GW_110

Global Summary

%DE = 0.15

genes with fdr < 0.2 = 1962 (1150 + / 812 −)

genes with fdr < 0.1 = 1656 (996 + / 660 −)

genes with fdr < 0.05 = 1387 (874 + / 513 −)

genes with fdr < 0.01 = 965 (643 + / 322 −)

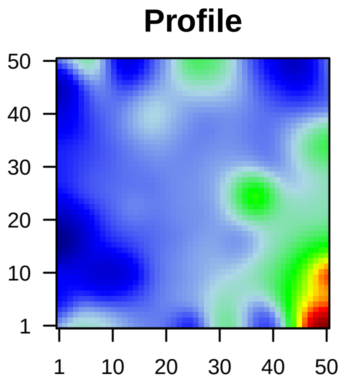
genes in genesets = 16332

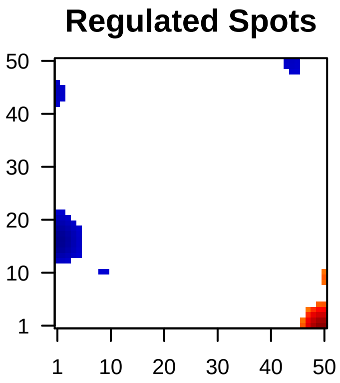
<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.08

<fdr> = 0.85



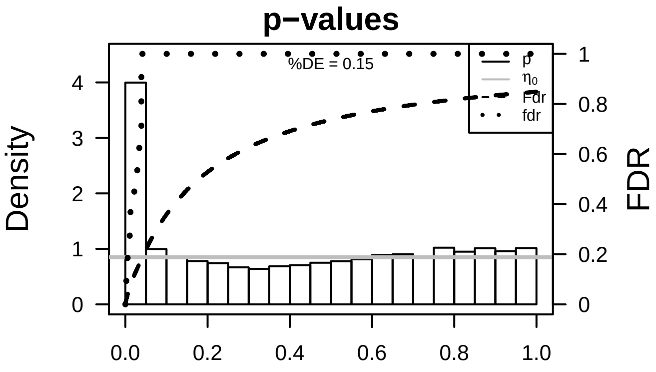


Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	154664	1.4	2e−16	2e−14	50 x 50	ATP−binding cassette, sub−family A (ABC1), member 13 [Sou
2	10551	1.31	2e−16	2e−14	50 x 10	anterior gradient 2 [Source:HGNC Symbol;Acc:328]
3	216	1.42	2e−16	2e−14	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGNC
4	241	1.35	2e−16	2e−14	50 x 1	arachidonate 5−lipoxygenase−activating protein [Source:HGN
5	306	1.56	2e−16	2e−14	4 x 42	annexin A3 [Source:HGNC Symbol;Acc:541]
6	348	1.39	2e−16	2e−14	50 x 1	apolipoprotein E [Source:HGNC Symbol;Acc:613]
7	92591	1.52	2e−16	2e−14	48 x 2	ankyrin repeat and SOCS box containing 16 [Source:HGNC S
8	23120	1.36	2e−16	2e−14	1 x 50	ATPase, class V, type 10B [Source:HGNC Symbol;Acc:13543
9	80341	1.77	2e−16	2e−14	50 x 10	BPI fold containing family B, member 2 [Source:HGNC Symb
10	387695	−1.42	2e−16	2e−14	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Symb
11	84419	1.57	2e−16	2e−14	5 x 50	chromosome 15 open reading frame 48 [Source:HGNC Symb
12	149563	1.34	2e−16	2e−14	34 x 23	chromosome 1 open reading frame 64 [Source:HGNC Symbo
13	92747	3.07	2e−16	2e−14	50 x 10	BPI fold containing family B, member 1 [Source:HGNC Symb
14	260436	3.4	2e−16	2e−14	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symbo
15	29923	−1.36	2e−16	2e−14	4 x 44	hypoxia inducible lipid droplet−associated [Source:HGNC Syr
16	56892	1.36	2e−16	2e−14	50 x 7	chromosome 8 open reading frame 4 [Source:HGNC Symbol
17	57172	2.41	2e−16	2e−14	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
18	92291	1.37	2e−16	2e−14	50 x 11	calpain 13 [Source:HGNC Symbol;Acc:16663]
19	6363	1.53	2e−16	2e−14	50 x 1	chemokine (C−C motif) ligand 19 [Source:HGNC Symbol;Acc
20	6352	1.42	2e−16	2e−14	48 x 1	chemokine (C−C motif) ligand 5 [Source:HGNC Symbol;Acc:

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	22.16	NULL	553	Cancer	Lembcke_Colonic Inflammation
2	20.25	NULL	417	H.Tiss	WIRTH_Immune system
3	17.48	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_D
4	13.52	NULL	312	BP	immune response
5	12.05	NULL	316	Cancer	SPANG_BCL6−index2
6	11.09	NULL	265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
7	11.09	NULL	265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
8	11.09	NULL	265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
9	11.09	NULL	265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
10	11.01	NULL	162	CC	external side of plasma membrane
11	9.6	NULL	1182	CC	extracellular region
12	8.95	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
13	8.74	NULL	683	CC	extracellular space
14	8.55	NULL	74	BP	regulation of immune response
15	8.36	NULL	185	Cancer	SPANG_LPS−index2
16	8.26	NULL	11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
17	8.26	NULL	15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
18	8.25	NULL	51	Glio	willscher_GBM_Verhaak−PNmut_expression_G_down
19	8.02	NULL	12	GSEA C2	ZHAN_MULTIPLE_MYELOMA_DN
20	7.97	NULL	5	GSEA C2	WONG_ENDOMETRIAL_CANCER_LATE
Underexpressed					
1	−12.45	NULL	142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
2	−12.45	NULL	142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
3	−10.51	NULL	530	Cancer	Lembcke_Normal vs Adenoma
4	−9.44	NULL	717	Chr	Chr 16
5	−8.73	NULL	21	CC	cornified envelope
6	−7.85	NULL	42	BP	keratinization
7	−7.18	NULL	4640	CC	nucleus
8	−6.86	NULL	149	BP	DNA replication
9	−6.82	NULL	370	BP	mitotic cell cycle
10	−6.44	NULL	127	H.Tiss	WIRTH_Muscle
11	−6.33	NULL	949	CC	nucleoplasm
12	−6.08	NULL	15	GSEA C2	SMID_BREAST_CANCER_LUMINAL_A_DN
13	−6.05	NULL	76	BP	epidermis development
14	−5.86	NULL	16	GSEA C2	FRASOR_RESPONSE_TO_SERM_OR_FULVESTRANT_DN
15	−5.86	NULL	53	BP	keratinocyte differentiation
16	−5.85	NULL	57	Glio	developing astrocytes
17	−5.69	NULL	16	GSEA C2	GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
18	−5.69	NULL	232	BP	mitosis
19	−5.58	NULL	1749	MF	DNA binding
20	−5.31	NULL	8	GSEA C2	NIKOLSKY_BREAST_CANCER_5P15_AMPLICON



GW_110

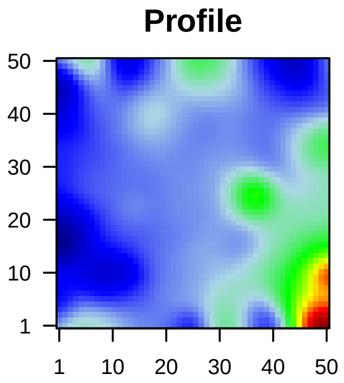
Local Summary

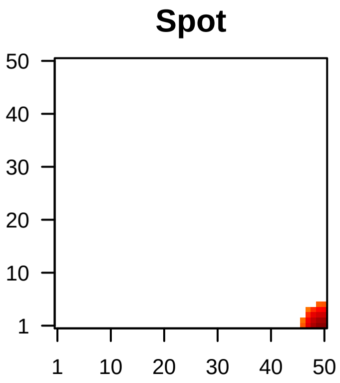
%DE = 0.97
metagenes = 20
genes = 311
genes in genesets = 309

genes with fdr < 0.1 = 286 (284 + / 2 −)
genes with fdr < 0.05 = 285 (283 + / 2 −)
genes with fdr < 0.01 = 267 (266 + / 1 −)

<r> metagenes = 0.98
<r> genes = 0.56

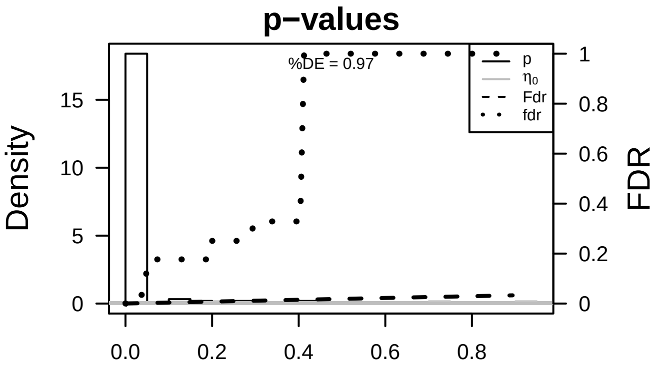
<FC> = 0.86
<shrinkage−t> = 29.96
<p−value> = 0
<fdr> = 0.13





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	241	1.35	2e−16	5e−17	50 x 1	arachidonate 5−lipoxygenase−activating protein [Source:HG
2	348	1.39	2e−16	5e−17	50 x 1	apolipoprotein E [Source:HGNC Symbol;Acc:613]
3	92591	1.52	2e−16	5e−17	48 x 2	ankyrin repeat and SOCS box containing 16 [Source:HGNC
4	260436	3.4	2e−16	5e−17	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symb
5	57172	2.41	2e−16	5e−17	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
6	6363	1.53	2e−16	5e−17	50 x 1	chemokine (C−C motif) ligand 19 [Source:HGNC Symbol;Acc
7	6352	1.42	2e−16	5e−17	48 x 1	chemokine (C−C motif) ligand 5 [Source:HGNC Symbol;Acc:
8	1236	1.43	2e−16	5e−17	50 x 1	chemokine (C−C motif) receptor 7 [Source:HGNC Symbol;Ac
9	930	2.07	2e−16	5e−17	49 x 1	CD19 molecule [Source:HGNC Symbol;Acc:1633]
10	915	1.41	2e−16	5e−17	49 x 1	CD3d molecule, delta (CD3−TCR complex) [Source:HGNC S
11	962	1.65	2e−16	5e−17	50 x 1	CD48 molecule [Source:HGNC Symbol;Acc:1683]
12	972	1.3	2e−16	5e−17	50 x 1	CD74 molecule, major histocompatibility complex, class II inv
13	925	1.29	2e−16	5e−17	48 x 1	CD8a molecule [Source:HGNC Symbol;Acc:1706]
14	51755	1.97	2e−16	5e−17	49 x 1	cyclin−dependent kinase 12 [Source:HGNC Symbol;Acc:242
15	10563	1.89	2e−16	5e−17	50 x 1	chemokine (C−X−C motif) ligand 13 [Source:HGNC Symbol;
16	1545	2.19	2e−16	5e−17	50 x 4	cytochrome P450, family 1, subfamily B, polypeptide 1 [Sourc
17	5168	1.68	2e−16	5e−17	50 x 2	ectonucleotide pyrophosphatase/phosphodiesterase 2 [Sourc
18	9214	1.37	2e−16	5e−17	49 x 1	Fas apoptotic inhibitory molecule 3 [Source:HGNC Symbol;A
19	54855	2.2	2e−16	5e−17	49 x 1	family with sequence similarity 46, member C [Source:HGNC
20	84824	1.29	2e−16	5e−17	49 x 1	Fc receptor−like A [Source:HGNC Symbol;Acc:18504]



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	30.94	NULL	95 / 417	H.Tiss	WIRTH_Immune system
2	27.6	NULL	103 / 553	Cancer	Lembcke_Colonic Inflammation
3	22.47	NULL	12 / 15	CC	MHC class II protein complex
4	21.46	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
5	21.34	NULL	3 / 5	GSEA C2	WONG_ENDOMETRIAL_CANCER_LATE
6	19.14	NULL	55 / 312	BP	immune response
7	17.95	NULL	7 / 11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
8	16.46	NULL	2 / 4	MMML CGS	MACIEJ_MMML 2
9	16.23	NULL	6 / 8	Glio	Donson−migration tethering and rolling−associated with LTS in HG
10	15.61	NULL	48 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
11	15.61	NULL	48 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
12	15.61	NULL	48 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
13	15.61	NULL	48 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
14	14.89	NULL	7 / 15	GSEA C2	FINAK_BREAST_CANCER_SDPP_SIGNATURE
15	14.89	NULL	8 / 16	GSEA C2	SU_THYMUS
16	14.86	NULL	7 / 13	Cancer	GENTLES_modul18
17	14.79	NULL	6 / 11	GSEA C2	BIOCARTA_THELPER_PATHWAY
18	14.31	NULL	15 / 47	BP	antigen processing and presentation
19	13.68	NULL	3 / 7	GSEA C2	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINE
20	13.61	NULL	18 / 74	BP	regulation of immune response
21	13.57	NULL	3 / 7	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
22	13.33	NULL	5 / 10	GSEA C2	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_
23	13.23	NULL	11 / 28	BP	B cell receptor signaling pathway
24	13.09	NULL	6 / 12	GSEA C2	BIOCARTA_CTL_PATHWAY
25	12.97	NULL	3 / 6	GSEA C2	SANA_RESPONSE_TO_IFNG_UP
26	12.69	NULL	6 / 15	Glio	Donson−chemokines/cytokines−associated with LTS in HGA
27	12.66	NULL	5 / 10	GSEA C2	LEE_DIFFERENTIATING_T_LYMPHOCYTE
28	12.53	NULL	25 / 162	CC	external side of plasma membrane
29	12.52	NULL	4 / 7	Glio	Donson−cytotoxic effectors−associated with LTS in HGA
30	12.42	NULL	5 / 13	GSEA C2	BIOCARTA_IL17_PATHWAY
31	12.3	NULL	6 / 12	GSEA C2	ZHAN_MULTIPLE_MYELOMA_DN
32	12.2	NULL	4 / 8	GSEA C2	GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_DN
33	12.03	NULL	4 / 13	BP	lymph node development
34	11.98	NULL	17 / 60	BP	T cell costimulation
35	11.81	NULL	4 / 9	GSEA C2	MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN
36	11.44	NULL	5 / 13	GSEA C2	HAHTOLA_CTCL_PATHOGENESIS
37	11.43	NULL	2 / 3	GSEA C2	KEGG_VIRAL_MYOCARDITIS
38	11.32	NULL	9 / 45	BP	T cell activation
39	11.2	NULL	17 / 84	BP	T cell receptor signaling pathway
40	11.15	NULL	7 / 27	MF	antigen binding

GW_110

Local Summary

%DE = 0.87

metagenes = 3

genes = 81

genes in genesets = 80

genes with fdr < 0.1 = 65 (65 + / 0 −)

genes with fdr < 0.05 = 60 (60 + / 0 −)

genes with fdr < 0.01 = 56 (56 + / 0 −)

<r> metagenes = 0.98

<r> genes = 0.39

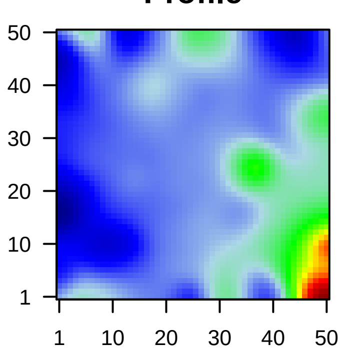
<FC> = 0.95

<shrinkage−t> = 33.14

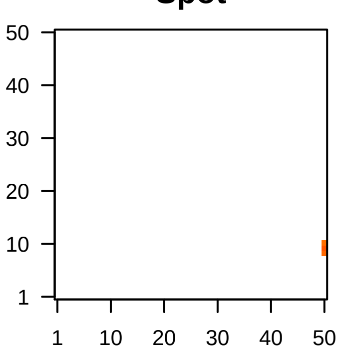
<p−value> = 0

<fdr> = 0.26

Profile



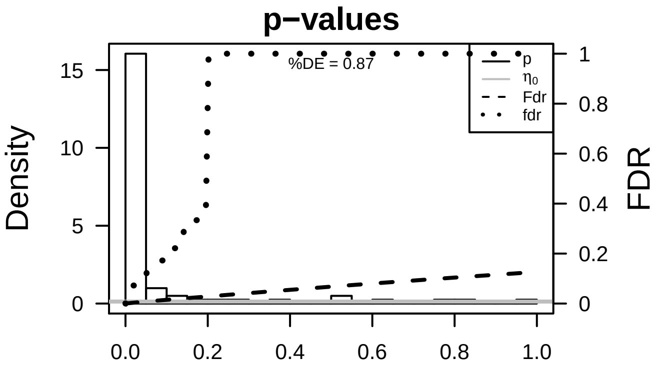
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	10551	1.31	2e−16	9e−17	50 x 10	anterior gradient 2 [Source:HGNC Symbol;Acc:328]
2	80341	1.77	2e−16	9e−17	50 x 10	BPI fold containing family B, member 2 [Source:HGNC Symb
3	92747	3.07	2e−16	9e−17	50 x 10	BPI fold containing family B, member 1 [Source:HGNC Symb
4	92291	1.37	2e−16	9e−17	50 x 11	calpain 13 [Source:HGNC Symbol;Acc:16663]
5	1675	1.62	2e−16	9e−17	50 x 9	complement factor D (adipsin) [Source:HGNC Symbol;Acc:27
6	54102	1.87	2e−16	9e−17	50 x 10	chloride intracellular channel 6 [Source:HGNC Symbol;Acc:2
7	1755	1.56	2e−16	9e−17	50 x 10	deleted in malignant brain tumors 1 [Source:HGNC Symbol;A
8	2327	1.53	2e−16	9e−17	50 x 11	flavin containing monooxygenase 2 (non−functional) [Source:
9	124220	2.44	2e−16	9e−17	50 x 10	zymogen granule protein 16B [Source:HGNC Symbol;Acc:30
10	389816	1.48	2e−16	9e−17	50 x 10	leucine rich repeat containing 26 [Source:HGNC Symbol;Acc:
11	4057	1.78	2e−16	9e−17	50 x 10	lactotransferrin [Source:HGNC Symbol;Acc:6720]
12	10232	2.55	2e−16	9e−17	50 x 11	mesothelin [Source:HGNC Symbol;Acc:7371]
13	4477	2.04	2e−16	9e−17	50 x 11	microseminoprotein, beta− [Source:HGNC Symbol;Acc:7372]
14	5284	1.87	2e−16	9e−17	50 x 10	polymeric immunoglobulin receptor [Source:HGNC Symbol;A
15	5304	1.86	2e−16	9e−17	50 x 10	prolactin−induced protein [Source:HGNC Symbol;Acc:8993]
16	51297	1.48	2e−16	9e−17	50 x 10	BPI fold containing family A, member 1 [Source:HGNC Symb
17	8842	1.64	2e−16	9e−17	50 x 10	prominin 1 [Source:HGNC Symbol;Acc:9454]
18	11272	2.7	2e−16	9e−17	50 x 10	proline rich 4 (lacrimal) [Source:HGNC Symbol;Acc:18020]
19	4246	1.34	2e−16	9e−17	50 x 10	secretoglobin, family 2A, member 1 [Source:HGNC Symbol;A
20	92304	2.64	2e−16	9e−17	50 x 10	secretoglobin, family 3A, member 1 [Source:HGNC Symbol;A

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset
1	55.7	NULL	11 / 16	GSEA C2 RICKMAN_HEAD_AND_NECK_CANCER_D
2	17.43	NULL	2 / 14	GSEA C2 SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_
3	16.5	NULL	1 / 5	GSEA C2 FERRARI_RESPONSE_TO_FENRETINIDE_DN
4	16.39	NULL	2 / 13	GSEA C2 NING_CHRONIC_OBSTRUCTIVE_PULMONARY_DISEASE_DN
5	15.68	NULL	2 / 13	GSEA C2 WONG_ENDMETRIUM_CANCER_UP
6	14.28	NULL	4 / 15	GSEA C2 POOLA_INVASIVE_BREAST_CANCER_DN
7	12.62	NULL	2 / 17	BP iron ion transport
8	12.45	NULL	2 / 10	GSEA C2 LUI_THYROID_CANCER_CLUSTER_5
9	12.04	NULL	3 / 16	GSEA C2 TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_LOBULAR_
10	11.55	NULL	1 / 5	GSEA C2 NAKAMURA_ALVEOLAR_EPITHELIUM
11	11.18	NULL	2 / 13	GSEA C2 BOYAULT_LIVER_CANCER_SUBCLASS_G3_DN
12	11.06	NULL	1 / 9	GSEA C2 GOUYER_TATI_TARGETS_UP
13	9.28	NULL	1 / 14	GSEA C2 WANG_BARRETTS_ESOPHAGUS_UP
14	9.28	NULL	1 / 14	GSEA C2 VALK_AML_WITH_11Q23_REARRANGED
15	9.25	NULL	1 / 7	GSEA C2 GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
16	9.22	NULL	1 / 15	GSEA C2 TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_16D_DN
17	9.22	NULL	1 / 15	GSEA C2 LOPES_METHYLATED_IN_COLON_CANCER_UP
18	9.12	NULL	1 / 7	GSEA C2 BIOCARTA_COMP_PATHWAY
19	8.97	NULL	23 / 1182	CC extracellular region
20	8.89	NULL	1 / 15	GSEA C2 RICKMAN_HEAD_AND_NECK_CANCER_E
21	8.81	NULL	2 / 16	GSEA C2 VALK_AML_CLUSTER_9
22	8.75	NULL	1 / 13	GSEA C2 YANG_BREAST_CANCER_ESR1_UP
23	8.55	NULL	1 / 16	GSEA C2 DOANE_BREAST_CANCER_ESR1_DN
24	8.34	NULL	1 / 12	H.Tiss WIRTH_Prim. lymphoid organs
25	8.34	NULL	1 / 12	GSEA C2 BERTUCCI_INVASIVE_CARCINOMA_DUCTAL_VS_LOBULAR_
26	8.34	NULL	1 / 12	GSEA C2 ASTON_MAJOR_DEPRESSIVE_DISORDER_DN
27	8.34	NULL	1 / 8	GSEA C2 REACTOME_COMPLEMENT_CASCADE
28	8.34	NULL	1 / 8	GSEA C2 REACTOME_INITIAL_TRIGGERING_OF_COMPLEMENT
29	8.06	NULL	15 / 683	CC extracellular space
30	8.05	NULL	1 / 10	BP negative regulation of blood coagulation
31	7.93	NULL	1 / 13	GSEA C2 CERVERA_SDHB_TARGETS_2
32	7.93	NULL	1 / 13	GSEA C2 REACTOME_FORMATION_OF_PLATELET_PLUG
33	7.93	NULL	1 / 13	GSEA C2 REACTOME_PLATELET_ACTIVATION
34	7.92	NULL	1 / 10	BP regulation of cytokine production
35	7.92	NULL	1 / 10	Glio willscher_ GBM_LTSwt_proteomics−G_UP
36	7.57	NULL	1 / 14	GSEA C2 REACTOME_FURTHER_PLATELET_RELEASATE
37	7.57	NULL	1 / 14	GSEA C2 REACTOME_PLATELET_DEGRANULATION
38	7.57	NULL	1 / 14	GSEA C2 ST_WNT_CA2_CYCLIC_GMP_PATHWAY
39	7.3	NULL	2 / 14	GSEA C2 PENG_RAPAMYCIN_RESPONSE_UP
40	7.25	NULL	1 / 15	GSEA C2 TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_DUCTAL_N

GW_110

Local Summary

%DE = 0.78

metagenes = 2

genes = 24

genes in genesets = 24

genes with fdr < 0.1 = 17 (0 + / 17 −)

genes with fdr < 0.05 = 17 (0 + / 17 −)

genes with fdr < 0.01 = 5 (0 + / 5 −)

<r> metagenes = 0.99

<r> genes = 0.41

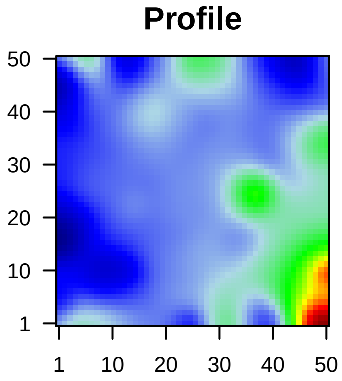
<FC> = −0.34

<shrinkage−t> = −11.91

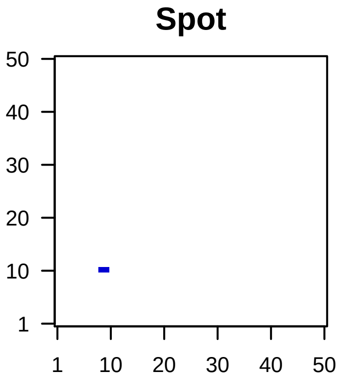
<p−value> = 0.02

<fdr> = 0.55

Profile



Spot



Local Genelist

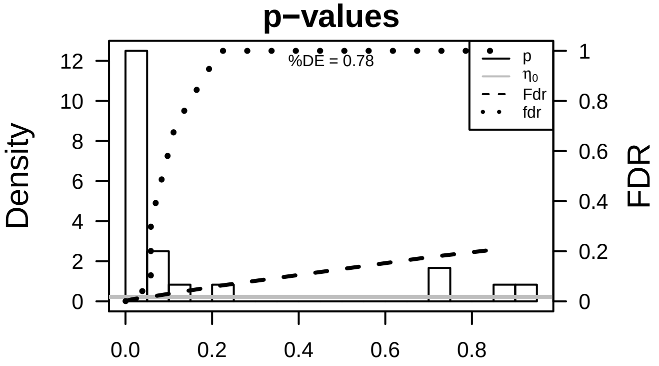
Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	30000	−0.66	3e−05	0.001	9 x 11	transportin 2 [Source:HGNC Symbol;Acc:19998]
2	27043	−0.58	2e−04	0.001	9 x 11	proline, glutamate and leucine rich protein 1 [Source:HGNC S
3	57176	−0.56	4e−04	0.001	9 x 11	Valine−−tRNA ligase, mitochondrial [Source:UniProtKB/TrEM
4	80728	−0.54	7e−04	0.001	10 x 11	Rho GTPase activating protein 39 [Source:HGNC Symbol;Ac
5	221927	−0.53	8e−04	0.001	9 x 11	BRCA1−associated ATM activator 1 [Source:HGNC Symbol;A
6	64710	−0.52	1e−03	0.015	9 x 11	nuclear casein kinase and cyclin−dependent kinase substrate
7	93643	−0.44	5e−03	0.015	9 x 11	tight junction associated protein 1 (peripheral) [Source:HGNC
8	5451	−0.43	7e−03	0.015	9 x 11	POU class 2 homeobox 1 [Source:HGNC Symbol;Acc:9212]
9	9091	−0.41	1e−02	0.018	9 x 11	phosphatidylinositol glycan anchor biosynthesis, class Q [Sou
10	339123	−0.39	1e−02	0.022	9 x 11	jumonji domain containing 8 [Source:HGNC Symbol;Acc:141
11	55764	−0.38	2e−02	0.026	10 x 11	intraflagellar transport 122 homolog (Chlamydomonas) [Sourc
12	11165	−0.36	2e−02	0.026	9 x 11	nudix (nucleoside diphosphate linked moiety X)−type motif 3 [
13	84939	−0.34	3e−02	0.026	10 x 11	melanoma associated antigen (mutated) 1 [Source:HGNC Sy
14	4832	−0.34	3e−02	0.041	9 x 11	NME/NM23 nucleoside diphosphate kinase 3 [Source:HGNC
15	10362	−0.32	4e−02	0.041	9 x 11	high mobility group 20B [Source:HGNC Symbol;Acc:5002]
16	11000	−0.31	5e−02	0.041	9 x 11	solute carrier family 27 (fatty acid transporter), member 3 [So
17	55051	−0.3	6e−02	0.041	9 x 11	NRDE−2, necessary for RNA interference, domain containing
18	10629	−0.3	6e−02	0.317	9 x 11	TAF6−like RNA polymerase II, p300/CBP−associated factor (I
19	54910	−0.25	1e−01	0.698	10 x 11	sema domain, immunoglobulin domain (Ig), transmembrane c
20	56996	−0.19	2e−01	1.000	10 x 11	solute carrier family 12, member 9 [Source:HGNC Symbol;Ac

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−15.35	NULL	2 / 15	GSEA C2	OLSSON_E2F3_TARGETS_DN
2	−14.72	NULL	1 / 11	GSEA C2	LAIHO_COLORECTAL_CANCER_SERRATED_DN
3	−14.01	NULL	1 / 12	GSEA C2	TIMOFEEVA_GROWTH_STRESS_VIA_STAT1_DN
4	−12.37	NULL	1 / 15	miRNA target starBase	hsa−miR−191*
5	−10.86	NULL	2 / 34	miRNA target starBase	hsa−miR−615−5p
6	−10.56	NULL	1 / 13	GSEA C2	ZHONG_RESPONSE_TO_AZACITIDINE_AND_TSA_DN
7	−10.56	NULL	1 / 13	GSEA C2	SPIRA_SMOKERS_LUNG_CANCER_DN
8	−10.34	NULL	1 / 5	GSEA C2	NAGY_PCAF_COMPONENTS_HUMAN
9	−10.27	NULL	1 / 14	GSEA C2	NIKOLSKY_BREAST_CANCER_7P22_AMPLICON
10	−10.26	NULL	2 / 21	BP	chromatin organization
11	−9.75	NULL	1 / 15	Pathw Ac	BENTINK_ras.6
12	−9.32	NULL	1 / 25	MF	Ran GTPase binding
13	−9.32	NULL	1 / 25	miRNA target starBase	hsa−miR−941
14	−8.97	NULL	2 / 70	miRNA target starBase	hsa−miR−622
15	−8.58	NULL	1 / 29	miRNA target starBase	hsa−miR−296−5p
16	−8.35	NULL	1 / 11	GSEA C2	DOANE_BREAST_CANCER_ESR1_UP
17	−8.26	NULL	1 / 13	GSEA C2	REACTOME_POST_TRANSLATIONAL_PROTEIN_MODIFICATIO
18	−8.24	NULL	3 / 132	miRNA target starBase	hsa−miR−28−5p
19	−8.21	NULL	1 / 23	Chr	Chr HSCHR6_MHC_DBB
20	−7.99	NULL	1 / 33	miRNA target starBase	hsa−miR−1231
21	−7.99	NULL	1 / 33	miRNA target starBase	hsa−miR−644
22	−7.94	NULL	1 / 10	BP	GTP biosynthetic process
23	−7.93	NULL	1 / 15	GSEA C2	REACTOME_RNA_POLYMERASE_III_TRANSCRIPTION
24	−7.93	NULL	1 / 15	GSEA C2	REACTOME_RNA_POLYMERASE_III_TRANSCRIPTION_INITIAT
25	−7.93	NULL	1 / 15	GSEA C2	REACTOME_RNA_POLYMERASE_III_TRANSCRIPTION_INITIAT
26	−7.93	NULL	1 / 14	GSEA C2	KEGG_GLYCOSYLPHOSPHATIDYLINOSITOL_GPI_ANCHOR_BI
27	−7.93	NULL	1 / 14	GSEA C2	REACTOME_SYNTHESIS_OF_GPI_ANCHORED_PROTEINS
28	−7.87	NULL	1 / 27	CC	MLL1 complex
29	−7.86	NULL	1 / 34	miRNA 3UTR	TCRA−517
30	−7.83	NULL	1 / 8	GSEA C2	NAGY_STAGA_COMPONENTS_HUMAN
31	−7.65	NULL	1 / 16	GSEA C2	COLLIS_PRKDC_SUBSTRATES
32	−7.62	NULL	1 / 15	GSEA C2	REACTOME_SYNTHESIS_OF_GLYCOSYLPHOSPHATIDYLINOS
33	−7.52	NULL	1 / 11	BP	CTP biosynthetic process
34	−7.52	NULL	1 / 11	BP	UTP biosynthetic process
35	−7.35	NULL	1 / 16	BP	preassembly of GPI anchor in ER membrane
36	−7.28	NULL	1 / 14	BP	embryonic heart tube development
37	−7.28	NULL	1 / 14	GSEA C2	DOANE_RESPONSE_TO_ANDROGEN_DN
38	−7.28	NULL	1 / 14	GSEA C2	SMID_BREAST_CANCER_LUMINAL_B_UP
39	−7.28	NULL	1 / 14	GSEA C2	BERNARD_PPAPDC1B_TARGETS_DN
40	−7.28	NULL	1 / 39	miRNA target starBase	hsa−miR−647

p−values



GW_110

Local Summary

%DE = 0.87

metagenes = 42

genes = 430

genes in genesets = 427

genes with fdr < 0.1 = 313 (4 + / 309 −)

genes with fdr < 0.05 = 224 (1 + / 223 −)

genes with fdr < 0.01 = 143 (1 + / 142 −)

<r> metagenes = 0.93

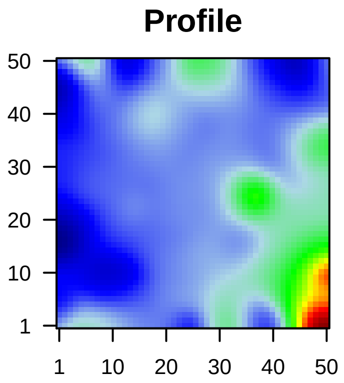
<r> genes = 0.26

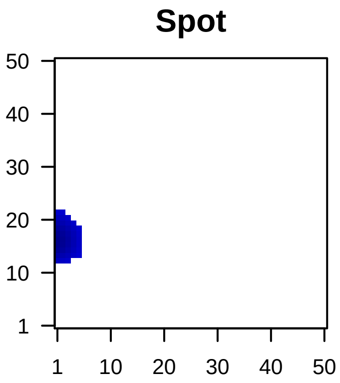
<FC> = −0.34

<shrinkage−t> = −12.02

<p−value> = 0.01

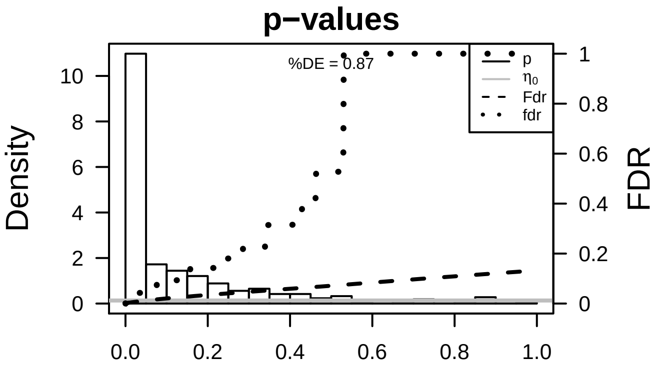
<fdr> = 0.59





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	10428	−1.34	2e−16	6e−15	1 x 15	craniofacial development protein 1 [Source:HGNC Symbol;Ac
2	283869	−1.34	2e−16	6e−15	1 x 17	neuropeptide W [Source:HGNC Symbol;Acc:30509]
3	230	−1.14	6e−13	3e−11	2 x 17	aldolase C, fructose−bisphosphate [Source:HGNC Symbol;A
4	23246	−1.13	1e−12	1e−09	1 x 16	block of proliferation 1 [Source:HGNC Symbol;Acc:15519]
5	26873	−1.05	3e−11	3e−09	1 x 17	5−oxoprolinase (ATP−hydrolysing) [Source:HGNC Symbol;Ac
6	3237	−1.03	9e−11	4e−07	1 x 16	homeobox D11 [Source:HGNC Symbol;Acc:5134]
7	2821	−0.92	7e−09	1e−06	3 x 17	glucose−6−phosphate isomerase [Source:HGNC Symbol;Acc
8	116447	−0.87	4e−08	1e−06	1 x 15	topoisomerase (DNA) I, mitochondrial [Source:HGNC Symbo
9	79080	−0.86	5e−08	2e−06	1 x 14	coiled−coil domain containing 86 [Source:HGNC Symbol;Acc
10	220064	−0.83	1e−07	2e−06	1 x 14	oral cancer overexpressed 1 [Source:HGNC Symbol;Acc:175
11	3217	−0.83	2e−07	2e−06	1 x 15	homeobox B7 [Source:HGNC Symbol;Acc:5118]
12	430	−0.83	2e−07	1e−05	2 x 20	achaete−scute family bHLH transcription factor 2 [Source:HG
13	2288	−0.8	4e−07	5e−05	1 x 19	FK506 binding protein 4, 59kDa [Source:HGNC Symbol;Acc:
14	89780	−0.76	2e−06	5e−05	4 x 15	wingless−type MMTV integration site family, member 3A [Sou
15	26519	−0.74	3e−06	5e−05	1 x 19	translocase of inner mitochondrial membrane 10 homolog (ye
16	991	−0.73	3e−06	1e−04	1 x 16	cell division cycle 20 [Source:HGNC Symbol;Acc:1723]
17	285958	−0.72	5e−06	1e−04	2 x 13	small nucleolar RNA host gene 15 (non−protein coding) [Sou
18	54976	−0.71	8e−06	1e−04	1 x 17	chromosome 20 open reading frame 27 [Source:HGNC Symb
19	118460	−0.7	8e−06	1e−04	1 x 13	exosome component 6 [Source:HGNC Symbol;Acc:19055]
20	84948	−0.69	1e−05	1e−04	1 x 16	tigger transposable element derived 5 [Source:HGNC Symbo



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−12.38	NULL	20 / 96	BP	rRNA processing
2	−10.38	NULL	5 / 13	GSEA C2	REACTOME_GLYCOLYSIS
3	−9.96	NULL	4 / 9	GSEA C2	BIOCARTA_GLYCOLYSIS_PATHWAY
4	−9.07	NULL	96 / 1318	CC	mitochondrion
5	−8.55	NULL	1 / 2	miRNA target	miR−16−1
6	−8.51	NULL	41 / 530	Cancer	Lembcke_Normal vs Adenoma
7	−8.34	NULL	5 / 10	GSEA C2	REACTOME_HIV_LIFE_CYCLE
8	−8.19	NULL	6 / 39	BP	glycolysis
9	−8.19	NULL	3 / 9	GSEA C2	MOREIRA_RESPONSE_TO_TSA_UP
10	−8.08	NULL	46 / 579	CC	nucleolus
11	−8.06	NULL	5 / 16	GSEA C2	BIOCARTA_PTDINS_PATHWAY
12	−7.62	NULL	4 / 14	CC	exosome (RNase complex)
13	−7.61	NULL	2 / 8	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_25
14	−7.53	NULL	4 / 11	GSEA C2	REACTOME_HIV_INFECTION
15	−7.31	NULL	25 / 153	MF	structural constituent of ribosome
16	−7.15	NULL	4 / 18	MF	ribonucleoprotein complex binding
17	−6.99	NULL	45 / 717	Chr	Chr 16
18	−6.89	NULL	4 / 15	GSEA C2	BASAKI_YBX1_TARGETS_UP
19	−6.88	NULL	3 / 10	GSEA C2	TOMIDA_METASTASIS_UP
20	−6.85	NULL	3 / 13	GSEA C2	SCHUHMACHER_MYC_TARGETS_UP
21	−6.84	NULL	5 / 14	GSEA C2	LOCKWOOD_AMPLIFIED_IN_LUNG_CANCER
22	−6.79	NULL	5 / 39	BP	gluconeogenesis
23	−6.52	NULL	5 / 15	GSEA C2	ZHANG_RESPONSE_TO_CANTHARIDIN_DN
24	−6.49	NULL	2 / 10	MF	monosaccharide binding
25	−6.37	NULL	21 / 167	CC	ribosome
26	−6.23	NULL	5 / 36	BP	ribosome biogenesis
27	−6.23	NULL	3 / 9	GSEA C2	CAFFAREL_RESPONSE_TO_THC_8HR_3_DN
28	−6.22	NULL	5 / 17	CC	proteasome accessory complex
29	−6.21	NULL	3 / 10	GSEA C2	REACTOME_MRNA_DECAY_BY_3_TO_5_EXORIBONUCLEASE
30	−6.21	NULL	1 / 5	miRNA target	hsa−miR−886−5p
31	−6.19	NULL	4 / 14	GSEA C2	KEGG_COLORECTAL_CANCER
32	−6.14	NULL	2 / 9	GSEA C2	KUMAMOTO_RESPONSE_TO_NUTLIN_3A_DN
33	−6.04	NULL	3 / 16	GSEA C2	GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
34	−6.01	NULL	3 / 13	GSEA C2	AUNG_GASTRIC_CANCER
35	−5.99	NULL	5 / 16	GSEA C2	WONG_EMBRYONIC_STEM_CELL_CORE
36	−5.95	NULL	4 / 14	GSEA C2	ELVIDGE_HYPOXIA_DN
37	−5.95	NULL	30 / 253	BP	translation
38	−5.93	NULL	5 / 28	BP	exonucleolytic nuclear−transcribed mRNA catabolic process involv
39	−5.9	NULL	29 / 304	CC	mitochondrial inner membrane
40	−5.86	NULL	12 / 66	BP	positive regulation of ubiquitin−protein ligase activity involved in mit

GW_110

Local Summary

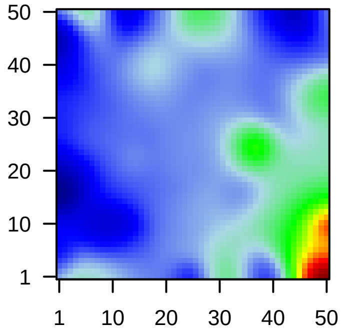
%DE = 0.76
metagenes = 8
genes = 144
genes in genesets = 143

genes with fdr < 0.1 = 104 (16 + / 88 −)
genes with fdr < 0.05 = 84 (10 + / 74 −)
genes with fdr < 0.01 = 70 (5 + / 65 −)

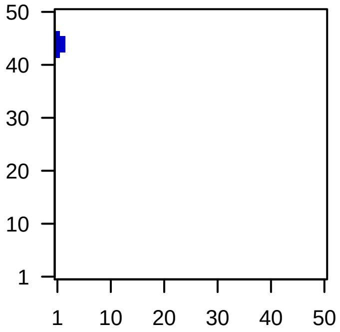
<r> metagenes = 0.97
<r> genes = 0.4

<FC> = −0.42
<shrinkage−t> = −14.66
<p−value> = 0
<fdr> = 0.39

Profile

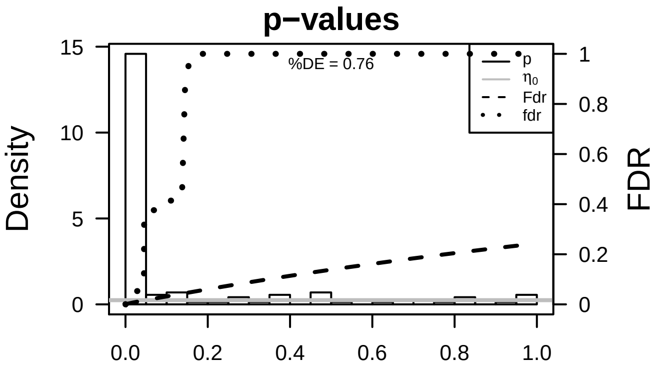


Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	3613	−1.41	2e−16	1e−15	1 x 46	inositol(myo)−1(or 4)−monophosphatase 2 [Source:HGNC Sy
2	50805	−1.7	2e−16	1e−15	1 x 43	iroquois homeobox 4 [Source:HGNC Symbol;Acc:6129]
3	10397	−1.32	2e−16	1e−15	1 x 42	N−myc downstream regulated 1 [Source:HGNC Symbol;Acc:
4	56901	−1.62	2e−16	1e−15	1 x 44	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4−li
5	5744	−1.47	2e−16	1e−15	1 x 43	parathyroid hormone−like hormone [Source:HGNC Symbol;A
6	6513	−1.46	2e−16	1e−15	1 x 43	solute carrier family 2 (facilitated glucose transporter), membe
7	8140	−1.47	2e−16	1e−15	1 x 43	solute carrier family 7 (amino acid transporter light chain, L sy
8	7280	−1.3	2e−16	1e−15	1 x 45	tubulin, beta 2A class IIa [Source:HGNC Symbol;Acc:12412]
9	56169	−1.19	5e−14	1e−12	1 x 46	gasdermin C [Source:HGNC Symbol;Acc:7151]
10	2152	1.19	6e−14	1e−12	1 x 43	coagulation factor III (thromboplastin, tissue factor) [Source:H
11	6665	−1.18	1e−13	6e−11	1 x 45	SRY (sex determining region Y)−box 15 [Source:HGNC Symb
12	1241	−1.11	2e−12	1e−10	1 x 46	leukotriene B4 receptor [Source:HGNC Symbol;Acc:6713]
13	5317	−1.08	9e−12	1e−10	1 x 46	plakophilin 1 (ectodermal dysplasia/skin fragility syndrome) [S
14	374918	−1.07	1e−11	1e−10	1 x 45	IGF−like family member 1 [Source:HGNC Symbol;Acc:24093
15	2167	−1.07	1e−11	7e−10	1 x 44	fatty acid binding protein 4, adipocyte [Source:HGNC Symbol
16	80115	−1.05	3e−11	4e−09	1 x 43	BAI1−associated protein 2−like 2 [Source:HGNC Symbol;Acc
17	664	−1.01	1e−10	2e−08	2 x 43	BCL2/adenovirus E1B 19kDa interacting protein 3 [Source:H
18	133	−0.9	6e−10	9e−08	1 x 42	adrenomedullin [Source:HGNC Symbol;Acc:259]
19	65124	−0.94	3e−09	1e−07	1 x 45	sosondowah ankyrin repeat domain family member C [Source
20	1041	−0.91	8e−09	1e−07	1 x 46	corneodesmosin [Source:HGNC Symbol;Acc:1802]



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−16.09	NULL	6 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
2	−12.48	NULL	1 / 5	GSEA C2	RODRIGUES_DCC_TARGETS_UP
3	−12.46	NULL	6 / 21	CC	desmosome
4	−12.26	NULL	1 / 5	GSEA C2	KYNG_ENVIRONMENTAL_STRESS_RESPONSE_NOT_BY_4NQ
5	−12.26	NULL	2 / 9	GSEA C2	KYNG_DNA_DAMAGE_UP
6	−12.26	NULL	2 / 9	GSEA C2	KYNG_ENVIRONMENTAL_STRESS_RESPONSE_UP
7	−11.88	NULL	3 / 16	GSEA C2	ELVIDGE_HIF1A_TARGETS_DN
8	−11.88	NULL	3 / 16	GSEA C2	ELVIDGE_HIF1A_AND_HIF2A_TARGETS_DN
9	−11.53	NULL	2 / 10	GSEA C2	RUGO_ENVIRONMENTAL_STRESS_RESPONSE_UP
10	−11.53	NULL	2 / 10	GSEA C2	KYNG_ENVIRONMENTAL_STRESS_RESPONSE_NOT_BY_GAM
11	−11.5	NULL	2 / 11	GSEA C2	BIOCARTA_VITCB_PATHWAY
12	−11.28	NULL	1 / 6	miRNA target set	hsa−miR−126
13	−11.09	NULL	2 / 15	GSEA C2	PRAMOONJAGO_SOX4_TARGETS_UP
14	−11.04	NULL	3 / 10	BP	negative regulation of interleukin−2 production
15	−11.03	NULL	1 / 8	GSEA C2	NIKOLSKY_BREAST_CANCER_5P15_AMPLICON
16	−10.98	NULL	1 / 6	GSEA C2	KYNG_ENVIRONMENTAL_STRESS_RESPONSE_NOT_BY_UV_
17	−10.93	NULL	2 / 15	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_3
18	−10.59	NULL	2 / 16	GSEA C2	SMITH_LIVER_CANCER
19	−10.53	NULL	2 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_4
20	−10.24	NULL	1 / 7	GSEA C2	BEGUM_TARGETS_OF_PAX3_FOXO1_FUSION_AND_PAX3
21	−9.87	NULL	2 / 13	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_BRAIN_UP
22	−9.76	NULL	2 / 9	GSEA C2	KORKOLA_CORRELATED_WITH_POU5F1
23	−9.68	NULL	2 / 11	BP	response to metal ion
24	−9.41	NULL	1 / 8	GSEA C2	REACTOME_FACILITATIVE_NA_INDEPENDENT_GLUCOSE_TR
25	−8.63	NULL	1 / 9	GSEA C2	KYNG_ENVIRONMENTAL_STRESS_RESPONSE_NOT_BY_GAM
26	−8.51	NULL	2 / 16	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_LUNG_UP
27	−8.44	NULL	2 / 15	GSEA C2	PARK_TRETINOIN_RESPONSE_AND_RARA_PLZF_FUSION
28	−8.33	NULL	1 / 10	MF	neutral amino acid transmembrane transporter activity
29	−8.33	NULL	1 / 10	GSEA C2	YOKOE_CANCER_TESTIS_ANTIGENS
30	−8.31	NULL	10 / 76	BP	epidermis development
31	−8.3	NULL	1 / 10	BP	surfactant homeostasis
32	−8.15	NULL	2 / 10	BP	skeletal muscle tissue regeneration
33	−8.13	NULL	2 / 16	GSEA C2	PARK_TRETINOIN_RESPONSE_AND_PML_RARA_FUSION
34	−8.12	NULL	38 / 572	Disease	GUDJ_psoriasis up
35	−8.11	NULL	1 / 10	GSEA C2	PARK_TRETINOIN_RESPONSE
36	−8.09	NULL	2 / 26	BP	positive regulation of cAMP biosynthetic process
37	−7.95	NULL	2 / 17	BP	cellular response to glucose starvation
38	−7.93	NULL	3 / 25	BP	brown fat cell differentiation
39	−7.8	NULL	1 / 11	MF	substrate−specific transmembrane transporter activity
40	−7.67	NULL	1 / 11	MMML CGS	MACIEJ_MMML 3

GW_110

Local Summary

%DE = 0.69

metagenes = 8

genes = 124

genes in genesets = 122

genes with fdr < 0.1 = 58 (1 + / 57 −)

genes with fdr < 0.05 = 55 (1 + / 54 −)

genes with fdr < 0.01 = 45 (1 + / 44 −)

<r> metagenes = 0.99

<r> genes = 0.52

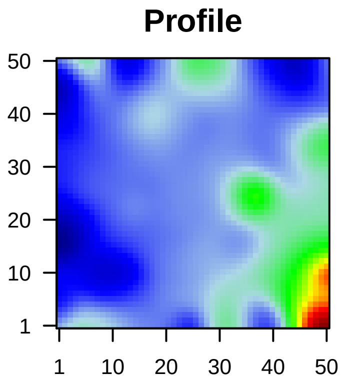
<FC> = −0.35

<shrinkage−t> = −12.33

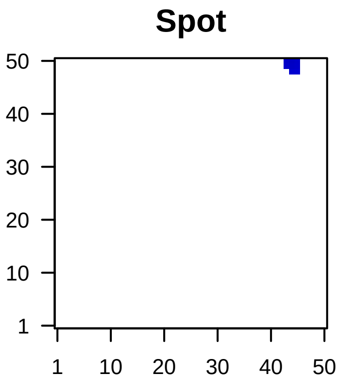
<p−value> = 0

<fdr> = 0.54

Profile



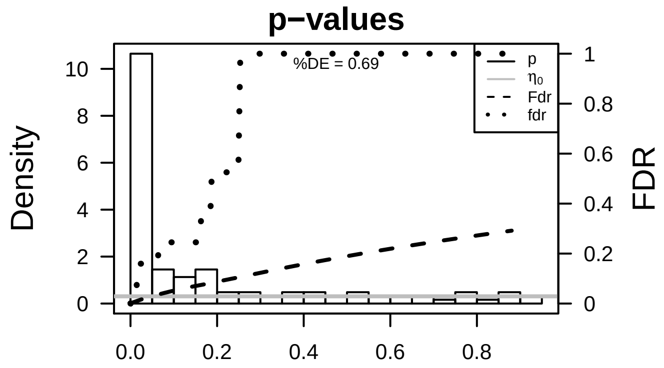
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	51659	−1.23	7e−15	5e−10	44 x 50	GINS complex subunit 2 (Psf2 homolog) [Source:HGNC Sym
2	113130	−1.07	1e−11	8e−10	44 x 49	cell division cycle associated 5 [Source:HGNC Symbol;Acc:1
3	8318	−1.05	3e−11	2e−09	45 x 49	cell division cycle 45 [Source:HGNC Symbol;Acc:1739]
4	1894	−1.02	1e−10	4e−06	45 x 50	epithelial cell transforming sequence 2 oncogene [Source:HG
5	7083	−0.83	2e−07	4e−06	45 x 49	thymidine kinase 1, soluble [Source:HGNC Symbol;Acc:1183
6	4173	−0.81	3e−07	4e−06	44 x 50	minichromosome maintenance complex component 4 [Source
7	259266	−0.81	3e−07	4e−06	45 x 49	asp (abnormal spindle) homolog, microcephaly associated (D
8	1163	−0.8	4e−07	3e−05	44 x 50	CDC28 protein kinase regulatory subunit 1B [Source:HGNC
9	79000	−0.74	3e−06	3e−05	44 x 49	aurora kinase A and ninein interacting protein [Source:HGNC
10	55839	−0.74	3e−06	3e−05	44 x 50	centromere protein N [Source:HGNC Symbol;Acc:30873]
11	29028	−0.74	3e−06	4e−05	44 x 50	ATPase family, AAA domain containing 2 [Source:HGNC Sym
12	387103	0.73	4e−06	1e−04	45 x 49	centromere protein W [Source:HGNC Symbol;Acc:21488]
13	9319	−0.69	1e−05	1e−04	43 x 50	thyroid hormone receptor interactor 13 [Source:HGNC Symbo
14	11065	−0.68	1e−05	1e−04	44 x 50	ubiquitin−conjugating enzyme E2C [Source:HGNC Symbol;A
15	150468	−0.68	2e−05	1e−04	43 x 50	cytoskeleton associated protein 2−like [Source:HGNC Symbo
16	55355	−0.67	2e−05	1e−04	44 x 49	Holliday junction recognition protein [Source:HGNC Symbol;
17	9928	−0.67	2e−05	4e−04	44 x 50	kinesin family member 14 [Source:HGNC Symbol;Acc:19181]
18	55143	−0.65	4e−05	4e−04	44 x 49	cell division cycle associated 8 [Source:HGNC Symbol;Acc:1
19	10635	−0.64	5e−05	4e−04	45 x 50	RAD51 associated protein 1 [Source:HGNC Symbol;Acc:169
20	3992	−0.64	5e−05	8e−04	45 x 50	fatty acid desaturase 1 [Source:HGNC Symbol;Acc:3574]

p−values



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−62.4	NULL	67 / 142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
2	−62.4	NULL	67 / 142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
3	−37.93	NULL	10 / 14	GSEA C2	ZHAN_MULTIPLE_MYELOMA_PR_UP
4	−34.93	NULL	12 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_2
5	−33.36	NULL	20 / 57	Glio	developing astrocytes
6	−31.87	NULL	8 / 10	GSEA C2	MONTERO_THYROID_CANCER_POOR_SURVIVAL_UP
7	−31.7	NULL	9 / 13	GSEA C2	CROONQUIST_IL6_DEPRIVATION_DN
8	−31.68	NULL	12 / 16	GSEA C2	FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
9	−31.51	NULL	11 / 15	GSEA C2	FINETTI_BREAST_CANCER_KINOME_RED
10	−31.45	NULL	10 / 16	GSEA C2	EGUCHI_CELL_CYCLE_RB1_TARGETS
11	−28.44	NULL	7 / 15	GSEA C2	SMID_BREAST_CANCER_LUMINAL_A_DN
12	−27.16	NULL	10 / 14	MMML CGS	MACIEJ_MMML 4
13	−27.1	NULL	9 / 15	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
14	−25.78	NULL	7 / 16	GSEA C2	CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_UP
15	−25.16	NULL	9 / 18	BP	spindle organization
16	−25.14	NULL	9 / 16	GSEA C2	KANG_DOXORUBICIN_RESISTANCE_UP
17	−25.02	NULL	8 / 15	GSEA C2	FOURNIER_ACINAR_DEVELOPMENT_LATE_DN
18	−24.94	NULL	3 / 11	GSEA C2	REACTOME_UNWINDING_OF_DNA
19	−24.16	NULL	54 / 530	Cancer	Lembcke_Normal vs Adenoma
20	−23.3	NULL	6 / 16	GSEA C2	CROONQUIST_NRAS_SIGNALING_DN
21	−23.05	NULL	5 / 14	GSEA C2	MISSIAGLIA_REGULATED_BY_METHYLATION_DN
22	−22.87	NULL	8 / 15	GSEA C2	LEE_EARLY_T_LYMPHOCYTE_UP
23	−22.52	NULL	4 / 12	GSEA C2	SHEPARD_BMYB_TARGETS
24	−21.95	NULL	5 / 16	GSEA C2	CROONQUIST_NRAS_VS_STROMAL_STIMULATION_DN
25	−21.85	NULL	7 / 14	GSEA C2	AMUNDSON_GAMMA_RADIATION_RESPONSE
26	−21.72	NULL	51 / 572	Disease	GUDJ_psoriasis up
27	−21.54	NULL	48 / 370	BP	mitotic cell cycle
28	−21.48	NULL	6 / 15	GSEA C2	TANG_SENESCENCE_TP53_TARGETS_DN
29	−20.55	NULL	6 / 15	GSEA C2	CHANG_CYCLING_GENES
30	−19.34	NULL	6 / 16	GSEA C2	GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
31	−18.98	NULL	6 / 16	Cancer	RHODES_UNDIFFERENTIATED_CANCER
32	−18.75	NULL	3 / 9	GSEA C2	SEMBA_FHIT_TARGETS_DN
33	−18.55	NULL	4 / 16	GSEA C2	REACTOME_DNA_STRAND_ELONGATION
34	−18.08	NULL	4 / 13	GSEA C2	NADERI_BREAST_CANCER_PROGNOSIS_UP
35	−17.98	NULL	31 / 232	BP	mitosis
36	−17.56	NULL	7 / 15	GSEA C2	LY_AGING_MIDDLE_DN
37	−17.35	NULL	15 / 56	CC	chromosome, centromeric region
38	−17.32	NULL	5 / 14	GSEA C2	LOPEZ_MESOTELIOMA_SURVIVAL_TIME_UP
39	−17.04	NULL	5 / 30	BP	DNA strand elongation involved in DNA replication
40	−17.03	NULL	5 / 13	GSEA C2	REN_BOUND_BY_E2F