GW_295

Global Summary

%DE = 0.15

genes with fdr < 0.2 = 2070 (1184 + / 886 −)

genes with fdr < 0.1 = 1512 (901 + / 611 −)

genes with fdr < 0.05 = 1334 (786 + / 548 −)

genes with fdr < 0.01 = 862 (557 + / 305 −)

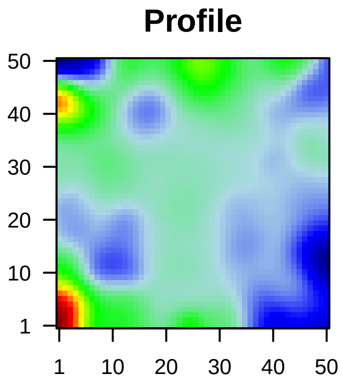
genes in genesets = 16332

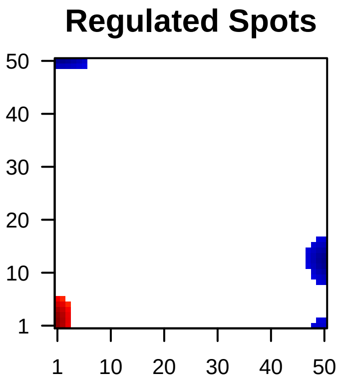
<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.1

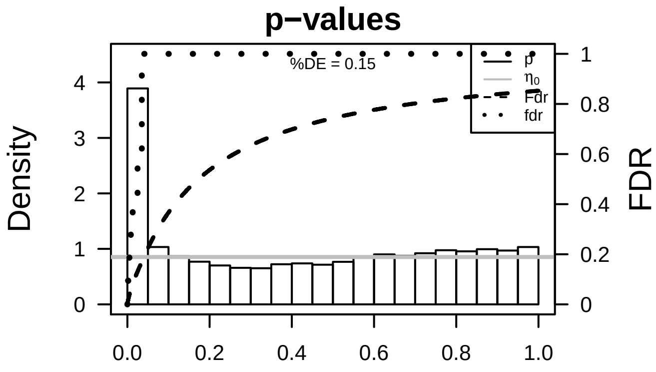
<fdr> = 0.85





Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	58	2.31	2e−16	4e−14	25 x 1	actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
2	70	1.92	2e−16	4e−14	25 x 1	actin, alpha, cardiac muscle 1 [Source:HGNC Symbol;Acc:14
3	131	−1.65	2e−16	4e−14	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
4	133	1.32	2e−16	4e−14	1 x 42	adrenomedullin [Source:HGNC Symbol;Acc:259]
5	216	−1.96	2e−16	4e−14	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGN
6	218	−1.68	2e−16	4e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
7	55107	2.3	2e−16	4e−14	1 x 5	anoctamin 1, calcium activated chloride channel [Source:HG
8	84002	1.34	2e−16	4e−14	13 x 50	UDP−GlcNAc:betaGal beta−1,3−N−acetylglucosaminyltransf
9	10950	−1.34	2e−16	4e−14	28 x 50	BTG family, member 3 [Source:HGNC Symbol;Acc:1132]
10	260436	−1.6	2e−16	4e−14	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symb
11	760	1.57	2e−16	4e−14	1 x 44	carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
12	768	1.48	2e−16	4e−14	1 x 6	carbonic anhydrase IX [Source:HGNC Symbol;Acc:1383]
13	22802	−1.68	2e−16	4e−14	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
14	1308	1.79	2e−16	4e−14	1 x 43	collagen, type XVII, alpha 1 [Source:HGNC Symbol;Acc:2194
15	1277	1.51	2e−16	4e−14	2 x 1	collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
16	1278	1.5	2e−16	4e−14	2 x 1	collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198]
17	1281	1.55	2e−16	4e−14	2 x 1	collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]
18	1287	1.33	2e−16	4e−14	15 x 50	collagen, type IV, alpha 5 [Source:HGNC Symbol;Acc:2207]
19	1288	1.93	2e−16	4e−14	1 x 43	collagen, type IV, alpha 6 [Source:HGNC Symbol;Acc:2208]
20	1289	1.41	2e−16	4e−14	2 x 1	collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209]



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	16.51	NULL	242	BP	extracellular matrix organization
2	15.34	NULL	64	BP	collagen catabolic process
3	15.13	NULL	69	BP	extracellular matrix disassembly
4	13.4	NULL	250	Lymphoma	LENZ_Stromal signature 1
5	13.25	NULL	190	CC	extracellular matrix
6	13.12	NULL	153	CC	endoplasmic reticulum lumen
7	13.08	NULL	699	Chr	Chr 5
8	11.81	NULL	83	CC	basement membrane
9	11.77	NULL	15	GSEA C2	CROMER_TUMORIGENESIS_UP
10	10.73	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
11	10.52	NULL	12	BP	hemidesmosome assembly
12	10.33	NULL	11	MF	platelet−derived growth factor binding
13	10.28	NULL	403	BP	cell adhesion
14	10.2	NULL	957	Chr	Chr 11
15	9.96	NULL	37	BP	collagen fibril organization
16	9.83	NULL	16	MMML CGS	MACIEJ_MMML 1
17	9.31	NULL	621	CC	endoplasmic reticulum
18	9.28	NULL	35	Glio	Colman_survival_associated
19	8.83	NULL	3274	CC	integral to membrane
20	8.78	NULL	15	GSEA C2	ONDER_CDH1_SIGNALING_VIA_CTNNB1
Underexpressed					
1	−9.93	NULL	1720	Chr	Chr 1
2	−8.64	NULL	135	H.Tiss	WIRTH_Mucosa
3	−7.13	NULL	15	CC	MHC class II protein complex
4	−6.96	NULL	9	GSEA C2	REACTOME_ETHANOL_OXIDATION
5	−6.47	NULL	1749	MF	DNA binding
6	−6.35	NULL	21	CC	cornified envelope
7	−6.35	NULL	1135	Chr	Chr 19
8	−5.84	NULL	940	MF	nucleic acid binding
9	−5.82	NULL	15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
10	−5.81	NULL	42	BP	keratinization
11	−5.73	NULL	15	GSEA C2	LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
12	−5.7	NULL	52	Chr	Chr HSCHR6_MHC_QBL
13	−5.66	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_D
14	−5.64	NULL	717	Chr	Chr 16
15	−5.49	NULL	14	GSEA C2	KIM_RESPONSE_TO_TSA_AND_DECITABINE_UP
16	−5.36	NULL	18	MF	acyl−CoA dehydrogenase activity
17	−5.28	NULL	417	H.Tiss	WIRTH_Immune system
18	−5.23	NULL	232	Chr	Chr 18
19	−5.15	NULL	18	BP	retinol metabolic process
20	−5.08	NULL	1574	BP	transcription, DNA−templated

GW_295

Local Summary

%DE = 0.89

metagenes = 17

genes = 259

genes in genesets = 257

genes with fdr < 0.1 = 215 (210 + / 5 −)

genes with fdr < 0.05 = 203 (199 + / 4 −)

genes with fdr < 0.01 = 177 (176 + / 1 −)

<r> metagenes = 0.96

<r> genes = 0.36

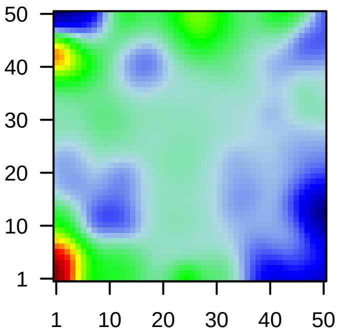
<FC> = 0.71

<shrinkage−t> = 24.84

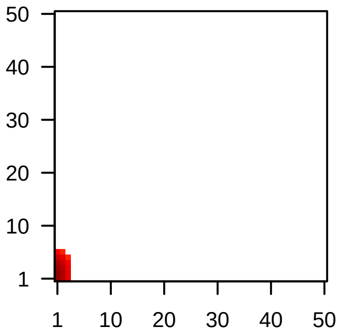
<p−value> = 0

<fdr> = 0.25

Profile



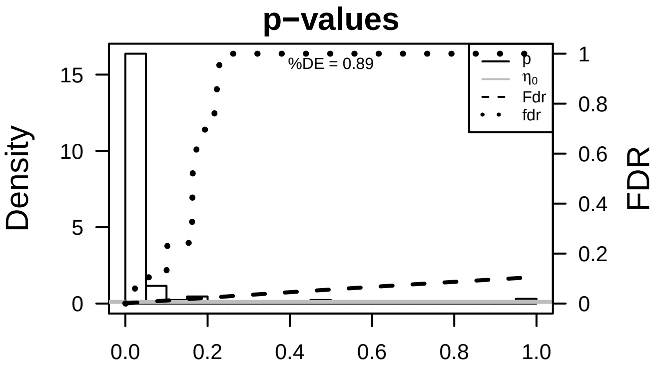
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	55107	2.3	2e−16	2e−16	1 x 5	anoctamin 1, calcium activated chloride channel [Source:HGI
2	768	1.48	2e−16	2e−16	1 x 6	carbonic anhydrase IX [Source:HGNC Symbol;Acc:1383]
3	1277	1.51	2e−16	2e−16	2 x 1	collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
4	1278	1.5	2e−16	2e−16	2 x 1	collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198]
5	1281	1.55	2e−16	2e−16	2 x 1	collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]
6	1289	1.41	2e−16	2e−16	2 x 1	collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209]
7	1291	1.53	2e−16	2e−16	2 x 1	collagen, type VI, alpha 1 [Source:HGNC Symbol;Acc:2211]
8	1293	1.54	2e−16	2e−16	2 x 1	collagen, type VI, alpha 3 [Source:HGNC Symbol;Acc:2213]
9	1437	1.53	2e−16	2e−16	1 x 4	colony stimulating factor 2 (granulocyte−macrophage) [Sourc
10	6374	2.05	2e−16	2e−16	1 x 1	chemokine (C−X−C motif) ligand 5 [Source:HGNC Symbol;A
11	1948	1.41	2e−16	2e−16	1 x 5	ephrin−B2 [Source:HGNC Symbol;Acc:3227]
12	11010	1.56	2e−16	2e−16	2 x 4	GLI pathogenesis−related 1 [Source:HGNC Symbol;Acc:170
13	3678	1.71	2e−16	2e−16	1 x 1	integrin, alpha 5 (fibronectin receptor, alpha polypeptide) [Sou
14	3918	1.91	2e−16	2e−16	1 x 4	laminin, gamma 2 [Source:HGNC Symbol;Acc:6493]
15	4312	2.03	2e−16	2e−16	1 x 1	matrix metallopeptidase 1 (interstitial collagenase) [Source:H
16	4319	1.93	2e−16	2e−16	1 x 3	matrix metallopeptidase 10 (stromelysin 2) [Source:HGNC Sy
17	4322	1.54	2e−16	2e−16	1 x 2	matrix metallopeptidase 13 (collagenase 3) [Source:HGNC S
18	4314	1.78	2e−16	2e−16	1 x 1	matrix metallopeptidase 3 (stromelysin 1, progelatinase) [Sou
19	4502	1.8	2e−16	2e−16	1 x 3	metallothionein 2A [Source:HGNC Symbol;Acc:7406]
20	644314	1.35	2e−16	2e−16	1 x 5	

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	32.05	NULL	11 / 15	GSEA C2	CROMER_TUMORIGENESIS_UP
2	31.16	NULL	24 / 64	BP	collagen catabolic process
3	30.27	NULL	25 / 69	BP	extracellular matrix disassembly
4	30.07	NULL	14 / 16	MMML CGS	MACIEJ_MMML 1
5	28.94	NULL	57 / 242	BP	extracellular matrix organization
6	28.82	NULL	7 / 11	MF	platelet−derived growth factor binding
7	27.62	NULL	46 / 190	CC	extracellular matrix
8	24.71	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
9	24.33	NULL	58 / 250	Lymphoma	LENZ_Stromal signature 1
10	22.36	NULL	14 / 37	BP	collagen fibril organization
11	21.94	NULL	7 / 12	miRNA target	miR−29c
12	20.49	NULL	9 / 15	GSEA C2	ONDER_CDH1_SIGNALING_VIA_CTNNB1
13	18.38	NULL	7 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_UP
14	18.03	NULL	38 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
15	18.03	NULL	38 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
16	18.03	NULL	38 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
17	18.03	NULL	38 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
18	17.8	NULL	32 / 183	CC	proteinaceous extracellular matrix
19	17.45	NULL	5 / 10	GSEA C2	KEGG_ECM_RECEPTOR_INTERACTION
20	17.37	NULL	68 / 683	CC	extracellular space
21	17.1	NULL	92 / 1182	CC	extracellular region
22	16.79	NULL	51 / 403	BP	cell adhesion
23	16.67	NULL	12 / 35	Glio	Colman_survival_associated
24	16.6	NULL	6 / 10	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C4
25	16.46	NULL	4 / 10	BP	protein heterotrimerization
26	16.44	NULL	10 / 40	BP	cellular response to amino acid stimulus
27	16.17	NULL	6 / 16	GSEA C2	CROONQUIST_STROMAL_STIMULATION_UP
28	16.07	NULL	23 / 153	CC	endoplasmic reticulum lumen
29	16	NULL	56 / 553	Cancer	Lembcke_Colonic Inflammation
30	15.7	NULL	5 / 11	GSEA C2	BIOCARTA_PLATELETAPP_PATHWAY
31	15.56	NULL	18 / 83	CC	basement membrane
32	15.28	NULL	17 / 57	MF	extracellular matrix structural constituent
33	14.96	NULL	7 / 14	GSEA C2	VERRECCHIA_EARLY_RESPONSE_TO_TGFB1
34	14.85	NULL	6 / 13	GSEA C2	FRIDMAN_SENESCENCE_UP
35	14.72	NULL	5 / 13	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
36	14.47	NULL	3 / 5	GSEA C2	VERNELL_RETINOBLASTOMA_PATHWAY_DN
37	14.24	NULL	8 / 16	GSEA C2	ROZANOV_MMP14_TARGETS_SUBSET
38	14.23	NULL	21 / 119	Lymphoma	ROSOLOWSKI_green total
39	14.14	NULL	14 / 68	CC	collagen
40	13.64	NULL	6 / 15	GSEA C2	LEE_LIVER_CANCER_HEPATOBLAST

GW_295

Local Summary

%DE = 0.86

metagenes = 5

genes = 154

genes in genesets = 152

genes with fdr < 0.1 = 109 (4 + / 105 −)

genes with fdr < 0.05 = 102 (4 + / 98 −)

genes with fdr < 0.01 = 52 (2 + / 50 −)

<r> metagenes = 1

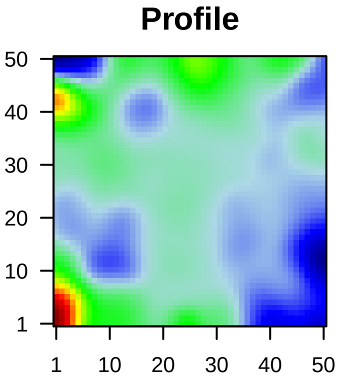
<r> genes = 0.66

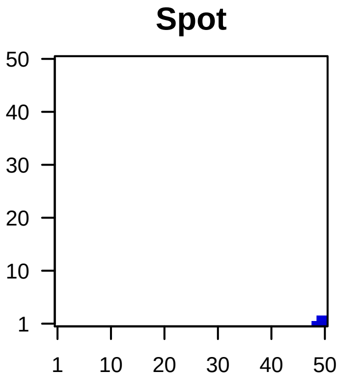
<FC> = −0.36

<shrinkage−t> = −12.61

<p−value> = 0.01

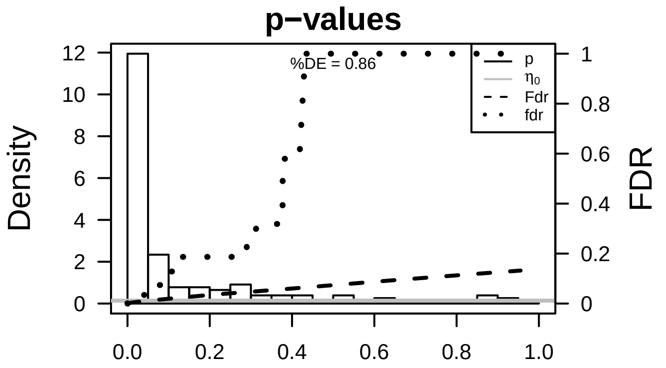
<fdr> = 0.56





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	260436	−1.6	2e−16	5e−15	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symbo
2	6363	−1.16	1e−12	1e−09	50 x 1	chemokine (C−C motif) ligand 19 [Source:HGNC Symbol;Acc
3	7351	−1.07	5e−11	3e−09	50 x 1	uncoupling protein 2 (mitochondrial, proton carrier) [Source:H
4	10537	−1.04	2e−10	3e−09	50 x 1	ubiquitin D [Source:HGNC Symbol;Acc:18795]
5	3575	1.03	3e−10	4e−09	50 x 2	interleukin 7 receptor [Source:HGNC Symbol;Acc:6024]
6	10628	−1	5e−10	2e−07	48 x 1	thioredoxin interacting protein [Source:HGNC Symbol;Acc:16
7	5920	−0.93	1e−08	6e−07	48 x 1	retinoic acid receptor responder (tazarotene induced) 3 [Sour
8	3122	−0.84	4e−08	3e−06	50 x 1	major histocompatibility complex, class II, DR alpha [Source:
9	5730	−0.85	2e−07	3e−06	50 x 1	prostaglandin D2 synthase 21kDa (brain) [Source:HGNC Syn
10	3820	−0.83	3e−07	3e−06	50 x 1	killer cell lectin−like receptor subfamily B, member 1 [Source:
11	3108	−0.83	4e−07	5e−05	50 x 1	major histocompatibility complex, class II, DM alpha [Source:
12	3125	−0.76	3e−06	5e−05	50 x 1	major histocompatibility complex, class II, DR beta 3 [Source:
13	6366	−0.73	8e−06	5e−05	50 x 2	chemokine (C−C motif) ligand 21 [Source:HGNC Symbol;Acc
14	7318	−0.72	1e−05	5e−05	48 x 1	ubiquitin−like modifier activating enzyme 7 [Source:HGNC Sy
15	25849	−0.72	1e−05	1e−04	50 x 2	prostate androgen−regulated mucin−like protein 1 [Source:H
16	4050	−0.69	2e−05	1e−04	50 x 1	lymphotoxin beta (TNF superfamily, member 3) [Source:HGN
17	115361	−0.69	2e−05	2e−04	48 x 1	guanylate binding protein 4 [Source:HGNC Symbol;Acc:2048
18	3512	−0.67	4e−05	2e−04	50 x 1	immunoglobulin J polypeptide, linker protein for immunoglobu
19	962	−0.67	4e−05	3e−04	50 x 1	CD48 molecule [Source:HGNC Symbol;Acc:1683]
20	919	−0.65	7e−05	3e−04	50 x 1	CD247 molecule [Source:HGNC Symbol;Acc:1677]



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−34.5	NULL	11 / 15	CC	MHC class II protein complex
2	−24.68	NULL	2 / 4	MMML CGS	MACIEJ_MMML 2
3	−22.44	NULL	3 / 6	GSEA C2	SANA_RESPONSE_TO_IFNG_UP
4	−21.94	NULL	66 / 417	H.Tiss	WIRTH_Immune system
5	−19.86	NULL	12 / 47	BP	antigen processing and presentation
6	−19.82	NULL	12 / 60	BP	T cell costimulation
7	−18.62	NULL	6 / 11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
8	−18.58	NULL	3 / 9	GSEA C2	MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN
9	−18.39	NULL	8 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
10	−17.66	NULL	38 / 312	BP	immune response
11	−17.62	NULL	2 / 3	GSEA C2	KEGG_VIRAL_MYOCARDITIS
12	−17.36	NULL	5 / 17	BP	positive regulation of neutrophil chemotaxis
13	−16.85	NULL	2 / 8	GSEA C2	NIELSEN_SYNOVIAL_SARCOMA_DN
14	−16.62	NULL	6 / 21	CC	clathrin−coated endocytic vesicle membrane
15	−16.61	NULL	2 / 3	MMML CGS	MACIEJ_MMML 7
16	−16.5	NULL	6 / 15	GSEA C2	FINAK_BREAST_CANCER_SDPP_SIGNATURE
17	−16.14	NULL	3 / 7	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
18	−15.86	NULL	5 / 11	GSEA C2	BIOCARTA_THELPER_PATHWAY
19	−15.85	NULL	61 / 553	Cancer	Lembcke_Colonic Inflammation
20	−15.81	NULL	6 / 23	CC	integral to lumenal side of endoplasmic reticulum membrane
21	−15.79	NULL	3 / 14	GSEA C2	WINNEPENNINCKX_MELANOMA_METASTASIS_DN
22	−15.71	NULL	5 / 12	GSEA C2	BIOCARTA_CTL_PATHWAY
23	−15.64	NULL	1 / 2	GSEA C2	KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUC
24	−15.64	NULL	1 / 2	GSEA C2	KEGG_AUTOIMMUNE_THYROID_DISEASE
25	−15.64	NULL	1 / 2	GSEA C2	KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS
26	−15.44	NULL	4 / 12	BP	dendritic cell chemotaxis
27	−14.85	NULL	2 / 4	GSEA C2	KEGG_LEISHMANIA_INFECTION
28	−14.51	NULL	5 / 12	BP	immunoglobulin mediated immune response
29	−14.19	NULL	6 / 28	CC	transport vesicle membrane
30	−14	NULL	2 / 10	BP	positive regulation of chemotaxis
31	−13.86	NULL	3 / 8	GSEA C2	LINDSTEDT_DENDRITIC_CELL_MATURATION_D
32	−13.47	NULL	7 / 52	Chr	Chr HSCHR6_MHC_QBL
33	−13.24	NULL	11 / 87	BP	antigen processing and presentation of exogenous peptide antigen
34	−13.17	NULL	6 / 32	CC	ER to Golgi transport vesicle membrane
35	−13.14	NULL	14 / 74	BP	regulation of immune response
36	−12.64	NULL	4 / 22	BP	positive regulation of interleukin−12 production
37	−12.63	NULL	2 / 12	BP	positive regulation of receptor−mediated endocytosis
38	−12.53	NULL	6 / 35	CC	trans−Golgi network membrane
39	−12.29	NULL	4 / 8	Glio	Donson−migration tethering and rolling−associated with LTS in HG
40	−12.22	NULL	3 / 10	GSEA C2	HOSHIDA_LIVER_CANCER_SUBCLASS_S1

GW_295

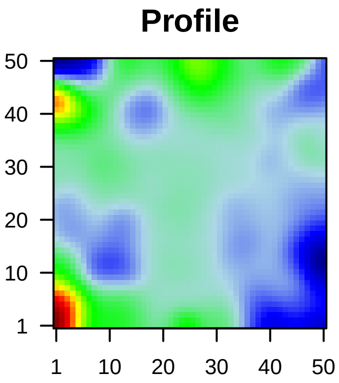
Local Summary

%DE = 0.72
metagenes = 29
genes = 330
genes in genesets = 326

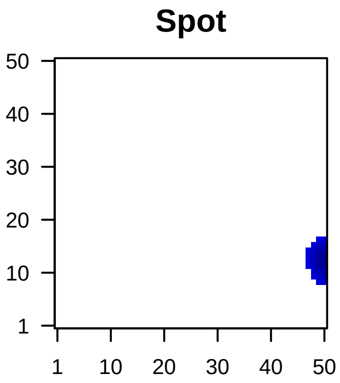
genes with fdr < 0.1 = 187 (9 + / 178 −)
genes with fdr < 0.05 = 166 (9 + / 157 −)
genes with fdr < 0.01 = 99 (6 + / 93 −)

<r> metagenes = 0.89
<r> genes = 0.25

<FC> = −0.36
<shrinkage−t> = −12.61
<p−value> = 0
<fdr> = 0.53



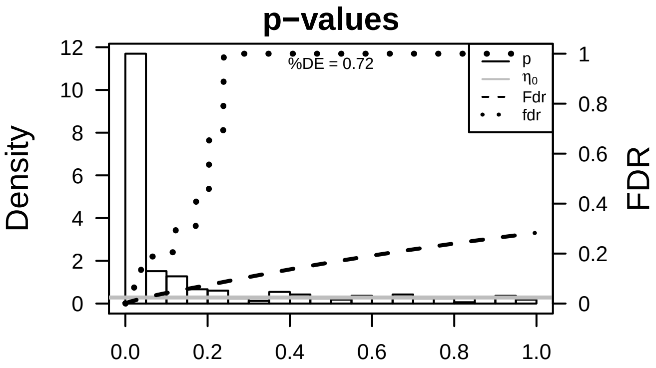
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	8857	−1.92	2e−16	5e−15	50 x 13	Fc fragment of IgG binding protein [Source:HGNC Symbol;Ac
2	2568	−1.35	2e−16	5e−15	50 x 13	gamma−aminobutyric acid (GABA) A receptor, pi [Source:HG
3	8543	−1.35	2e−16	5e−15	50 x 15	LIM domain only 4 [Source:HGNC Symbol;Acc:6644]
4	7033	−1.73	2e−16	5e−15	50 x 10	trefoil factor 3 (intestinal) [Source:HGNC Symbol;Acc:11757]
5	55930	−1.16	1e−12	3e−10	50 x 13	myosin VC [Source:HGNC Symbol;Acc:7604]
6	10551	1.12	6e−12	3e−10	50 x 10	anterior gradient 2 [Source:HGNC Symbol;Acc:328]
7	6920	−1.12	7e−12	4e−10	50 x 13	transcription elongation factor A (SII), 3 [Source:HGNC Symb
8	57523	−1.11	1e−11	7e−10	50 x 12	NYN domain and retroviral integrase containing [Source:HGN
9	3169	−1.1	2e−11	3e−08	50 x 12	forkhead box A1 [Source:HGNC Symbol;Acc:5021]
10	84952	−1.01	6e−10	3e−08	50 x 10	cingulin−like 1 [Source:HGNC Symbol;Acc:25931]
11	2762	−1.01	6e−10	7e−08	50 x 12	GDP−mannose 4,6−dehydratase [Source:HGNC Symbol;Acc
12	343990	−0.98	2e−09	7e−08	50 x 12	KIAA1211−like [Source:HGNC Symbol;Acc:33454]
13	83699	−0.97	2e−09	7e−08	50 x 11	SH3 domain binding glutamic acid−rich protein like 2 [Source
14	155066	−0.97	3e−09	7e−07	50 x 15	ATPase, H+ transporting V0 subunit e2 [Source:HGNC Symb
15	645296	−0.86	1e−08	8e−07	49 x 16	
16	498	−0.84	2e−08	2e−06	48 x 15	ATP synthase, H+ transporting, mitochondrial F1 complex, alp
17	2628	−0.9	4e−08	2e−06	50 x 14	glycine amidinotransferase (L−arginine:glycine amidinotransfe
18	7018	−0.89	5e−08	2e−06	50 x 10	transferrin [Source:HGNC Symbol;Acc:11740]
19	23171	−0.87	8e−08	2e−06	50 x 12	glycerol−3−phosphate dehydrogenase 1−like [Source:HGNC
20	7100	−0.87	9e−08	2e−06	50 x 14	toll−like receptor 5 [Source:HGNC Symbol;Acc:11851]



p−values

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−16.28	NULL	3 / 7	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_DN
2	−13.58	NULL	11 / 16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_D
3	−13.07	NULL	3 / 13	GSEA C2	WONG_ENDMETRIUM_CANCER_UP
4	−12.47	NULL	4 / 9	GSEA C2	REACTOME_ETHANOL_OXIDATION
5	−11.79	NULL	1 / 5	GSEA C2	FERRARI_RESPONSE_TO_FENRETINIDE_DN
6	−11.69	NULL	4 / 14	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_D
7	−10.01	NULL	4 / 16	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
8	−9.99	NULL	2 / 5	GSEA C2	SMID_BREAST_CANCER_ERBB2_DN
9	−9.8	NULL	5 / 16	GSEA C2	TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_LOBULAR_
10	−9.26	NULL	2 / 10	GSEA C2	LUI_THYROID_CANCER_CLUSTER_5
11	−8.97	NULL	3 / 16	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_
12	−8.96	NULL	6 / 15	GSEA C2	POOLA_INVASIVE_BREAST_CANCER_DN
13	−8.93	NULL	2 / 14	GSEA C2	WANG_BARRETTS_ESOPHAGUS_UP
14	−8.56	NULL	3 / 11	BP	DNA integration
15	−8.44	NULL	1 / 9	GSEA C2	GOUYER_TATI_TARGETS_UP
16	−8.3	NULL	3 / 16	GSEA C2	DOANE_BREAST_CANCER_ESR1_DN
17	−8.2	NULL	3 / 4	miRNA target	miR−204
18	−8	NULL	3 / 16	GSEA C2	BOYAULT_LIVER_CANCER_SUBCLASS_G1_UP
19	−7.99	NULL	3 / 16	GSEA C2	YANG_BREAST_CANCER_ESR1_BULK_UP
20	−7.87	NULL	1 / 3	miRNA 3UTR	ACGC−210
21	−7.68	NULL	2 / 11	MF	enhancer sequence−specific DNA binding
22	−7.63	NULL	1 / 13	GSEA C2	FONTAINE_FOLLICULAR_THYROID_ADENOMA_UP
23	−7.6	NULL	4 / 21	BP	drug metabolic process
24	−7.59	NULL	3 / 10	BP	epoxygenase P450 pathway
25	−7.29	NULL	2 / 6	GSEA C2	KAPOSI_LIVER_CANCER_POOR_SURVIVAL_DN
26	−7.26	NULL	2 / 14	BP	negative regulation of epithelial to mesenchymal transition
27	−7.16	NULL	2 / 10	BP	negative regulation of blood coagulation
28	−7.02	NULL	1 / 15	GSEA C2	FONTAINE_PAPILLARY_THYROID_CARCINOMA_DN
29	−6.99	NULL	1 / 8	GSEA C2	HEIDENBLAD_AMPLICON_12P11_12_UP
30	−6.79	NULL	2 / 16	GSEA C2	YANG_BREAST_CANCER_ESR1_DN
31	−6.76	NULL	6 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
32	−6.76	NULL	1 / 16	GSEA C2	WATTEL_AUTONOMOUS_THYROID_ADENOMA_UP
33	−6.74	NULL	2 / 7	GSEA C2	LOPEZ_MESOTELIOMA_SURVIVAL_TIME_DN
34	−6.72	NULL	2 / 12	CC	apical junction complex
35	−6.65	NULL	2 / 16	GSEA C2	ROY_WOUND_BLOOD_VESSEL_DN
36	−6.59	NULL	2 / 9	GSEA C2	MONTERO_THYROID_CANCER_POOR_SURVIVAL_DN
37	−6.49	NULL	4 / 15	GSEA C2	TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_DUCTAL_NO
38	−6.49	NULL	2 / 13	GSEA C2	YANG_BREAST_CANCER_ESR1_UP
39	−6.45	NULL	3 / 14	GSEA C2	LIEN_BREAST_CARCINOMA_METAPLASTIC_VS_DUCTAL_DN
40	−6.43	NULL	1 / 7	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_DN

GW_295

Local Summary

%DE = 0.85

metagenes = 12

genes = 209

genes in genesets = 205

genes with fdr < 0.1 = 152 (11 + / 141 −)

genes with fdr < 0.05 = 143 (8 + / 135 −)

genes with fdr < 0.01 = 117 (6 + / 111 −)

<r> metagenes = 0.98

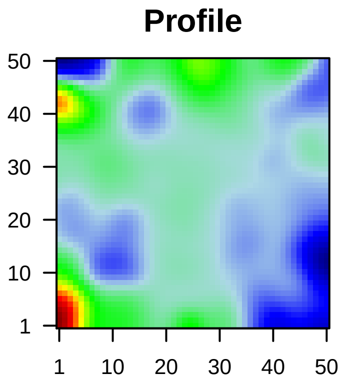
<r> genes = 0.46

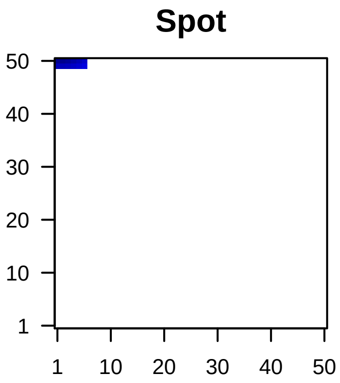
<FC> = −0.5

<shrinkage−t> = −17.69

<p−value> = 0

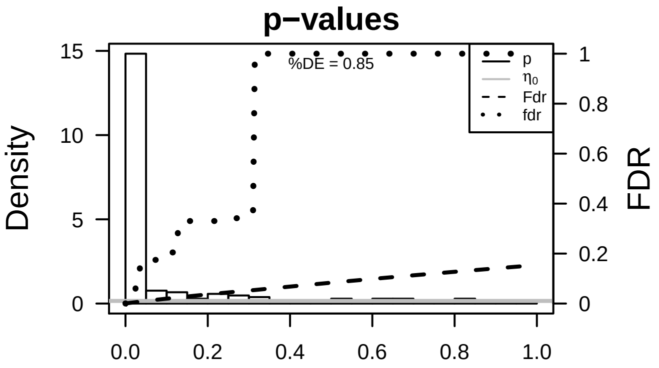
<fdr> = 0.33





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	131	−1.65	2e−16	8e−16	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	218	−1.68	2e−16	8e−16	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
3	22802	−1.68	2e−16	8e−16	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
4	1475	−1.74	2e−16	8e−16	1 x 50	cystatin A (stefin A) [Source:HGNC Symbol;Acc:2481]
5	192666	−1.83	2e−16	8e−16	1 x 50	keratin 24 [Source:HGNC Symbol;Acc:18527]
6	3851	−2.32	2e−16	8e−16	1 x 50	keratin 4 [Source:HGNC Symbol;Acc:6441]
7	5226	−1.34	2e−16	8e−16	6 x 50	phosphogluconate dehydrogenase [Source:HGNC Symbol;A
8	5275	−1.92	2e−16	8e−16	1 x 50	serpin peptidase inhibitor, clade B (ovalbumin), member 13 [
9	79755	−1.61	2e−16	8e−16	1 x 50	zinc finger protein 750 [Source:HGNC Symbol;Acc:25843]
10	1577	−1.29	3e−15	1e−13	4 x 50	cytochrome P450, family 3, subfamily A, polypeptide 5 [Sourc
11	387695	−1.27	8e−15	1e−13	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Sym
12	1672	−1.27	9e−15	8e−13	1 x 50	defensin, beta 1 [Source:HGNC Symbol;Acc:2766]
13	6702	−1.23	6e−14	8e−13	1 x 50	
14	163351	−1.23	6e−14	1e−11	1 x 50	guanylate binding protein family, member 6 [Source:HGNC S
15	79852	−1.18	4e−13	1e−11	3 x 50	epoxide hydrolase 3 [Source:HGNC Symbol;Acc:23760]
16	100134938	−1.17	7e−13	1e−11	6 x 50	polymerase (RNA) II (DNA directed) polypeptide J3 [Source:
17	5266	−1.07	1e−12	1e−11	1 x 49	peptidase inhibitor 3, skin−derived [Source:HGNC Symbol;Ac
18	9245	−1.16	1e−12	2e−10	4 x 50	glucosaminyl (N−acetyl) transferase 3, mucin type [Source:H
19	6337	−1.1	2e−11	2e−10	3 x 50	sodium channel, non−voltage−gated 1 alpha subunit [Source:
20	51228	−1	2e−11	2e−10	2 x 50	glycolipid transfer protein [Source:HGNC Symbol;Acc:24867]



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−40.27	NULL	65 / 135	H.Tiss	WIRTH_Mucosa
2	−21.17	NULL	12 / 21	CC	cornified envelope
3	−14.49	NULL	13 / 42	BP	keratinization
4	−14.44	NULL	5 / 10	GSEA C2	KEGG_LINOLEIC_ACID_METABOLISM
5	−14.23	NULL	16 / 53	BP	keratinocyte differentiation
6	−14.21	NULL	5 / 15	GSEA C2	LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
7	−12.96	NULL	17 / 76	BP	epidermis development
8	−12.89	NULL	3 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
9	−12.74	NULL	63 / 572	Disease	GUDJ_psoriasis up
10	−12.71	NULL	9 / 52	BP	negative regulation of endopeptidase activity
11	−12.08	NULL	6 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
12	−11.93	NULL	7 / 19	BP	peptide cross−linking
13	−11.84	NULL	5 / 15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
14	−11.77	NULL	5 / 13	BP	negative regulation of peptidase activity
15	−11.24	NULL	10 / 79	MF	serine−type endopeptidase inhibitor activity
16	−10.9	NULL	3 / 11	GSEA C2	REACTOME_XENOBIOTICS
17	−10.85	NULL	6 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
18	−10.45	NULL	4 / 23	MF	peptidase inhibitor activity
19	−10.28	NULL	2 / 8	GSEA C2	MCLACHLAN_DENTAL_CARIES_UP
20	−10.22	NULL	7 / 38	BP	epithelial cell differentiation
21	−10.22	NULL	5 / 29	BP	regulation of proteolysis
22	−9.69	NULL	1 / 6	GSEA C2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_B_DN
23	−9.67	NULL	3 / 14	GSEA C2	KIM_RESPONSE_TO_TSA_AND_DECITABINE_UP
24	−9.59	NULL	2 / 9	GSEA C2	MCLACHLAN_DENTAL_CARIES_DN
25	−9.59	NULL	13 / 186	MF	structural molecule activity
26	−9.34	NULL	2 / 9	GSEA C2	REACTOME_CYTOCHROME_P450_ARRANGED_BY_SUBSTRA
27	−9.34	NULL	2 / 9	GSEA C2	REACTOME_PHASE_1_FUNCTIONALIZATION_OF_COMPOUN
28	−9.14	NULL	4 / 16	GSEA C2	LEE_LIVER_CANCER_MYC_TGFA_UP
29	−9.08	NULL	4 / 16	GSEA C2	JAEGER_METASTASIS_DN
30	−9.03	NULL	6 / 82	CC	intermediate filament
31	−9.02	NULL	2 / 10	GSEA C2	NIKOLSKY_BREAST_CANCER_20Q12_Q13_AMPLICON
32	−8.73	NULL	3 / 11	GSEA C2	KEGG_DRUG_METABOLISM_CYTOCHROME_P450
33	−8.59	NULL	1 / 8	GSEA C2	GRAHAM_CML_QUIESCENT_VS_CML_DIVIDING_DN
34	−8.53	NULL	2 / 11	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_BONE_DN
35	−8.3	NULL	2 / 11	GSEA C2	REACTOME_BIOLOGICAL_OXIDATIONS
36	−8.29	NULL	5 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
37	−8.28	NULL	5 / 15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
38	−8.13	NULL	3 / 27	BP	response to bacterium
39	−8.12	NULL	3 / 13	GSEA C2	FARMER_BREAST_CANCER_APOCRINE VS LUMINAL
40	−7.91	NULL	3 / 13	GSEA C2	KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_