GW_111

Global Summary

%DE = 0.14

genes with fdr < 0.2 = 1812 (1103 + / 709 −)

genes with fdr < 0.1 = 1341 (878 + / 463 −)

genes with fdr < 0.05 = 1132 (761 + / 371 −)

genes with fdr < 0.01 = 816 (594 + / 222 −)

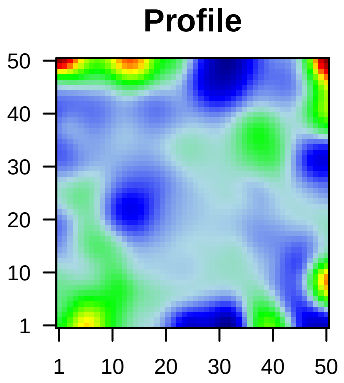
genes in genesets = 16332

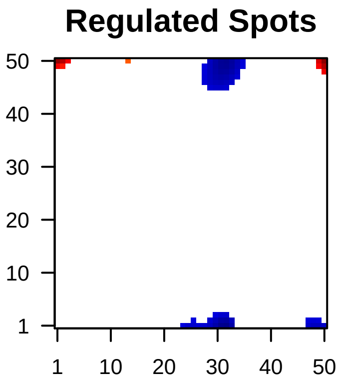
<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.1

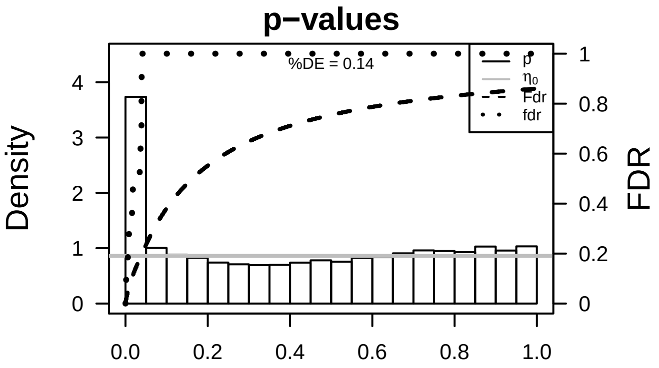
<fdr> = 0.86





Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	154664	1.59	2e−16	2e−14	50 x 50	ATP−binding cassette, sub−family A (ABC1), member 13 [Sou
2	24	1.44	2e−16	2e−14	16 x 50	ATP−binding cassette, sub−family A (ABC1), member 4 [Sour
3	79852	1.32	2e−16	2e−14	3 x 50	epoxide hydrolase 3 [Source:HGNC Symbol;Acc:23760]
4	8745	1.66	2e−16	2e−14	50 x 50	ADAM metallopeptidase domain 23 [Source:HGNC Symbol;A
5	9510	1.28	2e−16	2e−14	6 x 1	ADAM metallopeptidase with thrombospondin type 1 motif, 1
6	131	1.53	2e−16	2e−14	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
7	57016	2.28	2e−16	2e−14	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
8	441282	2.07	2e−16	2e−14	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC Sy
9	1646	1.28	2e−16	2e−14	13 x 50	aldo−keto reductase family 1, member C2 [Source:HGNC Sy
10	8644	1.91	2e−16	2e−14	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
11	1109	2.04	2e−16	2e−14	13 x 50	aldo−keto reductase family 1, member C4 [Source:HGNC Sy
12	214	1.79	2e−16	2e−14	50 x 50	activated leukocyte cell adhesion molecule [Source:HGNC Sy
13	218	2.79	2e−16	2e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
14	401138	2.09	2e−16	2e−14	1 x 5	amelotin [Source:HGNC Symbol;Acc:33188]
15	147463	1.34	2e−16	2e−14	25 x 50	ankyrin repeat domain 29 [Source:HGNC Symbol;Acc:27110]
16	347	2.24	2e−16	2e−14	50 x 7	apolipoprotein D [Source:HGNC Symbol;Acc:612]
17	9823	1.48	2e−16	2e−14	7 x 1	armadillo repeat containing, X−linked 2 [Source:HGNC Symb
18	25805	1.54	2e−16	2e−14	8 x 1	BMP and activin membrane−bound inhibitor [Source:HGNC S
19	92747	2.91	2e−16	2e−14	50 x 10	BPI fold containing family B, member 1 [Source:HGNC Symb
20	205428	1.34	2e−16	2e−14	50 x 50	chromosome 3 open reading frame 58 [Source:HGNC Symb



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	12.17	NULL	135	H.Tiss	WIRTH_Mucosa
2	10.23	NULL	743	Chr	Chr 7
3	9.21	NULL	918	Chr	Chr 17
4	8.82	NULL	11	GSEA C2	ITO_PTTG1_TARGETS_UP
5	7.91	NULL	1135	Chr	Chr 19
6	7.61	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_D
7	7.16	NULL	39	BP	retinoid metabolic process
8	7.12	NULL	9	GSEA C2	NIKOLSKY_BREAST_CANCER_17P11_AMPLICON
9	7.09	NULL	386	Chr	Chr 22
10	7.09	NULL	15	GSEA C2	LEE_LIVER_CANCER_HEPATOBLAST
11	7.04	NULL	13	GSEA C2	SINGH_NFE2L2_TARGETS
12	7.02	NULL	7	GSEA C2	MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
13	6.91	NULL	15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
14	6.79	NULL	1182	CC	extracellular region
15	6.69	NULL	6	GSEA C2	MURAKAMI_UV_RESPONSE_1HR_DN
16	6.59	NULL	683	CC	extracellular space
17	6.32	NULL	9	GSEA C2	GUTIERREZ_WALDENSTROEMS_MACROGLOBULINEMIA_1_D
18	6.29	NULL	55	BP	odontogenesis of dentin−containing tooth
19	6.19	NULL	5	GSEA C2	FERRARI_RESPONSE_TO_FENRETINIDE_DN
20	6.18	NULL	7	MMML CGS	MACIEJ_MMML 9
Underexpressed					
1	−8.15	NULL	957	Chr	Chr 11
2	−8.05	NULL	15	CC	MHC class II protein complex
3	−7.15	NULL	47	BP	antigen processing and presentation
4	−6.71	NULL	60	BP	interferon−gamma−mediated signaling pathway
5	−6.64	NULL	16	GSEA C2	MOSERLE_IFNA_RESPONSE
6	−6.21	NULL	127	H.Tiss	WIRTH_Muscle
7	−6.12	NULL	52	Chr	Chr HSCHR6_MHC_QBL
8	−6.06	NULL	602	Chr	Chr 10
9	−6.05	NULL	717	Chr	Chr 16
10	−5.97	NULL	23	CC	integral to lumenal side of endoplasmic reticulum membrane
11	−5.8	NULL	1720	Chr	Chr 1
12	−5.66	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_F
13	−5.62	NULL	51	BP	type I interferon signaling pathway
14	−5.49	NULL	10	BP	cellular response to zinc ion
15	−5.45	NULL	13	GSEA C2	BOWIE_RESPONSE_TO_TAMOXIFEN
16	−5.2	NULL	32	CC	ER to Golgi transport vesicle membrane
17	−5.19	NULL	7	MMML CGS	MACIEJ_MMML 13
18	−4.75	NULL	3	MMML CGS	MACIEJ_MMML 7
19	−4.73	NULL	153	MF	structural constituent of ribosome
20	−4.65	NULL	417	H.Tiss	WIRTH_Immune system

GW_111

Local Summary

%DE = 0.86

metagenes = 5

genes = 119

genes in genesets = 118

genes with fdr < 0.1 = 77 (71 + / 6 −)

genes with fdr < 0.05 = 74 (68 + / 6 −)

genes with fdr < 0.01 = 63 (59 + / 4 −)

<r> metagenes = 0.99

<r> genes = 0.31

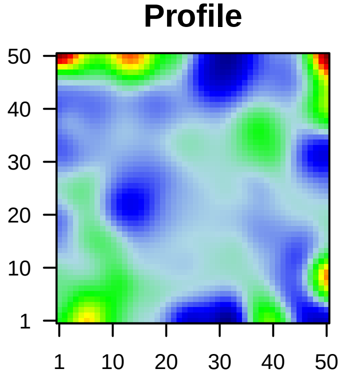
<FC> = 0.58

<shrinkage−t> = 20.24

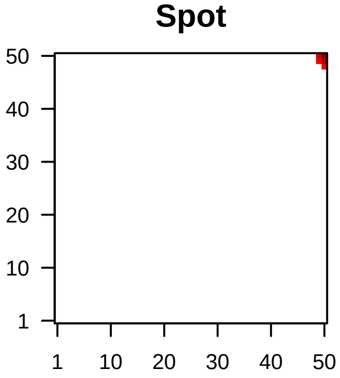
<p−value> = 0

<fdr> = 0.4

Profile



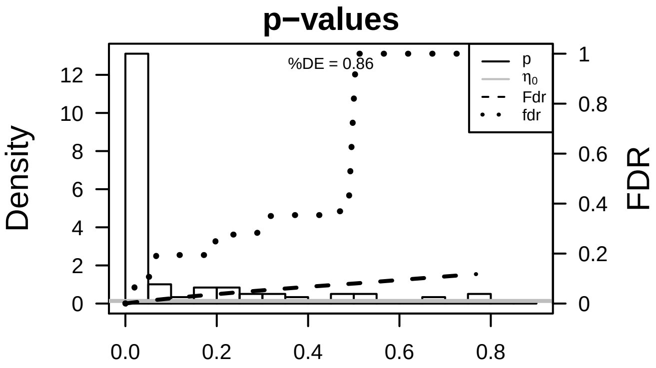
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	154664	1.59	2e−16	2e−16	50 x 50	ATP−binding cassette, sub−family A (ABC1), member 13 [Sou
2	8745	1.66	2e−16	2e−16	50 x 50	ADAM metallopeptidase domain 23 [Source:HGNC Symbol;A
3	214	1.79	2e−16	2e−16	50 x 50	activated leukocyte cell adhesion molecule [Source:HGNC Sy
4	205428	1.34	2e−16	2e−16	50 x 50	chromosome 3 open reading frame 58 [Source:HGNC Symbo
5	26256	1.61	2e−16	2e−16	50 x 50	calcium binding tyrosine−(Y)−phosphorylation regulated [Sou
6	56548	1.38	2e−16	2e−16	50 x 50	carbohydrate (N−acetylglucosamine 6−O) sulfotransferase 7 [
7	26047	2.14	2e−16	2e−16	50 x 50	contactin associated protein−like 2 [Source:HGNC Symbol;Ac
8	1592	1.25	2e−16	2e−16	50 x 50	cytochrome P450, family 26, subfamily A, polypeptide 1 [Sour
9	10655	1.48	2e−16	2e−16	50 x 50	doublesex and mab−3 related transcription factor 2 [Source:H
10	4072	1.73	2e−16	2e−16	50 x 50	epithelial cell adhesion molecule [Source:HGNC Symbol;Acc:
11	83888	1.53	2e−16	2e−16	50 x 50	fibroblast growth factor binding protein 2 [Source:HGNC Sym
12	2719	2.11	2e−16	2e−16	50 x 50	glypican 3 [Source:HGNC Symbol;Acc:4451]
13	2947	1.55	2e−16	2e−16	50 x 50	glutathione S−transferase mu 3 (brain) [Source:HGNC Symbo
14	4915	1.61	2e−16	2e−16	50 x 50	neurotrophic tyrosine kinase, receptor, type 2 [Source:HGNC
15	4922	2.24	2e−16	2e−16	50 x 50	neurotensin [Source:HGNC Symbol;Acc:8038]
16	4953	1.54	2e−16	2e−16	50 x 50	ornithine decarboxylase 1 [Source:HGNC Symbol;Acc:8109]
17	56963	1.56	2e−16	2e−16	50 x 50	repulsive guidance molecule family member a [Source:HGNC
18	6335	1.27	2e−16	2e−16	50 x 50	sodium channel, voltage−gated, type IX, alpha subunit [Sourc
19	6657	1.89	2e−16	2e−16	50 x 50	SRY (sex determining region Y)−box 2 [Source:HGNC Symbo
20	11166	1.63	2e−16	2e−16	50 x 50	SRY (sex determining region Y)−box 21 [Source:HGNC Symb

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset
1	24.95	NULL	2 / 7	GSEA C2 MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
2	21.08	NULL	5 / 15	GSEA C2 KEGG_GLUTATHIONE_METABOLISM
3	18.23	NULL	1 / 4	GSEA C2 MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_13
4	18.01	NULL	3 / 11	GSEA C2 ITO_PTTG1_TARGETS_UP
5	17.09	NULL	4 / 13	GSEA C2 KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_
6	16.33	NULL	3 / 13	BP regulation of blood vessel size
7	13.12	NULL	3 / 11	MF glutathione binding
8	13.12	NULL	3 / 11	GSEA C2 KEGG_DRUG_METABOLISM_CYTOCHROME_P450
9	12.55	NULL	2 / 10	GSEA C2 CONRAD_STEM_CELL
10	12.13	NULL	6 / 25	BP glutathione derivative biosynthetic process
11	11.56	NULL	2 / 11	GSEA C2 SMID_BREAST_CANCER_BASAL_UP
12	11.32	NULL	1 / 7	GSEA C2 REACTOME_G1_S_TRANSITION
13	11.32	NULL	1 / 7	miRNA target miR−145
14	11.28	NULL	2 / 9	GSEA C2 REACTOME_GLUCURONIDATION
15	11.22	NULL	3 / 48	BP cerebral cortex development
16	11.21	NULL	3 / 8	GSEA C2 LIU_CDX2_TARGETS_DN
17	11.05	NULL	3 / 12	GSEA C2 BROCKE_APOPTOSIS_REVERSED_BY_IL6
18	10.64	NULL	8 / 34	BP glutathione metabolic process
19	10.51	NULL	2 / 23	BP stem cell differentiation
20	10.42	NULL	2 / 15	MF glucuronosyltransferase activity
21	10.42	NULL	1 / 8	GSEA C2 REACTOME_E2F_TRANSCRIPTIONAL_TARGETS_AT_G1_S
22	10.42	NULL	1 / 8	miRNA 3UTR CTGCA−450
23	10.26	NULL	3 / 15	BP lipid glycosylation
24	10.22	NULL	1 / 2	miRNA target miR−127
25	10.2	NULL	1 / 11	Glio neurons_glio
26	10.17	NULL	2 / 19	BP anatomical structure formation involved in morphogenesis
27	10.01	NULL	11 / 119	BP xenobiotic metabolic process
28	9.73	NULL	1 / 11	CC axolemma
29	9.34	NULL	2 / 22	BP eye development
30	9.27	NULL	1 / 5	GSEA C2 KERLEY_RESPONSE_TO_CISPLATIN_DN
31	9.21	NULL	2 / 9	GSEA C2 REACTOME_METABOLISM_OF_AMINO_ACIDS
32	9.2	NULL	1 / 7	GSEA C2 REACTOME_REGULATION_OF_ORNITHINE_DECARBOXYLASE
33	9.14	NULL	2 / 10	GSEA C2 CERVERA_SDHB_TARGETS_1_DN
34	9.12	NULL	1 / 12	MF heparan sulfate proteoglycan binding
35	9.08	NULL	1 / 10	MF miRNA binding
36	8.89	NULL	1 / 3	GSEA C2 RUNNE_GENDER_EFFECT_DN
37	8.78	NULL	2 / 16	GSEA C2 GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_Y
38	8.69	NULL	1 / 13	BP positive regulation of endocytosis
39	8.57	NULL	1 / 11	BP neuronal stem cell maintenance
40	8.57	NULL	1 / 11	GSEA C2 REACTOME_E2F_MEDIATED_REGULATION_OF_DNA_REPLICA

GW_111

Local Summary

%DE = 0.79

metagenes = 5

genes = 112

genes in genesets = 109

genes with fdr < 0.1 = 82 (75 + / 7 −)

genes with fdr < 0.05 = 82 (75 + / 7 −)

genes with fdr < 0.01 = 72 (65 + / 7 −)

<r> metagenes = 1

<r> genes = 0.54

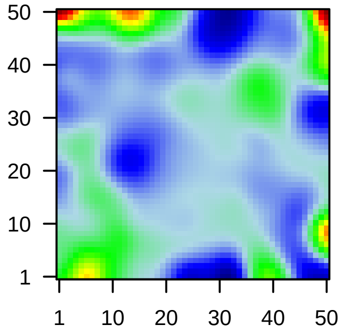
<FC> = 0.63

<shrinkage−t> = 22.42

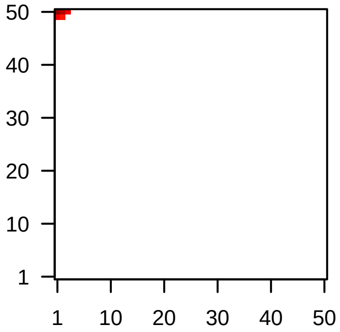
<p−value> = 0

<fdr> = 0.28

Profile



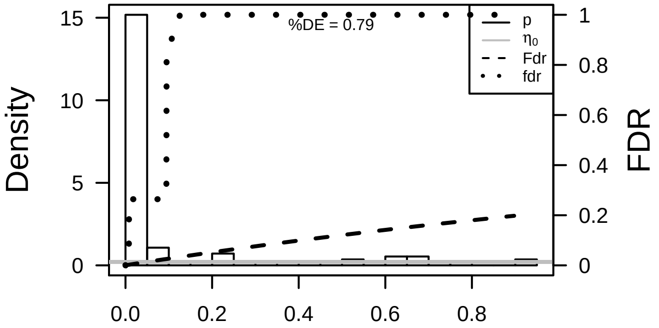
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	79852	1.32	2e−16	2e−16	3 x 50	epoxide hydrolase 3 [Source:HGNC Symbol;Acc:23760]
2	131	1.53	2e−16	2e−16	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
3	57016	2.28	2e−16	2e−16	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
4	441282	2.07	2e−16	2e−16	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC S
5	8644	1.91	2e−16	2e−16	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
6	218	2.79	2e−16	2e−16	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
7	810	1.29	2e−16	2e−16	1 x 50	calmodulin−like 3 [Source:HGNC Symbol;Acc:1452]
8	22802	1.3	2e−16	2e−16	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
9	49860	2.24	2e−16	2e−16	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
10	1673	−1.75	2e−16	2e−16	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
11	2877	1.89	2e−16	2e−16	1 x 50	glutathione peroxidase 2 (gastrointestinal) [Source:HGNC Sy
12	26085	2.06	2e−16	2e−16	1 x 50	kallikrein−related peptidase 13 [Source:HGNC Symbol;Acc:6
13	5653	2.53	2e−16	2e−16	1 x 50	kallikrein−related peptidase 6 [Source:HGNC Symbol;Acc:63
14	5650	1.73	2e−16	2e−16	1 x 49	kallikrein−related peptidase 7 [Source:HGNC Symbol;Acc:63
15	3860	1.26	2e−16	2e−16	1 x 50	keratin 13 [Source:HGNC Symbol;Acc:6415]
16	192666	2.8	2e−16	2e−16	1 x 50	keratin 24 [Source:HGNC Symbol;Acc:18527]
17	137797	1.46	2e−16	2e−16	1 x 50	LY6/PLAUR domain containing 2 [Source:HGNC Symbol;Acc
18	27076	1.28	2e−16	2e−16	1 x 50	LY6/PLAUR domain containing 3 [Source:HGNC Symbol;Acc
19	4118	1.59	2e−16	2e−16	1 x 50	mal, T−cell differentiation protein [Source:HGNC Symbol;Acc
20	7851	1.25	2e−16	2e−16	1 x 50	mal, T−cell differentiation protein−like [Source:HGNC Symbol

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	39.63	NULL	53 / 135	H.Tiss	WIRTH_Mucosa
2	22.44	NULL	7 / 19	BP	peptide cross−linking
3	21.73	NULL	4 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
4	20.21	NULL	5 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
5	20.13	NULL	3 / 12	BP	cellular aldehyde metabolic process
6	19.08	NULL	13 / 42	BP	keratinization
7	17.15	NULL	16 / 53	BP	keratinocyte differentiation
8	16.33	NULL	6 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
9	16.02	NULL	12 / 21	CC	cornified envelope
10	14.96	NULL	49 / 572	Disease	GUDJ_psoriasis up
11	14.11	NULL	2 / 16	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_LUNG_UP
12	13.9	NULL	4 / 15	MF	retinol dehydrogenase activity
13	13.02	NULL	2 / 11	GSEA C2	ROME_INSULIN_TARGETS_IN_MUSCLE_DN
14	12.96	NULL	1 / 9	GSEA C2	NIKOLSKY_BREAST_CANCER_17P11_AMPLICON
15	11.8	NULL	4 / 39	BP	retinoid metabolic process
16	11.77	NULL	10 / 122	MF	serine−type endopeptidase activity
17	11.29	NULL	14 / 76	BP	epidermis development
18	10.55	NULL	1 / 9	GSEA C2	GOUYER_TUMOR_INVASIVENESS
19	10.36	NULL	1 / 13	MF	oxidoreductase activity, acting on the aldehyde or oxo group of don
20	10.1	NULL	2 / 14	GSEA C2	KEGG_PHENYLALANINE_METABOLISM
21	10.02	NULL	2 / 16	GSEA C2	KOBAYASHI_EGFR_SIGNALING_24HR_UP
22	9.96	NULL	2 / 14	GSEA C2	CHIANG_LIVER_CANCER_SUBCLASS_POLYSOMY7_DN
23	9.88	NULL	1 / 10	GSEA C2	KEGG_LINOLEIC_ACID_METABOLISM
24	9.57	NULL	3 / 14	GSEA C2	CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U
25	9.31	NULL	2 / 15	GSEA C2	LI_AMPLIFIED_IN_LUNG_CANCER
26	9.11	NULL	1 / 6	GSEA C2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_B_DN
27	8.98	NULL	1 / 14	BP	tissue regeneration
28	8.87	NULL	1 / 12	GSEA C2	ODONNELL_METASTASIS_DN
29	8.87	NULL	1 / 12	GSEA C2	SYED_ESTRADIOL_RESPONSE
30	8.84	NULL	1 / 12	GSEA C2	ONDER_CDH1_TARGETS_1_UP
31	8.71	NULL	3 / 15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
32	8.62	NULL	1 / 15	BP	hormone metabolic process
33	8.61	NULL	1 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
34	8.55	NULL	3 / 10	GSEA C2	SMID_BREAST_CANCER_ERBB2_UP
35	8.53	NULL	1 / 18	MF	acyl−CoA dehydrogenase activity
36	8.42	NULL	1 / 13	GSEA C2	BRUECKNER_TARGETS_OF_MIRLET7A3_DN
37	8.42	NULL	1 / 13	GSEA C2	KEGG_BUTANOATE_METABOLISM
38	8.26	NULL	1 / 10	BP	positive regulation of endothelial cell apoptotic process
39	8.26	NULL	1 / 10	BP	retinal metabolic process
40	8.25	NULL	2 / 38	BP	myelination

GW_111

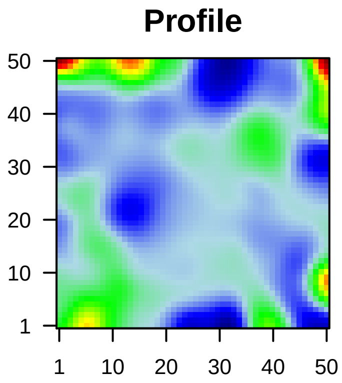
Local Summary

%DE = 0.87
metagenes = 1
genes = 28
genes in genesets = 28

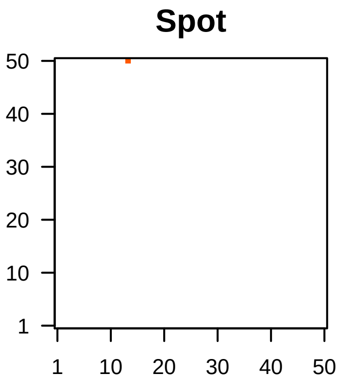
genes with fdr < 0.1 = 21 (18 + / 3 −)
genes with fdr < 0.05 = 15 (13 + / 2 −)
genes with fdr < 0.01 = 15 (13 + / 2 −)

<r> metagenes = NA
<r> genes = 0.31

<FC> = 0.42
<shrinkage−t> = 14.66
<p−value> = 0
<fdr> = 0.44



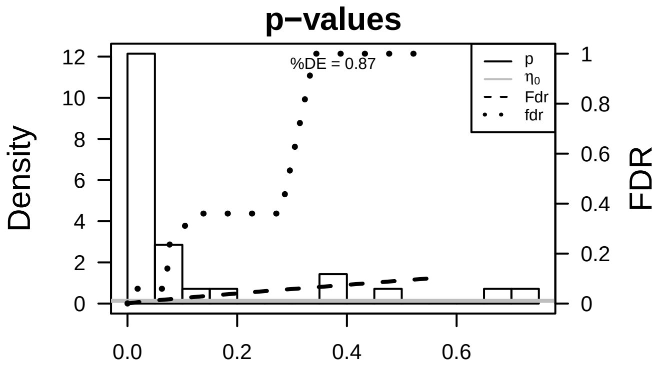
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	56666	1.44	2e−16	8e−16	14 x 50	pannexin 2 [Source:HGNC Symbol;Acc:8600]
2	493861	1.21	1e−15	6e−14	14 x 50	EP300 interacting inhibitor of differentiation 3 [Source:HGNC
3	7296	1.16	2e−14	5e−13	14 x 50	thioredoxin reductase 1 [Source:HGNC Symbol;Acc:12437]
4	57007	1.12	2e−13	8e−11	14 x 50	atypical chemokine receptor 3 [Source:HGNC Symbol;Acc:23
5	2817	1.01	3e−11	8e−11	14 x 50	glypican 1 [Source:HGNC Symbol;Acc:4449]
6	3005	1	5e−11	7e−10	14 x 50	H1 histone family, member 0 [Source:HGNC Symbol;Acc:471
7	8365	0.96	2e−10	1e−07	14 x 50	histone cluster 2, H4a [Source:HGNC Symbol;Acc:4794]
8	2736	0.83	5e−08	1e−07	14 x 50	GLI family zinc finger 2 [Source:HGNC Symbol;Acc:4318]
9	23657	0.82	6e−08	7e−05	14 x 50	solute carrier family 7 (anionic amino acid transporter light ch
10	5217	0.65	2e−05	5e−04	14 x 50	profilin 2 [Source:HGNC Symbol;Acc:8882]
11	1066	−0.58	1e−04	3e−03	14 x 50	carboxylesterase 1 [Source:HGNC Symbol;Acc:1863]
12	9048	0.51	8e−04	4e−03	14 x 50	artemin [Source:HGNC Symbol;Acc:727]
13	476	0.46	2e−03	4e−03	14 x 50	ATPase, Na+/K+ transporting, alpha 1 polypeptide [Source:H
14	8323	0.43	4e−03	4e−03	14 x 50	frizzled family receptor 6 [Source:HGNC Symbol;Acc:4044]
15	65055	−0.43	4e−03	4e−03	14 x 50	receptor accessory protein 1 [Source:HGNC Symbol;Acc:257
16	386757	0.42	5e−03	6e−02	14 x 50	solute carrier family 6 (neurotransmitter transporter), member
17	5909	−0.33	3e−02	6e−02	14 x 50	RAP1 GTPase activating protein [Source:HGNC Symbol;Acc:
18	23428	0.28	6e−02	6e−02	14 x 50	solute carrier family 7 (amino acid transporter light chain, L sy
19	131408	0.27	7e−02	6e−02	14 x 50	family with sequence similarity 131, member A [Source:HGN
20	100288413	0.26	9e−02	6e−02	14 x 50	endogenous retrovirus group MER34, member 1 [Source:HG



p−values

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	24.37	NULL	1 / 6	GSEA C2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_D_DN
2	20.26	NULL	1 / 12	MF	channel activity
3	19.18	NULL	1 / 13	BP	response to ischemia
4	18.24	NULL	1 / 14	GSEA C2	NIKOLSKY_BREAST_CANCER_22Q13_AMPLICON
5	16.2	NULL	1 / 10	BP	negative regulation of fibroblast growth factor receptor signaling pa
6	15.77	NULL	1 / 12	BP	negative regulation of intrinsic apoptotic signaling pathway in respo
7	14.23	NULL	1 / 12	MF	heparan sulfate proteoglycan binding
8	14.02	NULL	1 / 21	CC	gap junction
9	13.26	NULL	1 / 10	BP	anatomical structure development
10	12.96	NULL	1 / 17	BP	nucleobase−containing small molecule interconversion
11	12.91	NULL	2 / 11	GSEA C2	REACTOME_APOPTOSIS_INDUCED_DNA_FRAGMENTATION
12	12.81	NULL	1 / 14	GSEA C2	REACTOME_ACTIVATION_OF_RAC
13	12.35	NULL	2 / 17	MF	amino acid transmembrane transporter activity
14	12.07	NULL	1 / 19	BP	hydrogen peroxide catabolic process
15	11.64	NULL	1 / 12	BP	head development
16	11.5	NULL	2 / 19	BP	amino acid transmembrane transport
17	11.01	NULL	1 / 13	BP	regulation of smoothened signaling pathway
18	11.01	NULL	1 / 13	GSEA C2	BIOCARTA_SHH_PATHWAY
19	11	NULL	1 / 22	BP	response to axon injury
20	10.9	NULL	1 / 21	BP	chemokine−mediated signaling pathway
21	10.58	NULL	1 / 22	MF	coreceptor activity
22	10.48	NULL	1 / 19	MF	laminin binding
23	10.47	NULL	1 / 14	BP	hindbrain development
24	10.47	NULL	1 / 14	BP	negative regulation of chondrocyte differentiation
25	10.15	NULL	1 / 25	BP	gastrulation
26	10.15	NULL	1 / 25	BP	protein tetramerization
27	10.14	NULL	1 / 20	MF	fibroblast growth factor binding
28	10	NULL	1 / 15	BP	embryonic digestive tract development
29	9.68	NULL	1 / 27	MF	protein disulfide oxidoreductase activity
30	9.28	NULL	1 / 23	BP	glycosaminoglycan catabolic process
31	9.27	NULL	1 / 29	BP	positive regulation of cell death
32	9.2	NULL	1 / 17	BP	dorsal/ventral neural tube patterning
33	9.2	NULL	1 / 17	BP	morphogenesis of an epithelium
34	9.2	NULL	1 / 17	BP	osteoblast development
35	9.16	NULL	1 / 17	BP	platelet aggregation
36	9.08	NULL	1 / 30	BP	mesoderm formation
37	8.92	NULL	1 / 29	BP	receptor internalization
38	8.79	NULL	1 / 34	CC	chromosome, telomeric region
39	8.73	NULL	1 / 32	MF	NADP binding
40	8.64	NULL	4 / 147	CC	endosome

GW_111

Local Summary

%DE = 0.69

metagenes = 19

genes = 239

genes in genesets = 236

genes with fdr < 0.1 = 104 (6 + / 98 −)

genes with fdr < 0.05 = 102 (6 + / 96 −)

genes with fdr < 0.01 = 70 (3 + / 67 −)

<r> metagenes = 0.74

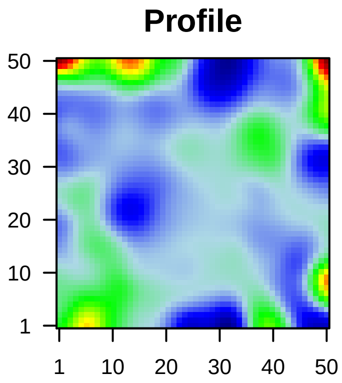
<r> genes = 0.26

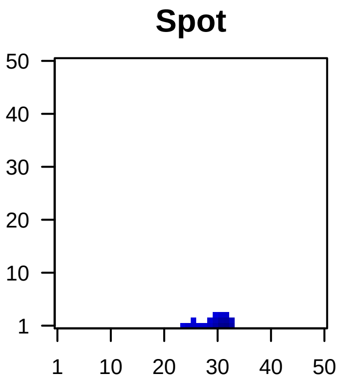
<FC> = −0.29

<shrinkage−t> = −10

<p−value> = 0.01

<fdr> = 0.6


Profile


Spot

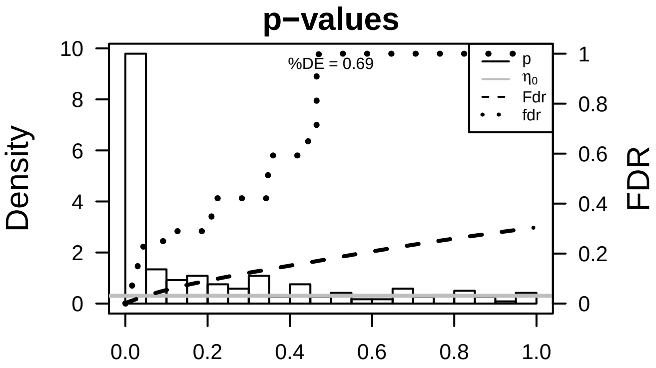
Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	3627	−1.42	2e−16	2e−14	32 x 1	chemokine (C−X−C motif) ligand 10 [Source:HGNC Symbol;A
2	58	−1.12	2e−13	4e−11	25 x 1	actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
3	1410	1.08	1e−12	4e−11	25 x 1	crystallin, alpha B [Source:HGNC Symbol;Acc:2389]
4	2318	−1.08	1e−12	1e−10	25 x 1	filamin C, gamma [Source:HGNC Symbol;Acc:3756]
5	10866	−1.06	3e−12	1e−08	32 x 1	HLA complex P5 (non−protein coding) [Source:HGNC Symbo
6	6890	−0.96	2e−10	3e−08	32 x 1	transporter 1, ATP−binding cassette, sub−family B (MDR/TAP
7	51296	−0.94	5e−10	3e−07	32 x 1	solute carrier family 15 (oligopeptide transporter), member 3 [
8	219285	−0.89	4e−09	9e−07	32 x 1	sterile alpha motif domain containing 9−like [Source:HGNC S
9	6373	−0.85	2e−08	9e−07	32 x 1	chemokine (C−X−C motif) ligand 11 [Source:HGNC Symbol;A
10	2273	0.83	4e−08	9e−07	25 x 1	four and a half LIM domains 1 [Source:HGNC Symbol;Acc:37
11	51191	−0.83	4e−08	2e−06	32 x 1	HECT and RLD domain containing E3 ubiquitin protein ligase
12	684	−0.81	9e−08	2e−06	32 x 1	bone marrow stromal cell antigen 2 [Source:HGNC Symbol;A
13	3433	−0.81	9e−08	3e−06	32 x 1	interferon−induced protein with tetratricopeptide repeats 2 [So
14	79156	−0.8	1e−07	7e−06	31 x 1	pleckstrin homology domain containing, family F (with FYVE d
15	8519	−0.78	3e−07	7e−06	32 x 1	interferon induced transmembrane protein 1 [Source:HGNC S
16	6588	−0.77	3e−07	2e−05	25 x 1	sarcolipin [Source:HGNC Symbol;Acc:11089]
17	1158	−0.76	6e−07	3e−05	25 x 1	creatine kinase, muscle [Source:HGNC Symbol;Acc:1994]
18	6355	−0.74	1e−06	3e−05	32 x 1	chemokine (C−C motif) ligand 8 [Source:HGNC Symbol;Acc:1
19	70	−0.73	1e−06	7e−05	25 x 1	actin, alpha, cardiac muscle 1 [Source:HGNC Symbol;Acc:14
20	4151	−0.7	4e−06	7e−05	25 x 1	myoglobin [Source:HGNC Symbol;Acc:6915]

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−37.6	NULL	13 / 16	GSEA C2	MOSERLE_IFNA_RESPONSE
2	−29.7	NULL	11 / 16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_F
3	−28.93	NULL	29 / 51	BP	type I interferon signaling pathway
4	−27.18	NULL	46 / 127	H.Tiss	WIRTH_Muscle
5	−26.56	NULL	2 / 2	MMML CGS	MACIEJ_MMML 27
6	−26.42	NULL	11 / 16	GSEA C2	UROSEVIC_RESPONSE_TO_IMIQUIMOD
7	−26.38	NULL	21 / 36	BP	muscle filament sliding
8	−24.48	NULL	9 / 10	GSEA C2	BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
9	−24.41	NULL	3 / 4	GSEA C2	KRASNOSELSKAYA_ILF3_TARGETS_UP
10	−24.34	NULL	9 / 16	H.Tiss	WIRTH_Hippocampus
11	−23.98	NULL	11 / 16	GSEA C2	ZHANG_INTERFERON_RESPONSE
12	−23.77	NULL	10 / 13	GSEA C2	BOWIE_RESPONSE_TO_TAMOXIFEN
13	−22.76	NULL	20 / 44	MF	structural constituent of muscle
14	−22.63	NULL	11 / 16	GSEA C2	EINAV_INTERFERON_SIGNATURE_IN_CANCER
15	−22.27	NULL	6 / 8	GSEA C2	ROETH_TERT_TARGETS_UP
16	−21.23	NULL	3 / 5	GSEA C2	KIM_LRRC3B_TARGETS
17	−20.61	NULL	6 / 6	Lymphoma	DAVE_MHCCII BL DN
18	−20.49	NULL	6 / 14	GSEA C2	RADAEVA_RESPONSE_TO_IFNA1_UP
19	−20.25	NULL	31 / 123	BP	defense response to virus
20	−19.45	NULL	5 / 15	GSEA C2	BECKER_TAMOXIFEN_RESISTANCE_UP
21	−19.28	NULL	4 / 12	GSEA C2	ZHU_CMV_8_HR_UP
22	−19.07	NULL	8 / 12	CC	myosin filament
23	−18.69	NULL	8 / 18	BP	positive regulation of T cell mediated cytotoxicity
24	−18.4	NULL	27 / 109	BP	response to virus
25	−18.18	NULL	8 / 11	GSEA C2	BENNETT_SYSTEMIC_LUPUS_ERYTHEMATOSUS
26	−18.06	NULL	7 / 10	CC	MHC class I protein complex
27	−17.52	NULL	6 / 12	GSEA C2	TSAI_DNAJB4_TARGETS_UP
28	−17.19	NULL	7 / 16	GSEA C2	MAHADEVAN_RESPONSE_TO_MP470_UP
29	−17.16	NULL	34 / 204	BP	cytokine−mediated signaling pathway
30	−16.88	NULL	7 / 18	MF	peptide antigen binding
31	−16.27	NULL	11 / 37	CC	sarcomere
32	−16.2	NULL	6 / 14	Glio	Donson−immune cell intra signaling−associated with LTS in HGA
33	−16.15	NULL	3 / 9	GSEA C2	DER_IFN_ALPHA_RESPONSE_UP
34	−16.15	NULL	3 / 9	GSEA C2	DER_IFN_GAMMA_RESPONSE_UP
35	−15.81	NULL	16 / 60	BP	interferon−gamma−mediated signaling pathway
36	−15.31	NULL	33 / 274	Lymphoma	SPANG_IL21 DN
37	−14.86	NULL	3 / 5	GSEA C2	BROWNE_INTERFERON_RESPONSIVE_GENES
38	−14.77	NULL	2 / 10	BP	positive regulation of cAMP−mediated signaling
39	−14.48	NULL	5 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
40	−14.33	NULL	3 / 8	GSEA C2	HUANG_DASATINIB_RESISTANCE_UP


p−values

GW_111

Local Summary

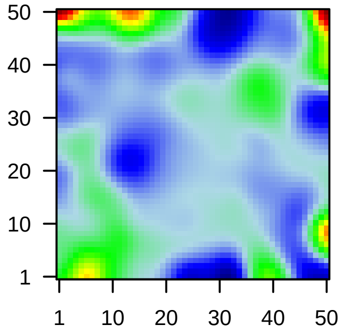
%DE = 0.67
metagenes = 7
genes = 178
genes in genesets = 176

genes with fdr < 0.1 = 73 (13 + / 60 −)
genes with fdr < 0.05 = 51 (10 + / 41 −)
genes with fdr < 0.01 = 31 (9 + / 22 −)

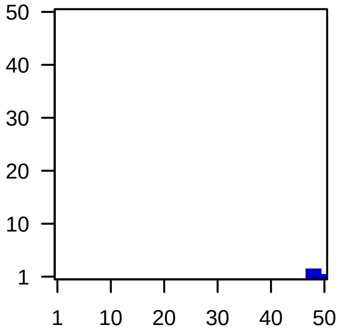
<r> metagenes = 1
<r> genes = 0.66

<FC> = −0.19
<shrinkage−t> = −6.8
<p−value> = 0.01
<fdr> = 0.65

Profile



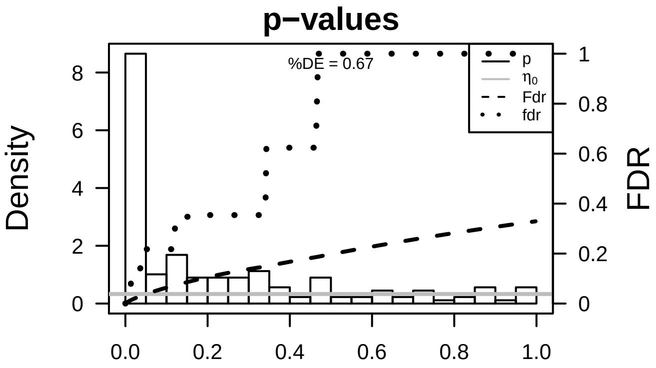
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	260436	−1.25	2e−16	7e−15	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symbo
2	5341	1.31	2e−16	7e−15	50 x 1	pleckstrin [Source:HGNC Symbol;Acc:9070]
3	3120	−0.94	5e−10	5e−08	47 x 1	major histocompatibility complex, class II, DQ beta 2 [Source:
4	4283	−0.92	2e−09	5e−08	49 x 1	chemokine (C−X−C motif) ligand 9 [Source:HGNC Symbol;Ac
5	3543	0.83	2e−09	2e−07	49 x 1	immunoglobulin lambda−like polypeptide 1 [Source:HGNC Sy
6	3108	−0.88	7e−09	9e−07	50 x 1	major histocompatibility complex, class II, DM alpha [Source:I
7	3125	−0.84	3e−08	9e−07	50 x 1	major histocompatibility complex, class II, DR beta 3 [Source:
8	3126	−0.83	4e−08	9e−07	50 x 1	major histocompatibility complex, class II, DR beta 4 [Source:
9	3113	−0.82	7e−08	9e−07	50 x 1	major histocompatibility complex, class II, DP alpha 1 [Source
10	11040	0.81	8e−08	9e−07	49 x 1	pim−2 oncogene [Source:HGNC Symbol;Acc:8987]
11	3620	−0.81	8e−08	3e−06	48 x 1	indoleamine 2,3−dioxygenase 1 [Source:HGNC Symbol;Acc:
12	3512	0.8	2e−07	3e−06	50 x 1	immunoglobulin J polypeptide, linker protein for immunoglobu
13	57172	0.79	2e−07	3e−06	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
14	10563	−0.79	2e−07	2e−04	50 x 1	chemokine (C−X−C motif) ligand 13 [Source:HGNC Symbol;
15	341	−0.7	4e−06	3e−04	50 x 1	apolipoprotein C−I [Source:HGNC Symbol;Acc:607]
16	3109	−0.67	9e−06	3e−04	50 x 1	major histocompatibility complex, class II, DM beta [Source:H
17	3122	−0.61	2e−05	3e−04	50 x 1	major histocompatibility complex, class II, DR alpha [Source:
18	51755	0.64	2e−05	3e−04	49 x 1	cyclin−dependent kinase 12 [Source:HGNC Symbol;Acc:242
19	2634	−0.64	3e−05	1e−03	47 x 1	guanylate binding protein 2, interferon−inducible [Source:HG
20	924	0.61	6e−05	1e−03	49 x 1	CD7 molecule [Source:HGNC Symbol;Acc:1695]

p−values



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all		Geneset
1	−49.13	NULL	12 / 15	CC	MHC class II protein complex
2	−29.87	NULL	14 / 47	BP	antigen processing and presentation
3	−25.65	NULL	7 / 21	CC	clathrin−coated endocytic vesicle membrane
4	−24.45	NULL	7 / 23	CC	integral to lumenal side of endoplasmic reticulum membrane
5	−24.12	NULL	3 / 6	GSEA C2	SANA_RESPONSE_TO_IFNG_UP
6	−22.04	NULL	7 / 28	CC	transport vesicle membrane
7	−21.74	NULL	2 / 3	MMML CGS	MACIEJ_MMML 7
8	−20.54	NULL	7 / 32	CC	ER to Golgi transport vesicle membrane
9	−19.59	NULL	7 / 35	CC	trans−Golgi network membrane
10	−19.16	NULL	12 / 60	BP	T cell costimulation
11	−19.1	NULL	12 / 87	BP	antigen processing and presentation of exogenous peptide antigen
12	−18.41	NULL	10 / 60	BP	interferon−gamma−mediated signaling pathway
13	−17.14	NULL	1 / 2	GSEA C2	KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUCT
14	−17.14	NULL	1 / 2	GSEA C2	KEGG_AUTOIMMUNE_THYROID_DISEASE
15	−17.14	NULL	1 / 2	GSEA C2	KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS
16	−16.94	NULL	7 / 46	CC	endocytic vesicle membrane
17	−16.85	NULL	4 / 15	Glio	Donson−chemokines/cytokines−associated with LTS in HGA
18	−16.52	NULL	39 / 312	BP	immune response
19	−14.84	NULL	8 / 52	Chr	Chr HSCHR6_MHC_QBL
20	−14.49	NULL	2 / 3	GSEA C2	KEGG_VIRAL_MYOCARDITIS
21	−14.02	NULL	11 / 84	BP	T cell receptor signaling pathway
22	−13.6	NULL	1 / 3	GSEA C2	KEGG_ANTIGEN_PROCESSING_AND_PRESENTATION
23	−13	NULL	4 / 7	Glio	Donson−cytotoxic effectors−associated with LTS in HGA
24	−12.39	NULL	12 / 215	CC	lysosomal membrane
25	−12.33	NULL	2 / 4	GSEA C2	KEGG_LEISHMANIA_INFECTION
26	−11.59	NULL	5 / 13	Cancer	GENTLES_modul18
27	−11.57	NULL	1 / 4	GSEA C2	REACTOME_COSTIMULATION_BY_THE_CD28_FAMILY
28	−11.57	NULL	1 / 4	GSEA C2	REACTOME_DOWNSTREAM_TCR_SIGNALING
29	−11.57	NULL	1 / 4	GSEA C2	REACTOME_TCR_SIGNALING
30	−10.99	NULL	5 / 43	MF	chemokine activity
31	−10.72	NULL	5 / 12	BP	immunoglobulin mediated immune response
32	−10.65	NULL	15 / 204	BP	cytokine−mediated signaling pathway
33	−10.5	NULL	5 / 77	CC	late endosome membrane
34	−10.34	NULL	2 / 11	GSEA C2	WILENSKY_RESPONSE_TO_DARAPLADIB
35	−10.17	NULL	2 / 6	GSEA C2	LUI_THYROID_CANCER_CLUSTER_4
36	−10.15	NULL	77 / 417	H.Tiss	WIRTH_Immune system
37	−10.11	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
38	−9.9	NULL	7 / 16	GSEA C2	SU_THYMUS
39	−9.79	NULL	3 / 16	GSEA C2	UROSEVIC_RESPONSE_TO_IMIQUIMOD
40	−9.62	NULL	1 / 6	GSEA C2	NIELSEN_LEIOMYOSARCOMA_UP

GW_111

Local Summary

%DE = 0.53

metagenes = 39

genes = 427

genes in genesets = 419

genes with fdr < 0.1 = 93 (7 + / 86 −)

genes with fdr < 0.05 = 58 (5 + / 53 −)

genes with fdr < 0.01 = 16 (3 + / 13 −)

<r> metagenes = 0.92

<r> genes = 0.24

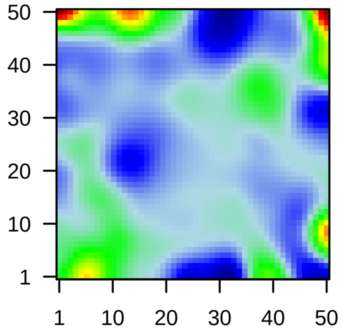
<FC> = −0.18

<shrinkage−t> = −6.35

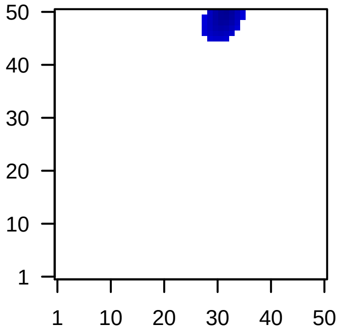
<p−value> = 0.09

<fdr> = 0.81

Profile



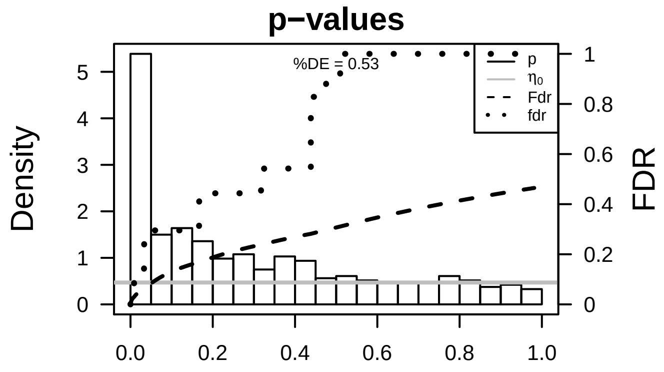
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	9111	−0.79	2e−07	2e−05	32 x 46	N−myc (and STAT) interactor [Source:HGNC Symbol;Acc:785
2	133383	−0.78	2e−07	4e−04	32 x 50	SET domain containing 9 [Source:HGNC Symbol;Acc:28508]
3	23471	−0.64	4e−06	4e−04	28 x 46	translocation associated membrane protein 1 [Source:HGNC
4	100093630	0.68	7e−06	4e−04	32 x 48	small nucleolar RNA host gene 8 (non−protein coding) [Sourc
5	80227	−0.68	7e−06	4e−04	31 x 47	proteasomal ATPase−associated factor 1 [Source:HGNC Syn
6	3988	−0.68	8e−06	4e−04	28 x 46	lipase A, lysosomal acid, cholesterol esterase [Source:HGNC
7	29922	−0.67	1e−05	6e−04	28 x 46	NME/NM23 family member 7 [Source:HGNC Symbol;Acc:20
8	10799	−0.66	1e−05	3e−03	34 x 50	ribonuclease P/MRP 40kDa subunit [Source:HGNC Symbol;
9	27069	−0.58	5e−05	3e−03	30 x 50	growth hormone inducible transmembrane protein [Source:H
10	10987	−0.6	7e−05	3e−03	33 x 50	COP9 signalosome subunit 5 [Source:HGNC Symbol;Acc:22
11	5318	0.6	7e−05	3e−03	29 x 45	plakophilin 2 [Source:HGNC Symbol;Acc:9024]
12	539	−0.59	9e−05	3e−03	32 x 50	ATP synthase, H+ transporting, mitochondrial F1 complex, O
13	6147	0.59	1e−04	3e−03	33 x 49	ribosomal protein L23a [Source:HGNC Symbol;Acc:10317]
14	29080	−0.58	1e−04	3e−03	31 x 50	coiled−coil domain containing 59 [Source:HGNC Symbol;Acc
15	522	−0.58	1e−04	4e−03	32 x 50	ATP synthase, H+ transporting, mitochondrial Fo complex, su
16	144363	−0.58	1e−04	6e−03	31 x 50	LYR motif containing 5 [Source:HGNC Symbol;Acc:27052]
17	23421	−0.57	2e−04	1e−02	32 x 50	integrin beta 3 binding protein (beta3−endonexin) [Source:HG
18	9978	−0.55	3e−04	1e−02	33 x 50	ring−box 1, E3 ubiquitin protein ligase [Source:HGNC Symbo
19	5728	−0.55	3e−04	1e−02	28 x 48	phosphatase and tensin homolog [Source:HGNC Symbol;Acc
20	84233	−0.54	4e−04	1e−02	31 x 49	transmembrane protein 126A [Source:HGNC Symbol;Acc:25

p−values



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−14.37	NULL	29 / 83	BP	respiratory electron transport chain
2	−13.74	NULL	9 / 19	CC	mitochondrial proton−transporting ATP synthase complex
3	−12.19	NULL	33 / 152	BP	cellular metabolic process
4	−11.54	NULL	7 / 15	BP	ATP synthesis coupled proton transport
5	−11.11	NULL	4 / 8	GSEA C2	REACTOME_REGULATION_OF_GENE_EXPRESSION_IN_BETA
6	−11.03	NULL	6 / 13	GSEA C2	REACTOME_FORMATION_OF_ATP_BY_CHEMIOSMOTIC_COU
7	−10.61	NULL	6 / 14	BP	mitochondrial ATP synthesis coupled proton transport
8	−10.45	NULL	4 / 9	GSEA C2	KEGG_RIBOSOME
9	−10.45	NULL	4 / 9	GSEA C2	REACTOME_FORMATION_OF_A_POOL_OF_FREE_40S_SUBU
10	−10.45	NULL	4 / 9	GSEA C2	REACTOME_GTP_HYDROLYSIS_AND_JOINING_OF_THE_60S_
11	−10.45	NULL	4 / 9	GSEA C2	REACTOME_INFLUENZA_VIRAL_RNA_TRANSCRIPTION_AND_
12	−10.45	NULL	4 / 9	GSEA C2	REACTOME_PEPTIDE_CHAIN_ELONGATION
13	−10.45	NULL	4 / 9	GSEA C2	REACTOME_REGULATION_OF_BETA_CELL_DEVELOPMENT
14	−10.45	NULL	4 / 9	GSEA C2	REACTOME_VIRAL_MRNA_TRANSLATION
15	−10.31	NULL	27 / 109	BP	SRP−dependent cotranslational protein targeting to membrane
16	−9.96	NULL	5 / 16	Cancer	GENTLES_modul10
17	−9.89	NULL	4 / 10	GSEA C2	REACTOME_TRANSLATION
18	−9.25	NULL	41 / 253	BP	translation
19	−9.07	NULL	22 / 81	BP	viral transcription
20	−9.04	NULL	32 / 153	MF	structural constituent of ribosome
21	−8.96	NULL	26 / 128	BP	translational initiation
22	−8.79	NULL	23 / 87	BP	translational termination
23	−8.59	NULL	23 / 92	BP	translational elongation
24	−8.52	NULL	1 / 2	TF	MYC_Signal transduction UP
25	−8.4	NULL	22 / 92	BP	viral life cycle
26	−8.31	NULL	29 / 167	CC	ribosome
27	−8.22	NULL	3 / 10	GSEA C2	POMEROY_MEDULLOBLASTOMA_PROGNOSIS_DN
28	−8.12	NULL	36 / 287	BP	viral process
29	−7.87	NULL	99 / 1318	CC	mitochondrion
30	−7.58	NULL	11 / 36	CC	mitochondrial respiratory chain complex I
31	−7.49	NULL	42 / 304	CC	mitochondrial inner membrane
32	−7.39	NULL	5 / 10	CC	large ribosomal subunit
33	−7.29	NULL	22 / 115	BP	nuclear−transcribed mRNA catabolic process, nonsense−mediated
34	−7.26	NULL	3 / 13	GSEA C2	LEE_LIVER_CANCER_SURVIVAL_DN
35	−7.26	NULL	4 / 11	Cancer	GENTLES_modul5
36	−7.08	NULL	6 / 25	MF	hydrogen ion transmembrane transporter activity
37	−6.96	NULL	10 / 34	MF	NADH dehydrogenase (ubiquinone) activity
38	−6.95	NULL	1 / 3	miRNA target	miR−19a
39	−6.95	NULL	1 / 3	miRNA target	miR−214
40	−6.85	NULL	78 / 1233	TF	KIM_MYC targets