GW_286

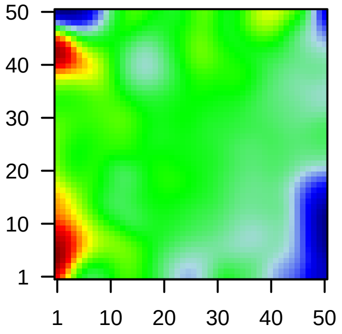
Global Summary

%DE = 0.14
genes with fdr < 0.2 = 1764 (985 + / 779 −)
genes with fdr < 0.1 = 1443 (831 + / 612 −)
genes with fdr < 0.05 = 1148 (677 + / 471 −)
genes with fdr < 0.01 = 674 (394 + / 280 −)

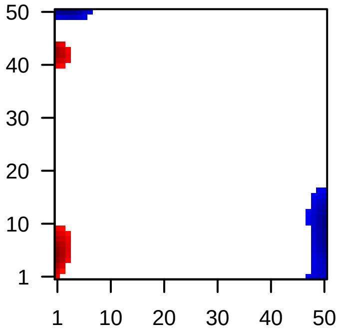
genes in genesets = 16332

<FC> = 0
<shrinkage−t> = 0
<p−value> = 0.12
<fdr> = 0.86

Profile



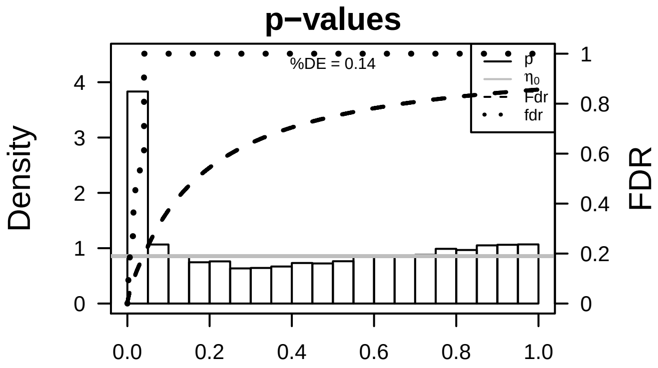
Regulated Spots



Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	8644	−2.32	2e−16	6e−14	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
2	1109	−1.88	2e−16	6e−14	13 x 50	aldo−keto reductase family 1, member C4 [Source:HGNC Sy
3	216	−2.41	2e−16	6e−14	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGN
4	218	−2.12	2e−16	6e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
5	401138	2.11	2e−16	6e−14	1 x 5	amelotin [Source:HGNC Symbol;Acc:33188]
6	260436	−1.57	2e−16	6e−14	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symb
7	8900	2.23	2e−16	6e−14	1 x 42	cyclin A1 [Source:HGNC Symbol;Acc:1577]
8	1000	1.54	2e−16	6e−14	4 x 1	cadherin 2, type 1, N−cadherin (neuronal) [Source:HGNC Sy
9	22802	−1.76	2e−16	6e−14	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
10	169044	2.02	2e−16	6e−14	45 x 1	collagen, type XXII, alpha 1 [Source:HGNC Symbol;Acc:229
11	51200	1.75	2e−16	6e−14	1 x 44	carboxypeptidase A4 [Source:HGNC Symbol;Acc:15740]
12	115908	1.61	2e−16	6e−14	3 x 1	collagen triple helix repeat containing 1 [Source:HGNC Symb
13	1515	2.34	2e−16	6e−14	1 x 44	cathepsin V [Source:HGNC Symbol;Acc:2538]
14	9547	1.94	2e−16	6e−14	1 x 46	chemokine (C−X−C motif) ligand 14 [Source:HGNC Symbol;
15	285761	2	2e−16	6e−14	1 x 4	discoidin, CUB and LCCL domain containing 1 [Source:HGN
16	131566	1.89	2e−16	6e−14	1 x 4	discoidin, CUB and LCCL domain containing 2 [Source:HGN
17	414325	1.78	2e−16	6e−14	1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
18	22943	1.6	2e−16	6e−14	1 x 7	dickkopf WNT signaling pathway inhibitor 1 [Source:HGNC S
19	27122	1.61	2e−16	6e−14	1 x 3	dickkopf WNT signaling pathway inhibitor 3 [Source:HGNC S
20	1823	2.49	2e−16	6e−14	1 x 45	desmocollin 1 [Source:HGNC Symbol;Acc:3035]

p−values



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	6.78	NULL	4	MMML CGS	MACIEJ_MMML 23
2	6.11	NULL	12	BP	hemidesmosome assembly
3	6.02	NULL	15	GSEA C2	CROMER_TUMORIGENESIS_UP
4	5.8	NULL	16	CC	lamellipodium membrane
5	5.79	NULL	10	CC	hemoglobin complex
6	5.73	NULL	1135	Chr	Chr 19
7	5.72	NULL	6	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_UP
8	5.61	NULL	1720	Chr	Chr 1
9	5.59	NULL	12	CC	fascia adherens
10	5.37	NULL	14	CC	endocytic vesicle lumen
11	5.21	NULL	940	MF	nucleic acid binding
12	5.05	NULL	16	GSEA C2	SESTO_RESPONSE_TO_UV_C8
13	4.81	NULL	16	GSEA C2	LANDEMAINE_LUNG_METASTASIS
14	4.78	NULL	11	GSEA C2	BIOCARTA_AHSP_PATHWAY
15	4.66	NULL	16	GSEA C2	ELVIDGE_HYPOXIA_BY_DMOG_UP
16	4.65	NULL	11	GSEA C2	LOPEZ_MESOTHELIOMA_SURVIVAL_DN
17	4.64	NULL	11	MF	oxygen transporter activity
18	4.61	NULL	12	GSEA C2	REACTOME_GAP_JUNCTION_ASSEMBLY
19	4.44	NULL	12	GSEA C2	REACTOME_INSULIN_SYNTHESIS_AND_SECRETION
20	4.44	NULL	21	CC	gap junction
Underexpressed					
1	−7.96	NULL	918	Chr	Chr 17
2	−7.88	NULL	135	H.Tiss	WIRTH_Mucosa
3	−6.96	NULL	15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
4	−6.94	NULL	16	GSEA C2	CROMER_TUMORIGENESIS_DN
5	−6.72	NULL	280	Chr	Chr 13
6	−6.13	NULL	553	Cancer	Lembcke_Colonic Inflammation
7	−6.11	NULL	6	GSEA C2	KAPOSI_LIVER_CANCER_POOR_SURVIVAL_DN
8	−5.61	NULL	9	GSEA C2	REACTOME_ETHANOL_OXIDATION
9	−5.51	NULL	12	BP	cellular aldehyde metabolic process
10	−5.41	NULL	327	Lymphoma	SPANG_CD40 6hrs UP
11	−5.31	NULL	21	CC	cornified envelope
12	−5.27	NULL	119	BP	xenobiotic metabolic process
13	−5.25	NULL	13	BP	negative regulation of peptidase activity
14	−5.24	NULL	16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
15	−5.19	NULL	699	Chr	Chr 5
16	−5.08	NULL	9	GSEA C2	GOUYER_TATI_TARGETS_UP
17	−5.07	NULL	15	CC	MHC class II protein complex
18	−4.95	NULL	15	GSEA C2	LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
19	−4.95	NULL	12	GSEA C2	MOROSETTI_FACIOSCAPULOHUMERAL_MUSCULAR_DISTRO
20	−4.83	NULL	16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN

GW_286

Local Summary

%DE = 0.64

metagenes = 25

genes = 354

genes in genesets = 351

genes with fdr < 0.1 = 191 (174 + / 17 −)

genes with fdr < 0.05 = 186 (170 + / 16 −)

genes with fdr < 0.01 = 140 (128 + / 12 −)

<r> metagenes = 0.92

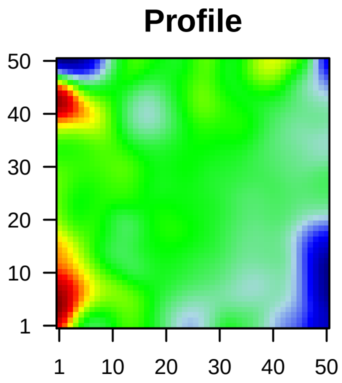
<r> genes = 0.31

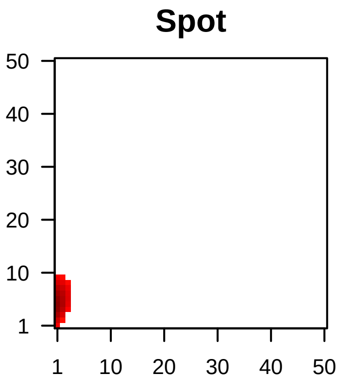
<FC> = 0.46

<shrinkage−t> = 16.08

<p−value> = 0

<fdr> = 0.47


Profile


Spot

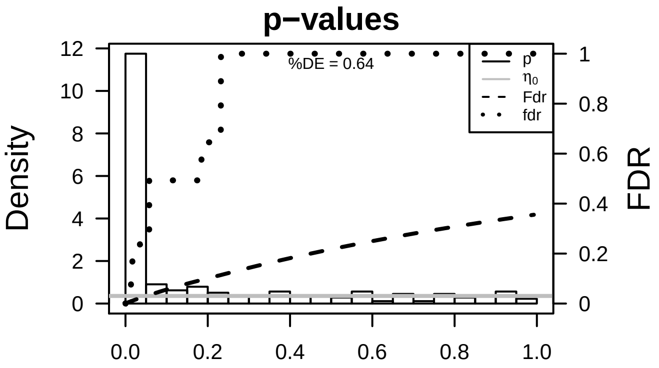
Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	401138	2.11	2e−16	2e−15	1 x 5	amelotin [Source:HGNC Symbol;Acc:33188]
2	285761	2	2e−16	2e−15	1 x 4	discoidin, CUB and LCCL domain containing 1 [Source:HGN
3	131566	1.89	2e−16	2e−15	1 x 4	discoidin, CUB and LCCL domain containing 2 [Source:HGN
4	22943	1.6	2e−16	2e−15	1 x 7	dickkopf WNT signaling pathway inhibitor 1 [Source:HGNC S
5	27122	1.61	2e−16	2e−15	1 x 3	dickkopf WNT signaling pathway inhibitor 3 [Source:HGNC S
6	84141	1.87	2e−16	2e−15	1 x 2	eva−1 homolog A (C. elegans) [Source:HGNC Symbol;Acc:2
7	8988	2.8	2e−16	2e−15	1 x 4	heat shock 27kDa protein 3 [Source:HGNC Symbol;Acc:524
8	3956	1.74	2e−16	2e−15	1 x 1	lectin, galactoside−binding, soluble, 1 [Source:HGNC Symbol
9	55714	1.59	2e−16	2e−15	1 x 1	teneurin transmembrane protein 3 [Source:HGNC Symbol;Ac
10	6447	1.76	2e−16	2e−15	1 x 1	secretogranin V (7B2 protein) [Source:HGNC Symbol;Acc:10
11	12	3.25	2e−16	2e−15	1 x 1	
12	5054	1.84	2e−16	2e−15	1 x 2	serpin peptidase inhibitor, clade E (nexin, plasminogen activa
13	284111	1.71	2e−16	2e−15	1 x 7	solute carrier family 13 (sodium−dependent citrate transporte
14	6695	1.59	2e−16	2e−15	1 x 2	sparc/osteonectin, cwcv and kazal−like domains proteoglycar
15	7045	1.81	2e−16	2e−15	1 x 2	transforming growth factor, beta−induced, 68kDa [Source:HG
16	10381	1.71	2e−16	2e−15	1 x 4	tubulin, beta 3 class III [Source:HGNC Symbol;Acc:20772]
17	153572	1.53	4e−16	6e−14	1 x 5	iroquois homeobox 2 [Source:HGNC Symbol;Acc:14359]
18	857	1.52	9e−16	8e−13	1 x 4	caveolin 1, caveolae protein, 22kDa [Source:HGNC Symbol;
19	205860	1.47	7e−15	1e−12	1 x 8	tripartite motif family−like 2 [Source:HGNC Symbol;Acc:2637
20	23768	1.45	1e−14	1e−12	1 x 4	fibronectin leucine rich transmembrane protein 2 [Source:HG

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	15.65	NULL	8 / 15	GSEA C2	CROMER_TUMORIGENESIS_UP
2	14.46	NULL	10 / 35	Glio	Colman_survival_associated
3	12.78	NULL	47 / 403	BP	cell adhesion
4	11.1	NULL	1 / 3	Glio	willscher_GBM_Verhaak−PNwt_expression_N_down
5	11.1	NULL	1 / 3	Glio	willscher_GBM_Verhaak−PNmut_expression_N_up
6	11.06	NULL	5 / 15	GSEA C2	ONDER_CDH1_SIGNALING_VIA_CTNNB1
7	10.97	NULL	46 / 242	BP	extracellular matrix organization
8	10.07	NULL	3 / 11	GSEA C2	BIOCARTA_PLATELETAPP_PATHWAY
9	10	NULL	5 / 11	Glio	Phillips MES up vs Prolif & PN
10	9.93	NULL	6 / 12	BP	hemidesmosome assembly
11	9.84	NULL	2 / 10	BP	negative regulation of cell−substrate adhesion
12	9.57	NULL	5 / 16	GSEA C2	BEGUM_TARGETS_OF_PAX3_FOXO1_FUSION_DN
13	9.56	NULL	4 / 10	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C4
14	9.25	NULL	3 / 16	CC	lamellipodium membrane
15	9.18	NULL	2 / 5	GSEA C2	VERNELL_RETINOBLASTOMA_PATHWAY_DN
16	9.11	NULL	1 / 4	GSEA C2	DACOSTA_LOW_DOSE_UV_RESPONSE_VIA_ERCC3_XPCS_D
17	8.84	NULL	3 / 16	Glio	VERHAAK_MES subtype
18	8.59	NULL	4 / 16	GSEA C2	SESTO_RESPONSE_TO_UV_C8
19	8.58	NULL	12 / 72	CC	extracellular vesicular exosome
20	8.48	NULL	3 / 14	GSEA C2	DANG_MYC_TARGETS_DN
21	8.47	NULL	2 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_UP
22	8.16	NULL	3 / 13	GSEA C2	BRUECKNER_TARGETS_OF_MIRLET7A3_DN
23	8.1	NULL	18 / 183	CC	proteinaceous extracellular matrix
24	8.05	NULL	16 / 117	Glio	GIEZELT_GBM_WT_up_VS_mut
25	7.72	NULL	2 / 15	GSEA C2	OSADA_ASCL1_TARGETS_DN
26	7.67	NULL	2 / 13	GSEA C2	CHARAFE_BREAST_CANCER_LUMINAL_VS_BASAL_DN
27	7.65	NULL	2 / 10	BP	regulation of receptor activity
28	7.65	NULL	2 / 10	GSEA C2	BIOCARTA_FIBRINOLYSIS_PATHWAY
29	7.43	NULL	4 / 16	GSEA C2	AMIT_EGF_RESPONSE_480_MCF10A
30	7.42	NULL	3 / 10	BP	positive regulation of peptidase activity
31	7.33	NULL	7 / 77	BP	negative regulation of canonical Wnt signaling pathway
32	7.33	NULL	6 / 19	MF	laminin binding
33	7.31	NULL	4 / 16	GSEA C2	AMIT_EGF_RESPONSE_60_HELA
34	7.31	NULL	4 / 16	GSEA C2	KERLEY_RESPONSE_TO_CISPLATIN_UP
35	7.28	NULL	3 / 14	GSEA C2	CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_
36	7.27	NULL	3 / 11	GSEA C2	ITO_PTTG1_TARGETS_UP
37	7.22	NULL	4 / 16	GSEA C2	AMUNDSON_POOR_SURVIVAL_AFTER_GAMMA_RADIATION_
38	7.19	NULL	4 / 13	GSEA C2	FRIDMAN_SENESCENCE_UP
39	7.18	NULL	1 / 6	GSEA C2	MAINA_HYPOXIA_VHL_TARGETS_UP
40	7.17	NULL	4 / 15	GSEA C2	SAGIV_CD24_TARGETS_DN


p−values

GW_286

Local Summary

%DE = 0.83

metagenes = 13

genes = 169

genes in genesets = 166

genes with fdr < 0.1 = 119 (108 + / 11 −)

genes with fdr < 0.05 = 108 (99 + / 9 −)

genes with fdr < 0.01 = 89 (84 + / 5 −)

<r> metagenes = 0.98

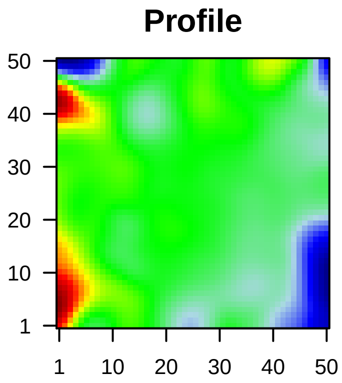
<r> genes = 0.36

<FC> = 0.56

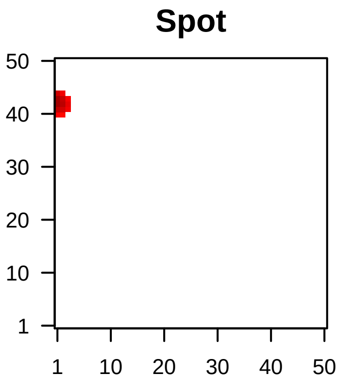
<shrinkage−t> = 19.54

<p−value> = 0

<fdr> = 0.38



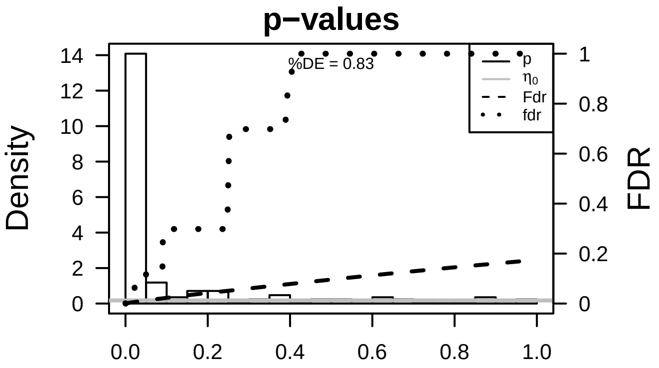
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	8900	2.23	2e−16	7e−16	1 x 42	cyclin A1 [Source:HGNC Symbol;Acc:1577]
2	51200	1.75	2e−16	7e−16	1 x 44	carboxypeptidase A4 [Source:HGNC Symbol;Acc:15740]
3	1515	2.34	2e−16	7e−16	1 x 44	cathepsin V [Source:HGNC Symbol;Acc:2538]
4	2697	2	2e−16	7e−16	1 x 44	gap junction protein, alpha 1, 43kDa [Source:HGNC Symbol;
5	9119	1.6	2e−16	7e−16	1 x 44	keratin 75 [Source:HGNC Symbol;Acc:24431]
6	387882	2.28	2e−16	7e−16	2 x 41	chromosome 12 open reading frame 75 [Source:HGNC Symb
7	81706	1.67	2e−16	7e−16	1 x 43	protein phosphatase 1, regulatory (inhibitor) subunit 14C [Sou
8	5947	1.61	2e−16	7e−16	1 x 43	retinol binding protein 1, cellular [Source:HGNC Symbol;Acc:
9	6513	1.58	2e−16	7e−16	1 x 43	solute carrier family 2 (facilitated glucose transporter), membe
10	116211	1.62	2e−16	7e−16	1 x 43	Transmembrane 4 L6 family member 19 [Source:UniProtKB/
11	143686	1.53	4e−16	1e−12	1 x 44	sestrin 3 [Source:HGNC Symbol;Acc:23060]
12	147920	1.42	5e−14	1e−12	2 x 43	IGF−like family member 2 [Source:HGNC Symbol;Acc:32929
13	1001	1.41	8e−14	1e−11	1 x 43	cadherin 3, type 1, P−cadherin (placental) [Source:HGNC Sy
14	6273	1.36	5e−13	2e−11	1 x 44	S100 calcium binding protein A2 [Source:HGNC Symbol;Acc:
15	4330	1.34	1e−12	2e−11	1 x 42	meningioma (disrupted in balanced translocation) 1 [Source:
16	2167	1.33	2e−12	5e−11	1 x 44	fatty acid binding protein 4, adipocyte [Source:HGNC Symbol
17	4753	1.3	4e−12	5e−11	1 x 44	NEL−like 2 (chicken) [Source:HGNC Symbol;Acc:7751]
18	2150	1.3	5e−12	1e−10	1 x 44	coagulation factor II (thrombin) receptor−like 1 [Source:HGN
19	80115	1.28	1e−11	4e−10	1 x 43	BAI1−associated protein 2−like 2 [Source:HGNC Symbol;Acc
20	23767	1.25	4e−11	4e−10	1 x 43	fibronectin leucine rich transmembrane protein 3 [Source:HG



p−values

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	15.7	NULL	2 / 6	GSEA C2	WALLACE_PROSTATE_CANCER_DN
2	12.42	NULL	1 / 2	miRNA target	miR−346
3	12.41	NULL	2 / 11	GSEA C2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_G_UP
4	11.79	NULL	4 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
5	11.52	NULL	2 / 16	GSEA C2	BECKER_TAMOXIFEN_RESISTANCE_DN
6	11.42	NULL	2 / 16	GSEA C2	WILLERT_WNT_SIGNALING
7	11.22	NULL	1 / 6	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_UP
8	10.86	NULL	2 / 15	GSEA C2	SENESE_HDAC1_AND_HDAC2_TARGETS_DN
9	10.62	NULL	7 / 85	Glio	laffaire_hypermeth_LGG_vs_control
10	10.42	NULL	3 / 16	GSEA C2	ELVIDGE_HYPOXIA_BY_DMOG_UP
11	10.31	NULL	4 / 16	GSEA C2	ELVIDGE_HIF1A_AND_HIF2A_TARGETS_DN
12	10.27	NULL	4 / 16	GSEA C2	ELVIDGE_HIF1A_TARGETS_DN
13	9.85	NULL	1 / 5	GSEA C2	RODRIGUES_DCC_TARGETS_UP
14	9.79	NULL	8 / 112	Glio	Christensen_hypermethylated_in_grade2_oligoastrocytoma
15	9.63	NULL	2 / 10	MF	gap junction channel activity
16	9.59	NULL	2 / 18	BP	male meiosis I
17	9.59	NULL	1 / 4	GSEA C2	NIELSEN_LEIOMYOSARCOMA_DN
18	9.26	NULL	2 / 15	GSEA C2	NGUYEN_NOTCH1_TARGETS_UP
19	9.24	NULL	1 / 10	GSEA C2	BIOCARTA_SKP2E2F_PATHWAY
20	9.12	NULL	2 / 10	GSEA C2	DAZARD_UV_RESPONSE_CLUSTER_G3
21	8.98	NULL	1 / 6	GSEA C2	OHM_EMBRYONIC_CARCINOMA_DN
22	8.85	NULL	2 / 8	GSEA C2	SIMBULAN_UV_RESPONSE_NORMAL_UP
23	8.74	NULL	1 / 11	GSEA C2	LOPEZ_MESOTHELIOMA_SURVIVAL_DN
24	8.73	NULL	2 / 2	miRNA target	miR−199a*
25	8.7	NULL	9 / 132	Glio	Christensen_hypermethylated_in_grade3_oligoastrocytoma
26	8.42	NULL	2 / 16	GSEA C2	LI_CISPLATIN_RESISTANCE_UP
27	8.38	NULL	2 / 12	GSEA C2	REACTOME_GAP_JUNCTION_ASSEMBLY
28	8.37	NULL	2 / 16	GSEA C2	ELVIDGE_HYPOXIA_UP
29	8.34	NULL	1 / 13	BP	nerve development
30	8.28	NULL	2 / 13	GSEA C2	VALK_AML_WITH_EVI1
31	8.26	NULL	1 / 10	BP	chronic inflammatory response
32	8.26	NULL	1 / 10	CC	Golgi−associated vesicle membrane
33	8.26	NULL	1 / 10	BP	regulation of ventricular cardiac muscle cell membrane repolarizati
34	8.26	NULL	1 / 10	BP	skeletal muscle tissue regeneration
35	8.26	NULL	1 / 10	GSEA C2	CONRAD_STEM_CELL
36	8.26	NULL	1 / 10	GSEA C2	REACTOME_GAP_JUNCTION_DEGRADATION
37	7.99	NULL	1 / 14	BP	multicellular organismal aging
38	7.93	NULL	2 / 14	GSEA C2	VALK_AML_CLUSTER_10
39	7.92	NULL	1 / 13	GSEA C2	SA_REG_CASCADE_OF_CYCLIN_EXPR
40	7.91	NULL	2 / 15	GSEA C2	STOSSI_RESPONSE_TO_ESTRADIOL

GW_286

Local Summary

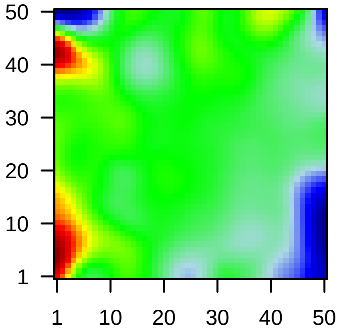
%DE = 0.77
metagenes = 54
genes = 711
genes in genesets = 705

genes with fdr < 0.1 = 354 (21 + / 333 −)
genes with fdr < 0.05 = 316 (20 + / 296 −)
genes with fdr < 0.01 = 172 (14 + / 158 −)

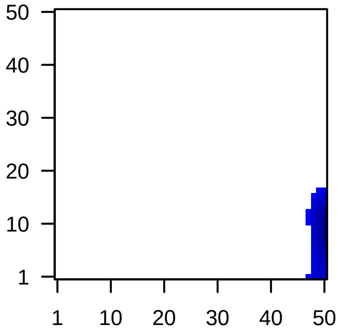
<r> metagenes = 0.77
<r> genes = 0.27

<FC> = −0.33
<shrinkage−t> = −11.56
<p−value> = 0.01
<fdr> = 0.62

Profile



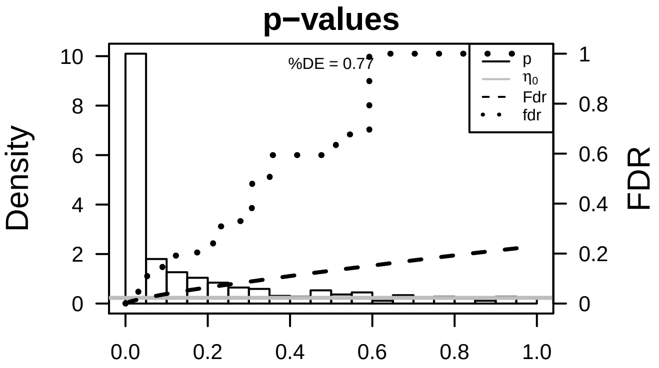
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	260436	−1.57	2e−16	2e−14	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symbc
2	6578	1.6	2e−16	2e−14	50 x 4	solute carrier organic anion transporter family, member 2A1 [S
3	7033	−1.47	7e−15	1e−11	50 x 10	trefoil factor 3 (intestinal) [Source:HGNC Symbol;Acc:11757]
4	348	1.4	1e−13	2e−10	50 x 1	apolipoprotein E [Source:HGNC Symbol;Acc:613]
5	10551	−1.32	2e−12	2e−10	50 x 10	anterior gradient 2 [Source:HGNC Symbol;Acc:328]
6	29116	−1.31	4e−12	2e−10	50 x 14	myosin regulatory light chain interacting protein [Source:HGN
7	3169	−1.3	5e−12	1e−09	50 x 12	forkhead box A1 [Source:HGNC Symbol;Acc:5021]
8	10232	−1.28	1e−11	1e−09	50 x 11	mesothelin [Source:HGNC Symbol;Acc:7371]
9	1363	−1.27	2e−11	2e−09	50 x 7	carboxypeptidase E [Source:HGNC Symbol;Acc:2303]
10	1675	−1.25	3e−11	2e−09	50 x 9	complement factor D (adipsin) [Source:HGNC Symbol;Acc:27
11	23231	−1.25	4e−11	1e−08	48 x 2	sel−1 suppressor of lin−12−like 3 (C. elegans) [Source:HGNC
12	5920	−1.21	1e−10	1e−08	48 x 1	retinoic acid receptor responder (tazarotene induced) 3 [Sour
13	79085	−1.2	2e−10	5e−08	50 x 13	solute carrier family 25 (mitochondrial carrier; phosphate carr
14	7018	−1.16	6e−10	5e−08	50 x 10	transferrin [Source:HGNC Symbol;Acc:11740]
15	6867	−1.16	8e−10	5e−08	50 x 6	transforming, acidic coiled−coil containing protein 1 [Source:H
16	6228	−1.15	1e−09	9e−07	50 x 14	ribosomal protein S23 [Source:HGNC Symbol;Acc:10410]
17	6192	1.09	7e−09	9e−07	50 x 9	ribosomal protein S4, Y−linked 1 [Source:HGNC Symbol;Acc:
18	6920	−1.08	1e−08	1e−06	50 x 13	transcription elongation factor A (SII), 3 [Source:HGNC Symb
19	65982	1.06	2e−08	1e−05	50 x 7	zinc finger and SCAN domain containing 18 [Source:HGNC S
20	21	1	1e−07	1e−05	50 x 17	ATP−binding cassette, sub−family A (ABC1), member 3 [Sour

p−values



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−11.95	NULL	12 / 15	CC	MHC class II protein complex
2	−11.5	NULL	14 / 16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_D
3	−10.82	NULL	108 / 553	Cancer	Lembcke_Colonic Inflammation
4	−10.52	NULL	6 / 12	GSEA C2	BERTUCCI_INVASIVE_CARCINOMA_DUCTAL_VS_LOBULAR_D
5	−10.16	NULL	3 / 6	GSEA C2	SANA_RESPONSE_TO_IFNG_UP
6	−9.94	NULL	7 / 14	GSEA C2	WU_SILENCED_BY_METHYLATION_IN_BLADDER_CANCER
7	−9.55	NULL	2 / 4	MMML CGS	MACIEJ_MMML 2
8	−9.48	NULL	7 / 8	Glio	Donson−migration tethering and rolling−associated with LTS in HG
9	−9.16	NULL	5 / 7	GSEA C2	LOPEZ_MESOTHELIOMA_SURVIVAL_WORST_VS_BEST_DN
10	−8.95	NULL	4 / 10	GSEA C2	ODONNELL_TARGETS_OF_MYC_AND_TFRC_UP
11	−8.95	NULL	5 / 14	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_D
12	−8.93	NULL	3 / 9	GSEA C2	GOUYER_TATI_TARGETS_UP
13	−8.88	NULL	8 / 15	GSEA C2	NAKAJIMA_MAST_CELL
14	−8.58	NULL	88 / 417	H.Tiss	WIRTH_Immune system
15	−8.46	NULL	4 / 11	GSEA C2	FUJII_YBX1_TARGETS_UP
16	−8.31	NULL	9 / 20	BP	complement activation
17	−8.28	NULL	5 / 16	GSEA C2	KORKOLA_TERATOMA_UP
18	−8.23	NULL	6 / 15	GSEA C2	POOLA_INVASIVE_BREAST_CANCER_DN
19	−8.22	NULL	5 / 9	GSEA C2	MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN
20	−8.17	NULL	5 / 8	GSEA C2	NIELSEN_SYNOVIAL_SARCOMA_DN
21	−8.17	NULL	4 / 9	GSEA C2	REACTOME_ETHANOL_OXIDATION
22	−8.13	NULL	4 / 7	GSEA C2	LOPEZ_MESOTHELIOMA_SURVIVAL_OVERALL_UP
23	−8.04	NULL	17 / 47	BP	antigen processing and presentation
24	−8.03	NULL	5 / 16	GSEA C2	TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_LOBULAR_N
25	−8	NULL	7 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
26	−7.96	NULL	2 / 5	GSEA C2	FERRARI_RESPONSE_TO_FENRETINIDE_DN
27	−7.94	NULL	5 / 10	GSEA C2	FERRANDO_LYL1_NEIGHBORS
28	−7.88	NULL	2 / 6	GSEA C2	TRAYNOR_RETT_SYNDROM_DN
29	−7.79	NULL	5 / 12	GSEA C2	HADDAD_T_LYMPHOCYTE_AND_NK_PROGENITOR_DN
30	−7.72	NULL	5 / 12	GSEA C2	ZHAN_V1_LATE_DIFFERENTIATION_GENES_UP
31	−7.6	NULL	4 / 13	GSEA C2	NING_CHRONIC_OBSTRUCTIVE_PULMONARY_DISEASE_DN
32	−7.55	NULL	6 / 7	GSEA C2	LOPEZ_MESOTELIOMA_SURVIVAL_TIME_DN
33	−7.52	NULL	12 / 49	Glio	Donson−innate immunity−associated with LTS in HGA
34	−7.41	NULL	50 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
35	−7.41	NULL	50 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
36	−7.41	NULL	50 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
37	−7.41	NULL	50 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
38	−7.38	NULL	3 / 13	GSEA C2	WONG_ENDMETRIUM_CANCER_UP
39	−7.38	NULL	58 / 312	BP	immune response
40	−7.38	NULL	5 / 14	BP	ruffle organization

GW_286

Local Summary

%DE = 0.78

metagenes = 13

genes = 241

genes in genesets = 237

genes with fdr < 0.1 = 161 (10 + / 151 −)

genes with fdr < 0.05 = 134 (9 + / 125 −)

genes with fdr < 0.01 = 108 (6 + / 102 −)

<r> metagenes = 0.98

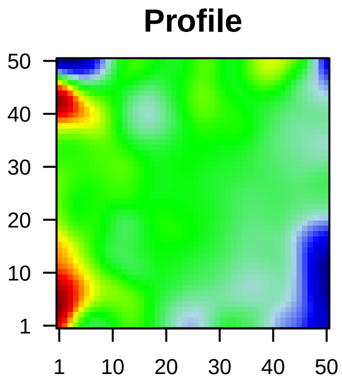
<r> genes = 0.43

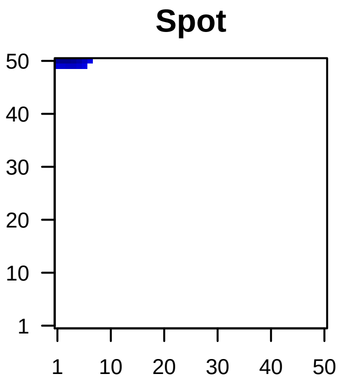
<FC> = −0.5

<shrinkage−t> = −17.52

<p−value> = 0

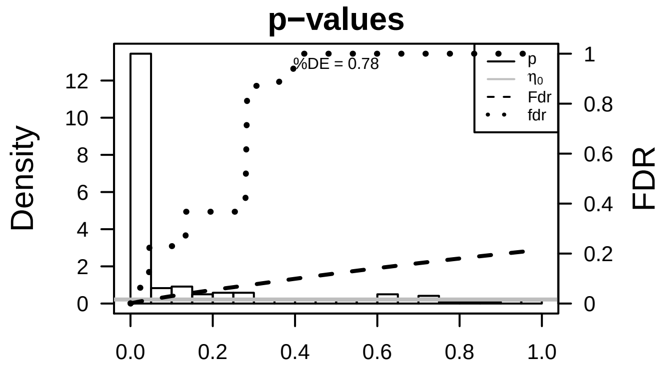
<fdr> = 0.43


Profile


Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	8644	−2.32	2e−16	2e−15	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
2	218	−2.12	2e−16	2e−15	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
3	22802	−1.76	2e−16	2e−15	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
4	192666	−1.81	2e−16	2e−15	1 x 50	keratin 24 [Source:HGNC Symbol;Acc:18527]
5	3934	−1.69	2e−16	2e−15	1 x 50	lipocalin 2 [Source:HGNC Symbol;Acc:6526]
6	7851	−1.78	2e−16	2e−15	1 x 50	mal, T−cell differentiation protein−like [Source:HGNC Symbol
7	6337	−1.62	2e−16	2e−15	3 x 50	sodium channel, non−voltage−gated 1 alpha subunit [Source:
8	92196	−1.52	7e−16	2e−14	3 x 50	death associated protein−like 1 [Source:HGNC Symbol;Acc:2
9	5275	−1.52	9e−16	3e−14	1 x 50	serpin peptidase inhibitor, clade B (ovalbumin), member 13 [S
10	2012	−1.38	2e−15	3e−13	3 x 50	epithelial membrane protein 1 [Source:HGNC Symbol;Acc:33
11	5266	−1.34	8e−15	6e−13	1 x 49	peptidase inhibitor 3, skin−derived [Source:HGNC Symbol;Ac
12	1673	1.44	3e−14	6e−13	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
13	6702	−1.43	3e−14	4e−12	1 x 50	
14	114569	−1.4	1e−13	1e−11	4 x 50	mal, T−cell differentiation protein 2 (gene/pseudogene) [Sour
15	5307	−1.3	5e−13	1e−11	3 x 50	paired−like homeodomain 1 [Source:HGNC Symbol;Acc:900
16	200958	−1.35	7e−13	2e−11	6 x 50	mucin 20, cell surface associated [Source:HGNC Symbol;Acc
17	9368	−1.34	1e−12	7e−11	5 x 50	solute carrier family 9, subfamily A (NHE3, cation proton anti
18	5055	−1.32	2e−12	1e−10	1 x 50	serpin peptidase inhibitor, clade B (ovalbumin), member 2 [Sc
19	6317	−1.3	5e−12	3e−10	1 x 49	serpin peptidase inhibitor, clade B (ovalbumin), member 3 [Sc
20	5493	−1.28	1e−11	9e−10	1 x 50	periplakin [Source:HGNC Symbol;Acc:9273]


p−values

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−34.52	NULL	67 / 135	H.Tiss	WIRTH_Mucosa
2	−21.84	NULL	12 / 21	CC	cornified envelope
3	−18.48	NULL	7 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
4	−16.33	NULL	16 / 53	BP	keratinocyte differentiation
5	−14.79	NULL	13 / 42	BP	keratinization
6	−14.54	NULL	66 / 572	Disease	GUDJ_psoriasis up
7	−14.52	NULL	6 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
8	−14.09	NULL	7 / 15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
9	−13.87	NULL	6 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
10	−13.57	NULL	10 / 52	BP	negative regulation of endopeptidase activity
11	−12.96	NULL	4 / 16	GSEA C2	JAEGER_METASTASIS_DN
12	−12.73	NULL	5 / 15	GSEA C2	LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
13	−11.73	NULL	17 / 76	BP	epidermis development
14	−11.69	NULL	3 / 13	GSEA C2	FARMER_BREAST_CANCER_APOCRINE VS LUMINAL
15	−11.06	NULL	3 / 13	GSEA C2	WONG_ENDMETRIUM_CANCER_UP
16	−11	NULL	2 / 8	TF Tissue	VAQUERIZAS_Tongue
17	−10.95	NULL	5 / 29	BP	regulation of proteolysis
18	−10.83	NULL	3 / 14	GSEA C2	KEGG_PHENYLALANINE_METABOLISM
19	−10.79	NULL	3 / 12	BP	cellular aldehyde metabolic process
20	−10.67	NULL	3 / 16	GSEA C2	CHEOK_RESPONSE_TO_MERCAPTOPURINE_AND_LD_MTX_
21	−10.59	NULL	2 / 8	GSEA C2	MCLACHLAN_DENTAL_CARIES_UP
22	−10.42	NULL	5 / 15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
23	−10.27	NULL	4 / 24	TF Tissue	VAQUERIZAS_Trachea
24	−10.25	NULL	4 / 15	MF	retinol dehydrogenase activity
25	−10.13	NULL	10 / 79	MF	serine−type endopeptidase inhibitor activity
26	−9.95	NULL	3 / 16	CC	microvillus membrane
27	−9.91	NULL	5 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
28	−9.89	NULL	2 / 9	GSEA C2	MCLACHLAN_DENTAL_CARIES_DN
29	−9.85	NULL	2 / 15	GSEA C2	KORKOLA_TERATOMA
30	−9.73	NULL	3 / 13	GSEA C2	HAN_SATB1_TARGETS_DN
31	−9.64	NULL	4 / 10	GSEA C2	SMID_BREAST_CANCER_ERBB2_UP
32	−9.55	NULL	4 / 16	GSEA C2	LEE_LIVER_CANCER_MYC_TGFA_UP
33	−9.51	NULL	3 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
34	−9.3	NULL	2 / 10	GSEA C2	NIKOLSKY_BREAST_CANCER_20Q12_Q13_AMPLICON
35	−9.24	NULL	5 / 13	BP	negative regulation of peptidase activity
36	−8.96	NULL	1 / 10	BP	positive regulation of endothelial cell apoptotic process
37	−8.96	NULL	1 / 10	BP	retinal metabolic process
38	−8.81	NULL	2 / 11	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_BONE_DN
39	−8.73	NULL	3 / 15	GSEA C2	LEE_LIVER_CANCER_MYC_E2F1_UP
40	−8.66	NULL	1 / 9	GSEA C2	NIKOLSKY_BREAST_CANCER_17P11_AMPLICON