GW_097

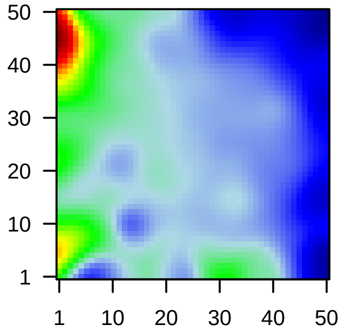
Global Summary

%DE = 0.13
genes with fdr < 0.2 = 1314 (835 + / 479 −)
genes with fdr < 0.1 = 1112 (718 + / 394 −)
genes with fdr < 0.05 = 891 (608 + / 283 −)
genes with fdr < 0.01 = 567 (418 + / 149 −)

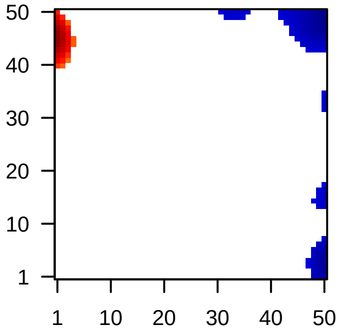
genes in genesets = 16332

<FC> = 0
<shrinkage−t> = 0
<p−value> = 0.14
<fdr> = 0.87

Profile



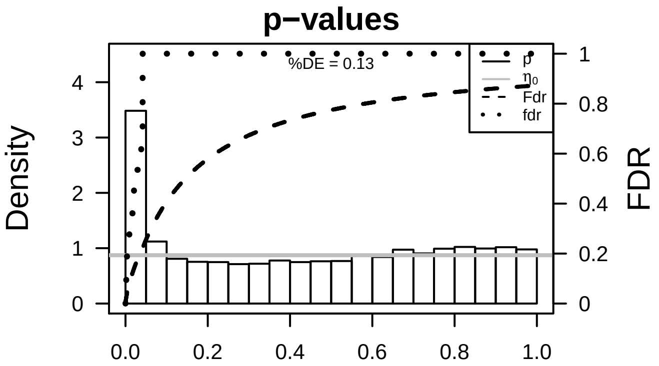
Regulated Spots



Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	218	−1.38	2e−16	6e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
2	650	1.42	2e−16	6e−14	1 x 4	bone morphogenetic protein 2 [Source:HGNC Symbol;Acc:1
3	768	1.4	2e−16	6e−14	1 x 6	carbonic anhydrase IX [Source:HGNC Symbol;Acc:1383]
4	57172	−1.46	2e−16	6e−14	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
5	1041	1.41	2e−16	6e−14	1 x 46	corneodesmosin [Source:HGNC Symbol;Acc:1802]
6	51200	1.55	2e−16	6e−14	1 x 44	carboxypeptidase A4 [Source:HGNC Symbol;Acc:15740]
7	1464	1.7	2e−16	6e−14	1 x 3	chondroitin sulfate proteoglycan 4 [Source:HGNC Symbol;Ac
8	1474	1.59	2e−16	6e−14	1 x 47	cystatin E/M [Source:HGNC Symbol;Acc:2478]
9	9547	2.45	2e−16	6e−14	1 x 46	chemokine (C−X−C motif) ligand 14 [Source:HGNC Symbol;
10	1577	−1.37	2e−16	6e−14	4 x 50	cytochrome P450, family 3, subfamily A, polypeptide 5 [Sourc
11	27065	1.84	2e−16	6e−14	1 x 46	Homo sapiens neuron specific gene family member 1 (NSG1
12	54541	1.49	2e−16	6e−14	1 x 4	DNA−damage−inducible transcript 4 [Source:HGNC Symbol;
13	414325	1.44	2e−16	6e−14	1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
14	1828	1.59	2e−16	6e−14	1 x 48	desmoglein 1 [Source:HGNC Symbol;Acc:3048]
15	2152	1.86	2e−16	6e−14	1 x 43	coagulation factor III (thromboplastin, tissue factor) [Source:H
16	2167	2.14	2e−16	6e−14	1 x 44	fatty acid binding protein 4, adipocyte [Source:HGNC Symbol
17	115572	1.63	2e−16	6e−14	1 x 48	family with sequence similarity 46, member B [Source:HGNC
18	10804	1.65	2e−16	6e−14	1 x 47	gap junction protein, beta 6, 30kDa [Source:HGNC Symbol;A
19	283120	−1.97	2e−16	6e−14	25 x 1	H19, imprinted maternally expressed transcript (non−protein
20	374918	2	2e−16	6e−14	1 x 45	IGF−like family member 1 [Source:HGNC Symbol;Acc:24093

p−values



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	19.35	NULL	135	H.Tiss	WIRTH_Mucosa
2	16.17	NULL	572	Disease	GUDJ_psoriasis up
3	12.87	NULL	76	BP	epidermis development
4	11.75	NULL	21	CC	cornified envelope
5	9.87	NULL	53	BP	keratinocyte differentiation
6	9.81	NULL	957	Chr	Chr 11
7	8.36	NULL	42	BP	keratinization
8	8.09	NULL	2659	CC	plasma membrane
9	8.03	NULL	16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
10	7.95	NULL	15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
11	7.87	NULL	21	CC	desmosome
12	7.52	NULL	186	MF	structural molecule activity
13	7.5	NULL	9	GSEA C2	WANG_RESPONSE_TO_PACLITAXEL_VIA_MAPK8_UP
14	7.47	NULL	15	GSEA C2	LEE_LIVER_CANCER_HEPATOBLAST
15	7.45	NULL	15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_DN
16	7.44	NULL	82	CC	intermediate filament
17	7.26	NULL	12	BP	hemidesmosome assembly
18	7.14	NULL	16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
19	7.02	NULL	6	Lymphoma	DAVE_MHCCII BL DN
20	6.89	NULL	16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
Underexpressed					
1	−6.53	NULL	153	MF	structural constituent of ribosome
2	−6.53	NULL	1318	CC	mitochondrion
3	−6.4	NULL	595	MF	RNA binding
4	−6.2	NULL	128	BP	translational initiation
5	−6.17	NULL	92	BP	translational elongation
6	−6.09	NULL	81	BP	viral transcription
7	−6.02	NULL	87	BP	translational termination
8	−5.78	NULL	8	GSEA C2	RUNNE_GENDER_EFFECT_UP
9	−5.67	NULL	109	BP	SRP−dependent cotranslational protein targeting to membrane
10	−5.67	NULL	167	CC	ribosome
11	−5.66	NULL	37	CC	cytosolic small ribosomal subunit
12	−5.64	NULL	7	MMML CGS	MACIEJ_MMML 5
13	−5.58	NULL	83	BP	respiratory electron transport chain
14	−5.33	NULL	92	BP	viral life cycle
15	−5.33	NULL	1233	TF	KIM_MYC targets
16	−5.29	NULL	115	BP	nuclear−transcribed mRNA catabolic process, nonsense−mediated
17	−5.23	NULL	9	GSEA C2	KEGG_RIBOSOME
18	−5.18	NULL	12	GSEA C2	REACTOME_FORMATION_OF_THE_TERNARY_COMPLEX_AN
19	−5.15	NULL	12	GSEA C2	REACTOME_TRANSLATION_INITIATION_COMPLEX_FORMATI
20	−5.13	NULL	9	GSEA C2	REACTOME_FORMATION_OF_A_POOL_OF_FREE_40S_SUBU

GW_097

Local Summary

%DE = 0.88

metagenes = 31

genes = 409

genes in genesets = 400

genes with fdr < 0.1 = 314 (303 + / 11 −)

genes with fdr < 0.05 = 296 (287 + / 9 −)

genes with fdr < 0.01 = 250 (243 + / 7 −)

<r> metagenes = 0.87

<r> genes = 0.34

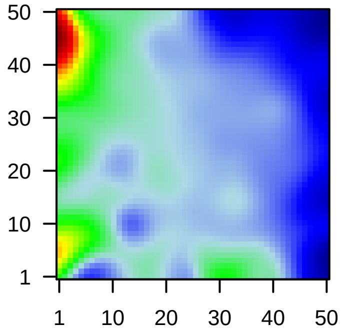
<FC> = 0.62

<shrinkage−t> = 21.87

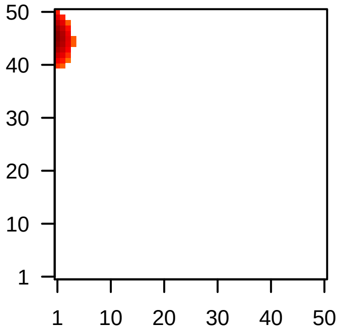
<p−value> = 0

<fdr> = 0.31

Profile



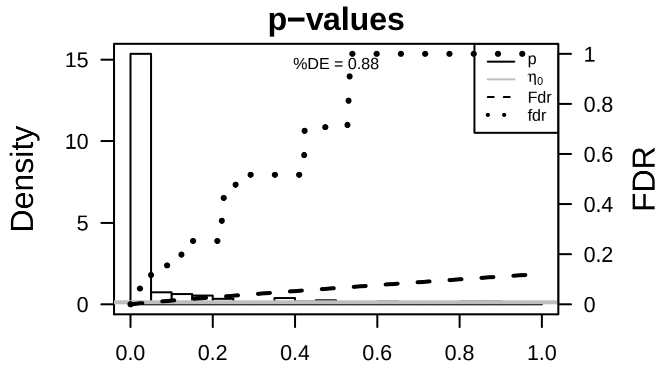
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	218	−1.38	2e−16	4e−16	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
2	1041	1.41	2e−16	4e−16	1 x 46	corneodesmosin [Source:HGNC Symbol;Acc:1802]
3	51200	1.55	2e−16	4e−16	1 x 44	carboxypeptidase A4 [Source:HGNC Symbol;Acc:15740]
4	1474	1.59	2e−16	4e−16	1 x 47	cystatin E/M [Source:HGNC Symbol;Acc:2478]
5	9547	2.45	2e−16	4e−16	1 x 46	chemokine (C−X−C motif) ligand 14 [Source:HGNC Symbol;
6	27065	1.84	2e−16	4e−16	1 x 46	Homo sapiens neuron specific gene family member 1 (NSG1
7	414325	1.44	2e−16	4e−16	1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
8	1828	1.59	2e−16	4e−16	1 x 48	desmoglein 1 [Source:HGNC Symbol;Acc:3048]
9	2152	1.86	2e−16	4e−16	1 x 43	coagulation factor III (thromboplastin, tissue factor) [Source:H
10	2167	2.14	2e−16	4e−16	1 x 44	fatty acid binding protein 4, adipocyte [Source:HGNC Symbol
11	115572	1.63	2e−16	4e−16	1 x 48	family with sequence similarity 46, member B [Source:HGNC
12	10804	1.65	2e−16	4e−16	1 x 47	gap junction protein, beta 6, 30kDa [Source:HGNC Symbol;A
13	374918	2	2e−16	4e−16	1 x 45	IGF−like family member 1 [Source:HGNC Symbol;Acc:24093
14	26085	1.81	2e−16	4e−16	1 x 50	kallikrein−related peptidase 13 [Source:HGNC Symbol;Acc:6
15	5653	1.83	2e−16	4e−16	1 x 50	kallikrein−related peptidase 6 [Source:HGNC Symbol;Acc:63
16	5650	1.61	2e−16	4e−16	1 x 49	kallikrein−related peptidase 7 [Source:HGNC Symbol;Acc:63
17	3848	2.67	2e−16	4e−16	1 x 47	keratin 1 [Source:HGNC Symbol;Acc:6412]
18	3861	1.41	2e−16	4e−16	1 x 45	keratin 14 [Source:HGNC Symbol;Acc:6416]
19	3868	1.63	2e−16	4e−16	1 x 46	keratin 16 [Source:HGNC Symbol;Acc:6423]
20	8581	1.81	2e−16	4e−16	1 x 48	lymphocyte antigen 6 complex, locus D [Source:HGNC Symb

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	38.26	NULL	86 / 135	H.Tiss	WIRTH_Mucosa
2	29.82	NULL	131 / 572	Disease	GUDJ_psoriasis up
3	26.23	NULL	18 / 21	CC	cornified envelope
4	23.41	NULL	29 / 76	BP	epidermis development
5	19.58	NULL	25 / 53	BP	keratinocyte differentiation
6	17.15	NULL	20 / 42	BP	keratinization
7	16.53	NULL	8 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
8	16.12	NULL	4 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
9	14.96	NULL	13 / 21	CC	desmosome
10	14.61	NULL	6 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
11	14.35	NULL	24 / 82	CC	intermediate filament
12	14.04	NULL	10 / 19	BP	peptide cross−linking
13	13.71	NULL	13 / 44	CC	keratin filament
14	13.58	NULL	8 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
15	13.28	NULL	7 / 15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL
16	12.45	NULL	32 / 186	MF	structural molecule activity
17	11.7	NULL	7 / 15	GSEA C2	AIGNER_ZEB1_TARGETS
18	11.7	NULL	6 / 16	GSEA C2	COLDREN_GEFITINIB_RESISTANCE_DN
19	11	NULL	3 / 6	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_UP
20	10.94	NULL	4 / 13	GSEA C2	REACTOME_GAP_JUNCTION_TRAFFICKING
21	10.69	NULL	11 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
22	10.42	NULL	4 / 16	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_LUNG_UP
23	9.6	NULL	3 / 15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
24	9.6	NULL	7 / 38	BP	epithelial cell differentiation
25	9.43	NULL	4 / 12	GSEA C2	REACTOME_GAP_JUNCTION_ASSEMBLY
26	9.42	NULL	3 / 11	GSEA C2	LEI_MYB_TARGETS
27	9.31	NULL	4 / 15	GSEA C2	KARAKAS_TGFB1_SIGNALING
28	9.1	NULL	74 / 1182	CC	extracellular region
29	9.09	NULL	3 / 10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
30	9.06	NULL	6 / 15	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_3
31	8.91	NULL	13 / 82	MF	structural constituent of cytoskeleton
32	8.84	NULL	4 / 10	GSEA C2	REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION_
33	8.73	NULL	6 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_4
34	8.72	NULL	3 / 10	GSEA C2	DAZARD_UV_RESPONSE_CLUSTER_G3
35	8.56	NULL	4 / 13	BP	intermediate filament cytoskeleton organization
36	8.41	NULL	4 / 15	BP	fibrinolysis
37	8.41	NULL	4 / 15	GSEA C2	LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
38	8.27	NULL	4 / 15	CC	connexon complex
39	8.08	NULL	3 / 15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_DN
40	8.05	NULL	5 / 21	CC	gap junction

GW_097

Local Summary

%DE = 0.64

metagenes = 23

genes = 386

genes in genesets = 384

genes with fdr < 0.1 = 148 (14 + / 134 −)

genes with fdr < 0.05 = 117 (11 + / 106 −)

genes with fdr < 0.01 = 69 (8 + / 61 −)

<r> metagenes = 0.93

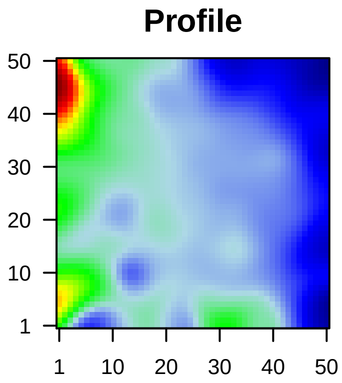
<r> genes = 0.45

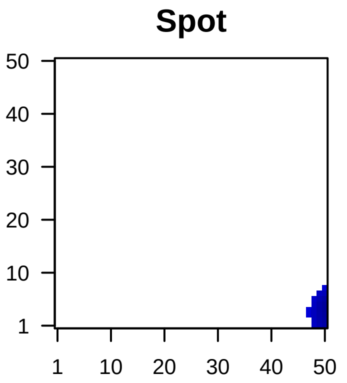
<FC> = −0.27

<shrinkage−t> = −9.54

<p−value> = 0.01

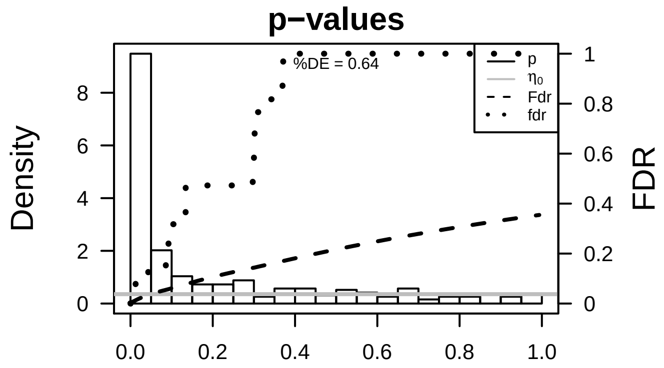
<fdr> = 0.64





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	57172	−1.46	2e−16	8e−15	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
2	3512	−1.54	2e−16	8e−15	50 x 1	immunoglobulin J polypeptide, linker protein for immunoglobu
3	3543	−1.95	2e−16	8e−15	49 x 1	immunoglobulin lambda−like polypeptide 1 [Source:HGNC Sy
4	10628	−1.61	2e−16	8e−15	48 x 1	thioredoxin interacting protein [Source:HGNC Symbol;Acc:16
5	10365	−1.31	7e−15	6e−12	50 x 3	Kruppel−like factor 2 [Source:HGNC Symbol;Acc:6347]
6	6578	1.27	5e−14	3e−09	50 x 4	solute carrier organic anion transporter family, member 2A1 [
7	3575	1.11	4e−11	3e−09	50 x 2	interleukin 7 receptor [Source:HGNC Symbol;Acc:6024]
8	338773	−1.11	4e−11	1e−08	50 x 5	transmembrane protein 119 [Source:HGNC Symbol;Acc:278
9	894	1.08	1e−10	2e−08	50 x 4	cyclin D2 [Source:HGNC Symbol;Acc:1583]
10	5176	−1.07	2e−10	3e−08	50 x 5	serpin peptidase inhibitor, clade F (alpha−2 antiplasmin, pigm
11	1396	−1.05	5e−10	1e−07	50 x 5	cysteine−rich protein 1 (intestinal) [Source:HGNC Symbol;Ac
12	54855	−1.01	2e−09	1e−07	49 x 1	family with sequence similarity 46, member C [Source:HGNC
13	51755	−1.01	2e−09	8e−07	49 x 1	cyclin−dependent kinase 12 [Source:HGNC Symbol;Acc:242
14	5730	−0.95	2e−08	8e−07	50 x 1	prostaglandin D2 synthase 21kDa (brain) [Source:HGNC Syn
15	25849	−0.95	2e−08	8e−07	50 x 2	prostate androgen−regulated mucin−like protein 1 [Source:H
16	5175	−0.94	2e−08	3e−06	50 x 4	platelet/endothelial cell adhesion molecule 1 [Source:HGNC
17	10537	−0.91	5e−08	3e−06	50 x 1	ubiquitin D [Source:HGNC Symbol;Acc:18795]
18	23643	−0.91	6e−08	4e−06	50 x 3	lymphocyte antigen 96 [Source:HGNC Symbol;Acc:17156]
19	8404	−0.9	9e−08	4e−06	50 x 6	SPARC−like 1 (hevin) [Source:HGNC Symbol;Acc:11220]
20	4239	−0.89	1e−07	4e−06	50 x 6	microfibrillar−associated protein 4 [Source:HGNC Symbol;Ac



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−15.8	NULL	3 / 5	GSEA C2	WONG_ENDOMETRIAL_CANCER_LATE
2	−13.82	NULL	110 / 553	Cancer	Lembcke_Colonic Inflammation
3	−13.19	NULL	7 / 8	Glio	Donson−migration tethering and rolling−associated with LTS in HG
4	−13.03	NULL	1 / 6	H.Tiss	WIRTH_Bone marrow
5	−11.8	NULL	50 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
6	−11.8	NULL	50 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
7	−11.8	NULL	50 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
8	−11.8	NULL	50 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
9	−11.15	NULL	3 / 14	GSEA C2	WINNEPENNINCKX_MELANOMA_METASTASIS_DN
10	−10.68	NULL	5 / 10	GSEA C2	BIOCARTA_LYM_PATHWAY
11	−10.63	NULL	7 / 12	GSEA C2	ZHAN_MULTIPLE_MYELOMA_DN
12	−10.42	NULL	5 / 9	GSEA C2	GUTIERREZ_WALDENSTROEMS_MACROGLOBULINEMIA_1_D
13	−10.37	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
14	−10.33	NULL	5 / 9	GSEA C2	MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN
15	−10.21	NULL	6 / 15	Glio	Donson−chemokines/cytokines−associated with LTS in HGA
16	−10.11	NULL	2 / 7	Cancer	ZHANG_MGUS up
17	−9.96	NULL	4 / 15	GSEA C2	SHIPP_DLBCL_VS_FOLLICULAR_LYMPHOMA_DN
18	−9.82	NULL	6 / 15	GSEA C2	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_GRANULO
19	−9.68	NULL	3 / 10	GSEA C2	LEE_EARLY_T_LYMPHOCYTE_DN
20	−9.56	NULL	3 / 15	GSEA C2	NADERI_BREAST_CANCER_PROGNOSIS_DN
21	−9.41	NULL	2 / 11	GSEA C2	AMIT_EGF_RESPONSE_20_HELA
22	−9.21	NULL	3 / 15	GSEA C2	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_
23	−9.19	NULL	3 / 7	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
24	−8.82	NULL	6 / 15	GSEA C2	FINAK_BREAST_CANCER_SDPP_SIGNATURE
25	−8.8	NULL	10 / 28	BP	B cell receptor signaling pathway
26	−8.61	NULL	3 / 11	GSEA C2	GUTIERREZ_CHRONIC_LYMPHOCYTIC_LEUKEMIA_UP
27	−8.58	NULL	5 / 10	GSEA C2	BIOCARTA_MONOCYTE_PATHWAY
28	−8.4	NULL	4 / 12	GSEA C2	ZHAN_V1_LATE_DIFFERENTIATION_GENES_UP
29	−8.14	NULL	10 / 43	MF	chemokine activity
30	−8.02	NULL	4 / 8	GSEA C2	BIOCARTA_GRANULOCYTES_PATHWAY
31	−7.96	NULL	2 / 12	GSEA C2	MCCABE_HOXC6_TARGETS_CANCER_UP
32	−7.94	NULL	6 / 43	BP	cellular response to organic cyclic compound
33	−7.93	NULL	17 / 74	BP	regulation of immune response
34	−7.87	NULL	2 / 15	GSEA C2	MARKS_HDAC_TARGETS_UP
35	−7.85	NULL	3 / 12	GSEA C2	HADDAD_T_LYMPHOCYTE_AND_NK_PROGENITOR_DN
36	−7.68	NULL	4 / 7	GSEA C2	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINE
37	−7.68	NULL	4 / 7	GSEA C2	LOPEZ_MESOTELIOMA_SURVIVAL_TIME_DN
38	−7.66	NULL	2 / 10	BP	cellular response to antibiotic
39	−7.61	NULL	3 / 14	BP	regulation of Wnt signaling pathway
40	−7.6	NULL	4 / 13	Cancer	GENTLES_modul17

GW_097

Local Summary

%DE = 0.68

metagenes = 10

genes = 155

genes in genesets = 154

genes with fdr < 0.1 = 73 (5 + / 68 −)

genes with fdr < 0.05 = 45 (4 + / 41 −)

genes with fdr < 0.01 = 23 (2 + / 21 −)

<r> metagenes = 0.97

<r> genes = 0.35

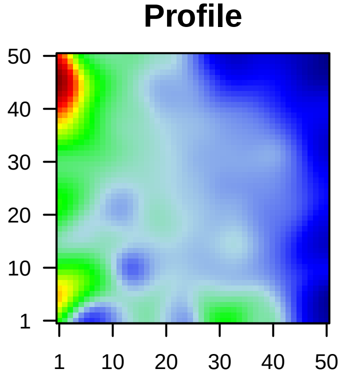
<FC> = −0.24

<shrinkage−t> = −8.4

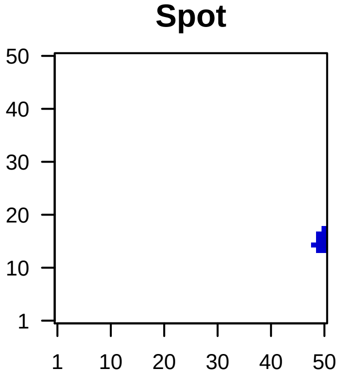
<p−value> = 0.03

<fdr> = 0.7

Profile



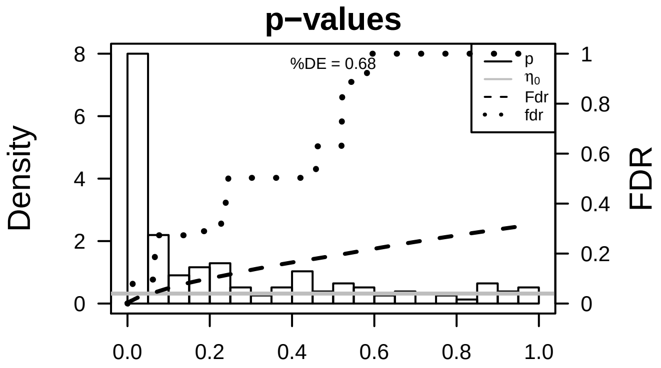
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	8543	−0.91	6e−08	3e−05	50 x 15	LIM domain only 4 [Source:HGNC Symbol;Acc:6644]
2	10439	0.83	8e−07	3e−05	50 x 17	olfactomedin 1 [Source:HGNC Symbol;Acc:17187]
3	9603	−0.81	1e−06	7e−05	50 x 18	nuclear factor, erythroid 2−like 3 [Source:HGNC Symbol;Acc:
4	26471	−0.79	3e−06	1e−04	49 x 14	nuclear protein, transcriptional regulator, 1 [Source:HGNC Sy
5	28951	−0.77	5e−06	1e−04	50 x 17	tribbles pseudokinase 2 [Source:HGNC Symbol;Acc:30809]
6	3033	−0.74	1e−05	1e−04	50 x 14	hydroxyacyl−CoA dehydrogenase [Source:HGNC Symbol;Ac
7	56997	−0.74	1e−05	4e−04	50 x 16	aarF domain containing kinase 3 [Source:HGNC Symbol;Acc
8	7915	−0.72	2e−05	4e−04	50 x 16	aldehyde dehydrogenase 5 family, member A1 [Source:HGN
9	29116	−0.71	3e−05	4e−04	50 x 14	myosin regulatory light chain interacting protein [Source:HGN
10	641638	−0.7	3e−05	4e−04	50 x 18	small nucleolar RNA host gene 6 (non−protein coding) [Sourc
11	29997	−0.63	4e−05	1e−03	50 x 15	glioma tumor suppressor candidate region gene 2 [Source:H
12	60436	−0.67	7e−05	1e−03	50 x 18	TGFB−induced factor homeobox 2 [Source:HGNC Symbol;Ac
13	79191	0.66	8e−05	4e−03	50 x 15	iroquois homeobox 3 [Source:HGNC Symbol;Acc:14360]
14	4602	−0.63	2e−04	4e−03	50 x 16	v−myb avian myeloblastosis viral oncogene homolog [Source
15	2879	−0.61	3e−04	4e−03	50 x 18	glutathione peroxidase 4 [Source:HGNC Symbol;Acc:4556]
16	23401	−0.6	4e−04	4e−03	50 x 14	frequently rearranged in advanced T−cell lymphomas 2 [Sour
17	79161	−0.6	4e−04	7e−03	49 x 16	transmembrane protein 243, mitochondrial [Source:HGNC Sy
18	7716	−0.58	6e−04	7e−03	50 x 16	vascular endothelial zinc finger 1 [Source:HGNC Symbol;Acc
19	6118	−0.55	1e−03	7e−03	49 x 16	replication protein A2, 32kDa [Source:HGNC Symbol;Acc:10
20	54780	−0.55	1e−03	7e−03	49 x 15	non−SMC element 4 homolog A (S. cerevisiae) [Source:HGN

p−values



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−12.7	NULL	2 / 11	MF	enhancer sequence−specific DNA binding
2	−11.9	NULL	1 / 3	miRNA target	miR−148a
3	−10.99	NULL	2 / 16	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL
4	−9.94	NULL	2 / 16	GSEA C2	SASAKI_ADULT_T_CELL_LEUKEMIA
5	−9.51	NULL	1 / 2	miRNA target	miR−153
6	−9.51	NULL	1 / 6	GSEA C2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_B_DN
7	−9.51	NULL	1 / 6	GSEA C2	LUI_THYROID_CANCER_CLUSTER_4
8	−9.46	NULL	3 / 15	GSEA C2	DAVICIONI_PAX_FOXO1_SIGNATURE_IN_ARMS_DN
9	−9.42	NULL	2 / 19	BP	spinal cord motor neuron differentiation
10	−9.34	NULL	3 / 34	BP	thymus development
11	−8.35	NULL	1 / 8	GSEA C2	BENPORATH_ES_CORE_NINE
12	−7.82	NULL	2 / 16	GSEA C2	HOEBEKE_LYMPHOID_STEM_CELL_UP
13	−7.52	NULL	1 / 3	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_18
14	−7.18	NULL	1 / 13	BP	negative regulation of protein complex assembly
15	−7.18	NULL	1 / 13	GSEA C2	BENPORATH_ES_CORE_NINE_CORRELATED
16	−7.18	NULL	1 / 13	GSEA C2	SPIRA_SMOKERS_LUNG_CANCER_DN
17	−7.16	NULL	1 / 10	GSEA C2	CAFFAREL_RESPONSE_TO_THC_24HR_3_DN
18	−6.98	NULL	2 / 10	BP	positive regulation of histone H3−K4 methylation
19	−6.96	NULL	1 / 10	GSEA C2	BASSO_CD40_SIGNALING_DN
20	−6.96	NULL	1 / 10	GSEA C2	KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_UP
21	−6.83	NULL	2 / 16	GSEA C2	DAVICIONI_TARGETS_OF_PAX_FOXO1_FUSIONS_DN
22	−6.75	NULL	1 / 10	GSEA C2	REACTOME_MITOCHONDRIAL_FATTY_ACID_BETA_OXIDATION
23	−6.67	NULL	2 / 15	GSEA C2	SHIPP_DLBCL_VS_FOLLICULAR_LYMPHOMA_DN
24	−6.63	NULL	1 / 15	GSEA C2	DOANE_BREAST_CANCER_CLASSES_DN
25	−6.63	NULL	1 / 15	GSEA C2	PUJANA_BREAST_CANCER_LIT_INT_NETWORK
26	−6.63	NULL	1 / 15	GSEA C2	SUNG_METASTASIS_STROMA_UP
27	−6.63	NULL	1 / 15	GSEA C2	FAELT_B_CLL_WITH_VH3_21_DN
28	−6.63	NULL	1 / 15	GSEA C2	MMS_MOUSE_LYMPH_HIGH_4HRS_UP
29	−6.6	NULL	1 / 11	GSEA C2	FUJII_YBX1_TARGETS_UP
30	−6.6	NULL	1 / 11	GSEA C2	ACEVEDO_LIVER_TUMOR_VS_NORMAL_ADJACENT_TISSUE_
31	−6.59	NULL	1 / 2	TF	MYC_Cell cycle DOWN
32	−6.48	NULL	2 / 14	GSEA C2	VANTVEER_BREAST_CANCER_METASTASIS_UP
33	−6.47	NULL	2 / 16	GSEA C2	HADDAD_B_LYMPHOCYTE_PROGENITOR
34	−6.47	NULL	1 / 12	BP	acute inflammatory response
35	−6.44	NULL	1 / 8	GSEA C2	ADDYA_ERYTHROID_DIFFERENTIATION_BY_HEMIN
36	−6.42	NULL	1 / 10	GSEA C2	FRASOR_TAMOXIFEN_RESPONSE_DN
37	−6.39	NULL	1 / 16	BP	ventricular septum development
38	−6.39	NULL	1 / 16	GSEA C2	OUELLET_CULTURED_OVARIAN_CANCER_INVASIVE_VS_LMP
39	−6.39	NULL	1 / 16	GSEA C2	BEGUM_TARGETS_OF_PAX3_FOXO1_FUSION_UP
40	−6.38	NULL	1 / 4	miRNA target	let−7c

GW_097

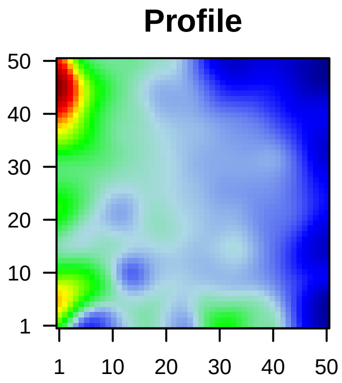
Local Summary

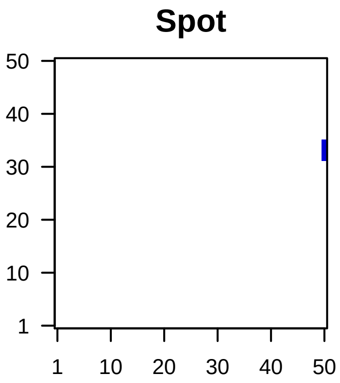
%DE = 0.69
metagenes = 4
genes = 126
genes in genesets = 126

genes with fdr < 0.1 = 46 (0 + / 46 −)
genes with fdr < 0.05 = 33 (0 + / 33 −)
genes with fdr < 0.01 = 2 (0 + / 2 −)

<r> metagenes = 0.99
<r> genes = 0.34

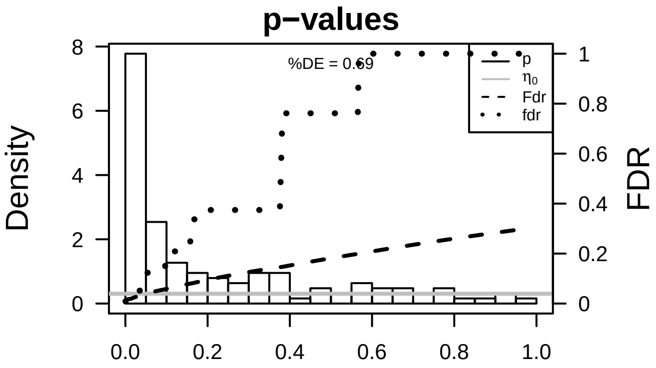
<FC> = −0.25
<shrinkage−t> = −8.93
<p−value> = 0.08
<fdr> = 0.75





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	728026	−0.61	3e−04	0.009	50 x 35	prothymosin, alpha [Source:HGNC Symbol;Acc:9623]
2	57092	−0.58	6e−04	0.009	50 x 35	PEST proteolytic signal containing nuclear protein [Source:H
3	4677	−0.57	7e−04	0.020	50 x 33	asparaginyl−tRNA synthetase [Source:HGNC Symbol;Acc:76
4	51124	−0.51	2e−03	0.020	50 x 34	Immediate early response 3−interacting protein 1 [Source:Ur
5	84191	−0.5	3e−03	0.020	50 x 34	family with sequence similarity 96, member A [Source:HGNC
6	1429	−0.49	3e−03	0.020	50 x 34	crystallin, zeta (quinone reductase) [Source:HGNC Symbol;A
7	10314	−0.49	4e−03	0.020	50 x 35	LanC lantibiotic synthetase component C−like 1 (bacterial) [S
8	55074	−0.47	5e−03	0.020	50 x 33	oxidation resistance 1 [Source:HGNC Symbol;Acc:15822]
9	10473	−0.47	5e−03	0.020	50 x 33	high mobility group nucleosomal binding domain 4 [Source:H
10	79366	−0.46	6e−03	0.020	50 x 32	high mobility group nucleosome binding domain 5 [Source:H
11	64431	−0.46	6e−03	0.020	50 x 32	ARP6 actin−related protein 6 homolog (yeast) [Source:HGNC
12	6139	−0.46	6e−03	0.020	50 x 33	RPL17−C18orf32 readthrough [Source:HGNC Symbol;Acc:4
13	23484	−0.45	7e−03	0.020	50 x 33	leptin receptor overlapping transcript−like 1 [Source:HGNC S
14	27292	−0.45	8e−03	0.020	50 x 32	DIM1 dimethyladenosine transferase 1 homolog (S. cerevisia
15	221294	−0.44	9e−03	0.020	50 x 33	5'−nucleotidase domain containing 1 [Source:HGNC Symbol;
16	8493	−0.44	9e−03	0.020	50 x 33	protein phosphatase, Mg2+/Mn2+ dependent, 1D [Source:HG
17	7485	−0.43	1e−02	0.020	50 x 34	tryptophan rich basic protein [Source:HGNC Symbol;Acc:127
18	7334	−0.43	1e−02	0.020	50 x 33	ubiquitin−conjugating enzyme E2N [Source:HGNC Symbol;A
19	51015	−0.43	1e−02	0.020	50 x 33	isochorismatase domain containing 1 [Source:HGNC Symbol
20	10224	−0.43	1e−02	0.020	50 x 33	zinc finger protein 443 [Source:HGNC Symbol;Acc:20878]



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−10.65	NULL	2 / 10	MF	NADPH binding
2	−10.22	NULL	3 / 14	GSEA C2	REACTOME_MRNA_3_END_PROCESSING
3	−10.11	NULL	1 / 2	miRNA target	miR−98
4	−8.12	NULL	9 / 232	Chr	Chr 18
5	−8.01	NULL	2 / 12	GSEA C2	CHEOK_RESPONSE_TO_MERCAPTOPURINE_UP
6	−7.83	NULL	1 / 10	Cancer	LIU_BREAST_CANCER
7	−7.55	NULL	2 / 11	GSEA C2	TURJANSKI_MAPK1_AND_MAPK2_TARGETS
8	−7.54	NULL	2 / 13	BP	response to salt stress
9	−7.43	NULL	3 / 15	GSEA C2	BIOCARTA_CTCF_PATHWAY
10	−7.43	NULL	1 / 3	TF	MYC_Tumor supressor genes UP
11	−6.96	NULL	1 / 4	miRNA target	let−7c
12	−6.96	NULL	1 / 4	miRNA target	let−7g
13	−6.88	NULL	3 / 27	MF	nucleotidyltransferase activity
14	−6.85	NULL	2 / 15	BP	3'−phosphoadenosine 5'−phosphosulfate metabolic process
15	−6.82	NULL	5 / 78	miRNA target−starBase	hsa−miR−365
16	−6.77	NULL	6 / 80	CC	chromatin
17	−6.58	NULL	2 / 6	GSEA C2	BIOCARTA_PML_PATHWAY
18	−6.52	NULL	5 / 80	miRNA target−starBase	hsa−miR−30a*
19	−6.39	NULL	5 / 122	miRNA target−starBase	hsa−miR−195
20	−6.36	NULL	1 / 4	TF	MYC_Apoptosis UP
21	−6.34	NULL	2 / 11	MF	mismatched DNA binding
22	−6.22	NULL	2 / 14	GSEA C2	BIOCARTA_TEL_PATHWAY
23	−5.98	NULL	3 / 38	miRNA target−starBase	hsa−miR−1277
24	−5.95	NULL	1 / 6	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_7
25	−5.81	NULL	3 / 50	miRNA target−starBase	hsa−miR−504
26	−5.63	NULL	1 / 5	TF	MYC_TF and cofactors
27	−5.63	NULL	1 / 5	GSEA C2	DING_LUNG_CANCER_MUTATED_RECURRENTLY
28	−5.62	NULL	3 / 41	BP	mRNA 3'−end processing
29	−5.61	NULL	6 / 45	miRNA target−starBase	hsa−miR−411
30	−5.58	NULL	1 / 6	miRNA target	let−7b
31	−5.58	NULL	1 / 6	miRNA target	let−7d
32	−5.58	NULL	1 / 6	miRNA target	miR−26a
33	−5.48	NULL	1 / 14	GSEA C2	REACTOME_CYTOSOLIC_TRNA_AMINOACYLATION
34	−5.47	NULL	4 / 55	miRNA target−starBase	hsa−miR−28−3p
35	−5.42	NULL	3 / 33	miRNA target−starBase	hsa−miR−892b
36	−5.4	NULL	1 / 8	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_25
37	−5.39	NULL	3 / 44	BP	termination of RNA polymerase II transcription
38	−5.36	NULL	11 / 264	miRNA target−starBase	hsa−miR−449a
39	−5.33	NULL	2 / 35	miRNA target−starBase	hsa−miR−1274b
40	−5.32	NULL	1 / 11	MF	glutathione binding

GW_097

Local Summary

%DE = 0.63

metagenes = 55

genes = 635

genes in genesets = 630

genes with fdr < 0.1 = 209 (19 + / 190 −)

genes with fdr < 0.05 = 163 (12 + / 151 −)

genes with fdr < 0.01 = 74 (4 + / 70 −)

<r> metagenes = 0.86

<r> genes = 0.24

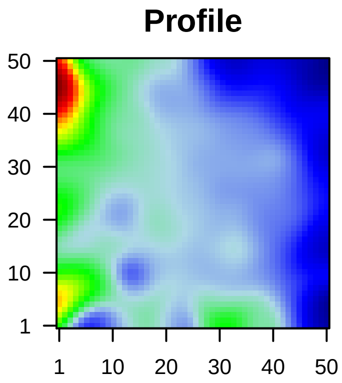
<FC> = −0.23

<shrinkage−t> = −8.04

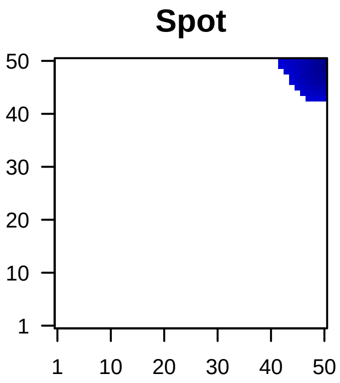
<p−value> = 0.04

<fdr> = 0.71

Profile



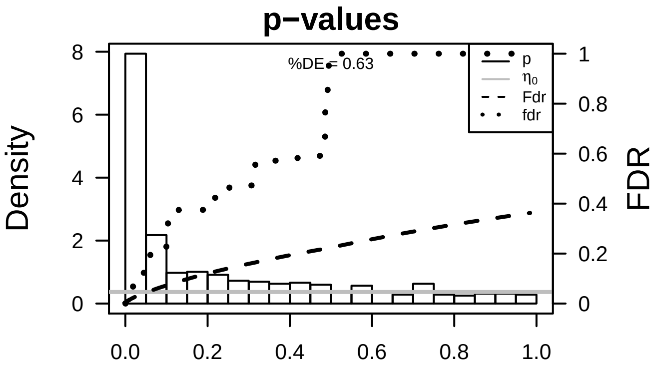
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	84223	1.46	2e−16	3e−14	47 x 46	IQ motif containing G [Source:HGNC Symbol;Acc:25251]
2	3866	−1.45	2e−16	3e−14	50 x 50	keratin 15 [Source:HGNC Symbol;Acc:6421]
3	11166	−1.35	9e−16	8e−10	50 x 50	SRY (sex determining region Y)−box 21 [Source:HGNC Symb
4	4072	−1.17	3e−12	2e−09	50 x 50	epithelial cell adhesion molecule [Source:HGNC Symbol;Acc:
5	216	−1.14	1e−11	5e−08	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGNC
6	154664	−1.06	2e−10	3e−06	50 x 50	ATP−binding cassette, sub−family A (ABC1), member 13 [Sou
7	4922	−0.95	1e−08	8e−06	50 x 50	neurotensin [Source:HGNC Symbol;Acc:8038]
8	3015	−0.84	5e−08	4e−05	45 x 48	H2A histone family, member Z [Source:HGNC Symbol;Acc:47
9	6657	−0.87	2e−07	7e−05	50 x 50	SRY (sex determining region Y)−box 2 [Source:HGNC Symbo
10	51804	−0.85	5e−07	9e−05	50 x 46	SIX homeobox 4 [Source:HGNC Symbol;Acc:10890]
11	84707	−0.83	9e−07	9e−05	50 x 48	brain expressed X−linked 2 [Source:HGNC Symbol;Acc:3093
12	1891	−0.81	1e−06	3e−04	50 x 45	enoyl CoA hydratase 1, peroxisomal [Source:HGNC Symbol;
13	440	−0.78	3e−06	3e−04	50 x 46	asparagine synthetase (glutamine−hydrolyzing) [Source:HGN
14	79844	−0.77	4e−06	3e−04	50 x 50	zinc finger, DHHC−type containing 11 [Source:HGNC Symbo
15	142	−0.77	5e−06	3e−04	47 x 46	poly (ADP−ribose) polymerase 1 [Source:HGNC Symbol;Acc
16	7345	−0.76	6e−06	4e−04	50 x 46	ubiquitin carboxyl−terminal esterase L1 (ubiquitin thiolesteras
17	25975	−0.75	8e−06	4e−04	48 x 50	EGF−like−domain, multiple 6 [Source:HGNC Symbol;Acc:323
18	6659	−0.74	9e−06	4e−04	50 x 45	SRY (sex determining region Y)−box 4 [Source:HGNC Symbo
19	26047	0.74	1e−05	4e−04	50 x 50	contactin associated protein−like 2 [Source:HGNC Symbol;Ac
20	94234	−0.73	1e−05	4e−04	50 x 50	forkhead box Q1 [Source:HGNC Symbol;Acc:20951]

p−values



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−17.16	NULL	93 / 142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
2	−17.16	NULL	93 / 142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
3	−13.23	NULL	10 / 16	Cancer	WOLFER_overlap genes
4	−12.23	NULL	18 / 30	BP	DNA strand elongation involved in DNA replication
5	−11.92	NULL	47 / 149	BP	DNA replication
6	−11.84	NULL	14 / 16	GSEA C2	FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
7	−11.44	NULL	6 / 8	GSEA C2	REACTOME_E2F_TRANSCRIPTIONAL_TARGETS_AT_G1_S
8	−11.43	NULL	98 / 370	BP	mitotic cell cycle
9	−10.85	NULL	24 / 66	CC	condensed chromosome kinetochore
10	−10.51	NULL	8 / 11	GSEA C2	REACTOME_UNWINDING_OF_DNA
11	−10.46	NULL	13 / 15	GSEA C2	FINETTI_BREAST_CANCER_KINOME_RED
12	−9.75	NULL	16 / 16	GSEA C2	EGUCHI_CELL_CYCLE_RB1_TARGETS
13	−9.68	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
14	−9.67	NULL	12 / 22	BP	DNA replication initiation
15	−9.63	NULL	2 / 7	GSEA C2	MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
16	−9.37	NULL	7 / 11	GSEA C2	REACTOME_E2F_MEDIATED_REGULATION_OF_DNA_REPLICA
17	−9.37	NULL	8 / 16	GSEA C2	KEGG_MISMATCH_REPAIR
18	−9.23	NULL	10 / 16	GSEA C2	REACTOME_G2_M_CHECKPOINTS
19	−9.22	NULL	4 / 13	BP	regulation of blood vessel size
20	−9.16	NULL	3 / 14	GSEA C2	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINEI
21	−9.12	NULL	19 / 61	CC	kinetochore
22	−9.03	NULL	9 / 15	GSEA C2	WU_APOPTOSIS_BY_CDKN1A_VIA_TP53
23	−9	NULL	17 / 49	BP	telomere maintenance
24	−9	NULL	6 / 7	GSEA C2	REACTOME_G1_S_TRANSITION
25	−8.95	NULL	5 / 16	GSEA C2	KAN_RESPONSE_TO_ARSENIC_TRIOXIDE
26	−8.91	NULL	4 / 12	GSEA C2	HELLER_SILENCED_BY_METHYLATION_DN
27	−8.89	NULL	9 / 11	GSEA C2	KALMA_E2F1_TARGETS
28	−8.89	NULL	10 / 14	GSEA C2	ZHAN_MULTIPLE_MYELOMA_PR_UP
29	−8.85	NULL	9 / 18	BP	nucleotide−excision repair, DNA gap filling
30	−8.81	NULL	13 / 24	BP	telomere maintenance via recombination
31	−8.64	NULL	8 / 15	GSEA C2	REACTOME_REPAIR_SYNTHESIS_OF_PATCH_27_30_BASES_
32	−8.46	NULL	110 / 530	Cancer	Lembcke_Normal vs Adenoma
33	−8.35	NULL	12 / 21	BP	telomere maintenance via semi−conservative replication
34	−8.3	NULL	2 / 6	GSEA C2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_D_DN
35	−8.01	NULL	11 / 16	GSEA C2	REACTOME_DNA_STRAND_ELONGATION
36	−8	NULL	3 / 12	GSEA C2	BROCKE_APOPTOSIS_REVERSED_BY_IL6
37	−8	NULL	9 / 15	GSEA C2	ODONNELL_TARGETS_OF_MYC_AND_TFRC_DN
38	−7.96	NULL	7 / 16	GSEA C2	RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIA
39	−7.94	NULL	5 / 9	GSEA C2	SEMBA_FHIT_TARGETS_DN
40	−7.93	NULL	10 / 22	BP	CENP−A containing nucleosome assembly at centromere

GW_097

Local Summary

%DE = 0.71

metagenes = 10

genes = 180

genes in genesets = 175

genes with fdr < 0.1 = 72 (2 + / 70 −)

genes with fdr < 0.05 = 32 (0 + / 32 −)

genes with fdr < 0.01 = 5 (0 + / 5 −)

<r> metagenes = 0.96

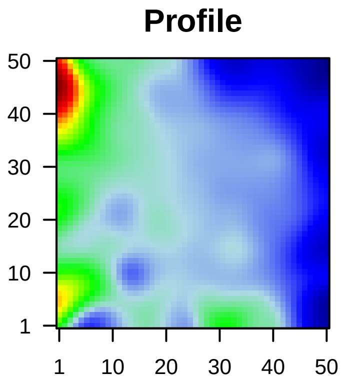
<r> genes = 0.29

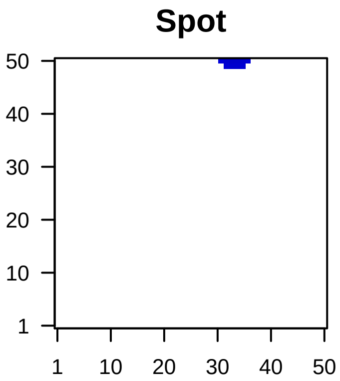
<FC> = −0.25

<shrinkage−t> = −8.62

<p−value> = 0.08

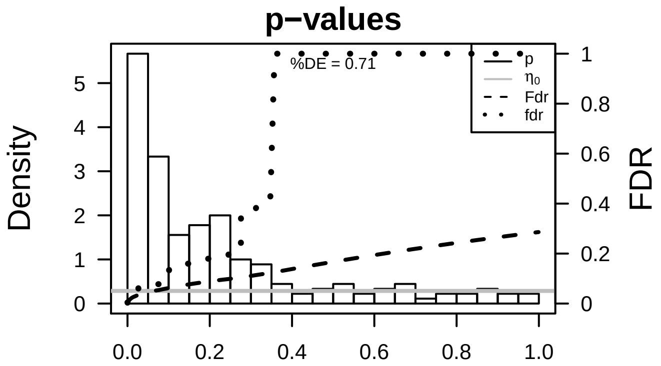
<fdr> = 0.82





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	10799	−0.68	6e−05	0.004	34 x 50	ribonuclease P/MRP 40kDa subunit [Source:HGNC Symbol;A
2	84833	−0.64	2e−04	0.004	33 x 50	up−regulated during skeletal muscle growth 5 homolog (mous
3	51110	−0.63	2e−04	0.005	32 x 50	lactamase, beta 2 [Source:HGNC Symbol;Acc:18512]
4	27257	−0.6	4e−04	0.005	34 x 50	LSM1 homolog, U6 small nuclear RNA associated (S. cerevis
5	441951	−0.6	4e−04	0.005	33 x 49	ZNFX1 antisense RNA 1 [Source:HGNC Symbol;Acc:33101]
6	401466	−0.59	5e−04	0.012	32 x 50	chromosome 8 open reading frame 59 [Source:HGNC Symbo
7	7386	−0.54	1e−03	0.012	34 x 50	ubiquinol−cytochrome c reductase, Rieske iron−sulfur polype
8	9352	−0.53	1e−03	0.012	31 x 50	thioredoxin−like 1 [Source:HGNC Symbol;Acc:12436]
9	388722	−0.53	2e−03	0.012	36 x 50	chromosome 1 open reading frame 53 [Source:HGNC Symbo
10	81853	−0.52	2e−03	0.012	32 x 50	transmembrane protein 14B [Source:HGNC Symbol;Acc:213
11	55856	−0.52	2e−03	0.012	34 x 50	acyl−CoA thioesterase 13 [Source:HGNC Symbol;Acc:20999
12	29078	−0.52	2e−03	0.012	34 x 50	NADH dehydrogenase (ubiquinone) complex I, assembly fact
13	548644	−0.52	2e−03	0.012	36 x 50	polymerase (RNA) II (DNA directed) polypeptide J3 [Source:
14	127018	−0.51	2e−03	0.028	31 x 50	lysophospholipase−like 1 [Source:HGNC Symbol;Acc:20440]
15	2287	−0.5	3e−03	0.044	35 x 49	FK506 binding protein 3, 25kDa [Source:HGNC Symbol;Acc:
16	6390	−0.48	4e−03	0.044	34 x 49	succinate dehydrogenase complex, subunit B, iron sulfur (Ip)
17	79675	−0.47	5e−03	0.044	35 x 50	FAST kinase domains 1 [Source:HGNC Symbol;Acc:26150]
18	29074	−0.47	6e−03	0.044	36 x 50	mitochondrial ribosomal protein L18 [Source:HGNC Symbol;
19	5321	−0.46	6e−03	0.044	35 x 50	phospholipase A2, group IVA (cytosolic, calcium−dependent)
20	29080	−0.45	7e−03	0.046	31 x 50	coiled−coil domain containing 59 [Source:HGNC Symbol;Acc



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all		Geneset
1	−22.72	NULL	27 / 83	BP	respiratory electron transport chain
2	−17.31	NULL	28 / 152	BP	cellular metabolic process
3	−16.6	NULL	37 / 304	CC	mitochondrial inner membrane
4	−15.26	NULL	8 / 19	CC	mitochondrial proton−transporting ATP synthase complex
5	−13.73	NULL	71 / 1318	CC	mitochondrion
6	−13.5	NULL	6 / 11	Cancer	GENTLES_modul5
7	−13.38	NULL	7 / 26	MF	cytochrome−c oxidase activity
8	−11.44	NULL	4 / 16	Cancer	GENTLES_modul10
9	−11.26	NULL	3 / 15	MMML CGS	MACIEJ_MMML 22
10	−11.08	NULL	11 / 34	MF	NADH dehydrogenase (ubiquinone) activity
11	−10.73	NULL	11 / 36	CC	mitochondrial respiratory chain complex I
12	−10.51	NULL	6 / 15	BP	ATP synthesis coupled proton transport
13	−10.14	NULL	4 / 12	BP	oxidative phosphorylation
14	−10.07	NULL	10 / 35	BP	mitochondrial electron transport, NADH to ubiquinone
15	−10	NULL	3 / 11	GSEA C2	BIOCARTA_ETC_PATHWAY
16	−9.97	NULL	5 / 10	CC	large ribosomal subunit
17	−9.94	NULL	3 / 15	GSEA C2	MOOTHA_TCA
18	−9.92	NULL	21 / 153	MF	structural constituent of ribosome
19	−9.91	NULL	21 / 167	CC	ribosome
20	−9.7	NULL	5 / 13	GSEA C2	REACTOME_FORMATION_OF_ATP_BY_CHEMIOSMOTIC_COU
21	−9.33	NULL	3 / 13	CC	mitochondrial respiratory chain
22	−9.32	NULL	5 / 14	BP	mitochondrial ATP synthesis coupled proton transport
23	−9.15	NULL	2 / 10	GSEA C2	CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_1
24	−8.99	NULL	3 / 16	GSEA C2	BARIS_THYROID_CANCER_UP
25	−8.8	NULL	2 / 12	MF	lysophospholipase activity
26	−8.39	NULL	6 / 62	Glio	Stuehler_Proteins_up_in_STS
27	−8.37	NULL	12 / 87	BP	translational termination
28	−8.22	NULL	23 / 253	BP	translation
29	−8.1	NULL	1 / 2	miRNA target	miR−375
30	−8.05	NULL	2 / 15	GSEA C2	NIKOLSKY_BREAST_CANCER_8P12_P11_AMPLICON
31	−8.01	NULL	2 / 11	GSEA C2	REACTOME_MRNA_DECAY_BY_5_TO_3_EXORIBONUCLEASE
32	−7.98	NULL	12 / 92	BP	translational elongation
33	−7.76	NULL	11 / 81	BP	viral transcription
34	−7.63	NULL	2 / 7	MMML CGS	MACIEJ_MMML 48
35	−7.46	NULL	3 / 20	BP	aerobic respiration
36	−7.18	NULL	11 / 92	BP	viral life cycle
37	−7.09	NULL	13 / 128	BP	translational initiation
38	−7.04	NULL	3 / 28	BP	tricarboxylic acid cycle
39	−6.94	NULL	4 / 18	MF	2 iron, 2 sulfur cluster binding
40	−6.81	NULL	3 / 8	GSEA C2	REACTOME_REGULATION_OF_GENE_EXPRESSION_IN_BETA