GW_034

Global Summary

%DE = 0.14

genes with fdr < 0.2 = 1715 (791 + / 924 −)

genes with fdr < 0.1 = 1323 (583 + / 740 −)

genes with fdr < 0.05 = 1012 (426 + / 586 −)

genes with fdr < 0.01 = 657 (272 + / 385 −)

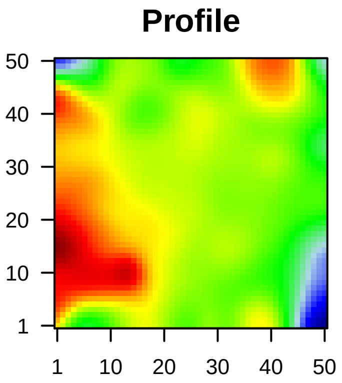
genes in genesets = 16332

<FC> = 0

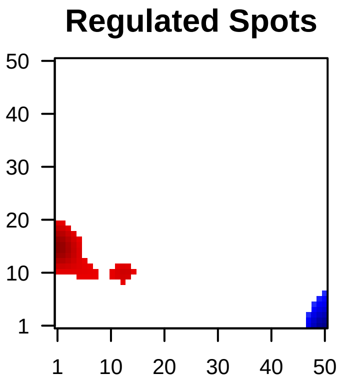
<shrinkage−t> = 0

<p−value> = 0.12

<fdr> = 0.87



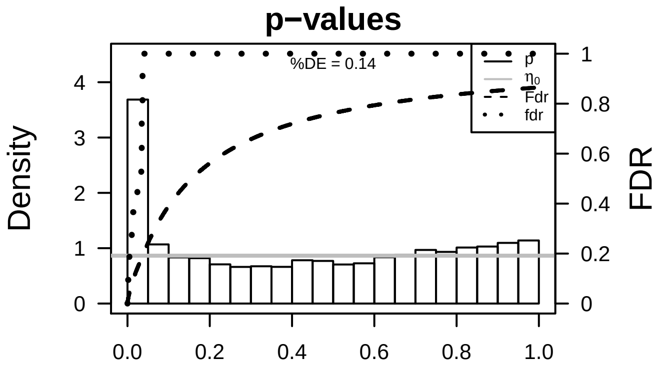
Profile



Regulated Spots

Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	131	−2.15	2e−16	5e−14	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	216	−1.84	2e−16	5e−14	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGNC
3	218	−1.93	2e−16	5e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
4	55107	2.09	2e−16	5e−14	1 x 5	anoctamin 1, calcium activated chloride channel [Source:HGN
5	164284	1.79	2e−16	5e−14	1 x 3	adenomatosis polyposis coli down−regulated 1−like [Source:
6	713	−1.74	2e−16	5e−14	50 x 1	complement component 1, q subcomponent, B chain [Source
7	768	1.91	2e−16	5e−14	1 x 6	carbonic anhydrase IX [Source:HGNC Symbol;Acc:1383]
8	919	−1.86	2e−16	5e−14	50 x 1	CD247 molecule [Source:HGNC Symbol;Acc:1677]
9	972	−1.82	2e−16	5e−14	50 x 1	CD74 molecule, major histocompatibility complex, class II inv
10	22802	−1.76	2e−16	5e−14	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
11	1396	1.78	2e−16	5e−14	50 x 5	cysteine−rich protein 1 (intestinal) [Source:HGNC Symbol;Ac
12	4283	−1.82	2e−16	5e−14	49 x 1	chemokine (C−X−C motif) ligand 9 [Source:HGNC Symbol;Ac
13	92196	−1.9	2e−16	5e−14	3 x 50	death associated protein−like 1 [Source:HGNC Symbol;Acc:2
14	414325	1.81	2e−16	5e−14	1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
15	1673	−1.92	2e−16	5e−14	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
16	26298	−1.72	2e−16	5e−14	4 x 50	ets homologous factor [Source:HGNC Symbol;Acc:3246]
17	2012	−1.95	2e−16	5e−14	3 x 50	epithelial membrane protein 1 [Source:HGNC Symbol;Acc:33
18	2354	−2.13	2e−16	5e−14	22 x 50	FBJ murine osteosarcoma viral oncogene homolog B [Source
19	10468	1.82	2e−16	5e−14	1 x 5	follistatin [Source:HGNC Symbol;Acc:3971]
20	729428	1.96	2e−16	5e−14	14 x 11	G antigen 12C [Source:HGNC Symbol;Acc:28402]



p−values

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	10	NULL	4	MMML CGS	MACIEJ_MMML 23
2	9.09	NULL	519	Chr	Chr 14
3	8.45	NULL	717	Chr	Chr 16
4	8.15	NULL	4640	CC	nucleus
5	7.91	NULL	1135	Chr	Chr 19
6	7.79	NULL	530	Cancer	Lembcke_Normal vs Adenoma
7	7.72	NULL	142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
8	7.72	NULL	142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
9	7.7	NULL	8	GSEA C2	NIKOLSKY_BREAST_CANCER_5P15_AMPLICON
10	7.41	NULL	940	MF	nucleic acid binding
11	6.9	NULL	10	CC	hemoglobin complex
12	6.73	NULL	949	CC	nucleoplasm
13	6.42	NULL	1749	MF	DNA binding
14	6.29	NULL	649	BP	gene expression
15	6.28	NULL	370	BP	mitotic cell cycle
16	6.26	NULL	449	Chr	Chr 20
17	6.21	NULL	96	BP	rRNA processing
18	6.14	NULL	579	CC	nucleolus
19	6.05	NULL	1574	BP	transcription, DNA−templated
20	5.93	NULL	743	Chr	Chr 7
Underexpressed					
1	−13.81	NULL	553	Cancer	Lembcke_Colonic Inflammation
2	−13.2	NULL	15	CC	MHC class II protein complex
3	−12.2	NULL	914	Chr	Chr 3
4	−11.24	NULL	312	BP	immune response
5	−10.82	NULL	417	H.Tiss	WIRTH_Immune system
6	−10.34	NULL	47	BP	antigen processing and presentation
7	−10.22	NULL	135	H.Tiss	WIRTH_Mucosa
8	−9.55	NULL	316	Cancer	SPANG_BCL6−index2
9	−8.93	NULL	1182	CC	extracellular region
10	−8.45	NULL	162	CC	external side of plasma membrane
11	−8.34	NULL	23	CC	integral to lumenal side of endoplasmic reticulum membrane
12	−8.3	NULL	32	CC	ER to Golgi transport vesicle membrane
13	−8.07	NULL	265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
14	−8.07	NULL	265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
15	−8.07	NULL	265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
16	−8.07	NULL	265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
17	−8.02	NULL	60	BP	T cell costimulation
18	−7.99	NULL	12	GSEA C2	BIOCARTA_CTL_PATHWAY
19	−7.93	NULL	250	Lymphoma	LENZ_Stromal signature 1
20	−7.79	NULL	6	GSEA C2	SANA_RESPONSE_TO_IFNG_UP

GW_034

Local Summary

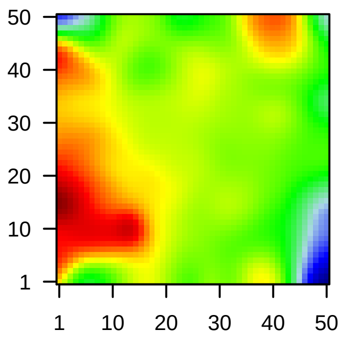
%DE = 0.64
metagenes = 13
genes = 78
genes in genesets = 61

genes with fdr < 0.1 = 46 (45 + / 1 −)
genes with fdr < 0.05 = 44 (44 + / 0 −)
genes with fdr < 0.01 = 35 (35 + / 0 −)

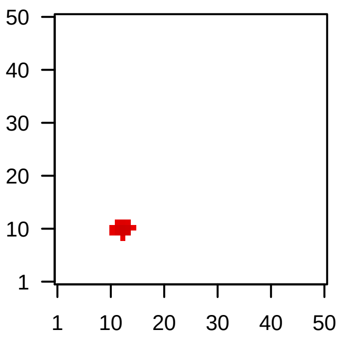
<r> metagenes = 0.95
<r> genes = 0.3

<FC> = 0.76
<shrinkage−t> = 26.7
<p−value> = 0
<fdr> = 0.41

Profile



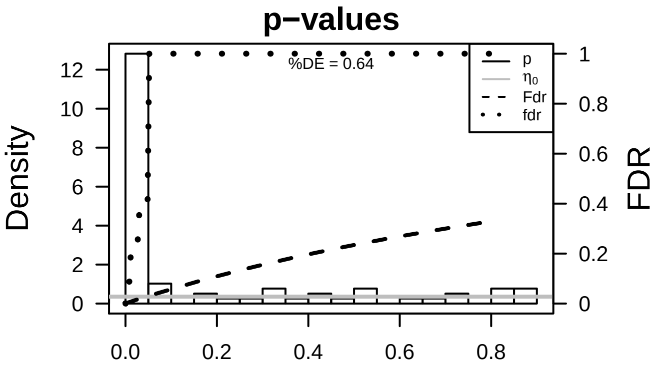
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	729428	1.96	2e−16	4e−16	14 x 11	G antigen 12C [Source:HGNC Symbol;Acc:28402]
2	729422	2.39	2e−16	4e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
3	100008586	2.02	2e−16	4e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
4	645073	1.88	2e−16	4e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
5	729442	2.21	2e−16	4e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
6	26748	2.41	2e−16	4e−16	14 x 11	G antigen 12I [Source:HGNC Symbol;Acc:4105]
7	645037	2.43	2e−16	4e−16	14 x 11	G antigen 2C [Source:HGNC Symbol;Acc:31958]
8	2576	2	2e−16	4e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
9	2577	2.27	2e−16	4e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
10	2579	2.3	2e−16	4e−16	14 x 11	G antigen 12I [Source:HGNC Symbol;Acc:4105]
11	4100	1.73	2e−16	4e−16	14 x 11	melanoma antigen family A, 1 (directs expression of antigen
12	4109	2.26	2e−16	4e−16	14 x 11	melanoma antigen family A, 10 [Source:HGNC Symbol;Acc:6
13	4103	1.81	2e−16	4e−16	14 x 10	melanoma antigen family A, 4 [Source:HGNC Symbol;Acc:68
14	8277	3.53	2e−16	4e−16	14 x 10	transketolase−like 1 [Source:HGNC Symbol;Acc:11835]
15	26749	1.5	7e−13	3e−10	14 x 11	G antigen 2E [Source:HGNC Symbol;Acc:31960]
16	729447	1.42	1e−11	1e−09	14 x 11	G antigen 2A [Source:HGNC Symbol;Acc:4099]
17	729396	1.36	7e−11	1e−09	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
18	84944	1.35	1e−10	6e−08	15 x 11	maelstrom spermatogenic transposon silencer [Source:HGN
19	24150	1.23	4e−09	6e−08	14 x 11	TP53 target 3D [Source:HGNC Symbol;Acc:44657]
20	440905	1.23	4e−09	1e−07	14 x 10	fatty acyl CoA reductase 2 pseudogene 1 [Source:HGNC Sy

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	24.35	NULL	1 / 9	GSEA C2	ABE_VEGFA_TARGETS_30MIN
2	21.41	NULL	1 / 11	GSEA C2	ABE_VEGFA_TARGETS_2HR
3	18.43	NULL	1 / 14	GSEA C2	VALK_AML_WITH_11Q23_REARRANGED
4	17.67	NULL	1 / 15	GSEA C2	VALK_AML_CLUSTER_16
5	17.67	NULL	1 / 15	GSEA C2	KEGG_PENTOSE_PHOSPHATE_PATHWAY
6	16.58	NULL	24 / 630	Chr	Chr X
7	13.66	NULL	1 / 11	GSEA C2	SU_PLACENTA
8	13.47	NULL	1 / 12	GSEA C2	RAY_TARGETS_OF_P210_BCR_ABL_FUSION_UP
9	11.75	NULL	1 / 14	GSEA C2	NIELSEN_GIST
10	11.26	NULL	1 / 15	GSEA C2	BROWNE_HCMV_INFECTION_8HR_DN
11	9.58	NULL	3 / 15	GSEA C2	MATTIOLI_MULTIPLE_MYELOMA_SUBGROUPS
12	9.34	NULL	1 / 14	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_B
13	9.23	NULL	1 / 4	GSEA C2	WEBER_METHYLATED_ICP_IN_SPERM_DN
14	8.62	NULL	1 / 10	BP	piRNA metabolic process
15	8.62	NULL	1 / 10	CC	XY body
16	8.11	NULL	1 / 11	BP	regulation of organ growth
17	7.82	NULL	7 / 120	H.Tiss	WIRTH_Testis
18	7.68	NULL	1 / 5	GSEA C2	CHOI_ATL_ACUTE_STAGE
19	7.29	NULL	1 / 13	BP	synapsis
20	6.95	NULL	1 / 14	BP	DNA methylation involved in gamete generation
21	6.95	NULL	1 / 21	BP	negative regulation of Notch signaling pathway
22	6.76	NULL	1 / 6	GSEA C2	NIELSEN_GIST_VS_SYNOVIAL_SARCOMA_UP
23	6.56	NULL	2 / 8	GSEA C2	WEBER_METHYLATED_ICP_IN_FIBROBLAST
24	6.41	NULL	8 / 419	CC	cellular_component
25	6.08	NULL	1 / 11	BP	positive regulation of synapse maturation
26	6.06	NULL	1 / 7	GSEA C2	NIELSEN_SYNOVIAL_SARCOMA_UP
27	5.86	NULL	8 / 481	BP	biological_process
28	5.74	NULL	1 / 12	BP	calcium−mediated signaling using intracellular calcium source
29	5.74	NULL	1 / 12	GSEA C2	PEPPER_CHRONIC_LYMPHOCYTIC_LEUKEMIA_UP
30	5.69	NULL	1 / 12	GSEA C2	HO_LIVER_CANCER_VASCULAR_INVASION
31	5.64	NULL	1 / 10	BP	paraxial mesoderm development
32	5.46	NULL	1 / 13	GSEA C2	VALK_AML_WITH_EVI1
33	5.25	NULL	1 / 22	BP	male meiosis
34	5.2	NULL	1 / 14	GSEA C2	VALK_AML_CLUSTER_10
35	5.03	NULL	8 / 549	MF	molecular_function
36	5.01	NULL	1 / 12	Glio	Phillips PN up vs MES & Prolif
37	4.78	NULL	1 / 16	GSEA C2	SHEDDEN_LUNG_CANCER_GOOD_SURVIVAL_A5
38	4.75	NULL	1 / 13	GSEA C2	GUENTHER_GROWTH_SPHERICAL_VS_ADHERENT_UP
39	4.71	NULL	1 / 10	GSEA C2	TSUNODA_CISPLATIN_RESISTANCE_DN
40	4.63	NULL	1 / 27	BP	gene silencing by RNA

GW_034

Local Summary

%DE = 0.73

metagenes = 54

genes = 546

genes in genesets = 543

genes with fdr < 0.1 = 299 (299 + / 0 −)

genes with fdr < 0.05 = 228 (228 + / 0 −)

genes with fdr < 0.01 = 122 (122 + / 0 −)

<r> metagenes = 0.86

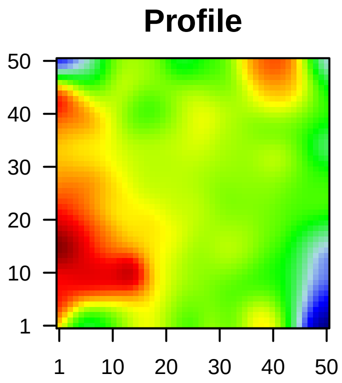
<r> genes = 0.23

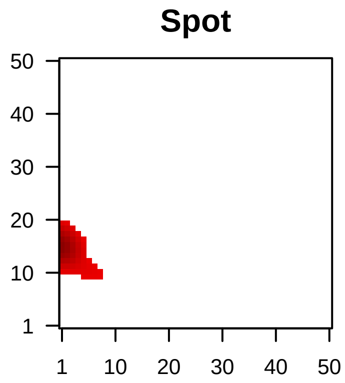
<FC> = 0.43

<shrinkage−t> = 15.02

<p−value> = 0.01

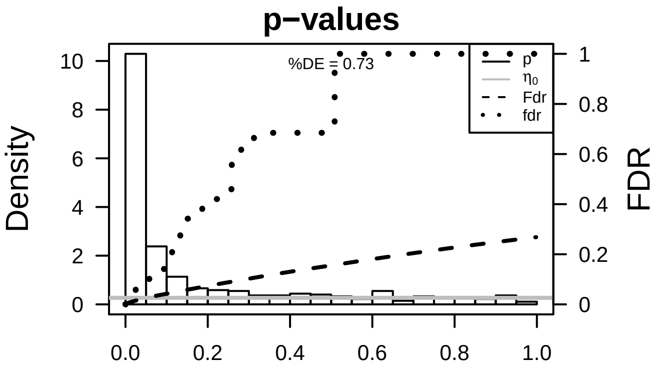
<fdr> = 0.61





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	51083	2.28	2e−16	2e−14	1 x 15	galanin/GMAP prepropeptide [Source:HGNC Symbol;Acc:41
2	283869	2.38	2e−16	2e−14	1 x 17	neuropeptide W [Source:HGNC Symbol;Acc:30509]
3	142678	1.5	7e−13	2e−10	1 x 17	mindbomb E3 ubiquitin protein ligase 2 [Source:HGNC Symb
4	4495	1.46	2e−12	2e−10	1 x 16	metallothionein 1G [Source:HGNC Symbol;Acc:7399]
5	23246	1.45	4e−12	1e−09	1 x 16	block of proliferation 1 [Source:HGNC Symbol;Acc:15519]
6	991	1.42	1e−11	3e−09	1 x 16	cell division cycle 20 [Source:HGNC Symbol;Acc:1723]
7	8772	1.39	3e−11	8e−07	1 x 14	Fas (TNFRSF6)−associated via death domain [Source:HGNC
8	55210	1.22	6e−09	6e−06	1 x 18	ATPase family, AAA domain containing 3A [Source:HGNC Sy
9	10202	1.12	9e−08	6e−06	1 x 15	dehydrogenase/reductase (SDR family) member 2 [Source:H
10	4715	1.11	1e−07	6e−06	1 x 17	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9, 22
11	79581	1.09	2e−07	6e−06	1 x 15	solute carrier family 52 (riboflavin transporter), member 2 [So
12	116444	1.09	2e−07	6e−06	1 x 11	glutamate receptor, ionotropic, N−methyl−D−aspartate 3B [So
13	27161	1.09	2e−07	2e−05	8 x 10	argonaute RISC catalytic component 2 [Source:HGNC Symb
14	285958	1.07	3e−07	4e−05	2 x 13	small nucleolar RNA host gene 15 (non−protein coding) [Sou
15	84310	1.03	8e−07	4e−05	6 x 10	chromosome 7 open reading frame 50 [Source:HGNC Symbo
16	26233	1.02	1e−06	4e−05	1 x 15	F−box and leucine−rich repeat protein 6 [Source:HGNC Sym
17	5442	1.02	1e−06	4e−05	8 x 11	polymerase (RNA) mitochondrial (DNA directed) [Source:HG
18	116447	1.01	2e−06	4e−05	1 x 15	topoisomerase (DNA) I, mitochondrial [Source:HGNC Symbo
19	7407	1	2e−06	1e−04	3 x 15	valyl−tRNA synthetase [Source:HGNC Symbol;Acc:12651]
20	10963	0.94	6e−06	1e−04	1 x 16	stress−induced−phosphoprotein 1 [Source:HGNC Symbol;Ac



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset
1	10.86	NULL	2 / 7	GSEA C2 CAFFAREL_RESPONSE_TO_THC_24HR_5_UP
2	10.48	NULL	2 / 10	GSEA C2 ZHU_CMV_24_HR_UP
3	10.48	NULL	2 / 10	GSEA C2 ZHU_CMV_ALL_UP
4	10.12	NULL	2 / 21	BP feeding behavior
5	9.73	NULL	1 / 6	GSEA C2 REACTOME_CLASS_A1_RHODOPSIN_LIKE_RECEPTORS
6	9.73	NULL	1 / 6	GSEA C2 REACTOME_GPCR_LIGAND_BINDING
7	9.54	NULL	5 / 12	GSEA C2 CREIGHTON_AKT1_SIGNALING_VIA_MTOR_UP
8	9.42	NULL	15 / 96	BP rRNA processing
9	8.92	NULL	1 / 7	GSEA C2 REACTOME_PEPTIDE_LIGAND_BINDING_RECEPTORS
10	8.4	NULL	2 / 11	GSEA C2 SCIBETTA_KDM5B_TARGETS_DN
11	8.31	NULL	4 / 10	GSEA C2 HOFMANN_MYELODYSPLASTIC_SYNDROM_LOW_RISK_DN
12	8.27	NULL	1 / 8	GSEA C2 SAMOLS_TARGETS_OF_KHSV_MIRNAS_UP
13	8.27	NULL	1 / 8	GSEA C2 REACTOME_G_ALPHA_I_SIGNALLING_EVENTS
14	8.18	NULL	2 / 16	GSEA C2 FRASOR_RESPONSE_TO_SERM_OR_FULVESTRANT_DN
15	8.06	NULL	2 / 13	GSEA C2 RICKMAN_HEAD_AND_NECK_CANCER_C
16	8.05	NULL	2 / 14	GSEA C2 KRASNOSELSKAYA_ILF3_TARGETS_DN
17	7.99	NULL	2 / 12	GSEA C2 BHATTACHARYA_EMBRYONIC_STEM_CELL
18	7.72	NULL	2 / 10	GSEA C2 TAKAO_RESPONSE_TO_UVB_RADIATION_UP
19	7.65	NULL	2 / 15	MF neuropeptide hormone activity
20	7.53	NULL	4 / 13	GSEA C2 REACTOME_GLYCOLYSIS
21	7.43	NULL	2 / 18	BP smooth muscle contraction
22	7.43	NULL	5 / 18	MF ribonucleoprotein complex binding
23	7.34	NULL	47 / 530	Cancer Lembcke_Normal vs Adenoma
24	7.26	NULL	1 / 10	GSEA C2 WELCSH_BRCA1_TARGETS_1_DN
25	6.87	NULL	1 / 11	GSEA C2 SMID_BREAST_CANCER_RELAPSE_IN_BONE_DN
26	6.87	NULL	1 / 11	GSEA C2 PARK_APL_PATHOGENESIS_DN
27	6.67	NULL	22 / 167	CC ribosome
28	6.66	NULL	5 / 16	GSEA C2 KORKOLA_EMBRYONAL_CARCINOMA_UP
29	6.63	NULL	5 / 14	GSEA C2 NIKOLSKY_BREAST_CANCER_7P22_AMPLICON
30	6.61	NULL	2 / 9	GSEA C2 KUMAMOTO_RESPONSE_TO_NUTLIN_3A_DN
31	6.61	NULL	49 / 579	CC nucleolus
32	6.56	NULL	2 / 8	GSEA C2 NIKOLSKY_BREAST_CANCER_5P15_AMPLICON
33	6.54	NULL	7 / 19	CC mitochondrial small ribosomal subunit
34	6.51	NULL	4 / 15	Cancer GENTLES_modul1
35	6.44	NULL	2 / 16	GSEA C2 BROWNE_HCMV_INFECTION_24HR_UP
36	6.43	NULL	3 / 15	GSEA C2 LY_AGING_MIDDLE_DN
37	6.4	NULL	23 / 153	MF structural constituent of ribosome
38	6.33	NULL	92 / 1318	CC mitochondrion
39	6.32	NULL	12 / 66	BP positive regulation of ubiquitin−protein ligase activity involved in mit
40	6.31	NULL	3 / 9	GSEA C2 BIOCARTA_GLYCOLYSIS_PATHWAY

GW_034

Local Summary

%DE = 0.91

metagenes = 21

genes = 366

genes in genesets = 364

genes with fdr < 0.1 = 298 (8 + / 290 −)

genes with fdr < 0.05 = 298 (8 + / 290 −)

genes with fdr < 0.01 = 224 (6 + / 218 −)

<r> metagenes = 0.95

<r> genes = 0.48

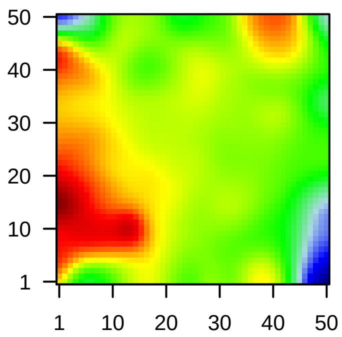
<FC> = −0.71

<shrinkage−t> = −24.73

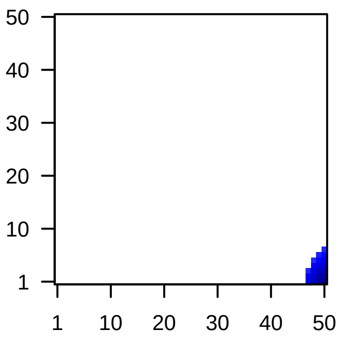
<p−value> = 0

<fdr> = 0.31

Profile

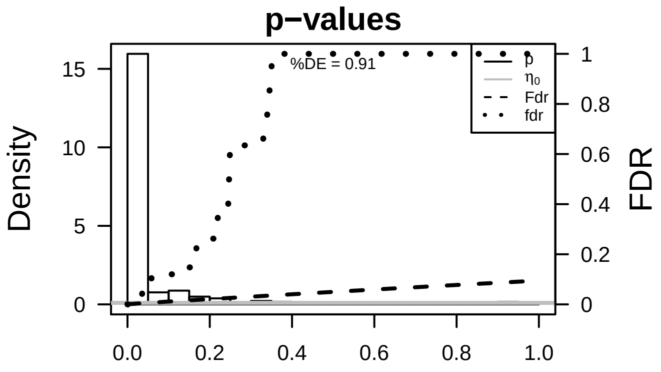


Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	713	−1.74	2e−16	6e−16	50 x 1	complement component 1, q subcomponent, B chain [Source
2	919	−1.86	2e−16	6e−16	50 x 1	CD247 molecule [Source:HGNC Symbol;Acc:1677]
3	972	−1.82	2e−16	6e−16	50 x 1	CD74 molecule, major histocompatibility complex, class II inv
4	1396	1.78	2e−16	6e−16	50 x 5	cysteine−rich protein 1 (intestinal) [Source:HGNC Symbol;Ac
5	4283	−1.82	2e−16	6e−16	49 x 1	chemokine (C−X−C motif) ligand 9 [Source:HGNC Symbol;A
6	3001	−1.74	2e−16	6e−16	48 x 1	granzyme A (granzyme 1, cytotoxic T−lymphocyte−associate
7	3002	−1.84	2e−16	6e−16	49 x 1	granzyme B (granzyme 2, cytotoxic T−lymphocyte−associate
8	3109	−1.96	2e−16	6e−16	50 x 1	major histocompatibility complex, class II, DM beta [Source:H
9	3113	−2.05	2e−16	6e−16	50 x 1	major histocompatibility complex, class II, DP alpha 1 [Source
10	3122	−2.23	2e−16	6e−16	50 x 1	major histocompatibility complex, class II, DR alpha [Source:
11	5920	−2.17	2e−16	6e−16	48 x 1	retinoic acid receptor responder (tazarotene induced) 3 [Sour
12	5996	−1.76	2e−16	6e−16	50 x 1	regulator of G−protein signaling 1 [Source:HGNC Symbol;Ac
13	10537	−1.72	2e−16	6e−16	50 x 1	ubiquitin D [Source:HGNC Symbol;Acc:18795]
14	2634	−1.67	1e−15	8e−14	47 x 1	guanylate binding protein 2, interferon−inducible [Source:HG
15	915	−1.64	4e−15	2e−13	49 x 1	CD3d molecule, delta (CD3−TCR complex) [Source:HGNC S
16	3108	−1.61	1e−14	2e−13	50 x 1	major histocompatibility complex, class II, DM alpha [Source:
17	397	−1.59	1e−14	8e−13	50 x 1	Rho GDP dissociation inhibitor (GDI) beta [Source:HGNC Sy
18	3512	−1.58	4e−14	2e−12	50 x 1	immunoglobulin J polypeptide, linker protein for immunoglobu
19	6451	−1.56	9e−14	5e−12	50 x 5	SH3 domain binding glutamic acid−rich protein like [Source:H
20	2745	−1.51	4e−13	5e−12	50 x 3	glutaredoxin (thioltransferase) [Source:HGNC Symbol;Acc:43



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−34.55	NULL	12 / 15	CC	MHC class II protein complex
2	−23.49	NULL	89 / 417	H.Tiss	WIRTH_Immune system
3	−21.75	NULL	15 / 47	BP	antigen processing and presentation
4	−21.43	NULL	55 / 312	BP	immune response
5	−21.25	NULL	104 / 553	Cancer	Lembcke_Colonic Inflammation
6	−20.22	NULL	3 / 6	GSEA C2	SANA_RESPONSE_TO_IFNG_UP
7	−19.53	NULL	6 / 11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
8	−18.89	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
9	−17.61	NULL	5 / 12	GSEA C2	BIOCARTA_CTL_PATHWAY
10	−17.58	NULL	7 / 21	CC	clathrin−coated endocytic vesicle membrane
11	−17.18	NULL	4 / 7	Glio	Donson−cytotoxic effectors−associated with LTS in HGA
12	−17.1	NULL	5 / 11	GSEA C2	BIOCARTA_THELPER_PATHWAY
13	−16.93	NULL	2 / 4	MMML CGS	MACIEJ_MMML 2
14	−16.7	NULL	7 / 23	CC	integral to lumenal side of endoplasmic reticulum membrane
15	−16.51	NULL	8 / 28	CC	transport vesicle membrane
16	−16.43	NULL	7 / 8	Glio	Donson−migration tethering and rolling−associated with LTS in HG
17	−16.32	NULL	47 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
18	−16.32	NULL	47 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
19	−16.32	NULL	47 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
20	−16.32	NULL	47 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
21	−16.06	NULL	2 / 3	GSEA C2	KEGG_VIRAL_MYOCARDITIS
22	−15.5	NULL	14 / 60	BP	T cell costimulation
23	−15.46	NULL	3 / 5	GSEA C2	WONG_ENDOMETRIAL_CANCER_LATE
24	−15.29	NULL	4 / 8	GSEA C2	GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_DN
25	−14.27	NULL	9 / 35	CC	trans−Golgi network membrane
26	−14.02	NULL	5 / 10	GSEA C2	LEE_DIFFERENTIATING_T_LYMPHOCYTE
27	−13.99	NULL	6 / 13	Cancer	GENTLES_modul18
28	−13.93	NULL	5 / 12	BP	immunoglobulin mediated immune response
29	−13.86	NULL	7 / 32	CC	ER to Golgi transport vesicle membrane
30	−13.83	NULL	5 / 13	GSEA C2	BIOCARTA_IL17_PATHWAY
31	−13.68	NULL	4 / 8	GSEA C2	NIELSEN_SYNOVIAL_SARCOMA_DN
32	−13.61	NULL	6 / 15	Glio	Donson−chemokines/cytokines−associated with LTS in HGA
33	−13.56	NULL	6 / 15	GSEA C2	FINAK_BREAST_CANCER_SDPP_SIGNATURE
34	−13.54	NULL	2 / 4	GSEA C2	KEGG_LEISHMANIA_INFECTION
35	−13.47	NULL	15 / 84	BP	T cell receptor signaling pathway
36	−13.43	NULL	6 / 13	GSEA C2	HAHTOLA_CTCL_PATHOGENESIS
37	−13.31	NULL	2 / 6	GSEA C2	LUI_THYROID_CANCER_CLUSTER_4
38	−13.28	NULL	13 / 87	BP	antigen processing and presentation of exogenous peptide antigen
39	−13.27	NULL	2 / 5	GSEA C2	WEST_ADRENOCORTICAL_CARCINOMA_VS_ADENOMA_DN
40	−13.24	NULL	2 / 4	GSEA C2	REACTOME_CLASSICAL_ANTIBODY_MEDIATED_COMPLEMEN