GW_211

Global Summary

%DE = 0.13

genes with fdr < 0.2 = 1753 (955 + / 798 −)

genes with fdr < 0.1 = 1408 (796 + / 612 −)

genes with fdr < 0.05 = 972 (560 + / 412 −)

genes with fdr < 0.01 = 755 (447 + / 308 −)

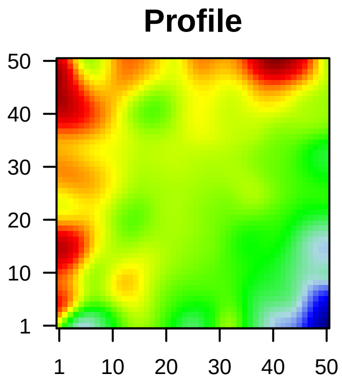
genes in genesets = 16332

<FC> = 0

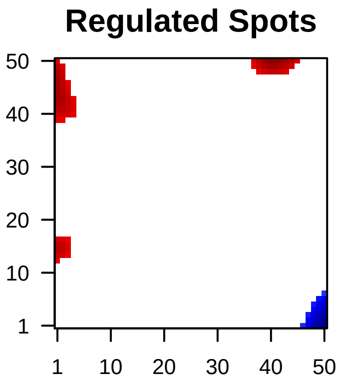
<shrinkage−t> = 0

<p−value> = 0.12

<fdr> = 0.87



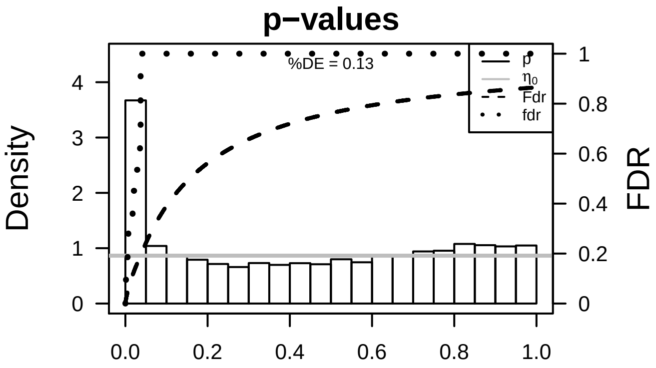
Profile



Regulated Spots

Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	242	1.56	2e−16	4e−14	1 x 48	arachidonate 12−lipoxygenase, 12R type [Source:HGNC Sym
2	55107	2.36	2e−16	4e−14	1 x 5	anoctamin 1, calcium activated chloride channel [Source:HGN
3	92747	2.45	2e−16	4e−14	50 x 10	BPI fold containing family B, member 1 [Source:HGNC Symb
4	760	1.91	2e−16	4e−14	1 x 44	carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
5	92291	1.48	2e−16	4e−14	50 x 11	calpain 13 [Source:HGNC Symbol;Acc:16663]
6	6363	−1.51	2e−16	4e−14	50 x 1	chemokine (C−C motif) ligand 19 [Source:HGNC Symbol;Acc
7	894	−1.46	2e−16	4e−14	50 x 4	cyclin D2 [Source:HGNC Symbol;Acc:1583]
8	908	1.68	2e−16	4e−14	40 x 50	chaperonin containing TCP1, subunit 6A (zeta 1) [Source:HG
9	1382	2.07	2e−16	4e−14	1 x 48	cellular retinoic acid binding protein 2 [Source:HGNC Symbol
10	2919	1.5	2e−16	4e−14	1 x 1	chemokine (C−X−C motif) ligand 1 (melanoma growth stimul
11	9547	−1.56	2e−16	4e−14	1 x 46	chemokine (C−X−C motif) ligand 14 [Source:HGNC Symbol;
12	6372	2.61	2e−16	4e−14	1 x 1	chemokine (C−X−C motif) ligand 6 [Source:HGNC Symbol;A
13	1673	2.52	2e−16	4e−14	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
14	1809	−1.92	2e−16	4e−14	6 x 1	dihydropyrimidinase−like 3 [Source:HGNC Symbol;Acc:3015]
15	2354	−2.44	2e−16	4e−14	22 x 50	FBJ murine osteosarcoma viral oncogene homolog B [Source
16	10468	1.44	2e−16	4e−14	1 x 5	follistatin [Source:HGNC Symbol;Acc:3971]
17	51083	2.04	2e−16	4e−14	1 x 15	galanin/GMAP prepropeptide [Source:HGNC Symbol;Acc:41
18	2631	1.52	2e−16	4e−14	39 x 50	glioblastoma amplified sequence [Source:HGNC Symbol;Acc
19	3040	−1.57	2e−16	4e−14	4 x 1	hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
20	3043	−1.44	2e−16	4e−14	5 x 1	hemoglobin, beta [Source:HGNC Symbol;Acc:4827]



p−values

Global Geneset Analysis

Overexpressed

Rank	GSZ	p−value	#all	Geneset	
1	15.34	NULL	572	Disease	GUDJ_psoriasis up
2	10.05	NULL	21	CC	cornified envelope
3	9.72	NULL	42	BP	keratinization
4	9.6	NULL	76	BP	epidermis development
5	9.52	NULL	530	Cancer	Lembcke_Normal vs Adenoma
6	9.03	NULL	10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
7	8.38	NULL	534	Chr	Chr 8
8	7.29	NULL	1720	Chr	Chr 1
9	7.12	NULL	15	GSEA C2	SNIJDERS_AMPLIFIED_IN_HEAD_AND_NECK_TUMORS
10	7.04	NULL	142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
11	7.04	NULL	142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
12	6.94	NULL	717	Chr	Chr 16
13	6.77	NULL	53	BP	keratinocyte differentiation
14	6.69	NULL	10	BP	cellular response to zinc ion
15	6.57	NULL	135	H.Tiss	WIRTH_Mucosa
16	6.52	NULL	7	MMML CGS	MACIEJ_MMML 13
17	6.44	NULL	15	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_3
18	6.28	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_4
19	6.27	NULL	15	MF	interleukin−1 receptor binding
20	5.89	NULL	13	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_C

Underexpressed

Rank	GSZ	p−value	#all	Geneset	
1	−10.95	NULL	16	GSEA C2	CROONQUIST_STROMAL_STIMULATION_UP
2	−9.9	NULL	15	CC	MHC class II protein complex
3	−9.67	NULL	417	H.Tiss	WIRTH_Immune system
4	−9.67	NULL	250	Lymphoma	LENZ_Stromal signature 1
5	−8.62	NULL	8	GSEA C2	RUNNE_GENDER_EFFECT_UP
6	−8.32	NULL	10	GSEA C2	CHASSOT_SKIN_WOUND
7	−8.29	NULL	714	Chr	Chr 6
8	−8.25	NULL	7	MMML CGS	MACIEJ_MMML 5
9	−7.43	NULL	553	Cancer	Lembcke_Colonic Inflammation
10	−7.22	NULL	9	GSEA C2	GUTIERREZ_WALDENSTROEMS_MACROGLOBULINEMIA_1_D
11	−7.08	NULL	504	Chr	Chr 15
12	−6.65	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
13	−6.52	NULL	327	Lymphoma	SPANG_CD40 6hrs UP
14	−6.47	NULL	190	CC	extracellular matrix
15	−6.44	NULL	24	TF Tissue	VAQUERIZAS_Trachea
16	−6.41	NULL	316	Cancer	SPANG_BCL6−index2
17	−6.39	NULL	11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
18	−6.36	NULL	11	MF	platelet−derived growth factor binding
19	−6.31	NULL	162	CC	external side of plasma membrane
20	−6.3	NULL	60	BP	T cell costimulation

GW_211

Local Summary

%DE = 0.61

metagenes = 13

genes = 164

genes in genesets = 164

genes with fdr < 0.1 = 70 (70 + / 0 −)

genes with fdr < 0.05 = 50 (50 + / 0 −)

genes with fdr < 0.01 = 30 (30 + / 0 −)

<r> metagenes = 0.98

<r> genes = 0.3

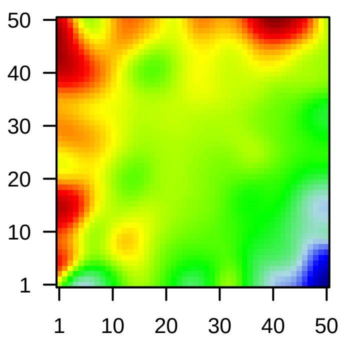
<FC> = 0.4

<shrinkage−t> = 14.17

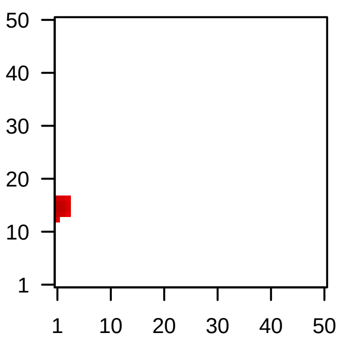
<p−value> = 0

<fdr> = 0.62

Profile



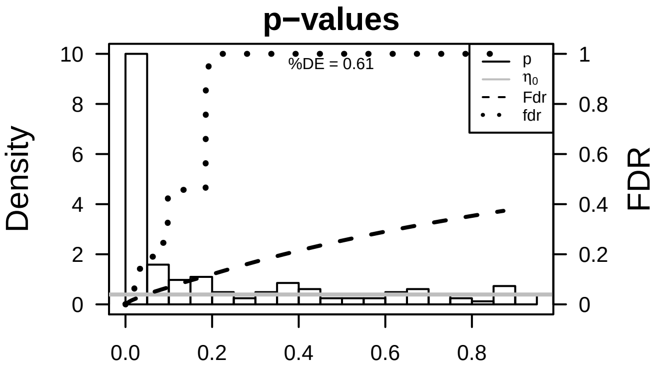
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	51083	2.04	2e−16	4e−15	1 x 15	galanin/GMAP prepropeptide [Source:HGNC Symbol;Acc:41
2	93273	1.58	2e−16	4e−15	2 x 15	LEM domain containing 1 [Source:HGNC Symbol;Acc:18725]
3	51373	1.94	2e−16	4e−15	1 x 16	28S ribosomal protein S17, mitochondrial; HCG1984214, isof
4	283869	2.03	2e−16	4e−15	1 x 17	neuropeptide W [Source:HGNC Symbol;Acc:30509]
5	4495	1.29	3e−13	3e−11	1 x 16	metallothionein 1G [Source:HGNC Symbol;Acc:7399]
6	142678	1.27	7e−13	2e−10	1 x 17	mindbomb E3 ubiquitin protein ligase 2 [Source:HGNC Symb
7	131076	1.23	4e−12	2e−07	1 x 16	coiled−coil domain containing 58 [Source:HGNC Symbol;Acc
8	27294	1.04	3e−09	4e−07	1 x 16	dihydrodiol dehydrogenase (dimeric) [Source:HGNC Symbol;
9	4728	1.01	9e−09	6e−07	2 x 17	NADH dehydrogenase (ubiquinone) Fe−S protein 8, 23kDa (
10	26094	0.99	2e−08	4e−06	1 x 13	DDB1 and CUL4 associated factor 4 [Source:HGNC Symbol;
11	7205	0.94	1e−07	4e−06	2 x 16	thyroid hormone receptor interactor 6 [Source:HGNC Symbol
12	388581	0.92	2e−07	4e−06	1 x 15	family with sequence similarity 132, member A [Source:HGN
13	116447	0.91	2e−07	4e−06	1 x 15	topoisomerase (DNA) I, mitochondrial [Source:HGNC Symbo
14	118460	0.91	3e−07	5e−06	1 x 13	exosome component 6 [Source:HGNC Symbol;Acc:19055]
15	10552	0.9	4e−07	5e−06	1 x 15	actin related protein 2/3 complex, subunit 1A, 41kDa [Source:
16	78999	0.89	4e−07	5e−06	1 x 14	leucine rich repeat and fibronectin type III domain containing
17	55630	0.89	5e−07	3e−05	1 x 16	solute carrier family 39 (zinc transporter), member 4 [Source:
18	5499	0.86	1e−06	3e−05	1 x 13	protein phosphatase 1, catalytic subunit, alpha isozyme [Sou
19	8772	0.85	1e−06	4e−05	1 x 14	Fas (TNFRSF6)−associated via death domain [Source:HGNC
20	26233	0.84	2e−06	5e−05	1 x 15	F−box and leucine−rich repeat protein 6 [Source:HGNC Sym

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	19.55	NULL	1 / 3	GSEA C2	WEBER_METHYLATED_LCP_IN_SPERM_DN
2	16.76	NULL	1 / 6	GSEA C2	REACTOME_CLASS_A1_RHODOPSIN_LIKE_RECEPTORS
3	16.76	NULL	1 / 6	GSEA C2	REACTOME_GPCR_LIGAND_BINDING
4	16.7	NULL	2 / 21	BP	feeding behavior
5	15.92	NULL	2 / 7	GSEA C2	CAFFAREL_RESPONSE_TO_THC_24HR_5_UP
6	15.33	NULL	1 / 7	GSEA C2	REACTOME_PEPTIDE_LIGAND_BINDING_RECEPTORS
7	14.39	NULL	1 / 5	GSEA C2	WEBER_METHYLATED_LCP_IN_FIBROBLAST_DN
8	14.2	NULL	1 / 8	GSEA C2	SAMOLS_TARGETS_OF_KHSV_MIRNAS_UP
9	14.2	NULL	1 / 8	GSEA C2	REACTOME_G_ALPHA_I_SIGNALLING_EVENTS
10	12.52	NULL	1 / 3	GSEA C2	KEGG_OXIDATIVE_PHOSPHORYLATION
11	12.52	NULL	1 / 3	GSEA C2	KEGG_PARKINSONS_DISEASE
12	12.51	NULL	1 / 10	GSEA C2	WELCSH_BRCA1_TARGETS_1_DN
13	12.51	NULL	1 / 10	GSEA C2	TAKAO_RESPONSE_TO_UVB_RADIATION_UP
14	12.3	NULL	2 / 11	GSEA C2	SCIBETTA_KDM5B_TARGETS_DN
15	12.21	NULL	2 / 13	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_C
16	12.1	NULL	2 / 10	GSEA C2	ZHU_CMV_24_HR_UP
17	12.1	NULL	2 / 10	GSEA C2	ZHU_CMV_ALL_UP
18	11.85	NULL	1 / 11	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_BONE_DN
19	11.85	NULL	1 / 11	GSEA C2	PARK_APL_PATHOGENESIS_DN
20	11.71	NULL	2 / 12	GSEA C2	BHATTACHARYA_EMBRYONIC_STEM_CELL
21	10.77	NULL	1 / 13	GSEA C2	KORKOLA_EMBRYONIC_CARCINOMA_VS_SEMINOMA_UP
22	10.7	NULL	2 / 14	GSEA C2	KRASNOSELSKAYA_ILF3_TARGETS_DN
23	10.5	NULL	1 / 4	GSEA C2	REACTOME_GLUCOSE_REGULATION_OF_INSULIN_SECRETI
24	10.5	NULL	1 / 4	GSEA C2	REACTOME_INTEGRATION_OF_ENERGY_METABOLISM
25	10.5	NULL	1 / 4	GSEA C2	REACTOME_REGULATION_OF_INSULIN_SECRETION
26	10.33	NULL	1 / 14	GSEA C2	FARMER_BREAST_CANCER_BASAL_VS_LULMINAL
27	10.33	NULL	1 / 14	GSEA C2	LIEN_BREAST_CARCINOMA_METAPLASTIC_VS_DUCTAL_UP
28	10.26	NULL	2 / 18	BP	smooth muscle contraction
29	9.93	NULL	1 / 15	MF	neuropeptide hormone activity
30	9.93	NULL	1 / 15	GSEA C2	NAGASHIMA_NRG1_SIGNALING_UP
31	9.93	NULL	1 / 15	GSEA C2	FERNANDEZ_BOUND_BY_MYC
32	9.61	NULL	1 / 7	MMML CGS	MACIEJ_MMML 13
33	9.57	NULL	1 / 16	GSEA C2	DOANE_BREAST_CANCER_ESR1_DN
34	9.57	NULL	1 / 16	GSEA C2	TAVOR_CEBPA_TARGETS_DN
35	9.57	NULL	1 / 16	GSEA C2	FRASOR_RESPONSE_TO_SERM_OR_FULVESTRANT_DN
36	9.57	NULL	1 / 16	GSEA C2	BROWNE_HCMV_INFECTION_24HR_UP
37	9.46	NULL	2 / 10	GSEA C2	KEGG_HUNTINGTONS_DISEASE
38	9.41	NULL	4 / 18	MF	ribonucleoprotein complex binding
39	9.25	NULL	1 / 17	Disease	BCHETNIA_EBM up
40	9.19	NULL	1 / 5	GSEA C2	REACTOME_ELECTRON_TRANSPORT_CHAIN

GW_211

Local Summary

%DE = 0.72

metagenes = 34

genes = 433

genes in genesets = 424

genes with fdr < 0.1 = 213 (179 + / 34 −)

genes with fdr < 0.05 = 201 (171 + / 30 −)

genes with fdr < 0.01 = 163 (147 + / 16 −)

<r> metagenes = 0.87

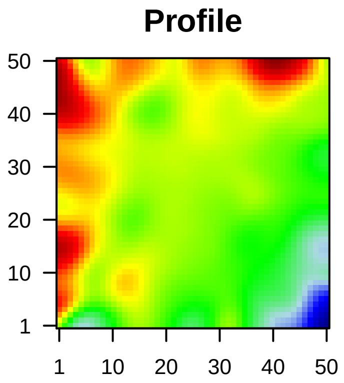
<r> genes = 0.32

<FC> = 0.39

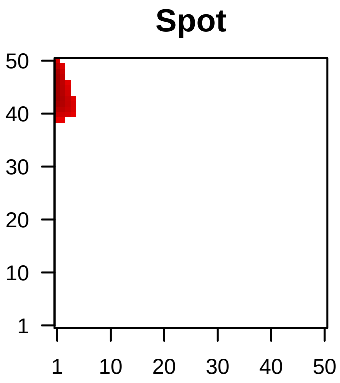
<shrinkage−t> = 13.66

<p−value> = 0

<fdr> = 0.51



Profile



Spot

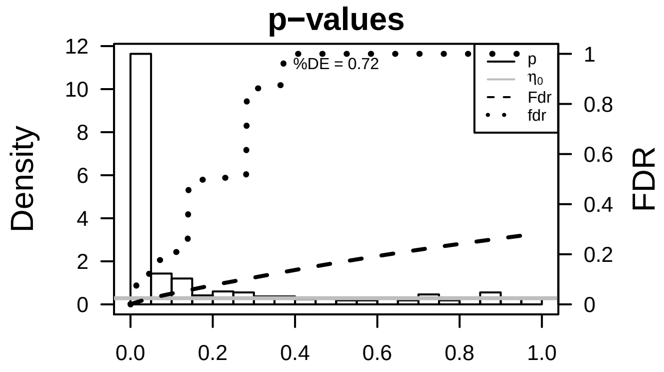
Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	242	1.56	2e−16	8e−16	1 x 48	arachidonate 12−lipoxygenase, 12R type [Source:HGNC Sym
2	760	1.91	2e−16	8e−16	1 x 44	carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
3	1382	2.07	2e−16	8e−16	1 x 48	cellular retinoic acid binding protein 2 [Source:HGNC Symbol
4	9547	−1.56	2e−16	8e−16	1 x 46	chemokine (C−X−C motif) ligand 14 [Source:HGNC Symbol;
5	1673	2.52	2e−16	8e−16	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
6	3489	2.56	2e−16	8e−16	1 x 44	insulin−like growth factor binding protein 6 [Source:HGNC Sy
7	3552	2.09	2e−16	8e−16	1 x 43	interleukin 1, alpha [Source:HGNC Symbol;Acc:5991]
8	56300	2.27	2e−16	8e−16	1 x 47	interleukin 36, gamma [Source:HGNC Symbol;Acc:15741]
9	26085	2.17	2e−16	8e−16	1 x 50	kallikrein−related peptidase 13 [Source:HGNC Symbol;Acc:6
10	3851	−1.6	2e−16	8e−16	1 x 50	keratin 4 [Source:HGNC Symbol;Acc:6441]
11	286887	1.44	2e−16	8e−16	1 x 47	keratin 6C [Source:HGNC Symbol;Acc:20406]
12	388533	1.64	2e−16	8e−16	1 x 49	keratinocyte differentiation−associated protein [Source:HGNC
13	84648	2.13	2e−16	8e−16	1 x 48	late cornified envelope 3D [Source:HGNC Symbol;Acc:16615
14	643479	1.62	2e−16	8e−16	1 x 49	
15	23682	1.9	2e−16	8e−16	1 x 46	RAB38, member RAS oncogene family [Source:HGNC Symb
16	6283	2.39	2e−16	8e−16	1 x 49	S100 calcium binding protein A12 [Source:HGNC Symbol;Ac
17	6278	2.11	2e−16	8e−16	1 x 49	S100 calcium binding protein A7 [Source:HGNC Symbol;Acc:
18	338324	2.16	2e−16	8e−16	1 x 48	S100 calcium binding protein A7A [Source:HGNC Symbol;Ac
19	374897	1.49	2e−16	8e−16	1 x 49	suprabasin [Source:HGNC Symbol;Acc:24950]
20	6317	1.51	2e−16	8e−16	1 x 49	serpin peptidase inhibitor, clade B (ovalbumin), member 3 [Sc

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	26.25	NULL	18 / 21	CC	cornified envelope
2	25.35	NULL	31 / 76	BP	epidermis development
3	24.06	NULL	130 / 572	Disease	GUDJ_psoriasis up
4	22.33	NULL	20 / 42	BP	keratinization
5	19.09	NULL	3 / 10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
6	18	NULL	27 / 53	BP	keratinocyte differentiation
7	15.27	NULL	83 / 135	H.Tiss	WIRTH_Mucosa
8	12.69	NULL	5 / 16	GSEA C2	AMIT_SERUM_RESPONSE_480_MCF10A
9	12.44	NULL	4 / 10	MF	RAGE receptor binding
10	12.05	NULL	3 / 15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
11	11.78	NULL	3 / 15	MF	interleukin−1 receptor binding
12	10.78	NULL	7 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
13	10.17	NULL	1 / 5	GSEA C2	BUSA_SAM68_TARGETS_UP
14	9.47	NULL	2 / 7	GSEA C2	YE_METASTATIC_LIVER_CANCER
15	9.4	NULL	1 / 4	GSEA C2	BUDHU_LIVER_CANCER_METASTASIS_DN
16	9.23	NULL	5 / 16	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_DN
17	9.2	NULL	7 / 15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL
18	8.9	NULL	4 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_DN
19	8.72	NULL	7 / 15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
20	8.33	NULL	15 / 79	MF	serine−type endopeptidase inhibitor activity
21	8.15	NULL	76 / 1182	CC	extracellular region
22	8.02	NULL	4 / 16	GSEA C2	SESTO_RESPONSE_TO_UV_C7
23	7.99	NULL	6 / 16	GSEA C2	COLDREN_GEFITINIB_RESISTANCE_DN
24	7.69	NULL	3 / 8	GSEA C2	MCLACHLAN_DENTAL_CARIES_UP
25	7.44	NULL	1 / 6	GSEA C2	SEIKE_LUNG_CANCER_POOR_SURVIVAL
26	7.3	NULL	4 / 15	GSEA C2	CHANG_IMMORTALIZED_BY_HPV31_DN
27	7.26	NULL	9 / 73	BP	defense response to bacterium
28	7.24	NULL	4 / 15	GSEA C2	LEE_LIVER_CANCER_DENA_UP
29	7.24	NULL	3 / 8	GSEA C2	MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_UP
30	7.22	NULL	4 / 15	GSEA C2	LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
31	7.16	NULL	5 / 14	GSEA C2	CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U
32	7.06	NULL	4 / 25	BP	response to zinc ion
33	6.92	NULL	2 / 10	BP	lipoxygenase pathway
34	6.92	NULL	2 / 2	miRNA target	miR−199a*
35	6.8	NULL	14 / 122	MF	serine−type endopeptidase activity
36	6.8	NULL	11 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
37	6.77	NULL	3 / 10	GSEA C2	NIKOLSKY_BREAST_CANCER_20Q12_Q13_AMPLICON
38	6.76	NULL	3 / 11	GSEA C2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_G_UP
39	6.75	NULL	10 / 19	BP	peptide cross−linking
40	6.6	NULL	10 / 52	BP	negative regulation of endopeptidase activity



p−values

GW_211

Local Summary

%DE = 0.73

metagenes = 23

genes = 379

genes in genesets = 374

genes with fdr < 0.1 = 191 (191 + / 0 −)

genes with fdr < 0.05 = 153 (153 + / 0 −)

genes with fdr < 0.01 = 112 (112 + / 0 −)

<r> metagenes = 0.94

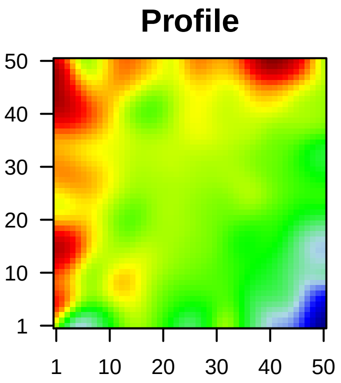
<r> genes = 0.34

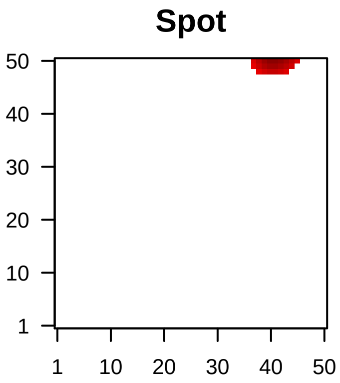
<FC> = 0.4

<shrinkage−t> = 13.86

<p−value> = 0.01

<fdr> = 0.59





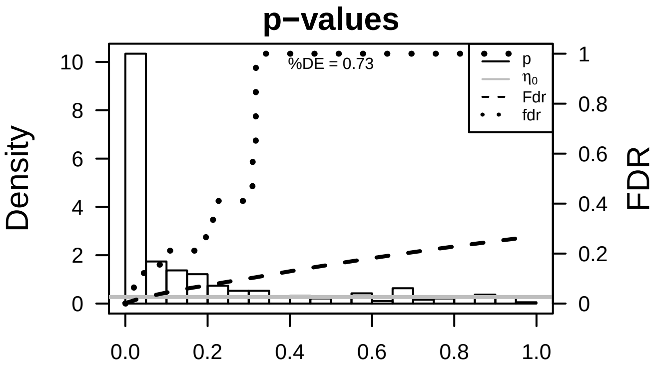
Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	908	1.68	2e−16	8e−15	40 x 50	chaperonin containing TCP1, subunit 6A (zeta 1) [Source:HG
2	2631	1.52	2e−16	8e−15	39 x 50	glioblastoma amplified sequence [Source:HGNC Symbol;Acc
3	23480	1.52	2e−16	8e−15	39 x 50	Sec61 gamma subunit [Source:HGNC Symbol;Acc:18277]
4	643253	1.38	6e−15	7e−12	40 x 50	
5	54517	1.32	7e−14	4e−10	41 x 50	pseudouridylate synthase 7 homolog (S. cerevisiae) [Source:
6	55915	1.22	4e−12	6e−09	38 x 50	LanC lantibiotic synthetase component C−like 2 (bacterial) [S
7	51142	1.06	6e−11	1e−08	38 x 50	coiled−coil−helix−coiled−coil−helix domain containing 2 [Sour
8	8500	1.13	2e−10	2e−08	42 x 50	protein tyrosine phosphatase, receptor type, f polypeptide (PT
9	6611	1.1	5e−10	2e−08	42 x 50	spermine synthase [Source:HGNC Symbol;Acc:11123]
10	5723	1.09	6e−10	1e−07	37 x 50	phosphoserine phosphatase [Source:HGNC Symbol;Acc:957
11	83787	1.06	2e−09	1e−07	39 x 50	armadillo repeat containing 10 [Source:HGNC Symbol;Acc:21
12	54928	1.04	3e−09	2e−06	40 x 50	inositol monophosphatase domain containing 1 [Source:HGN
13	84284	0.98	3e−08	2e−06	38 x 50	nucleoside−triphosphatase, cancer−related [Source:HGNC S
14	10165	0.97	4e−08	3e−06	40 x 50	solute carrier family 25 (aspartate/glutamate carrier), member
15	220042	0.95	8e−08	3e−06	42 x 50	chromosome 11 open reading frame 82 [Source:HGNC Symb
16	55353	0.94	9e−08	5e−06	42 x 50	lysosomal protein transmembrane 4 beta [Source:HGNC Sym
17	29028	0.92	2e−07	5e−06	44 x 50	ATPase family, AAA domain containing 2 [Source:HGNC Sym
18	100130742	0.91	3e−07	5e−06	37 x 49	leucine rich repeat containing 69 [Source:HGNC Symbol;Acc:
19	157769	0.91	3e−07	5e−06	40 x 50	family with sequence similarity 91, member A1 [Source:HGN
20	5701	0.9	3e−07	5e−06	41 x 50	proteasome (prosome, macropain) 26S subunit, ATPase, 2 [S

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all		Geneset
1	21.28	NULL	50 / 142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
2	21.28	NULL	50 / 142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
3	14.8	NULL	7 / 16	Cancer	RHODES_UNDIFFERENTIATED_CANCER
4	12.88	NULL	8 / 13	GSEA C2	CROONQUIST_IL6_DEPRIVATION_DN
5	12.75	NULL	6 / 15	GSEA C2	SMID_BREAST_CANCER_LUMINAL_A_DN
6	12.04	NULL	10 / 16	GSEA C2	FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
7	11.14	NULL	6 / 15	Cancer	GENTLES_modul6
8	11.08	NULL	7 / 15	GSEA C2	FOURNIER_ACINAR_DEVELOPMENT_LATE_DN
9	10.89	NULL	59 / 530	Cancer	Lembcke_Normal vs Adenoma
10	10.83	NULL	7 / 15	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP
11	10.38	NULL	9 / 15	GSEA C2	FINETTI_BREAST_CANCER_KINOME_RED
12	10.23	NULL	7 / 18	Lymphoma	DAVE_c−myc BL UP
13	10.15	NULL	53 / 370	BP	mitotic cell cycle
14	10.03	NULL	13 / 57	Glio	developing astrocytes
15	10.02	NULL	5 / 14	GSEA C2	XU_HGF_TARGETS_INDUCED_BY_AKT1_48HR_DN
16	9.76	NULL	4 / 14	GSEA C2	MAYBURD_RESPONSE_TO_L663536_DN
17	9.76	NULL	6 / 15	GSEA C2	REACTOME_FORMATION_OF_TUBULIN_FOLDING_INTERMED
18	9.74	NULL	5 / 10	CC	zona pellucida receptor complex
19	9.56	NULL	6 / 16	Cancer	WOLFER_overlap genes
20	9.25	NULL	9 / 36	BP	'de novo' posttranslational protein folding
21	9.19	NULL	38 / 534	Chr	Chr 8
22	8.8	NULL	5 / 9	GSEA C2	BIOCARTA_RANMS_PATHWAY
23	8.68	NULL	71 / 1233	TF	KIM_MYC targets
24	8.66	NULL	6 / 14	MMML CGS	MACIEJ_MMML 4
25	8.64	NULL	39 / 743	Chr	Chr 7
26	8.55	NULL	7 / 16	Cancer	RHODES_UNDIFFERENTIATED_CANCER
27	8.54	NULL	30 / 232	BP	mitosis
28	8.45	NULL	10 / 18	BP	spindle organization
29	8.42	NULL	22 / 148	BP	G1/S transition of mitotic cell cycle
30	8.38	NULL	7 / 16	GSEA C2	KANG_DOXORUBICIN_RESISTANCE_UP
31	8.38	NULL	4 / 16	GSEA C2	PUJANA_BREAST_CANCER_WITH_BRCA1_MUTATED_UP
32	8.25	NULL	3 / 13	GSEA C2	BOYAULT_LIVER_CANCER_SUBCLASS_G3_UP
33	8.24	NULL	48 / 572	Disease	GUDJ_psoriasis up
34	7.98	NULL	3 / 15	GSEA C2	TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_LOBULAR_
35	7.88	NULL	4 / 16	GSEA C2	LY_AGING_PREMATURE_DN
36	7.51	NULL	5 / 15	GSEA C2	LY_AGING_OLD_DN
37	7.46	NULL	2 / 19	BP	ATP biosynthetic process
38	7.43	NULL	4 / 11	GSEA C2	REACTOME_PURINE_RIBONUCLEOSIDE_MONOPHOSPHATE_
39	7.37	NULL	6 / 16	GSEA C2	EGUCHI_CELL_CYCLE_RB1_TARGETS
40	7.23	NULL	4 / 10	GSEA C2	MONTERO_THYROID_CANCER_POOR_SURVIVAL_UP



GW_211

Local Summary

%DE = 0.94

metagenes = 22

genes = 378

genes in genesets = 376

genes with fdr < 0.1 = 340 (10 + / 330 −)

genes with fdr < 0.05 = 317 (8 + / 309 −)

genes with fdr < 0.01 = 258 (4 + / 254 −)

<r> metagenes = 0.95

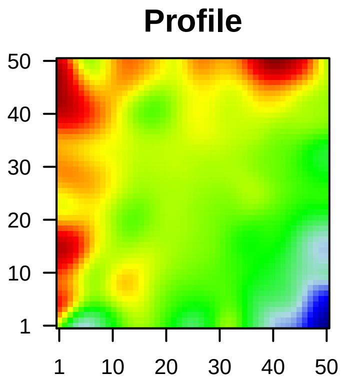
<r> genes = 0.48

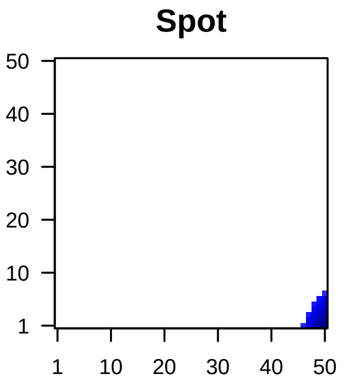
<FC> = −0.54

<shrinkage−t> = −18.93

<p−value> = 0

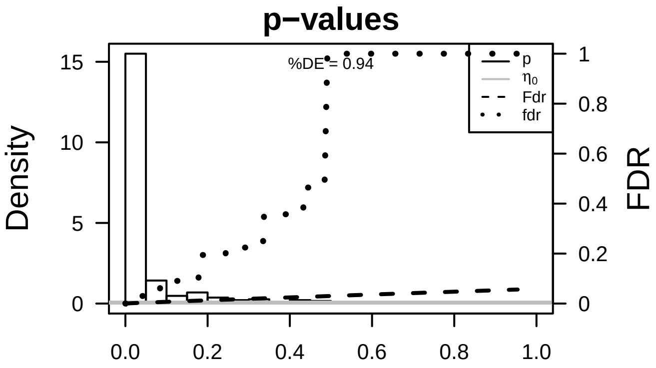
<fdr> = 0.33





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	6363	−1.51	2e−16	1e−15	50 x 1	chemokine (C−C motif) ligand 19 [Source:HGNC Symbol;Acc
2	894	−1.46	2e−16	1e−15	50 x 4	cyclin D2 [Source:HGNC Symbol;Acc:1583]
3	10365	−1.46	2e−16	1e−15	50 x 3	Kruppel−like factor 2 [Source:HGNC Symbol;Acc:6347]
4	5996	−1.53	2e−16	1e−15	50 x 1	regulator of G−protein signaling 1 [Source:HGNC Symbol;Acc
5	713	−1.39	4e−15	6e−13	50 x 1	complement component 1, q subcomponent, B chain [Source
6	3109	−1.34	3e−14	1e−12	50 x 1	major histocompatibility complex, class II, DM beta [Source:H
7	10537	−1.32	8e−14	6e−11	50 x 1	ubiquitin D [Source:HGNC Symbol;Acc:18795]
8	25849	−1.23	3e−12	7e−11	50 x 2	prostate androgen−regulated mucin−like protein 1 [Source:HG
9	6451	−1.21	7e−12	7e−11	50 x 5	SH3 domain binding glutamic acid−rich protein like [Source:H
10	3113	−1.2	9e−12	2e−10	50 x 1	major histocompatibility complex, class II, DP alpha 1 [Source
11	3122	−1.11	2e−11	9e−10	50 x 1	major histocompatibility complex, class II, DR alpha [Source:H
12	3059	−1.15	7e−11	9e−10	50 x 1	hematopoietic cell−specific Lyn substrate 1 [Source:HGNC Sy
13	55303	−1.13	1e−10	9e−10	50 x 1	GTPase, IMAP family member 4 [Source:HGNC Symbol;Acc:
14	6925	−1.13	2e−10	9e−10	50 x 6	transcription factor 4 [Source:HGNC Symbol;Acc:11634]
15	919	−1.13	2e−10	1e−09	50 x 1	CD247 molecule [Source:HGNC Symbol;Acc:1677]
16	51176	−1.11	3e−10	1e−09	50 x 5	lymphoid enhancer−binding factor 1 [Source:HGNC Symbol;A
17	962	−1.11	3e−10	1e−09	50 x 1	CD48 molecule [Source:HGNC Symbol;Acc:1683]
18	5920	−1.11	3e−10	4e−09	48 x 1	retinoic acid receptor responder (tazarotene induced) 3 [Sour
19	5730	−1.09	6e−10	4e−09	50 x 1	prostaglandin D2 synthase 21kDa (brain) [Source:HGNC Syn
20	30061	−1.08	8e−10	4e−09	50 x 5	solute carrier family 40 (iron−regulated transporter), member



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−28.31	NULL	12 / 15	CC	MHC class II protein complex
2	−22.28	NULL	91 / 417	H.Tiss	WIRTH_Immune system
3	−20.63	NULL	108 / 553	Cancer	Lembcke_Colonic Inflammation
4	−18.92	NULL	59 / 312	BP	immune response
5	−17.98	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
6	−17.32	NULL	15 / 47	BP	antigen processing and presentation
7	−16.28	NULL	7 / 12	GSEA C2	ZHAN_MULTIPLE_MYELOMA_DN
8	−16.04	NULL	6 / 11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
9	−14.92	NULL	3 / 6	GSEA C2	SANA_RESPONSE_TO_IFNG_UP
10	−14.53	NULL	15 / 60	BP	T cell costimulation
11	−14.21	NULL	7 / 15	GSEA C2	FINAK_BREAST_CANCER_SDPP_SIGNATURE
12	−13.82	NULL	2 / 4	MMML CGS	MACIEJ_MMML 2
13	−13.74	NULL	5 / 11	GSEA C2	BIOCARTA_THELPER_PATHWAY
14	−13.62	NULL	7 / 8	Glio	Donson−migration tethering and rolling−associated with LTS in HG
15	−13.54	NULL	7 / 21	CC	clathrin−coated endocytic vesicle membrane
16	−13.07	NULL	2 / 4	GSEA C2	REACTOME_CLASSICAL_ANTIBODY_MEDIATED_COMPLEMEN
17	−12.86	NULL	7 / 23	CC	integral to lumenal side of endoplasmic reticulum membrane
18	−12.85	NULL	4 / 7	Glio	Donson−cytotoxic effectors−associated with LTS in HGA
19	−12.57	NULL	7 / 16	Lymphoma	WRIGHT_ABC UP
20	−12.54	NULL	5 / 10	GSEA C2	LEE_DIFFERENTIATING_T_LYMPHOCYTE
21	−12.45	NULL	18 / 74	BP	regulation of immune response
22	−12.25	NULL	29 / 162	CC	external side of plasma membrane
23	−12.21	NULL	5 / 12	GSEA C2	BIOCARTA_CTL_PATHWAY
24	−12.01	NULL	5 / 13	GSEA C2	BIOCARTA_IL17_PATHWAY
25	−12	NULL	9 / 35	CC	trans−Golgi network membrane
26	−11.92	NULL	48 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
27	−11.92	NULL	48 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
28	−11.92	NULL	48 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
29	−11.92	NULL	48 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
30	−11.76	NULL	4 / 16	GSEA C2	KORKOLA_TERATOMA_UP
31	−11.75	NULL	8 / 16	GSEA C2	SU_THYMUS
32	−11.74	NULL	8 / 28	CC	transport vesicle membrane
33	−11.65	NULL	6 / 13	Cancer	GENTLES_modul18
34	−11.63	NULL	4 / 9	GSEA C2	MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN
35	−11.58	NULL	16 / 84	BP	T cell receptor signaling pathway
36	−11.26	NULL	2 / 3	GSEA C2	KEGG_VIRAL_MYOCARDITIS
37	−11.01	NULL	5 / 10	GSEA C2	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_
38	−10.86	NULL	14 / 87	BP	antigen processing and presentation of exogenous peptide antigen
39	−10.66	NULL	11 / 60	BP	interferon−gamma−mediated signaling pathway
40	−10.62	NULL	7 / 32	CC	ER to Golgi transport vesicle membrane