GW_271

Global Summary

%DE = 0.16

genes with fdr < 0.2 = 2086 (1128 + / 958 −)

genes with fdr < 0.1 = 1526 (870 + / 656 −)

genes with fdr < 0.05 = 1176 (694 + / 482 −)

genes with fdr < 0.01 = 848 (530 + / 318 −)

genes in genesets = 16332

<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.1

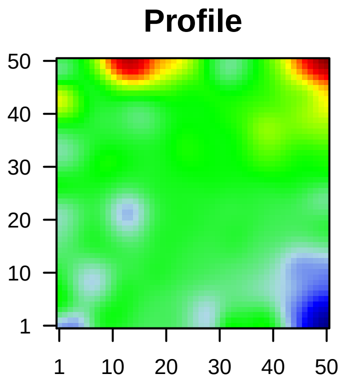
<fdr> = 0.84

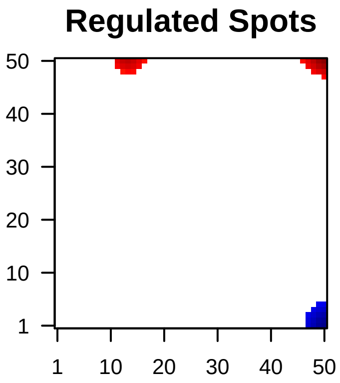
Global Genelist

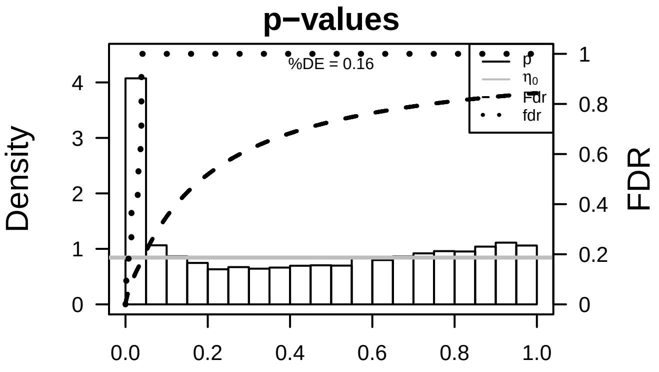
Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	131	2.48	2e−16	4e−14	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	57016	2.28	2e−16	4e−14	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
3	441282	2.15	2e−16	4e−14	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC Sy
4	8644	2.58	2e−16	4e−14	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
5	1109	2.59	2e−16	4e−14	13 x 50	aldo−keto reductase family 1, member C4 [Source:HGNC Sy
6	216	1.86	2e−16	4e−14	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGN
7	218	2.79	2e−16	4e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
8	501	−2.22	2e−16	4e−14	6 x 46	aldehyde dehydrogenase 7 family, member A1 [Source:HGN
9	11199	1.57	2e−16	4e−14	15 x 50	annexin A10 [Source:HGNC Symbol;Acc:534]
10	23780	1.71	2e−16	4e−14	32 x 1	apolipoprotein L, 2 [Source:HGNC Symbol;Acc:619]
11	25805	2.63	2e−16	4e−14	8 x 1	BMP and activin membrane−bound inhibitor [Source:HGNC
12	84707	1.74	2e−16	4e−14	50 x 48	brain expressed X−linked 2 [Source:HGNC Symbol;Acc:3093
13	339512	2.23	2e−16	4e−14	50 x 50	chromosome 1 open reading frame 110 [Source:HGNC Sym
14	760	1.76	2e−16	4e−14	1 x 44	carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
15	26256	1.79	2e−16	4e−14	50 x 50	calcium binding tyrosine−(Y)−phosphorylation regulated [Sou
16	928	1.59	2e−16	4e−14	50 x 50	CD9 molecule [Source:HGNC Symbol;Acc:1709]
17	1066	2.79	2e−16	4e−14	14 x 50	carboxylesterase 1 [Source:HGNC Symbol;Acc:1863]
18	629	−1.58	2e−16	4e−14	32 x 1	complement factor B [Source:HGNC Symbol;Acc:1037]
19	9073	2.47	2e−16	4e−14	8 x 50	claudin 8 [Source:HGNC Symbol;Acc:2050]
20	1396	−1.57	2e−16	4e−14	50 x 5	cysteine−rich protein 1 (intestinal) [Source:HGNC Symbol;Ac

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	10.25	NULL	866	Chr	Chr 12
2	9.72	NULL	534	Chr	Chr 8
3	9.13	NULL	633	Chr	Chr 9
4	8.91	NULL	743	Chr	Chr 7
5	7.78	NULL	603	miRNA target−starBase	hsa−miR−20a
6	7.6	NULL	14	GSEA C2	NIKOLSKY_BREAST_CANCER_12Q13_Q21_AMPLICON
7	7.44	NULL	494	miRNA target−starBase	hsa−miR−107
8	7.38	NULL	495	miRNA target−starBase	hsa−miR−103
9	7.12	NULL	436	miRNA target−starBase	hsa−miR−548n
10	7.06	NULL	39	BP	retinoid metabolic process
11	7.04	NULL	538	miRNA target−starBase	hsa−miR−17
12	6.99	NULL	368	miRNA target−starBase	hsa−miR−144
13	6.92	NULL	565	miRNA target−starBase	hsa−miR−20b
14	6.75	NULL	517	miRNA target−starBase	hsa−miR−106a
15	6.53	NULL	310	miRNA target−starBase	hsa−miR−340
16	6.45	NULL	545	miRNA target−starBase	hsa−miR−93
17	6.39	NULL	341	miRNA target−starBase	hsa−let−7a
18	6.37	NULL	13	GSEA C2	SINGH_NFE2L2_TARGETS
19	6.32	NULL	318	miRNA target−starBase	hsa−miR−590−3p
20	6.21	NULL	271	miRNA target−starBase	hsa−miR−520b
Underexpressed					
1	−11.85	NULL	1135	Chr	Chr 19
2	−9.76	NULL	553	Cancer	Lembcke_Colonic Inflammation
3	−7.09	NULL	10	BP	cellular response to zinc ion
4	−6.73	NULL	417	H.Tiss	WIRTH_Immune system
5	−6.59	NULL	7	MMML CGS	MACIEJ_MMML 13
6	−6.58	NULL	253	BP	translation
7	−6.06	NULL	699	Chr	Chr 5
8	−5.77	NULL	109	BP	SRP−dependent cotranslational protein targeting to membrane
9	−5.68	NULL	1182	CC	extracellular region
10	−5.64	NULL	312	BP	immune response
11	−5.59	NULL	10	MF	RAGE receptor binding
12	−5.48	NULL	957	Chr	Chr 11
13	−5.38	NULL	92	BP	translational elongation
14	−5.36	NULL	167	CC	ribosome
15	−5.33	NULL	714	Chr	Chr 6
16	−5.28	NULL	1720	Chr	Chr 1
17	−5.27	NULL	87	BP	translational termination
18	−5.25	NULL	15	BP	negative regulation of growth
19	−5.24	NULL	153	MF	structural constituent of ribosome
20	−5.15	NULL	81	BP	viral transcription







GW_271

Local Summary

%DE = 0.7

metagenes = 13

genes = 207

genes in genesets = 206

genes with fdr < 0.1 = 127 (121 + / 6 −)

genes with fdr < 0.05 = 111 (105 + / 6 −)

genes with fdr < 0.01 = 82 (78 + / 4 −)

<r> metagenes = 0.95

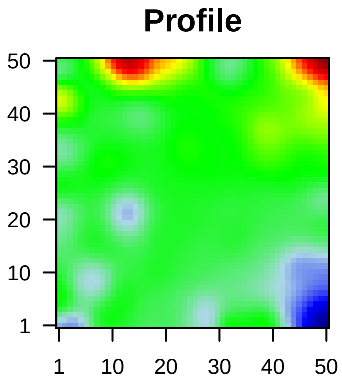
<r> genes = 0.28

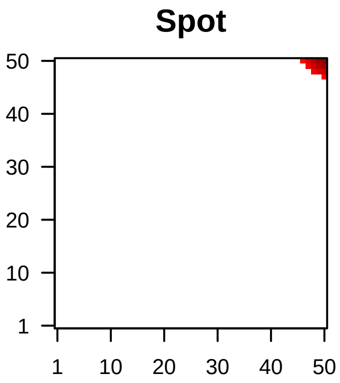
<FC> = 0.56

<shrinkage−t> = 19.64

<p−value> = 0

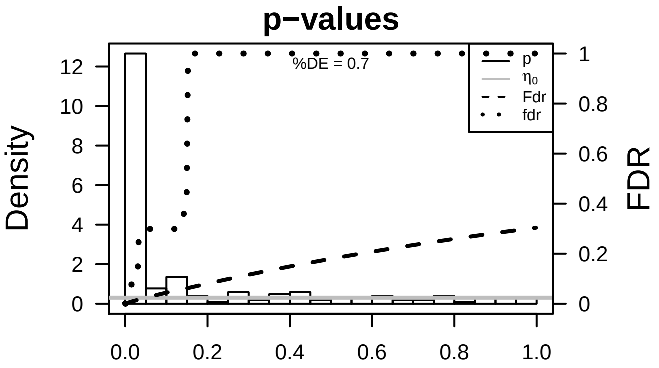
<fdr> = 0.43





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	216	1.86	2e−16	1e−15	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGN
2	84707	1.74	2e−16	1e−15	50 x 48	brain expressed X−linked 2 [Source:HGNC Symbol;Acc:3093
3	339512	2.23	2e−16	1e−15	50 x 50	chromosome 1 open reading frame 110 [Source:HGNC Sym
4	26256	1.79	2e−16	1e−15	50 x 50	calcium binding tyrosine−(Y)−phosphorylation regulated [Sou
5	928	1.59	2e−16	1e−15	50 x 50	CD9 molecule [Source:HGNC Symbol;Acc:1709]
6	10655	2.02	2e−16	1e−15	50 x 50	doublesex and mab−3 related transcription factor 2 [Source:H
7	2944	2.06	2e−16	1e−15	50 x 50	glutathione S−transferase mu 1 [Source:HGNC Symbol;Acc:4
8	2946	1.64	2e−16	1e−15	50 x 50	glutathione S−transferase mu 2 (muscle) [Source:HGNC Sym
9	2947	2.09	2e−16	1e−15	50 x 50	glutathione S−transferase mu 3 (brain) [Source:HGNC Symb
10	3880	−2.86	2e−16	1e−15	50 x 49	keratin 19 [Source:HGNC Symbol;Acc:6436]
11	84171	1.98	2e−16	1e−15	50 x 49	lysyl oxidase−like 4 [Source:HGNC Symbol;Acc:17171]
12	7348	2.19	2e−16	1e−15	50 x 50	uroplakin 1B [Source:HGNC Symbol;Acc:12578]
13	256764	1.68	2e−16	1e−15	50 x 50	WD repeat domain 72 [Source:HGNC Symbol;Acc:26790]
14	4915	1.54	9e−16	5e−12	50 x 50	neurotrophic tyrosine kinase, receptor, type 2 [Source:HGNC
15	7358	1.42	8e−14	6e−12	50 x 50	UDP−glucose 6−dehydrogenase [Source:HGNC Symbol;Acc
16	2730	1.4	2e−13	6e−12	50 x 50	glutamate−cysteine ligase, modifier subunit [Source:HGNC S
17	10643	1.39	3e−13	1e−11	48 x 50	insulin−like growth factor 2 mRNA binding protein 3 [Source:
18	55190	1.38	4e−13	3e−11	47 x 50	nudix (nucleoside diphosphate linked moiety X)−type motif 11
19	3790	1.36	8e−13	3e−11	50 x 50	potassium voltage−gated channel, delayed−rectifier, subfamil
20	200634	1.35	1e−12	6e−11	50 x 49	keratinocyte associated protein 3 [Source:HGNC Symbol;Acc



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset
1	22.4	NULL	5 / 15	GSEA C2 KEGG_GLUTATHIONE_METABOLISM
2	20.91	NULL	4 / 13	GSEA C2 KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_
3	20.1	NULL	3 / 11	MF glutathione binding
4	20.1	NULL	3 / 11	GSEA C2 KEGG_DRUG_METABOLISM_CYTOCHROME_P450
5	17.99	NULL	6 / 25	BP glutathione derivative biosynthetic process
6	15.58	NULL	8 / 34	BP glutathione metabolic process
7	14.05	NULL	4 / 15	GSEA C2 RICKMAN_HEAD_AND_NECK_CANCER_E
8	13.71	NULL	11 / 119	BP xenobiotic metabolic process
9	13.51	NULL	5 / 20	MF glutathione transferase activity
10	12.68	NULL	3 / 16	GSEA C2 BOYAULT_LIVER_CANCER_SUBCLASS_G1_DN
11	10.66	NULL	2 / 15	GSEA C2 LEE_LIVER_CANCER_MYC_UP
12	10.66	NULL	2 / 15	GSEA C2 LEE_LIVER_CANCER_E2F1_UP
13	10.6	NULL	2 / 7	GSEA C2 FREDERICK_PRKCI_TARGETS
14	10.14	NULL	2 / 9	GSEA C2 REACTOME_GLUCURONIDATION
15	9.95	NULL	2 / 15	GSEA C2 REACTOME_PHASE_II_CONJUGATION
16	9.6	NULL	3 / 16	GSEA C2 GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_
17	9.47	NULL	2 / 12	GSEA C2 LEE_METASTASIS_AND_ALTERNATIVE_SPLICING_DN
18	8.98	NULL	1 / 6	GSEA C2 GAUSSMANN_MLL_AF4_FUSION_TARGETS_D_DN
19	8.98	NULL	1 / 6	GSEA C2 KAPOSI_LIVER_CANCER_POOR_SURVIVAL_DN
20	8.95	NULL	4 / 15	GSEA C2 REACTOME_GLUTATHIONE_CONJUGATION
21	8.37	NULL	2 / 10	GSEA C2 CONRAD_STEM_CELL
22	8.27	NULL	2 / 12	BP glutamate metabolic process
23	8.23	NULL	1 / 8	GSEA C2 NIELSEN_LIPOSARCOMA_UP
24	7.89	NULL	2 / 13	GSEA C2 SINGH_NFE2L2_TARGETS
25	7.85	NULL	1 / 9	GSEA C2 GOERING_BLOOD_HDL_CHOLESTEROL_QTL_CIS
26	7.79	NULL	3 / 11	GSEA C2 ITO_PTTG1_TARGETS_UP
27	7.76	NULL	1 / 4	GSEA C2 MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_13
28	7.65	NULL	1 / 6	GSEA C2 KORKOLA_CHORIOCARCINOMA_UP
29	7.61	NULL	2 / 12	BP cellular aldehyde metabolic process
30	7.4	NULL	3 / 13	BP regulation of blood vessel size
31	7.12	NULL	2 / 15	GSEA C2 BIOCARTA_ACTINY_PATHWAY
32	7.05	NULL	1 / 9	GSEA C2 ABDULRAHMAN_KIDNEY_CANCER_VHL_DN
33	7.05	NULL	1 / 9	GSEA C2 REACTOME_ETHANOL_OXIDATION
34	7.05	NULL	1 / 12	GSEA C2 DAZARD_RESPONSE_TO_UV_SCC_UP
35	6.99	NULL	2 / 16	BP glutathione biosynthetic process
36	6.86	NULL	2 / 10	GSEA C2 KEGG_ASCORBATE_AND_ALDARATE_METABOLISM
37	6.84	NULL	4 / 32	BP glycosaminoglycan biosynthetic process
38	6.81	NULL	59 / 914	Chr Chr 3
39	6.74	NULL	1 / 12	GSEA C2 SMID_BREAST_CANCER_RELAPSE_IN_BRAIN_DN
40	6.71	NULL	2 / 16	GSEA C2 KOKKINAKIS_METHIONINE_DEPRIVATION_48HR_DN

GW_271

Local Summary

%DE = 0.69

metagenes = 14

genes = 161

genes in genesets = 160

genes with fdr < 0.1 = 97 (96 + / 1 −)

genes with fdr < 0.05 = 83 (83 + / 0 −)

genes with fdr < 0.01 = 70 (70 + / 0 −)

<r> metagenes = 0.98

<r> genes = 0.25

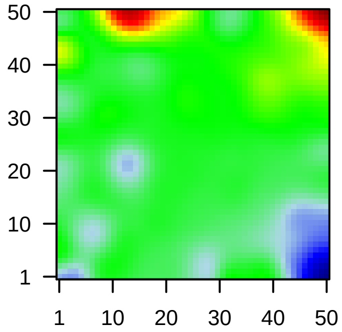
<FC> = 0.61

<shrinkage−t> = 21.38

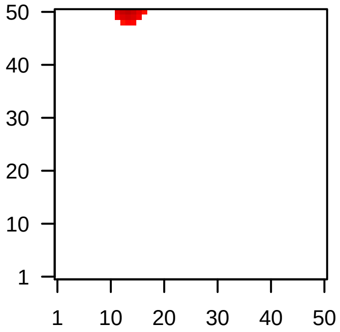
<p−value> = 0

<fdr> = 0.42

Profile



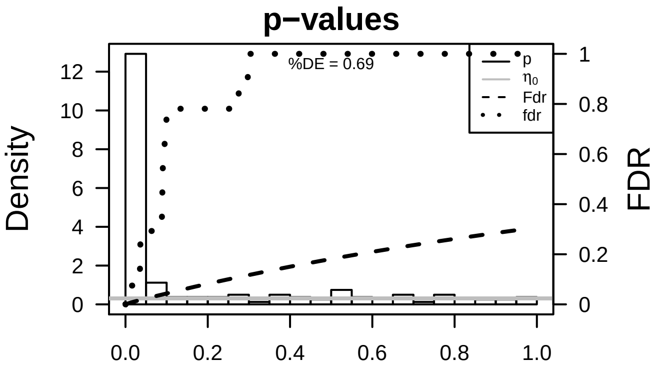
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	1109	2.59	2e−16	9e−16	13 x 50	aldo−keto reductase family 1, member C4 [Source:HGNC Sy
2	11199	1.57	2e−16	9e−16	15 x 50	annexin A10 [Source:HGNC Symbol;Acc:534]
3	1066	2.79	2e−16	9e−16	14 x 50	carboxylesterase 1 [Source:HGNC Symbol;Acc:1863]
4	57007	1.74	2e−16	9e−16	14 x 50	atypical chemokine receptor 3 [Source:HGNC Symbol;Acc:23
5	57834	2.71	2e−16	9e−16	13 x 50	cytochrome P450, family 4, subfamily F, polypeptide 11 [Sour
6	1749	1.76	2e−16	9e−16	13 x 50	distal−less homeobox 5 [Source:HGNC Symbol;Acc:2918]
7	493861	1.6	2e−16	9e−16	14 x 50	EP300 interacting inhibitor of differentiation 3 [Source:HGNC
8	2690	1.67	2e−16	9e−16	15 x 50	growth hormone receptor [Source:HGNC Symbol;Acc:4263]
9	56666	1.6	2e−16	9e−16	14 x 50	pannexin 2 [Source:HGNC Symbol;Acc:8600]
10	140809	2.04	2e−16	9e−16	13 x 50	sulfiredoxin 1 [Source:HGNC Symbol;Acc:16132]
11	7102	2.39	2e−16	9e−16	15 x 50	tetraspanin 7 [Source:HGNC Symbol;Acc:11854]
12	7296	1.56	2e−16	9e−16	14 x 50	thioredoxin reductase 1 [Source:HGNC Symbol;Acc:12437]
13	63928	1.54	4e−16	1e−14	13 x 50	calcineurin−like EF−hand protein 2 [Source:HGNC Symbol;A
14	2564	1.54	7e−16	2e−13	13 x 50	gamma−aminobutyric acid (GABA) A receptor, epsilon [Sourc
15	27333	1.49	6e−15	2e−13	16 x 50	golgi integral membrane protein 4 [Source:HGNC Symbol;Ac
16	83857	1.48	7e−15	2e−12	16 x 50	transmembrane and tetratricopeptide repeat containing 1 [So
17	4051	1.43	6e−14	2e−12	12 x 50	cytochrome P450, family 4, subfamily F, polypeptide 3 [Sourc
18	57214	1.42	9e−14	2e−12	17 x 50	KIAA1199 [Source:HGNC Symbol;Acc:29213]
19	4147	1.42	1e−13	1e−11	15 x 50	matrilin 2 [Source:HGNC Symbol;Acc:6908]
20	1646	1.38	4e−13	1e−10	13 x 50	aldo−keto reductase family 1, member C2 [Source:HGNC Sy

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	13.85	NULL	1 / 7	Glio	Donson−cytotoxic effectors−associated with LTS in HGA
2	10.93	NULL	2 / 10	BP	response to food
3	10.51	NULL	2 / 12	BP	head development
4	10.39	NULL	3 / 19	BP	anatomical structure formation involved in morphogenesis
5	10.32	NULL	2 / 14	BP	bile acid and bile salt transport
6	10.13	NULL	4 / 39	BP	retinoid metabolic process
7	9.96	NULL	3 / 14	MF	phospholipid−translocating ATPase activity
8	9.87	NULL	1 / 10	GSEA C2	AMUNDSON_GAMMA_RADIATION_RESISTANCE
9	9.83	NULL	1 / 6	GSEA C2	ZAIDI_OSTEOBLAST_TRANSCRIPTION_FACTORS
10	9.83	NULL	1 / 6	GSEA C2	NIELSEN_GIST_VS_SYNOVIAL_SARCOMA_UP
11	9.62	NULL	1 / 12	BP	androgen metabolic process
12	8.61	NULL	3 / 13	GSEA C2	SINGH_NFE2L2_TARGETS
13	8.55	NULL	5 / 35	miRNA target−miRBase	hsa−miR−127−3p
14	8.52	NULL	1 / 16	GSEA C2	BOYAULT_LIVER_CANCER_SUBCLASS_G1_DN
15	8.41	NULL	2 / 35	MF	monooxygenase activity
16	8.18	NULL	2 / 15	GSEA C2	COLIN_PILOCYTIC_ASTROCYTOMA_VS_GLIOBLASTOMA_UP
17	8.14	NULL	5 / 32	MF	ATPase activity, coupled to transmembrane movement of substanc
18	7.95	NULL	1 / 18	MF	aromatase activity
19	7.81	NULL	4 / 51	BP	osteoblast differentiation
20	7.81	NULL	2 / 22	BP	response to axon injury
21	7.77	NULL	1 / 15	Cancer	GENTLES_modul13
22	7.77	NULL	1 / 15	GSEA C2	VALK_AML_CLUSTER_4
23	7.65	NULL	4 / 63	BP	phototransduction, visible light
24	7.65	NULL	2 / 29	BP	receptor internalization
25	7.59	NULL	1 / 18	BP	bile acid biosynthetic process
26	7.55	NULL	2 / 16	BP	hormone−mediated signaling pathway
27	7.48	NULL	1 / 16	GSEA C2	DUNNE_TARGETS_OF_AML1_MTG8_FUSION_DN
28	7.48	NULL	1 / 16	GSEA C2	BONOME_OVARIAN_CANCER_POOR_SURVIVAL_UP
29	7.45	NULL	3 / 32	MF	NADP binding
30	7.34	NULL	14 / 434	BP	oxidation−reduction process
31	7.32	NULL	2 / 14	GSEA C2	MAYBURD_RESPONSE_TO_L663536_DN
32	7.17	NULL	2 / 12	BP	positive regulation of protein import into nucleus
33	7.09	NULL	2 / 15	BP	leukotriene metabolic process
34	7.04	NULL	3 / 31	BP	bile acid metabolic process
35	7.04	NULL	2 / 44	BP	steroid metabolic process
36	6.92	NULL	5 / 63	MF	oxidoreductase activity, acting on paired donors, with incorporation
37	6.82	NULL	1 / 11	BP	ear development
38	6.82	NULL	1 / 11	GSEA C2	SU_PLACENTA
39	6.81	NULL	1 / 10	BP	creatine metabolic process
40	6.81	NULL	1 / 10	BP	oxaloacetate metabolic process

GW_271

Local Summary

%DE = 0.95

metagenes = 17

genes = 283

genes in genesets = 281

genes with fdr < 0.1 = 241 (5 + / 236 −)

genes with fdr < 0.05 = 241 (5 + / 236 −)

genes with fdr < 0.01 = 170 (3 + / 167 −)

<r> metagenes = 0.98

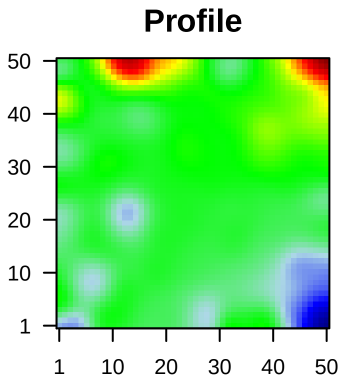
<r> genes = 0.56

<FC> = −0.49

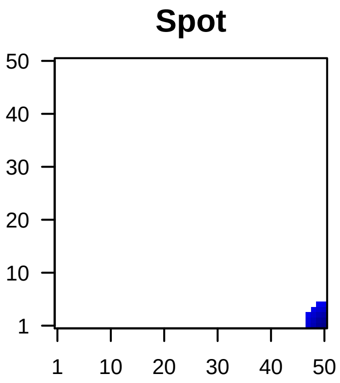
<shrinkage−t> = −17.25

<p−value> = 0

<fdr> = 0.46



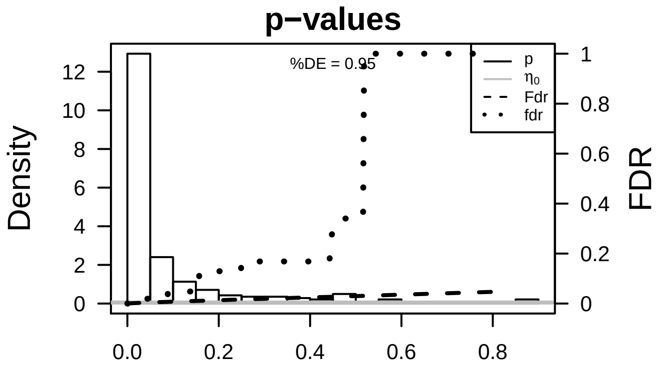
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	1396	−1.57	2e−16	1e−15	50 x 5	cysteine−rich protein 1 (intestinal) [Source:HGNC Symbol;Ac
2	3512	−1.57	2e−16	1e−15	50 x 1	immunoglobulin J polypeptide, linker protein for immunoglobu
3	3543	−2.21	2e−16	1e−15	49 x 1	immunoglobulin lambda−like polypeptide 1 [Source:HGNC Sy
4	57172	−1.53	1e−15	3e−14	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
5	5920	1.5	3e−15	6e−12	48 x 1	retinoic acid receptor responder (tazarotene induced) 3 [Sour
6	260436	−1.38	4e−13	3e−11	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symbo
7	3936	−1.34	2e−12	3e−10	50 x 1	lymphocyte cytosolic protein 1 (L−plastin) [Source:HGNC Syr
8	51755	−1.27	3e−11	3e−10	49 x 1	cyclin−dependent kinase 12 [Source:HGNC Symbol;Acc:242
9	54855	−1.25	5e−11	4e−09	49 x 1	family with sequence similarity 46, member C [Source:HGNC
10	347733	−1.2	3e−10	7e−09	50 x 5	tubulin, beta 2B class IIb [Source:HGNC Symbol;Acc:30829]
11	91607	−1.17	8e−10	9e−09	48 x 4	schlafen family member 11 [Source:HGNC Symbol;Acc:2663
12	241	−1.15	1e−09	7e−08	50 x 1	arachidonate 5−lipoxygenase−activating protein [Source:HGN
13	3385	−1.11	6e−09	3e−07	50 x 1	intercellular adhesion molecule 3 [Source:HGNC Symbol;Acc
14	3059	−1.06	3e−08	3e−07	50 x 1	hematopoietic cell−specific Lyn substrate 1 [Source:HGNC S
15	23643	−1.04	5e−08	5e−07	50 x 3	lymphocyte antigen 96 [Source:HGNC Symbol;Acc:17156]
16	10550	−1.02	8e−08	5e−07	50 x 3	ADP−ribosylation−like factor 6 interacting protein 5 [Source:H
17	10628	−0.99	1e−07	5e−07	48 x 1	thioredoxin interacting protein [Source:HGNC Symbol;Acc:16
18	23180	−1	2e−07	5e−07	50 x 1	raftlin, lipid raft linker 1 [Source:HGNC Symbol;Acc:30278]
19	6347	−1	2e−07	6e−07	50 x 4	chemokine (C−C motif) ligand 2 [Source:HGNC Symbol;Acc:
20	1545	−0.99	2e−07	5e−06	50 x 4	cytochrome P450, family 1, subfamily B, polypeptide 1 [Sourc



p−values

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−26.94	NULL	89 / 417	H.Tiss	WIRTH_Immune system
2	−21.55	NULL	92 / 553	Cancer	Lembcke_Colonic Inflammation
3	−20.05	NULL	12 / 15	CC	MHC class II protein complex
4	−18.21	NULL	6 / 8	Glio	Donson−migration tethering and rolling−associated with LTS in HG
5	−18.09	NULL	50 / 312	BP	immune response
6	−16.92	NULL	6 / 15	GSEA C2	FINAK_BREAST_CANCER_SDPP_SIGNATURE
7	−16.86	NULL	3 / 5	GSEA C2	WONG_ENDOMETRIAL_CANCER_LATE
8	−16.66	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
9	−14.72	NULL	4 / 9	GSEA C2	MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN
10	−14.13	NULL	3 / 7	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
11	−13.51	NULL	15 / 47	BP	antigen processing and presentation
12	−13.5	NULL	5 / 12	BP	dendritic cell chemotaxis
13	−13.44	NULL	43 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
14	−13.44	NULL	43 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
15	−13.44	NULL	43 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
16	−13.44	NULL	43 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
17	−13.21	NULL	1 / 6	H.Tiss	WIRTH_Bone marrow
18	−13.1	NULL	6 / 11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
19	−12.9	NULL	3 / 7	GSEA C2	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINE
20	−12.31	NULL	6 / 16	GSEA C2	FERRANDO_TAL1_NEIGHBORS
21	−12.03	NULL	5 / 11	GSEA C2	BIOCARTA_THELPER_PATHWAY
22	−12.01	NULL	4 / 8	GSEA C2	GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_DN
23	−11.66	NULL	14 / 60	BP	T cell costimulation
24	−11.59	NULL	4 / 13	Lymphoma	BENTINK_mBL DOWN
25	−11.58	NULL	17 / 74	BP	regulation of immune response
26	−11.5	NULL	5 / 10	GSEA C2	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_
27	−11.41	NULL	5 / 17	BP	positive regulation of neutrophil chemotaxis
28	−11	NULL	5 / 15	Glio	Donson−chemokines/cytokines−associated with LTS in HGA
29	−10.95	NULL	6 / 27	MF	antigen binding
30	−10.72	NULL	5 / 12	GSEA C2	BIOCARTA_CTL_PATHWAY
31	−10.69	NULL	4 / 15	GSEA C2	HUMMEL_BURKITTS_LYMPHOMA_DN
32	−10.59	NULL	4 / 13	BP	lymph node development
33	−10.45	NULL	23 / 204	BP	cell surface receptor signaling pathway
34	−10.29	NULL	5 / 10	GSEA C2	LEE_DIFFERENTIATING_T_LYMPHOCYTE
35	−10.27	NULL	5 / 13	GSEA C2	HAHTOLA_CTCL_PATHOGENESIS
36	−10.25	NULL	29 / 316	Cancer	SPANG_BCL6−index2
37	−10.23	NULL	2 / 12	GSEA C2	MCCABE_HOXC6_TARGETS_CANCER_UP
38	−10.2	NULL	4 / 14	BP	ruffle organization
39	−10.15	NULL	6 / 13	Cancer	GENTLES_modul18
40	−10.12	NULL	8 / 16	GSEA C2	SU_THYMUS