GW_018

Global Summary

%DE = 0.13

genes with fdr < 0.2 = 1564 (781 + / 783 −)

genes with fdr < 0.1 = 1108 (550 + / 558 −)

genes with fdr < 0.05 = 864 (431 + / 433 −)

genes with fdr < 0.01 = 653 (329 + / 324 −)

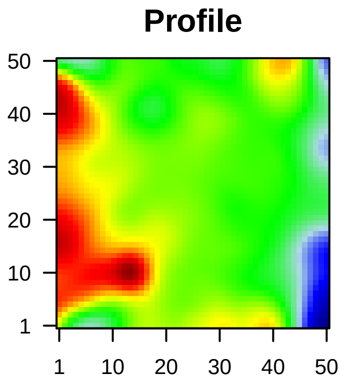
genes in genesets = 16332

<FC> = 0

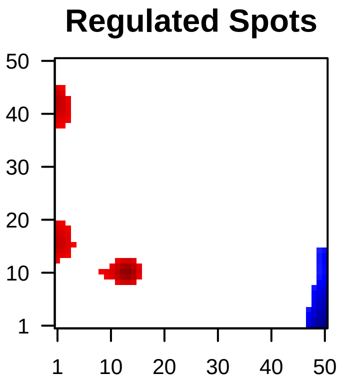
<shrinkage−t> = 0

<p−value> = 0.13

<fdr> = 0.87



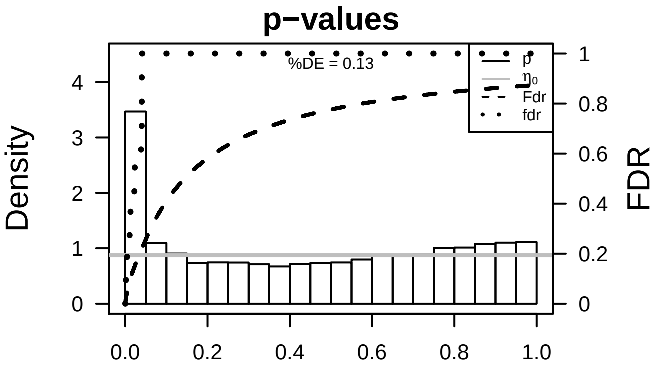
Profile



Regulated Spots

Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	131	−2.69	2e−16	5e−14	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	218	−2.32	2e−16	5e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
3	810	−2.01	2e−16	5e−14	1 x 50	calmodulin−like 3 [Source:HGNC Symbol;Acc:1452]
4	51806	−1.83	2e−16	5e−14	4 x 50	calmodulin−like 5 [Source:HGNC Symbol;Acc:18180]
5	57172	−2.31	2e−16	5e−14	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
6	1041	2.22	2e−16	5e−14	1 x 46	corneodesmosin [Source:HGNC Symbol;Acc:1802]
7	1675	1.86	2e−16	5e−14	50 x 9	complement factor D (adipsin) [Source:HGNC Symbol;Acc:27
8	22802	−2.21	2e−16	5e−14	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
9	1281	−1.71	2e−16	5e−14	2 x 1	collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]
10	49860	−2.67	2e−16	5e−14	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
11	441520	3.1	2e−16	5e−14	14 x 11	cancer/testis antigen family 45, member A2 [Source:HGNC S
12	55894	1.8	2e−16	5e−14	1 x 47	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
13	414325	1.91	2e−16	5e−14	1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
14	1809	−1.96	2e−16	5e−14	6 x 1	dihydropyrimidinase−like 3 [Source:HGNC Symbol;Acc:3015]
15	1917	1.82	2e−16	5e−14	25 x 1	eukaryotic translation elongation factor 1 alpha 2 [Source:HG
16	2152	1.98	2e−16	5e−14	1 x 43	coagulation factor III (thromboplastin, tissue factor) [Source:H
17	2201	1.76	2e−16	5e−14	1 x 5	fibrillin 2 [Source:HGNC Symbol;Acc:3604]
18	8857	−1.87	2e−16	5e−14	50 x 13	Fc fragment of IgG binding protein [Source:HGNC Symbol;Ac
19	2312	2.63	2e−16	5e−14	1 x 49	filaggrin [Source:HGNC Symbol;Acc:3748]
20	2318	1.96	2e−16	5e−14	25 x 1	filamin C, gamma [Source:HGNC Symbol;Acc:3756]



p−values

Global Geneset Analysis

Rank	GSZ	p−value	#all		Geneset
Overexpressed					
1	9.65	NULL	1135	Chr	Chr 19
2	8.39	NULL	530	Cancer	Lembcke_Normal vs Adenoma
3	7.51	NULL	142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
4	7.51	NULL	142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
5	7.14	NULL	6	GSEA C2	SEIKE_LUNG_CANCER_POOR_SURVIVAL
6	7.02	NULL	4	MMML CGS	MACIEJ_MMML 23
7	6.88	NULL	8	GSEA C2	NIKOLSKY_BREAST_CANCER_5P15_AMPLICON
8	6.64	NULL	572	Disease	GUDJ_psoriasis up
9	5.98	NULL	21	CC	cornified envelope
10	5.57	NULL	15	MF	interleukin−1 receptor binding
11	5.34	NULL	10	GSEA C2	BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
12	5.29	NULL	4	GSEA C2	BUDHU_LIVER_CANCER_METASTASIS_DN
13	5.29	NULL	1720	Chr	Chr 1
14	5.26	NULL	76	BP	epidermis development
15	5.12	NULL	13	GSEA C2	BOWIE_RESPONSE_TO_TAMOXIFEN
16	5.1	NULL	16	GSEA C2	XU_HGF_TARGETS_INDUCED_BY_AKT1_6HR
17	5.08	NULL	12	BP	hemidesmosome assembly
18	5.05	NULL	9	GSEA C2	HEDVAT_ELF4_TARGETS_UP
19	5	NULL	11	MF	substrate−specific transmembrane transporter activity
20	4.9	NULL	10	CC	hemoglobin complex
Underexpressed					
1	−10.32	NULL	250	Lymphoma	LENZ_Stromal signature 1
2	−10.2	NULL	15	CC	MHC class II protein complex
3	−9	NULL	553	Cancer	Lembcke_Colonic Inflammation
4	−8.46	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
5	−7.85	NULL	1033	Chr	Chr 2
6	−7.81	NULL	417	H.Tiss	WIRTH_Immune system
7	−7.47	NULL	190	CC	extracellular matrix
8	−7.35	NULL	602	Chr	Chr 10
9	−7.08	NULL	16	MMML CGS	MACIEJ_MMML 1
10	−6.85	NULL	13	GSEA C2	LINDGREN_BLADDER_CANCER_CLUSTER_2B
11	−6.48	NULL	119	BP	xenobiotic metabolic process
12	−6.41	NULL	463	miRNA target sites	hsa−miR−301a
13	−6.33	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_D
14	−6.18	NULL	47	BP	antigen processing and presentation
15	−6.14	NULL	12	GSEA C2	ZHAN_MULTIPLE_MYELOMA_DN
16	−6.06	NULL	456	miRNA target sites	hsa−miR−130a
17	−5.91	NULL	9	GSEA C2	REACTOME_ETHANOL_OXIDATION
18	−5.71	NULL	232	Chr	Chr 18
19	−5.64	NULL	6	GSEA C2	SANA_RESPONSE_TO_IFNG_UP
20	−5.63	NULL	449	miRNA target sites	hsa−miR−130b

GW_018

Local Summary

%DE = 0.6

metagenes = 29

genes = 143

genes in genesets = 118

genes with fdr < 0.1 = 62 (61 + / 1 −)

genes with fdr < 0.05 = 61 (60 + / 1 −)

genes with fdr < 0.01 = 48 (48 + / 0 −)

<r> metagenes = 0.91

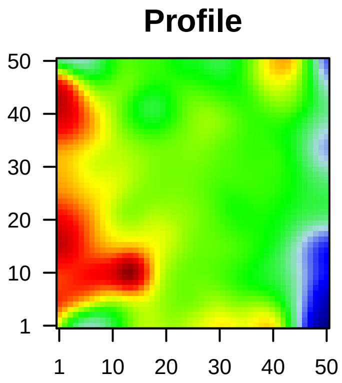
<r> genes = 0.22

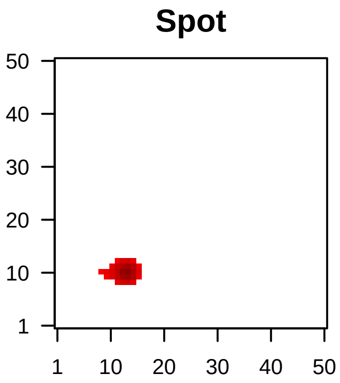
<FC> = 0.67

<shrinkage−t> = 23.46

<p−value> = 0

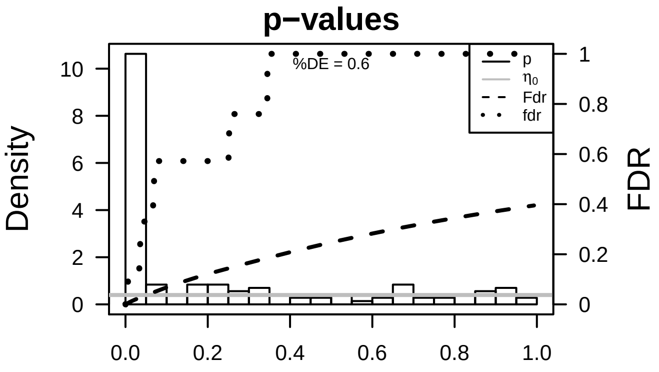
<fdr> = 0.53





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	441520	3.1	2e−16	7e−16	14 x 11	cancer/testis antigen family 45, member A2 [Source:HGNC S
2	729428	2.54	2e−16	7e−16	14 x 11	G antigen 12C [Source:HGNC Symbol;Acc:28402]
3	729422	2.75	2e−16	7e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
4	100008586	2.43	2e−16	7e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
5	645073	2.56	2e−16	7e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
6	729442	2.74	2e−16	7e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
7	26748	2.07	2e−16	7e−16	14 x 11	G antigen 12I [Source:HGNC Symbol;Acc:4105]
8	729396	2.07	2e−16	7e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
9	729447	2.16	2e−16	7e−16	14 x 11	G antigen 2A [Source:HGNC Symbol;Acc:4099]
10	645037	2.91	2e−16	7e−16	14 x 11	G antigen 2C [Source:HGNC Symbol;Acc:31958]
11	26749	2.08	2e−16	7e−16	14 x 11	G antigen 2E [Source:HGNC Symbol;Acc:31960]
12	2576	2.62	2e−16	7e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
13	2577	2.28	2e−16	7e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
14	4100	2.29	2e−16	7e−16	14 x 11	melanoma antigen family A, 1 (directs expression of antigen
15	4109	3.11	2e−16	7e−16	14 x 11	melanoma antigen family A, 10 [Source:HGNC Symbol;Acc:6
16	4103	1.77	2e−16	7e−16	14 x 10	melanoma antigen family A, 4 [Source:HGNC Symbol;Acc:68
17	653219	2.43	2e−16	7e−16	14 x 11	X antigen family, member 1B [Source:HGNC Symbol;Acc:254
18	84944	1.71	2e−15	8e−13	15 x 11	maelstrom spermatogenic transposon silencer [Source:HGN
19	100101629	1.64	2e−14	8e−13	14 x 11	G antigen 2E [Source:HGNC Symbol;Acc:31960]
20	653048	1.63	3e−14	3e−11	14 x 11	X antigen family, member 1B [Source:HGNC Symbol;Acc:254



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	15.46	NULL	30 / 630	Chr	Chr X
2	14.8	NULL	1 / 11	GSEA C2	SU_PLACENTA
3	12.87	NULL	1 / 14	GSEA C2	NIELSEN_GIST
4	12.27	NULL	2 / 15	GSEA C2	BROWNE_HCMV_INFECTION_8HR_DN
5	8.53	NULL	1 / 10	BP	piRNA metabolic process
6	8.53	NULL	1 / 10	CC	XY body
7	8.45	NULL	3 / 15	GSEA C2	MATTIOLI_MULTIPLE_MYELOMA_SUBGROUPS
8	8.07	NULL	1 / 6	GSEA C2	NIELSEN_LEIOMYOSARCOMA_UP
9	8.06	NULL	1 / 11	BP	regulation of organ growth
10	7.44	NULL	1 / 21	BP	negative regulation of Notch signaling pathway
11	7.3	NULL	1 / 13	BP	synapsis
12	7.24	NULL	1 / 14	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_B
13	6.98	NULL	1 / 14	BP	DNA methylation involved in gamete generation
14	6.85	NULL	1 / 5	GSEA C2	CHOI_ATL_ACUTE_STAGE
15	6.76	NULL	1 / 2	GSEA C2	KUROKAWA_LIVER_CANCER_EARLY_RECURRENCE_UP
16	6.7	NULL	1 / 4	GSEA C2	WEBER_METHYLATED_ICP_IN_SPERM_DN
17	6.14	NULL	1 / 12	GSEA C2	RAY_TARGETS_OF_P210_BCR_ABL_FUSION_UP
18	5.75	NULL	2 / 8	GSEA C2	WEBER_METHYLATED_ICP_IN_FIBROBLAST
19	5.18	NULL	2 / 22	BP	male meiosis
20	5.17	NULL	3 / 21	BP	chromatin organization
21	5.15	NULL	1 / 6	GSEA C2	NIELSEN_GIST_VS_SYNOVIAL_SARCOMA_UP
22	4.99	NULL	1 / 8	GSEA C2	HEIDENBLAD_AMPLIFIED_IN_PANCREATIC_CANCER
23	4.94	NULL	2 / 68	MF	histone deacetylase binding
24	4.86	NULL	9 / 120	H.Tiss	WIRTH_Testis
25	4.72	NULL	1 / 27	BP	gene silencing by RNA
26	4.67	NULL	1 / 7	GSEA C2	NIELSEN_SYNOVIAL_SARCOMA_UP
27	4.43	NULL	1 / 10	GSEA C2	TSUNODA_CISPLATIN_RESISTANCE_DN
28	4.23	NULL	9 / 419	CC	cellular_component
29	4.21	NULL	2 / 10	GSEA C2	XU_GH1_AUTOCRINE_TARGETS_DN
30	4.2	NULL	2 / 13	CC	STAGA complex
31	4.18	NULL	1 / 33	BP	fertilization
32	4	NULL	1 / 15	GSEA C2	KEGG_INOSITOL_PHOSPHATE_METABOLISM
33	3.91	NULL	1 / 12	GSEA C2	HOSHIDA_LIVER_CANCER_SURVIVAL_UP
34	3.88	NULL	1 / 12	MF	calcium−dependent cysteine−type endopeptidase activity
35	3.88	NULL	1 / 12	miRNA target−starBase	hsa−miR−671−3p
36	3.88	NULL	11 / 481	BP	biological_process
37	3.8	NULL	2 / 16	GSEA C2	DAVICIONI_TARGETS_OF_PAX_FOXO1_FUSIONS_DN
38	3.72	NULL	1 / 10	BP	paraxial mesoderm development
39	3.7	NULL	1 / 12	GSEA C2	HO_LIVER_CANCER_VASCULAR_INVASION
40	3.59	NULL	2 / 48	Cancer	KUIPER_MM poor survival

GW_018

Local Summary

%DE = 0.67

metagenes = 22

genes = 277

genes in genesets = 276

genes with fdr < 0.1 = 105 (105 + / 0 −)

genes with fdr < 0.05 = 90 (90 + / 0 −)

genes with fdr < 0.01 = 35 (35 + / 0 −)

<r> metagenes = 0.95

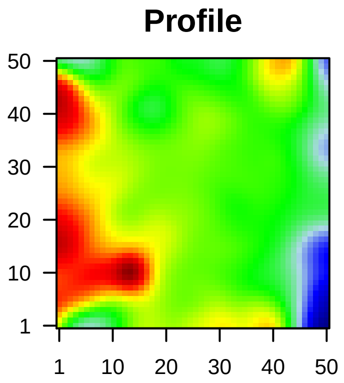
<r> genes = 0.29

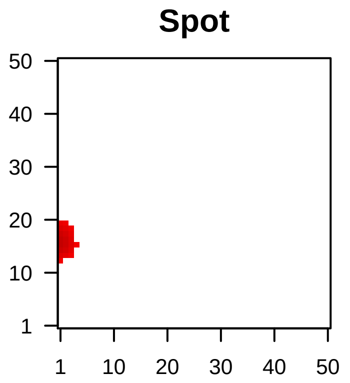
<FC> = 0.37

<shrinkage−t> = 13.05

<p−value> = 0.03

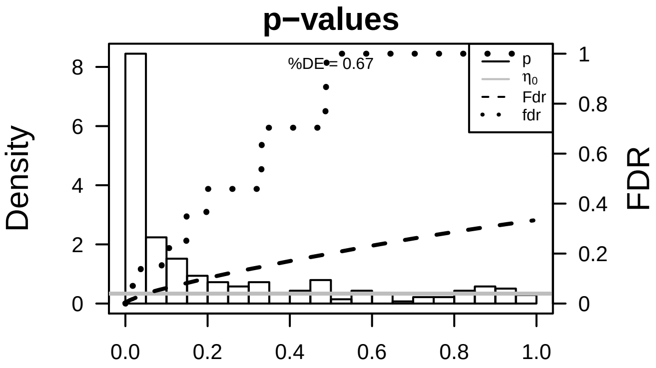
<fdr> = 0.69





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	51083	2	2e−16	2e−14	1 x 15	galanin/GMAP prepropeptide [Source:HGNC Symbol;Acc:41
2	10202	1.51	2e−12	8e−06	1 x 15	dehydrogenase/reductase (SDR family) member 2 [Source:H
3	23246	1.13	2e−07	8e−06	1 x 16	block of proliferation 1 [Source:HGNC Symbol;Acc:15519]
4	6535	1.13	2e−07	9e−06	1 x 16	solute carrier family 6 (neurotransmitter transporter), member
5	4728	1.11	3e−07	2e−04	2 x 17	NADH dehydrogenase (ubiquinone) Fe−S protein 8, 23kDa (
6	1152	1.02	2e−06	3e−04	1 x 17	creatine kinase, brain [Source:HGNC Symbol;Acc:1991]
7	430	0.95	1e−05	3e−04	2 x 20	achaete−scute family bHLH transcription factor 2 [Source:HG
8	92856	0.94	1e−05	3e−04	1 x 18	IMP4, U3 small nucleolar ribonucleoprotein, homolog (yeast)
9	3237	0.94	1e−05	3e−04	1 x 16	homeobox D11 [Source:HGNC Symbol;Acc:5134]
10	219931	0.93	1e−05	4e−04	1 x 14	two pore segment channel 2 [Source:HGNC Symbol;Acc:208
11	2194	0.91	2e−05	4e−04	1 x 17	fatty acid synthase [Source:HGNC Symbol;Acc:3594]
12	131076	0.91	3e−05	4e−04	1 x 16	coiled−coil domain containing 58 [Source:HGNC Symbol;Acc
13	10428	0.9	3e−05	1e−03	1 x 15	craniofacial development protein 1 [Source:HGNC Symbol;Ac
14	7407	0.87	5e−05	1e−03	3 x 15	valyl−tRNA synthetase [Source:HGNC Symbol;Acc:12651]
15	7422	0.84	9e−05	1e−03	1 x 13	vascular endothelial growth factor A [Source:HGNC Symbol;
16	81037	0.84	1e−04	1e−03	1 x 14	CLPTM1−like [Source:HGNC Symbol;Acc:24308]
17	2932	0.83	1e−04	1e−03	1 x 17	glycogen synthase kinase 3 beta [Source:HGNC Symbol;Acc
18	51042	0.83	1e−04	1e−03	1 x 19	zinc finger protein 593 [Source:HGNC Symbol;Acc:30943]
19	113655	0.83	1e−04	1e−03	1 x 18	major facilitator superfamily domain containing 3 [Source:HG
20	55257	0.82	1e−04	1e−03	1 x 15	MRG/MORF4L binding protein [Source:HGNC Symbol;Acc:1



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	14.78	NULL	2 / 7	GSEA C2	CAFFAREL_RESPONSE_TO_THC_24HR_5_UP
2	13.43	NULL	1 / 6	GSEA C2	REACTOME_CLASS_A1_RHODOPSIN_LIKE_RECEPTORS
3	13.43	NULL	1 / 6	GSEA C2	REACTOME_GPCR_LIGAND_BINDING
4	12.77	NULL	2 / 10	GSEA C2	ZHU_CMV_24_HR_UP
5	12.77	NULL	2 / 10	GSEA C2	ZHU_CMV_ALL_UP
6	12.34	NULL	1 / 7	GSEA C2	REACTOME_PEPTIDE_LIGAND_BINDING_RECEPTORS
7	11.54	NULL	2 / 11	GSEA C2	SCIBETTA_KDM5B_TARGETS_DN
8	11.47	NULL	1 / 8	GSEA C2	SAMOLS_TARGETS_OF_KHSV_MIRNAS_UP
9	11.47	NULL	1 / 8	GSEA C2	REACTOME_G_ALPHA_I_SIGNALLING_EVENTS
10	11	NULL	2 / 12	GSEA C2	BHATTACHARYA_EMBRYONIC_STEM_CELL
11	10.93	NULL	2 / 10	BP	creatine metabolic process
12	10.89	NULL	2 / 18	BP	smooth muscle contraction
13	10.82	NULL	1 / 3	GSEA C2	KEGG_OXIDATIVE_PHOSPHORYLATION
14	10.82	NULL	1 / 3	GSEA C2	KEGG_PARKINSONS_DISEASE
15	10.14	NULL	1 / 10	GSEA C2	WELCSH_BRCA1_TARGETS_1_DN
16	10.14	NULL	1 / 10	GSEA C2	TAKAO_RESPONSE_TO_UVB_RADIATION_UP
17	9.92	NULL	2 / 14	GSEA C2	KRASNOSELSKAYA_ILF3_TARGETS_DN
18	9.92	NULL	2 / 15	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_7
19	9.62	NULL	1 / 11	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_BONE_DN
20	9.62	NULL	1 / 11	GSEA C2	PARK_APL_PATHOGENESIS_DN
21	9.38	NULL	14 / 96	BP	rRNA processing
22	9.28	NULL	2 / 16	GSEA C2	BROWNE_HCMV_INFECTION_24HR_UP
23	9.21	NULL	1 / 4	GSEA C2	REACTOME_GLUCOSE_REGULATION_OF_INSULIN_SECRETI
24	9.21	NULL	1 / 4	GSEA C2	REACTOME_INTEGRATION_OF_ENERGY_METABOLISM
25	9.21	NULL	1 / 4	GSEA C2	REACTOME_REGULATION_OF_INSULIN_SECRETION
26	9.06	NULL	3 / 10	GSEA C2	KEGG_HUNTINGTONS_DISEASE
27	9.01	NULL	2 / 13	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_C
28	8.94	NULL	2 / 8	GSEA C2	NIKOLSKY_BREAST_CANCER_5P15_AMPLICON
29	8.76	NULL	1 / 13	GSEA C2	KORKOLA_EMBRYONIC_CARCINOMA_VS_SEMINOMA_UP
30	8.4	NULL	1 / 14	GSEA C2	FARMER_BREAST_CANCER_BASAL_VS_LULMINAL
31	8.4	NULL	1 / 14	GSEA C2	LIEN_BREAST_CARCINOMA_METAPLASTIC_VS_DUCTAL_UP
32	8.13	NULL	1 / 5	GSEA C2	REACTOME_ELECTRON_TRANSPORT_CHAIN
33	8.08	NULL	1 / 15	MF	neuropeptide hormone activity
34	8.08	NULL	1 / 15	GSEA C2	NAGASHIMA_NRG1_SIGNALING_UP
35	8.08	NULL	1 / 15	GSEA C2	FERNANDEZ_BOUND_BY_MYC
36	8.03	NULL	2 / 11	BP	positive regulation of protein complex assembly
37	7.91	NULL	4 / 13	GSEA C2	XU_RESPONSE_TO_TRETINOIN_AND_NSC682994_DN
38	7.89	NULL	3 / 14	GSEA C2	KEGG_COLORECTAL_CANCER
39	7.79	NULL	1 / 16	GSEA C2	DOANE_BREAST_CANCER_ESR1_DN
40	7.79	NULL	1 / 16	GSEA C2	TAVOR_CEBPA_TARGETS_DN

GW_018

Local Summary

%DE = 0.68

metagenes = 21

genes = 255

genes in genesets = 250

genes with fdr < 0.1 = 119 (109 + / 10 −)

genes with fdr < 0.05 = 101 (92 + / 9 −)

genes with fdr < 0.01 = 87 (80 + / 7 −)

<r> metagenes = 0.97

<r> genes = 0.33

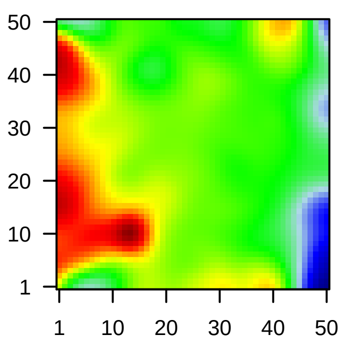
<FC> = 0.4

<shrinkage−t> = 14.09

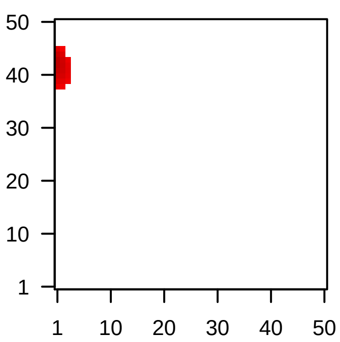
<p−value> = 0

<fdr> = 0.56

Profile



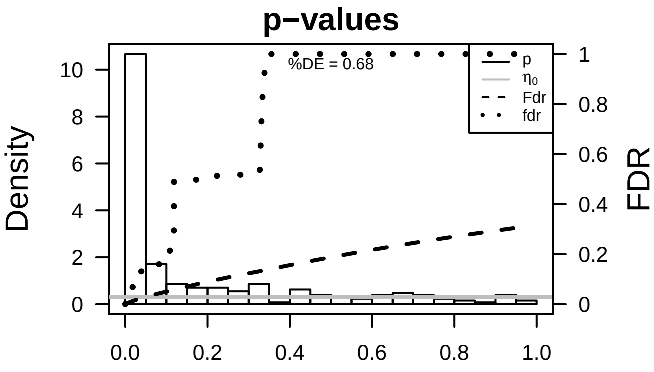
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	2152	1.98	2e−16	4e−15	1 x 43	coagulation factor III (thromboplastin, tissue factor) [Source:H
2	2731	1.76	2e−16	4e−15	1 x 38	glycine dehydrogenase (decarboxylating) [Source:HGNC Syn
3	3552	2.27	2e−16	4e−15	1 x 43	interleukin 1, alpha [Source:HGNC Symbol;Acc:5991]
4	5947	−2.25	2e−16	4e−15	1 x 43	retinol binding protein 1, cellular [Source:HGNC Symbol;Acc:
5	6339	1.76	2e−16	4e−15	1 x 45	sodium channel, non−voltage−gated 1, delta subunit [Source:
6	760	1.75	4e−16	3e−13	1 x 44	carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
7	154	1.69	4e−15	8e−12	1 x 40	adrenoceptor beta 2, surface [Source:HGNC Symbol;Acc:28
8	2352	1.6	1e−13	1e−10	1 x 42	folate receptor 3 (gamma) [Source:HGNC Symbol;Acc:3795]
9	7280	1.52	2e−12	1e−10	1 x 45	tubulin, beta 2A class IIa [Source:HGNC Symbol;Acc:12412]
10	5744	1.5	3e−12	3e−09	1 x 43	parathyroid hormone−like hormone [Source:HGNC Symbol;A
11	3861	1.31	3e−11	5e−09	1 x 45	keratin 14 [Source:HGNC Symbol;Acc:6416]
12	80115	1.39	9e−11	8e−09	1 x 43	BAI1−associated protein 2−like 2 [Source:HGNC Symbol;Acc
13	56901	1.37	2e−10	2e−08	1 x 44	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4−li
14	8942	−1.34	5e−10	2e−08	1 x 40	kynureninase [Source:HGNC Symbol;Acc:6469]
15	116211	1.33	6e−10	3e−08	1 x 43	Transmembrane 4 L6 family member 19 [Source:UniProtKB/
16	25819	1.31	1e−09	1e−07	1 x 41	CCR4 carbon catabolite repression 4−like (S. cerevisiae) [Sou
17	6513	1.28	2e−09	4e−07	1 x 43	solute carrier family 2 (facilitated glucose transporter), membe
18	9052	1.24	7e−09	4e−07	1 x 40	G protein−coupled receptor, family C, group 5, member A [So
19	50805	1.22	1e−08	4e−07	1 x 43	iroquois homeobox 4 [Source:HGNC Symbol;Acc:6129]
20	693159	1.21	2e−08	1e−06	1 x 39	microRNA 574 [Source:HGNC Symbol;Acc:32830]

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset
1	14.9	NULL	1 / 4	GSEA C2 BUDHU_LIVER_CANCER_METASTASIS_DN
2	12.53	NULL	5 / 12	BP hemidesmosome assembly
3	11.78	NULL	1 / 6	GSEA C2 SEIKE_LUNG_CANCER_POOR_SURVIVAL
4	11.57	NULL	4 / 15	GSEA C2 KOBAYASHI_EGFR_SIGNALING_6HR_DN
5	11.09	NULL	2 / 2	miRNA target miR−199a*
6	10.52	NULL	3 / 16	GSEA C2 UZONYI_RESPONSE_TO_LEUKOTRIENE_AND_THROMBIN
7	10.28	NULL	1 / 6	GSEA C2 MAINA_HYPOXIA_VHL_TARGETS_UP
8	10.13	NULL	2 / 13	GSEA C2 HASINA_NOL7_TARGETS_UP
9	9.98	NULL	3 / 16	GSEA C2 HARRIS_HYPOXIA
10	9.29	NULL	2 / 11	BP positive regulation of positive chemotaxis
11	8.8	NULL	1 / 10	GSEA C2 BIOCARTA_LYM_PATHWAY
12	8.8	NULL	3 / 13	GSEA C2 WANG_METHYLATED_IN_BREAST_CANCER
13	8.68	NULL	2 / 14	GSEA C2 HOEGERKORP_CD44_TARGETS_DIRECT_UP
14	8.63	NULL	3 / 16	GSEA C2 LEONARD_HYPOXIA
15	8.51	NULL	2 / 15	GSEA C2 HINATA_NFKB_TARGETS_KERATINOCYTE_DN
16	8.31	NULL	2 / 13	BP response to copper ion
17	8.28	NULL	2 / 15	GSEA C2 NAGASHIMA_NRG1_SIGNALING_DN
18	8.24	NULL	2 / 6	GSEA C2 KORKOLA_EMBRYONAL_CARCINOMA
19	8.13	NULL	3 / 12	GSEA C2 MIZUKAMI_HYPOXIA_UP
20	7.97	NULL	4 / 78	BP positive regulation of angiogenesis
21	7.96	NULL	2 / 14	GSEA C2 MAINA_VHL_TARGETS_DN
22	7.93	NULL	1 / 12	GSEA C2 BIOCARTA_ERYTH_PATHWAY
23	7.67	NULL	1 / 10	GSEA C2 REACTOME_FORMATION_OF_FIBRIN_CLOT_CLOTTING_CAS
24	7.63	NULL	2 / 14	BP positive regulation of osteoclast differentiation
25	7.58	NULL	1 / 13	BP positive regulation of interleukin−2 biosynthetic process
26	7.45	NULL	2 / 8	GSEA C2 SIMBULAN_UV_RESPONSE_NORMAL_UP
27	7.42	NULL	2 / 25	BP response to zinc ion
28	7.35	NULL	3 / 15	GSEA C2 REACTOME_FORMATION_OF_TUBULIN_FOLDING_INTERMED
29	7.35	NULL	3 / 15	GSEA C2 REACTOME_POST_CHAPERONIN_TUBULIN_FOLDING_PATHW
30	7.33	NULL	1 / 5	GSEA C2 RODRIGUES_DCC_TARGETS_UP
31	7.26	NULL	1 / 11	GSEA C2 BIOCARTA_EXTRINSIC_PATHWAY
32	7.18	NULL	1 / 9	GSEA C2 HEDVAT_ELF4_TARGETS_UP
33	7.15	NULL	2 / 8	GSEA C2 MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_UP
34	7.11	NULL	3 / 15	GSEA C2 AMIT_EGF_RESPONSE_240_MCF10A
35	7.08	NULL	2 / 15	BP response to osmotic stress
36	7.07	NULL	8 / 76	BP epidermis development
37	7.07	NULL	1 / 7	GSEA C2 BEGUM_TARGETS_OF_PAX3_FOXO1_FUSION_AND_PAX3
38	7	NULL	2 / 8	GSEA C2 LIU_CDX2_TARGETS_DN
39	6.98	NULL	2 / 17	BP morphogenesis of an epithelium
40	6.98	NULL	1 / 15	MF interleukin−1 receptor binding

GW_018

Local Summary

%DE = 0.86

metagenes = 42

genes = 606

genes in genesets = 603

genes with fdr < 0.1 = 397 (12 + / 385 −)

genes with fdr < 0.05 = 367 (11 + / 356 −)

genes with fdr < 0.01 = 237 (9 + / 228 −)

<r> metagenes = 0.78

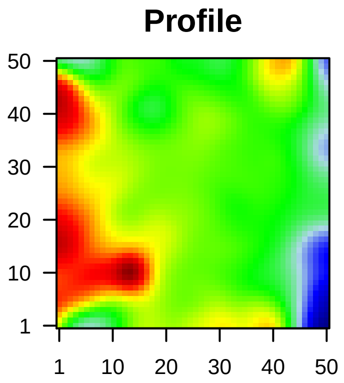
<r> genes = 0.3

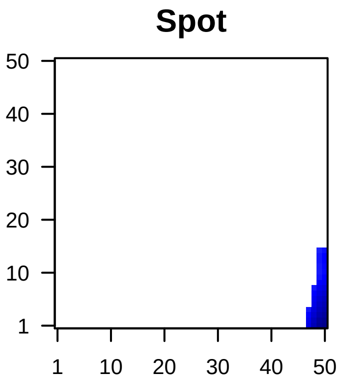
<FC> = −0.53

<shrinkage−t> = −18.47

<p−value> = 0

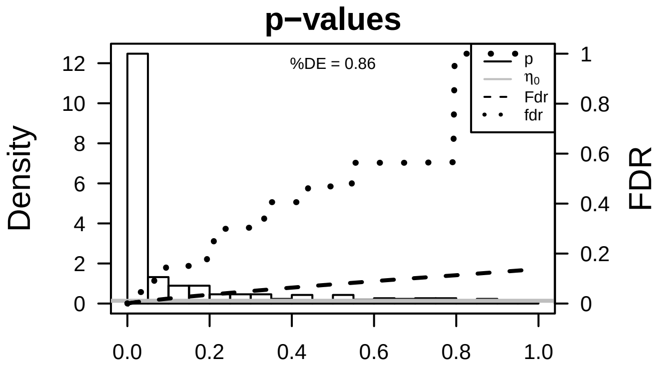
<fdr> = 0.49





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	57172	−2.31	2e−16	2e−15	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
2	1675	1.86	2e−16	2e−15	50 x 9	complement factor D (adipsin) [Source:HGNC Symbol;Acc:27
3	8857	−1.87	2e−16	2e−15	50 x 13	Fc fragment of IgG binding protein [Source:HGNC Symbol;Ac
4	3109	−1.84	2e−16	2e−15	50 x 1	major histocompatibility complex, class II, DM beta [Source:H
5	3113	−1.84	2e−16	2e−15	50 x 1	major histocompatibility complex, class II, DP alpha 1 [Source
6	3122	−1.97	2e−16	2e−15	50 x 1	major histocompatibility complex, class II, DR alpha [Source:
7	3512	−2.03	2e−16	2e−15	50 x 1	immunoglobulin J polypeptide, linker protein for immunoglobu
8	3543	−3.25	2e−16	2e−15	49 x 1	immunoglobulin lambda−like polypeptide 1 [Source:HGNC Sy
9	10232	3.42	2e−16	2e−15	50 x 11	mesothelin [Source:HGNC Symbol;Acc:7371]
10	5341	1.77	2e−16	2e−15	50 x 1	pleckstrin [Source:HGNC Symbol;Acc:9070]
11	10537	−1.74	4e−16	4e−13	50 x 1	ubiquitin D [Source:HGNC Symbol;Acc:18795]
12	51755	−1.68	5e−15	3e−12	49 x 1	cyclin−dependent kinase 12 [Source:HGNC Symbol;Acc:242
13	3108	−1.62	5e−14	3e−12	50 x 1	major histocompatibility complex, class II, DM alpha [Source:
14	2568	−1.61	8e−14	3e−12	50 x 13	gamma−aminobutyric acid (GABA) A receptor, pi [Source:HG
15	894	−1.6	1e−13	6e−12	50 x 4	cyclin D2 [Source:HGNC Symbol;Acc:1583]
16	260436	−1.58	2e−13	6e−12	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symbo
17	6363	−1.57	3e−13	6e−12	50 x 1	chemokine (C−C motif) ligand 19 [Source:HGNC Symbol;Acc
18	5920	−1.57	3e−13	2e−11	48 x 1	retinoic acid receptor responder (tazarotene induced) 3 [Sour
19	5996	−1.55	6e−13	2e−11	50 x 1	regulator of G−protein signaling 1 [Source:HGNC Symbol;Acc
20	972	−1.54	8e−13	2e−10	50 x 1	CD74 molecule, major histocompatibility complex, class II inv



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−28.95	NULL	12 / 15	CC	MHC class II protein complex
2	−17.62	NULL	16 / 47	BP	antigen processing and presentation
3	−17.32	NULL	60 / 312	BP	immune response
4	−15.98	NULL	121 / 553	Cancer	Lembcke_Colonic Inflammation
5	−15.59	NULL	3 / 6	GSEA C2	SANA_RESPONSE_TO_IFNG_UP
6	−15.54	NULL	3 / 5	GSEA C2	WONG_ENDOMETRIAL_CANCER_LATE
7	−15.46	NULL	14 / 16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_D
8	−14.84	NULL	9 / 28	CC	transport vesicle membrane
9	−14.83	NULL	7 / 21	CC	clathrin−coated endocytic vesicle membrane
10	−14.09	NULL	7 / 23	CC	integral to lumenal side of endoplasmic reticulum membrane
11	−14.01	NULL	94 / 417	H.Tiss	WIRTH_Immune system
12	−13.72	NULL	4 / 7	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
13	−13.11	NULL	5 / 9	GSEA C2	MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN
14	−12.85	NULL	6 / 7	GSEA C2	LOPEZ_MESOTELIOMA_SURVIVAL_TIME_DN
15	−12.78	NULL	2 / 4	MMML CGS	MACIEJ_MMML 2
16	−12.72	NULL	9 / 35	CC	trans−Golgi network membrane
17	−12.56	NULL	14 / 60	BP	T cell costimulation
18	−12.28	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
19	−11.77	NULL	4 / 8	GSEA C2	GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_DN
20	−11.65	NULL	7 / 32	CC	ER to Golgi transport vesicle membrane
21	−11.12	NULL	6 / 11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
22	−10.96	NULL	3 / 6	GSEA C2	LUI_THYROID_CANCER_CLUSTER_4
23	−10.91	NULL	7 / 8	Glio	Donson−migration tethering and rolling−associated with LTS in HG
24	−10.91	NULL	1 / 6	H.Tiss	WIRTH_Bone marrow
25	−10.69	NULL	4 / 7	Glio	Donson−cytotoxic effectors−associated with LTS in HGA
26	−10.67	NULL	13 / 87	BP	antigen processing and presentation of exogenous peptide antigen
27	−10.19	NULL	10 / 46	CC	endocytic vesicle membrane
28	−9.94	NULL	5 / 8	GSEA C2	NIELSEN_SYNOVIAL_SARCOMA_DN
29	−9.74	NULL	5 / 12	BP	immunoglobulin mediated immune response
30	−9.7	NULL	5 / 12	GSEA C2	BIOCARTA_CTL_PATHWAY
31	−9.68	NULL	11 / 60	BP	interferon−gamma−mediated signaling pathway
32	−9.65	NULL	8 / 52	Chr	Chr HSCHR6_MHC_QBL
33	−9.64	NULL	5 / 11	GSEA C2	BIOCARTA_THELPER_PATHWAY
34	−9.62	NULL	6 / 15	Glio	Donson−chemokines/cytokines−associated with LTS in HGA
35	−9.55	NULL	2 / 3	GSEA C2	KEGG_VIRAL_MYOCARDITIS
36	−9.44	NULL	15 / 84	BP	T cell receptor signaling pathway
37	−9.34	NULL	3 / 9	GSEA C2	GUTIERREZ_WALDENSTROEMS_MACROGLOBULINEMIA_2
38	−9.26	NULL	4 / 11	GSEA C2	GUTIERREZ_CHRONIC_LYMPHOCYTIC_LEUKEMIA_UP
39	−9.23	NULL	5 / 17	BP	positive regulation of neutrophil chemotaxis
40	−9.17	NULL	1 / 2	GSEA C2	KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUCT