GW_126

Global Summary

%DE = 0.14

genes with fdr < 0.2 = 1771 (956 + / 815 −)

genes with fdr < 0.1 = 1420 (789 + / 631 −)

genes with fdr < 0.05 = 1174 (661 + / 513 −)

genes with fdr < 0.01 = 815 (478 + / 337 −)

genes in genesets = 16332

<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.11

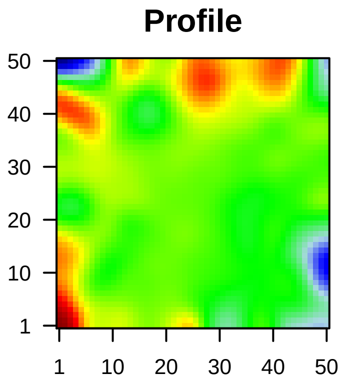
<fdr> = 0.86

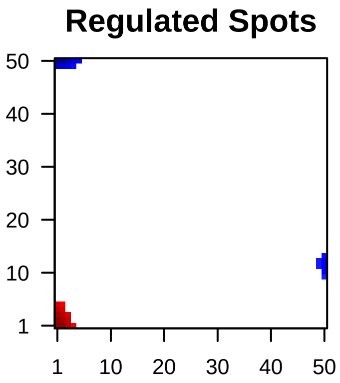
Global Genelist

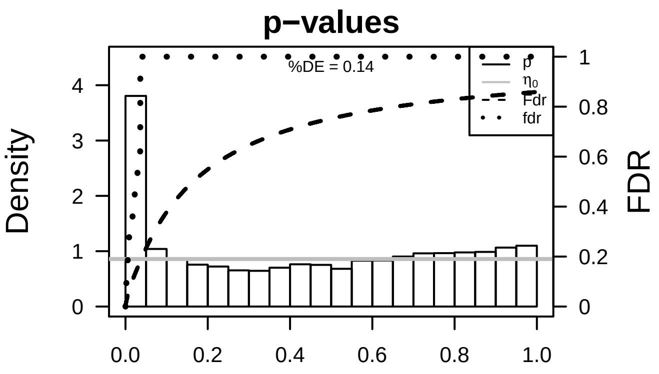
Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	24	1.53	2e−16	4e−14	16 x 50	ATP−binding cassette, sub−family A (ABC1), member 4 [Sour
2	70	1.45	2e−16	4e−14	25 x 1	actin, alpha, cardiac muscle 1 [Source:HGNC Symbol;Acc:14
3	163782	1.45	2e−16	4e−14	1 x 2	KN motif and ankyrin repeat domains 4 [Source:HGNC Symb
4	164284	1.5	2e−16	4e−14	1 x 3	adenomatosis polyposis coli down−regulated 1−like [Source:H
5	329	1.56	2e−16	4e−14	27 x 46	baculoviral IAP repeat containing 2 [Source:HGNC Symbol;A
6	655	−1.44	2e−16	4e−14	50 x 50	bone morphogenetic protein 7 [Source:HGNC Symbol;Acc:10
7	810	−1.83	2e−16	4e−14	1 x 50	calmodulin−like 3 [Source:HGNC Symbol;Acc:1452]
8	6347	−1.41	2e−16	4e−14	50 x 4	chemokine (C−C motif) ligand 2 [Source:HGNC Symbol;Acc:
9	1021	2.05	2e−16	4e−14	1 x 6	cyclin−dependent kinase 6 [Source:HGNC Symbol;Acc:1777]
10	30850	1.7	2e−16	4e−14	3 x 5	cerebellar degeneration−related protein 2−like [Source:HGNC
11	4680	−2.13	2e−16	4e−14	1 x 50	carcinoembryonic antigen−related cell adhesion molecule 6 (
12	22802	−2.32	2e−16	4e−14	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
13	1289	1.76	2e−16	4e−14	2 x 1	collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209]
14	51200	1.58	2e−16	4e−14	1 x 44	carboxypeptidase A4 [Source:HGNC Symbol;Acc:15740]
15	49860	−2.32	2e−16	4e−14	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
16	1595	1.76	2e−16	4e−14	12 x 50	cytochrome P450, family 51, subfamily A, polypeptide 1 [Sour
17	92196	−1.55	2e−16	4e−14	3 x 50	death associated protein−like 1 [Source:HGNC Symbol;Acc:2
18	84259	2.28	2e−16	4e−14	5 x 42	DCN1, defective in cullin neddylation 1, domain containing 5 [
19	1673	−1.5	2e−16	4e−14	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
20	55268	−1.56	2e−16	4e−14	50 x 14	enoyl CoA hydratase domain containing 2 [Source:HGNC Sy

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	15.59	NULL	957	Chr	Chr 11
2	12.97	NULL	519	Chr	Chr 14
3	10.67	NULL	64	BP	collagen catabolic process
4	10.62	NULL	69	BP	extracellular matrix disassembly
5	10.18	NULL	242	BP	extracellular matrix organization
6	9.7	NULL	190	CC	extracellular matrix
7	8.62	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
8	8.32	NULL	449	Chr	Chr 20
9	8.07	NULL	16	MMML CGS	MACIEJ_MMML 1
10	8.04	NULL	15	GSEA C2	SNIJDERS_AMPLIFIED_IN_HEAD_AND_NECK_TUMORS
11	7.77	NULL	37	BP	collagen fibril organization
12	7.43	NULL	250	Lymphoma	LENZ_Stromal signature 1
13	7.26	NULL	13	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
14	6.9	NULL	7	MMML CGS	MACIEJ_MMML 13
15	6.89	NULL	15	GSEA C2	CROMER_TUMORIGENESIS_UP
16	6.88	NULL	595	MF	RNA binding
17	6.57	NULL	68	CC	collagen
18	6.55	NULL	649	BP	gene expression
19	6.24	NULL	16	CC	lamellipodium membrane
20	6.16	NULL	10	BP	cellular response to zinc ion
Underexpressed					
1	−11.96	NULL	135	H.Tiss	WIRTH_Mucosa
2	−11.7	NULL	1135	Chr	Chr 19
3	−9.19	NULL	572	Disease	GUDJ_psoriasis up
4	−7.4	NULL	16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
5	−6.86	NULL	13	GSEA C2	WONG_ENDMETRIUM_CANCER_UP
6	−6.69	NULL	9	GSEA C2	GOUYER_TATI_TARGETS_UP
7	−6.6	NULL	714	Chr	Chr 6
8	−6.18	NULL	16	GSEA C2	CROMER_TUMORIGENESIS_DN
9	−6.16	NULL	24	TF Tissue	VAQUERIZAS_Trachea
10	−5.9	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_D
11	−5.9	NULL	16	GSEA C2	UROSEVIC_RESPONSE_TO_IMIQUIMOD
12	−5.78	NULL	630	Chr	Chr X
13	−5.74	NULL	918	Chr	Chr 17
14	−5.57	NULL	312	BP	immune response
15	−5.56	NULL	42	BP	keratinization
16	−5.56	NULL	16	GSEA C2	MAHADEVAN_RESPONSE_TO_MP470_UP
17	−5.52	NULL	21	CC	cornified envelope
18	−5.5	NULL	76	BP	epidermis development
19	−5.48	NULL	10	GSEA C2	CHASSOT_SKIN_WOUND
20	−5.46	NULL	16	GSEA C2	ZHANG_INTERFERON_RESPONSE







GW_126

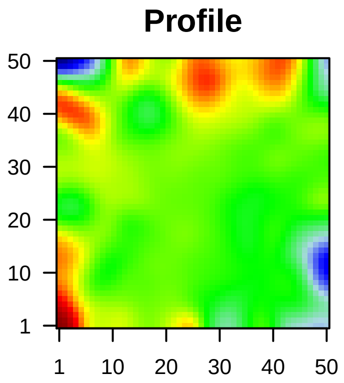
Local Summary

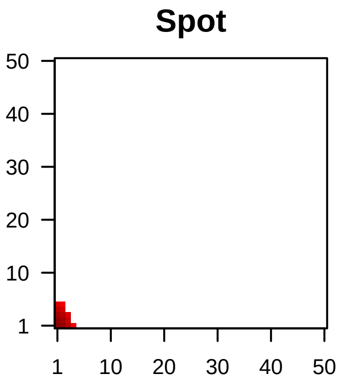
%DE = 0.71
metagenes = 14
genes = 247
genes in genesets = 245

genes with fdr < 0.1 = 143 (117 + / 26 −)
genes with fdr < 0.05 = 143 (117 + / 26 −)
genes with fdr < 0.01 = 112 (94 + / 18 −)

<r> metagenes = 0.96
<r> genes = 0.38

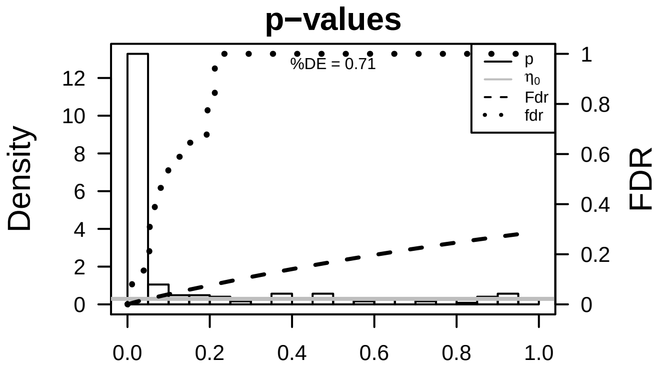
<FC> = 0.36
<shrinkage−t> = 12.82
<p−value> = 0
<fdr> = 0.41





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	163782	1.45	2e−16	1e−15	1 x 2	KN motif and ankyrin repeat domains 4 [Source:HGNC Symb
2	164284	1.5	2e−16	1e−15	1 x 3	adenomatosis polyposis coli down−regulated 1−like [Source:H
3	1289	1.76	2e−16	1e−15	2 x 1	collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209]
4	2619	1.4	2e−16	1e−15	2 x 1	growth arrest−specific 1 [Source:HGNC Symbol;Acc:4165]
5	3040	−1.7	2e−16	1e−15	4 x 1	hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
6	8870	−1.45	2e−16	1e−15	1 x 3	immediate early response 3 [Source:HGNC Symbol;Acc:5392
7	4312	2.19	2e−16	1e−15	1 x 1	matrix metallopeptidase 1 (interstitial collagenase) [Source:H
8	4319	1.99	2e−16	1e−15	1 x 3	matrix metallopeptidase 10 (stromelysin 2) [Source:HGNC Sy
9	4320	1.84	2e−16	1e−15	3 x 1	matrix metallopeptidase 11 (stromelysin 3) [Source:HGNC Sy
10	4316	2.46	2e−16	1e−15	2 x 1	matrix metallopeptidase 7 (matrilysin, uterine) [Source:HGNC
11	10630	1.49	2e−16	1e−15	1 x 2	podoplanin [Source:HGNC Symbol;Acc:29602]
12	10631	1.47	2e−16	1e−15	2 x 1	periostin, osteoblast specific factor [Source:HGNC Symbol;Ac
13	11098	1.4	2e−16	1e−15	1 x 1	protease, serine, 23 [Source:HGNC Symbol;Acc:14370]
14	6696	1.65	2e−16	1e−15	2 x 1	secreted phosphoprotein 1 [Source:HGNC Symbol;Acc:1125
15	7045	1.33	2e−16	1e−15	1 x 2	transforming growth factor, beta−induced, 68kDa [Source:HG
16	6591	1.38	4e−16	1e−13	1 x 4	snail family zinc finger 2 [Source:HGNC Symbol;Acc:11094]
17	1300	1.34	2e−15	4e−13	3 x 1	collagen, type X, alpha 1 [Source:HGNC Symbol;Acc:2185]
18	8076	1.31	1e−14	4e−13	4 x 1	microfibrillar associated protein 5 [Source:HGNC Symbol;Acc
19	12	−1.31	1e−14	2e−12	1 x 1	
20	1281	1.17	6e−14	2e−12	2 x 1	collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	35.13	NULL	27 / 64	BP	collagen catabolic process
2	34.45	NULL	30 / 69	BP	extracellular matrix disassembly
3	30.47	NULL	15 / 16	MMML CGS	MACIEJ_MMML 1
4	30.43	NULL	56 / 190	CC	extracellular matrix
5	29.82	NULL	65 / 242	BP	extracellular matrix organization
6	29.53	NULL	12 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
7	25.29	NULL	66 / 250	Lymphoma	LENZ_Stromal signature 1
8	23.52	NULL	6 / 13	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
9	23.12	NULL	12 / 19	MF	extracellular matrix binding
10	22.84	NULL	12 / 15	GSEA C2	CROMER_TUMORIGENESIS_UP
11	22.63	NULL	7 / 11	MF	platelet−derived growth factor binding
12	22.12	NULL	13 / 37	BP	collagen fibril organization
13	20.63	NULL	6 / 10	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C4
14	18.94	NULL	6 / 10	GSEA C2	JEON_SMAD6_TARGETS_UP
15	17.98	NULL	19 / 57	MF	extracellular matrix structural constituent
16	17.61	NULL	5 / 13	GSEA C2	BRUECKNER_TARGETS_OF_MIRLET7A3_DN
17	17.2	NULL	5 / 15	GSEA C2	TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_DUCTAL_NO
18	17.08	NULL	8 / 12	miRNA target	miR−29c
19	16.9	NULL	4 / 5	GSEA C2	COLLER_MYC_TARGETS_DN
20	16.7	NULL	4 / 7	GSEA C2	WANG_ESOPHAGUS_CANCER_PROGRESSION_UP
21	16.58	NULL	33 / 183	CC	proteinaceous extracellular matrix
22	16.14	NULL	7 / 16	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_N
23	15.74	NULL	10 / 40	BP	cellular response to amino acid stimulus
24	15.27	NULL	15 / 68	CC	collagen
25	15.03	NULL	2 / 13	GSEA C2	SUZUKI_AMPLIFIED_IN_ORAL_CANCER
26	15	NULL	5 / 10	GSEA C2	KEGG_ECM_RECEPTOR_INTERACTION
27	14.76	NULL	5 / 15	GSEA C2	CHANG_POU5F1_TARGETS_UP
28	14.34	NULL	23 / 119	Lymphoma	ROSOLOWSKI_green total
29	14.12	NULL	24 / 153	CC	endoplasmic reticulum lumen
30	14.02	NULL	4 / 14	GSEA C2	COWLING_MYCN_TARGETS
31	13.92	NULL	9 / 81	MF	metalloendopeptidase activity
32	13.66	NULL	5 / 14	BP	chondrocyte development
33	13.6	NULL	1 / 5	GSEA C2	ZEMBUTSU_SENSITIVITY_TO_NIMUSTINE
34	13.57	NULL	15 / 85	MF	integrin binding
35	13.54	NULL	6 / 11	MMML CGS	MACIEJ_MMML 31
36	13.09	NULL	12 / 35	Glio	Colman_survival_associated
37	12.99	NULL	12 / 68	Glio	cultured astroglia vs. in vivo astrocytes
38	12.86	NULL	3 / 11	BP	innervation
39	12.66	NULL	4 / 16	CC	lamellipodium membrane
40	12.64	NULL	8 / 73	MF	metallopeptidase activity

GW_126

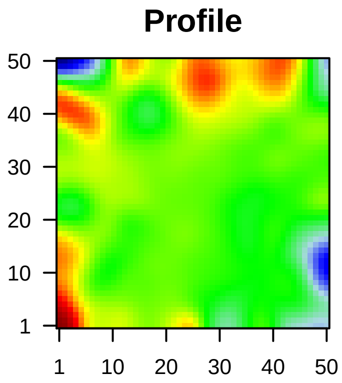
Local Summary

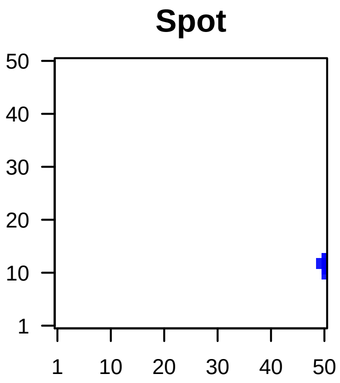
%DE = 0.85
metagenes = 7
genes = 133
genes in genesets = 132

genes with fdr < 0.1 = 89 (5 + / 84 −)
genes with fdr < 0.05 = 72 (4 + / 68 −)
genes with fdr < 0.01 = 62 (3 + / 59 −)

<r> metagenes = 0.96
<r> genes = 0.32

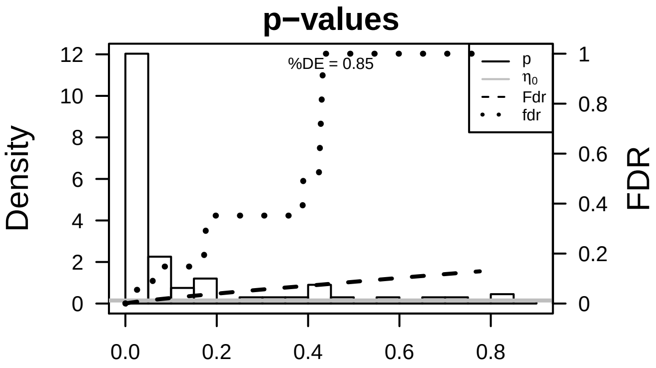
<FC> = −0.39
<shrinkage−t> = −13.7
<p−value> = 0
<fdr> = 0.49





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	55268	−1.56	2e−16	1e−15	50 x 14	enoyl CoA hydratase domain containing 2 [Source:HGNC Syı
2	10232	2.76	2e−16	1e−15	50 x 11	mesothelin [Source:HGNC Symbol;Acc:7371]
3	135112	−1.56	2e−16	1e−15	50 x 13	nuclear receptor coactivator 7 [Source:HGNC Symbol;Acc:21
4	6228	−1.79	2e−16	1e−15	50 x 14	ribosomal protein S23 [Source:HGNC Symbol;Acc:10410]
5	2568	−1.11	6e−11	5e−10	50 x 13	gamma−aminobutyric acid (GABA) A receptor, pi [Source:HG
6	83699	−1.11	7e−11	5e−10	50 x 11	SH3 domain binding glutamic acid−rich protein like 2 [Source
7	634	−1.1	8e−11	8e−10	50 x 12	carcinoembryonic antigen−related cell adhesion molecule 1 (l
8	3169	−1.09	1e−10	2e−08	50 x 12	forkhead box A1 [Source:HGNC Symbol;Acc:5021]
9	29116	−1.03	2e−09	2e−08	50 x 14	myosin regulatory light chain interacting protein [Source:HGN
10	9249	−1.02	2e−09	2e−08	50 x 13	dehydrogenase/reductase (SDR family) member 3 [Source:H
11	7018	−1	4e−09	2e−08	50 x 10	transferrin [Source:HGNC Symbol;Acc:11740]
12	7033	−1	4e−09	6e−07	50 x 10	trefoil factor 3 (intestinal) [Source:HGNC Symbol;Acc:11757]
13	8857	−0.93	5e−08	6e−07	50 x 13	Fc fragment of IgG binding protein [Source:HGNC Symbol;Ac
14	260293	−0.92	7e−08	2e−06	50 x 14	cytochrome P450, family 4, subfamily X, polypeptide 1 [Sourc
15	92747	−0.89	2e−07	2e−06	50 x 10	BPI fold containing family B, member 1 [Source:HGNC Symb
16	84952	−0.88	2e−07	2e−05	50 x 10	cingulin−like 1 [Source:HGNC Symbol;Acc:25931]
17	79083	−0.79	3e−06	2e−05	50 x 10	melanophilin [Source:HGNC Symbol;Acc:29643]
18	7100	−0.79	4e−06	2e−05	50 x 14	toll−like receptor 5 [Source:HGNC Symbol;Acc:11851]
19	92304	−0.79	4e−06	5e−05	50 x 10	secretoglobin, family 3A, member 1 [Source:HGNC Symbol;A
20	55930	−0.75	9e−06	5e−05	50 x 13	myosin VC [Source:HGNC Symbol;Acc:7604]



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset
1	−24.09	NULL	11 / 16	GSEA C2 RICKMAN_HEAD_AND_NECK_CANCER_D
2	−17.04	NULL	3 / 7	GSEA C2 HUPER_BREAST_BASAL_VS_LUMINAL_DN
3	−17	NULL	1 / 4	GSEA C2 NICK_RESPONSE_TO_PROC_TREATMENT_UP
4	−15.2	NULL	3 / 14	GSEA C2 SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_
5	−13.73	NULL	3 / 10	GSEA C2 YAMASHITA_LIVER_CANCER_WITH_EPCAM_DN
6	−12.6	NULL	3 / 13	GSEA C2 WONG_ENDMETRIUM_CANCER_UP
7	−11.28	NULL	3 / 15	GSEA C2 CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_DN
8	−10.8	NULL	3 / 16	GSEA C2 TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_
9	−10.8	NULL	3 / 16	GSEA C2 TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
10	−10.5	NULL	1 / 5	GSEA C2 SMID_BREAST_CANCER_ERBB2_DN
11	−10.17	NULL	2 / 11	CC photoreceptor outer segment membrane
12	−9.85	NULL	3 / 15	GSEA C2 TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_DUCTAL_N
13	−9.78	NULL	1 / 10	GSEA C2 NAKAMURA_TUMOR_ZONE_PERIPHERAL_VS_CENTRAL_DN
14	−9.46	NULL	4 / 15	GSEA C2 POOLA_INVASIVE_BREAST_CANCER_DN
15	−9.45	NULL	1 / 5	GSEA C2 FERRARI_RESPONSE_TO_FENRETINIDE_DN
16	−9.31	NULL	1 / 14	GSEA C2 RODRIGUES_THYROID_CARCINOMA_UP
17	−9.29	NULL	1 / 11	GSEA C2 LAIHO_COLORECTAL_CANCER_SERRATED_DN
18	−9.26	NULL	1 / 11	BP cell wall macromolecule catabolic process
19	−9.26	NULL	1 / 11	MF nuclear hormone receptor binding
20	−9.02	NULL	2 / 15	GSEA C2 DOANE_BREAST_CANCER_CLASSES_UP
21	−8.88	NULL	2 / 16	GSEA C2 YANG_BREAST_CANCER_ESR1_BULK_UP
22	−8.76	NULL	3 / 15	GSEA C2 SABATES_COLORECTAL_ADENOMA_UP
23	−8.63	NULL	2 / 16	GSEA C2 ROY_WOUND_BLOOD_VESSEL_DN
24	−8.43	NULL	1 / 7	GSEA C2 NEBEN_AML_WITH_FLT3_OR_NRAS_UP
25	−8.4	NULL	1 / 13	GSEA C2 WANG_LMO4_TARGETS_DN
26	−8.4	NULL	1 / 13	GSEA C2 ZHANG_RESPONSE_TO_IKK_INHIBITOR_AND_TNF_UP
27	−8.19	NULL	3 / 16	GSEA C2 CROMER_TUMORIGENESIS_DN
28	−8.17	NULL	2 / 15	GSEA C2 NEWMAN_ERCC6_TARGETS_UP
29	−8.15	NULL	2 / 12	GSEA C2 BERTUCCI_INVASIVE_CARCINOMA_DUCTAL_VS_LOBULAR_
30	−8.07	NULL	2 / 14	GSEA C2 VANTVEER_BREAST_CANCER_METASTASIS_UP
31	−8.07	NULL	1 / 14	GSEA C2 BOYAULT_LIVER_CANCER_SUBCLASS_G123_DN
32	−8.05	NULL	1 / 14	GSEA C2 TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_3D_UP
33	−8.05	NULL	1 / 14	GSEA C2 ZHOU_INFLAMMATORY_RESPONSE_LPS_UP
34	−7.91	NULL	1 / 8	GSEA C2 HEIDENBLAD_AMPLICON_12P11_12_UP
35	−7.85	NULL	1 / 8	GSEA C2 HASLINGER_B_CLL_WITH_6Q21_DELETION
36	−7.76	NULL	2 / 15	BP hormone metabolic process
37	−7.76	NULL	1 / 15	Cancer SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
38	−7.76	NULL	1 / 15	Cancer SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
39	−7.76	NULL	1 / 15	GSEA C2 GAUSSMANN_MLL_AF4_FUSION_TARGETS_F_UP
40	−7.76	NULL	1 / 15	GSEA C2 VALK_AML_CLUSTER_15

GW_126

Local Summary

%DE = 0.91

metagenes = 9

genes = 168

genes in genesets = 164

genes with fdr < 0.1 = 142 (18 + / 124 −)

genes with fdr < 0.05 = 129 (16 + / 113 −)

genes with fdr < 0.01 = 109 (13 + / 96 −)

<r> metagenes = 0.99

<r> genes = 0.49

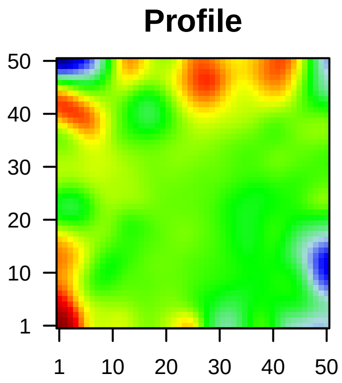
<FC> = −0.6

<shrinkage−t> = −21.31

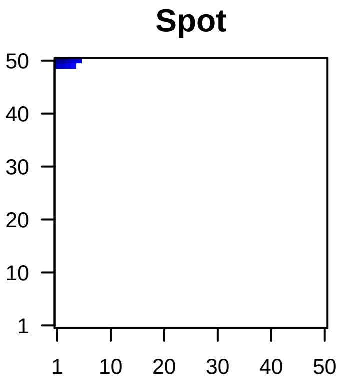
<p−value> = 0

<fdr> = 0.31

Profile



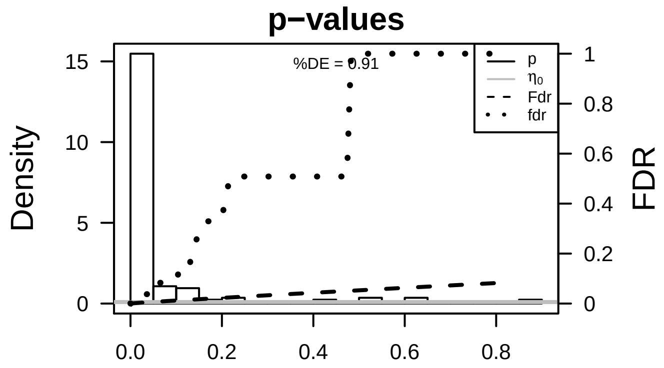
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	810	−1.83	2e−16	1e−16	1 x 50	calmodulin−like 3 [Source:HGNC Symbol;Acc:1452]
2	4680	−2.13	2e−16	1e−16	1 x 50	carcinoembryonic antigen−related cell adhesion molecule 6 (
3	22802	−2.32	2e−16	1e−16	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
4	49860	−2.32	2e−16	1e−16	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
5	92196	−1.55	2e−16	1e−16	3 x 50	death associated protein−like 1 [Source:HGNC Symbol;Acc:2
6	1673	−1.5	2e−16	1e−16	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
7	1999	−1.4	2e−16	1e−16	5 x 50	E74−like factor 3 (ets domain transcription factor, epithelial−s
8	2877	1.55	2e−16	1e−16	1 x 50	glutathione peroxidase 2 (gastrointestinal) [Source:HGNC Sy
9	9314	−1.39	2e−16	1e−16	4 x 50	Kruppel−like factor 4 (gut) [Source:HGNC Symbol;Acc:6348]
10	26085	−1.39	2e−16	1e−16	1 x 50	kallikrein−related peptidase 13 [Source:HGNC Symbol;Acc:6
11	5653	−1.46	2e−16	1e−16	1 x 50	kallikrein−related peptidase 6 [Source:HGNC Symbol;Acc:63
12	3860	−3.12	2e−16	1e−16	1 x 50	keratin 13 [Source:HGNC Symbol;Acc:6415]
13	192666	−1.45	2e−16	1e−16	1 x 50	keratin 24 [Source:HGNC Symbol;Acc:18527]
14	388533	1.55	2e−16	1e−16	1 x 49	keratinocyte differentiation−associated protein [Source:HGNC
15	3934	−3	2e−16	1e−16	1 x 50	lipocalin 2 [Source:HGNC Symbol;Acc:6526]
16	4118	−2.11	2e−16	1e−16	1 x 50	mal, T−cell differentiation protein [Source:HGNC Symbol;Acc
17	342897	−1.43	2e−16	1e−16	1 x 50	non−specific cytotoxic cell receptor protein 1 homolog (zebraf
18	220963	−1.57	2e−16	1e−16	4 x 50	solute carrier family 16, member 9 [Source:HGNC Symbol;Ac
19	6700	−1.86	2e−16	1e−16	1 x 50	small proline−rich protein 2A [Source:HGNC Symbol;Acc:112
20	6702	−1.58	2e−16	1e−16	1 x 50	

p−values



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−36.93	NULL	61 / 135	H.Tiss	WIRTH_Mucosa
2	−20.19	NULL	4 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
3	−19.81	NULL	13 / 42	BP	keratinization
4	−19.11	NULL	12 / 21	CC	cornified envelope
5	−18.81	NULL	16 / 53	BP	keratinocyte differentiation
6	−17.76	NULL	7 / 19	BP	peptide cross−linking
7	−17.75	NULL	17 / 76	BP	epidermis development
8	−16.38	NULL	6 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
9	−16.37	NULL	1 / 6	GSEA C2	SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_DN
10	−15.95	NULL	60 / 572	Disease	GUDJ_psoriasis up
11	−15.95	NULL	5 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
12	−15.87	NULL	1 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
13	−15.46	NULL	3 / 16	GSEA C2	CHEOK_RESPONSE_TO_MERCAPTOPURINE_AND_LD_MTX_
14	−14.27	NULL	5 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
15	−12.11	NULL	1 / 8	GSEA C2	MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_UP
16	−12.06	NULL	1 / 10	GSEA C2	MURAKAMI_UV_RESPONSE_1HR_UP
17	−11.4	NULL	1 / 11	GSEA C2	MURAKAMI_UV_RESPONSE_6HR_DN
18	−11.36	NULL	2 / 13	GSEA C2	WONG_ENDMETRIUM_CANCER_UP
19	−11.32	NULL	3 / 16	GSEA C2	LEE_LIVER_CANCER_ACOX1_UP
20	−11.28	NULL	1 / 9	GSEA C2	GOUYER_TATI_TARGETS_UP
21	−11.27	NULL	12 / 122	MF	serine−type endopeptidase activity
22	−11.18	NULL	4 / 15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
23	−11.1	NULL	2 / 15	GSEA C2	LEE_LIVER_CANCER_MYC_UP
24	−10.85	NULL	3 / 15	GSEA C2	LEE_LIVER_CANCER_MYC_E2F1_UP
25	−10.6	NULL	1 / 10	Glio	willscher_ GBM_LTSwt_proteomics−G_UP
26	−10.19	NULL	3 / 16	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_LUNG_UP
27	−10.18	NULL	12 / 186	MF	structural molecule activity
28	−10.17	NULL	2 / 12	GSEA C2	ZHAN_MULTIPLE_MYELOMA_DN
29	−10.07	NULL	2 / 11	GSEA C2	ROME_INSULIN_TARGETS_IN_MUSCLE_DN
30	−9.76	NULL	7 / 38	BP	epithelial cell differentiation
31	−9.68	NULL	4 / 10	MF	RAGE receptor binding
32	−9.52	NULL	1 / 12	GSEA C2	BROWNE_HCMV_INFECTION_4HR_UP
33	−9.12	NULL	2 / 15	GSEA C2	KORKOLA_TERATOMA
34	−9.08	NULL	1 / 13	GSEA C2	VALK_AML_WITH_CEBPA
35	−8.7	NULL	1 / 14	BP	protein homotrimerization
36	−8.54	NULL	4 / 44	CC	keratin filament
37	−8.54	NULL	3 / 14	GSEA C2	ZHAN_MULTIPLE_MYELOMA_MF_UP
38	−8.4	NULL	5 / 13	BP	negative regulation of peptidase activity
39	−8.39	NULL	6 / 82	CC	intermediate filament
40	−8.35	NULL	1 / 15	GSEA C2	MUELLER_METHYLATED_IN_GLIOBLASTOMA