GW_239

Global Summary

%DE = 0.15

genes with fdr < 0.2 = 1927 (1185 + / 742 −)

genes with fdr < 0.1 = 1686 (1067 + / 619 −)

genes with fdr < 0.05 = 1382 (893 + / 489 −)

genes with fdr < 0.01 = 1008 (698 + / 310 −)

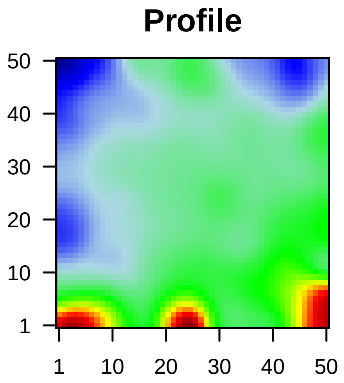
genes in genesets = 16332

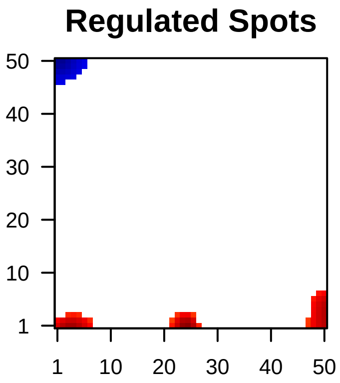
<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.08

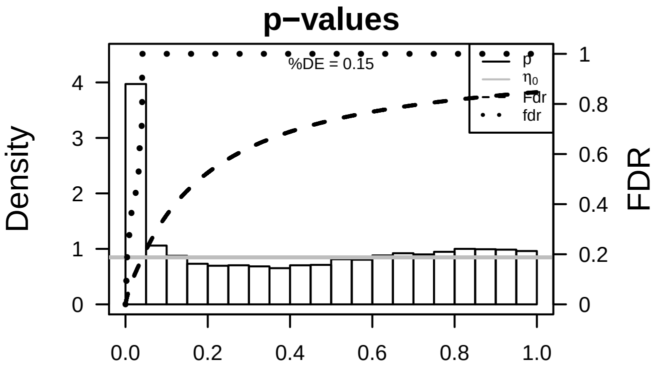
<fdr> = 0.85





Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	79852	−1.47	2e−16	2e−14	3 x 50	epoxide hydrolase 3 [Source:HGNC Symbol;Acc:23760]
2	58	4.54	2e−16	2e−14	25 x 1	actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
3	59	1.47	2e−16	2e−14	3 x 1	actin, alpha 2, smooth muscle, aorta [Source:HGNC Symbol;
4	70	2.73	2e−16	2e−14	25 x 1	actin, alpha, cardiac muscle 1 [Source:HGNC Symbol;Acc:14
5	88	1.59	2e−16	2e−14	25 x 1	actinin, alpha 2 [Source:HGNC Symbol;Acc:164]
6	131	−1.53	2e−16	2e−14	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
7	165	1.65	2e−16	2e−14	3 x 1	AE binding protein 1 [Source:HGNC Symbol;Acc:303]
8	1646	1.43	2e−16	2e−14	13 x 50	aldo−keto reductase family 1, member C2 [Source:HGNC Sy
9	8644	2.67	2e−16	2e−14	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
10	1109	2.38	2e−16	2e−14	13 x 50	aldo−keto reductase family 1, member C4 [Source:HGNC Sy
11	218	1.57	2e−16	2e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
12	270	1.65	2e−16	2e−14	50 x 7	adenosine monophosphate deaminase 1 [Source:HGNC Sym
13	401138	3.36	2e−16	2e−14	1 x 5	amelotin [Source:HGNC Symbol;Acc:33188]
14	163782	1.47	2e−16	2e−14	1 x 2	KN motif and ankyrin repeat domains 4 [Source:HGNC Symb
15	10930	1.52	2e−16	2e−14	25 x 1	apolipoprotein B mRNA editing enzyme, catalytic polypeptide
16	347	1.94	2e−16	2e−14	50 x 7	apolipoprotein D [Source:HGNC Symbol;Acc:612]
17	140458	1.65	2e−16	2e−14	25 x 1	ankyrin repeat and SOCS box containing 5 [Source:HGNC Sy
18	633	1.41	2e−16	2e−14	3 x 1	biglycan [Source:HGNC Symbol;Acc:1044]
19	387695	−1.48	2e−16	2e−14	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Sym
20	57172	2.17	2e−16	2e−14	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	31.88	NULL	127	H.Tiss	WIRTH_Muscle
2	25.44	NULL	36	BP	muscle filament sliding
3	22.25	NULL	190	CC	extracellular matrix
4	21.16	NULL	250	Lymphoma	LENZ_Stromal signature 1
5	21.08	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_F
6	19.84	NULL	16	H.Tiss	WIRTH_Hippocampus
7	19.3	NULL	553	Cancer	Lembcke_Colonic Inflammation
8	19.16	NULL	44	MF	structural constituent of muscle
9	16.49	NULL	84	BP	muscle contraction
10	15.5	NULL	37	CC	sarcomere
11	15.41	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
12	15.14	NULL	242	BP	extracellular matrix organization
13	14.74	NULL	16	MMML CGS	MACIEJ_MMML 1
14	13.95	NULL	183	CC	proteinaceous extracellular matrix
15	13.77	NULL	69	BP	extracellular matrix disassembly
16	13.71	NULL	12	CC	myosin filament
17	13.61	NULL	34	CC	myofibril
18	12.82	NULL	13	CC	muscle myosin complex
19	12.26	NULL	64	BP	collagen catabolic process
20	12.25	NULL	683	CC	extracellular space
Underexpressed					
1	−21.35	NULL	135	H.Tiss	WIRTH_Mucosa
2	−15.62	NULL	572	Disease	GUDJ_psoriasis up
3	−13.66	NULL	142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
4	−13.66	NULL	142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
5	−10.71	NULL	530	Cancer	Lembcke_Normal vs Adenoma
6	−9.76	NULL	21	CC	cornified envelope
7	−9.69	NULL	370	BP	mitotic cell cycle
8	−9.37	NULL	76	BP	epidermis development
9	−8.15	NULL	8	GSEA C2	LIU_CDX2_TARGETS_DN
10	−7.53	NULL	42	BP	keratinization
11	−7.32	NULL	949	CC	nucleoplasm
12	−6.73	NULL	232	BP	mitosis
13	−6.45	NULL	1233	TF	KIM_MYC targets
14	−6.42	NULL	53	BP	keratinocyte differentiation
15	−6.3	NULL	13	H.Tiss	WIRTH_Tonsil
16	−6.16	NULL	15	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_3
17	−6.05	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_4
18	−5.92	NULL	15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
19	−5.86	NULL	16	GSEA C2	EGUCHI_CELL_CYCLE_RB1_TARGETS
20	−5.86	NULL	15	GSEA C2	AIGNER_ZEB1_TARGETS

GW_239

Local Summary

%DE = 0.97

metagenes = 17

genes = 281

genes in genesets = 280

genes with fdr < 0.1 = 259 (255 + / 4 −)

genes with fdr < 0.05 = 253 (249 + / 4 −)

genes with fdr < 0.01 = 244 (241 + / 3 −)

<r> metagenes = 0.96

<r> genes = 0.42

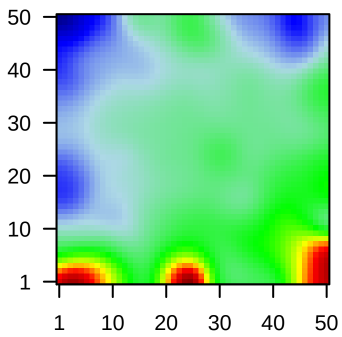
<FC> = 0.87

<shrinkage−t> = 30.54

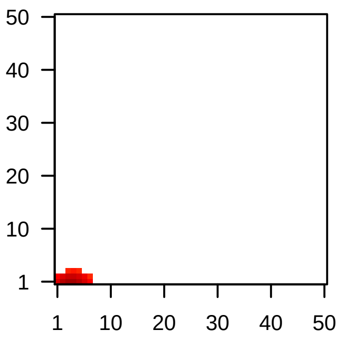
<p−value> = 0

<fdr> = 0.12

Profile



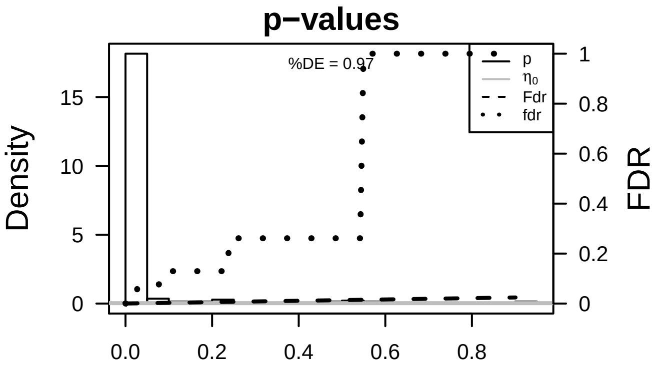
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	59	1.47	2e−16	3e−17	3 x 1	actin, alpha 2, smooth muscle, aorta [Source:HGNC Symbol;
2	165	1.65	2e−16	3e−17	3 x 1	AE binding protein 1 [Source:HGNC Symbol;Acc:303]
3	163782	1.47	2e−16	3e−17	1 x 2	KN motif and ankyrin repeat domains 4 [Source:HGNC Symb
4	633	1.41	2e−16	3e−17	3 x 1	biglycan [Source:HGNC Symbol;Acc:1044]
5	22918	1.41	2e−16	3e−17	4 x 1	CD93 molecule [Source:HGNC Symbol;Acc:15855]
6	1009	1.44	2e−16	3e−17	3 x 1	cadherin 11, type 2, OB−cadherin (osteoblast) [Source:HGN
7	1306	1.48	2e−16	3e−17	4 x 1	collagen, type XV, alpha 1 [Source:HGNC Symbol;Acc:2192]
8	1277	1.9	2e−16	3e−17	2 x 1	collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
9	1278	2.14	2e−16	3e−17	2 x 1	collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198]
10	1281	1.86	2e−16	3e−17	2 x 1	collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]
11	1289	1.61	2e−16	3e−17	2 x 1	collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209]
12	1290	1.66	2e−16	3e−17	2 x 1	collagen, type V, alpha 2 [Source:HGNC Symbol;Acc:2210]
13	1291	1.54	2e−16	3e−17	2 x 1	collagen, type VI, alpha 1 [Source:HGNC Symbol;Acc:2211]
14	1293	1.79	2e−16	3e−17	2 x 1	collagen, type VI, alpha 3 [Source:HGNC Symbol;Acc:2213]
15	1490	1.49	2e−16	3e−17	3 x 1	connective tissue growth factor [Source:HGNC Symbol;Acc:2
16	1513	1.8	2e−16	3e−17	4 x 1	cathepsin K [Source:HGNC Symbol;Acc:2536]
17	1634	1.45	2e−16	3e−17	4 x 1	decorin [Source:HGNC Symbol;Acc:2705]
18	2202	1.38	2e−16	3e−17	5 x 1	EGF containing fibulin−like extracellular matrix protein 1 [Sou
19	2191	1.37	2e−16	3e−17	1 x 1	fibroblast activation protein, alpha [Source:HGNC Symbol;Ac
20	2199	1.95	2e−16	3e−17	4 x 1	fibulin 2 [Source:HGNC Symbol;Acc:3601]

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	43.91	NULL	66 / 190	CC	extracellular matrix
2	43.72	NULL	14 / 16	MMML CGS	MACIEJ_MMML 1
3	40.74	NULL	79 / 250	Lymphoma	LENZ_Stromal signature 1
4	39.53	NULL	12 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
5	34.44	NULL	30 / 69	BP	extracellular matrix disassembly
6	33.63	NULL	8 / 11	MF	platelet−derived growth factor binding
7	33.2	NULL	61 / 242	BP	extracellular matrix organization
8	32.36	NULL	26 / 64	BP	collagen catabolic process
9	30.15	NULL	8 / 12	miRNA target	miR−29c
10	28.79	NULL	21 / 57	MF	extracellular matrix structural constituent
11	25.48	NULL	11 / 19	MF	extracellular matrix binding
12	24.62	NULL	14 / 37	BP	collagen fibril organization
13	24.04	NULL	11 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_UP
14	22.81	NULL	37 / 183	CC	proteinaceous extracellular matrix
15	21.64	NULL	4 / 5	GSEA C2	COLLER_MYC_TARGETS_DN
16	21.51	NULL	6 / 13	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
17	21.03	NULL	7 / 16	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_
18	19.83	NULL	8 / 15	GSEA C2	DASU_IL6_SIGNALING_SCAR_DN
19	19.1	NULL	21 / 119	Lymphoma	ROSOLOWSKI_green total
20	18.9	NULL	73 / 683	CC	extracellular space
21	18.89	NULL	4 / 8	GSEA C2	HAEGERSTRAND_RESPONSE_TO_IMATINIB
22	18.73	NULL	10 / 15	GSEA C2	CROMER_TUMORIGENESIS_UP
23	18.45	NULL	5 / 15	GSEA C2	CHANG_POU5F1_TARGETS_UP
24	18.43	NULL	5 / 10	GSEA C2	KEGG_ECM_RECEPTOR_INTERACTION
25	18.43	NULL	7 / 16	GSEA C2	LIEN_BREAST_CARCINOMA_METAPLASTIC
26	18.18	NULL	7 / 16	GSEA C2	CROONQUIST_STROMAL_STIMULATION_UP
27	17.99	NULL	15 / 68	CC	collagen
28	17.66	NULL	10 / 40	BP	cellular response to amino acid stimulus
29	17.56	NULL	101 / 1182	CC	extracellular region
30	17.42	NULL	5 / 10	GSEA C2	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
31	16.97	NULL	6 / 11	MMML CGS	MACIEJ_MMML 31
32	16.89	NULL	20 / 83	CC	basement membrane
33	16.72	NULL	5 / 15	GSEA C2	TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_DUCTAL_NO
34	16.61	NULL	5 / 13	GSEA C2	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
35	16.47	NULL	4 / 13	GSEA C2	CHIBA_RESPONSE_TO_TSA_UP
36	16.36	NULL	68 / 553	Cancer	Lembcke_Colonic Inflammation
37	15.9	NULL	4 / 10	BP	protein heterotrimerization
38	15.76	NULL	7 / 16	GSEA C2	GU_PDEF_TARGETS_UP
39	15.74	NULL	23 / 153	CC	endoplasmic reticulum lumen
40	15.58	NULL	5 / 10	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C4

GW_239

Local Summary

%DE = 0.98

metagenes = 15

genes = 127

genes in genesets = 126

genes with fdr < 0.1 = 124 (124 + / 0 −)

genes with fdr < 0.05 = 121 (121 + / 0 −)

genes with fdr < 0.01 = 118 (118 + / 0 −)

<r> metagenes = 0.99

<r> genes = 0.6

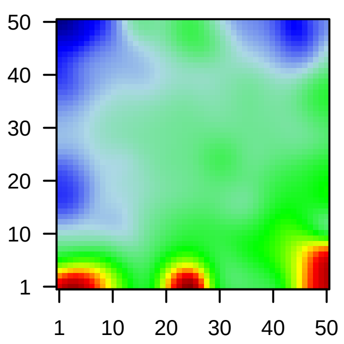
<FC> = 1.31

<shrinkage−t> = 45.72

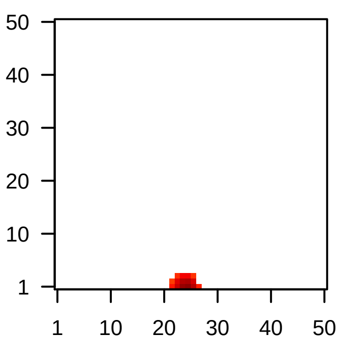
<p−value> = 0

<fdr> = 0.07

Profile



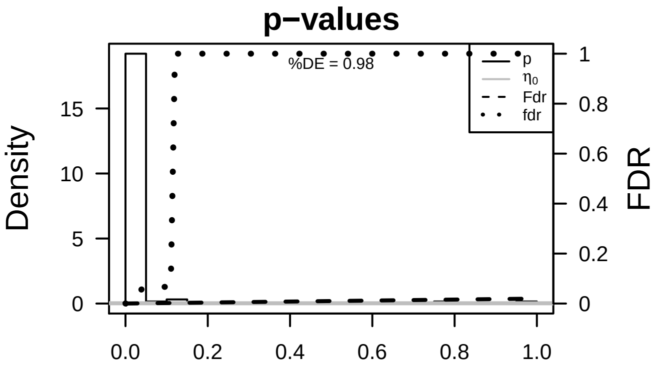
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	58	4.54	2e−16	1e−17	25 x 1	actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
2	70	2.73	2e−16	1e−17	25 x 1	actin, alpha, cardiac muscle 1 [Source:HGNC Symbol;Acc:14
3	88	1.59	2e−16	1e−17	25 x 1	actinin, alpha 2 [Source:HGNC Symbol;Acc:164]
4	10930	1.52	2e−16	1e−17	25 x 1	apolipoprotein B mRNA editing enzyme, catalytic polypeptide
5	140458	1.65	2e−16	1e−17	25 x 1	ankyrin repeat and SOCS box containing 5 [Source:HGNC Sy
6	10486	1.61	2e−16	1e−17	24 x 1	CAP, adenylate cyclase−associated protein, 2 (yeast) [Source
7	844	1.5	2e−16	1e−17	24 x 1	calsequestrin 1 (fast−twitch, skeletal muscle) [Source:HGNC
8	845	1.37	2e−16	1e−17	25 x 1	calsequestrin 2 (cardiac muscle) [Source:HGNC Symbol;Acc:
9	1158	3.52	2e−16	1e−17	25 x 1	creatine kinase, muscle [Source:HGNC Symbol;Acc:1994]
10	1160	1.59	2e−16	1e−17	25 x 1	creatine kinase, mitochondrial 2 (sarcomeric) [Source:HGNC
11	202333	2.05	2e−16	1e−17	25 x 1	cardiomyopathy associated 5 [Source:HGNC Symbol;Acc:14
12	1410	1.73	2e−16	1e−17	25 x 1	crystallin, alpha B [Source:HGNC Symbol;Acc:2389]
13	1674	1.43	2e−16	1e−17	25 x 1	desmin [Source:HGNC Symbol;Acc:2770]
14	1917	2.07	2e−16	1e−17	25 x 1	eukaryotic translation elongation factor 1 alpha 2 [Source:HG
15	2027	2.41	2e−16	1e−17	25 x 1	enolase 3 (beta, muscle) [Source:HGNC Symbol;Acc:3354]
16	2273	2.44	2e−16	1e−17	25 x 1	four and a half LIM domains 1 [Source:HGNC Symbol;Acc:37
17	2318	1.84	2e−16	1e−17	25 x 1	filamin C, gamma [Source:HGNC Symbol;Acc:3756]
18	126393	1.68	2e−16	1e−17	25 x 1	heat shock protein, alpha−crystallin−related, B6 [Source:HG
19	10324	3.07	2e−16	1e−17	25 x 1	kelch−like family member 41 [Source:HGNC Symbol;Acc:169
20	4151	3.11	2e−16	1e−17	25 x 1	myoglobin [Source:HGNC Symbol;Acc:6915]

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	69.28	NULL	65 / 127	H.Tiss	WIRTH_Muscle
2	63.65	NULL	23 / 36	BP	muscle filament sliding
3	53	NULL	12 / 16	H.Tiss	WIRTH_Hippocampus
4	52.74	NULL	11 / 16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_F
5	49.06	NULL	23 / 44	MF	structural constituent of muscle
6	39.6	NULL	10 / 12	CC	myosin filament
7	35.65	NULL	12 / 37	CC	sarcomere
8	34.38	NULL	8 / 13	CC	muscle myosin complex
9	33.5	NULL	15 / 34	CC	myofibril
10	32.97	NULL	8 / 14	CC	contractile fiber
11	31.59	NULL	23 / 84	BP	muscle contraction
12	27.55	NULL	9 / 16	CC	M band
13	26.2	NULL	22 / 88	CC	Z disc
14	25.57	NULL	10 / 20	CC	I band
15	24.62	NULL	6 / 12	BP	skeletal muscle contraction
16	23.37	NULL	9 / 37	BP	cardiac muscle contraction
17	22.76	NULL	7 / 12	MF	titin binding
18	22.11	NULL	5 / 11	BP	cardiac muscle tissue morphogenesis
19	21.05	NULL	6 / 18	BP	regulation of muscle contraction
20	20.56	NULL	7 / 15	GSEA C2	REACTOME_STRIATED_MUSCLE_CONTRACTION
21	20.12	NULL	7 / 15	BP	striated muscle contraction
22	19.11	NULL	4 / 16	MF	microfilament motor activity
23	18.81	NULL	2 / 6	GSEA C2	BIOCARTA_HSP27_PATHWAY
24	18.15	NULL	5 / 11	CC	A band
25	18.09	NULL	8 / 42	CC	myosin complex
26	17.64	NULL	5 / 26	BP	ventricular cardiac muscle tissue morphogenesis
27	17.27	NULL	3 / 15	Cancer	BEN−PORATH_UP
28	16.66	NULL	25 / 297	MF	actin binding
29	16.2	NULL	4 / 14	BP	adult heart development
30	15.41	NULL	2 / 10	BP	heart contraction
31	14.77	NULL	3 / 13	CC	pseudopodium
32	13.51	NULL	2 / 10	BP	creatine metabolic process
33	13.3	NULL	7 / 21	BP	sarcomere organization
34	13.29	NULL	2 / 14	GSEA C2	BIOCARTA_UCALPAIN_PATHWAY
35	13.26	NULL	2 / 16	GSEA C2	SASSON_RESPONSE_TO_GONADOTROPHINS_DN
36	13.26	NULL	2 / 16	GSEA C2	SASSON_RESPONSE_TO_FORSKOLIN_DN
37	12.86	NULL	4 / 14	MF	tropomyosin binding
38	12.82	NULL	2 / 20	MF	myosin binding
39	12.78	NULL	1 / 9	GSEA C2	PENG_GLUCOSE_DEPRIVATION_UP
40	12.78	NULL	1 / 9	GSEA C2	PENG_GLUCOSE_DEPRIVATION_DN

GW_239

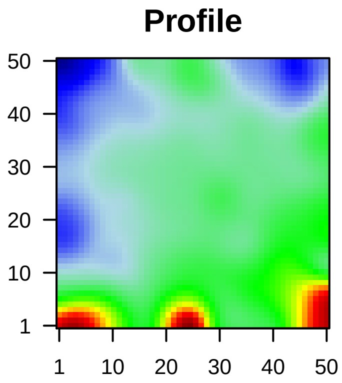
Local Summary

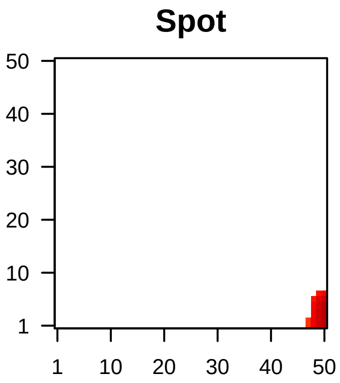
%DE = 0.96
metagenes = 22
genes = 373
genes in genesets = 371

genes with fdr < 0.1 = 341 (337 + / 4 −)
genes with fdr < 0.05 = 321 (320 + / 1 −)
genes with fdr < 0.01 = 297 (296 + / 1 −)

<r> metagenes = 0.95
<r> genes = 0.47

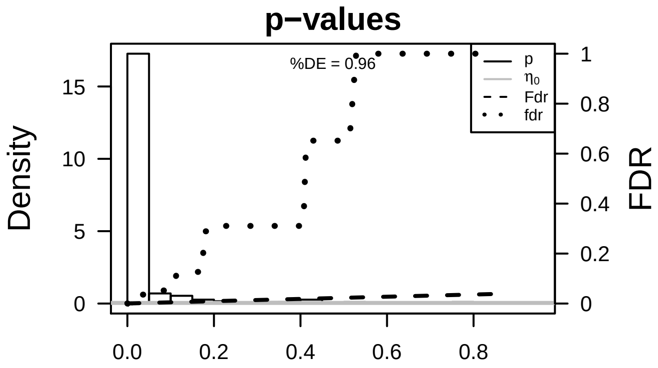
<FC> = 0.74
<shrinkage−t> = 25.94
<p−value> = 0
<fdr> = 0.2


Profile


Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	270	1.65	2e−16	1e−16	50 x 7	adenosine monophosphate deaminase 1 [Source:HGNC Sym
2	347	1.94	2e−16	1e−16	50 x 7	apolipoprotein D [Source:HGNC Symbol;Acc:612]
3	57172	2.17	2e−16	1e−16	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
4	6358	1.58	2e−16	1e−16	50 x 7	chemokine (C−C motif) ligand 14 [Source:HGNC Symbol;Acc
5	6363	1.97	2e−16	1e−16	50 x 1	chemokine (C−C motif) ligand 19 [Source:HGNC Symbol;Acc
6	1359	2	2e−16	1e−16	50 x 7	carboxypeptidase A3 (mast cell) [Source:HGNC Symbol;Acc:
7	1363	1.51	2e−16	1e−16	50 x 7	carboxypeptidase E [Source:HGNC Symbol;Acc:2303]
8	51755	1.91	2e−16	1e−16	49 x 1	cyclin−dependent kinase 12 [Source:HGNC Symbol;Acc:242
9	1511	1.47	2e−16	1e−16	50 x 7	cathepsin G [Source:HGNC Symbol;Acc:2532]
10	10563	2	2e−16	1e−16	50 x 1	chemokine (C−X−C motif) ligand 13 [Source:HGNC Symbol;
11	79901	1.44	2e−16	1e−16	50 x 7	cytochrome b reductase 1 [Source:HGNC Symbol;Acc:20797
12	2532	1.73	2e−16	1e−16	50 x 5	Duffy blood group, atypical chemokine receptor [Source:HGN
13	54855	1.97	2e−16	1e−16	49 x 1	family with sequence similarity 46, member C [Source:HGNC
14	51303	1.41	2e−16	1e−16	49 x 3	FK506 binding protein 11, 19 kDa [Source:HGNC Symbol;Ac
15	3488	1.94	2e−16	1e−16	50 x 7	insulin−like growth factor binding protein 5 [Source:HGNC Sy
16	3543	1.26	2e−16	1e−16	49 x 1	immunoglobulin lambda−like polypeptide 1 [Source:HGNC Sy
17	3394	1.57	2e−16	1e−16	50 x 1	interferon regulatory factor 8 [Source:HGNC Symbol;Acc:535
18	10365	1.41	2e−16	1e−16	50 x 3	Kruppel−like factor 2 [Source:HGNC Symbol;Acc:6347]
19	4239	1.57	2e−16	1e−16	50 x 6	microfibrillar−associated protein 4 [Source:HGNC Symbol;Ac
20	4256	1.5	2e−16	1e−16	50 x 6	matrix Gla protein [Source:HGNC Symbol;Acc:7060]


p−values

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	22.98	NULL	104 / 553	Cancer	Lembcke_Colonic Inflammation
2	20.02	NULL	5 / 9	GSEA C2	MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN
3	18.75	NULL	88 / 417	H.Tiss	WIRTH_Immune system
4	15.72	NULL	55 / 312	BP	immune response
5	14.61	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
6	14.38	NULL	7 / 8	Glio	Donson−migration tethering and rolling−associated with LTS in HG
7	13.28	NULL	6 / 15	GSEA C2	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_GRANULO
8	11.76	NULL	3 / 16	GSEA C2	GRAHAM_CML_QUIESCENT_VS_CML_DIVIDING_UP
9	11.73	NULL	12 / 15	CC	MHC class II protein complex
10	11.42	NULL	3 / 5	GSEA C2	WONG_ENDOMETRIAL_CANCER_LATE
11	11.21	NULL	6 / 16	Lymphoma	WRIGHT_ABC UP
12	11.13	NULL	6 / 15	Glio	Donson−chemokines/cytokines−associated with LTS in HGA
13	11.11	NULL	10 / 43	MF	chemokine activity
14	10.95	NULL	4 / 12	GSEA C2	BERTUCCI_INVASIVE_CARCINOMA_DUCTAL_VS_LOBULAR_D
15	10.94	NULL	3 / 9	GSEA C2	GUTIERREZ_WALDENSTROEMS_MACROGLOBULINEMIA_2
16	10.93	NULL	8 / 16	GSEA C2	SU_THYMUS
17	10.65	NULL	4 / 7	GSEA C2	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINE
18	10.62	NULL	29 / 162	CC	external side of plasma membrane
19	10.56	NULL	7 / 12	GSEA C2	ZHAN_MULTIPLE_MYELOMA_DN
20	10.41	NULL	2 / 6	GSEA C2	TRAYNOR_RETT_SYNDROM_DN
21	10.17	NULL	45 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
22	10.17	NULL	45 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
23	10.17	NULL	45 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
24	10.17	NULL	45 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
25	10.17	NULL	4 / 13	Cancer	GENTLES_modul17
26	9.95	NULL	19 / 74	BP	regulation of immune response
27	9.7	NULL	5 / 10	GSEA C2	BIOCARTA_LYM_PATHWAY
28	9.65	NULL	4 / 10	BP	germ cell migration
29	9.64	NULL	6 / 15	GSEA C2	FINAK_BREAST_CANCER_SDPP_SIGNATURE
30	9.43	NULL	4 / 13	BP	lymph node development
31	9.39	NULL	5 / 12	BP	dendritic cell chemotaxis
32	9.32	NULL	32 / 316	Cancer	SPANG_BCL6−index2
33	9.31	NULL	14 / 60	BP	T cell costimulation
34	9.24	NULL	4 / 13	BP	positive regulation of endocytosis
35	9.18	NULL	3 / 7	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
36	9.1	NULL	5 / 17	BP	positive regulation of neutrophil chemotaxis
37	9.06	NULL	5 / 12	GSEA C2	BIOCARTA_CTL_PATHWAY
38	9.05	NULL	6 / 13	GSEA C2	HAHTOLA_CTCL_PATHOGENESIS
39	9.02	NULL	4 / 16	GSEA C2	GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_UP
40	8.94	NULL	3 / 17	MF	metallocarboxypeptidase activity

GW_239

Local Summary

%DE = 0.95

metagenes = 23

genes = 327

genes in genesets = 318

genes with fdr < 0.1 = 270 (25 + / 245 −)

genes with fdr < 0.05 = 256 (22 + / 234 −)

genes with fdr < 0.01 = 209 (17 + / 192 −)

<r> metagenes = 0.95

<r> genes = 0.42

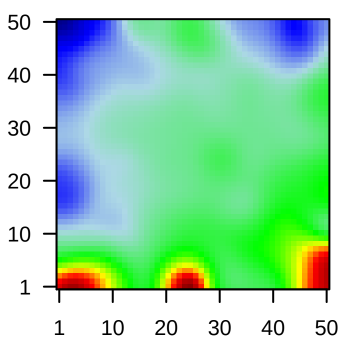
<FC> = −0.53

<shrinkage−t> = −18.53

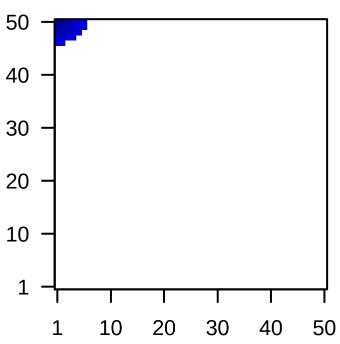
<p−value> = 0

<fdr> = 0.33

Profile



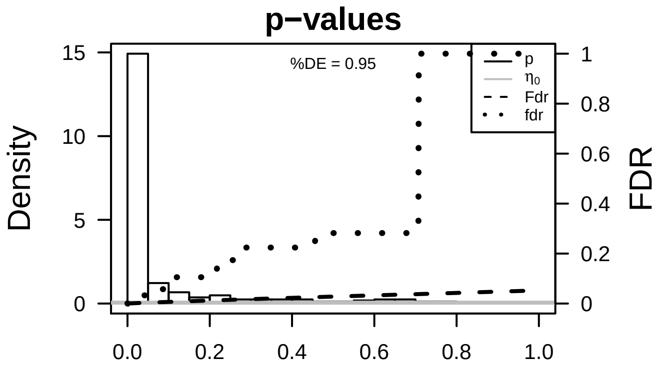
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	79852	−1.47	2e−16	1e−16	3 x 50	epoxide hydrolase 3 [Source:HGNC Symbol;Acc:23760]
2	131	−1.53	2e−16	1e−16	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
3	8644	2.67	2e−16	1e−16	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
4	218	1.57	2e−16	1e−16	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
5	387695	−1.48	2e−16	1e−16	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Sym
6	22802	−1.94	2e−16	1e−16	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
7	84518	−1.59	2e−16	1e−16	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
8	54544	−1.44	2e−16	1e−16	1 x 50	cysteine−rich C−terminal 1 [Source:HGNC Symbol;Acc:2987
9	49860	−2.16	2e−16	1e−16	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
10	1475	−1.91	2e−16	1e−16	1 x 50	cystatin A (stefin A) [Source:HGNC Symbol;Acc:2481]
11	1673	−2.4	2e−16	1e−16	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
12	1999	−1.65	2e−16	1e−16	5 x 50	E74−like factor 3 (ets domain transcription factor, epithelial−s
13	9982	−1.88	2e−16	1e−16	1 x 47	fibroblast growth factor binding protein 1 [Source:HGNC Sym
14	56169	−1.4	2e−16	1e−16	1 x 46	gasdermin C [Source:HGNC Symbol;Acc:7151]
15	26085	−1.46	2e−16	1e−16	1 x 50	kallikrein−related peptidase 13 [Source:HGNC Symbol;Acc:6
16	3934	−1.83	2e−16	1e−16	1 x 50	lipocalin 2 [Source:HGNC Symbol;Acc:6526]
17	4014	1.7	2e−16	1e−16	2 x 48	loricrin [Source:HGNC Symbol;Acc:6663]
18	10874	−1.37	2e−16	1e−16	4 x 50	neuromedin U [Source:HGNC Symbol;Acc:7859]
19	5307	−1.42	2e−16	1e−16	3 x 50	paired−like homeodomain 1 [Source:HGNC Symbol;Acc:900
20	6283	−2.01	2e−16	1e−16	1 x 49	S100 calcium binding protein A12 [Source:HGNC Symbol;Ac

p−values



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−53.91	NULL	97 / 135	H.Tiss	WIRTH_Mucosa
2	−31.35	NULL	19 / 21	CC	cornified envelope
3	−26	NULL	107 / 572	Disease	GUDJ_psoriasis up
4	−22.03	NULL	19 / 42	BP	keratinization
5	−21.54	NULL	27 / 76	BP	epidermis development
6	−20.86	NULL	12 / 19	BP	peptide cross−linking
7	−20.02	NULL	25 / 53	BP	keratinocyte differentiation
8	−15.45	NULL	5 / 10	MF	RAGE receptor binding
9	−12.84	NULL	6 / 13	BP	negative regulation of peptidase activity
10	−12.82	NULL	5 / 16	GSEA C2	LEE_LIVER_CANCER_MYC_TGFA_UP
11	−12.48	NULL	7 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
12	−12.35	NULL	7 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
13	−12.01	NULL	10 / 15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
14	−11.84	NULL	12 / 52	BP	negative regulation of endopeptidase activity
15	−11.82	NULL	8 / 15	GSEA C2	LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
16	−11.75	NULL	14 / 79	MF	serine−type endopeptidase inhibitor activity
17	−11.64	NULL	6 / 13	H.Tiss	WIRTH_Tonsil
18	−11.27	NULL	7 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
19	−11.2	NULL	8 / 29	BP	regulation of proteolysis
20	−10.79	NULL	3 / 16	GSEA C2	CHEOK_RESPONSE_TO_MERCAPTOPURINE_AND_LD_MTX_
21	−10.75	NULL	7 / 16	GSEA C2	COLDREN_GEFITINIB_RESISTANCE_DN
22	−10.65	NULL	7 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
23	−10.48	NULL	7 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
24	−10.37	NULL	5 / 15	GSEA C2	CHANG_IMMORTALIZED_BY_HPV31_DN
25	−10.3	NULL	66 / 1182	CC	extracellular region
26	−10.25	NULL	4 / 15	GSEA C2	LEE_LIVER_CANCER_MYC_E2F1_UP
27	−10.18	NULL	3 / 10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
28	−10.01	NULL	3 / 16	GSEA C2	LEE_LIVER_CANCER_ACOX1_UP
29	−9.64	NULL	6 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
30	−9.63	NULL	3 / 14	GSEA C2	ZHAN_MULTIPLE_MYELOMA_MF_UP
31	−9.61	NULL	9 / 38	BP	epithelial cell differentiation
32	−9.34	NULL	5 / 15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
33	−9.17	NULL	3 / 13	GSEA C2	WONG_ENDMETRIUM_CANCER_UP
34	−8.31	NULL	24 / 186	MF	structural molecule activity
35	−8.21	NULL	3 / 15	GSEA C2	LEE_LIVER_CANCER_MYC_UP
36	−8.14	NULL	15 / 122	MF	serine−type endopeptidase activity
37	−7.9	NULL	4 / 22	MF	cysteine−type endopeptidase inhibitor activity
38	−7.81	NULL	8 / 73	BP	defense response to bacterium
39	−7.81	NULL	4 / 24	TF Tissue	VAQUERIZAS_Trachea
40	−7.71	NULL	5 / 23	MF	peptidase inhibitor activity