GW_083

Global Summary

%DE = 0.15

genes with fdr < 0.2 = 2002 (1006 + / 996 −)

genes with fdr < 0.1 = 1471 (737 + / 734 −)

genes with fdr < 0.05 = 1291 (647 + / 644 −)

genes with fdr < 0.01 = 888 (458 + / 430 −)

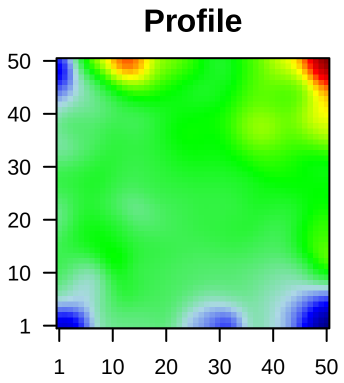
genes in genesets = 16332

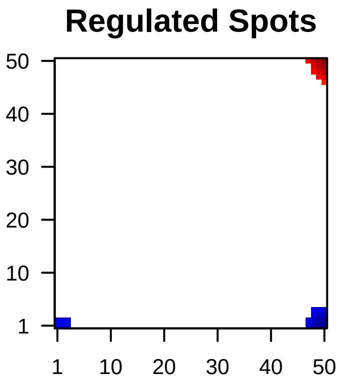
<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.1

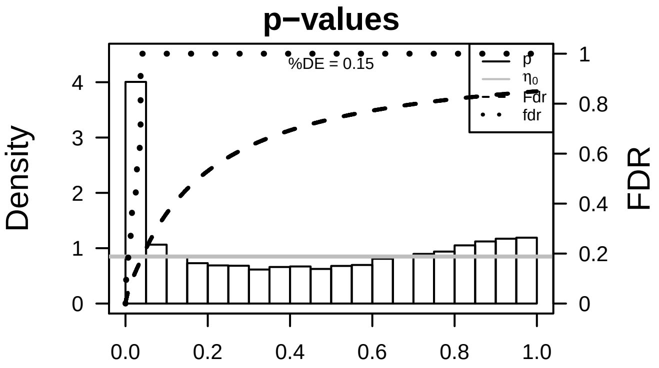
<fdr> = 0.85





Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	154664	2.2	2e−16	4e−14	50 x 50	ATP−binding cassette, sub−family A (ABC1), member 13 [Sou
2	8745	2.11	2e−16	4e−14	50 x 50	ADAM metallopeptidase domain 23 [Source:HGNC Symbol;A
3	124	2.67	2e−16	4e−14	50 x 11	alcohol dehydrogenase 1A (class I), alpha polypeptide [Sourc
4	126	2.6	2e−16	4e−14	50 x 12	alcohol dehydrogenase 1C (class I), gamma polypeptide [Sou
5	10551	1.85	2e−16	4e−14	50 x 10	anterior gradient 2 [Source:HGNC Symbol;Acc:328]
6	57016	2.7	2e−16	4e−14	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
7	441282	2.55	2e−16	4e−14	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC Sy
8	1109	3.06	2e−16	4e−14	13 x 50	aldo−keto reductase family 1, member C4 [Source:HGNC Sy
9	216	2.82	2e−16	4e−14	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGN
10	218	2.47	2e−16	4e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
11	501	−1.86	2e−16	4e−14	6 x 46	aldehyde dehydrogenase 7 family, member A1 [Source:HGN
12	445	2.18	2e−16	4e−14	50 x 47	argininosuccinate synthase 1 [Source:HGNC Symbol;Acc:75
13	8702	1.84	2e−16	4e−14	50 x 50	UDP−Gal:betaGlcNAc beta 1,4− galactosyltransferase, polyp
14	10409	−2.01	2e−16	4e−14	1 x 2	brain abundant, membrane attached signal protein 1 [Source:
15	633	−2.02	2e−16	4e−14	3 x 1	biglycan [Source:HGNC Symbol;Acc:1044]
16	684	−2.16	2e−16	4e−14	32 x 1	bone marrow stromal cell antigen 2 [Source:HGNC Symbol;A
17	375791	−2.03	2e−16	4e−14	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Symb
18	760	−2.22	2e−16	4e−14	1 x 44	carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
19	26256	2.03	2e−16	4e−14	50 x 50	calcium binding tyrosine−(Y)−phosphorylation regulated [Sou
20	51806	−2.4	2e−16	4e−14	4 x 50	calmodulin−like 5 [Source:HGNC Symbol;Acc:18180]



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	10.53	NULL	743	Chr	Chr 7
2	9.16	NULL	633	Chr	Chr 9
3	8.93	NULL	914	Chr	Chr 3
4	7.48	NULL	232	Chr	Chr 18
5	7.28	NULL	34	BP	glutathione metabolic process
6	6.95	NULL	13	GSEA C2	SINGH_NFE2L2_TARGETS
7	6.93	NULL	1033	Chr	Chr 2
8	6.67	NULL	9	GSEA C2	REACTOME_ETHANOL_OXIDATION
9	6.32	NULL	15	GSEA C2	KEGG_GLUTATHIONE_METABOLISM
10	6.29	NULL	1749	MF	DNA binding
11	5.96	NULL	7	GSEA C2	FREDERICK_PRKCI_TARGETS
12	5.71	NULL	368	miRNA target−starBase	hsa−miR−144
13	5.5	NULL	24	TF Tissue	VAQUERIZAS_Trachea
14	5.43	NULL	1581	BP	regulation of transcription, DNA−dependent
15	5.24	NULL	311	miRNA target−starBase	hsa−miR−302c
16	5	NULL	39	Cancer	ZHANG_MM up
17	4.99	NULL	1574	BP	transcription, DNA−templated
18	4.93	NULL	4640	CC	nucleus
19	4.92	NULL	438	miRNA target−starBase	hsa−miR−424
20	4.91	NULL	180	miRNA target−starBase	hsa−miR−374a
Underexpressed					
1	−16.12	NULL	553	Cancer	Lembcke_Colonic Inflammation
2	−13.14	NULL	250	Lymphoma	LENZ_Stromal signature 1
3	−12.72	NULL	312	BP	immune response
4	−12.15	NULL	190	CC	extracellular matrix
5	−12	NULL	265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
6	−12	NULL	265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
7	−12	NULL	265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
8	−12	NULL	265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
9	−11.92	NULL	572	Disease	GUDJ_psoriasis up
10	−11.91	NULL	618	Chr	Chr 4
11	−11.57	NULL	135	H.Tiss	WIRTH_Mucosa
12	−10.85	NULL	1182	CC	extracellular region
13	−10.76	NULL	602	Chr	Chr 10
14	−10.55	NULL	717	Chr	Chr 16
15	−9.69	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
16	−9.28	NULL	51	BP	type I interferon signaling pathway
17	−8.86	NULL	683	CC	extracellular space
18	−8.85	NULL	10	MF	RAGE receptor binding
19	−8.85	NULL	866	Chr	Chr 12
20	−8.59	NULL	13	GSEA C2	BOWIE_RESPONSE_TO_TAMOXIFEN

GW_083

Local Summary

%DE = 0.88

metagenes = 13

genes = 208

genes in genesets = 206

genes with fdr < 0.1 = 182 (175 + / 7 −)

genes with fdr < 0.05 = 159 (156 + / 3 −)

genes with fdr < 0.01 = 144 (142 + / 2 −)

<r> metagenes = 0.97

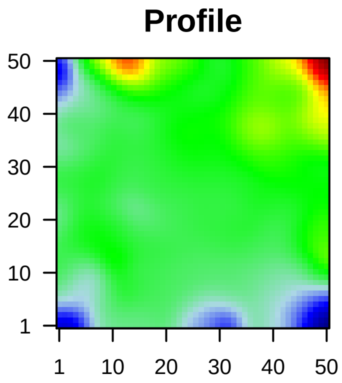
<r> genes = 0.28

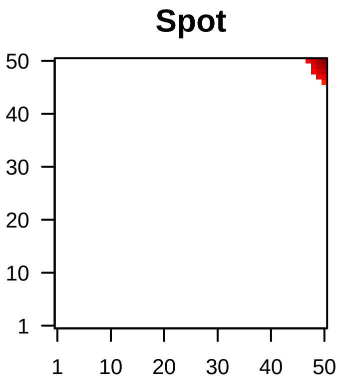
<FC> = 0.93

<shrinkage−t> = 32.46

<p−value> = 0

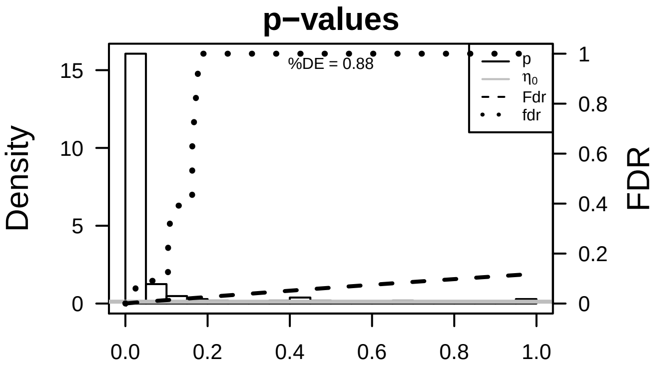
<fdr> = 0.26





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	154664	2.2	2e−16	2e−16	50 x 50	ATP−binding cassette, sub−family A (ABC1), member 13 [Sou
2	8745	2.11	2e−16	2e−16	50 x 50	ADAM metallopeptidase domain 23 [Source:HGNC Symbol;A
3	216	2.82	2e−16	2e−16	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGN
4	445	2.18	2e−16	2e−16	50 x 47	argininosuccinate synthase 1 [Source:HGNC Symbol;Acc:75
5	8702	1.84	2e−16	2e−16	50 x 50	UDP−Gal:betaGlcNAc beta 1,4− galactosyltransferase, polyp
6	26256	2.03	2e−16	2e−16	50 x 50	calcium binding tyrosine−(Y)−phosphorylation regulated [Sou
7	4072	2.23	2e−16	2e−16	50 x 50	epithelial cell adhesion molecule [Source:HGNC Symbol;Acc:
8	83888	2.44	2e−16	2e−16	50 x 50	fibroblast growth factor binding protein 2 [Source:HGNC Sym
9	94234	2.17	2e−16	2e−16	50 x 50	forkhead box Q1 [Source:HGNC Symbol;Acc:20951]
10	2719	1.87	2e−16	2e−16	50 x 50	glypican 3 [Source:HGNC Symbol;Acc:4451]
11	2938	2.71	2e−16	2e−16	50 x 50	glutathione S−transferase alpha 2 [Source:HGNC Symbol;Ac
12	2944	2.58	2e−16	2e−16	50 x 50	glutathione S−transferase mu 1 [Source:HGNC Symbol;Acc:
13	2946	1.94	2e−16	2e−16	50 x 50	glutathione S−transferase mu 2 (muscle) [Source:HGNC Sym
14	10643	1.96	2e−16	2e−16	48 x 50	insulin−like growth factor 2 mRNA binding protein 3 [Source:
15	3880	2.71	2e−16	2e−16	50 x 49	keratin 19 [Source:HGNC Symbol;Acc:6436]
16	4915	2.4	2e−16	2e−16	50 x 50	neurotrophic tyrosine kinase, receptor, type 2 [Source:HGNC
17	4922	2.09	2e−16	2e−16	50 x 50	neurotensin [Source:HGNC Symbol;Acc:8038]
18	6657	1.9	2e−16	2e−16	50 x 50	SRY (sex determining region Y)−box 2 [Source:HGNC Symb
19	7345	2.98	2e−16	2e−16	50 x 46	ubiquitin carboxyl−terminal esterase L1 (ubiquitin thiolesteras
20	54578	1.99	2e−16	2e−16	50 x 50	UDP glucuronosyltransferase 1 family, polypeptide A6 [Sourc



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	18.03	NULL	8 / 34	BP	glutathione metabolic process
2	17.68	NULL	6 / 25	BP	glutathione derivative biosynthetic process
3	16.23	NULL	4 / 13	GSEA C2	KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_
4	15.67	NULL	5 / 15	GSEA C2	KEGG_GLUTATHIONE_METABOLISM
5	15.52	NULL	5 / 20	MF	glutathione transferase activity
6	14.7	NULL	3 / 11	MF	glutathione binding
7	14.7	NULL	3 / 11	GSEA C2	KEGG_DRUG_METABOLISM_CYTOCHROME_P450
8	14.52	NULL	4 / 15	GSEA C2	REACTOME_GLUTATHIONE_CONJUGATION
9	14.18	NULL	4 / 13	BP	regulation of blood vessel size
10	13.89	NULL	4 / 15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
11	13.88	NULL	3 / 11	GSEA C2	ITO_PTTG1_TARGETS_UP
12	13.32	NULL	2 / 7	GSEA C2	FREDERICK_PRKCI_TARGETS
13	13.3	NULL	2 / 7	GSEA C2	MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
14	12.88	NULL	2 / 6	GSEA C2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_D_DN
15	12.76	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
16	12.5	NULL	11 / 119	BP	xenobiotic metabolic process
17	12.22	NULL	2 / 12	GSEA C2	MOROSETTI_FACIOSCAPULOHUMERAL_MUSCULAR_DISTRO
18	11.47	NULL	3 / 6	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_7
19	11.14	NULL	3 / 16	GSEA C2	BOYAULT_LIVER_CANCER_SUBCLASS_G1_DN
20	10.55	NULL	3 / 9	GSEA C2	BROWNE_HCMV_INFECTION_8HR_UP
21	10.41	NULL	50 / 914	Chr	Chr 3
22	10.23	NULL	1 / 6	GSEA C2	KAPOSI_LIVER_CANCER_POOR_SURVIVAL_DN
23	9.64	NULL	2 / 15	GSEA C2	LEE_LIVER_CANCER_MYC_UP
24	9.64	NULL	2 / 15	GSEA C2	LEE_LIVER_CANCER_E2F1_UP
25	9.48	NULL	3 / 12	GSEA C2	BROCKE_APOPTOSIS_REVERSED_BY_IL6
26	9.13	NULL	2 / 12	BP	cellular aldehyde metabolic process
27	9.09	NULL	1 / 8	GSEA C2	MUNSHI_MULTIPLE_MYELOMA_DN
28	8.78	NULL	1 / 5	GSEA C2	NIELSEN_SCHWANNOMA_DN
29	8.63	NULL	1 / 4	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_13
30	8.55	NULL	2 / 15	GSEA C2	REACTOME_PHASE_II_CONJUGATION
31	8.53	NULL	1 / 2	miRNA target	miR−127
32	8.36	NULL	2 / 13	Lymphoma	BENTINK_mBL UP
33	8.34	NULL	3 / 15	BP	lipid glycosylation
34	8.01	NULL	1 / 9	GSEA C2	ABDULRAHMAN_KIDNEY_CANCER_VHL_DN
35	8.01	NULL	1 / 9	GSEA C2	REACTOME_ETHANOL_OXIDATION
36	7.95	NULL	1 / 10	MF	omega peptidase activity
37	7.93	NULL	2 / 10	GSEA C2	CONRAD_STEM_CELL
38	7.57	NULL	2 / 12	BP	glutamate metabolic process
39	7.52	NULL	1 / 10	GSEA C2	MAINA_VHL_TARGETS_UP
40	7.52	NULL	1 / 10	GSEA C2	FRIDMAN_SENESCENCE_DN

GW_083

Local Summary

%DE = 0.9

metagenes = 6

genes = 110

genes in genesets = 110

genes with fdr < 0.1 = 97 (6 + / 91 −)

genes with fdr < 0.05 = 84 (5 + / 79 −)

genes with fdr < 0.01 = 78 (5 + / 73 −)

<r> metagenes = 0.99

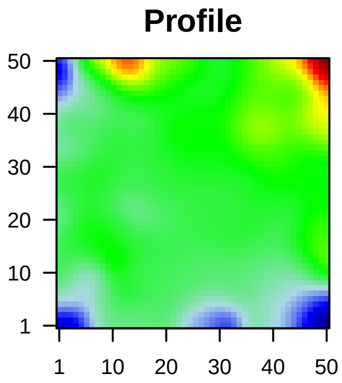
<r> genes = 0.48

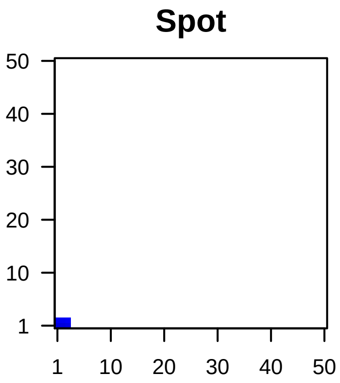
<FC> = −0.77

<shrinkage−t> = −27.01

<p−value> = 0

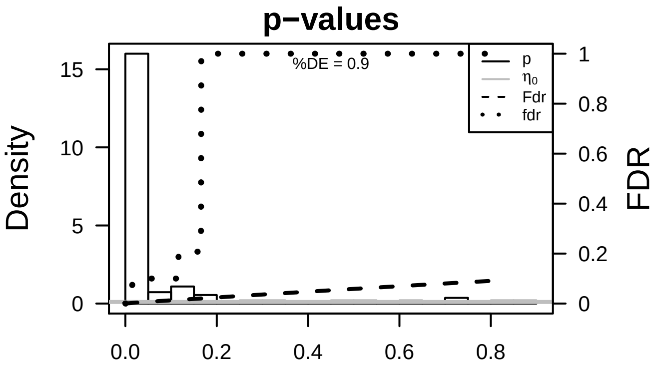
<fdr> = 0.26





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	10409	−2.01	2e−16	8e−16	1 x 2	brain abundant, membrane attached signal protein 1 [Source:
2	633	−2.02	2e−16	8e−16	3 x 1	biglycan [Source:HGNC Symbol;Acc:1044]
3	6696	3.17	2e−16	8e−16	2 x 1	secreted phosphoprotein 1 [Source:HGNC Symbol;Acc:1125
4	3956	−1.81	4e−16	5e−15	1 x 1	lectin, galactoside−binding, soluble, 1 [Source:HGNC Symbol
5	25878	−1.81	4e−16	5e−15	3 x 1	matrix−remodelling associated 5 [Source:HGNC Symbol;Acc:
6	12	−1.79	9e−16	6e−14	1 x 1	
7	1293	−1.74	7e−15	7e−14	2 x 1	collagen, type VI, alpha 3 [Source:HGNC Symbol;Acc:2213]
8	1289	−1.72	1e−14	3e−12	2 x 1	collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209]
9	1462	−1.63	3e−13	2e−11	3 x 1	versican [Source:HGNC Symbol;Acc:2464]
10	6423	−1.56	3e−12	2e−11	3 x 1	secreted frizzled−related protein 2 [Source:HGNC Symbol;Ac
11	3569	1.55	4e−12	8e−11	1 x 1	interleukin 6 (interferon, beta 2) [Source:HGNC Symbol;Acc:
12	1290	−1.52	1e−11	2e−10	2 x 1	collagen, type V, alpha 2 [Source:HGNC Symbol;Acc:2210]
13	4318	−1.48	4e−11	2e−10	1 x 1	matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 9
14	4060	−1.47	5e−11	4e−10	2 x 1	lumican [Source:HGNC Symbol;Acc:6724]
15	1291	−1.45	9e−11	7e−10	2 x 1	collagen, type VI, alpha 1 [Source:HGNC Symbol;Acc:2211]
16	112464	−1.43	2e−10	7e−10	1 x 1	protein kinase C, delta binding protein [Source:HGNC Symbo
17	7058	−1.41	3e−10	7e−10	2 x 1	thrombospondin 2 [Source:HGNC Symbol;Acc:11786]
18	4312	−1.4	3e−10	7e−10	1 x 1	matrix metallopeptidase 1 (interstitial collagenase) [Source:H
19	55714	−1.4	4e−10	7e−10	1 x 1	teneurin transmembrane protein 3 [Source:HGNC Symbol;Ac
20	9315	−1.4	4e−10	7e−10	3 x 1	neuronal regeneration related protein [Source:HGNC Symbol



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−41.78	NULL	13 / 16	MMML CGS	MACIEJ_MMML 1
2	−38.55	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
3	−36.07	NULL	7 / 11	MF	platelet−derived growth factor binding
4	−33.22	NULL	39 / 190	CC	extracellular matrix
5	−31.7	NULL	42 / 250	Lymphoma	LENZ_Stromal signature 1
6	−30.67	NULL	21 / 64	BP	collagen catabolic process
7	−29.76	NULL	22 / 69	BP	extracellular matrix disassembly
8	−28.87	NULL	4 / 5	GSEA C2	COLLER_MYC_TARGETS_DN
9	−25.96	NULL	9 / 15	GSEA C2	CROMER_TUMORIGENESIS_UP
10	−25.16	NULL	5 / 10	GSEA C2	KEGG_ECM_RECEPTOR_INTERACTION
11	−24.16	NULL	7 / 12	miRNA target	miR−29c
12	−24.09	NULL	7 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_UP
13	−23.71	NULL	7 / 16	GSEA C2	ROZANOV_MMP14_TARGETS_SUBSET
14	−22.9	NULL	14 / 57	MF	extracellular matrix structural constituent
15	−22.69	NULL	12 / 37	BP	collagen fibril organization
16	−22.25	NULL	5 / 13	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
17	−21.9	NULL	5 / 16	GSEA C2	URS_ADIPOCYTE_DIFFERENTIATION_DN
18	−21.52	NULL	38 / 242	BP	extracellular matrix organization
19	−21.41	NULL	5 / 16	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_
20	−20.38	NULL	4 / 10	BP	protein heterotrimerization
21	−20.34	NULL	5 / 10	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C4
22	−19.43	NULL	6 / 16	GSEA C2	CROONQUIST_STROMAL_STIMULATION_UP
23	−19.13	NULL	5 / 16	GSEA C2	REACTOME_SIGNALING_BY_PDGF
24	−18.92	NULL	18 / 119	Lymphoma	ROSOLOWSKI_green total
25	−18.88	NULL	5 / 16	GSEA C2	GU_PDEF_TARGETS_UP
26	−18.87	NULL	3 / 8	GSEA C2	HAEGERSTRAND_RESPONSE_TO_IMATINIB
27	−18.65	NULL	5 / 16	GSEA C2	LIEN_BREAST_CARCINOMA_METAPLASTIC
28	−18.25	NULL	4 / 13	GSEA C2	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
29	−17.92	NULL	7 / 15	GSEA C2	ONDER_CDH1_SIGNALING_VIA_CTNNB1
30	−17.6	NULL	2 / 5	GSEA C2	DASU_IL6_SIGNALING_UP
31	−17.58	NULL	8 / 40	BP	cellular response to amino acid stimulus
32	−17.42	NULL	9 / 35	Glio	Colman_survival_associated
33	−17.27	NULL	22 / 183	CC	proteinaceous extracellular matrix
34	−17.22	NULL	5 / 13	GSEA C2	FRIDMAN_SENESCENCE_UP
35	−17.21	NULL	4 / 15	GSEA C2	REACTOME_NCAM1_INTERACTIONS
36	−17	NULL	6 / 13	GSEA C2	TSAI_RESPONSE_TO_RADIATION_THERAPY
37	−16.86	NULL	1 / 2	miRNA target	miR−18
38	−16.58	NULL	4 / 16	GSEA C2	REACTOME_AXON_GUIDANCE
39	−16.58	NULL	4 / 16	GSEA C2	REACTOME_NCAM_SIGNALING_FOR_NEURITE_OUT_GROWT
40	−16.36	NULL	5 / 15	GSEA C2	LINDGREN_BLADDER_CANCER_HIGH_RECURRENCE

GW_083

Local Summary

%DE = 0.98

metagenes = 14

genes = 253

genes in genesets = 251

genes with fdr < 0.1 = 235 (7 + / 228 −)

genes with fdr < 0.05 = 235 (7 + / 228 −)

genes with fdr < 0.01 = 203 (6 + / 197 −)

<r> metagenes = 0.99

<r> genes = 0.59

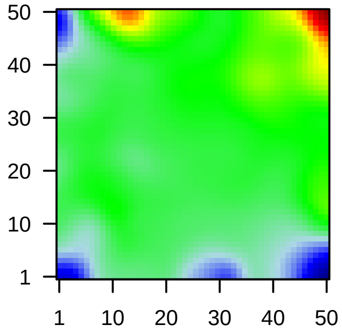
<FC> = −0.7

<shrinkage−t> = −24.59

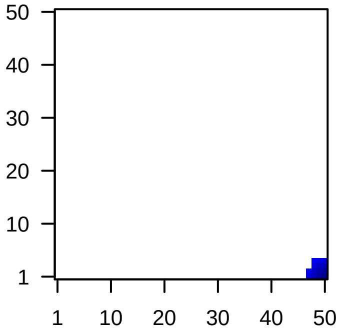
<p−value> = 0

<fdr> = 0.31

Profile



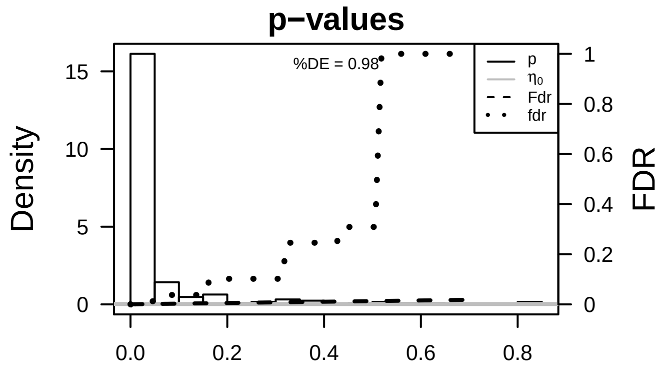
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	3122	−1.88	2e−16	1e−15	50 x 1	major histocompatibility complex, class II, DR alpha [Source:H
2	3108	−1.8	9e−16	9e−15	50 x 1	major histocompatibility complex, class II, DM alpha [Source:I
3	3512	−1.77	3e−15	9e−15	50 x 1	immunoglobulin J polypeptide, linker protein for immunoglobu
4	23180	−1.75	4e−15	7e−13	50 x 1	raftlin, lipid raft linker 1 [Source:HGNC Symbol;Acc:30278]
5	54855	−1.66	1e−13	3e−12	49 x 1	family with sequence similarity 46, member C [Source:HGNC
6	3936	−1.6	9e−13	3e−12	50 x 1	lymphocyte cytosolic protein 1 (L−plastin) [Source:HGNC Syr
7	3109	−1.59	1e−12	4e−12	50 x 1	major histocompatibility complex, class II, DM beta [Source:H
8	3113	−1.57	2e−12	4e−12	50 x 1	major histocompatibility complex, class II, DP alpha 1 [Source
9	3128	−1.56	3e−12	6e−11	50 x 1	major histocompatibility complex, class II, DR beta 6 (pseudo
10	972	−1.51	1e−11	4e−10	50 x 1	CD74 molecule, major histocompatibility complex, class II inva
11	23643	−1.44	1e−10	4e−10	50 x 3	lymphocyte antigen 96 [Source:HGNC Symbol;Acc:17156]
12	10537	−1.43	1e−10	5e−10	50 x 1	ubiquitin D [Source:HGNC Symbol;Acc:18795]
13	3669	−1.42	2e−10	8e−10	48 x 1	interferon stimulated exonuclease gene 20kDa [Source:HGN
14	260436	−1.4	4e−10	8e−10	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symbo
15	51303	−1.39	5e−10	3e−09	49 x 3	FK506 binding protein 11, 19 kDa [Source:HGNC Symbol;Ac
16	152007	−1.37	1e−09	1e−08	50 x 3	GLI pathogenesis−related 2 [Source:HGNC Symbol;Acc:180
17	3002	−1.32	3e−09	1e−08	49 x 1	granzyme B (granzyme 2, cytotoxic T−lymphocyte−associate
18	9404	−1.29	7e−09	1e−08	50 x 1	leupaxin [Source:HGNC Symbol;Acc:14061]
19	57172	−1.29	8e−09	2e−08	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
20	6352	−1.27	1e−08	2e−08	48 x 1	chemokine (C−C motif) ligand 5 [Source:HGNC Symbol;Acc:

p−values



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all		Geneset
1	−37.18	NULL	12 / 15	CC	MHC class II protein complex
2	−25.87	NULL	87 / 417	H.Tiss	WIRTH_Immune system
3	−23.97	NULL	88 / 553	Cancer	Lembcke_Colonic Inflammation
4	−22.32	NULL	3 / 5	GSEA C2	WONG_ENDOMETRIAL_CANCER_LATE
5	−21.69	NULL	15 / 47	BP	antigen processing and presentation
6	−21.48	NULL	47 / 312	BP	immune response
7	−19.88	NULL	2 / 3	GSEA C2	KEGG_VIRAL_MYOCARDITIS
8	−18.88	NULL	6 / 8	Glio	Donson−migration tethering and rolling−associated with LTS in HG
9	−18.74	NULL	7 / 21	CC	clathrin−coated endocytic vesicle membrane
10	−17.94	NULL	40 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
11	−17.94	NULL	40 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
12	−17.94	NULL	40 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
13	−17.94	NULL	40 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
14	−17.85	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
15	−17.82	NULL	7 / 23	CC	integral to lumenal side of endoplasmic reticulum membrane
16	−17.3	NULL	14 / 60	BP	T cell costimulation
17	−16.93	NULL	4 / 8	GSEA C2	GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_DN
18	−16.75	NULL	2 / 4	GSEA C2	KEGG_LEISHMANIA_INFECTION
19	−15.97	NULL	7 / 28	CC	transport vesicle membrane
20	−15.89	NULL	3 / 7	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
21	−15.82	NULL	3 / 6	GSEA C2	SANA_RESPONSE_TO_IFNG_UP
22	−15.66	NULL	6 / 15	GSEA C2	FINAK_BREAST_CANCER_SDPP_SIGNATURE
23	−15.63	NULL	6 / 11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
24	−15.24	NULL	5 / 12	BP	immunoglobulin mediated immune response
25	−15.07	NULL	5 / 12	GSEA C2	BIOCARTA_CTL_PATHWAY
26	−15	NULL	1 / 2	GSEA C2	KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUCT
27	−15	NULL	1 / 2	GSEA C2	KEGG_AUTOIMMUNE_THYROID_DISEASE
28	−15	NULL	1 / 2	GSEA C2	KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS
29	−14.81	NULL	7 / 32	CC	ER to Golgi transport vesicle membrane
30	−14.66	NULL	5 / 11	GSEA C2	BIOCARTA_THELPER_PATHWAY
31	−14.65	NULL	8 / 35	CC	trans−Golgi network membrane
32	−14.62	NULL	17 / 74	BP	regulation of immune response
33	−14.51	NULL	5 / 15	Glio	Donson−chemokines/cytokines−associated with LTS in HGA
34	−14.37	NULL	3 / 8	GSEA C2	LINDSTEDT_DENDRITIC_CELL_MATURATION_D
35	−13.97	NULL	12 / 87	BP	antigen processing and presentation of exogenous peptide antigen
36	−13.94	NULL	5 / 12	GSEA C2	ZHAN_MULTIPLE_MYELOMA_DN
37	−13.63	NULL	5 / 12	BP	dendritic cell chemotaxis
38	−13.6	NULL	5 / 13	GSEA C2	HAHTOLA_CTCL_PATHOGENESIS
39	−13.47	NULL	8 / 52	Chr	Chr HSCHR6_MHC_QBL
40	−13.41	NULL	2 / 6	GSEA C2	LUI_THYROID_CANCER_CLUSTER_4