GW_125

Global Summary

%DE = 0.15

genes with fdr < 0.2 = 1812 (974 + / 838 −)

genes with fdr < 0.1 = 1530 (818 + / 712 −)

genes with fdr < 0.05 = 1193 (645 + / 548 −)

genes with fdr < 0.01 = 865 (468 + / 397 −)

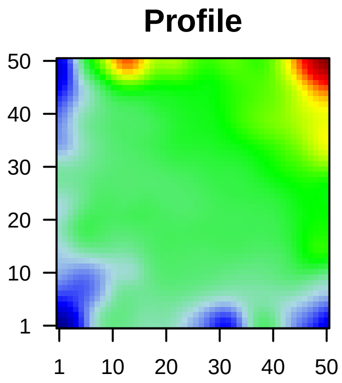
genes in genesets = 16332

<FC> = 0

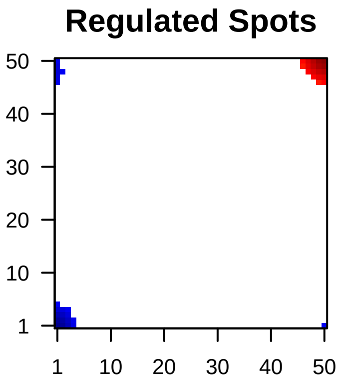
<shrinkage−t> = 0

<p−value> = 0.1

<fdr> = 0.85



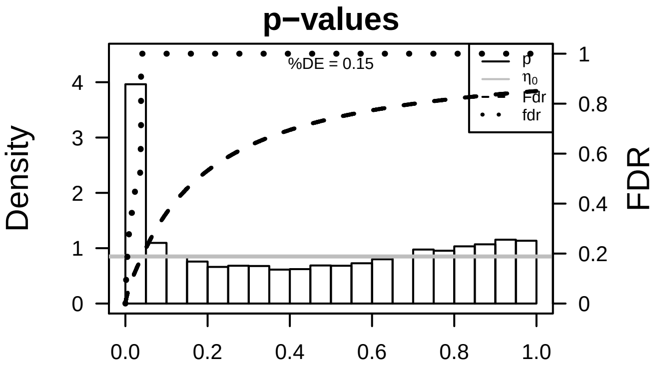
Profile



Regulated Spots

Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	8745	1.79	2e−16	3e−14	50 x 50	ADAM metallopeptidase domain 23 [Source:HGNC Symbol;A
2	131	3.04	2e−16	3e−14	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
3	57016	3.19	2e−16	3e−14	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
4	441282	3.05	2e−16	3e−14	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC Sy
5	8644	3.18	2e−16	3e−14	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
6	1109	3.27	2e−16	3e−14	13 x 50	aldo−keto reductase family 1, member C4 [Source:HGNC Sy
7	214	1.76	2e−16	3e−14	50 x 50	activated leukocyte cell adhesion molecule [Source:HGNC Sy
8	216	2.35	2e−16	3e−14	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGN
9	218	2.31	2e−16	3e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
10	84002	1.88	2e−16	3e−14	13 x 50	UDP−GlcNAc:betaGal beta−1,3−N−acetylglucosaminyltransf
11	25805	1.76	2e−16	3e−14	8 x 1	BMP and activin membrane−bound inhibitor [Source:HGNC S
12	84707	1.77	2e−16	3e−14	50 x 48	brain expressed X−linked 2 [Source:HGNC Symbol;Acc:3093
13	633	−1.71	2e−16	3e−14	3 x 1	biglycan [Source:HGNC Symbol;Acc:1044]
14	684	−1.77	2e−16	3e−14	32 x 1	bone marrow stromal cell antigen 2 [Source:HGNC Symbol;A
15	399948	1.91	2e−16	3e−14	50 x 15	colorectal cancer associated 1 [Source:HGNC Symbol;Acc:3
16	205428	1.75	2e−16	3e−14	50 x 50	chromosome 3 open reading frame 58 [Source:HGNC Symb
17	29113	2.15	2e−16	3e−14	2 x 47	chromosome 6 open reading frame 15 [Source:HGNC Symb
18	26256	1.89	2e−16	3e−14	50 x 50	calcium binding tyrosine−(Y)−phosphorylation regulated [Sou
19	84290	−1.73	2e−16	3e−14	1 x 50	calpain, small subunit 2 [Source:HGNC Symbol;Acc:16371]
20	874	1.7	2e−16	3e−14	6 x 50	carbonyl reductase 3 [Source:HGNC Symbol;Acc:1549]



p−values

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	18.14	NULL	914	Chr	Chr 3
2	13.11	NULL	633	Chr	Chr 9
3	10.62	NULL	232	Chr	Chr 18
4	10.05	NULL	13	GSEA C2	SINGH_NFE2L2_TARGETS
5	9.18	NULL	34	BP	glutathione metabolic process
6	7.98	NULL	463	miRNA target−starBase	hsa−miR−301a
7	7.73	NULL	433	miRNA target−starBase	hsa−miR−19b
8	7.73	NULL	456	miRNA target−starBase	hsa−miR−130a
9	7.47	NULL	142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
10	7.47	NULL	142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
11	7.35	NULL	4	MMML CGS	MACIEJ_MMML 23
12	7.3	NULL	440	miRNA target−starBase	hsa−miR−19a
13	7.17	NULL	15	GSEA C2	KEGG_GLUTATHIONE_METABOLISM
14	6.96	NULL	436	miRNA target−starBase	hsa−miR−548n
15	6.93	NULL	242	miRNA target−starBase	hsa−miR−26b
16	6.93	NULL	396	miRNA target−starBase	hsa−miR−301b
17	6.89	NULL	603	miRNA target−starBase	hsa−miR−20a
18	6.84	NULL	234	miRNA target−starBase	hsa−miR−26a
19	6.78	NULL	13	BP	regulation of blood vessel size
20	6.76	NULL	25	BP	glutathione derivative biosynthetic process
Underexpressed					
1	−13.57	NULL	553	Cancer	Lembcke_Colonic Inflammation
2	−13.47	NULL	190	CC	extracellular matrix
3	−13.42	NULL	250	Lymphoma	LENZ_Stromal signature 1
4	−12.93	NULL	717	Chr	Chr 16
5	−12.72	NULL	1182	CC	extracellular region
6	−12.27	NULL	265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
7	−12.27	NULL	265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
8	−12.27	NULL	265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
9	−12.27	NULL	265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
10	−12.14	NULL	21	CC	cornified envelope
11	−11.64	NULL	64	BP	collagen catabolic process
12	−11.51	NULL	135	H.Tiss	WIRTH_Mucosa
13	−11.42	NULL	69	BP	extracellular matrix disassembly
14	−10.97	NULL	242	BP	extracellular matrix organization
15	−10.86	NULL	572	Disease	GUDJ_psoriasis up
16	−10.71	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
17	−10.6	NULL	683	CC	extracellular space
18	−10.53	NULL	76	BP	epidermis development
19	−10.09	NULL	11	MF	platelet−derived growth factor binding
20	−9.88	NULL	42	BP	keratinization

GW_125

Local Summary

%DE = 0.88

metagenes = 19

genes = 250

genes in genesets = 248

genes with fdr < 0.1 = 204 (197 + / 7 −)

genes with fdr < 0.05 = 183 (178 + / 5 −)

genes with fdr < 0.01 = 155 (152 + / 3 −)

<r> metagenes = 0.94

<r> genes = 0.27

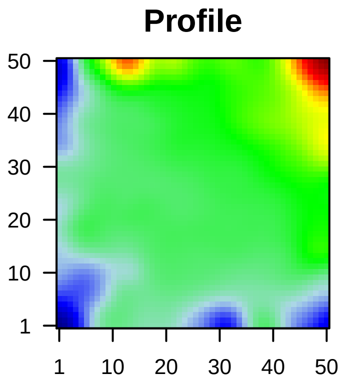
<FC> = 0.72

<shrinkage−t> = 25.31

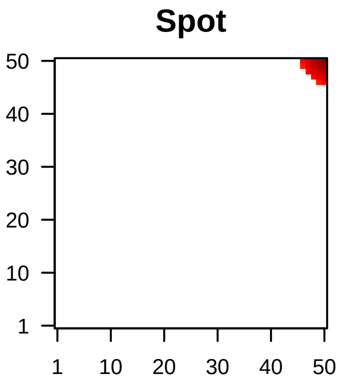
<p−value> = 0

<fdr> = 0.31

Profile



Spot



Local Genelist

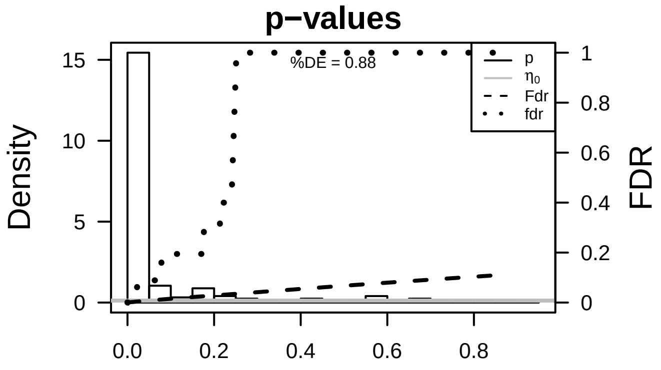
Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	8745	1.79	2e−16	3e−16	50 x 50	ADAM metallopeptidase domain 23 [Source:HGNC Symbol;A
2	214	1.76	2e−16	3e−16	50 x 50	activated leukocyte cell adhesion molecule [Source:HGNC Sy
3	216	2.35	2e−16	3e−16	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGNC
4	84707	1.77	2e−16	3e−16	50 x 48	brain expressed X−linked 2 [Source:HGNC Symbol;Acc:3093
5	205428	1.75	2e−16	3e−16	50 x 50	chromosome 3 open reading frame 58 [Source:HGNC Symbo
6	26256	1.89	2e−16	3e−16	50 x 50	calcium binding tyrosine−(Y)−phosphorylation regulated [Sou
7	26047	2.15	2e−16	3e−16	50 x 50	contactin associated protein−like 2 [Source:HGNC Symbol;Ac
8	10655	1.69	2e−16	3e−16	50 x 50	doublesex and mab−3 related transcription factor 2 [Source:H
9	4072	1.98	2e−16	3e−16	50 x 50	epithelial cell adhesion molecule [Source:HGNC Symbol;Acc:
10	2729	1.89	2e−16	3e−16	50 x 50	glutamate−cysteine ligase, catalytic subunit [Source:HGNC S
11	2730	1.7	2e−16	3e−16	50 x 50	glutamate−cysteine ligase, modifier subunit [Source:HGNC S
12	2938	2.4	2e−16	3e−16	50 x 50	glutathione S−transferase alpha 2 [Source:HGNC Symbol;Ac
13	2944	2.49	2e−16	3e−16	50 x 50	glutathione S−transferase mu 1 [Source:HGNC Symbol;Acc:4
14	2946	1.77	2e−16	3e−16	50 x 50	glutathione S−transferase mu 2 (muscle) [Source:HGNC Sym
15	2947	2.24	2e−16	3e−16	50 x 50	glutathione S−transferase mu 3 (brain) [Source:HGNC Symbo
16	3880	2.57	2e−16	3e−16	50 x 49	keratin 19 [Source:HGNC Symbol;Acc:6436]
17	4922	3.5	2e−16	3e−16	50 x 50	neurotensin [Source:HGNC Symbol;Acc:8038]
18	8544	1.73	2e−16	3e−16	50 x 50	pirin (iron−binding nuclear protein) [Source:HGNC Symbol;Ac
19	6657	1.85	2e−16	3e−16	50 x 50	SRY (sex determining region Y)−box 2 [Source:HGNC Symbo
20	7345	3	2e−16	3e−16	50 x 46	ubiquitin carboxyl−terminal esterase L1 (ubiquitin thiolesteras

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	22.06	NULL	4 / 13	BP	regulation of blood vessel size
2	20.93	NULL	6 / 25	BP	glutathione derivative biosynthetic process
3	20.72	NULL	5 / 15	GSEA C2	KEGG_GLUTATHIONE_METABOLISM
4	20.62	NULL	8 / 34	BP	glutathione metabolic process
5	19.13	NULL	2 / 7	GSEA C2	MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
6	18.35	NULL	5 / 20	MF	glutathione transferase activity
7	18.02	NULL	3 / 11	MF	glutathione binding
8	18.02	NULL	3 / 11	GSEA C2	KEGG_DRUG_METABOLISM_CYTOCHROME_P450
9	18	NULL	4 / 13	GSEA C2	KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_
10	16.03	NULL	4 / 15	GSEA C2	REACTOME_GLUTATHIONE_CONJUGATION
11	14.8	NULL	3 / 11	GSEA C2	ITO_PTTG1_TARGETS_UP
12	14.58	NULL	13 / 119	BP	xenobiotic metabolic process
13	14.19	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
14	13.31	NULL	67 / 914	Chr	Chr 3
15	11.71	NULL	2 / 7	GSEA C2	FREDERICK_PRKCI_TARGETS
16	11.3	NULL	2 / 6	GSEA C2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_D_DN
17	10.33	NULL	3 / 6	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_7
18	10.32	NULL	3 / 15	GSEA C2	REACTOME_PHASE_II_CONJUGATION
19	10.27	NULL	3 / 16	GSEA C2	BOYAULT_LIVER_CANCER_SUBCLASS_G1_DN
20	10.24	NULL	3 / 11	GSEA C2	ODONNELL_TFRC_TARGETS_DN
21	9.82	NULL	1 / 8	GSEA C2	MUNSHI_MULTIPLE_MYELOMA_DN
22	9.79	NULL	3 / 16	GSEA C2	KAN_RESPONSE_TO_ARSENIC_TRIOXIDE
23	9.77	NULL	2 / 15	GSEA C2	LEE_LIVER_CANCER_MYC_UP
24	9.77	NULL	2 / 15	GSEA C2	LEE_LIVER_CANCER_E2F1_UP
25	9.53	NULL	1 / 11	Glio	neurons_glio
26	9.43	NULL	4 / 15	GSEA C2	UDAYAKUMAR_MED1_TARGETS_UP
27	9.32	NULL	2 / 12	BP	glutamate metabolic process
28	9.28	NULL	4 / 26	BP	sulfur amino acid metabolic process
29	9.09	NULL	3 / 16	GSEA C2	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_Y
30	9.05	NULL	1 / 6	GSEA C2	KAPOSI_LIVER_CANCER_POOR_SURVIVAL_DN
31	9.05	NULL	2 / 12	BP	cellular aldehyde metabolic process
32	8.9	NULL	2 / 13	GSEA C2	SINGH_NFE2L2_TARGETS
33	8.79	NULL	2 / 13	Lymphoma	BENTINK_mBL UP
34	8.61	NULL	1 / 10	MF	omega peptidase activity
35	8.57	NULL	4 / 23	BP	apoptotic mitochondrial changes
36	8.53	NULL	5 / 14	GSEA C2	PUJANA_BRCA_CENTERED_NETWORK
37	8.37	NULL	3 / 12	GSEA C2	KAYO_AGING_MUSCLE_UP
38	8.24	NULL	4 / 16	GSEA C2	RODWELL_AGING_KIDNEY_DN
39	8.11	NULL	3 / 12	GSEA C2	LI_WILMS_TUMOR_VS_FETAL_KIDNEY_1_DN
40	7.95	NULL	1 / 15	MF	neuropeptide hormone activity

p−values



GW_125

Local Summary

%DE = 0.87

metagenes = 15

genes = 251

genes in genesets = 249

genes with fdr < 0.1 = 189 (16 + / 173 −)

genes with fdr < 0.05 = 189 (16 + / 173 −)

genes with fdr < 0.01 = 155 (11 + / 144 −)

<r> metagenes = 0.96

<r> genes = 0.38

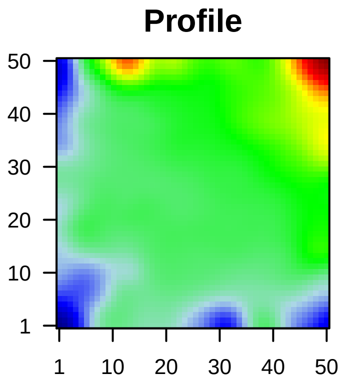
<FC> = −0.61

<shrinkage−t> = −21.59

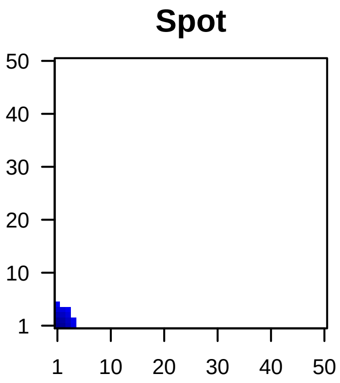
<p−value> = 0

<fdr> = 0.31

Profile



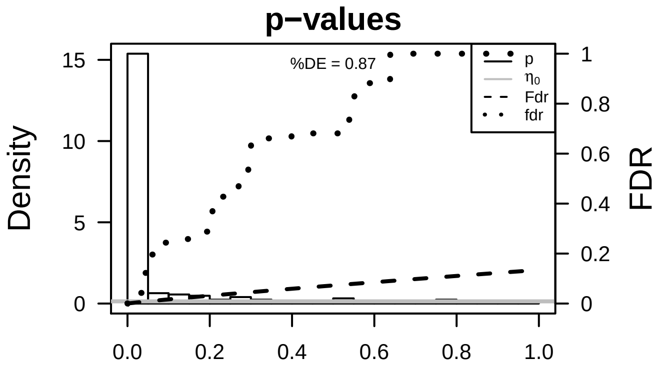
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	633	−1.71	2e−16	6e−16	3 x 1	biglycan [Source:HGNC Symbol;Acc:1044]
2	1277	−2.26	2e−16	6e−16	2 x 1	collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
3	1278	−1.76	2e−16	6e−16	2 x 1	collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198]
4	1289	−2.11	2e−16	6e−16	2 x 1	collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209]
5	1290	−1.84	2e−16	6e−16	2 x 1	collagen, type V, alpha 2 [Source:HGNC Symbol;Acc:2210]
6	1291	−2.11	2e−16	6e−16	2 x 1	collagen, type VI, alpha 1 [Source:HGNC Symbol;Acc:2211]
7	54541	−1.78	2e−16	6e−16	1 x 4	DNA−damage−inducible transcript 4 [Source:HGNC Symbol;
8	3040	2.21	2e−16	6e−16	4 x 1	hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
9	4312	−2.31	2e−16	6e−16	1 x 1	matrix metallopeptidase 1 (interstitial collagenase) [Source:H
10	4314	−1.92	2e−16	6e−16	1 x 1	matrix metallopeptidase 3 (stromelysin 1, progelatinase) [Sou
11	6696	3.4	2e−16	6e−16	2 x 1	secreted phosphoprotein 1 [Source:HGNC Symbol;Acc:1125
12	3371	−1.88	2e−16	6e−16	1 x 3	tenascin C [Source:HGNC Symbol;Acc:5318]
13	1281	−1.5	3e−15	7e−13	2 x 1	collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]
14	10630	−1.58	2e−14	8e−13	1 x 2	podoplanin [Source:HGNC Symbol;Acc:29602]
15	25878	−1.56	5e−14	5e−12	3 x 1	matrix−remodelling associated 5 [Source:HGNC Symbol;Acc:
16	55107	−1.51	2e−13	5e−12	1 x 5	anoctamin 1, calcium activated chloride channel [Source:HG
17	1293	−1.49	5e−13	5e−12	2 x 1	collagen, type VI, alpha 3 [Source:HGNC Symbol;Acc:2213]
18	3956	−1.48	6e−13	5e−12	1 x 1	lectin, galactoside−binding, soluble, 1 [Source:HGNC Symbol
19	12	−1.48	7e−13	9e−12	1 x 1	
20	4316	−1.47	1e−12	9e−12	2 x 1	matrix metallopeptidase 7 (matrilysin, uterine) [Source:HGNC

p−values



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−37.72	NULL	12 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
2	−37.34	NULL	58 / 190	CC	extracellular matrix
3	−36.03	NULL	32 / 69	BP	extracellular matrix disassembly
4	−35.76	NULL	29 / 64	BP	collagen catabolic process
5	−35.44	NULL	7 / 11	MF	platelet−derived growth factor binding
6	−34.48	NULL	15 / 16	MMML CGS	MACIEJ_MMML 1
7	−31.36	NULL	68 / 250	Lymphoma	LENZ_Stromal signature 1
8	−30.19	NULL	67 / 242	BP	extracellular matrix organization
9	−28.21	NULL	12 / 15	GSEA C2	CROMER_TUMORIGENESIS_UP
10	−24.73	NULL	14 / 37	BP	collagen fibril organization
11	−23.52	NULL	20 / 57	MF	extracellular matrix structural constituent
12	−23.13	NULL	8 / 12	miRNA target	miR−29c
13	−22.74	NULL	8 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_UP
14	−22.45	NULL	11 / 40	BP	cellular response to amino acid stimulus
15	−21.98	NULL	6 / 10	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C4
16	−21.37	NULL	36 / 183	CC	proteinaceous extracellular matrix
17	−20.89	NULL	4 / 10	BP	protein heterotrimerization
18	−20.12	NULL	5 / 10	GSEA C2	KEGG_ECM_RECEPTOR_INTERACTION
19	−19.81	NULL	4 / 8	GSEA C2	HAEGERSTRAND_RESPONSE_TO_IMATINIB
20	−19.72	NULL	7 / 16	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_
21	−18.25	NULL	5 / 13	GSEA C2	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
22	−18.14	NULL	5 / 11	BP	dermatan sulfate biosynthetic process
23	−18.14	NULL	8 / 16	GSEA C2	ROZANOV_MMP14_TARGETS_SUBSET
24	−18.04	NULL	4 / 12	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C2
25	−17.85	NULL	12 / 35	Glio	Colman_survival_associated
26	−17.73	NULL	38 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
27	−17.73	NULL	38 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
28	−17.73	NULL	38 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
29	−17.73	NULL	38 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
30	−17.69	NULL	6 / 13	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
31	−17.43	NULL	8 / 15	GSEA C2	LEE_LIVER_CANCER_HEPATOBLAST
32	−16.75	NULL	59 / 553	Cancer	Lembcke_Colonic Inflammation
33	−16.37	NULL	5 / 16	GSEA C2	BEGUM_TARGETS_OF_PAX3_FOXO1_FUSION_DN
34	−16.27	NULL	4 / 15	GSEA C2	REACTOME_NCAM1_INTERACTIONS
35	−16.15	NULL	99 / 1182	CC	extracellular region
36	−16.12	NULL	16 / 68	CC	collagen
37	−16.07	NULL	2 / 5	GSEA C2	DASU_IL6_SIGNALING_UP
38	−16.04	NULL	73 / 683	CC	extracellular space
39	−15.94	NULL	23 / 83	CC	basement membrane
40	−15.92	NULL	25 / 153	CC	endoplasmic reticulum lumen

GW_125

Local Summary

%DE = 0.93

metagenes = 1

genes = 74

genes in genesets = 73

genes with fdr < 0.1 = 65 (0 + / 65 −)

genes with fdr < 0.05 = 59 (0 + / 59 −)

genes with fdr < 0.01 = 52 (0 + / 52 −)

<r> metagenes = NA

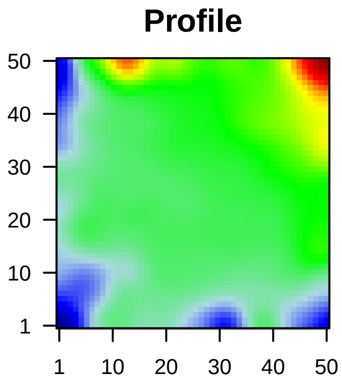
<r> genes = 0.71

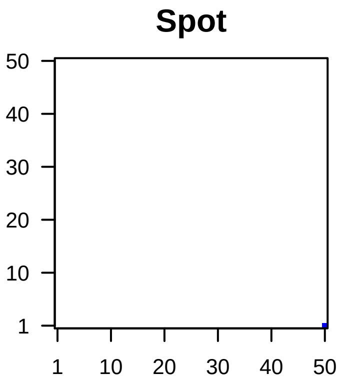
<FC> = −0.6

<shrinkage−t> = −20.9

<p−value> = 0

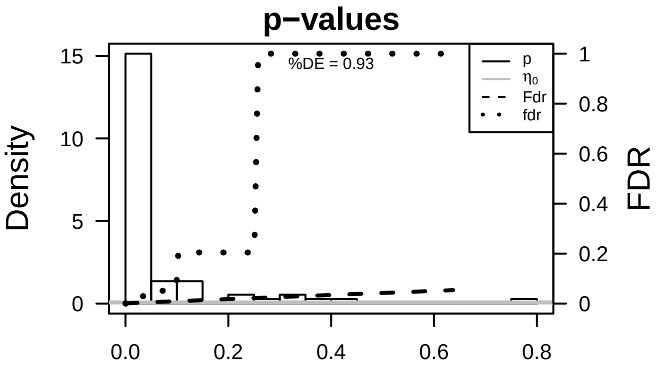
<fdr> = 0.38





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	23180	−1.21	4e−09	7e−08	50 x 1	raftlin, lipid raft linker 1 [Source:HGNC Symbol;Acc:30278]
2	3126	−1.16	2e−08	1e−07	50 x 1	major histocompatibility complex, class II, DR beta 4 [Source:
3	348	−1.11	7e−08	1e−07	50 x 1	apolipoprotein E [Source:HGNC Symbol;Acc:613]
4	260436	−1.11	8e−08	5e−07	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symb
5	8764	−1.06	3e−07	5e−07	50 x 1	tumor necrosis factor receptor superfamily, member 14 [Sour
6	83641	−1.06	3e−07	8e−07	50 x 1	family with sequence similarity 107, member B [Source:HGN
7	10537	−1.04	5e−07	8e−07	50 x 1	ubiquitin D [Source:HGNC Symbol;Acc:18795]
8	5880	−1.03	6e−07	8e−07	50 x 1	ras−related C3 botulinum toxin substrate 2 (rho family, small
9	972	−1.02	8e−07	1e−06	50 x 1	CD74 molecule, major histocompatibility complex, class II inv
10	5341	−1.01	1e−06	6e−06	50 x 1	pleckstrin [Source:HGNC Symbol;Acc:9070]
11	3109	−0.98	2e−06	2e−05	50 x 1	major histocompatibility complex, class II, DM beta [Source:H
12	3689	−0.93	7e−06	2e−05	50 x 1	integrin, beta 2 (complement component 3 receptor 3 and 4 s
13	3108	−0.92	8e−06	4e−05	50 x 1	major histocompatibility complex, class II, DM alpha [Source:
14	7133	−0.87	3e−05	4e−05	50 x 1	tumor necrosis factor receptor superfamily, member 1B [Sour
15	713	−0.86	3e−05	4e−05	50 x 1	complement component 1, q subcomponent, B chain [Source
16	3936	−0.86	3e−05	1e−04	50 x 1	lymphocyte cytosolic protein 1 (L−plastin) [Source:HGNC Sy
17	9806	−0.83	6e−05	4e−04	50 x 1	sparc/osteonectin, cwcv and kazal−like domains proteoglyca
18	3113	−0.79	1e−04	4e−04	50 x 1	major histocompatibility complex, class II, DP alpha 1 [Source
19	3512	−0.76	2e−04	4e−04	50 x 1	immunoglobulin J polypeptide, linker protein for immunoglobu
20	3059	−0.74	3e−04	4e−04	50 x 1	hematopoietic cell−specific Lyn substrate 1 [Source:HGNC Sy



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−41.31	NULL	8 / 15	CC	MHC class II protein complex
2	−31.79	NULL	2 / 3	GSEA C2	KEGG_VIRAL_MYOCARDITIS
3	−26.2	NULL	2 / 4	GSEA C2	KEGG_LEISHMANIA_INFECTION
4	−21.94	NULL	8 / 47	BP	antigen processing and presentation
5	−21.61	NULL	3 / 8	GSEA C2	LINDSTEDT_DENDRITIC_CELL_MATURATION_D
6	−21.26	NULL	1 / 2	GSEA C2	KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUC
7	−21.26	NULL	1 / 2	GSEA C2	KEGG_AUTOIMMUNE_THYROID_DISEASE
8	−21.26	NULL	1 / 2	GSEA C2	KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS
9	−21.24	NULL	5 / 15	GSEA C2	FINAK_BREAST_CANCER_SDPP_SIGNATURE
10	−21.16	NULL	2 / 4	GSEA C2	REACTOME_CLASSICAL_ANTIBODY_MEDIATED_COMPLEMEN
11	−21.09	NULL	5 / 21	CC	clathrin−coated endocytic vesicle membrane
12	−20.04	NULL	5 / 23	CC	integral to lumenal side of endoplasmic reticulum membrane
13	−19.83	NULL	2 / 6	GSEA C2	LUI_THYROID_CANCER_CLUSTER_4
14	−19.44	NULL	3 / 12	GSEA C2	ZHAN_MULTIPLE_MYELOMA_DN
15	−18.93	NULL	3 / 10	GSEA C2	HOSHIDA_LIVER_CANCER_SUBCLASS_S1
16	−18.71	NULL	2 / 6	GSEA C2	SANA_RESPONSE_TO_IFNG_UP
17	−18.19	NULL	21 / 312	BP	immune response
18	−17.95	NULL	5 / 28	CC	transport vesicle membrane
19	−17.73	NULL	2 / 8	GSEA C2	GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_DN
20	−17	NULL	2 / 8	GSEA C2	KEGG_CELL_ADHESION_MOLECULES_CAMS
21	−16.65	NULL	5 / 32	CC	ER to Golgi transport vesicle membrane
22	−16.61	NULL	2 / 11	GSEA C2	ABE_VEGFA_TARGETS_2HR
23	−16.48	NULL	3 / 10	BP	negative thymic T cell selection
24	−16.42	NULL	9 / 87	BP	antigen processing and presentation of exogenous peptide antigen
25	−16.41	NULL	3 / 12	BP	immunoglobulin mediated immune response
26	−16.38	NULL	8 / 60	BP	T cell costimulation
27	−16.21	NULL	3 / 11	GSEA C2	KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY
28	−15.84	NULL	5 / 35	CC	trans−Golgi network membrane
29	−15.82	NULL	3 / 14	BP	ruffle organization
30	−15.77	NULL	1 / 3	GSEA C2	KEGG_ANTIGEN_PROCESSING_AND_PRESENTATION
31	−15.55	NULL	3 / 16	GSEA C2	FERRANDO_TAL1_NEIGHBORS
32	−15.5	NULL	2 / 11	GSEA C2	WILENSKY_RESPONSE_TO_DARAPLADIB
33	−15.1	NULL	22 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
34	−15.1	NULL	22 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
35	−15.1	NULL	22 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
36	−15.1	NULL	22 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
37	−14.9	NULL	2 / 3	MMML CGS	MACIEJ_MMML 7
38	−14.87	NULL	2 / 7	GSEA C2	BIOCARTA_COMP_PATHWAY
39	−14.86	NULL	1 / 5	GSEA C2	NAKAMURA_ALVEOLAR_EPITHELIUM
40	−14.8	NULL	2 / 11	BP	chaperone mediated protein folding requiring cofactor

GW_125

Local Summary

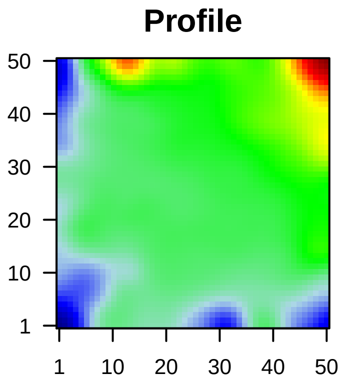
%DE = 0.95
metagenes = 6
genes = 153
genes in genesets = 149

genes with fdr < 0.1 = 125 (18 + / 107 −)
genes with fdr < 0.05 = 125 (18 + / 107 −)
genes with fdr < 0.01 = 112 (16 + / 96 −)

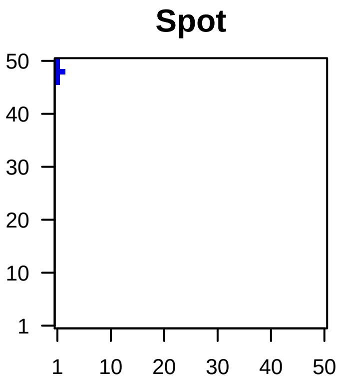
<r> metagenes = 0.97
<r> genes = 0.49

<FC> = −0.71
<shrinkage−t> = −25.12
<p−value> = 0
<fdr> = 0.22

Profile



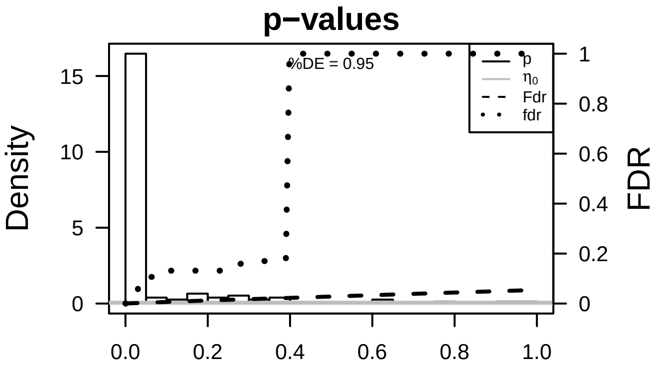
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	131	3.04	2e−16	6e−17	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	57016	3.19	2e−16	6e−17	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
3	441282	3.05	2e−16	6e−17	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC S
4	8644	3.18	2e−16	6e−17	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
5	218	2.31	2e−16	6e−17	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
6	84290	−1.73	2e−16	6e−17	1 x 50	calpain, small subunit 2 [Source:HGNC Symbol;Acc:16371]
7	54544	−1.8	2e−16	6e−17	1 x 50	cysteine−rich C−terminal 1 [Source:HGNC Symbol;Acc:2987
8	49860	−2.59	2e−16	6e−17	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
9	1672	−1.83	2e−16	6e−17	1 x 50	defensin, beta 1 [Source:HGNC Symbol;Acc:2766]
10	414325	−2.34	2e−16	6e−17	1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
11	115572	−2.04	2e−16	6e−17	1 x 48	family with sequence similarity 46, member B [Source:HGNC
12	2706	−2.62	2e−16	6e−17	1 x 47	gap junction protein, beta 2, 26kDa [Source:HGNC Symbol;A
13	2877	3.1	2e−16	6e−17	1 x 50	glutathione peroxidase 2 (gastrointestinal) [Source:HGNC Sy
14	26085	−1.99	2e−16	6e−17	1 x 50	kallikrein−related peptidase 13 [Source:HGNC Symbol;Acc:6
15	3851	−2.81	2e−16	6e−17	1 x 50	keratin 4 [Source:HGNC Symbol;Acc:6441]
16	8581	−2.2	2e−16	6e−17	1 x 48	lymphocyte antigen 6 complex, locus D [Source:HGNC Symb
17	4118	−1.93	2e−16	6e−17	1 x 50	mal, T−cell differentiation protein [Source:HGNC Symbol;Acc
18	51458	−2.23	2e−16	6e−17	1 x 50	Rh family, C glycoprotein [Source:HGNC Symbol;Acc:18140]
19	84659	−1.99	2e−16	6e−17	1 x 48	ribonuclease, RNase A family, 7 [Source:HGNC Symbol;Acc:
20	6278	−3.91	2e−16	6e−17	1 x 49	S100 calcium binding protein A7 [Source:HGNC Symbol;Acc:

p−values



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−40.12	NULL	17 / 21	CC	cornified envelope
2	−29.98	NULL	64 / 135	H.Tiss	WIRTH_Mucosa
3	−28.41	NULL	4 / 10	MF	RAGE receptor binding
4	−27.65	NULL	18 / 42	BP	keratinization
5	−25.57	NULL	21 / 76	BP	epidermis development
6	−22.11	NULL	22 / 53	BP	keratinocyte differentiation
7	−20.69	NULL	3 / 10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
8	−19.61	NULL	74 / 572	Disease	GUDJ_psoriasis up
9	−14.28	NULL	3 / 16	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_DN
10	−12.94	NULL	5 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
11	−12.82	NULL	9 / 19	BP	peptide cross−linking
12	−10.47	NULL	2 / 12	GSEA C2	REACTOME_GAP_JUNCTION_ASSEMBLY
13	−10.1	NULL	5 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
14	−9.99	NULL	2 / 13	GSEA C2	REACTOME_GAP_JUNCTION_TRAFFICKING
15	−9.94	NULL	3 / 15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
16	−9.67	NULL	4 / 15	GSEA C2	CHANG_IMMORTALIZED_BY_HPV31_DN
17	−9.19	NULL	2 / 15	CC	connexon complex
18	−9.16	NULL	6 / 73	BP	defense response to bacterium
19	−8.76	NULL	1 / 16	BP	response to reactive oxygen species
20	−8.61	NULL	1 / 5	miRNA target	miR−196a
21	−8.5	NULL	3 / 16	GSEA C2	AMIT_SERUM_RESPONSE_480_MCF10A
22	−8.35	NULL	2 / 14	BP	defense response to fungus
23	−8.19	NULL	3 / 15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL
24	−8.16	NULL	4 / 15	GSEA C2	AIGNER_ZEB1_TARGETS
25	−8.08	NULL	6 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
26	−7.93	NULL	1 / 19	BP	defense response to Gram−negative bacterium
27	−7.68	NULL	1 / 10	MF	gap junction channel activity
28	−7.56	NULL	2 / 21	CC	gap junction
29	−7.53	NULL	2 / 15	GSEA C2	KARAKAS_TGFB1_SIGNALING
30	−7.44	NULL	4 / 16	GSEA C2	LEE_LIVER_CANCER_MYC_TGFA_UP
31	−7.24	NULL	5 / 13	BP	negative regulation of peptidase activity
32	−7.21	NULL	6 / 15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
33	−7.1	NULL	5 / 38	BP	epithelial cell differentiation
34	−7.04	NULL	19 / 186	MF	structural molecule activity
35	−6.89	NULL	1 / 12	GSEA C2	SCHLESINGER_METHYLATED_DE_NOVO_IN_CANCER
36	−6.49	NULL	2 / 15	MF	interleukin−1 receptor binding
37	−6.33	NULL	9 / 44	CC	keratin filament
38	−6.29	NULL	1 / 14	GSEA C2	ZHAN_MULTIPLE_MYELOMA_CD2_DN
39	−6.12	NULL	2 / 16	GSEA C2	MURATA_VIRULENCE_OF_H_PILORI
40	−6.09	NULL	4 / 15	GSEA C2	LEE_LIVER_CANCER_MYC_E2F1_UP