GW_287

Global Summary

%DE = 0.16

genes with fdr < 0.2 = 2006 (1187 + / 819 −)

genes with fdr < 0.1 = 1730 (1028 + / 702 −)

genes with fdr < 0.05 = 1379 (846 + / 533 −)

genes with fdr < 0.01 = 1051 (666 + / 385 −)

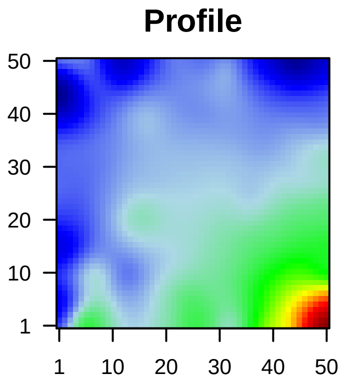
genes in genesets = 16332

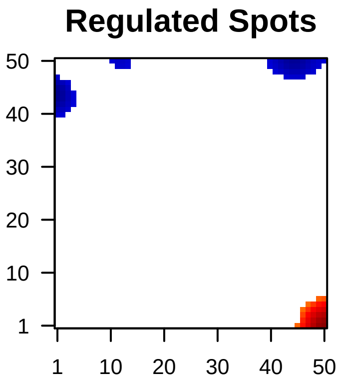
<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.08

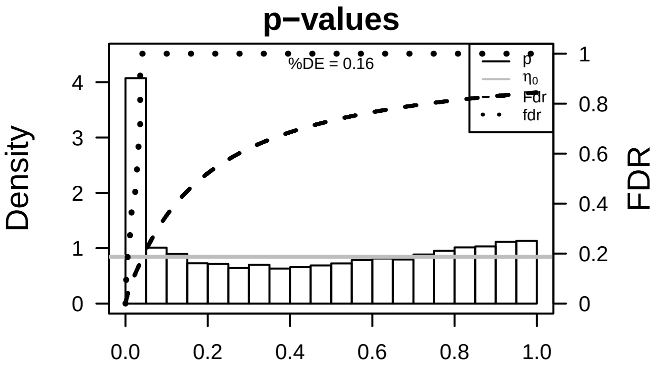
<fdr> = 0.85





Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	25890	2	2e−16	3e−14	50 x 4	ABI family, member 3 (NESH) binding protein [Source:HGNC
2	9744	1.92	2e−16	3e−14	49 x 1	ArfGAP with coiled−coil, ankyrin repeat and PH domains 1 [S
3	58	2.45	2e−16	3e−14	25 x 1	actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
4	57016	−3	2e−16	3e−14	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
5	441282	−2.21	2e−16	3e−14	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC Sy
6	115701	1.92	2e−16	3e−14	50 x 3	alpha−kinase 2 [Source:HGNC Symbol;Acc:20565]
7	55107	−2.27	2e−16	3e−14	1 x 5	anoctamin 1, calcium activated chloride channel [Source:HGN
8	347	2.17	2e−16	3e−14	50 x 7	apolipoprotein D [Source:HGNC Symbol;Acc:612]
9	55843	1.92	2e−16	3e−14	50 x 1	Rho GTPase activating protein 15 [Source:HGNC Symbol;Ac
10	9459	2.03	2e−16	3e−14	50 x 1	Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6 [Sou
11	260436	2.32	2e−16	3e−14	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symbo
12	730	2.22	2e−16	3e−14	49 x 7	complement component 7 [Source:HGNC Symbol;Acc:1346]
13	6358	2.45	2e−16	3e−14	50 x 7	chemokine (C−C motif) ligand 14 [Source:HGNC Symbol;Acc
14	6363	3.84	2e−16	3e−14	50 x 1	chemokine (C−C motif) ligand 19 [Source:HGNC Symbol;Acc
15	6366	3.07	2e−16	3e−14	50 x 2	chemokine (C−C motif) ligand 21 [Source:HGNC Symbol;Acc
16	6355	1.85	2e−16	3e−14	32 x 1	chemokine (C−C motif) ligand 8 [Source:HGNC Symbol;Acc:
17	1236	2.55	2e−16	3e−14	50 x 1	chemokine (C−C motif) receptor 7 [Source:HGNC Symbol;Ac
18	930	3.26	2e−16	3e−14	49 x 1	CD19 molecule [Source:HGNC Symbol;Acc:1633]
19	919	2.17	2e−16	3e−14	50 x 1	CD247 molecule [Source:HGNC Symbol;Acc:1677]
20	939	1.99	2e−16	3e−14	49 x 1	CD27 molecule [Source:HGNC Symbol;Acc:11922]



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	23	NULL	417	H.Tiss	WIRTH_Immune system
2	20.52	NULL	553	Cancer	Lembcke_Colonic Inflammation
3	13.54	NULL	312	BP	immune response
4	11.04	NULL	327	Lymphoma	SPANG_CD40 6hrs UP
5	11.02	NULL	162	CC	external side of plasma membrane
6	10.46	NULL	9	GSEA C2	MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN
7	9.57	NULL	74	BP	regulation of immune response
8	9.49	NULL	8	Glio	Donson−migration tethering and rolling−associated with LTS in HG
9	9.47	NULL	60	BP	T cell costimulation
10	9.26	NULL	11	GSEA C2	BIOCARTA_THELPER_PATHWAY
11	9.25	NULL	11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
12	9.07	NULL	28	BP	B cell receptor signaling pathway
13	8.86	NULL	15	CC	MHC class II protein complex
14	8.55	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
15	8.36	NULL	12	BP	dendritic cell chemotaxis
16	8.27	NULL	16	GSEA C2	SU_THYMUS
17	8.17	NULL	265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
18	8.17	NULL	265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
19	8.17	NULL	265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
20	8.17	NULL	265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
Underexpressed					
1	−17.57	NULL	142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
2	−17.57	NULL	142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
3	−15.65	NULL	530	Cancer	Lembcke_Normal vs Adenoma
4	−13.14	NULL	572	Disease	GUDJ_psoriasis up
5	−12.05	NULL	370	BP	mitotic cell cycle
6	−10.12	NULL	135	H.Tiss	WIRTH_Mucosa
7	−9.05	NULL	76	BP	epidermis development
8	−8.73	NULL	15	GSEA C2	SMID_BREAST_CANCER_LUMINAL_A_DN
9	−8.68	NULL	1233	TF	KIM_MYC targets
10	−8.66	NULL	12	BP	hemidesmosome assembly
11	−8.35	NULL	64	BP	collagen catabolic process
12	−8.06	NULL	232	BP	mitosis
13	−8.02	NULL	69	BP	extracellular matrix disassembly
14	−7.32	NULL	16	GSEA C2	FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
15	−7.28	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_2
16	−7.23	NULL	14	MMML CGS	MACIEJ_MMML 4
17	−7.2	NULL	16	GSEA C2	CROONQUIST_NRAS_VS_STROMAL_STIMULATION_DN
18	−7.15	NULL	148	BP	G1/S transition of mitotic cell cycle
19	−7.14	NULL	10	GSEA C2	MONTERO_THYROID_CANCER_POOR_SURVIVAL_UP
20	−7.13	NULL	13	GSEA C2	CROONQUIST_IL6_DEPRIVATION_DN

GW_287

Local Summary

%DE = 0.98

metagenes = 27

genes = 394

genes in genesets = 391

genes with fdr < 0.1 = 375 (373 + / 2 −)

genes with fdr < 0.05 = 370 (368 + / 2 −)

genes with fdr < 0.01 = 363 (361 + / 2 −)

<r> metagenes = 0.97

<r> genes = 0.52

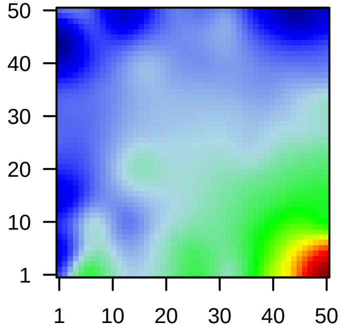
<FC> = 1.31

<shrinkage−t> = 45.71

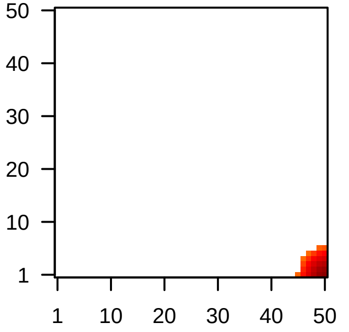
<p−value> = 0

<fdr> = 0.08

Profile



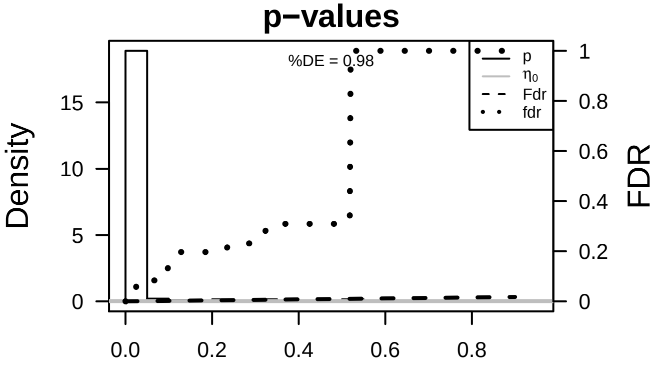
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	25890	2	2e−16	3e−17	50 x 4	ABI family, member 3 (NESH) binding protein [Source:HGNC
2	9744	1.92	2e−16	3e−17	49 x 1	ArfGAP with coiled−coil, ankyrin repeat and PH domains 1 [S
3	115701	1.92	2e−16	3e−17	50 x 3	alpha−kinase 2 [Source:HGNC Symbol;Acc:20565]
4	55843	1.92	2e−16	3e−17	50 x 1	Rho GTPase activating protein 15 [Source:HGNC Symbol;Ac
5	9459	2.03	2e−16	3e−17	50 x 1	Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6 [Sou
6	260436	2.32	2e−16	3e−17	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symbo
7	6363	3.84	2e−16	3e−17	50 x 1	chemokine (C−C motif) ligand 19 [Source:HGNC Symbol;Acc
8	6366	3.07	2e−16	3e−17	50 x 2	chemokine (C−C motif) ligand 21 [Source:HGNC Symbol;Acc
9	1236	2.55	2e−16	3e−17	50 x 1	chemokine (C−C motif) receptor 7 [Source:HGNC Symbol;Ac
10	930	3.26	2e−16	3e−17	49 x 1	CD19 molecule [Source:HGNC Symbol;Acc:1633]
11	919	2.17	2e−16	3e−17	50 x 1	CD247 molecule [Source:HGNC Symbol;Acc:1677]
12	939	1.99	2e−16	3e−17	49 x 1	CD27 molecule [Source:HGNC Symbol;Acc:11922]
13	915	2.13	2e−16	3e−17	49 x 1	CD3d molecule, delta (CD3−TCR complex) [Source:HGNC S
14	962	2.92	2e−16	3e−17	50 x 1	CD48 molecule [Source:HGNC Symbol;Acc:1683]
15	1043	2.31	2e−16	3e−17	50 x 1	CD52 molecule [Source:HGNC Symbol;Acc:1804]
16	969	1.91	2e−16	3e−17	50 x 1	CD69 molecule [Source:HGNC Symbol;Acc:1694]
17	974	1.89	2e−16	3e−17	48 x 1	CD79b molecule, immunoglobulin−associated beta [Source:H
18	7122	1.96	2e−16	3e−17	50 x 6	claudin 5 [Source:HGNC Symbol;Acc:2047]
19	25999	1.89	2e−16	3e−17	50 x 4	CAP−GLY domain containing linker protein 3 [Source:HGNC
20	11151	2.11	2e−16	3e−17	50 x 1	coronin, actin binding protein, 1A [Source:HGNC Symbol;Acc

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	32.29	NULL	106 / 417	H.Tiss	WIRTH_Immune system
2	31.25	NULL	125 / 553	Cancer	Lembcke_Colonic Inflammation
3	19.83	NULL	67 / 312	BP	immune response
4	19.54	NULL	13 / 15	CC	MHC class II protein complex
5	19.24	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
6	18.56	NULL	4 / 9	GSEA C2	MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN
7	18.49	NULL	6 / 8	Glio	Donson−migration tethering and rolling−associated with LTS in HG
8	17.12	NULL	56 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
9	17.12	NULL	56 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
10	17.12	NULL	56 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
11	17.12	NULL	56 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
12	16.23	NULL	7 / 15	GSEA C2	FINAK_BREAST_CANCER_SDPP_SIGNATURE
13	15.93	NULL	7 / 11	GSEA C2	BIOCARTA_THELPER_PATHWAY
14	15.92	NULL	7 / 11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
15	15.76	NULL	7 / 12	GSEA C2	ZHAN_MULTIPLE_MYELOMA_DN
16	15.62	NULL	13 / 28	BP	B cell receptor signaling pathway
17	15.55	NULL	5 / 12	BP	dendritic cell chemotaxis
18	14.83	NULL	20 / 60	BP	T cell costimulation
19	14.78	NULL	19 / 74	BP	regulation of immune response
20	14.69	NULL	8 / 16	GSEA C2	SU_THYMUS
21	14.68	NULL	31 / 162	CC	external side of plasma membrane
22	14.33	NULL	5 / 17	BP	positive regulation of neutrophil chemotaxis
23	14.17	NULL	6 / 10	GSEA C2	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_
24	14.15	NULL	6 / 12	GSEA C2	BIOCARTA_CTL_PATHWAY
25	13.43	NULL	8 / 13	Cancer	GENTLES_modul18
26	13.38	NULL	5 / 10	GSEA C2	LEE_DIFFERENTIATING_T_LYMPHOCYTE
27	12.28	NULL	7 / 13	GSEA C2	BIOCARTA_IL17_PATHWAY
28	12.12	NULL	16 / 47	BP	antigen processing and presentation
29	12.09	NULL	5 / 10	GSEA C2	BIOCARTA_LYM_PATHWAY
30	11.71	NULL	2 / 3	GSEA C2	KEGG_VIRAL_MYOCARDITIS
31	11.57	NULL	5 / 8	GSEA C2	BIOCARTA_TCRA_PATHWAY
32	11.2	NULL	5 / 11	BP	positive regulation of B cell differentiation
33	11.09	NULL	10 / 43	MF	chemokine activity
34	11.08	NULL	4 / 14	BP	ruffle organization
35	11.06	NULL	10 / 28	Lymphoma	DAVE_Immune response 1
36	10.85	NULL	7 / 15	Glio	Donson−chemokines/cytokines−associated with LTS in HGA
37	10.78	NULL	5 / 10	GSEA C2	LEE_EARLY_T_LYMPHOCYTE_DN
38	10.72	NULL	27 / 204	BP	cell surface receptor signaling pathway
39	10.7	NULL	14 / 49	Glio	Donson−innate immunity−associated with LTS in HGA
40	10.66	NULL	6 / 13	GSEA C2	HAHTOLA_CTCL_PATHOGENESIS

GW_287

Local Summary

%DE = 0.85

metagenes = 24

genes = 288

genes in genesets = 282

genes with fdr < 0.1 = 207 (4 + / 203 −)

genes with fdr < 0.05 = 194 (4 + / 190 −)

genes with fdr < 0.01 = 156 (4 + / 152 −)

<r> metagenes = 0.94

<r> genes = 0.36

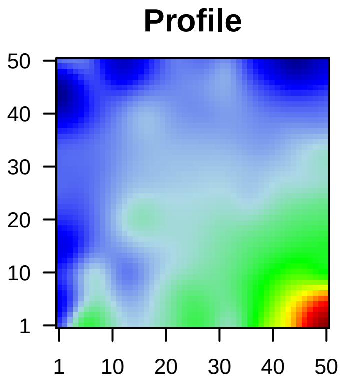
<FC> = −0.74

<shrinkage−t> = −26.11

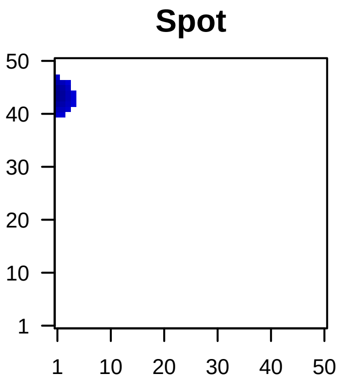
<p−value> = 0

<fdr> = 0.37

Profile

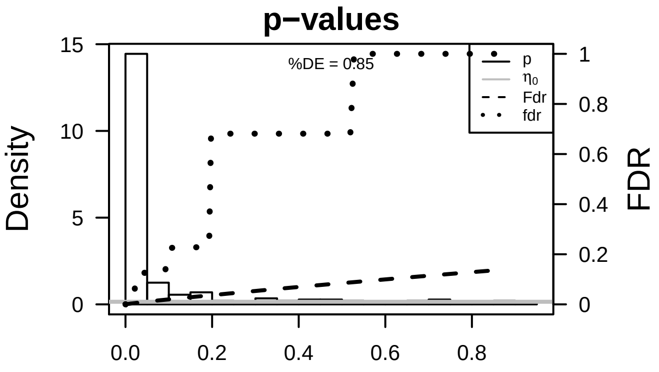


Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	1001	−1.87	2e−16	6e−16	1 x 43	cadherin 3, type 1, P−cadherin (placental) [Source:HGNC Sy
2	9635	−2.03	2e−16	6e−16	1 x 46	chloride channel accessory 2 [Source:HGNC Symbol;Acc:20
3	1825	−1.9	2e−16	6e−16	1 x 45	desmocollin 3 [Source:HGNC Symbol;Acc:3037]
4	2171	−1.87	2e−16	6e−16	1 x 46	fatty acid binding protein 5 (psoriasis−associated) [Source:H
5	10804	−1.92	2e−16	6e−16	1 x 47	gap junction protein, beta 6, 30kDa [Source:HGNC Symbol;A
6	3861	−2.45	2e−16	6e−16	1 x 45	keratin 14 [Source:HGNC Symbol;Acc:6416]
7	3868	−3.14	2e−16	6e−16	1 x 46	keratin 16 [Source:HGNC Symbol;Acc:6423]
8	3872	−2.21	2e−16	6e−16	1 x 43	keratin 17 [Source:HGNC Symbol;Acc:6427]
9	3852	−2.11	2e−16	6e−16	1 x 44	keratin 5 [Source:HGNC Symbol;Acc:6442]
10	55214	−2.14	2e−16	6e−16	1 x 42	leprecan−like 1 [Source:HGNC Symbol;Acc:19317]
11	3963	−2.48	2e−16	6e−16	1 x 47	lectin, galactoside−binding, soluble, 7 [Source:HGNC Symbol
12	653499	−2.28	2e−16	6e−16	1 x 47	lectin, galactoside−binding, soluble, 7 [Source:HGNC Symbol
13	5317	−1.93	2e−16	6e−16	1 x 46	plakophilin 1 (ectodermal dysplasia/skin fragility syndrome) [S
14	5744	−2.18	2e−16	6e−16	1 x 43	parathyroid hormone−like hormone [Source:HGNC Symbol;A
15	5947	−2.21	2e−16	6e−16	1 x 43	retinol binding protein 1, cellular [Source:HGNC Symbol;Acc:
16	144406	−2.14	2e−16	6e−16	1 x 42	WD repeat domain 66 [Source:HGNC Symbol;Acc:28506]
17	1308	−1.84	4e−16	2e−13	1 x 43	collagen, type XVII, alpha 1 [Source:HGNC Symbol;Acc:2194
18	6513	−1.77	5e−15	7e−13	1 x 43	solute carrier family 2 (facilitated glucose transporter), membe
19	3613	−1.72	3e−14	7e−13	1 x 46	inositol(myo)−1(or 4)−monophosphatase 2 [Source:HGNC Sy
20	8140	−1.71	4e−14	7e−13	1 x 43	solute carrier family 7 (amino acid transporter light chain, L sy



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−25.93	NULL	26 / 135	H.Tiss	WIRTH_Mucosa
2	−21.39	NULL	19 / 82	CC	intermediate filament
3	−20.58	NULL	16 / 76	BP	epidermis development
4	−20.18	NULL	5 / 12	BP	hemidesmosome assembly
5	−18.62	NULL	7 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
6	−18.37	NULL	9 / 44	CC	keratin filament
7	−17.62	NULL	4 / 13	BP	intermediate filament cytoskeleton organization
8	−15.72	NULL	66 / 572	Disease	GUDJ_psoriasis up
9	−15.67	NULL	8 / 21	CC	desmosome
10	−14.3	NULL	11 / 82	MF	structural constituent of cytoskeleton
11	−13.77	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
12	−13.74	NULL	5 / 15	GSEA C2	AIGNER_ZEB1_TARGETS
13	−13.1	NULL	2 / 8	GSEA C2	DORN_ADENOVIRUS_INFECTION_24HR_UP
14	−12.53	NULL	18 / 186	MF	structural molecule activity
15	−12.17	NULL	3 / 25	BP	response to zinc ion
16	−11.59	NULL	4 / 12	GSEA C2	REACTOME_GAP_JUNCTION_ASSEMBLY
17	−11.27	NULL	3 / 17	BP	morphogenesis of an epithelium
18	−11.15	NULL	3 / 35	CC	cell periphery
19	−10.99	NULL	4 / 38	BP	epithelial cell differentiation
20	−10.59	NULL	2 / 15	GSEA C2	SMID_BREAST_CANCER_LUMINAL_A_DN
21	−10.55	NULL	4 / 13	GSEA C2	REACTOME_GAP_JUNCTION_TRAFFICKING
22	−10.5	NULL	3 / 16	GSEA C2	BECKER_TAMOXIFEN_RESISTANCE_DN
23	−10.2	NULL	4 / 15	CC	connexon complex
24	−10.11	NULL	2 / 2	miRNA target	miR−199a*
25	−9.6	NULL	3 / 12	BP	keratinocyte proliferation
26	−9.51	NULL	6 / 70	BP	cell junction assembly
27	−9.5	NULL	5 / 21	CC	gap junction
28	−9.21	NULL	2 / 15	GSEA C2	NGUYEN_NOTCH1_TARGETS_UP
29	−8.95	NULL	8 / 44	BP	skin development
30	−8.93	NULL	1 / 5	miRNA target	miR−196a
31	−8.86	NULL	2 / 9	GSEA C2	RODWELL_AGING_KIDNEY_UP
32	−8.8	NULL	2 / 16	GSEA C2	DORN_ADENOVIRUS_INFECTION_12HR_UP
33	−8.72	NULL	5 / 32	CC	cell−cell adherens junction
34	−8.53	NULL	2 / 15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
35	−8.46	NULL	4 / 20	MF	scaffold protein binding
36	−8.3	NULL	3 / 16	BP	ectoderm development
37	−8.29	NULL	2 / 16	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_LUNG_UP
38	−8.17	NULL	3 / 11	GSEA C2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_G_UP
39	−7.96	NULL	3 / 16	GSEA C2	YANG_BREAST_CANCER_ESR1_DN
40	−7.79	NULL	3 / 10	MF	gap junction channel activity

GW_287

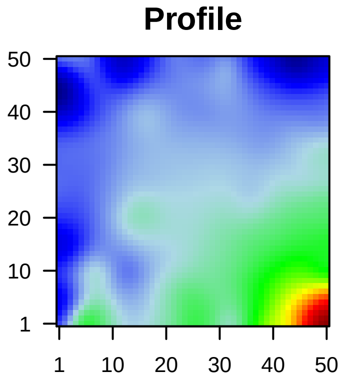
Local Summary

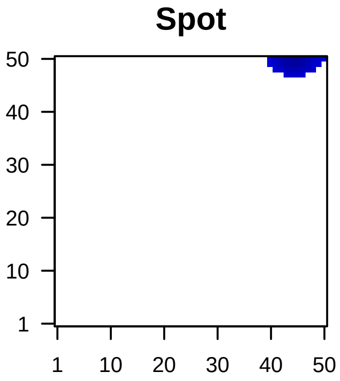
%DE = 0.88
metagenes = 33
genes = 505
genes in genesets = 501

genes with fdr < 0.1 = 418 (5 + / 413 −)
genes with fdr < 0.05 = 326 (2 + / 324 −)
genes with fdr < 0.01 = 222 (2 + / 220 −)

<r> metagenes = 0.87
<r> genes = 0.29

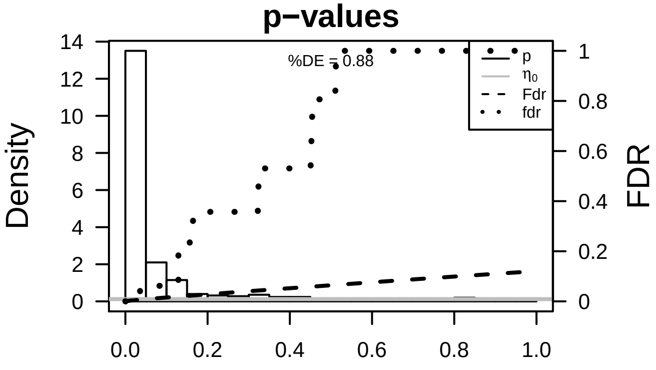
<FC> = −0.6
<shrinkage−t> = −21.15
<p−value> = 0
<fdr> = 0.46


Profile


Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	4072	−1.92	2e−16	7e−15	50 x 50	epithelial cell adhesion molecule [Source:HGNC Symbol;Acc:
2	256764	−2.81	2e−16	7e−15	50 x 50	WD repeat domain 72 [Source:HGNC Symbol;Acc:26790]
3	54443	−1.74	2e−14	4e−10	43 x 50	anillin, actin binding protein [Source:HGNC Symbol;Acc:1408
4	51659	−1.56	6e−12	6e−10	44 x 50	GINS complex subunit 2 (Psf2 homolog) [Source:HGNC Sym
5	7083	−1.52	2e−11	3e−09	45 x 49	thymidine kinase 1, soluble [Source:HGNC Symbol;Acc:1183
6	1894	−1.47	9e−11	3e−09	45 x 50	epithelial cell transforming sequence 2 oncogene [Source:HG
7	55165	−1.46	1e−10	3e−09	44 x 50	centrosomal protein 55kDa [Source:HGNC Symbol;Acc:1161
8	22974	−1.45	2e−10	3e−09	44 x 50	TPX2, microtubule−associated [Source:HGNC Symbol;Acc:1
9	9055	−1.43	2e−10	3e−09	45 x 49	protein regulator of cytokinesis 1 [Source:HGNC Symbol;Acc:
10	9319	−1.43	2e−10	2e−08	43 x 50	thyroid hormone receptor interactor 13 [Source:HGNC Symbo
11	116832	−1.39	8e−10	2e−08	46 x 50	ribosomal protein L39−like [Source:HGNC Symbol;Acc:1709
12	655	−1.39	8e−10	3e−08	50 x 50	bone morphogenetic protein 7 [Source:HGNC Symbol;Acc:10
13	81831	−1.37	1e−09	3e−08	42 x 50	neuropilin (NRP) and tolloid (TLL)−like 2 [Source:HGNC Sym
14	7153	−1.36	2e−09	6e−08	45 x 49	topoisomerase (DNA) II alpha 170kDa [Source:HGNC Symbo
15	339512	−1.34	3e−09	6e−08	50 x 50	chromosome 1 open reading frame 110 [Source:HGNC Symb
16	113130	−1.33	4e−09	6e−08	44 x 49	cell division cycle associated 5 [Source:HGNC Symbol;Acc:1
17	29968	−1.32	5e−09	1e−07	49 x 50	phosphoserine aminotransferase 1 [Source:HGNC Symbol;A
18	8318	−1.31	8e−09	1e−07	45 x 49	cell division cycle 45 [Source:HGNC Symbol;Acc:1739]
19	9833	−1.3	9e−09	1e−07	44 x 50	maternal embryonic leucine zipper kinase [Source:HGNC Sy
20	136	−1.29	1e−08	1e−07	41 x 50	adenosine A2b receptor [Source:HGNC Symbol;Acc:264]


p−values

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−53.41	NULL	87 / 142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
2	−53.41	NULL	87 / 142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
3	−25.95	NULL	15 / 16	GSEA C2	FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
4	−25.92	NULL	13 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_2
5	−25.61	NULL	23 / 57	Glio	developing astrocytes
6	−25.44	NULL	94 / 370	BP	mitotic cell cycle
7	−24.81	NULL	11 / 13	GSEA C2	CROONQUIST_IL6_DEPRIVATION_DN
8	−24.36	NULL	14 / 15	GSEA C2	FINETTI_BREAST_CANCER_KINOME_RED
9	−23.93	NULL	92 / 530	Cancer	Lembcke_Normal vs Adenoma
10	−23.86	NULL	11 / 14	MMML CGS	MACIEJ_MMML 4
11	−23.67	NULL	8 / 10	GSEA C2	MONTERO_THYROID_CANCER_POOR_SURVIVAL_UP
12	−22.97	NULL	12 / 16	GSEA C2	EGUCHI_CELL_CYCLE_RB1_TARGETS
13	−20.89	NULL	10 / 14	GSEA C2	ZHAN_MULTIPLE_MYELOMA_PR_UP
14	−19.96	NULL	12 / 18	BP	spindle organization
15	−19.35	NULL	11 / 15	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
16	−19.34	NULL	10 / 15	GSEA C2	LEE_EARLY_T_LYMPHOCYTE_UP
17	−19.2	NULL	10 / 16	GSEA C2	KANG_DOXORUBICIN_RESISTANCE_UP
18	−18.89	NULL	69 / 572	Disease	GUDJ_psoriasis up
19	−18.85	NULL	10 / 16	GSEA C2	CROONQUIST_NRAS_SIGNALING_DN
20	−18.66	NULL	11 / 16	Cancer	WOLFER_overlap genes
21	−18.3	NULL	8 / 15	GSEA C2	SMID_BREAST_CANCER_LUMINAL_A_DN
22	−18.02	NULL	9 / 16	GSEA C2	GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
23	−17.64	NULL	47 / 232	BP	mitosis
24	−17.59	NULL	9 / 14	GSEA C2	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
25	−17.1	NULL	8 / 14	GSEA C2	AMUNDSON_GAMMA_RADIATION_RESPONSE
26	−16.88	NULL	11 / 15	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
27	−16.87	NULL	36 / 149	BP	DNA replication
28	−16.77	NULL	10 / 15	GSEA C2	FOURNIER_ACINAR_DEVELOPMENT_LATE_DN
29	−16.77	NULL	8 / 15	GSEA C2	WU_APOPTOSIS_BY_CDKN1A_VIA_TP53
30	−16.29	NULL	8 / 16	GSEA C2	CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_UP
31	−16.22	NULL	10 / 16	GSEA C2	REACTOME_G2_M_CHECKPOINTS
32	−16.11	NULL	7 / 11	GSEA C2	KALMA_E2F1_TARGETS
33	−15.94	NULL	5 / 8	GSEA C2	REACTOME_E2F_TRANSCRIPTIONAL_TARGETS_AT_G1_S
34	−15.78	NULL	8 / 15	GSEA C2	BOYAULT_LIVER_CANCER_SUBCLASS_G23_UP
35	−15.61	NULL	7 / 16	GSEA C2	FRASOR_RESPONSE_TO_SERM_OR_FULVESTRANT_DN
36	−15.61	NULL	7 / 11	GSEA C2	ODONNELL_TFRC_TARGETS_DN
37	−15.59	NULL	8 / 15	GSEA C2	CHANG_CYCLING_GENES
38	−15.22	NULL	8 / 13	GSEA C2	WINNEPENNINCKX_MELANOMA_METASTASIS_UP
39	−15.09	NULL	20 / 56	CC	chromosome, centromeric region
40	−15.02	NULL	8 / 15	GSEA C2	LY_AGING_MIDDLE_DN

GW_287

Local Summary

%DE = 0.96

metagenes = 7

genes = 118

genes in genesets = 118

genes with fdr < 0.1 = 110 (0 + / 110 −)

genes with fdr < 0.05 = 94 (0 + / 94 −)

genes with fdr < 0.01 = 87 (0 + / 87 −)

<r> metagenes = 0.98

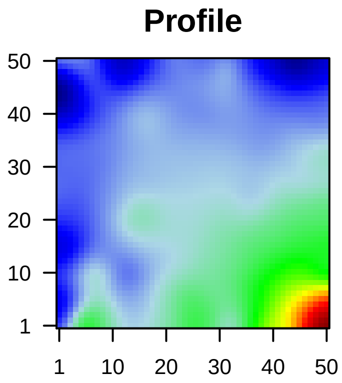
<r> genes = 0.29

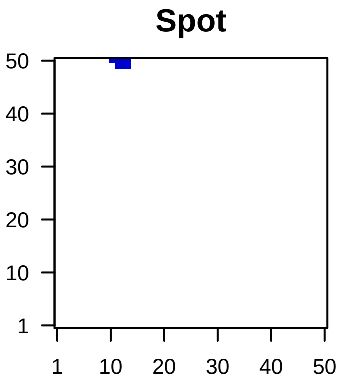
<FC> = −0.69

<shrinkage−t> = −24.22

<p−value> = 0

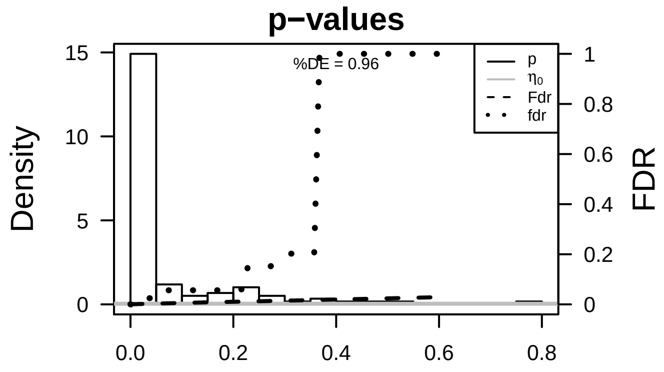
<fdr> = 0.38





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	483	−1.55	8e−12	2e−11	13 x 50	ATPase, Na+/K+ transporting, beta 3 polypeptide [Source:HG
2	5217	−1.54	1e−11	2e−11	14 x 50	profilin 2 [Source:HGNC Symbol;Acc:8882]
3	1109	−1.53	1e−11	2e−09	13 x 50	aldo−keto reductase family 1, member C4 [Source:HGNC Sy
4	8626	−1.41	4e−10	2e−09	13 x 50	tumor protein p63 [Source:HGNC Symbol;Acc:15979]
5	55971	−1.39	9e−10	2e−08	13 x 50	BAI1−associated protein 2−like 1 [Source:HGNC Symbol;Acc
6	3321	−1.33	5e−09	2e−08	13 x 50	immunoglobulin superfamily, member 3 [Source:HGNC Symb
7	57834	−1.3	9e−09	4e−08	13 x 50	cytochrome P450, family 4, subfamily F, polypeptide 11 [Sour
8	57007	−1.26	3e−08	4e−08	14 x 50	atypical chemokine receptor 3 [Source:HGNC Symbol;Acc:23
9	2817	−1.26	3e−08	4e−08	14 x 50	glypican 1 [Source:HGNC Symbol;Acc:4449]
10	140809	−1.25	4e−08	2e−07	13 x 50	sulfiredoxin 1 [Source:HGNC Symbol;Acc:16132]
11	10610	−1.22	7e−08	4e−07	12 x 50	ST6 (alpha−N−acetyl−neuraminyl−2,3−beta−galactosyl−1,3)−
12	6319	−1.18	2e−07	4e−07	12 x 50	stearoyl−CoA desaturase (delta−9−desaturase) [Source:HGN
13	53637	−1.16	3e−07	4e−07	12 x 50	sphingosine−1−phosphate receptor 5 [Source:HGNC Symbol
14	406988	−1.15	4e−07	4e−07	12 x 50	MIR205 host gene (non−protein coding) [Source:HGNC Syml
15	1717	−1.15	4e−07	1e−06	13 x 50	7−dehydrocholesterol reductase [Source:HGNC Symbol;Acc:
16	10653	−1.06	6e−07	1e−06	12 x 50	serine peptidase inhibitor, Kunitz type, 2 [Source:HGNC Syml
17	2950	−1.02	1e−06	1e−06	12 x 50	glutathione S−transferase pi 1 [Source:HGNC Symbol;Acc:46
18	9069	−1.1	1e−06	1e−06	14 x 50	claudin 12 [Source:HGNC Symbol;Acc:2034]
19	4055	−1.09	1e−06	1e−06	14 x 50	lymphotoxin beta receptor (TNFR superfamily, member 3) [Sc
20	8323	−1.09	2e−06	2e−06	14 x 50	frizzled family receptor 6 [Source:HGNC Symbol;Acc:4044]



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−11.88	NULL	3 / 15	GSEA C2	PODAR_RESPONSE_TO_ADAPHOSTIN_DN
2	−11.48	NULL	2 / 13	GSEA C2	KEGG_PROXIMAL_TUBULE_BICARBONATE_RECLAMATION
3	−11.06	NULL	2 / 9	Glio	Colman_survival_robust
4	−10.96	NULL	2 / 12	miRNA target-starBase	hsa-miR-1249
5	−10.59	NULL	1 / 2	Cancer	GENTLES_modul8
6	−10.57	NULL	2 / 15	GSEA C2	KEGG_ALDOSTERONE_REGULATED_SODIUM_REABSORPTIO
7	−10.03	NULL	3 / 13	GSEA C2	SINGH_NFE2L2_TARGETS
8	−10.01	NULL	3 / 15	GSEA C2	WAMUNYOKOLI_OVARIAN_CANCER_LMP_UP
9	−9.94	NULL	2 / 10	GSEA C2	REACTOME_TRANSFORMATION_OF_LANOSTEROL_TO_CHOL
10	−9.86	NULL	1 / 2	miRNA target	miR−124a
11	−9.74	NULL	2 / 13	GSEA C2	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_MONOCYT
12	−9.33	NULL	2 / 14	GSEA C2	RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_DN
13	−9	NULL	2 / 14	GSEA C2	REACTOME_ACTIVATION_OF_RAC
14	−8.97	NULL	2 / 15	GSEA C2	RUTELLA_RESPONSE_TO_HGF_UP
15	−8.93	NULL	3 / 31	BP	positive regulation of actin filament polymerization
16	−8.83	NULL	1 / 6	GSEA C2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_D_DN
17	−8.74	NULL	3 / 19	BP	anatomical structure formation involved in morphogenesis
18	−8.68	NULL	1 / 5	GSEA C2	OHM_EMBRYONIC_CARCINOMA_UP
19	−8.64	NULL	2 / 16	GSEA C2	RUTELLA_RESPONSE_TO_CSF2RB_AND_IL4_UP
20	−8.38	NULL	1 / 8	TF Tissue	VAQUERIZAS_Tongue
21	−8.33	NULL	1 / 7	Glio	Donson−cytotoxic effectors−associated with LTS in HGA
22	−8.19	NULL	2 / 16	GSEA C2	SESTO_RESPONSE_TO_UV_C7
23	−8.08	NULL	2 / 12	GSEA C2	TIMOFEEVA_GROWTH_STRESS_VIA_STAT1_DN
24	−8.08	NULL	2 / 12	GSEA C2	LI_LUNG_CANCER
25	−8.05	NULL	1 / 10	GSEA C2	TARTE_PLASMA_CELL_VS_PLASMABLAST_DN
26	−8.05	NULL	1 / 10	GSEA C2	HOSHIDA_LIVER_CANCER_SUBCLASS_S1
27	−8	NULL	1 / 5	GSEA C2	SHARMA_ASTROCYTOMA_WITH_NF1_SYNDROM
28	−7.99	NULL	3 / 39	BP	retinoid metabolic process
29	−7.9	NULL	3 / 12	GSEA C2	DELLA_RESPONSE_TO_TSA_AND_BUTYRATE
30	−7.85	NULL	2 / 16	GSEA C2	REACTOME_BASIGIN_INTERACTIONS
31	−7.84	NULL	2 / 15	GSEA C2	REACTOME_CHOLESTEROL_BIOSYNTHESIS
32	−7.65	NULL	2 / 15	GSEA C2	KANG_FLUOROURACIL_RESISTANCE_UP
33	−7.64	NULL	2 / 13	BP	smooth muscle tissue development
34	−7.6	NULL	2 / 10	H.Tiss	WIRTH_B−cells
35	−7.55	NULL	2 / 16	GSEA C2	KEGG_STEROID_BIOSYNTHESIS
36	−7.31	NULL	2 / 14	GSEA C2	SHAFFER_IRF4_TARGETS_IN_ACTIVATED_B_LYMPHOCYTE
37	−7.24	NULL	2 / 15	GSEA C2	JEON_SMAD6_TARGETS_DN
38	−7.23	NULL	1 / 12	GSEA C2	SCHLOSSER_MYC_TARGETS_AND_SERUM_RESPONSE_UP
39	−7.23	NULL	1 / 12	GSEA C2	KEGG_CARDIAC_MUSCLE_CONTRACTION
40	−7.19	NULL	1 / 8	GSEA C2	JAZAG_TGFB1_SIGNALING_VIA_SMAD4_DN