GW_038

Global Summary

%DE = 0.14

genes with fdr < 0.2 = 1738 (806 + / 932 −)

genes with fdr < 0.1 = 1319 (591 + / 728 −)

genes with fdr < 0.05 = 1010 (434 + / 576 −)

genes with fdr < 0.01 = 656 (265 + / 391 −)

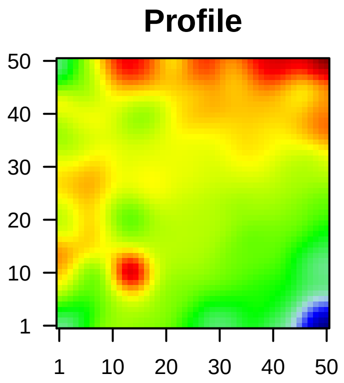
genes in genesets = 16332

<FC> = 0

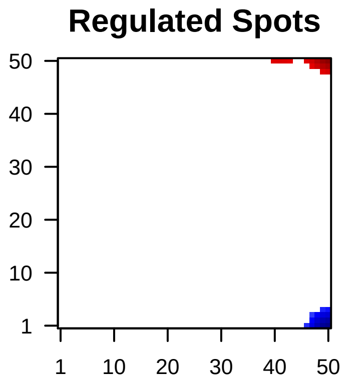
<shrinkage−t> = 0

<p−value> = 0.12

<fdr> = 0.86



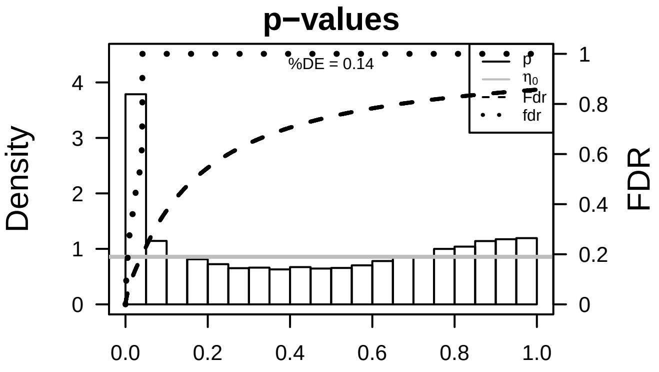
Profile



Regulated Spots

Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	8745	2.03	2e−16	5e−14	50 x 50	ADAM metallopeptidase domain 23 [Source:HGNC Symbol;A
2	154	−2.02	2e−16	5e−14	1 x 40	adrenoceptor beta 2, surface [Source:HGNC Symbol;Acc:286
3	57016	2.18	2e−16	5e−14	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
4	441282	2.07	2e−16	5e−14	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC Sy
5	8644	2.92	2e−16	5e−14	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Syı
6	1109	3.11	2e−16	5e−14	13 x 50	aldo−keto reductase family 1, member C4 [Source:HGNC Syı
7	344905	2.34	2e−16	5e−14	50 x 50	ATPase type 13A5 [Source:HGNC Symbol;Acc:31789]
8	10409	−2.24	2e−16	5e−14	1 x 2	brain abundant, membrane attached signal protein 1 [Source:
9	339512	2.5	2e−16	5e−14	50 x 50	chromosome 1 open reading frame 110 [Source:HGNC Symb
10	713	−1.99	2e−16	5e−14	50 x 1	complement component 1, q subcomponent, B chain [Source
11	57172	−2.13	2e−16	5e−14	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
12	972	−2.06	2e−16	5e−14	50 x 1	CD74 molecule, major histocompatibility complex, class II inv
13	22802	−2.24	2e−16	5e−14	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
14	84518	−2.18	2e−16	5e−14	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
15	1308	−2.17	2e−16	5e−14	1 x 43	collagen, type XVII, alpha 1 [Source:HGNC Symbol;Acc:2194
16	1288	1.92	2e−16	5e−14	1 x 43	collagen, type IV, alpha 6 [Source:HGNC Symbol;Acc:2208]
17	1396	−2.34	2e−16	5e−14	50 x 5	cysteine−rich protein 1 (intestinal) [Source:HGNC Symbol;Ac
18	3627	−2.01	2e−16	5e−14	32 x 1	chemokine (C−X−C motif) ligand 10 [Source:HGNC Symbol;
19	57834	2.39	2e−16	5e−14	13 x 50	cytochrome P450, family 4, subfamily F, polypeptide 11 [Sour
20	1672	−2.37	2e−16	5e−14	1 x 50	defensin, beta 1 [Source:HGNC Symbol;Acc:2766]



p−values

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	13.8	NULL	1033	Chr	Chr 2
2	7.27	NULL	34	BP	glutathione metabolic process
3	6.99	NULL	15	GSEA C2	KEGG_GLUTATHIONE_METABOLISM
4	6.9	NULL	1720	Chr	Chr 1
5	6.79	NULL	25	BP	glutathione derivative biosynthetic process
6	6.48	NULL	530	Cancer	Lembcke_Normal vs Adenoma
7	6.23	NULL	7	GSEA C2	MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
8	6.05	NULL	20	MF	glutathione transferase activity
9	5.94	NULL	142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
10	5.94	NULL	142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
11	5.63	NULL	187	Chr	Chr 21
12	5.61	NULL	15	GSEA C2	REACTOME_GLUTATHIONE_CONJUGATION
13	5.44	NULL	13	BP	regulation of blood vessel size
14	5.38	NULL	15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
15	5.29	NULL	119	BP	xenobiotic metabolic process
16	4.87	NULL	1253	BP	small molecule metabolic process
17	4.86	NULL	1233	TF	KIM_MYC targets
18	4.75	NULL	142	miRNA target−starBase	hsa−miR−522
19	4.73	NULL	717	Chr	Chr 16
20	4.63	NULL	15	Cancer	GENTLES_modul6
Underexpressed					
1	−17.08	NULL	553	Cancer	Lembcke_Colonic Inflammation
2	−16.83	NULL	866	Chr	Chr 12
3	−14.08	NULL	519	Chr	Chr 14
4	−13.13	NULL	312	BP	immune response
5	−12.84	NULL	265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
6	−12.84	NULL	265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
7	−12.84	NULL	265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
8	−12.84	NULL	265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
9	−12.57	NULL	15	CC	MHC class II protein complex
10	−12.19	NULL	1182	CC	extracellular region
11	−11.36	NULL	417	H.Tiss	WIRTH_Immune system
12	−8.65	NULL	1135	Chr	Chr 19
13	−8.55	NULL	683	CC	extracellular space
14	−8.31	NULL	316	Cancer	SPANG_BCL6−index2
15	−8.28	NULL	47	BP	antigen processing and presentation
16	−8.17	NULL	250	Lymphoma	LENZ_Stromal signature 1
17	−7.89	NULL	5	GSEA C2	WONG_ENDOMETRIAL_CANCER_LATE
18	−7.86	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
19	−7.83	NULL	699	Chr	Chr 5
20	−7.2	NULL	6	GSEA C2	SANA_RESPONSE_TO_IFNG_UP

GW_038

Local Summary

%DE = 0.73

metagenes = 11

genes = 190

genes in genesets = 189

genes with fdr < 0.1 = 116 (106 + / 10 −)

genes with fdr < 0.05 = 112 (103 + / 9 −)

genes with fdr < 0.01 = 87 (81 + / 6 −)

<r> metagenes = 0.95

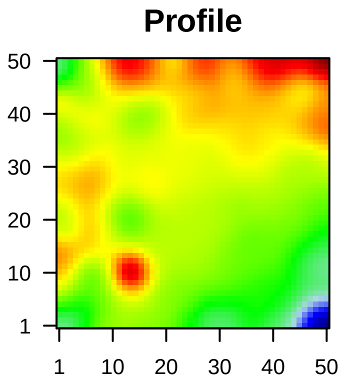
<r> genes = 0.29

<FC> = 0.64

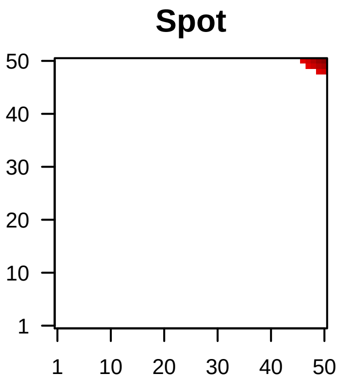
<shrinkage−t> = 22.52

<p−value> = 0

<fdr> = 0.41



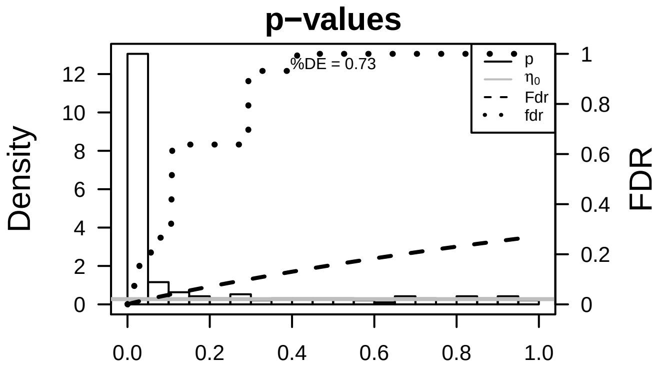
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	8745	2.03	2e−16	9e−16	50 x 50	ADAM metallopeptidase domain 23 [Source:HGNC Symbol;A
2	344905	2.34	2e−16	9e−16	50 x 50	ATPase type 13A5 [Source:HGNC Symbol;Acc:31789]
3	339512	2.5	2e−16	9e−16	50 x 50	chromosome 1 open reading frame 110 [Source:HGNC Symb
4	94234	−2.39	2e−16	9e−16	50 x 50	forkhead box Q1 [Source:HGNC Symbol;Acc:20951]
5	2719	2.36	2e−16	9e−16	50 x 50	glypican 3 [Source:HGNC Symbol;Acc:4451]
6	2938	1.97	2e−16	9e−16	50 x 50	glutathione S−transferase alpha 2 [Source:HGNC Symbol;Ac
7	2944	2.61	2e−16	9e−16	50 x 50	glutathione S−transferase mu 1 [Source:HGNC Symbol;Acc:4
8	3880	−2.18	2e−16	9e−16	50 x 49	keratin 19 [Source:HGNC Symbol;Acc:6436]
9	4922	3.68	2e−16	9e−16	50 x 50	neurotensin [Source:HGNC Symbol;Acc:8038]
10	4953	2.05	2e−16	9e−16	50 x 50	ornithine decarboxylase 1 [Source:HGNC Symbol;Acc:8109]
11	6657	2.15	2e−16	9e−16	50 x 50	SRY (sex determining region Y)−box 2 [Source:HGNC Symbo
12	11166	2.55	2e−16	9e−16	50 x 50	SRY (sex determining region Y)−box 21 [Source:HGNC Symb
13	7348	2.29	2e−16	9e−16	50 x 50	uroplakin 1B [Source:HGNC Symbol;Acc:12578]
14	26047	1.79	3e−14	5e−12	50 x 50	contactin associated protein−like 2 [Source:HGNC Symbol;Ac
15	2947	1.74	1e−13	5e−12	50 x 50	glutathione S−transferase mu 3 (brain) [Source:HGNC Symbo
16	2729	1.72	3e−13	5e−12	50 x 50	glutamate−cysteine ligase, catalytic subunit [Source:HGNC S
17	2946	1.7	4e−13	5e−12	50 x 50	glutathione S−transferase mu 2 (muscle) [Source:HGNC Sym
18	80896	1.7	5e−13	5e−12	50 x 50	N−acetylneuraminate pyruvate lyase (dihydrodipicolinate synt
19	4072	1.7	5e−13	5e−11	50 x 50	epithelial cell adhesion molecule [Source:HGNC Symbol;Acc:
20	28978	1.66	1e−12	2e−10	49 x 50	transmembrane protein 14A [Source:HGNC Symbol;Acc:210



p−values

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	23.18	NULL	2 / 7	GSEA C2	MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
2	21.95	NULL	5 / 15	GSEA C2	KEGG_GLUTATHIONE_METABOLISM
3	18.67	NULL	6 / 25	BP	glutathione derivative biosynthetic process
4	18.58	NULL	8 / 34	BP	glutathione metabolic process
5	18.57	NULL	3 / 11	MF	glutathione binding
6	18.57	NULL	3 / 11	GSEA C2	KEGG_DRUG_METABOLISM_CYTOCHROME_P450
7	18.14	NULL	5 / 20	MF	glutathione transferase activity
8	16.97	NULL	4 / 13	GSEA C2	KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_
9	16.11	NULL	3 / 13	BP	regulation of blood vessel size
10	13.5	NULL	4 / 15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
11	13.28	NULL	4 / 15	GSEA C2	REACTOME_GLUTATHIONE_CONJUGATION
12	13.01	NULL	1 / 4	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_13
13	11.38	NULL	11 / 119	BP	xenobiotic metabolic process
14	11.19	NULL	1 / 11	Glio	neurons_glio
15	11.02	NULL	2 / 15	GSEA C2	LEE_LIVER_CANCER_MYC_UP
16	11.02	NULL	2 / 15	GSEA C2	LEE_LIVER_CANCER_E2F1_UP
17	10.06	NULL	3 / 12	GSEA C2	BROCKE_APOPTOSIS_REVERSED_BY_IL6
18	9.79	NULL	2 / 9	GSEA C2	REACTOME_METABOLISM_OF_AMINO_ACIDS
19	9.43	NULL	2 / 23	BP	stem cell differentiation
20	9.36	NULL	1 / 15	MF	neuropeptide hormone activity
21	8.85	NULL	1 / 9	GSEA C2	GOERING_BLOOD_HDL_CHOLESTEROL_QTL_CIS
22	8.74	NULL	3 / 11	GSEA C2	ITO_PTTG1_TARGETS_UP
23	8.58	NULL	2 / 9	GSEA C2	REACTOME_GLUCURONIDATION
24	8.42	NULL	1 / 7	GSEA C2	REACTOME_G1_S_TRANSITION
25	8.42	NULL	1 / 7	miRNA target	miR−145
26	8.33	NULL	3 / 16	GSEA C2	SANA_RESPONSE_TO_IFNG_DN
27	8.12	NULL	2 / 20	TF	MYC_Metabolism UP
28	8.01	NULL	1 / 7	GSEA C2	REACTOME_REGULATION_OF_ORNITHINE_DECARBOXYLASE
29	7.96	NULL	2 / 10	GSEA C2	CERVERA_SDHB_TARGETS_1_DN
30	7.84	NULL	2 / 7	GSEA C2	FREDERICK_PRKCI_TARGETS
31	7.77	NULL	1 / 8	GSEA C2	REACTOME_E2F_TRANSCRIPTIONAL_TARGETS_AT_G1_S
32	7.77	NULL	1 / 8	miRNA 3UTR	CTGCA−450
33	7.62	NULL	2 / 11	GSEA C2	DANG_MYC_TARGETS_UP
34	7.58	NULL	2 / 10	GSEA C2	CONRAD_STEM_CELL
35	7.55	NULL	2 / 15	GSEA C2	REACTOME_PHASE_II_CONJUGATION
36	7.41	NULL	2 / 15	GSEA C2	KEGG_ARGININE_AND_PROLINE_METABOLISM
37	7.4	NULL	1 / 8	GSEA C2	PUJANA_CHEK2_PCC_NETWORK
38	7.34	NULL	3 / 15	BP	lipid glycosylation
39	7.32	NULL	3 / 48	BP	cerebral cortex development
40	7.29	NULL	2 / 12	GSEA C2	LEE_METASTASIS_AND_ALTERNATIVE_SPLICING_DN

GW_038

Local Summary

%DE = 0.78

metagenes = 4

genes = 138

genes in genesets = 137

genes with fdr < 0.1 = 90 (87 + / 3 −)

genes with fdr < 0.05 = 72 (71 + / 1 −)

genes with fdr < 0.01 = 41 (41 + / 0 −)

<r> metagenes = 0.98

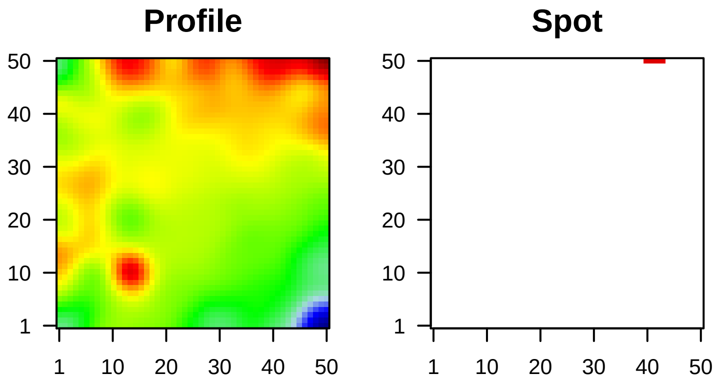
<r> genes = 0.38

<FC> = 0.48

<shrinkage−t> = 16.74

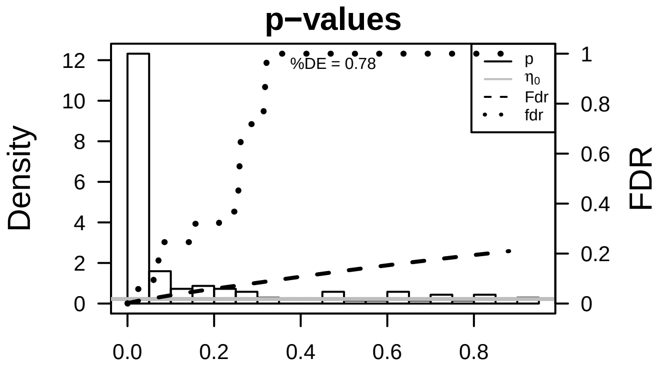
<p−value> = 0.01

<fdr> = 0.51



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	9319	1.19	4e−07	9e−06	43 x 50	thyroid hormone receptor interactor 13 [Source:HGNC Symbo
2	84365	1.17	6e−07	2e−05	40 x 50	nucleolar protein interacting with the FHA domain of MKI67 [S
3	29097	1.14	1e−06	2e−05	40 x 50	cornichon family AMPA receptor auxiliary protein 4 [Source:H
4	154807	1.13	2e−06	2e−04	40 x 50	vitamin K epoxide reductase complex, subunit 1−like 1 [Sourc
5	152559	1.05	8e−06	2e−04	40 x 50	progestin and adipoQ receptor family member III [Source:HG
6	23366	1	2e−05	2e−04	40 x 50	KIAA0895 [Source:HGNC Symbol;Acc:22206]
7	54888	0.98	3e−05	2e−04	40 x 50	NOP2/Sun RNA methyltransferase family, member 2 [Source:
8	26872	0.97	3e−05	2e−04	40 x 50	six transmembrane epithelial antigen of the prostate 1 [Sourc
9	9128	0.97	4e−05	2e−04	43 x 50	pre−mRNA processing factor 4 [Source:HGNC Symbol;Acc:1
10	54443	0.96	5e−05	2e−04	43 x 50	anillin, actin binding protein [Source:HGNC Symbol;Acc:1408
11	7027	0.95	5e−05	7e−04	43 x 50	transcription factor Dp−1 [Source:HGNC Symbol;Acc:11749]
12	9631	0.92	8e−05	7e−04	42 x 50	nucleoporin 155kDa [Source:HGNC Symbol;Acc:8063]
13	55699	0.91	1e−04	7e−04	40 x 50	isoleucyl−tRNA synthetase 2, mitochondrial [Source:HGNC S
14	7804	0.9	1e−04	1e−03	41 x 50	low density lipoprotein receptor−related protein 8, apolipoprot
15	29899	0.89	2e−04	1e−03	41 x 50	G−protein signaling modulator 2 [Source:HGNC Symbol;Acc:
16	64216	0.86	2e−04	1e−03	40 x 50	transcription factor B2, mitochondrial [Source:HGNC Symbol;
17	54517	0.86	2e−04	1e−03	41 x 50	pseudouridylate synthase 7 homolog (S. cerevisiae) [Source:
18	5433	0.85	3e−04	1e−03	40 x 50	polymerase (RNA) II (DNA directed) polypeptide D [Source:H
19	52	0.84	4e−04	1e−03	41 x 50	acid phosphatase 1, soluble [Source:HGNC Symbol;Acc:122]
20	137392	0.83	4e−04	1e−03	40 x 50	family with sequence similarity 92, member A1 [Source:HGN



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	13.88	NULL	4 / 13	GSEA C2	SCHUHMACHER_MYC_TARGETS_UP
2	13.28	NULL	4 / 14	GSEA C2	MAYBURD_RESPONSE_TO_L663536_DN
3	13.17	NULL	4 / 18	Lymphoma	DAVE_c−myc BL UP
4	10.12	NULL	4 / 16	GSEA C2	BIDUS_METASTASIS_UP
5	10.04	NULL	3 / 15	GSEA C2	REACTOME_MITOCHONDRIAL_TRNA_AMINOACYLATION
6	9.52	NULL	3 / 18	BP	spindle organization
7	9.36	NULL	3 / 16	GSEA C2	REACTOME_REV_MEDIATED_NUCLEAR_EXPORT_OF_HIV1_F
8	9.18	NULL	2 / 16	CC	male germ cell nucleus
9	9.03	NULL	2 / 8	GSEA C2	KEGG_VALINE_LEUCINE_AND_ISOLEUCINE_BIOSYNTHESIS
10	8.96	NULL	2 / 6	GSEA C2	LOPEZ_MBD_TARGETS
11	8.89	NULL	3 / 15	GSEA C2	NAKAYAMA_SOFT_TISSUE_TUMORS_PCA2_UP
12	8.78	NULL	3 / 37	miRNA target−starBase	hsa−miR−518e
13	8.76	NULL	3 / 16	GSEA C2	REACTOME_TRANSPORT_OF_THE_SLBP_INDEPENDENT_MA
14	8.65	NULL	2 / 10	CC	microtubule plus−end
15	8.54	NULL	0 / 15	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
16	8.34	NULL	3 / 11	BP	mitotic metaphase plate congression
17	8.17	NULL	3 / 16	Cancer	WOLFER_overlap genes
18	8.07	NULL	1 / 8	GSEA C2	NIKOLSKY_BREAST_CANCER_5P15_AMPLICON
19	8.06	NULL	3 / 13	GSEA C2	WINNEPENNINCKX_MELANOMA_METASTASIS_UP
20	7.99	NULL	2 / 11	GSEA C2	REACTOME_PURINE_RIBONUCLEOSIDE_MONOPHOSPHATE_
21	7.91	NULL	2 / 10	GSEA C2	MONTERO_THYROID_CANCER_POOR_SURVIVAL_UP
22	7.88	NULL	2 / 12	GSEA C2	LI_WILMS_TUMOR_VS_FETAL_KIDNEY_1_DN
23	7.82	NULL	5 / 44	BP	tRNA aminoacylation for protein translation
24	7.81	NULL	2 / 8	TF	MYC_RNA processing binding UP
25	7.76	NULL	3 / 13	GSEA C2	CROONQUIST_IL6_DEPRIVATION_DN
26	7.74	NULL	1 / 8	GSEA C2	EHLERS_ANEUPLOIDY_DN
27	7.7	NULL	4 / 15	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP
28	7.69	NULL	1 / 4	MMML CGS	MACIEJ_MMML 41
29	7.51	NULL	4 / 35	MF	aminoacyl−tRNA ligase activity
30	7.44	NULL	3 / 14	GSEA C2	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
31	7.3	NULL	2 / 9	GSEA C2	FUNG_IL2_SIGNALING_1
32	7.23	NULL	3 / 17	CC	proteasome accessory complex
33	7.19	NULL	1 / 6	GSEA C2	FOURNIER_ACINAR_DEVELOPMENT_EARLY_DN
34	7.13	NULL	3 / 53	miRNA target−starBase	hsa−miR−518f
35	7.09	NULL	2 / 13	GSEA C2	LEE_LIVER_CANCER_SURVIVAL_DN
36	7.06	NULL	2 / 16	BP	mitotic cytokinesis
37	7	NULL	3 / 16	GSEA C2	FUJII_YBX1_TARGETS_DN
38	6.97	NULL	5 / 29	BP	regulation of glucose transport
39	6.97	NULL	2 / 13	GSEA C2	ALONSO_METASTASIS_UP
40	6.96	NULL	2 / 14	BP	purine ribonucleoside monophosphate biosynthetic process

GW_038

Local Summary

%DE = 0.99

metagenes = 15

genes = 264

genes in genesets = 262

genes with fdr < 0.1 = 255 (7 + / 248 −)

genes with fdr < 0.05 = 251 (4 + / 247 −)

genes with fdr < 0.01 = 235 (3 + / 232 −)

<r> metagenes = 0.99

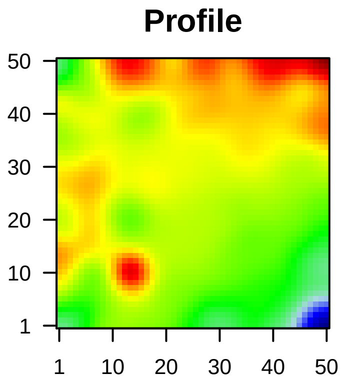
<r> genes = 0.6

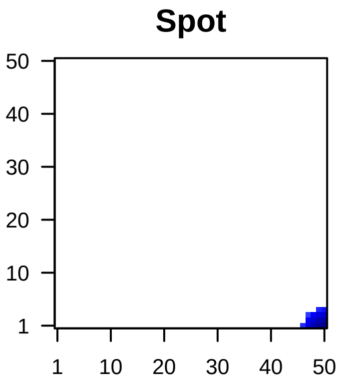
<FC> = −0.92

<shrinkage−t> = −32.18

<p−value> = 0

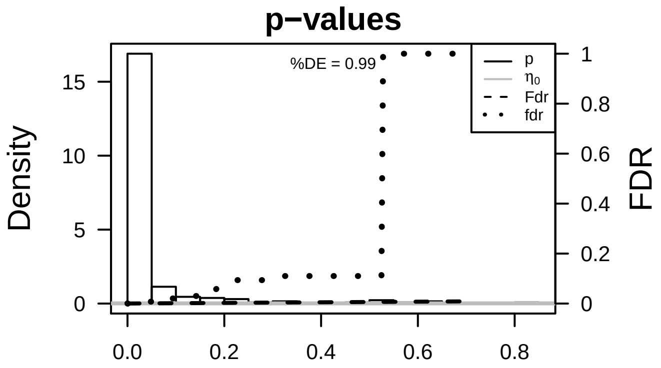
<fdr> = 0.22





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	713	−1.99	2e−16	5e−17	50 x 1	complement component 1, q subcomponent, B chain [Source
2	57172	−2.13	2e−16	5e−17	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
3	972	−2.06	2e−16	5e−17	50 x 1	CD74 molecule, major histocompatibility complex, class II inv
4	54855	−2.28	2e−16	5e−17	49 x 1	family with sequence similarity 46, member C [Source:HGNC
5	3108	−2.36	2e−16	5e−17	50 x 1	major histocompatibility complex, class II, DM alpha [Source:
6	3109	−2.32	2e−16	5e−17	50 x 1	major histocompatibility complex, class II, DM beta [Source:H
7	3113	−2.37	2e−16	5e−17	50 x 1	major histocompatibility complex, class II, DP alpha 1 [Source
8	3122	−2.66	2e−16	5e−17	50 x 1	major histocompatibility complex, class II, DR alpha [Source:
9	3128	−2.08	2e−16	5e−17	50 x 1	major histocompatibility complex, class II, DR beta 6 (pseudo
10	3512	−2.46	2e−16	5e−17	50 x 1	immunoglobulin J polypeptide, linker protein for immunoglobu
11	3543	−4.05	2e−16	5e−17	49 x 1	immunoglobulin lambda−like polypeptide 1 [Source:HGNC Sy
12	3936	−2.05	2e−16	5e−17	50 x 1	lymphocyte cytosolic protein 1 (L−plastin) [Source:HGNC Syr
13	23231	−1.93	2e−16	5e−17	48 x 2	sel−1 suppressor of lin−12−like 3 (C. elegans) [Source:HGNC
14	51466	−1.73	2e−13	5e−13	48 x 1	Enah/Vasp−like [Source:HGNC Symbol;Acc:20234]
15	2745	−1.7	4e−13	5e−13	50 x 3	glutaredoxin (thioltransferase) [Source:HGNC Symbol;Acc:43
16	83641	−1.69	5e−13	1e−12	50 x 1	family with sequence similarity 107, member B [Source:HGN
17	915	−1.66	1e−12	1e−12	49 x 1	CD3d molecule, delta (CD3−TCR complex) [Source:HGNC S
18	962	−1.66	2e−12	7e−12	50 x 1	CD48 molecule [Source:HGNC Symbol;Acc:1683]
19	397	−1.6	5e−12	7e−12	50 x 1	Rho GDP dissociation inhibitor (GDI) beta [Source:HGNC Sy
20	260436	−1.61	6e−12	2e−11	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symb



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−37.38	NULL	12 / 15	CC	MHC class II protein complex
2	−28.78	NULL	90 / 417	H.Tiss	WIRTH_Immune system
3	−23.73	NULL	52 / 312	BP	immune response
4	−23.53	NULL	3 / 5	GSEA C2	WONG_ENDOMETRIAL_CANCER_LATE
5	−23.3	NULL	15 / 47	BP	antigen processing and presentation
6	−22.49	NULL	94 / 553	Cancer	Lembcke_Colonic Inflammation
7	−19.82	NULL	3 / 6	GSEA C2	SANA_RESPONSE_TO_IFNG_UP
8	−19.3	NULL	7 / 21	CC	clathrin−coated endocytic vesicle membrane
9	−18.68	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
10	−18.34	NULL	7 / 23	CC	integral to lumenal side of endoplasmic reticulum membrane
11	−17.02	NULL	6 / 11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
12	−16.97	NULL	7 / 15	GSEA C2	FINAK_BREAST_CANCER_SDPP_SIGNATURE
13	−16.8	NULL	43 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
14	−16.8	NULL	43 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
15	−16.8	NULL	43 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
16	−16.8	NULL	43 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
17	−16.78	NULL	2 / 3	GSEA C2	KEGG_VIRAL_MYOCARDITIS
18	−16.55	NULL	14 / 60	BP	T cell costimulation
19	−16.42	NULL	7 / 28	CC	transport vesicle membrane
20	−15.95	NULL	4 / 8	GSEA C2	GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_DN
21	−15.55	NULL	8 / 35	CC	trans−Golgi network membrane
22	−15.42	NULL	3 / 7	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
23	−15.37	NULL	1 / 2	GSEA C2	KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUC
24	−15.37	NULL	1 / 2	GSEA C2	KEGG_AUTOIMMUNE_THYROID_DISEASE
25	−15.37	NULL	1 / 2	GSEA C2	KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS
26	−15.23	NULL	7 / 32	CC	ER to Golgi transport vesicle membrane
27	−14.85	NULL	5 / 11	GSEA C2	BIOCARTA_THELPER_PATHWAY
28	−14.81	NULL	2 / 6	GSEA C2	LUI_THYROID_CANCER_CLUSTER_4
29	−14.73	NULL	1 / 6	H.Tiss	WIRTH_Bone marrow
30	−14.56	NULL	13 / 87	BP	antigen processing and presentation of exogenous peptide antigen
31	−14.06	NULL	2 / 4	GSEA C2	KEGG_LEISHMANIA_INFECTION
32	−14.05	NULL	17 / 74	BP	regulation of immune response
33	−13.82	NULL	2 / 4	GSEA C2	REACTOME_CLASSICAL_ANTIBODY_MEDIATED_COMPLEMEN
34	−13.8	NULL	5 / 12	GSEA C2	BIOCARTA_CTL_PATHWAY
35	−13.65	NULL	5 / 12	BP	immunoglobulin mediated immune response
36	−13.47	NULL	6 / 8	Glio	Donson−migration tethering and rolling−associated with LTS in HG
37	−13.22	NULL	2 / 5	GSEA C2	WEST_ADRENOCORTICAL_CARCINOMA_VS_ADENOMA_DN
38	−13.12	NULL	4 / 7	Glio	Donson−cytotoxic effectors−associated with LTS in HGA
39	−13.05	NULL	6 / 13	Cancer	GENTLES_modul18
40	−12.92	NULL	8 / 46	CC	endocytic vesicle membrane