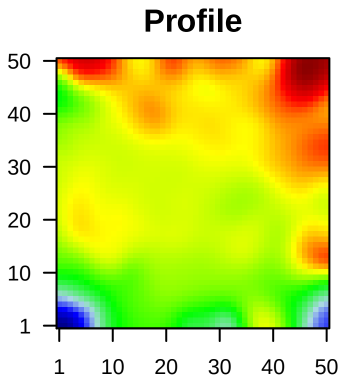
GW_212

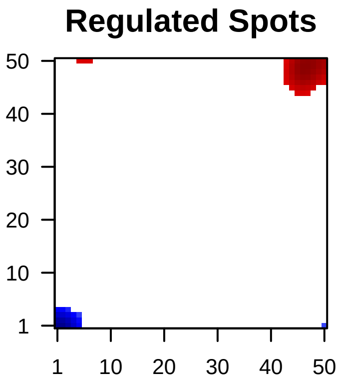
Global Summary

%DE = 0.14
genes with fdr < 0.2 = 1717 (798 + / 919 −)
genes with fdr < 0.1 = 1520 (691 + / 829 −)
genes with fdr < 0.05 = 1170 (528 + / 642 −)
genes with fdr < 0.01 = 836 (362 + / 474 −)

genes in genesets = 16332

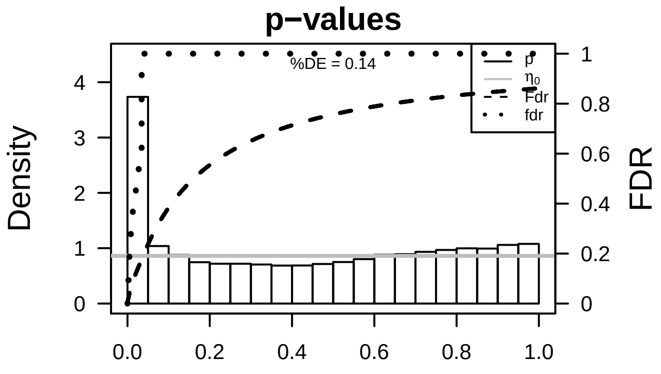
<FC> = 0
<shrinkage−t> = 0
<p−value> = 0.11
<fdr> = 0.86


Profile


Regulated Spots

Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	59	−1.83	2e−16	5e−14	3 x 1	actin, alpha 2, smooth muscle, aorta [Source:HGNC Symbol;
2	124	1.67	2e−16	5e−14	50 x 11	alcohol dehydrogenase 1A (class I), alpha polypeptide [Sourc
3	131	1.6	2e−16	5e−14	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
4	165	−1.62	2e−16	5e−14	3 x 1	AE binding protein 1 [Source:HGNC Symbol;Acc:303]
5	216	2.02	2e−16	5e−14	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGN
6	55107	−1.83	2e−16	5e−14	1 x 5	anoctamin 1, calcium activated chloride channel [Source:HG
7	23120	1.62	2e−16	5e−14	1 x 50	ATPase, class V, type 10B [Source:HGNC Symbol;Acc:13543
8	633	−1.7	2e−16	5e−14	3 x 1	biglycan [Source:HGNC Symbol;Acc:1044]
9	260436	1.65	2e−16	5e−14	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symb
10	56892	2.2	2e−16	5e−14	50 x 7	chromosome 8 open reading frame 4 [Source:HGNC Symbol
11	51806	2.17	2e−16	5e−14	4 x 50	calmodulin−like 5 [Source:HGNC Symbol;Acc:18180]
12	6347	−1.73	2e−16	5e−14	50 x 4	chemokine (C−C motif) ligand 2 [Source:HGNC Symbol;Acc:
13	6364	2.37	2e−16	5e−14	46 x 1	chemokine (C−C motif) ligand 20 [Source:HGNC Symbol;Acc
14	1056	1.65	2e−16	5e−14	50 x 50	carboxyl ester lipase [Source:HGNC Symbol;Acc:1848]
15	22802	2.29	2e−16	5e−14	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
16	1308	−1.62	2e−16	5e−14	1 x 43	collagen, type XVII, alpha 1 [Source:HGNC Symbol;Acc:2194
17	1277	−1.71	2e−16	5e−14	2 x 1	collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
18	1278	−1.56	2e−16	5e−14	2 x 1	collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198]
19	1289	−2.05	2e−16	5e−14	2 x 1	collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209]
20	1290	−1.59	2e−16	5e−14	2 x 1	collagen, type V, alpha 2 [Source:HGNC Symbol;Acc:2210]


p−values

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	16.36	NULL	914	Chr	Chr 3
2	14.33	NULL	142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
3	14.33	NULL	142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
4	10.9	NULL	4640	CC	nucleus
5	10.47	NULL	949	CC	nucleoplasm
6	10.26	NULL	370	BP	mitotic cell cycle
7	9.99	NULL	135	H.Tiss	WIRTH_Mucosa
8	8.91	NULL	149	BP	DNA replication
9	8.58	NULL	86	BP	nucleosome assembly
10	8.35	NULL	298	BP	DNA repair
11	8.29	NULL	1749	MF	DNA binding
12	7.44	NULL	16	GSEA C2	EGUCHI_CELL_CYCLE_RB1_TARGETS
13	7.19	NULL	30	BP	DNA strand elongation involved in DNA replication
14	7.18	NULL	16	Cancer	WOLFER_overlap genes
15	6.91	NULL	15	GSEA C2	BOYAULT_LIVER_CANCER_SUBCLASS_G23_UP
16	6.82	NULL	11	GSEA C2	KALMA_E2F1_TARGETS
17	6.76	NULL	232	BP	mitosis
18	6.47	NULL	39	miRNA target starBase	hsa−miR−95
19	6.46	NULL	47	CC	nucleosome
20	6.25	NULL	16	GSEA C2	PUJANA_BREAST_CANCER_WITH_BRCA1_MUTATED_UP
Underexpressed					
1	−19.57	NULL	190	CC	extracellular matrix
2	−19.57	NULL	250	Lymphoma	LENZ_Stromal signature 1
3	−18.23	NULL	553	Cancer	Lembcke_Colonic Inflammation
4	−17.17	NULL	242	BP	extracellular matrix organization
5	−16.06	NULL	683	CC	extracellular space
6	−15.54	NULL	69	BP	extracellular matrix disassembly
7	−15.47	NULL	1182	CC	extracellular region
8	−14.82	NULL	64	BP	collagen catabolic process
9	−14.07	NULL	265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
10	−14.07	NULL	265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
11	−14.07	NULL	265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
12	−14.07	NULL	265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
13	−12.69	NULL	403	BP	cell adhesion
14	−12.17	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
15	−12.11	NULL	312	BP	immune response
16	−12.09	NULL	183	CC	proteinaceous extracellular matrix
17	−11.55	NULL	15	GSEA C2	CROMER_TUMORIGENESIS_UP
18	−11.33	NULL	16	MMML CGS	MACIEJ_MMML 1
19	−11	NULL	11	MF	platelet−derived growth factor binding
20	−10.55	NULL	57	MF	extracellular matrix structural constituent

GW_212

Local Summary

%DE = 0.82

metagenes = 48

genes = 575

genes in genesets = 571

genes with fdr < 0.1 = 354 (340 + / 14 −)

genes with fdr < 0.05 = 312 (301 + / 11 −)

genes with fdr < 0.01 = 233 (224 + / 9 −)

<r> metagenes = 0.87

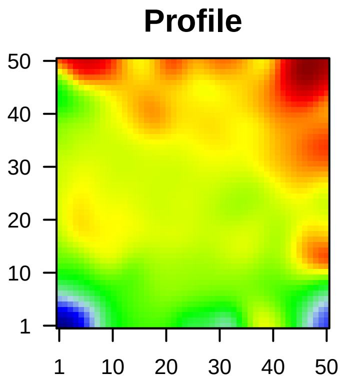
<r> genes = 0.26

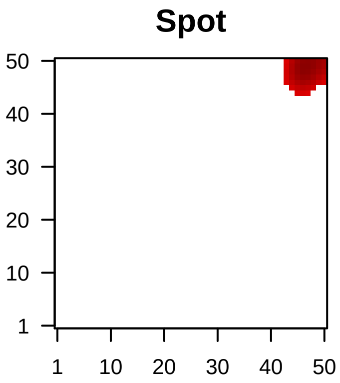
<FC> = 0.44

<shrinkage−t> = 15.5

<p−value> = 0

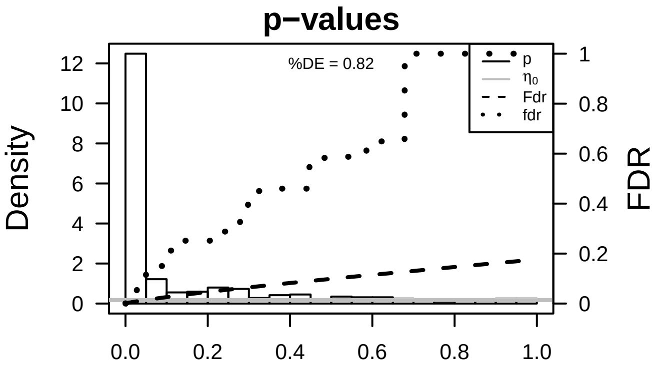
<fdr> = 0.5





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	216	2.02	2e−16	3e−15	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGNC
2	1056	1.65	2e−16	3e−15	50 x 50	carboxyl ester lipase [Source:HGNC Symbol;Acc:1848]
3	94234	1.64	2e−16	3e−15	50 x 50	forkhead box Q1 [Source:HGNC Symbol;Acc:20951]
4	3880	1.74	2e−16	3e−15	50 x 49	keratin 19 [Source:HGNC Symbol;Acc:6436]
5	4922	3.33	2e−16	3e−15	50 x 50	neurotensin [Source:HGNC Symbol;Acc:8038]
6	256764	−1.77	2e−16	3e−15	50 x 50	WD repeat domain 72 [Source:HGNC Symbol;Acc:26790]
7	7546	2.12	2e−16	3e−15	48 x 50	Zic family member 2 [Source:HGNC Symbol;Acc:12873]
8	4171	1.46	4e−15	6e−11	46 x 48	minichromosome maintenance complex component 2 [Source
9	11166	1.34	6e−13	7e−10	50 x 50	SRY (sex determining region Y)−box 21 [Source:HGNC Symb
10	5357	1.27	9e−12	7e−10	50 x 50	plastin 1 [Source:HGNC Symbol;Acc:9090]
11	10388	1.26	2e−11	9e−10	47 x 46	synaptonemal complex protein 2 [Source:HGNC Symbol;Acc:
12	6565	1.25	2e−11	2e−09	50 x 50	solute carrier family 15 (oligopeptide transporter), member 2 [
13	79682	1.22	6e−11	2e−09	46 x 47	centromere protein U [Source:HGNC Symbol;Acc:21348]
14	1894	1.22	6e−11	2e−09	45 x 50	epithelial cell transforming sequence 2 oncogene [Source:HG
15	6657	1.22	7e−11	5e−09	50 x 50	SRY (sex determining region Y)−box 2 [Source:HGNC Symbo
16	4072	1.19	2e−10	5e−09	50 x 50	epithelial cell adhesion molecule [Source:HGNC Symbol;Acc:
17	286676	1.19	2e−10	6e−09	50 x 49	immunoglobulin−like domain containing receptor 1 [Source:H
18	53820	1.18	2e−10	6e−09	49 x 47	ripply transcriptional repressor 3 [Source:HGNC Symbol;Acc:
19	51203	1.18	3e−10	5e−08	45 x 48	nucleolar and spindle associated protein 1 [Source:HGNC Sy
20	5984	1.13	1e−09	5e−08	46 x 50	replication factor C (activator 1) 4, 37kDa [Source:HGNC Sym



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	37.44	NULL	93 / 142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
2	37.44	NULL	93 / 142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
3	23.26	NULL	16 / 16	GSEA C2	EGUCHI_CELL_CYCLE_RB1_TARGETS
4	21.64	NULL	99 / 370	BP	mitotic cell cycle
5	19.34	NULL	48 / 149	BP	DNA replication
6	18.81	NULL	9 / 11	GSEA C2	KALMA_E2F1_TARGETS
7	17.87	NULL	18 / 30	BP	DNA strand elongation involved in DNA replication
8	17.68	NULL	11 / 16	GSEA C2	GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
9	17.59	NULL	109 / 530	Cancer	Lembcke_Normal vs Adenoma
10	17.1	NULL	9 / 16	Cancer	WOLFER_overlap genes
11	16.99	NULL	10 / 15	GSEA C2	LEE_EARLY_T_LYMPHOCYTE_UP
12	16.95	NULL	12 / 16	GSEA C2	KANG_DOXORUBICIN_RESISTANCE_UP
13	16.82	NULL	6 / 7	GSEA C2	REACTOME_G1_S_TRANSITION
14	16.8	NULL	12 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_2
15	16.76	NULL	26 / 57	Glio	developing astrocytes
16	16.35	NULL	10 / 16	GSEA C2	PUJANA_BREAST_CANCER_WITH_BRCA1_MUTATED_UP
17	16.21	NULL	8 / 11	GSEA C2	REACTOME_UNWINDING_OF_DNA
18	16	NULL	2 / 7	GSEA C2	MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
19	15.67	NULL	8 / 11	GSEA C2	LIANG_SILENCED_BY_METHYLATION_DN
20	15.35	NULL	10 / 14	GSEA C2	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
21	15.1	NULL	9 / 15	GSEA C2	BOYAULT_LIVER_CANCER_SUBCLASS_G23_UP
22	15.08	NULL	12 / 22	BP	DNA replication initiation
23	15.02	NULL	8 / 12	GSEA C2	REACTOME_CELL_CYCLE_MITOTIC
24	14.9	NULL	10 / 15	GSEA C2	WU_APOPTOSIS_BY_CDKN1A_VIA_TP53
25	14.89	NULL	11 / 13	GSEA C2	CROONQUIST_IL6_DEPRIVATION_DN
26	14.83	NULL	11 / 16	GSEA C2	REACTOME_DNA_STRAND_ELONGATION
27	14.8	NULL	11 / 16	GSEA C2	FRASOR_RESPONSE_TO_SERM_OR_FULVESTRANT_DN
28	14.7	NULL	11 / 16	GSEA C2	SONG_TARGETS_OF_IE86_CMV_PROTEIN
29	14.41	NULL	8 / 10	GSEA C2	MONTERO_THYROID_CANCER_POOR_SURVIVAL_UP
30	14.22	NULL	6 / 8	GSEA C2	REACTOME_E2F_TRANSCRIPTIONAL_TARGETS_AT_G1_S
31	14.22	NULL	6 / 9	GSEA C2	SEMBA_FHIT_TARGETS_DN
32	14.16	NULL	11 / 14	GSEA C2	ZHAN_MULTIPLE_MYELOMA_PR_UP
33	13.92	NULL	8 / 13	GSEA C2	PUJANA_XPRSS_INT_NETWORK
34	13.4	NULL	9 / 14	GSEA C2	PUJANA_BRCA_CENTERED_NETWORK
35	13.3	NULL	7 / 15	GSEA C2	KAUFFMANN_DNA_REPLICATION_GENES
36	13.27	NULL	7 / 11	GSEA C2	REACTOME_E2F_MEDIATED_REGULATION_OF_DNA_REPLIC
37	13.26	NULL	12 / 15	GSEA C2	CHANG_CYCLING_GENES
38	13.08	NULL	6 / 14	GSEA C2	SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_UP
39	13.01	NULL	11 / 15	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
40	12.88	NULL	13 / 24	BP	telomere maintenance via recombination

GW_212

Local Summary

%DE = 0.75

metagenes = 3

genes = 95

genes in genesets = 95

genes with fdr < 0.1 = 60 (55 + / 5 −)

genes with fdr < 0.05 = 55 (51 + / 4 −)

genes with fdr < 0.01 = 48 (44 + / 4 −)

<r> metagenes = 0.99

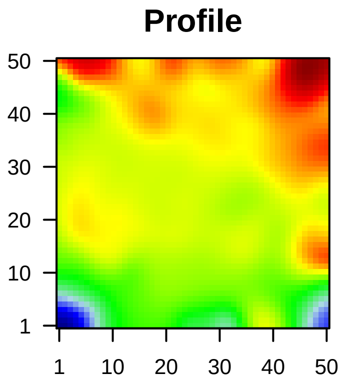
<r> genes = 0.39

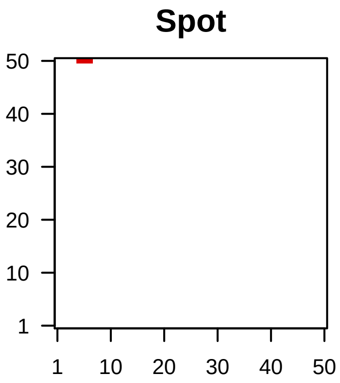
<FC> = 0.42

<shrinkage−t> = 14.54

<p−value> = 0

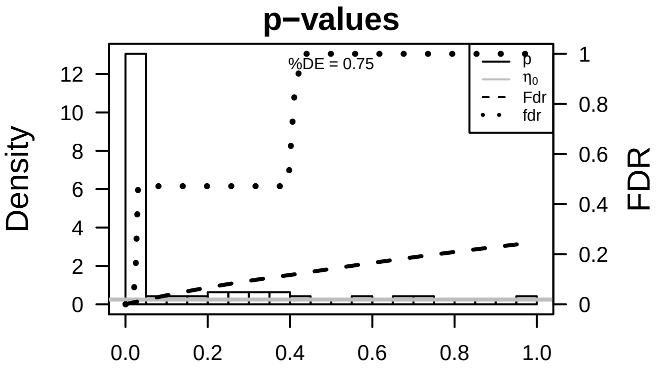
<fdr> = 0.41





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	1999	1.48	3e−15	7e−13	5 x 50	E74−like factor 3 (ets domain transcription factor, epithelial−s
2	284340	1.42	3e−14	2e−11	6 x 50	chemokine (C−X−C motif) ligand 17 [Source:HGNC Symbol;
3	26353	−1.34	8e−13	2e−11	5 x 50	heat shock 22kDa protein 8 [Source:HGNC Symbol;Acc:3017
4	58528	1.32	2e−12	5e−09	6 x 50	Ras−related GTP binding D [Source:HGNC Symbol;Acc:199
5	200958	1.18	3e−10	5e−09	6 x 50	mucin 20, cell surface associated [Source:HGNC Symbol;Ac
6	9957	1.17	4e−10	6e−08	7 x 50	heparan sulfate (glucosamine) 3−O−sulfotransferase 1 [Sour
7	10161	−1.11	3e−09	8e−08	6 x 50	lysophosphatidic acid receptor 6 [Source:HGNC Symbol;Acc:
8	55808	1.08	6e−09	2e−07	7 x 50	ST6 (alpha−N−acetyl−neuraminyl−2,3−beta−galactosyl−1,3)−
9	6338	1.05	2e−08	4e−07	5 x 50	sodium channel, non−voltage−gated 1, beta subunit [Source:
10	5226	1.03	3e−08	4e−07	6 x 50	phosphogluconate dehydrogenase [Source:HGNC Symbol;A
11	201501	1.02	5e−08	5e−07	7 x 50	zinc finger and BTB domain containing 7C [Source:HGNC Sy
12	7113	1.01	7e−08	2e−06	5 x 50	transmembrane protease, serine 2 [Source:HGNC Symbol;A
13	84419	0.98	1e−07	6e−06	5 x 50	chromosome 15 open reading frame 48 [Source:HGNC Sym
14	51195	0.95	4e−07	6e−06	5 x 50	Rap guanine nucleotide exchange factor (GEF)−like 1 [Sourc
15	54101	0.93	6e−07	1e−05	6 x 50	receptor−interacting serine−threonine kinase 4 [Source:HGN
16	79007	0.89	2e−06	1e−05	6 x 50	dysbindin (dystrobrevin binding protein 1) domain containing
17	26578	0.89	2e−06	1e−05	6 x 50	osteoclast stimulating factor 1 [Source:HGNC Symbol;Acc:85
18	54502	0.88	2e−06	1e−05	6 x 50	RNA binding motif protein 47 [Source:HGNC Symbol;Acc:30
19	22837	0.87	3e−06	1e−05	6 x 50	cordon−bleu WH2 repeat protein−like 1 [Source:HGNC Sym
20	5627	0.87	3e−06	1e−04	7 x 50	protein S (alpha) [Source:HGNC Symbol;Acc:9456]



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	15.3	NULL	2 / 16	GSEA C2	ELVIDGE_HYPOXIA_BY_DMOG_UP
2	12.72	NULL	1 / 2	Cancer	GENTLES_modul8
3	12.01	NULL	1 / 8	GSEA C2	DORN_ADENOVIRUS_INFECTION_24HR_UP
4	11.56	NULL	2 / 15	GSEA C2	KONDO_EZH2_TARGETS
5	11.19	NULL	1 / 9	GSEA C2	DORN_ADENOVIRUS_INFECTION_32HR_UP
6	10.51	NULL	1 / 10	GSEA C2	DORN_ADENOVIRUS_INFECTION_12HR_DN
7	9.64	NULL	2 / 16	CC	microvillus membrane
8	9.44	NULL	1 / 12	GSEA C2	YAMASHITA_LIVER_CANCER_STEM_CELL_UP
9	9.44	NULL	1 / 12	GSEA C2	DORN_ADENOVIRUS_INFECTION_48HR_UP
10	9.19	NULL	3 / 15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
11	9.01	NULL	1 / 13	GSEA C2	HATADA_METHYLATED_IN_LUNG_CANCER_DN
12	8.62	NULL	1 / 14	GSEA C2	HALMOS_CEBPA_TARGETS_DN
13	8.54	NULL	4 / 63	CC	Golgi lumen
14	8.54	NULL	1 / 8	GSEA C2	KEGG_TASTE_TRANSDUCTION
15	8.29	NULL	2 / 14	GSEA C2	KEGG_BIOSYNTHESIS_OF_UNSATURATED_FATTY_ACIDS
16	8.28	NULL	1 / 15	GSEA C2	KIM_MYC_AMPLIFICATION_TARGETS_DN
17	8.18	NULL	1 / 9	GSEA C2	MCCOLLUM_GELDANAMYCIN_RESISTANCE_UP
18	8.03	NULL	1 / 13	GSEA C2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_F_DN
19	7.98	NULL	1 / 16	GSEA C2	FRASOR_TAMOXIFEN_RESPONSE_UP
20	7.98	NULL	1 / 16	GSEA C2	TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_LOBULAR_
21	7.98	NULL	1 / 16	GSEA C2	STREICHER_LSM1_TARGETS_UP
22	7.98	NULL	1 / 16	GSEA C2	OLSSON_E2F3_TARGETS_UP
23	7.98	NULL	1 / 16	GSEA C2	RODRIGUES_NTN1_AND_DCC_TARGETS
24	7.98	NULL	1 / 16	GSEA C2	SCHWAB_TARGETS_OF_BMYB_S427G_DN
25	7.98	NULL	1 / 16	GSEA C2	SCHWAB_TARGETS_OF_BMYB_I624M_DN
26	7.98	NULL	1 / 16	GSEA C2	LEE_LIVER_CANCER_MYC_TGFA_UP
27	7.98	NULL	1 / 16	GSEA C2	GEISS_RESPONSE_TO_DSRNA_UP
28	7.98	NULL	1 / 16	TF Tissue	VAQUERIZAS_Pancreas
29	7.95	NULL	1 / 9	GSEA C2	BALLIF_DEVELOPMENTAL_DISABILITY_P16_P12_DELETION
30	7.94	NULL	1 / 15	GSEA C2	CHANG_POU5F1_TARGETS_UP
31	7.87	NULL	3 / 13	H.Tiss	WIRTH_Tonsil
32	7.68	NULL	1 / 14	GSEA C2	VANTVEER_BREAST_CANCER_METASTASIS_DN
33	7.68	NULL	1 / 14	GSEA C2	ZHAN_MULTIPLE_MYELOMA_CD2_DN
34	7.68	NULL	1 / 10	BP	sialylation
35	7.4	NULL	2 / 17	BP	long−chain fatty−acyl−CoA biosynthetic process
36	7.38	NULL	1 / 15	GSEA C2	SMIRNOV_CIRCULATING_ENDOTHELIOCYTES_IN_CANCER_
37	7.38	NULL	1 / 15	GSEA C2	NAKAMURA_METASTASIS_MODEL_DN
38	7.38	NULL	1 / 15	GSEA C2	BOYAULT_LIVER_CANCER_SUBCLASS_G23_UP
39	7.31	NULL	2 / 27	CC	basal plasma membrane
40	7.1	NULL	1 / 16	BP	positive regulation of TOR signaling

GW_212

Local Summary

%DE = 0.98

metagenes = 18

genes = 270

genes in genesets = 269

genes with fdr < 0.1 = 262 (5 + / 257 −)

genes with fdr < 0.05 = 261 (5 + / 256 −)

genes with fdr < 0.01 = 243 (3 + / 240 −)

<r> metagenes = 0.96

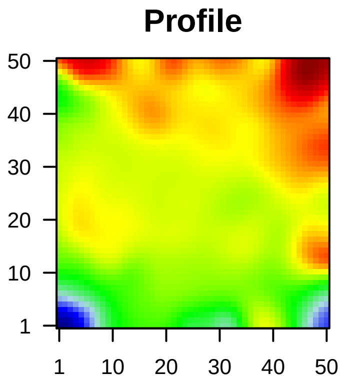
<r> genes = 0.39

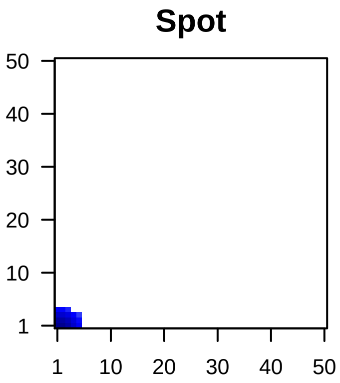
<FC> = −0.83

<shrinkage−t> = −29.16

<p−value> = 0

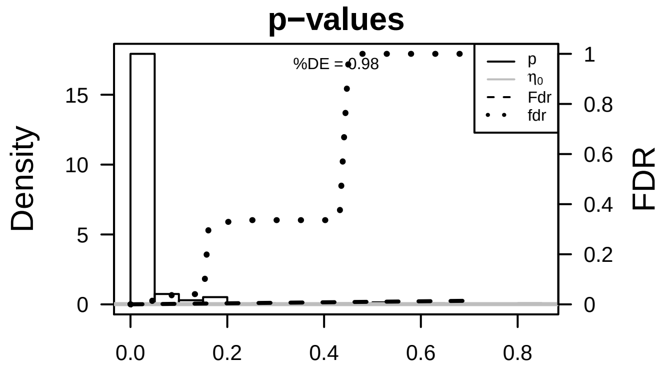
<fdr> = 0.19





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	59	−1.83	2e−16	5e−17	3 x 1	actin, alpha 2, smooth muscle, aorta [Source:HGNC Symbol;
2	165	−1.62	2e−16	5e−17	3 x 1	AE binding protein 1 [Source:HGNC Symbol;Acc:303]
3	633	−1.7	2e−16	5e−17	3 x 1	biglycan [Source:HGNC Symbol;Acc:1044]
4	1277	−1.71	2e−16	5e−17	2 x 1	collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
5	1278	−1.56	2e−16	5e−17	2 x 1	collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198]
6	1289	−2.05	2e−16	5e−17	2 x 1	collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209]
7	1290	−1.59	2e−16	5e−17	2 x 1	collagen, type V, alpha 2 [Source:HGNC Symbol;Acc:2210]
8	1291	−1.7	2e−16	5e−17	2 x 1	collagen, type VI, alpha 1 [Source:HGNC Symbol;Acc:2211]
9	1293	−1.73	2e−16	5e−17	2 x 1	collagen, type VI, alpha 3 [Source:HGNC Symbol;Acc:2213]
10	1687	−1.84	2e−16	5e−17	1 x 4	deafness, autosomal dominant 5 [Source:HGNC Symbol;Acc
11	27122	−1.54	2e−16	5e−17	1 x 3	dickkopf WNT signaling pathway inhibitor 3 [Source:HGNC S
12	3956	−1.78	2e−16	5e−17	1 x 1	lectin, galactoside−binding, soluble, 1 [Source:HGNC Symbol
13	4312	−2.71	2e−16	5e−17	1 x 1	matrix metallopeptidase 1 (interstitial collagenase) [Source:H
14	4319	−1.73	2e−16	5e−17	1 x 3	matrix metallopeptidase 10 (stromelysin 2) [Source:HGNC Sy
15	4314	−2.53	2e−16	5e−17	1 x 1	matrix metallopeptidase 3 (stromelysin 1, progelatinase) [Sou
16	4318	−1.53	2e−16	5e−17	1 x 1	matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 9
17	12	−1.99	2e−16	5e−17	1 x 1	
18	23213	−1.65	2e−16	5e−17	2 x 1	sulfatase 1 [Source:HGNC Symbol;Acc:20391]
19	7045	−2.28	2e−16	5e−17	1 x 2	transforming growth factor, beta−induced, 68kDa [Source:HG
20	7058	−1.63	2e−16	5e−17	2 x 1	thrombospondin 2 [Source:HGNC Symbol;Acc:11786]



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−41.28	NULL	63 / 190	CC	extracellular matrix
2	−36.44	NULL	31 / 69	BP	extracellular matrix disassembly
3	−36.38	NULL	73 / 250	Lymphoma	LENZ_Stromal signature 1
4	−34.95	NULL	28 / 64	BP	collagen catabolic process
5	−34.61	NULL	15 / 16	MMML CGS	MACIEJ_MMML 1
6	−34.52	NULL	67 / 242	BP	extracellular matrix organization
7	−32.51	NULL	12 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
8	−31.62	NULL	8 / 11	MF	platelet−derived growth factor binding
9	−30.3	NULL	11 / 15	GSEA C2	CROMER_TUMORIGENESIS_UP
10	−27.39	NULL	6 / 10	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C4
11	−24.07	NULL	8 / 12	miRNA target	miR−29c
12	−24.01	NULL	10 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_UP
13	−23.44	NULL	20 / 57	MF	extracellular matrix structural constituent
14	−23.22	NULL	38 / 183	CC	proteinaceous extracellular matrix
15	−22.25	NULL	7 / 15	GSEA C2	LEE_LIVER_CANCER_HEPATOBLAST
16	−21.95	NULL	12 / 35	Glio	Colman_survival_associated
17	−21.75	NULL	15 / 37	BP	collagen fibril organization
18	−21.55	NULL	79 / 683	CC	extracellular space
19	−20.56	NULL	11 / 19	MF	extracellular matrix binding
20	−20.53	NULL	106 / 1182	CC	extracellular region
21	−20.29	NULL	5 / 10	GSEA C2	KEGG_ECM_RECEPTOR_INTERACTION
22	−20.27	NULL	12 / 40	BP	cellular response to amino acid stimulus
23	−19.51	NULL	22 / 83	CC	basement membrane
24	−19.3	NULL	7 / 15	GSEA C2	MISHRA_CARCINOMA_ASSOCIATED_FIBROBLAST_UP
25	−19.22	NULL	6 / 10	GSEA C2	JEON_SMAD6_TARGETS_UP
26	−18.73	NULL	4 / 8	GSEA C2	HAEGERSTRAND_RESPONSE_TO_IMATINIB
27	−18.67	NULL	42 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
28	−18.67	NULL	42 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
29	−18.67	NULL	42 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
30	−18.67	NULL	42 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
31	−18.48	NULL	64 / 553	Cancer	Lembcke_Colonic Inflammation
32	−18.34	NULL	7 / 16	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_
33	−18.27	NULL	8 / 15	GSEA C2	DASU_IL6_SIGNALING_SCAR_DN
34	−17.69	NULL	5 / 16	GSEA C2	URS_ADIPOCYTE_DIFFERENTIATION_DN
35	−17.54	NULL	7 / 16	GSEA C2	CROONQUIST_STROMAL_STIMULATION_UP
36	−17.39	NULL	5 / 10	GSEA C2	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
37	−17.04	NULL	5 / 13	GSEA C2	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
38	−16.94	NULL	8 / 15	GSEA C2	ONDER_CDH1_SIGNALING_VIA_CTNNB1
39	−16.77	NULL	23 / 119	Lymphoma	ROSOLOWSKI_green total
40	−16.65	NULL	18 / 85	MF	integrin binding

GW_212

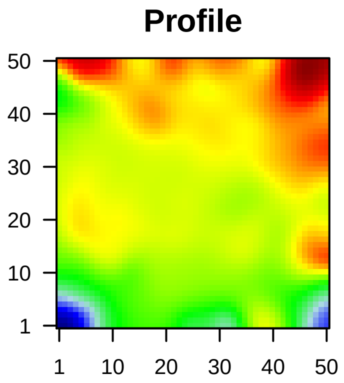
Local Summary

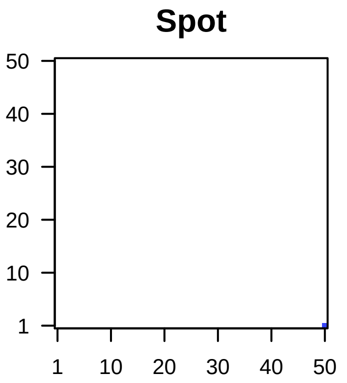
%DE = 0.95
metagenes = 1
genes = 74
genes in genesets = 73

genes with fdr < 0.1 = 66 (2 + / 64 −)
genes with fdr < 0.05 = 63 (2 + / 61 −)
genes with fdr < 0.01 = 49 (2 + / 47 −)

<r> metagenes = NA
<r> genes = 0.71

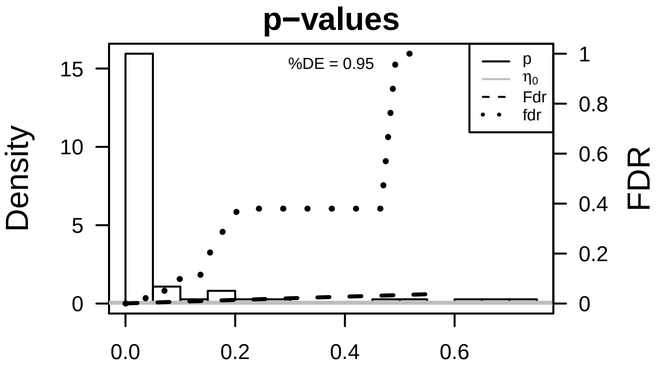
<FC> = −0.52
<shrinkage−t> = −18.11
<p−value> = 0
<fdr> = 0.37





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	260436	1.65	2e−16	8e−16	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symbo
2	23180	−1.47	4e−15	1e−12	50 x 1	raftlin, lipid raft linker 1 [Source:HGNC Symbol;Acc:30278]
3	10537	−1.36	3e−13	2e−08	50 x 1	ubiquitin D [Source:HGNC Symbol;Acc:18795]
4	3512	−1.07	1e−08	2e−08	50 x 1	immunoglobulin J polypeptide, linker protein for immunoglobu
5	3128	−1.04	2e−08	2e−08	50 x 1	major histocompatibility complex, class II, DR beta 6 (pseudo
6	55303	−1.04	2e−08	2e−08	50 x 1	GTPase, IMAP family member 4 [Source:HGNC Symbol;Acc:
7	5552	−1.04	2e−08	4e−08	50 x 1	serglycin [Source:HGNC Symbol;Acc:9361]
8	5341	−1.03	3e−08	3e−07	50 x 1	pleckstrin [Source:HGNC Symbol;Acc:9070]
9	5880	−0.99	1e−07	6e−07	50 x 1	ras−related C3 botulinum toxin substrate 2 (rho family, small
10	3936	−0.96	3e−07	2e−06	50 x 1	lymphocyte cytosolic protein 1 (L−plastin) [Source:HGNC Sy
11	9404	−0.92	8e−07	8e−06	50 x 1	leupaxin [Source:HGNC Symbol;Acc:14061]
12	7133	−0.87	3e−06	8e−06	50 x 1	tumor necrosis factor receptor superfamily, member 1B [Sour
13	3059	−0.85	5e−06	4e−05	50 x 1	hematopoietic cell−specific Lyn substrate 1 [Source:HGNC S
14	9806	−0.79	2e−05	4e−05	50 x 1	sparc/osteonectin, cwcv and kazal−like domains proteoglyca
15	7412	−0.78	3e−05	4e−05	50 x 1	vascular cell adhesion molecule 1 [Source:HGNC Symbol;Ac
16	241	−0.77	4e−05	5e−05	50 x 1	arachidonate 5−lipoxygenase−activating protein [Source:HG
17	7805	−0.76	5e−05	8e−05	50 x 1	lysosomal protein transmembrane 5 [Source:HGNC Symbol;
18	713	−0.73	9e−05	8e−05	50 x 1	complement component 1, q subcomponent, B chain [Source
19	3394	−0.73	1e−04	9e−05	50 x 1	interferon regulatory factor 8 [Source:HGNC Symbol;Acc:535
20	1236	−0.71	1e−04	9e−05	50 x 1	chemokine (C−C motif) receptor 7 [Source:HGNC Symbol;Ac



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−22.39	NULL	5 / 15	GSEA C2	FINAK_BREAST_CANCER_SDPP_SIGNATURE
2	−20.26	NULL	1 / 4	MMML CGS	MACIEJ_MMML 2
3	−19.82	NULL	22 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
4	−19.82	NULL	22 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
5	−19.82	NULL	22 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
6	−19.82	NULL	22 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
7	−18.78	NULL	1 / 5	GSEA C2	NAKAMURA_ALVEOLAR_EPITHELIUM
8	−17.29	NULL	29 / 417	H.Tiss	WIRTH_Immune system
9	−17.03	NULL	2 / 3	MMML CGS	MACIEJ_MMML 7
10	−16.86	NULL	2 / 4	GSEA C2	REACTOME_CLASSICAL_ANTIBODY_MEDIATED_COMPLEMEN
11	−16.54	NULL	8 / 15	CC	MHC class II protein complex
12	−16.09	NULL	2 / 6	GSEA C2	BUDHU_LIVER_CANCER_METASTASIS_UP
13	−15.07	NULL	2 / 7	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
14	−14.87	NULL	3 / 14	BP	ruffle organization
15	−13.8	NULL	2 / 10	GSEA C2	PARK_TRETINOIN_RESPONSE
16	−13.64	NULL	1 / 5	GSEA C2	WONG_ENDOMETRIAL_CANCER_LATE
17	−13.48	NULL	2 / 8	GSEA C2	GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_DN
18	−13.19	NULL	3 / 12	GSEA C2	ZHAN_MULTIPLE_MYELOMA_DN
19	−12.83	NULL	8 / 74	BP	regulation of immune response
20	−12.79	NULL	28 / 553	Cancer	Lembcke_Colonic Inflammation
21	−12.74	NULL	3 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
22	−12.29	NULL	3 / 10	BP	negative thymic T cell selection
23	−12.18	NULL	21 / 312	BP	immune response
24	−11.9	NULL	2 / 10	GSEA C2	AMUNDSON_GAMMA_RADIATION_RESISTANCE
25	−11.87	NULL	3 / 11	GSEA C2	KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY
26	−11.68	NULL	2 / 9	GSEA C2	BIOCARTA_LAIR_PATHWAY
27	−11.66	NULL	3 / 16	GSEA C2	FERRANDO_TAL1_NEIGHBORS
28	−11.65	NULL	2 / 7	GSEA C2	BIOCARTA_COMP_PATHWAY
29	−11.56	NULL	2 / 10	BP	chronic inflammatory response
30	−11.54	NULL	2 / 3	GSEA C2	KEGG_VIRAL_MYOCARDITIS
31	−11.45	NULL	4 / 17	BP	positive regulation of neutrophil chemotaxis
32	−11.39	NULL	8 / 60	BP	T cell costimulation
33	−11.14	NULL	3 / 8	GSEA C2	LINDSTEDT_DENDRITIC_CELL_MATURATION_D
34	−11.01	NULL	3 / 12	MF	Rac GTPase activator activity
35	−10.95	NULL	2 / 10	GSEA C2	BIOCARTA_LYM_PATHWAY
36	−10.71	NULL	2 / 8	GSEA C2	BIOCARTA_CLASSIC_PATHWAY
37	−10.71	NULL	2 / 8	GSEA C2	REACTOME_COMPLEMENT_CASCADE
38	−10.71	NULL	2 / 8	GSEA C2	REACTOME_INITIAL_TRIGGERING_OF_COMPLEMENT
39	−10.59	NULL	2 / 12	CC	phagocytic cup
40	−10.51	NULL	5 / 21	CC	clathrin−coated endocytic vesicle membrane