GW_047

Global Summary

%DE = 0.15

genes with fdr < 0.2 = 1663 (1031 + / 632 −)

genes with fdr < 0.1 = 1370 (897 + / 473 −)

genes with fdr < 0.05 = 1131 (785 + / 346 −)

genes with fdr < 0.01 = 843 (626 + / 217 −)

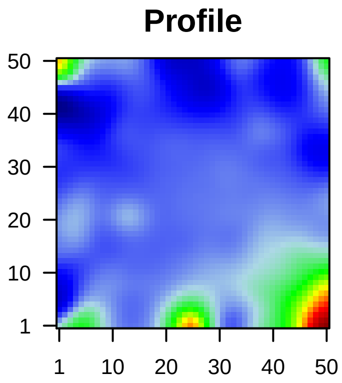
genes in genesets = 16332

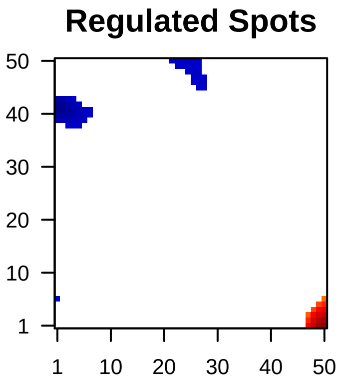
<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.09

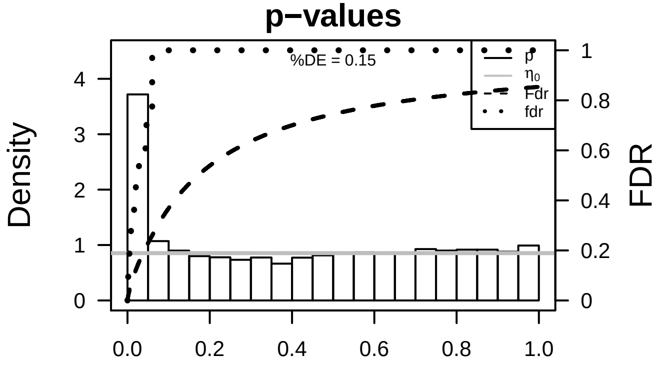
<fdr> = 0.85





Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	154664	1.19	2e−16	2e−14	50 x 50	ATP−binding cassette, sub−family A (ABC1), member 13 [Sou
2	58	3.81	2e−16	2e−14	25 x 1	actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
3	70	2.28	2e−16	2e−14	25 x 1	actin, alpha, cardiac muscle 1 [Source:HGNC Symbol;Acc:14
4	57016	1.75	2e−16	2e−14	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
5	441282	1.22	2e−16	2e−14	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC Sy
6	8644	1.31	2e−16	2e−14	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
7	1109	1.45	2e−16	2e−14	13 x 50	aldo−keto reductase family 1, member C4 [Source:HGNC Sy
8	216	1.6	2e−16	2e−14	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGN
9	218	1.14	2e−16	2e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
10	144193	1.23	2e−16	2e−14	15 x 50	amidohydrolase domain containing 1 [Source:HGNC Symbol;
11	187	1.3	2e−16	2e−14	5 x 1	apelin receptor [Source:HGNC Symbol;Acc:339]
12	347	1.43	2e−16	2e−14	50 x 7	apolipoprotein D [Source:HGNC Symbol;Acc:612]
13	151516	1.5	2e−16	2e−14	1 x 46	aspartic peptidase, retroviral−like 1 [Source:HGNC Symbol;A
14	479	1.37	2e−16	2e−14	7 x 50	ATPase, H+/K+ transporting, nongastric, alpha polypeptide [S
15	29113	3.16	2e−16	2e−14	2 x 47	chromosome 6 open reading frame 15 [Source:HGNC Symbo
16	760	−1.16	2e−16	2e−14	1 x 44	carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
17	810	1.09	2e−16	2e−14	1 x 50	calmodulin−like 3 [Source:HGNC Symbol;Acc:1452]
18	51806	2.3	2e−16	2e−14	4 x 50	calmodulin−like 5 [Source:HGNC Symbol;Acc:18180]
19	57172	1.37	2e−16	2e−14	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
20	845	1.22	2e−16	2e−14	25 x 1	calsequestrin 2 (cardiac muscle) [Source:HGNC Symbol;Acc:



Global Geneset Analysis

Rank	GSZ	p−value	#all		Geneset
Overexpressed					
1	18.6	NULL	42	BP	keratinization
2	18.51	NULL	36	BP	muscle filament sliding
3	17.05	NULL	553	Cancer	Lembcke_Colonic Inflammation
4	16.59	NULL	127	H.Tiss	WIRTH_Muscle
5	15.09	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_F
6	14.66	NULL	21	CC	cornified envelope
7	14.07	NULL	16	H.Tiss	WIRTH_Hippocampus
8	13.72	NULL	44	MF	structural constituent of muscle
9	13.16	NULL	12	CC	myosin filament
10	11.84	NULL	312	BP	immune response
11	11.53	NULL	9	GSEA C2	MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN
12	11.47	NULL	53	BP	keratinocyte differentiation
13	11.33	NULL	13	CC	muscle myosin complex
14	10.6	NULL	417	H.Tiss	WIRTH_Immune system
15	10.51	NULL	15	CC	MHC class II protein complex
16	10.14	NULL	19	BP	peptide cross−linking
17	10.11	NULL	37	CC	sarcomere
18	9.92	NULL	84	BP	muscle contraction
19	9.74	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_D
20	8.47	NULL	14	CC	contractile fiber
Underexpressed					
1	−8.35	NULL	4640	CC	nucleus
2	−8.14	NULL	488	miRNA target−starBase	hsa−miR−16
3	−7.93	NULL	313	miRNA target−starBase	hsa−miR−559
4	−7.89	NULL	436	miRNA target−starBase	hsa−miR−548n
5	−7.8	NULL	512	miRNA target−starBase	hsa−miR−15a
6	−7.6	NULL	262	miRNA target−starBase	hsa−miR−548l
7	−7.6	NULL	336	miRNA target−starBase	hsa−miR−548d−5p
8	−7.54	NULL	479	miRNA target−starBase	hsa−miR−15b
9	−7.54	NULL	312	miRNA target−starBase	hsa−miR−32
10	−7.52	NULL	495	miRNA target−starBase	hsa−miR−103
11	−7.49	NULL	12	BP	hemidesmosome assembly
12	−7.39	NULL	494	miRNA target−starBase	hsa−miR−107
13	−7.34	NULL	319	miRNA target−starBase	hsa−miR−367
14	−7.23	NULL	464	miRNA target−starBase	hsa−miR−195
15	−7.21	NULL	336	miRNA target−starBase	hsa−miR−548b−5p
16	−7.11	NULL	414	miRNA target−starBase	hsa−miR−497
17	−7.1	NULL	302	miRNA target−starBase	hsa−miR−548i
18	−7.02	NULL	321	miRNA target−starBase	hsa−miR−548a−5p
19	−6.91	NULL	438	miRNA target−starBase	hsa−miR−424
20	−6.82	NULL	293	miRNA target−starBase	hsa−miR−186

GW_047

Local Summary

%DE = 0.94

metagenes = 18

genes = 307

genes in genesets = 305

genes with fdr < 0.1 = 252 (245 + / 7 −)

genes with fdr < 0.05 = 240 (234 + / 6 −)

genes with fdr < 0.01 = 229 (223 + / 6 −)

<r> metagenes = 0.97

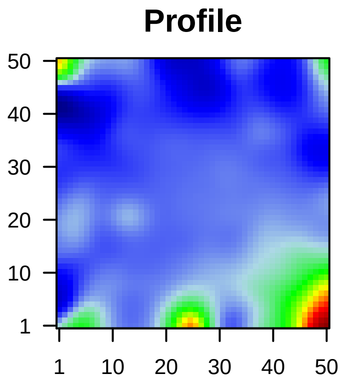
<r> genes = 0.53

<FC> = 0.59

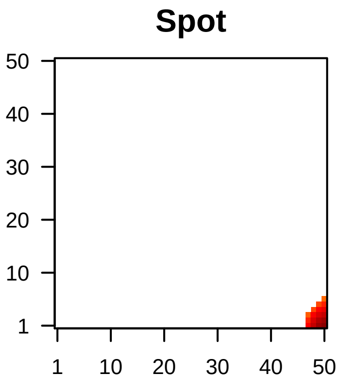
<shrinkage−t> = 20.63

<p−value> = 0

<fdr> = 0.24



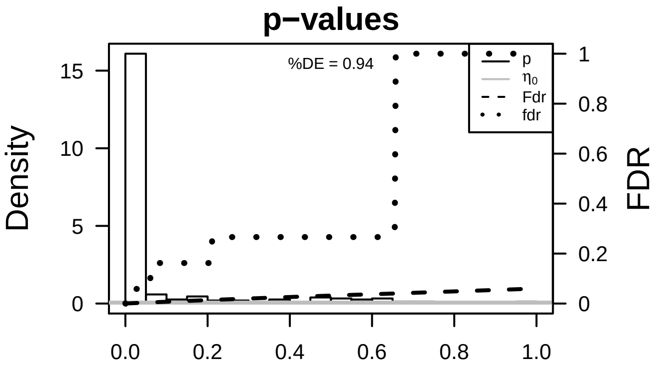
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	57172	1.37	2e−16	1e−16	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
2	6363	2.66	2e−16	1e−16	50 x 1	chemokine (C−C motif) ligand 19 [Source:HGNC Symbol;Acc
3	6366	1.25	2e−16	1e−16	50 x 2	chemokine (C−C motif) ligand 21 [Source:HGNC Symbol;Acc
4	1236	1.5	2e−16	1e−16	50 x 1	chemokine (C−C motif) receptor 7 [Source:HGNC Symbol;Ac
5	930	1.85	2e−16	1e−16	49 x 1	CD19 molecule [Source:HGNC Symbol;Acc:1633]
6	939	1.13	2e−16	1e−16	49 x 1	CD27 molecule [Source:HGNC Symbol;Acc:11922]
7	962	1.49	2e−16	1e−16	50 x 1	CD48 molecule [Source:HGNC Symbol;Acc:1683]
8	1043	1.26	2e−16	1e−16	50 x 1	CD52 molecule [Source:HGNC Symbol;Acc:1804]
9	974	1.2	2e−16	1e−16	48 x 1	CD79b molecule, immunoglobulin−associated beta [Source:H
10	11151	1.15	2e−16	1e−16	50 x 1	coronin, actin binding protein, 1A [Source:HGNC Symbol;Acc
11	51755	1.22	2e−16	1e−16	49 x 1	cyclin−dependent kinase 12 [Source:HGNC Symbol;Acc:242
12	10563	2.09	2e−16	1e−16	50 x 1	chemokine (C−X−C motif) ligand 13 [Source:HGNC Symbol;
13	2532	2.09	2e−16	1e−16	50 x 5	Duffy blood group, atypical chemokine receptor [Source:HGN
14	9214	1.4	2e−16	1e−16	49 x 1	Fas apoptotic inhibitory molecule 3 [Source:HGNC Symbol;A
15	54855	1.62	2e−16	1e−16	49 x 1	family with sequence similarity 46, member C [Source:HGNC
16	84824	1.55	2e−16	1e−16	49 x 1	Fc receptor−like A [Source:HGNC Symbol;Acc:18504]
17	9535	1.2	2e−16	1e−16	50 x 1	glia maturation factor, gamma [Source:HGNC Symbol;Acc:43
18	3385	1.25	2e−16	1e−16	50 x 1	intercellular adhesion molecule 3 [Source:HGNC Symbol;Acc
19	3512	1.76	2e−16	1e−16	50 x 1	immunoglobulin J polypeptide, linker protein for immunoglobu
20	3543	1.5	2e−16	1e−16	49 x 1	immunoglobulin lambda−like polypeptide 1 [Source:HGNC Sy



p−values

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	28.98	NULL	4 / 9	GSEA C2	MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN
2	27.08	NULL	89 / 417	H.Tiss	WIRTH_Immune system
3	25.84	NULL	99 / 553	Cancer	Lembcke_Colonic Inflammation
4	20.11	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
5	18.39	NULL	6 / 8	Glio	Donson−migration tethering and rolling−associated with LTS in HG
6	17.28	NULL	5 / 12	BP	dendritic cell chemotaxis
7	16.54	NULL	3 / 7	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
8	16.45	NULL	12 / 15	CC	MHC class II protein complex
9	16.42	NULL	5 / 17	BP	positive regulation of neutrophil chemotaxis
10	16.04	NULL	51 / 312	BP	immune response
11	15.18	NULL	6 / 15	GSEA C2	FINAK_BREAST_CANCER_SDPP_SIGNATURE
12	13.79	NULL	5 / 10	GSEA C2	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_
13	13.66	NULL	6 / 11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
14	13.66	NULL	3 / 5	GSEA C2	WONG_ENDOMETRIAL_CANCER_LATE
15	13.55	NULL	5 / 15	Glio	Donson−chemokines/cytokines−associated with LTS in HGA
16	13.31	NULL	18 / 74	BP	regulation of immune response
17	13.04	NULL	7 / 12	GSEA C2	ZHAN_MULTIPLE_MYELOMA_DN
18	12.99	NULL	2 / 10	BP	positive regulation of chemotaxis
19	12.8	NULL	26 / 162	CC	external side of plasma membrane
20	12.7	NULL	4 / 13	BP	lymph node development
21	12.67	NULL	45 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
22	12.67	NULL	45 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
23	12.67	NULL	45 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
24	12.67	NULL	45 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
25	12.63	NULL	5 / 10	GSEA C2	LEE_DIFFERENTIATING_T_LYMPHOCYTE
26	12.47	NULL	3 / 11	GSEA C2	TARTE_PLASMA_CELL_VS_B_LYMPHOCYTE_DN
27	12.33	NULL	5 / 11	GSEA C2	BIOCARTA_THELPER_PATHWAY
28	12.32	NULL	3 / 16	GSEA C2	GRAHAM_CML_QUIESCENT_VS_CML_DIVIDING_UP
29	12.17	NULL	14 / 60	BP	T cell costimulation
30	12.1	NULL	8 / 43	MF	chemokine activity
31	12.08	NULL	7 / 28	BP	B cell receptor signaling pathway
32	11.88	NULL	3 / 16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_D
33	11.87	NULL	5 / 12	GSEA C2	BIOCARTA_CTL_PATHWAY
34	11.7	NULL	2 / 12	BP	positive regulation of receptor−mediated endocytosis
35	11.64	NULL	4 / 27	BP	release of sequestered calcium ion into cytosol
36	11.59	NULL	3 / 22	BP	positive regulation of phosphatidylinositol 3−kinase activity
37	11.27	NULL	23 / 204	BP	cell surface receptor signaling pathway
38	11.07	NULL	4 / 13	BP	positive regulation of endocytosis
39	10.99	NULL	6 / 13	Cancer	GENTLES_modul18
40	10.91	NULL	5 / 11	BP	positive regulation of B cell differentiation

GW_047

Local Summary

%DE = 0.86

metagenes = 1

genes = 27

genes in genesets = 27

genes with fdr < 0.1 = 19 (2 + / 17 −)

genes with fdr < 0.05 = 14 (1 + / 13 −)

genes with fdr < 0.01 = 9 (1 + / 8 −)

<r> metagenes = NA

<r> genes = 0.38

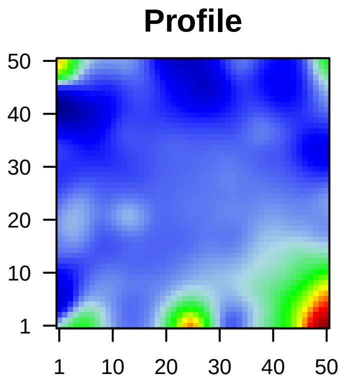
<FC> = −0.27

<shrinkage−t> = −9.51

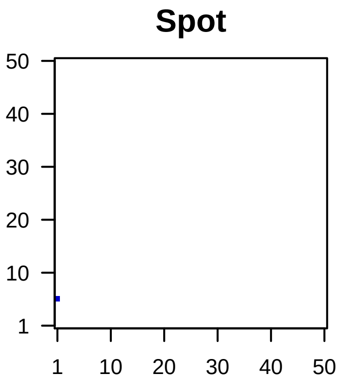
<p−value> = 0

<fdr> = 0.53

Profile



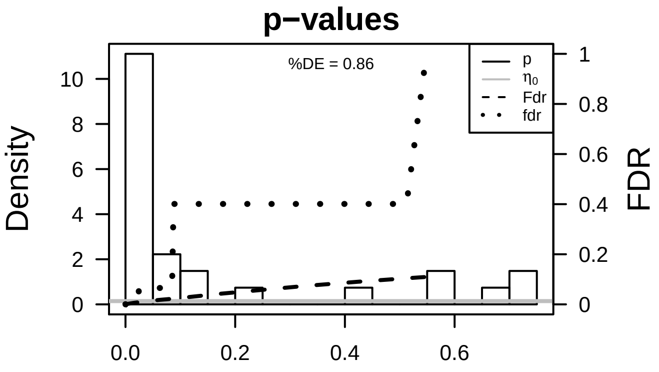
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	768	−1.04	2e−14	2e−07	1 x 6	carbonic anhydrase IX [Source:HGNC Symbol;Acc:1383]
2	24147	−0.74	6e−08	8e−05	1 x 6	four jointed box 1 (Drosophila) [Source:HGNC Symbol;Acc:17
3	8614	−0.56	3e−05	8e−05	1 x 6	stanniocalcin 2 [Source:HGNC Symbol;Acc:11374]
4	1594	−0.56	4e−05	2e−04	1 x 6	cytochrome P450, family 27, subfamily B, polypeptide 1 [Sour
5	4000	−0.52	1e−04	2e−04	1 x 6	lamin A/C [Source:HGNC Symbol;Acc:6636]
6	351	−0.51	2e−04	2e−04	1 x 6	amyloid beta (A4) precursor protein [Source:HGNC Symbol;A
7	114793	−0.5	2e−04	1e−03	1 x 6	formin−like 2 [Source:HGNC Symbol;Acc:18267]
8	595	0.43	6e−04	1e−03	1 x 6	cyclin D1 [Source:HGNC Symbol;Acc:1582]
9	11014	−0.46	7e−04	8e−03	1 x 6	KDEL (Lys−Asp−Glu−Leu) endoplasmic reticulum protein rete
10	4651	−0.4	3e−03	1e−02	1 x 6	myosin X [Source:HGNC Symbol;Acc:7593]
11	3675	−0.37	6e−03	3e−02	1 x 6	integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA−3 r
12	1021	−0.32	2e−02	3e−02	1 x 6	cyclin−dependent kinase 6 [Source:HGNC Symbol;Acc:1777]
13	4627	−0.28	2e−02	3e−02	1 x 6	myosin, heavy chain 9, non−muscle [Source:HGNC Symbol;A
14	6624	−0.27	3e−02	3e−02	1 x 6	fascin homolog 1, actin−bundling protein (Strongylocentrotus
15	5829	−0.29	3e−02	7e−02	1 x 6	paxillin [Source:HGNC Symbol;Acc:9718]
16	84230	−0.26	6e−02	7e−02	1 x 6	leucine rich repeat containing 8 family, member C [Source:HG
17	3486	0.24	8e−02	7e−02	1 x 6	insulin−like growth factor binding protein 3 [Source:HGNC Sy
18	5228	−0.23	8e−02	7e−02	1 x 6	placental growth factor [Source:HGNC Symbol;Acc:8893]
19	57048	−0.21	1e−01	7e−02	1 x 6	TMEM256−PLSCR3 readthrough (NMD candidate) [Source:H
20	51776	−0.21	1e−01	4e−01	1 x 6	Mitogen−activated protein kinase kinase kinase MLT [Source

p−values



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−28.26	NULL	1 / 3	GSEA C2	VICENT_METASTASIS_DN
2	−26.68	NULL	1 / 5	GSEA C2	CHEN_HOXA5_TARGETS_6HR_DN
3	−22.17	NULL	2 / 12	miRNA target starBase	hsa−miR−1249
4	−21.99	NULL	2 / 13	BP	response to vitamin D
5	−21.79	NULL	1 / 4	miRNA target	miR−106b
6	−21	NULL	3 / 13	GSEA C2	MAHADEVAN_GIST_MORPHOLOGICAL_SWITCH
7	−19.44	NULL	2 / 16	BP	decidualization
8	−19.39	NULL	1 / 2	miRNA target	miR−124a
9	−18.76	NULL	2 / 17	BP	calcium ion homeostasis
10	−18.53	NULL	1 / 5	miRNA 3UTR	TCGA−213
11	−18.09	NULL	1 / 9	GSEA C2	KANG_GIST_WITH_PDGFRA_UP
12	−18.09	NULL	1 / 9	miRNA 3UTR	GTAT−127
13	−18.04	NULL	1 / 16	CC	microvillus membrane
14	−17.75	NULL	1 / 6	GSEA C2	REACTOME_STEROID_HORMONES
15	−17.4	NULL	1 / 17	BP	morphogenesis of an epithelium
16	−15.47	NULL	2 / 11	MF	actin−dependent ATPase activity
17	−15.15	NULL	3 / 79	BP	cellular response to hypoxia
18	−14.98	NULL	1 / 22	BP	bicarbonate transport
19	−14.98	NULL	1 / 22	BP	response to testosterone
20	−14.89	NULL	1 / 8	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_LIVER_DN
21	−14.25	NULL	1 / 24	BP	regulation of transcription from RNA polymerase II promoter in resp
22	−13.92	NULL	1 / 25	BP	one−carbon metabolic process
23	−13.8	NULL	2 / 27	miRNA target starBase	hsa−miR−483−3p
24	−13.41	NULL	1 / 4	miRNA target	let−7c
25	−13.41	NULL	1 / 4	miRNA target	let−7g
26	−13.41	NULL	1 / 4	miRNA target	miR−34b
27	−12.76	NULL	1 / 10	BP	positive regulation of keratinocyte differentiation
28	−12.19	NULL	1 / 11	BP	negative regulation of multicellular organism growth
29	−11.98	NULL	1 / 10	BP	mitotic nuclear envelope reassembly
30	−11.75	NULL	1 / 10	BP	ionotropic glutamate receptor signaling pathway
31	−11.75	NULL	1 / 10	BP	positive regulation of peptidase activity
32	−11.75	NULL	1 / 10	GSEA C2	BIOCARTA_P35ALZHEIMERS_PATHWAY
33	−11.4	NULL	1 / 12	BP	regulation of bone mineralization
34	−11.29	NULL	1 / 11	BP	nuclear envelope organization
35	−11.29	NULL	1 / 11	GSEA C2	MOREAUX_B_LYMPHOCYTE_MATURATION_BY_TACI_UP
36	−11.29	NULL	1 / 11	GSEA C2	BIOCARTA_HIVNEF_PATHWAY
37	−11.07	NULL	1 / 11	BP	cellular copper ion homeostasis
38	−11.07	NULL	1 / 11	GSEA C2	AKL_HTLV1_INFECTION_UP
39	−11.07	NULL	1 / 11	GSEA C2	PARK_APL_PATHOGENESIS_DN
40	−11.07	NULL	1 / 11	GSEA C2	BIOCARTA_PLATELETAPP_PATHWAY

GW_047

Local Summary

%DE = 0.68

metagenes = 32

genes = 297

genes in genesets = 291

genes with fdr < 0.1 = 132 (7 + / 125 −)

genes with fdr < 0.05 = 118 (7 + / 111 −)

genes with fdr < 0.01 = 71 (3 + / 68 −)

<r> metagenes = 0.97

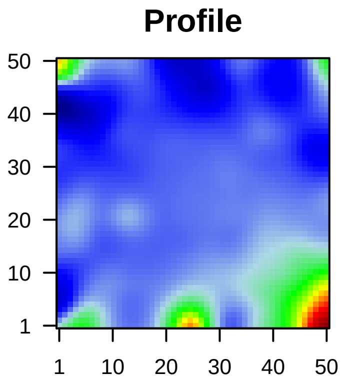
<r> genes = 0.31

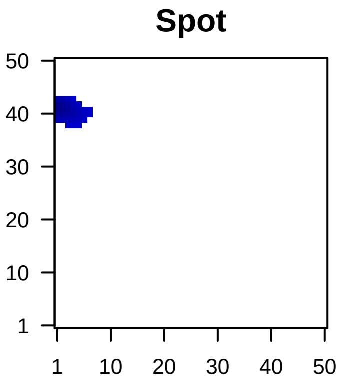
<FC> = −0.26

<shrinkage−t> = −9.19

<p−value> = 0.01

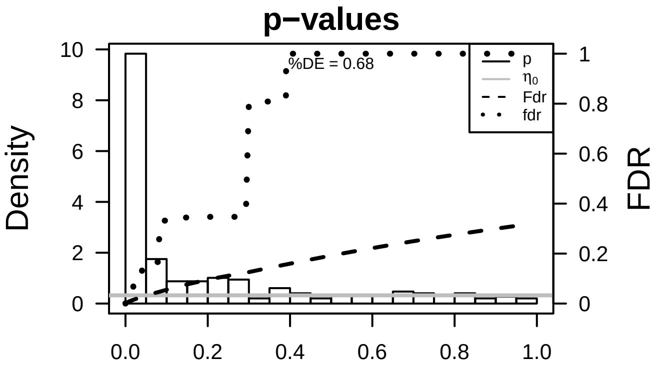
<fdr> = 0.59





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	1308	−2.02	2e−16	3e−15	1 x 43	collagen, type XVII, alpha 1 [Source:HGNC Symbol;Acc:2194
2	2152	−1.23	2e−16	3e−15	1 x 43	coagulation factor III (thromboplastin, tissue factor) [Source:H
3	55214	−1.36	2e−16	3e−15	1 x 42	leprecan−like 1 [Source:HGNC Symbol;Acc:19317]
4	10397	−1.28	2e−16	3e−15	1 x 42	N−myc downstream regulated 1 [Source:HGNC Symbol;Acc:
5	5744	−1.2	2e−16	3e−15	1 x 43	parathyroid hormone−like hormone [Source:HGNC Symbol;A
6	6513	−1.18	2e−16	3e−15	1 x 43	solute carrier family 2 (facilitated glucose transporter), membe
7	780854	−1.15	2e−16	3e−15	2 x 39	small nucleolar RNA, C/D box 3D [Source:HGNC Symbol;Acc
8	306	−1.07	2e−15	4e−11	4 x 42	annexin A3 [Source:HGNC Symbol;Acc:541]
9	1001	−0.98	4e−13	2e−10	1 x 43	cadherin 3, type 1, P−cadherin (placental) [Source:HGNC Sy
10	3552	−0.95	2e−12	4e−09	1 x 43	interleukin 1, alpha [Source:HGNC Symbol;Acc:5991]
11	26499	−0.89	6e−11	4e−09	1 x 42	pleckstrin 2 [Source:HGNC Symbol;Acc:19238]
12	664	−0.88	9e−11	2e−08	2 x 43	BCL2/adenovirus E1B 19kDa interacting protein 3 [Source:H
13	4015	−0.85	3e−10	6e−08	1 x 41	lysyl oxidase [Source:HGNC Symbol;Acc:6664]
14	148304	−0.83	1e−09	1e−06	1 x 41	chromosome 1 open reading frame 74 [Source:HGNC Symbo
15	135398	−0.76	2e−08	1e−06	1 x 40	chromosome 6 open reading frame 141 [Source:HGNC Symb
16	84632	−0.74	5e−08	1e−06	1 x 41	actin filament associated protein 1−like 2 [Source:HGNC Sym
17	25819	−0.73	6e−08	1e−06	1 x 41	CCR4 carbon catabolite repression 4−like (S. cerevisiae) [Sou
18	205	−0.73	7e−08	1e−06	2 x 42	adenylate kinase 4 [Source:HGNC Symbol;Acc:363]
19	7162	−0.73	8e−08	1e−06	1 x 42	trophoblast glycoprotein [Source:HGNC Symbol;Acc:12004]
20	55236	−0.73	9e−08	1e−05	4 x 41	ubiquitin−like modifier activating enzyme 6 [Source:HGNC Sy



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−17.33	NULL	3 / 12	BP	hemidesmosome assembly
2	−14.54	NULL	3 / 15	GSEA C2	PRAMOONJAGO_SOX4_TARGETS_UP
3	−14.03	NULL	3 / 16	GSEA C2	ELVIDGE_HIF1A_TARGETS_DN
4	−13.58	NULL	3 / 16	GSEA C2	ELVIDGE_HIF1A_AND_HIF2A_TARGETS_DN
5	−13.27	NULL	3 / 16	GSEA C2	LEONARD_HYPOXIA
6	−12.23	NULL	2 / 16	GSEA C2	UZONYI_RESPONSE_TO_LEUKOTRIENE_AND_THROMBIN
7	−12.14	NULL	1 / 5	GSEA C2	KYNG_ENVIRONMENTAL_STRESS_RESPONSE_NOT_BY_4NQ
8	−11.02	NULL	2 / 16	GSEA C2	WATTEL_AUTONOMOUS_THYROID_ADENOMA_UP
9	−10.97	NULL	1 / 6	GSEA C2	KYNG_ENVIRONMENTAL_STRESS_RESPONSE_NOT_BY_UV_
10	−10.66	NULL	4 / 32	CC	cell−cell adherens junction
11	−10.66	NULL	3 / 9	GSEA C2	WANG_RESPONSE_TO_PACLITAXEL_VIA_MAPK8_UP
12	−10.52	NULL	2 / 14	GSEA C2	MAINA_VHL_TARGETS_DN
13	−10.24	NULL	1 / 5	GSEA C2	RODRIGUES_DCC_TARGETS_UP
14	−9.77	NULL	2 / 16	GSEA C2	HARRIS_HYPOXIA
15	−9.7	NULL	1 / 6	GSEA C2	MAINA_HYPOXIA_VHL_TARGETS_UP
16	−9.37	NULL	2 / 16	GSEA C2	ELVIDGE_HYPOXIA_BY_DMOG_UP
17	−9.37	NULL	2 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
18	−9.35	NULL	1 / 4	GSEA C2	BUDHU_LIVER_CANCER_METASTASIS_DN
19	−9.3	NULL	6 / 83	CC	basement membrane
20	−9.22	NULL	3 / 15	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_3
21	−9.21	NULL	3 / 15	GSEA C2	BROWNE_HCMV_INFECTION_2HR_DN
22	−8.9	NULL	3 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_4
23	−8.8	NULL	2 / 8	GSEA C2	MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_UP
24	−8.75	NULL	3 / 13	GSEA C2	WANG_METHYLATED_IN_BREAST_CANCER
25	−8.75	NULL	1 / 9	GSEA C2	KYNG_ENVIRONMENTAL_STRESS_RESPONSE_NOT_BY_GAM
26	−8.75	NULL	1 / 9	GSEA C2	KYNG_DNA_DAMAGE_UP
27	−8.75	NULL	1 / 9	GSEA C2	KYNG_ENVIRONMENTAL_STRESS_RESPONSE_UP
28	−8.65	NULL	1 / 7	GSEA C2	BEGUM_TARGETS_OF_PAX3_FOXO1_FUSION_AND_PAX3
29	−8.63	NULL	2 / 8	GSEA C2	REACTOME_FACILITATIVE_NA_INDEPENDENT_GLUCOSE_TR
30	−8.57	NULL	8 / 76	BP	epidermis development
31	−8.44	NULL	4 / 22	MF	cadherin binding
32	−8.44	NULL	2 / 11	GSEA C2	BIOCARTA_VITCB_PATHWAY
33	−8.33	NULL	2 / 13	H.Tiss	WIRTH_Thymus
34	−8.25	NULL	1 / 10	GSEA C2	RUGO_ENVIRONMENTAL_STRESS_RESPONSE_UP
35	−8.25	NULL	1 / 10	GSEA C2	KYNG_ENVIRONMENTAL_STRESS_RESPONSE_NOT_BY_GAM
36	−8.25	NULL	1 / 10	GSEA C2	PARK_TRETINOIN_RESPONSE
37	−8.18	NULL	2 / 15	BP	response to osmotic stress
38	−7.9	NULL	2 / 5	GSEA C2	FERRARI_RESPONSE_TO_FENRETINIDE_DN
39	−7.84	NULL	2 / 15	GSEA C2	NAGASHIMA_NRG1_SIGNALING_DN
40	−7.82	NULL	1 / 11	BP	response to metal ion

GW_047

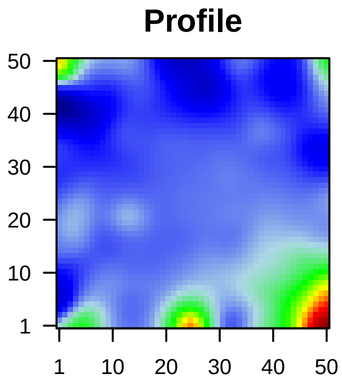
Local Summary

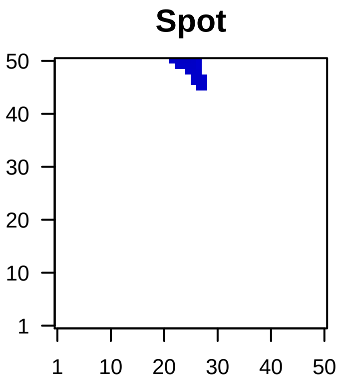
%DE = 0.64
metagenes = 22
genes = 321
genes in genesets = 318

genes with fdr < 0.1 = 128 (8 + / 120 −)
genes with fdr < 0.05 = 71 (2 + / 69 −)
genes with fdr < 0.01 = 26 (1 + / 25 −)

<r> metagenes = 0.94
<r> genes = 0.25

<FC> = −0.2
<shrinkage−t> = −6.96
<p−value> = 0.04
<fdr> = 0.72





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	8553	−0.77	6e−10	3e−08	22 x 50	basic helix−loop−helix family, member e40 [Source:HGNC Sy
2	5366	−0.84	6e−10	6e−08	22 x 50	phorbol−12−myristate−13−acetate−induced protein 1 [Source
3	2354	−0.81	2e−09	6e−08	22 x 50	FBJ murine osteosarcoma viral oncogene homolog B [Source
4	6675	−0.82	2e−09	1e−07	28 x 45	UDP−N−acteylglucosamine pyrophosphorylase 1 [Source:HG
5	23645	−0.81	3e−09	1e−07	22 x 50	protein phosphatase 1, regulatory subunit 15A [Source:HGNC
6	57404	0.8	4e−09	5e−07	28 x 47	cytochrome P450, family 20, subfamily A, polypeptide 1 [Sour
7	3725	−0.78	8e−09	3e−05	22 x 50	jun proto−oncogene [Source:HGNC Symbol;Acc:6204]
8	25998	−0.68	5e−07	3e−05	28 x 45	inhibitor of Bruton agammaglobulinemia tyrosine kinase [Sour
9	100008589	−0.67	7e−07	3e−05	23 x 50	RNA, 28S ribosomal 5 [Source:HGNC Symbol;Acc:37659]
10	150094	−0.67	9e−07	2e−04	22 x 50	salt−inducible kinase 1 [Source:HGNC Symbol;Acc:11142]
11	56929	−0.62	4e−06	2e−04	22 x 50	fem−1 homolog c (C. elegans) [Source:HGNC Symbol;Acc:16
12	5782	−0.62	5e−06	6e−04	25 x 50	protein tyrosine phosphatase, non−receptor type 12 [Source:I
13	467	−0.59	1e−05	6e−04	22 x 50	activating transcription factor 3 [Source:HGNC Symbol;Acc:78
14	4609	−0.57	2e−05	6e−04	22 x 50	v−myc avian myelocytomatosis viral oncogene homolog [Sou
15	1958	−0.57	2e−05	6e−04	22 x 50	early growth response 1 [Source:HGNC Symbol;Acc:3238]
16	10492	−0.57	3e−05	1e−03	26 x 50	synaptotagmin binding, cytoplasmic RNA interacting protein [
17	1316	−0.55	5e−05	1e−03	22 x 50	Kruppel−like factor 6 [Source:HGNC Symbol;Acc:2235]
18	1647	−0.55	6e−05	1e−03	22 x 50	growth arrest and DNA−damage−inducible, alpha [Source:HG
19	58487	−0.54	6e−05	2e−03	26 x 48	CREB/ATF bZIP transcription factor [Source:HGNC Symbol;A
20	51014	−0.53	1e−04	2e−03	26 x 50	transmembrane emp24 protein transport domain containing 7

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−23.43	NULL	8 / 16	GSEA C2	NAGASHIMA_EGF_SIGNALING_UP
2	−20.36	NULL	5 / 10	GSEA C2	CHASSOT_SKIN_WOUND
3	−19.34	NULL	6 / 16	GSEA C2	AMIT_SERUM_RESPONSE_40_MCF10A
4	−17.73	NULL	4 / 14	GSEA C2	TIAN_TNF_SIGNALING_NOT_VIA_NFKB
5	−17.2	NULL	6 / 15	GSEA C2	AMIT_EGF_RESPONSE_40_HELA
6	−16.23	NULL	5 / 24	TF Tissue	VAQUERIZAS_Trachea
7	−15.64	NULL	6 / 16	TF Tissue	VAQUERIZAS_Pancreas
8	−15.59	NULL	5 / 16	GSEA C2	AMIT_EGF_RESPONSE_40_MCF10A
9	−15.21	NULL	3 / 11	GSEA C2	AMIT_EGF_RESPONSE_20_HELA
10	−13.72	NULL	3 / 12	GSEA C2	GENTILE_UV_HIGH_DOSE_UP
11	−13.58	NULL	5 / 16	GSEA C2	UZONYI_RESPONSE_TO_LEUKOTRIENE_AND_THROMBIN
12	−12.83	NULL	4 / 16	GSEA C2	AMIT_EGF_RESPONSE_60_MCF10A
13	−12.82	NULL	3 / 12	GSEA C2	SESTO_RESPONSE_TO_UV_C3
14	−12.65	NULL	3 / 14	GSEA C2	DAZARD_UV_RESPONSE_CLUSTER_G2
15	−12.2	NULL	3 / 16	GSEA C2	CROONQUIST_STROMAL_STIMULATION_UP
16	−12.18	NULL	6 / 16	GSEA C2	AMIT_DELAYED_EARLY_GENES
17	−12.15	NULL	4 / 16	GSEA C2	BIOCARTA_ETS_PATHWAY
18	−11.98	NULL	3 / 15	GSEA C2	KRIGE_AMINO_ACID_DEPRIVATION
19	−11.83	NULL	33 / 262	miRNA target starBase	hsa−miR−548l
20	−11.7	NULL	7 / 62	TF Tissue	VAQUERIZAS_Lung
21	−11.62	NULL	3 / 15	GSEA C2	INGA_TP53_TARGETS
22	−11.54	NULL	2 / 8	GSEA C2	YEMELYANOV_GR_TARGETS_DN
23	−11.33	NULL	19 / 172	miRNA target starBase	hsa−miR−607
24	−11.07	NULL	4 / 14	BP	response to light stimulus
25	−11.05	NULL	12 / 90	miRNA target starBase	hsa−miR−362−5p
26	−10.99	NULL	3 / 16	GSEA C2	GENTILE_UV_RESPONSE_CLUSTER_D4
27	−10.98	NULL	3 / 16	GSEA C2	AMIT_EGF_RESPONSE_60_HELA
28	−10.84	NULL	3 / 10	GSEA C2	REACTOME_ACTIVATION_OF_THE_AP1_FAMILY_OF_TRANSC
29	−10.82	NULL	6 / 39	BP	response to cAMP
30	−10.79	NULL	3 / 16	GSEA C2	MAHADEVAN_RESPONSE_TO_MP470_DN
31	−10.66	NULL	3 / 10	GSEA C2	BIOCARTA_CDMAC_PATHWAY
32	−10.64	NULL	4 / 16	GSEA C2	SCIAN_INVERSED_TARGETS_OF_TP53_AND_TP73_DN
33	−10.53	NULL	3 / 12	GSEA C2	BIOCARTA_CCR5_PATHWAY
34	−10.05	NULL	5 / 39	TF Tissue	VAQUERIZAS_Thyroid
35	−10.01	NULL	4 / 23	BP	negative regulation of fibroblast proliferation
36	−10	NULL	20 / 155	miRNA target starBase	hsa−miR−200b
37	−9.95	NULL	1 / 2	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_14
38	−9.95	NULL	2 / 15	GSEA C2	PRAMOONJAGO_SOX4_TARGETS_UP
39	−9.89	NULL	2 / 9	GSEA C2	GUTIERREZ_WALDENSTROEMS_MACROGLOBULINEMIA_1_D
40	−9.82	NULL	29 / 284	miRNA target starBase	hsa−miR−503