GW_290

Global Summary

%DE = 0.13

genes with fdr < 0.2 = 1686 (963 + / 723 −)

genes with fdr < 0.1 = 1371 (792 + / 579 −)

genes with fdr < 0.05 = 1112 (663 + / 449 −)

genes with fdr < 0.01 = 783 (488 + / 295 −)

genes in genesets = 16332

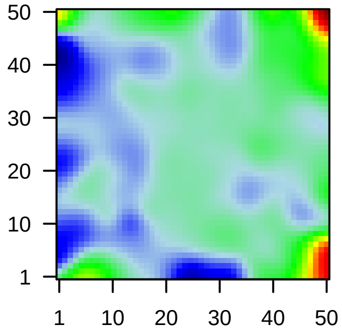
<FC> = 0

<shrinkage−t> = 0

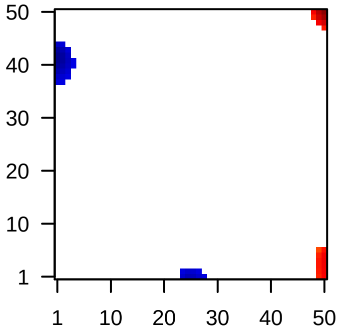
<p−value> = 0.11

<fdr> = 0.87

Profile



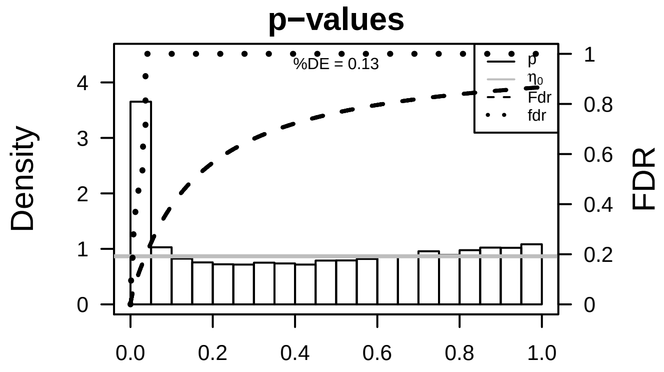
Regulated Spots



Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	154664	1.24	2e−16	3e−14	50 x 50	ATP−binding cassette, sub−family A (ABC1), member 13 [Sou
2	24	1.47	2e−16	3e−14	16 x 50	ATP−binding cassette, sub−family A (ABC1), member 4 [Sour
3	124	1.47	2e−16	3e−14	50 x 11	alcohol dehydrogenase 1A (class I), alpha polypeptide [Sourc
4	126	1.34	2e−16	3e−14	50 x 12	alcohol dehydrogenase 1C (class I), gamma polypeptide [Sou
5	242	2.68	2e−16	3e−14	1 x 48	arachidonate 12−lipoxygenase, 12R type [Source:HGNC Sym
6	59344	1.26	2e−16	3e−14	2 x 45	arachidonate lipoxygenase 3 [Source:HGNC Symbol;Acc:137
7	147495	1.29	2e−16	3e−14	2 x 44	adenomatosis polyposis coli down−regulated 1 [Source:HGN
8	440	1.75	2e−16	3e−14	50 x 46	asparagine synthetase (glutamine−hydrolyzing) [Source:HGN
9	479	1.3	2e−16	3e−14	7 x 50	ATPase, H+/K+ transporting, nongastric, alpha polypeptide [S
10	344905	1.34	2e−16	3e−14	50 x 50	ATPase type 13A5 [Source:HGNC Symbol;Acc:31789]
11	684	−1.49	2e−16	3e−14	32 x 1	bone marrow stromal cell antigen 2 [Source:HGNC Symbol;A
12	388115	−1.27	2e−16	3e−14	26 x 2	chromosome 15 open reading frame 52 [Source:HGNC Symb
13	260436	−1.59	2e−16	3e−14	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symbo
14	29113	2.46	2e−16	3e−14	2 x 47	chromosome 6 open reading frame 15 [Source:HGNC Symbo
15	810	1.48	2e−16	3e−14	1 x 50	calmodulin−like 3 [Source:HGNC Symbol;Acc:1452]
16	57172	2	2e−16	3e−14	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
17	84290	−1.48	2e−16	3e−14	1 x 50	calpain, small subunit 2 [Source:HGNC Symbol;Acc:16371]
18	875	1.78	2e−16	3e−14	49 x 47	cystathionine−beta−synthase [Source:HGNC Symbol;Acc:15
19	6347	1.26	2e−16	3e−14	50 x 4	chemokine (C−C motif) ligand 2 [Source:HGNC Symbol;Acc:
20	1048	1.85	2e−16	3e−14	2 x 50	carcinoembryonic antigen−related cell adhesion molecule 5 [

p−values



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	16.02	NULL	42	BP	keratinization
2	13.97	NULL	21	CC	cornified envelope
3	9.66	NULL	53	BP	keratinocyte differentiation
4	9.27	NULL	19	BP	peptide cross−linking
5	9.1	NULL	553	Cancer	Lembcke_Colonic Inflammation
6	8.92	NULL	918	Chr	Chr 17
7	8.4	NULL	9	GSEA C2	GUTIERREZ_WALDENSTROEMS_MACROGLOBULINEMIA_1_D
8	8.38	NULL	15	CC	MHC class II protein complex
9	8.36	NULL	76	BP	epidermis development
10	7.86	NULL	12	GSEA C2	HELLER_SILENCED_BY_METHYLATION_DN
11	7.43	NULL	16	GSEA C2	KAN_RESPONSE_TO_ARSENIC_TRIOXIDE
12	7.04	NULL	15	GSEA C2	AGUIRRE_PANCREATIC_CANCER_COPY_NUMBER_UP
13	6.95	NULL	602	Chr	Chr 10
14	6.94	NULL	21	CC	clathrin−coated endocytic vesicle membrane
15	6.59	NULL	9	GSEA C2	REACTOME_ETHANOL_OXIDATION
16	6.55	NULL	5	GSEA C2	WONG_ENDOMETRIAL_CANCER_LATE
17	6.49	NULL	572	Disease	GUDJ_psoriasis up
18	6.41	NULL	10	GSEA C2	NOJIMA_SFRP2_TARGETS_UP
19	6.36	NULL	16	MF	fibronectin binding
20	6.28	NULL	10	BP	lipoxygenase pathway
Underexpressed					
1	−9.52	NULL	957	Chr	Chr 11
2	−7.63	NULL	633	Chr	Chr 9
3	−7.05	NULL	127	H.Tiss	WIRTH_Muscle
4	−6.92	NULL	16	GSEA C2	EINAV_INTERFERON_SIGNATURE_IN_CANCER
5	−6.14	NULL	8	GSEA C2	ROETH_TERT_TARGETS_UP
6	−5.87	NULL	504	Chr	Chr 15
7	−5.82	NULL	519	Chr	Chr 14
8	−5.55	NULL	31	BP	negative regulation of viral genome replication
9	−5.36	NULL	16	GSEA C2	MOSERLE_IFNA_RESPONSE
10	−5.33	NULL	36	BP	muscle filament sliding
11	−5.29	NULL	16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
12	−5.23	NULL	12	GSEA C2	TSAI_DNAJB4_TARGETS_UP
13	−5.19	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_F
14	−5.01	NULL	15	GSEA C2	BECKER_TAMOXIFEN_RESISTANCE_UP
15	−4.94	NULL	4	MMML CGS	MACIEJ_MMML 47
16	−4.93	NULL	13	GSEA C2	BOWIE_RESPONSE_TO_TAMOXIFEN
17	−4.68	NULL	10	GSEA C2	BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
18	−4.64	NULL	16	H.Tiss	WIRTH_Hippocampus
19	−4.63	NULL	84	BP	muscle contraction
20	−4.49	NULL	15	GSEA C2	ONDER_CDH1_TARGETS_2_DN

GW_290

Local Summary

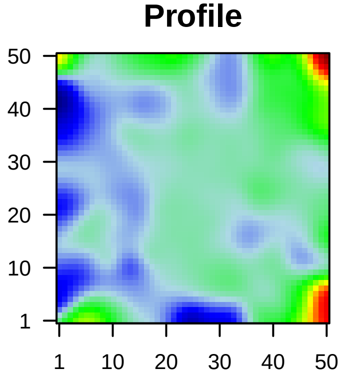
%DE = 0.49
metagenes = 12
genes = 230
genes in genesets = 229

genes with fdr < 0.1 = 83 (75 + / 8 −)
genes with fdr < 0.05 = 66 (60 + / 6 −)
genes with fdr < 0.01 = 48 (45 + / 3 −)

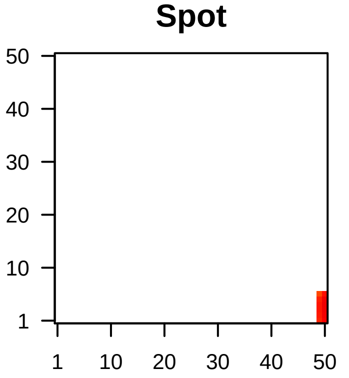
<r> metagenes = 0.96
<r> genes = 0.53

<FC> = 0.27
<shrinkage−t> = 9.57
<p−value> = 0
<fdr> = 0.65

Profile



Spot



Local Genelist

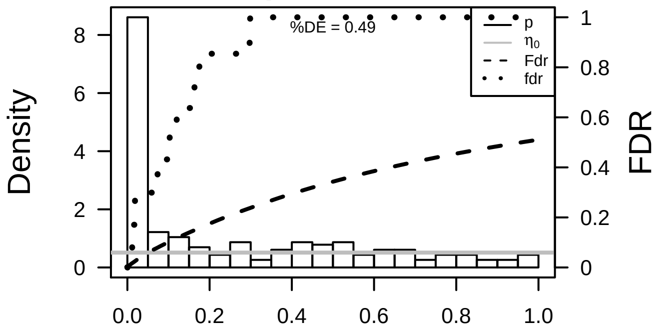
Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	260436	−1.59	2e−16	2e−15	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symbo
2	57172	2	2e−16	2e−15	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
3	6347	1.26	2e−16	2e−15	50 x 4	chemokine (C−C motif) ligand 2 [Source:HGNC Symbol;Acc:
4	51755	1.7	2e−16	2e−15	49 x 1	cyclin−dependent kinase 12 [Source:HGNC Symbol;Acc:242
5	54855	1.75	2e−16	2e−15	49 x 1	family with sequence similarity 46, member C [Source:HGNC
6	3512	2.92	2e−16	2e−15	50 x 1	immunoglobulin J polypeptide, linker protein for immunoglobu
7	3543	1.34	2e−16	2e−15	49 x 1	immunoglobulin lambda−like polypeptide 1 [Source:HGNC Sy
8	25849	1.26	2e−16	2e−15	50 x 2	prostate androgen−regulated mucin−like protein 1 [Source:H
9	11040	1.51	2e−16	2e−15	49 x 1	pim−2 oncogene [Source:HGNC Symbol;Acc:8987]
10	5996	1.48	2e−16	2e−15	50 x 1	regulator of G−protein signaling 1 [Source:HGNC Symbol;Ac
11	5552	1.34	2e−16	2e−15	50 x 1	serglycin [Source:HGNC Symbol;Acc:9361]
12	10537	1.73	2e−16	2e−15	50 x 1	ubiquitin D [Source:HGNC Symbol;Acc:18795]
13	2219	1.13	1e−13	7e−11	50 x 5	ficolin (collagen/fibrinogen domain containing) 1 [Source:HG
14	126306	1.09	7e−13	1e−10	49 x 1	junctional sarcoplasmic reticulum protein 1 [Source:HGNC Sy
15	7494	1.07	2e−12	4e−08	49 x 5	X−box binding protein 1 [Source:HGNC Symbol;Acc:12801]
16	347733	0.94	6e−10	4e−08	50 x 5	tubulin, beta 2B class IIb [Source:HGNC Symbol;Acc:30829]
17	3122	0.87	7e−10	3e−07	50 x 1	major histocompatibility complex, class II, DR alpha [Source:
18	953	0.89	4e−09	3e−07	50 x 4	ectonucleoside triphosphate diphosphohydrolase 1 [Source:
19	28984	0.87	8e−09	3e−07	50 x 6	regulator of cell cycle [Source:HGNC Symbol;Acc:20369]
20	1880	0.87	8e−09	3e−07	50 x 3	G protein−coupled receptor 183 [Source:HGNC Symbol;Acc:

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	37.15	NULL	3 / 5	GSEA C2	WONG_ENDOMETRIAL_CANCER_LATE
2	27.59	NULL	4 / 8	GSEA C2	GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_DN
3	22.11	NULL	3 / 7	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
4	16.52	NULL	2 / 11	GSEA C2	GUTIERREZ_CHRONIC_LYMPHOCYTIC_LEUKEMIA_UP
5	15.83	NULL	10 / 15	CC	MHC class II protein complex
6	15.08	NULL	1 / 4	MMML CGS	MACIEJ_MMML 2
7	14.84	NULL	5 / 10	GSEA C2	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_
8	14.45	NULL	2 / 9	GSEA C2	GUTIERREZ_WALDENSTROEMS_MACROGLOBULINEMIA_1_D
9	13.12	NULL	1 / 13	GSEA C2	LEE_INTRATHYMIC_T_PROGENITOR
10	13.01	NULL	2 / 13	GSEA C2	HAHTOLA_MYCOSIS_FUNGOIDES_DN
11	12.76	NULL	5 / 27	MF	antigen binding
12	12.45	NULL	39 / 312	BP	immune response
13	12.29	NULL	3 / 12	BP	negative regulation of cytokine secretion
14	12.14	NULL	2 / 6	GSEA C2	BUDHU_LIVER_CANCER_METASTASIS_UP
15	11.69	NULL	1 / 16	GSEA C2	HASLINGER_B_CLL_WITH_CHROMOSOME_12_TRISOMY
16	11.68	NULL	1 / 6	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_8
17	10.49	NULL	6 / 21	CC	clathrin−coated endocytic vesicle membrane
18	10.2	NULL	70 / 553	Cancer	Lembcke_Colonic Inflammation
19	10.19	NULL	2 / 7	Cancer	ZHANG_MGUS up
20	10.07	NULL	1 / 2	GSEA C2	GUTIERREZ_MULTIPLE_MYELOMA_UP
21	10.02	NULL	1 / 6	H.Tiss	WIRTH_Bone marrow
22	9.98	NULL	6 / 23	CC	integral to lumenal side of endoplasmic reticulum membrane
23	9.8	NULL	1 / 11	GSEA C2	BIOCARTA_CACAM_PATHWAY
24	9.46	NULL	1 / 7	GSEA C2	IIZUKA_LIVER_CANCER_PROGRESSION_G2_G3_DN
25	9.46	NULL	60 / 417	H.Tiss	WIRTH_Immune system
26	9.38	NULL	2 / 9	GSEA C2	GOUYER_TATI_TARGETS_UP
27	9.32	NULL	4 / 16	GSEA C2	CASORELLI_ACUTE_PROMYELOCYTIC_LEUKEMIA_UP
28	9.3	NULL	2 / 13	GSEA C2	ZIRN_TRETINOIN_RESPONSE_UP
29	9.26	NULL	6 / 8	Glio	Donson−migration tethering and rolling−associated with LTS in HG
30	9.21	NULL	4 / 12	BP	immunoglobulin mediated immune response
31	9.15	NULL	2 / 3	GSEA C2	KEGG_VIRAL_MYOCARDITIS
32	9.13	NULL	2 / 12	GSEA C2	BIOCARTA_HDAC_PATHWAY
33	9.13	NULL	2 / 12	GSEA C2	BIOCARTA_PGC1A_PATHWAY
34	9.04	NULL	2 / 12	GSEA C2	LEE_RECENT_THYMIC_EMIGRANT
35	8.94	NULL	6 / 28	CC	transport vesicle membrane
36	8.92	NULL	1 / 13	GSEA C2	BIOCARTA_NFAT_PATHWAY
37	8.82	NULL	2 / 8	GSEA C2	MCLACHLAN_DENTAL_CARIES_UP
38	8.69	NULL	37 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
39	8.69	NULL	37 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
40	8.69	NULL	37 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down

p−values



GW_290

Local Summary

%DE = 0.76

metagenes = 9

genes = 159

genes in genesets = 158

genes with fdr < 0.1 = 95 (82 + / 13 −)

genes with fdr < 0.05 = 84 (72 + / 12 −)

genes with fdr < 0.01 = 74 (66 + / 8 −)

<r> metagenes = 0.98

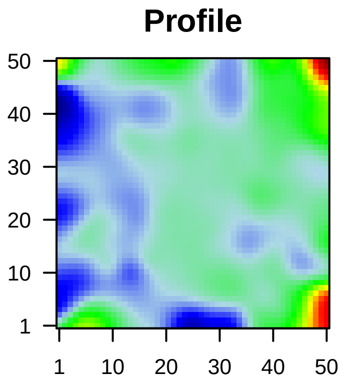
<r> genes = 0.29

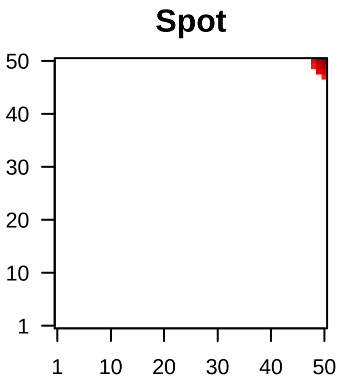
<FC> = 0.37

<shrinkage−t> = 12.93

<p−value> = 0

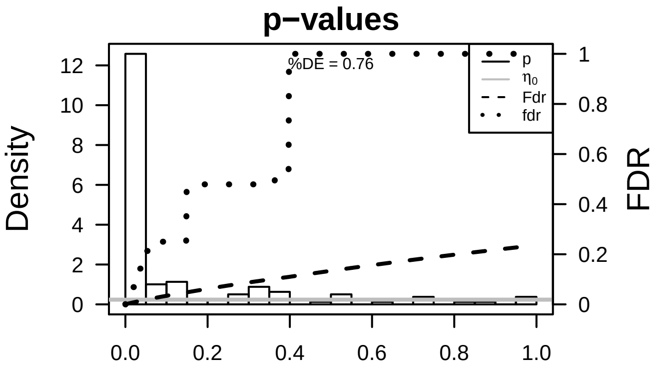
<fdr> = 0.45





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	154664	1.24	2e−16	8e−16	50 x 50	ATP−binding cassette, sub−family A (ABC1), member 13 [Sou
2	344905	1.34	2e−16	8e−16	50 x 50	ATPase type 13A5 [Source:HGNC Symbol;Acc:31789]
3	29785	1.56	2e−16	8e−16	50 x 50	cytochrome P450, family 2, subfamily S, polypeptide 1 [Sourc
4	10655	1.36	2e−16	8e−16	50 x 50	doublesex and mab−3 related transcription factor 2 [Source:H
5	94234	1.35	2e−16	8e−16	50 x 50	forkhead box Q1 [Source:HGNC Symbol;Acc:20951]
6	3304	1.35	2e−16	8e−16	49 x 49	heat shock 70kDa protein 1A [Source:HGNC Symbol;Acc:523
7	3866	1.72	2e−16	8e−16	50 x 50	keratin 15 [Source:HGNC Symbol;Acc:6421]
8	3880	1.28	2e−16	8e−16	50 x 49	keratin 19 [Source:HGNC Symbol;Acc:6436]
9	4922	1.66	2e−16	8e−16	50 x 50	neurotensin [Source:HGNC Symbol;Acc:8038]
10	79679	1.31	2e−16	8e−16	50 x 50	V−set domain containing T cell activation inhibitor 1 [Source:H
11	2938	1.22	7e−16	3e−14	50 x 50	glutathione S−transferase alpha 2 [Source:HGNC Symbol;Ac
12	216	1.21	2e−15	4e−14	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGN
13	3856	1.2	3e−15	4e−14	50 x 48	keratin 8 pseudogene 3 [Source:HGNC Symbol;Acc:31056]
14	84707	1.19	4e−15	5e−13	50 x 48	brain expressed X−linked 2 [Source:HGNC Symbol;Acc:3093
15	9076	1.16	2e−14	1e−12	49 x 50	claudin 1 [Source:HGNC Symbol;Acc:2032]
16	2944	1.14	4e−14	2e−12	50 x 50	glutathione S−transferase mu 1 [Source:HGNC Symbol;Acc:4
17	2730	1.12	2e−13	2e−12	50 x 50	glutamate−cysteine ligase, modifier subunit [Source:HGNC S
18	4915	1.12	2e−13	3e−12	50 x 50	neurotrophic tyrosine kinase, receptor, type 2 [Source:HGNC
19	57291	1.11	3e−13	1e−11	50 x 50	differentiation antagonizing non−protein coding RNA [Source:
20	79190	1.09	6e−13	3e−10	50 x 47	iroquois homeobox 6 [Source:HGNC Symbol;Acc:14675]



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	23.78	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
2	22.02	NULL	1 / 2	GSEA C2	KUROKAWA_LIVER_CANCER_EARLY_RECURRENCE_UP
3	17.96	NULL	5 / 15	GSEA C2	KEGG_GLUTATHIONE_METABOLISM
4	17.63	NULL	4 / 13	GSEA C2	KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_
5	16.45	NULL	2 / 7	GSEA C2	MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
6	15.26	NULL	3 / 13	BP	regulation of blood vessel size
7	15.05	NULL	6 / 25	BP	glutathione derivative biosynthetic process
8	14.83	NULL	4 / 15	GSEA C2	REACTOME_GLUTATHIONE_CONJUGATION
9	14.54	NULL	3 / 12	GSEA C2	BROCKE_APOPTOSIS_REVERSED_BY_IL6
10	14.15	NULL	2 / 9	GSEA C2	BROWNE_HCMV_INFECTION_8HR_UP
11	13.41	NULL	8 / 34	BP	glutathione metabolic process
12	12.62	NULL	2 / 11	GSEA C2	CONCANNON_APOPTOSIS_BY_EPOXOMICIN_UP
13	12.32	NULL	2 / 10	GSEA C2	CERVERA_SDHB_TARGETS_1_DN
14	12.15	NULL	1 / 5	GSEA C2	DASU_IL6_SIGNALING_UP
15	12.14	NULL	11 / 119	BP	xenobiotic metabolic process
16	12.11	NULL	5 / 20	MF	glutathione transferase activity
17	11.86	NULL	2 / 9	GSEA C2	NIKOLSKY_BREAST_CANCER_17P11_AMPLICON
18	11.11	NULL	3 / 11	MF	glutathione binding
19	11.11	NULL	3 / 11	GSEA C2	KEGG_DRUG_METABOLISM_CYTOCHROME_P450
20	10.97	NULL	2 / 12	BP	cellular aldehyde metabolic process
21	10.88	NULL	1 / 6	GSEA C2	SESTO_RESPONSE_TO_UV_C0
22	10.88	NULL	1 / 6	GSEA C2	BIOCARTA_TID_PATHWAY
23	10.82	NULL	1 / 5	GSEA C2	TURASHVILI_BREAST_CARCINOMA_DUCTAL_VS_LOBULAR_
24	10.16	NULL	2 / 7	GSEA C2	FREDERICK_PRKCI_TARGETS
25	9.92	NULL	1 / 7	GSEA C2	WEINMANN_ADAPTATION_TO_HYPOXIA_UP
26	9.88	NULL	2 / 15	GSEA C2	REACTOME_PHASE_II_CONJUGATION
27	9.22	NULL	2 / 10	GSEA C2	KEGG_ASCORBATE_AND_ALDARATE_METABOLISM
28	9.16	NULL	1 / 8	GSEA C2	BARRIER_CANCER_RELAPSE_NORMAL_SAMPLE_DN
29	9.16	NULL	1 / 8	GSEA C2	ADDYA_ERYTHROID_DIFFERENTIATION_BY_HEMIN
30	9.16	NULL	1 / 8	GSEA C2	CHANDRAN_METASTASIS_UP
31	9.16	NULL	1 / 8	GSEA C2	WU_APOPTOSIS_BY_CDKN1A_NOT_VIA_TP53
32	9.16	NULL	1 / 8	GSEA C2	KEGG_PRION_DISEASES
33	9.16	NULL	1 / 8	GSEA C2	REACTOME_INFLUENZA_LIFE_CYCLE
34	9.15	NULL	2 / 11	GSEA C2	SMID_BREAST_CANCER_BASAL_UP
35	9.15	NULL	2 / 9	GSEA C2	REACTOME_METABOLISM_OF_AMINO_ACIDS
36	9.08	NULL	1 / 9	GSEA C2	REACTOME_CYTOCHROME_P450_ARRANGED_BY_SUBSTRA
37	8.91	NULL	1 / 6	GSEA C2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_D_DN
38	8.91	NULL	1 / 6	GSEA C2	KAPOSI_LIVER_CANCER_POOR_SURVIVAL_DN
39	8.7	NULL	2 / 18	MF	acyl−CoA dehydrogenase activity
40	8.59	NULL	1 / 11	Glio	neurons_glio

GW_290

Local Summary

%DE = 0.82

metagenes = 9

genes = 93

genes in genesets = 93

genes with fdr < 0.1 = 51 (2 + / 49 −)

genes with fdr < 0.05 = 40 (1 + / 39 −)

genes with fdr < 0.01 = 32 (1 + / 31 −)

<r> metagenes = 0.95

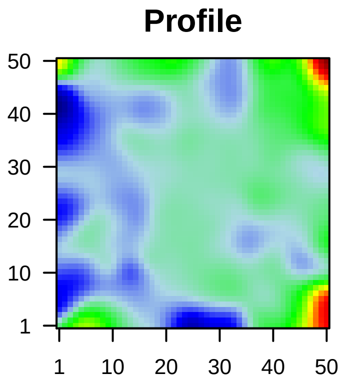
<r> genes = 0.62

<FC> = −0.33

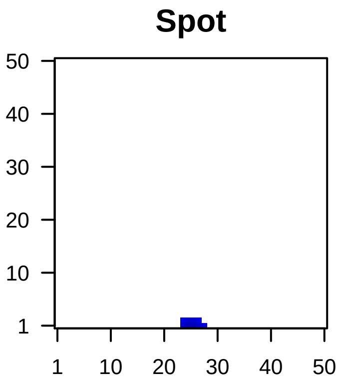
<shrinkage−t> = −11.55

<p−value> = 0.01

<fdr> = 0.58



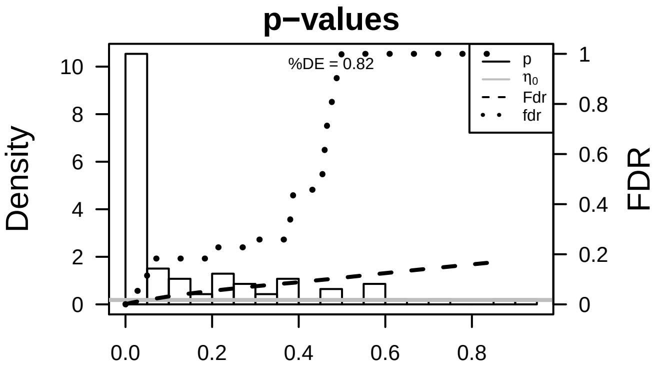
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	388115	−1.27	2e−16	4e−15	26 x 2	chromosome 15 open reading frame 52 [Source:HGNC Symb
2	58	−1.18	6e−15	4e−11	25 x 1	actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
3	6588	−1.06	2e−12	9e−08	25 x 1	sarcolipin [Source:HGNC Symbol;Acc:11089]
4	1410	−0.89	5e−09	9e−07	25 x 1	crystallin, alpha B [Source:HGNC Symbol;Acc:2389]
5	1158	−0.82	6e−08	3e−06	25 x 1	creatine kinase, muscle [Source:HGNC Symbol;Acc:1994]
6	1917	−0.78	2e−07	7e−06	25 x 1	eukaryotic translation elongation factor 1 alpha 2 [Source:HG
7	84448	−0.75	6e−07	3e−05	25 x 1	actin binding LIM protein family, member 2 [Source:HGNC Sy
8	70	−0.72	2e−06	4e−05	25 x 1	actin, alpha, cardiac muscle 1 [Source:HGNC Symbol;Acc:14
9	5269	−0.69	6e−06	4e−05	28 x 1	serpin peptidase inhibitor, clade B (ovalbumin), member 6 [Sc
10	7136	−0.68	6e−06	3e−04	25 x 1	troponin I type 2 (skeletal, fast) [Source:HGNC Symbol;Acc:1
11	4620	−0.64	3e−05	3e−04	25 x 1	myosin, heavy chain 2, skeletal muscle, adult [Source:HGNC
12	4151	−0.62	4e−05	4e−04	25 x 1	myoglobin [Source:HGNC Symbol;Acc:6915]
13	10324	−0.6	7e−05	9e−04	25 x 1	kelch−like family member 41 [Source:HGNC Symbol;Acc:169
14	2318	−0.57	2e−04	9e−04	25 x 1	filamin C, gamma [Source:HGNC Symbol;Acc:3756]
15	22998	−0.57	2e−04	2e−03	24 x 1	LIM and calponin homology domains 1 [Source:HGNC Symb
16	4608	−0.53	5e−04	2e−03	25 x 1	myosin binding protein H [Source:HGNC Symbol;Acc:7552]
17	4633	−0.53	5e−04	2e−03	25 x 1	myosin, light chain 2, regulatory, cardiac, slow [Source:HGNC
18	7138	−0.52	6e−04	2e−03	25 x 1	troponin T type 1 (skeletal, slow) [Source:HGNC Symbol;Acc:
19	22921	−0.52	6e−04	2e−03	28 x 1	methionine sulfoxide reductase B2 [Source:HGNC Symbol;Ac
20	9172	−0.51	7e−04	2e−03	24 x 1	myomesin 2 [Source:HGNC Symbol;Acc:7614]



p−values

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−45.78	NULL	11 / 16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_F
2	−45.5	NULL	47 / 127	H.Tiss	WIRTH_Muscle
3	−44.02	NULL	22 / 36	BP	muscle filament sliding
4	−41.41	NULL	9 / 16	H.Tiss	WIRTH_Hippocampus
5	−31.86	NULL	9 / 12	CC	myosin filament
6	−30.22	NULL	21 / 44	MF	structural constituent of muscle
7	−26.91	NULL	21 / 84	BP	muscle contraction
8	−25.26	NULL	11 / 37	CC	sarcomere
9	−24.74	NULL	6 / 12	BP	skeletal muscle contraction
10	−24.06	NULL	7 / 16	CC	M band
11	−22.81	NULL	13 / 34	CC	myofibril
12	−20.98	NULL	7 / 13	CC	muscle myosin complex
13	−20.89	NULL	9 / 20	CC	I band
14	−20.24	NULL	2 / 6	GSEA C2	BIOCARTA_HSP27_PATHWAY
15	−19.1	NULL	7 / 14	CC	contractile fiber
16	−17.78	NULL	9 / 37	BP	cardiac muscle contraction
17	−16.98	NULL	5 / 11	BP	cardiac muscle tissue morphogenesis
18	−16.82	NULL	3 / 15	Cancer	BEN−PORATH_UP
19	−16.33	NULL	6 / 12	MF	titin binding
20	−16.14	NULL	18 / 88	CC	Z disc
21	−14.1	NULL	6 / 18	BP	regulation of muscle contraction
22	−13.63	NULL	2 / 20	MF	myosin binding
23	−13.19	NULL	1 / 9	GSEA C2	PENG_GLUCOSE_DEPRIVATION_UP
24	−13.19	NULL	1 / 9	GSEA C2	PENG_GLUCOSE_DEPRIVATION_DN
25	−13.1	NULL	2 / 10	BP	heart contraction
26	−12.52	NULL	4 / 15	BP	striated muscle contraction
27	−12.44	NULL	1 / 6	GSEA C2	LY_AGING_OLD_UP
28	−12.42	NULL	1 / 10	GSEA C2	BIOCARTA_EPHA4_PATHWAY
29	−12.27	NULL	23 / 297	MF	actin binding
30	−12.16	NULL	4 / 11	CC	A band
31	−12.06	NULL	2 / 14	GSEA C2	BIOCARTA_UCALPAIN_PATHWAY
32	−11.96	NULL	4 / 14	MF	tropomyosin binding
33	−11.6	NULL	2 / 15	GSEA C2	BIOCARTA_INTEGRIN_PATHWAY
34	−11.21	NULL	1 / 5	GSEA C2	LIU_VAV3_PROSTATE_CARCINOGENESIS_UP
35	−11.2	NULL	2 / 14	BP	actomyosin structure organization
36	−11.19	NULL	1 / 12	GSEA C2	BIOCARTA_NO1_PATHWAY
37	−11.19	NULL	1 / 12	GSEA C2	BIOCARTA_RAB_PATHWAY
38	−11.01	NULL	1 / 14	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_
39	−10.99	NULL	2 / 15	BP	skeletal muscle fiber development
40	−10.85	NULL	4 / 36	CC	sarcoplasmic reticulum

GW_290

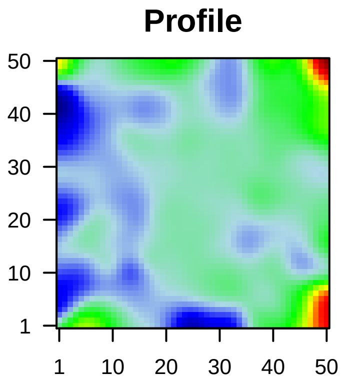
Local Summary

%DE = 0.61
metagenes = 24
genes = 271
genes in genesets = 266

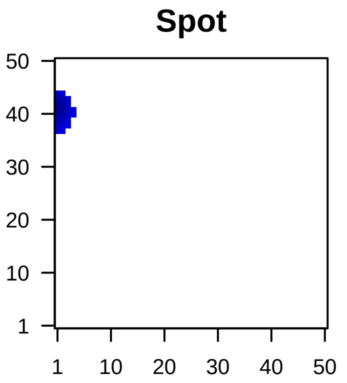
genes with fdr < 0.1 = 114 (25 + / 89 −)
genes with fdr < 0.05 = 113 (25 + / 88 −)
genes with fdr < 0.01 = 63 (14 + / 49 −)

<r> metagenes = 0.97
<r> genes = 0.31

<FC> = −0.18
<shrinkage−t> = −6.4
<p−value> = 0.01
<fdr> = 0.6



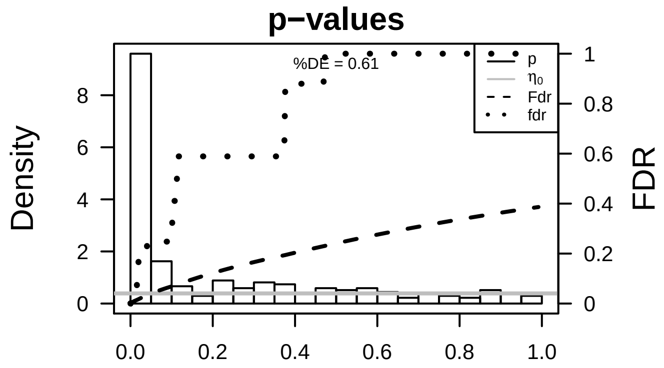
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	147495	1.29	2e−16	5e−15	2 x 44	adenomatosis polyposis coli down−regulated 1 [Source:HGN
2	118430	1.51	2e−16	5e−15	2 x 44	mucin−like 1 [Source:HGNC Symbol;Acc:30588]
3	56901	−1.25	2e−16	5e−15	1 x 44	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4−li
4	5744	1.35	2e−16	5e−15	1 x 43	parathyroid hormone−like hormone [Source:HGNC Symbol;A
5	5836	−1.34	2e−16	5e−15	1 x 44	phosphorylase, glycogen, liver [Source:HGNC Symbol;Acc:9
6	113146	−1.1	4e−13	3e−11	1 x 44	AHNAK nucleoprotein 2 [Source:HGNC Symbol;Acc:20125]
7	3552	−1.09	6e−13	1e−09	1 x 43	interleukin 1, alpha [Source:HGNC Symbol;Acc:5991]
8	1984	1.02	1e−11	2e−08	1 x 37	eukaryotic translation initiation factor 5A [Source:HGNC Sym
9	2152	−0.97	2e−10	3e−08	1 x 43	coagulation factor III (thromboplastin, tissue factor) [Source:H
10	303	−0.93	8e−10	3e−08	3 x 41	
11	79413	−0.93	8e−10	4e−08	1 x 43	zinc finger, BED−type containing 2 [Source:HGNC Symbol;A
12	27242	0.92	1e−09	8e−08	1 x 40	tumor necrosis factor receptor superfamily, member 21 [Sour
13	1515	−0.91	2e−09	1e−07	1 x 44	cathepsin V [Source:HGNC Symbol;Acc:2538]
14	347735	−0.9	3e−09	3e−07	1 x 43	serine incorporator 2 [Source:HGNC Symbol;Acc:23231]
15	858	−0.87	8e−09	3e−07	1 x 42	caveolin 2 [Source:HGNC Symbol;Acc:1528]
16	51200	−0.87	1e−08	3e−07	1 x 44	carboxypeptidase A4 [Source:HGNC Symbol;Acc:15740]
17	1288	−0.86	1e−08	5e−06	1 x 43	collagen, type IV, alpha 6 [Source:HGNC Symbol;Acc:2208]
18	10397	−0.73	1e−07	5e−06	1 x 42	N−myc downstream regulated 1 [Source:HGNC Symbol;Acc:
19	2150	−0.8	1e−07	5e−06	1 x 44	coagulation factor II (thrombin) receptor−like 1 [Source:HGN
20	6281	−0.73	2e−07	6e−06	1 x 42	S100 calcium binding protein A10 [Source:HGNC Symbol;Ac



p−values

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−10.5	NULL	1 / 4	GSEA C2	BUDHU_LIVER_CANCER_METASTASIS_DN
2	−10.46	NULL	4 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
3	−10.21	NULL	2 / 6	GSEA C2	WALLACE_PROSTATE_CANCER_DN
4	−9.76	NULL	2 / 11	BP	positive regulation of positive chemotaxis
5	−9.55	NULL	2 / 2	miRNA target	miR−199a*
6	−9.51	NULL	3 / 15	GSEA C2	BROWNE_HCMV_INFECTION_2HR_DN
7	−9.49	NULL	1 / 7	GSEA C2	BIOCARTA_FEEDER_PATHWAY
8	−8.78	NULL	2 / 14	GSEA C2	HOEGERKORP_CD44_TARGETS_DIRECT_UP
9	−8.51	NULL	2 / 11	GSEA C2	MIDORIKAWA_AMPLIFIED_IN_LIVER_CANCER
10	−8.37	NULL	1 / 6	GSEA C2	SEIKE_LUNG_CANCER_POOR_SURVIVAL
11	−7.95	NULL	2 / 16	GSEA C2	UZONYI_RESPONSE_TO_LEUKOTRIENE_AND_THROMBIN
12	−7.94	NULL	2 / 15	GSEA C2	KANG_CISPLATIN_RESISTANCE_UP
13	−7.82	NULL	3 / 16	GSEA C2	HARRIS_HYPOXIA
14	−7.79	NULL	2 / 15	GSEA C2	NAGASHIMA_NRG1_SIGNALING_DN
15	−7.71	NULL	2 / 11	BP	response to metal ion
16	−7.52	NULL	3 / 16	GSEA C2	ELVIDGE_HYPOXIA_BY_DMOG_UP
17	−7.39	NULL	1 / 6	GSEA C2	MAINA_HYPOXIA_VHL_TARGETS_UP
18	−7.39	NULL	1 / 11	MF	AMP binding
19	−7.12	NULL	2 / 11	GSEA C2	BIOCARTA_VITCB_PATHWAY
20	−7.1	NULL	3 / 15	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_3
21	−7.05	NULL	1 / 12	H.Tiss	WIRTH_Prim. lymphoid organs
22	−6.85	NULL	3 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_4
23	−6.74	NULL	1 / 13	GSEA C2	REACTOME_GLYCOGEN_BREAKDOWN_GLYCOGENOLYSIS
24	−6.74	NULL	1 / 5	GSEA C2	KYNG_ENVIRONMENTAL_STRESS_RESPONSE_NOT_BY_4NQ
25	−6.71	NULL	3 / 15	GSEA C2	LEE_LIVER_CANCER_DENA_UP
26	−6.69	NULL	2 / 15	GSEA C2	TAKAO_RESPONSE_TO_UVB_RADIATION_DN
27	−6.53	NULL	1 / 7	GSEA C2	FUNG_IL2_TARGETS_WITH_STAT5_BINDING_SITES_T1
28	−6.45	NULL	2 / 16	GSEA C2	LEE_LIVER_CANCER_MYC_TGFA_UP
29	−6.45	NULL	2 / 16	GSEA C2	LEE_LIVER_CANCER_ACOX1_UP
30	−6.44	NULL	2 / 16	CC	extrinsic to plasma membrane
31	−6.43	NULL	2 / 5	miRNA target−starBase	hsa−miR−1268
32	−6.36	NULL	1 / 4	miRNA target	miR−206
33	−6.36	NULL	2 / 13	BP	response to copper ion
34	−6.3	NULL	1 / 10	GSEA C2	BIOCARTA_LYM_PATHWAY
35	−6.29	NULL	3 / 12	GSEA C2	REACTOME_GAP_JUNCTION_ASSEMBLY
36	−6.28	NULL	4 / 16	GSEA C2	ELVIDGE_HIF1A_TARGETS_DN
37	−6.18	NULL	4 / 15	GSEA C2	KOBAYASHI_EGFR_SIGNALING_6HR_DN
38	−6.11	NULL	2 / 10	BP	positive regulation of Rho protein signal transduction
39	−6.08	NULL	1 / 6	GSEA C2	KYNG_ENVIRONMENTAL_STRESS_RESPONSE_NOT_BY_UV_
40	−6	NULL	2 / 16	GSEA C2	SESTO_RESPONSE_TO_UV_C2