GW_013

Global Summary

%DE = 0.14

genes with fdr < 0.2 = 1655 (1002 + / 653 −)

genes with fdr < 0.1 = 1386 (888 + / 498 −)

genes with fdr < 0.05 = 1155 (773 + / 382 −)

genes with fdr < 0.01 = 786 (594 + / 192 −)

genes in genesets = 16332

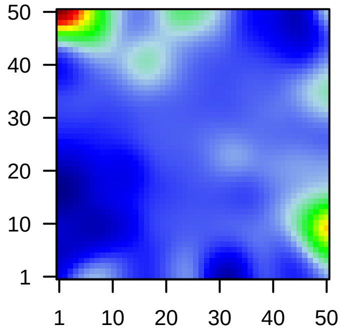
<FC> = 0

<shrinkage−t> = 0

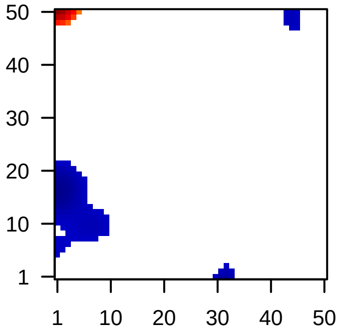
<p−value> = 0.1

<fdr> = 0.86

Profile



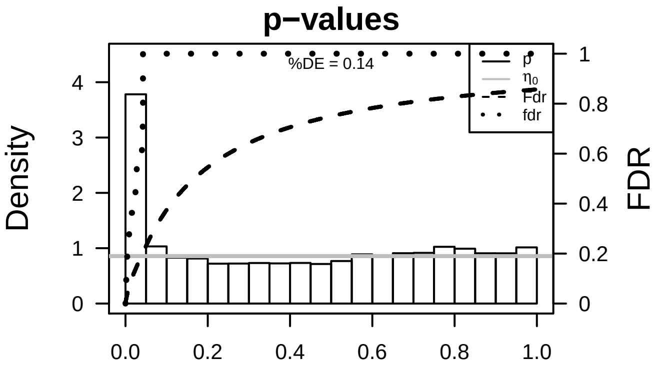
Regulated Spots



Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	144568	1.79	2e−16	2e−14	1 x 50	alpha−2−macroglobulin−like 1 [Source:HGNC Symbol;Acc:23
2	55	1.35	2e−16	2e−14	4 x 50	acid phosphatase, prostate [Source:HGNC Symbol;Acc:125]
3	131	2.69	2e−16	2e−14	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
4	57016	1.55	2e−16	2e−14	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
5	216	2.66	2e−16	2e−14	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGNC
6	220	1.3	2e−16	2e−14	4 x 46	aldehyde dehydrogenase 1 family, member A3 [Source:HGNC
7	218	2.02	2e−16	2e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
8	242	1.65	2e−16	2e−14	1 x 48	arachidonate 12−lipoxygenase, 12R type [Source:HGNC Sym
9	347	2.34	2e−16	2e−14	50 x 7	apolipoprotein D [Source:HGNC Symbol;Acc:612]
10	360	1.36	2e−16	2e−14	1 x 50	aquaporin 3 (Gill blood group) [Source:HGNC Symbol;Acc:63
11	23120	1.43	2e−16	2e−14	1 x 50	ATPase, class V, type 10B [Source:HGNC Symbol;Acc:13543
12	10331	1.28	2e−16	2e−14	15 x 40	UDP−GlcNAc:betaGal beta−1,3−N−acetylglucosaminyltransfe
13	80341	1.5	2e−16	2e−14	50 x 10	BPI fold containing family B, member 2 [Source:HGNC Symb
14	684	−1.33	2e−16	2e−14	32 x 1	bone marrow stromal cell antigen 2 [Source:HGNC Symbol;A
15	79949	1.34	2e−16	2e−14	50 x 10	pleckstrin homology domain containing, family S member 1 [S
16	92747	4.5	2e−16	2e−14	50 x 10	BPI fold containing family B, member 1 [Source:HGNC Symb
17	140683	1.76	2e−16	2e−14	18 x 37	BPI fold containing family A, member 2 [Source:HGNC Symb
18	391267	1.38	2e−16	2e−14	50 x 13	ankyrin repeat domain 20 family, member A11, pseudogene [
19	260436	1.42	2e−16	2e−14	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symb
20	389336	1.3	2e−16	2e−14	5 x 5	chromosome 5 open reading frame 46 [Source:HGNC Symb

p−values



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	31.06	NULL	135	H.Tiss	WIRTH_Mucosa
2	16.83	NULL	21	CC	cornified envelope
3	14.71	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_D
4	14.22	NULL	53	BP	keratinocyte differentiation
5	13.66	NULL	42	BP	keratinization
6	13.52	NULL	19	BP	peptide cross−linking
7	13.16	NULL	16	GSEA C2	CROMER_TUMORIGENESIS_DN
8	10.58	NULL	375	Disease	GUDJ_psoriasis down
9	9.15	NULL	24	TF Tissue	VAQUERIZAS_Trachea
10	8.7	NULL	572	Disease	GUDJ_psoriasis up
11	8.65	NULL	16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
12	8.46	NULL	1146	TF	HEBENSTREIT_low expression TF
13	8.38	NULL	1182	CC	extracellular region
14	8.05	NULL	15	GSEA C2	LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
15	7.78	NULL	16	GSEA C2	DAZARD_UV_RESPONSE_CLUSTER_G24
16	7.65	NULL	12	BP	cellular aldehyde metabolic process
17	7.55	NULL	38	BP	epithelial cell differentiation
18	7.49	NULL	186	MF	structural molecule activity
19	7.44	NULL	201	CC	apical plasma membrane
20	7.38	NULL	618	Chr	Chr 4
Underexpressed					
1	−12.53	NULL	142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
2	−12.53	NULL	142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
3	−9.58	NULL	370	BP	mitotic cell cycle
4	−9.37	NULL	51	BP	type I interferon signaling pathway
5	−8.64	NULL	4	MMML CGS	MACIEJ_MMML 23
6	−7.62	NULL	74	BP	antigen processing and presentation of exogenous peptide antigen
7	−7.52	NULL	949	CC	nucleoplasm
8	−7.51	NULL	13	GSEA C2	BOWIE_RESPONSE_TO_TAMOXIFEN
9	−7.5	NULL	16	GSEA C2	EINAV_INTERFERON_SIGNATURE_IN_CANCER
10	−7.4	NULL	123	BP	defense response to virus
11	−7.36	NULL	16	GSEA C2	UROSEVIC_RESPONSE_TO_IMIQUIMOD
12	−7.33	NULL	70	BP	antigen processing and presentation of exogenous peptide antigen
13	−7.17	NULL	530	Cancer	Lembcke_Normal vs Adenoma
14	−7.16	NULL	16	GSEA C2	ZHANG_INTERFERON_RESPONSE
15	−7.11	NULL	10	GSEA C2	BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
16	−6.91	NULL	74	BP	anaphase−promoting complex−dependent proteasomal ubiquitin−c
17	−6.86	NULL	4640	CC	nucleus
18	−6.46	NULL	298	BP	DNA repair
19	−6.33	NULL	16	GSEA C2	MOSERLE_IFNA_RESPONSE
20	−6.33	NULL	70	BP	regulation of ubiquitin−protein ligase activity involved in mitotic cell

GW_013

Local Summary

%DE = 0.99

metagenes = 12

genes = 196

genes in genesets = 192

genes with fdr < 0.1 = 192 (187 + / 5 −)

genes with fdr < 0.05 = 190 (185 + / 5 −)

genes with fdr < 0.01 = 190 (185 + / 5 −)

<r> metagenes = 0.98

<r> genes = 0.47

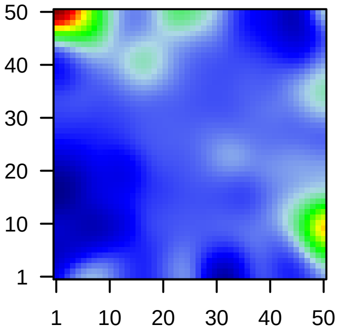
<FC> = 1.2

<shrinkage−t> = 42.14

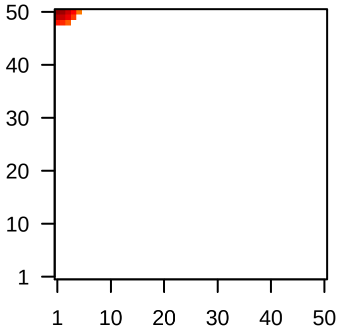
<p−value> = 0

<fdr> = 0.04

Profile



Spot



Local Genelist

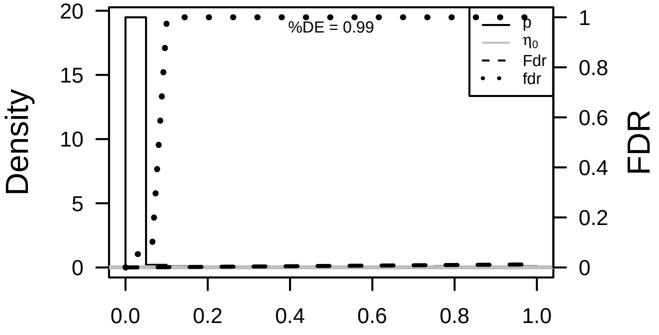
Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	144568	1.79	2e−16	7e−18	1 x 50	alpha−2−macroglobulin−like 1 [Source:HGNC Symbol;Acc:23
2	55	1.35	2e−16	7e−18	4 x 50	acid phosphatase, prostate [Source:HGNC Symbol;Acc:125]
3	131	2.69	2e−16	7e−18	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
4	57016	1.55	2e−16	7e−18	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
5	218	2.02	2e−16	7e−18	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
6	242	1.65	2e−16	7e−18	1 x 48	arachidonate 12−lipoxygenase, 12R type [Source:HGNC Sym
7	360	1.36	2e−16	7e−18	1 x 50	aquaporin 3 (Gill blood group) [Source:HGNC Symbol;Acc:63
8	23120	1.43	2e−16	7e−18	1 x 50	ATPase, class V, type 10B [Source:HGNC Symbol;Acc:13543
9	394263	2.01	2e−16	7e−18	3 x 50	
10	375791	2.3	2e−16	7e−18	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Symb
11	1048	2.19	2e−16	7e−18	2 x 50	carcinoembryonic antigen−related cell adhesion molecule 5 [
12	4680	1.72	2e−16	7e−18	1 x 50	carcinoembryonic antigen−related cell adhesion molecule 6 (
13	22802	2.75	2e−16	7e−18	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
14	9022	1.74	2e−16	7e−18	1 x 50	chloride intracellular channel 3 [Source:HGNC Symbol;Acc:2
15	84518	1.84	2e−16	7e−18	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
16	54544	1.85	2e−16	7e−18	1 x 50	cysteine−rich C−terminal 1 [Source:HGNC Symbol;Acc:2987
17	49860	2.99	2e−16	7e−18	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
18	1475	1.4	2e−16	7e−18	1 x 50	cystatin A (stefin A) [Source:HGNC Symbol;Acc:2481]
19	1562	1.94	2e−16	7e−18	1 x 50	cytochrome P450, family 2, subfamily C, polypeptide 18 [Sou
20	1577	2.28	2e−16	7e−18	4 x 50	cytochrome P450, family 3, subfamily A, polypeptide 5 [Sourc

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	57.88	NULL	72 / 135	H.Tiss	WIRTH_Mucosa
2	35.1	NULL	14 / 21	CC	cornified envelope
3	28.74	NULL	16 / 42	BP	keratinization
4	27.84	NULL	19 / 53	BP	keratinocyte differentiation
5	24.52	NULL	8 / 19	BP	peptide cross−linking
6	22.27	NULL	76 / 572	Disease	GUDJ_psoriasis up
7	20.22	NULL	6 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
8	17.32	NULL	19 / 76	BP	epidermis development
9	15.86	NULL	6 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
10	14.02	NULL	5 / 10	GSEA C2	KEGG_LINOLEIC_ACID_METABOLISM
11	13.01	NULL	7 / 38	BP	epithelial cell differentiation
12	12.58	NULL	6 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
13	11.54	NULL	6 / 13	BP	negative regulation of peptidase activity
14	11.31	NULL	4 / 15	MF	retinol dehydrogenase activity
15	10.91	NULL	4 / 15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
16	10.37	NULL	12 / 122	MF	serine−type endopeptidase activity
17	10.35	NULL	6 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
18	9.87	NULL	11 / 79	MF	serine−type endopeptidase inhibitor activity
19	9.76	NULL	6 / 15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
20	9.76	NULL	5 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
21	9.71	NULL	2 / 11	GSEA C2	ROME_INSULIN_TARGETS_IN_MUSCLE_DN
22	9.69	NULL	4 / 10	GSEA C2	SMID_BREAST_CANCER_ERBB2_UP
23	9.69	NULL	3 / 11	GSEA C2	REACTOME_XENOBIOTICS
24	9.54	NULL	5 / 21	CC	desmosome
25	9.46	NULL	3 / 14	GSEA C2	KIM_RESPONSE_TO_TSA_AND_DECITABINE_UP
26	9.45	NULL	49 / 1182	CC	extracellular region
27	9.29	NULL	5 / 16	GSEA C2	LEE_LIVER_CANCER_MYC_TGFA_UP
28	8.92	NULL	3 / 14	GSEA C2	CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U
29	8.89	NULL	3 / 12	BP	cellular aldehyde metabolic process
30	8.58	NULL	13 / 186	MF	structural molecule activity
31	8.42	NULL	4 / 23	MF	peptidase inhibitor activity
32	8.39	NULL	4 / 44	CC	keratin filament
33	8.29	NULL	1 / 6	GSEA C2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_B_DN
34	8.04	NULL	3 / 18	BP	retinol metabolic process
35	7.63	NULL	4 / 15	GSEA C2	LEE_LIVER_CANCER_MYC_E2F1_UP
36	7.51	NULL	2 / 15	GSEA C2	ALONSO_METASTASIS_NEURAL_UP
37	7.42	NULL	3 / 16	GSEA C2	COLDREN_GEFITINIB_RESISTANCE_DN
38	7.39	NULL	4 / 39	BP	retinoid metabolic process
39	7.3	NULL	5 / 10	MF	RAGE receptor binding
40	7.16	NULL	3 / 15	GSEA C2	CHANG_IMMORTALIZED_BY_HPV31_DN

p−values



GW_013

Local Summary

%DE = 0.92

metagenes = 8

genes = 127

genes in genesets = 124

genes with fdr < 0.1 = 104 (2 + / 102 −)

genes with fdr < 0.05 = 100 (2 + / 98 −)

genes with fdr < 0.01 = 75 (2 + / 73 −)

<r> metagenes = 0.99

<r> genes = 0.43

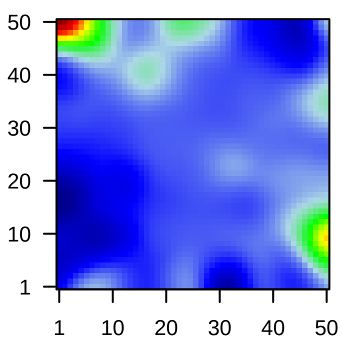
<FC> = −0.48

<shrinkage−t> = −16.77

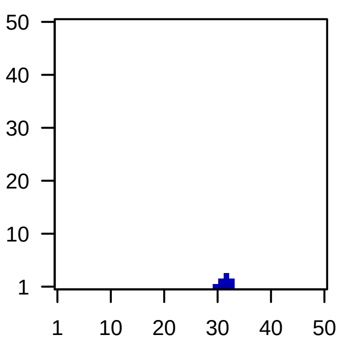
<p−value> = 0

<fdr> = 0.36

Profile



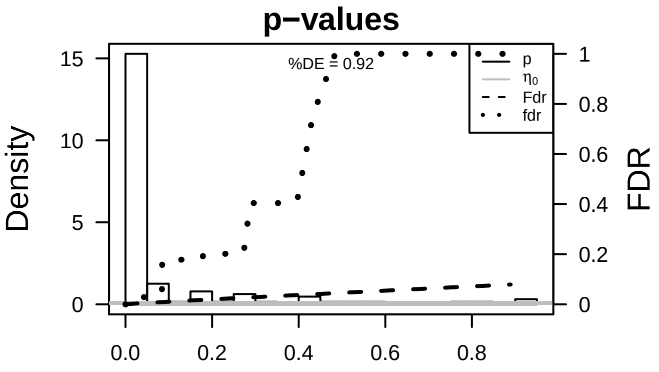
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	684	−1.33	2e−16	8e−16	32 x 1	bone marrow stromal cell antigen 2 [Source:HGNC Symbol;A
2	3627	−1.28	2e−16	8e−16	32 x 1	chemokine (C−X−C motif) ligand 10 [Source:HGNC Symbol;A
3	9636	−1.57	2e−16	8e−16	32 x 1	ISG15 ubiquitin−like modifier [Source:HGNC Symbol;Acc:405
4	1591	1.16	8e−14	1e−10	33 x 2	cytochrome P450, family 24, subfamily A, polypeptide 1 [Sour
5	51191	−1.06	1e−11	2e−10	32 x 1	HECT and RLD domain containing E3 ubiquitin protein ligase
6	4321	−1.02	5e−11	2e−10	32 x 1	matrix metallopeptidase 12 (macrophage elastase) [Source:H
7	7453	−1.02	6e−11	2e−10	32 x 1	tryptophanyl−tRNA synthetase [Source:HGNC Symbol;Acc:1
8	3430	−1.02	7e−11	3e−09	32 x 1	interferon−induced protein 35 [Source:HGNC Symbol;Acc:53
9	115362	−0.95	1e−09	3e−09	32 x 1	guanylate binding protein 5 [Source:HGNC Symbol;Acc:1989
10	10410	−0.87	1e−09	3e−09	32 x 1	interferon induced transmembrane protein 3 [Source:HGNC S
11	3433	−0.94	2e−09	3e−09	32 x 1	interferon−induced protein with tetratricopeptide repeats 2 [So
12	2537	−0.94	2e−09	3e−09	32 x 1	interferon, alpha−inducible protein 6 [Source:HGNC Symbol;A
13	10581	−0.86	2e−09	3e−09	32 x 1	interferon induced transmembrane protein 2 [Source:HGNC S
14	5699	−0.93	2e−09	5e−09	32 x 1	proteasome (prosome, macropain) subunit, beta type, 10 [Sou
15	8519	−0.92	3e−09	5e−09	32 x 1	interferon induced transmembrane protein 1 [Source:HGNC S
16	94240	−0.92	3e−09	2e−08	32 x 1	epithelial stromal interaction 1 (breast) [Source:HGNC Symbo
17	51296	−0.91	4e−09	3e−07	32 x 1	solute carrier family 15 (oligopeptide transporter), member 3 [
18	100	−0.85	4e−08	3e−07	30 x 1	adenosine deaminase [Source:HGNC Symbol;Acc:186]
19	5721	−0.84	6e−08	3e−07	32 x 1	proteasome (prosome, macropain) activator subunit 2 (PA28 I
20	4061	−0.83	8e−08	2e−06	32 x 1	lymphocyte antigen 6 complex, locus E [Source:HGNC Symb

p−values



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−52.02	NULL	29 / 51	BP	type I interferon signaling pathway
2	−45.92	NULL	9 / 10	GSEA C2	BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
3	−44.97	NULL	11 / 16	GSEA C2	EINAV_INTERFERON_SIGNATURE_IN_CANCER
4	−42.19	NULL	10 / 13	GSEA C2	BOWIE_RESPONSE_TO_TAMOXIFEN
5	−39.92	NULL	8 / 10	GSEA C2	GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
6	−38.69	NULL	13 / 16	GSEA C2	MOSERLE_IFNA_RESPONSE
7	−38.14	NULL	11 / 16	GSEA C2	UROSEVIC_RESPONSE_TO_IMIQUIMOD
8	−37.73	NULL	11 / 16	GSEA C2	ZHANG_INTERFERON_RESPONSE
9	−34.95	NULL	13 / 31	BP	negative regulation of viral genome replication
10	−34.38	NULL	3 / 4	GSEA C2	KRASNOSELSKAYA_ILF3_TARGETS_UP
11	−33.44	NULL	31 / 123	BP	defense response to virus
12	−33.3	NULL	8 / 11	GSEA C2	BENNETT_SYSTEMIC_LUPUS_ERYTHEMATOSUS
13	−31.2	NULL	6 / 6	Lymphoma	DAVE_MHCCII BL DN
14	−31.07	NULL	27 / 109	BP	response to virus
15	−29.61	NULL	6 / 12	GSEA C2	TSAI_DNAJB4_TARGETS_UP
16	−28.52	NULL	34 / 204	BP	cytokine−mediated signaling pathway
17	−27.45	NULL	3 / 5	GSEA C2	KIM_LRRC3B_TARGETS
18	−27.43	NULL	6 / 8	GSEA C2	ROETH_TERT_TARGETS_UP
19	−26.91	NULL	4 / 12	GSEA C2	ZHU_CMV_8_HR_UP
20	−25.37	NULL	6 / 14	GSEA C2	RADAEVA_RESPONSE_TO_IFNA1_UP
21	−24.84	NULL	6 / 14	GSEA C2	XU_AKT1_TARGETS_6HR
22	−24.68	NULL	7 / 10	CC	MHC class I protein complex
23	−24.64	NULL	7 / 16	GSEA C2	MAHADEVAN_RESPONSE_TO_MP470_UP
24	−24.04	NULL	4 / 10	GSEA C2	DAUER_STAT3_TARGETS_DN
25	−23.05	NULL	33 / 274	Lymphoma	SPANG_IL21 DN
26	−22.16	NULL	6 / 16	GSEA C2	XU_HGF_TARGETS_INDUCED_BY_AKT1_6HR
27	−21.95	NULL	5 / 18	BP	response to interferon−gamma
28	−21.63	NULL	6 / 14	Glio	Donson−immune cell intra signaling−associated with LTS in HGA
29	−21.24	NULL	5 / 14	GSEA C2	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_3D_UP
30	−21.07	NULL	4 / 15	GSEA C2	BECKER_TAMOXIFEN_RESISTANCE_UP
31	−20.96	NULL	5 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
32	−20.82	NULL	47 / 572	Disease	GUDJ_psoriasis up
33	−20.29	NULL	3 / 13	GSEA C2	TSAI_RESPONSE_TO_RADIATION_THERAPY
34	−20.08	NULL	4 / 14	GSEA C2	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_8D_UP
35	−20.04	NULL	2 / 2	MMML CGS	MACIEJ_MMML 27
36	−19.81	NULL	3 / 9	GSEA C2	DER_IFN_ALPHA_RESPONSE_UP
37	−19.81	NULL	3 / 9	GSEA C2	DER_IFN_GAMMA_RESPONSE_UP
38	−19.63	NULL	8 / 18	BP	positive regulation of T cell mediated cytotoxicity
39	−19.19	NULL	16 / 60	BP	interferon−gamma−mediated signaling pathway
40	−19.12	NULL	5 / 16	GSEA C2	ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_UP

GW_013

Local Summary

%DE = 0.89

metagenes = 109

genes = 1068

genes in genesets = 1059

genes with fdr < 0.1 = 721 (12 + / 709 −)

genes with fdr < 0.05 = 560 (8 + / 552 −)

genes with fdr < 0.01 = 189 (4 + / 185 −)

<r> metagenes = 0.74

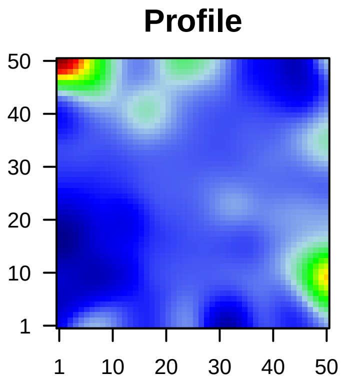
<r> genes = 0.19

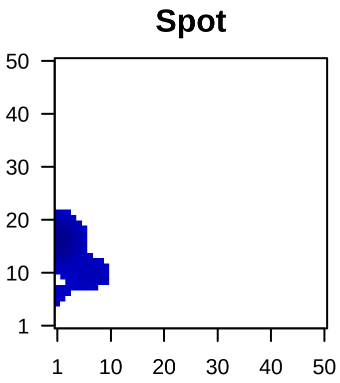
<FC> = −0.29

<shrinkage−t> = −10.04

<p−value> = 0.03

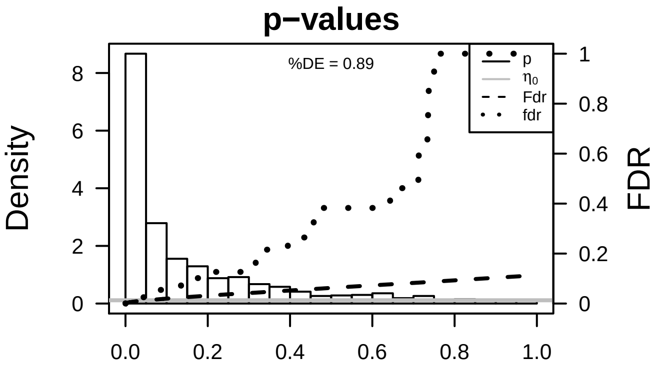
<fdr> = 0.7





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	768	−0.98	2e−10	1e−08	1 x 6	carbonic anhydrase IX [Source:HGNC Symbol;Acc:1383]
2	3237	−0.98	4e−10	1e−08	1 x 16	homeobox D11 [Source:HGNC Symbol;Acc:5134]
3	682	−0.97	4e−10	7e−08	4 x 11	basigin (Ok blood group) [Source:HGNC Symbol;Acc:1116]
4	375790	−0.95	1e−09	7e−08	1 x 7	agrin [Source:HGNC Symbol;Acc:329]
5	5690	−0.94	2e−09	2e−07	1 x 15	proteasome (prosome, macropain) subunit, beta type, 2 [Sou
6	28514	0.92	3e−09	3e−07	1 x 5	delta−like 1 (Drosophila) [Source:HGNC Symbol;Acc:2908]
7	10459	−0.9	6e−09	8e−07	8 x 9	MAD2 mitotic arrest deficient−like 2 (yeast) [Source:HGNC S
8	284111	0.87	2e−08	8e−07	1 x 7	solute carrier family 13 (sodium−dependent citrate transporte
9	3909	−0.87	2e−08	8e−07	1 x 5	laminin, alpha 3 [Source:HGNC Symbol;Acc:6483]
10	84058	−0.87	3e−08	2e−06	1 x 7	WD repeat domain 54 [Source:HGNC Symbol;Acc:25770]
11	10130	−0.85	4e−08	7e−06	1 x 13	protein disulfide isomerase family A, member 6 [Source:HGN
12	51373	−0.82	1e−07	7e−06	1 x 16	28S ribosomal protein S17, mitochondrial; HCG1984214, isof
13	3217	−0.8	3e−07	7e−06	1 x 15	homeobox B7 [Source:HGNC Symbol;Acc:5118]
14	2026	−0.8	3e−07	7e−06	10 x 10	enolase 2 (gamma, neuronal) [Source:HGNC Symbol;Acc:33
15	23338	−0.79	3e−07	7e−06	10 x 12	jade family PHD finger 2 [Source:HGNC Symbol;Acc:22984]
16	57109	−0.79	4e−07	7e−06	1 x 20	REX4, RNA exonuclease 4 homolog (S. cerevisiae) [Source:
17	3654	−0.79	4e−07	2e−05	3 x 13	interleukin−1 receptor−associated kinase 1 [Source:HGNC S
18	2131	−0.77	6e−07	2e−05	1 x 6	exostosin glycosyltransferase 1 [Source:HGNC Symbol;Acc:3
19	8772	−0.76	9e−07	2e−05	1 x 14	Fas (TNFRSF6)−associated via death domain [Source:HGNC
20	10981	−0.76	1e−06	3e−05	1 x 5	RAB32, member RAS oncogene family [Source:HGNC Symb



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−9.37	NULL	7 / 13	GSEA C2	REACTOME_GLYCOLYSIS
2	−9.02	NULL	4 / 8	GSEA C2	NIKOLSKY_BREAST_CANCER_5P15_AMPLICON
3	−8.8	NULL	15 / 66	BP	positive regulation of ubiquitin−protein ligase activity involved in mi
4	−8.8	NULL	14 / 55	CC	proteasome complex
5	−8.62	NULL	12 / 48	BP	regulation of cellular amino acid metabolic process
6	−8.6	NULL	14 / 62	BP	negative regulation of ubiquitin−protein ligase activity involved in m
7	−8.45	NULL	15 / 70	BP	regulation of ubiquitin−protein ligase activity involved in mitotic cell
8	−8.11	NULL	15 / 74	BP	anaphase−promoting complex−dependent proteasomal ubiquitin−
9	−7.99	NULL	15 / 70	BP	antigen processing and presentation of exogenous peptide antigen
10	−7.76	NULL	7 / 17	CC	proteasome accessory complex
11	−7.67	NULL	15 / 74	BP	antigen processing and presentation of exogenous peptide antigen
12	−7.67	NULL	6 / 12	BP	heparan sulfate proteoglycan biosynthetic process
13	−7.52	NULL	2 / 5	GSEA C2	DASU_IL6_SIGNALING_UP
14	−7.51	NULL	6 / 15	GSEA C2	HU_ANGIOGENESIS_UP
15	−7.48	NULL	5 / 17	CC	proteasome core complex
16	−7.37	NULL	3 / 8	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_25
17	−7.22	NULL	5 / 18	MF	threonine−type endopeptidase activity
18	−7.16	NULL	16 / 91	BP	antigen processing and presentation of peptide antigen via MHC c
19	−7.11	NULL	12 / 63	BP	DNA damage response, signal transduction by p53 class mediator
20	−6.94	NULL	4 / 10	GSEA C2	HONMA_DOCETAXEL_RESISTANCE
21	−6.93	NULL	28 / 153	MF	structural constituent of ribosome
22	−6.9	NULL	5 / 12	GSEA C2	CREIGHTON_AKT1_SIGNALING_VIA_MTOR_UP
23	−6.88	NULL	5 / 15	GSEA C2	DACOSTA_UV_RESPONSE_VIA_ERCC3_TTD_UP
24	−6.86	NULL	1 / 2	GSEA C2	PELLICCIOTTA_HDAC_IN_ANTIGEN_PRESENTATION_DN
25	−6.86	NULL	1 / 2	GSEA C2	REACTOME_DIABETES_PATHWAYS
26	−6.84	NULL	4 / 15	GSEA C2	BIOCARTA_PROTEASOME_PATHWAY
27	−6.73	NULL	4 / 12	BP	hemidesmosome assembly
28	−6.67	NULL	5 / 10	GSEA C2	HOFMANN_MYELODYSPLASTIC_SYNDROM_LOW_RISK_DN
29	−6.57	NULL	8 / 32	BP	glycosaminoglycan biosynthetic process
30	−6.53	NULL	6 / 25	BP	proteolysis involved in cellular protein catabolic process
31	−6.44	NULL	39 / 253	BP	translation
32	−6.4	NULL	6 / 16	GSEA C2	SHIPP_DLBCL_VS_FOLLICULAR_LYMPHOMA_UP
33	−6.23	NULL	7 / 16	GSEA C2	JIANG_HYPOXIA_VIA_VHL
34	−6.21	NULL	145 / 1318	CC	mitochondrion
35	−6.19	NULL	7 / 19	CC	mitochondrial small ribosomal subunit
36	−6.18	NULL	1 / 2	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_14
37	−6.17	NULL	76 / 530	Cancer	Lembcke_Normal vs Adenoma
38	−6.16	NULL	16 / 106	BP	protein polyubiquitination
39	−6.09	NULL	5 / 14	GSEA C2	RIZKI_TUMOR_INVASIVENESS_2D_DN
40	−6.09	NULL	101 / 717	Chr	Chr 16

GW_013

Local Summary

%DE = 0.84

metagenes = 11

genes = 149

genes in genesets = 147

genes with fdr < 0.1 = 98 (0 + / 98 −)

genes with fdr < 0.05 = 85 (0 + / 85 −)

genes with fdr < 0.01 = 47 (0 + / 47 −)

<r> metagenes = 0.98

<r> genes = 0.5

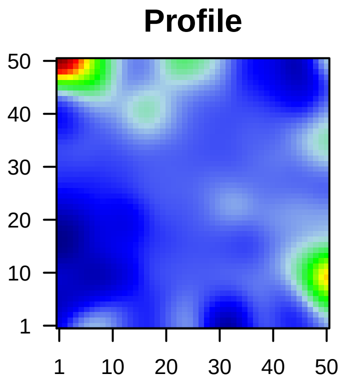
<FC> = −0.35

<shrinkage−t> = −12.36

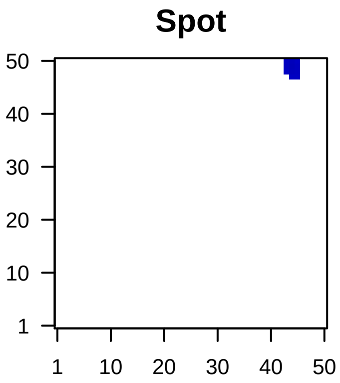
<p−value> = 0.01

<fdr> = 0.54

Profile



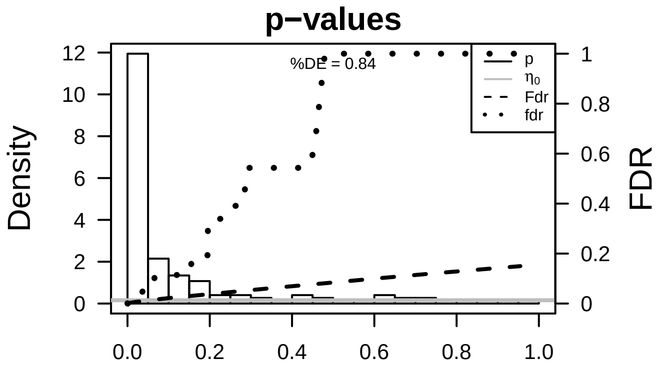
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	1163	−0.76	9e−07	4e−05	44 x 50	CDC28 protein kinase regulatory subunit 1B [Source:HGNC
2	7083	−0.73	3e−06	6e−05	45 x 49	thymidine kinase 1, soluble [Source:HGNC Symbol;Acc:1183
3	6790	−0.71	5e−06	2e−04	44 x 50	aurora kinase A [Source:HGNC Symbol;Acc:11393]
4	55355	−0.65	3e−05	2e−04	44 x 49	Holliday junction recognition protein [Source:HGNC Symbol;A
5	890	−0.65	3e−05	2e−04	44 x 50	cyclin A2 [Source:HGNC Symbol;Acc:1578]
6	9212	−0.64	3e−05	2e−04	45 x 48	aurora kinase B [Source:HGNC Symbol;Acc:11390]
7	83461	−0.64	4e−05	2e−04	44 x 50	cell division cycle associated 3 [Source:HGNC Symbol;Acc:1
8	2305	−0.63	5e−05	2e−04	44 x 49	forkhead box M1 [Source:HGNC Symbol;Acc:3818]
9	1033	−0.63	6e−05	2e−04	43 x 50	cyclin−dependent kinase inhibitor 3 [Source:HGNC Symbol;A
10	891	−0.62	6e−05	3e−04	44 x 49	cyclin B1 [Source:HGNC Symbol;Acc:1579]
11	22974	−0.61	8e−05	3e−04	44 x 50	TPX2, microtubule−associated [Source:HGNC Symbol;Acc:1
12	10797	−0.61	9e−05	3e−04	43 x 50	methylenetetrahydrofolate dehydrogenase (NADP+ depender
13	10112	−0.61	9e−05	3e−04	44 x 49	kinesin family member 20A [Source:HGNC Symbol;Acc:9787
14	10535	−0.6	1e−04	4e−04	45 x 47	ribonuclease H2, subunit A [Source:HGNC Symbol;Acc:1851
15	6119	−0.6	1e−04	4e−04	43 x 48	replication protein A3, 14kDa [Source:HGNC Symbol;Acc:102
16	29089	−0.58	2e−04	4e−04	45 x 49	ubiquitin−conjugating enzyme E2T (putative) [Source:HGNC
17	90390	−0.58	2e−04	4e−04	44 x 50	mediator complex subunit 30 [Source:HGNC Symbol;Acc:230
18	55143	−0.58	2e−04	4e−04	44 x 49	cell division cycle associated 8 [Source:HGNC Symbol;Acc:1
19	8317	−0.57	2e−04	4e−04	45 x 47	cell division cycle 7 [Source:HGNC Symbol;Acc:1745]
20	9133	−0.57	2e−04	4e−04	45 x 49	cyclin B2 [Source:HGNC Symbol;Acc:1580]

p−values



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−72.53	NULL	76 / 142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
2	−72.53	NULL	76 / 142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
3	−39.28	NULL	12 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_2
4	−36.22	NULL	13 / 16	GSEA C2	FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
5	−35.4	NULL	12 / 15	GSEA C2	FINETTI_BREAST_CANCER_KINOME_RED
6	−35	NULL	10 / 15	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
7	−34.05	NULL	10 / 14	GSEA C2	ZHAN_MULTIPLE_MYELOMA_PR_UP
8	−32.92	NULL	10 / 14	MMML CGS	MACIEJ_MMML 4
9	−32.03	NULL	9 / 13	GSEA C2	CROONQUIST_IL6_DEPRIVATION_DN
10	−30.63	NULL	10 / 16	GSEA C2	EGUCHI_CELL_CYCLE_RB1_TARGETS
11	−29.98	NULL	20 / 57	Glio	developing astrocytes
12	−28.89	NULL	8 / 10	GSEA C2	MONTERO_THYROID_CANCER_POOR_SURVIVAL_UP
13	−28.64	NULL	66 / 530	Cancer	Lembcke_Normal vs Adenoma
14	−28.4	NULL	9 / 15	GSEA C2	FOURNIER_ACINAR_DEVELOPMENT_LATE_DN
15	−27.11	NULL	58 / 370	BP	mitotic cell cycle
16	−26.74	NULL	10 / 18	BP	spindle organization
17	−25.07	NULL	9 / 16	GSEA C2	KANG_DOXORUBICIN_RESISTANCE_UP
18	−24.5	NULL	6 / 16	Cancer	RHODES_UNDIFFERENTIATED_CANCER
19	−24.16	NULL	7 / 15	GSEA C2	LY_AGING_MIDDLE_DN
20	−24.12	NULL	7 / 15	GSEA C2	CHANG_CYCLING_GENES
21	−24.04	NULL	7 / 16	GSEA C2	CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_UP
22	−23.48	NULL	7 / 16	GSEA C2	SCIAN_CELL_CYCLE_TARGETS_OF_TP53_AND_TP73_DN
23	−23.09	NULL	53 / 572	Disease	GUDJ_psoriasis up
24	−22.87	NULL	8 / 15	GSEA C2	LEE_EARLY_T_LYMPHOCYTE_UP
25	−22.84	NULL	7 / 14	GSEA C2	AMUNDSON_GAMMA_RADIATION_RESPONSE
26	−22.25	NULL	4 / 9	GSEA C2	KUMAMOTO_RESPONSE_TO_NUTLIN_3A_DN
27	−22.19	NULL	6 / 15	GSEA C2	TANG_SENESCENCE_TP53_TARGETS_DN
28	−21.98	NULL	7 / 15	GSEA C2	SMID_BREAST_CANCER_LUMINAL_A_DN
29	−21.48	NULL	6 / 16	GSEA C2	CROONQUIST_NRAS_SIGNALING_DN
30	−20.9	NULL	7 / 16	GSEA C2	GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
31	−20.18	NULL	16 / 56	CC	chromosome, centromeric region
32	−20.03	NULL	34 / 232	BP	mitosis
33	−19.76	NULL	5 / 14	GSEA C2	MISSIAGLIA_REGULATED_BY_METHYLATION_DN
34	−19.45	NULL	4 / 12	GSEA C2	SHEPARD_BMYB_TARGETS
35	−19.33	NULL	5 / 13	GSEA C2	REN_BOUND_BY_E2F
36	−18.83	NULL	5 / 16	GSEA C2	FRASOR_RESPONSE_TO_SERM_OR_FULVESTRANT_DN
37	−18.73	NULL	5 / 16	GSEA C2	CROONQUIST_NRAS_VS_STROMAL_STIMULATION_DN
38	−17.93	NULL	5 / 14	GSEA C2	LOPEZ_MESOTELIOMA_SURVIVAL_TIME_UP
39	−17.88	NULL	6 / 11	BP	mitotic metaphase plate congression
40	−17.62	NULL	4 / 11	GSEA C2	LIANG_SILENCED_BY_METHYLATION_DN