.65	NULL	1 / 9	GSEA C2	BROWNE_HCMV_INFECTION_18HR_UP
33	−7.65	NULL	1 / 9	GSEA C2	BIOCARTA_NUCLEARRS_PATHWAY
34	−7.57	NULL	2 / 35	MF	monooxygenase activity
35	−7.56	NULL	1 / 13	miRNA 3UTR	TGCA−517A−−517C
36	−7.38	NULL	1 / 16	miRNA target starBase	hsa−miR−1298
37	−7.24	NULL	1 / 12	GSEA C2	KAAB_FAILED_HEART_ATRIUM_UP
38	−7.24	NULL	1 / 12	GSEA C2	KEGG_DRUG_METABOLISM_OTHER_ENZYMES
39	−7.13	NULL	2 / 16	CC	microvillus membrane
40	−7	NULL	1 / 10	GSEA C2	BOYAULT_LIVER_CANCER_SUBCLASS_G23_DN