GW_028

Global Summary

%DE = 0.14

genes with fdr < 0.2 = 1760 (966 + / 794 −)

genes with fdr < 0.1 = 1278 (716 + / 562 −)

genes with fdr < 0.05 = 1100 (628 + / 472 −)

genes with fdr < 0.01 = 778 (460 + / 318 −)

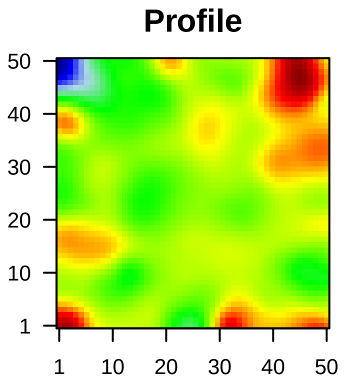
genes in genesets = 16332

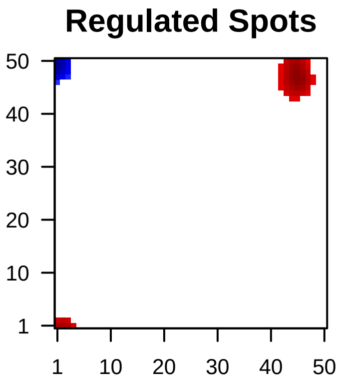
<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.11

<fdr> = 0.86



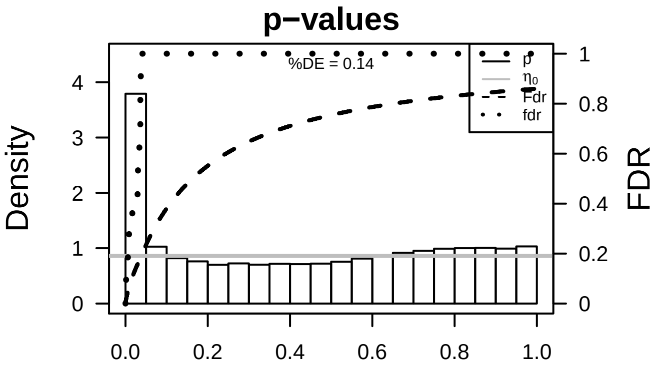


Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	131	1.78	2e−16	4e−14	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	165	1.43	2e−16	4e−14	3 x 1	AE binding protein 1 [Source:HGNC Symbol;Acc:303]
3	57016	−1.5	2e−16	4e−14	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
4	441282	−1.51	2e−16	4e−14	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC S
5	8644	−2.07	2e−16	4e−14	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
6	1109	−1.64	2e−16	4e−14	13 x 50	aldo−keto reductase family 1, member C4 [Source:HGNC Sy
7	501	−2.04	2e−16	4e−14	6 x 46	aldehyde dehydrogenase 7 family, member A1 [Source:HGN
8	445328	−1.86	2e−16	4e−14	4 x 46	Rho guanine nucleotide exchange factor (GEF) 35 [Source:H
9	260436	−1.58	2e−16	4e−14	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symb
10	768	1.87	2e−16	4e−14	1 x 6	carbonic anhydrase IX [Source:HGNC Symbol;Acc:1383]
11	131076	1.42	2e−16	4e−14	1 x 16	coiled−coil domain containing 58 [Source:HGNC Symbol;Acc
12	1152	1.51	2e−16	4e−14	1 x 17	creatine kinase, brain [Source:HGNC Symbol;Acc:1991]
13	9076	1.47	2e−16	4e−14	49 x 50	claudin 1 [Source:HGNC Symbol;Acc:2032]
14	1277	1.96	2e−16	4e−14	2 x 1	collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
15	1278	1.42	2e−16	4e−14	2 x 1	collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198]
16	1281	1.37	2e−16	4e−14	2 x 1	collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]
17	49860	−2.76	2e−16	4e−14	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
18	1410	−1.52	2e−16	4e−14	25 x 1	crystallin, alpha B [Source:HGNC Symbol;Acc:2389]
19	1475	1.95	2e−16	4e−14	1 x 50	cystatin A (stefin A) [Source:HGNC Symbol;Acc:2481]
20	3627	2.07	2e−16	4e−14	32 x 1	chemokine (C−X−C motif) ligand 10 [Source:HGNC Symbol;

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	12.11	NULL	633	Chr	Chr 9
2	11.65	NULL	190	CC	extracellular matrix
3	10.74	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
4	10.63	NULL	52	Chr	Chr HSCHR6_MHC_QBL
5	10.47	NULL	4640	CC	nucleus
6	10.2	NULL	37	BP	collagen fibril organization
7	9.56	NULL	242	BP	extracellular matrix organization
8	9.38	NULL	69	BP	extracellular matrix disassembly
9	8.99	NULL	7	MMML CGS	MACIEJ_MMML 9
10	8.89	NULL	16	MMML CGS	MACIEJ_MMML 1
11	8.87	NULL	142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
12	8.87	NULL	142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
13	8.75	NULL	11	MF	platelet−derived growth factor binding
14	8.61	NULL	13	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
15	8.19	NULL	64	BP	collagen catabolic process
16	8.04	NULL	68	Glio	cultured astroglia vs. in vivo astrocytes
17	7.95	NULL	949	CC	nucleoplasm
18	7.89	NULL	6	Lymphoma	DAVE_MHCCII BL DN
19	7.89	NULL	370	BP	mitotic cell cycle
20	7.47	NULL	57	MF	extracellular matrix structural constituent
Underexpressed					
1	−8.25	NULL	957	Chr	Chr 11
2	−8.2	NULL	3274	CC	integral to membrane
3	−7.79	NULL	743	Chr	Chr 7
4	−6.85	NULL	4	MMML CGS	MACIEJ_MMML 23
5	−6.45	NULL	135	H.Tiss	WIRTH_Mucosa
6	−6.29	NULL	449	Chr	Chr 20
7	−6	NULL	15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
8	−5.97	NULL	44	BP	steroid metabolic process
9	−5.8	NULL	11	MF	oxygen transporter activity
10	−5.79	NULL	1253	BP	small molecule metabolic process
11	−5.77	NULL	20	MF	glutathione transferase activity
12	−5.71	NULL	42	BP	keratinization
13	−5.68	NULL	26	MF	oxygen binding
14	−5.63	NULL	14	BP	cyclooxygenase pathway
15	−5.4	NULL	12	BP	cellular aldehyde metabolic process
16	−5.26	NULL	16	BP	response to reactive oxygen species
17	−5.21	NULL	621	CC	endoplasmic reticulum
18	−5.17	NULL	10	CC	hemoglobin complex
19	−5.06	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_D
20	−5.01	NULL	49	BP	arachidonic acid metabolic process



GW_028

Local Summary

%DE = 0.79

metagenes = 7

genes = 141

genes in genesets = 141

genes with fdr < 0.1 = 86 (70 + / 16 −)

genes with fdr < 0.05 = 86 (70 + / 16 −)

genes with fdr < 0.01 = 62 (55 + / 7 −)

<r> metagenes = 0.99

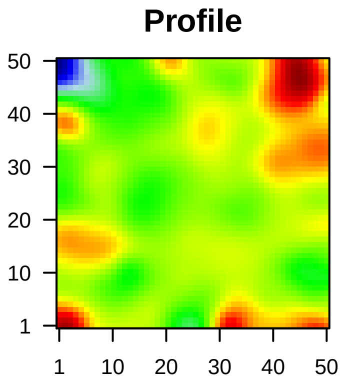
<r> genes = 0.48

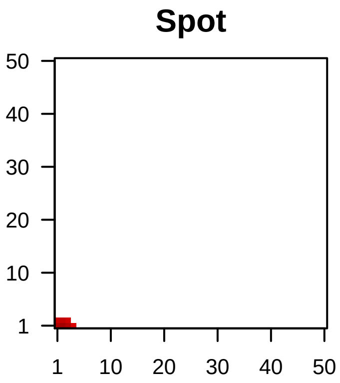
<FC> = 0.36

<shrinkage−t> = 12.69

<p−value> = 0

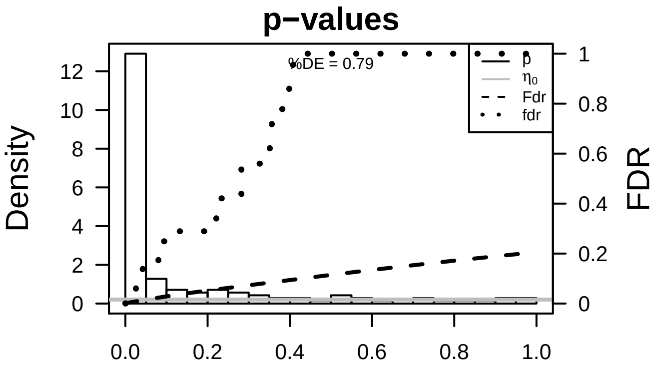
<fdr> = 0.43





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	165	1.43	2e−16	6e−16	3 x 1	AE binding protein 1 [Source:HGNC Symbol;Acc:303]
2	1277	1.96	2e−16	6e−16	2 x 1	collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
3	1278	1.42	2e−16	6e−16	2 x 1	collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198]
4	1281	1.37	2e−16	6e−16	2 x 1	collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]
5	3040	−1.9	2e−16	6e−16	4 x 1	hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
6	3576	1.67	2e−16	6e−16	1 x 1	interleukin 8 [Source:HGNC Symbol;Acc:6025]
7	8076	1.73	2e−16	6e−16	4 x 1	microfibrillar associated protein 5 [Source:HGNC Symbol;Acc
8	4320	2.37	2e−16	6e−16	3 x 1	matrix metallopeptidase 11 (stromelysin 3) [Source:HGNC Sy
9	10631	1.46	2e−16	6e−16	2 x 1	periostin, osteoblast specific factor [Source:HGNC Symbol;Ac
10	12	−1.92	2e−16	6e−16	1 x 1	
11	1290	1.21	3e−14	3e−13	2 x 1	collagen, type V, alpha 2 [Source:HGNC Symbol;Acc:2210]
12	3491	1.21	3e−14	3e−13	2 x 1	cysteine−rich, angiogenic inducer, 61 [Source:HGNC Symbol
13	1301	1.2	5e−14	3e−13	4 x 1	collagen, type XI, alpha 1 [Source:HGNC Symbol;Acc:2186]
14	1293	1.2	5e−14	3e−13	2 x 1	collagen, type VI, alpha 3 [Source:HGNC Symbol;Acc:2213]
15	1291	1.2	6e−14	4e−13	2 x 1	collagen, type VI, alpha 1 [Source:HGNC Symbol;Acc:2211]
16	115908	1.19	7e−14	6e−12	3 x 1	collagen triple helix repeat containing 1 [Source:HGNC Symb
17	6678	1.16	3e−13	2e−10	3 x 1	secreted protein, acidic, cysteine−rich (osteonectin) [Source:H
18	7058	1.07	1e−11	2e−10	2 x 1	thrombospondin 2 [Source:HGNC Symbol;Acc:11786]
19	4316	−1.07	2e−11	5e−10	2 x 1	matrix metallopeptidase 7 (matrilysin, uterine) [Source:HGNC
20	1300	1.05	5e−11	5e−10	3 x 1	collagen, type X, alpha 1 [Source:HGNC Symbol;Acc:2185]



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	49.13	NULL	12 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
2	42.06	NULL	14 / 16	MMML CGS	MACIEJ_MMML 1
3	41.29	NULL	7 / 11	MF	platelet−derived growth factor binding
4	37.18	NULL	50 / 190	CC	extracellular matrix
5	36.17	NULL	25 / 64	BP	collagen catabolic process
6	36	NULL	13 / 37	BP	collagen fibril organization
7	35.99	NULL	28 / 69	BP	extracellular matrix disassembly
8	31.87	NULL	51 / 250	Lymphoma	LENZ_Stromal signature 1
9	31.04	NULL	6 / 13	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
10	29.41	NULL	8 / 12	miRNA target	miR−29c
11	28.32	NULL	7 / 16	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_N
12	28.27	NULL	18 / 57	MF	extracellular matrix structural constituent
13	28.22	NULL	49 / 242	BP	extracellular matrix organization
14	27.21	NULL	4 / 10	BP	protein heterotrimerization
15	23.83	NULL	4 / 8	GSEA C2	HAEGERSTRAND_RESPONSE_TO_IMATINIB
16	22.77	NULL	4 / 5	GSEA C2	COLLER_MYC_TARGETS_DN
17	22.54	NULL	8 / 40	BP	cellular response to amino acid stimulus
18	22.52	NULL	5 / 10	GSEA C2	KEGG_ECM_RECEPTOR_INTERACTION
19	22.5	NULL	13 / 68	CC	collagen
20	22.16	NULL	5 / 15	GSEA C2	TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_DUCTAL_NO
21	21.76	NULL	4 / 12	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C2
22	21.11	NULL	10 / 15	GSEA C2	CROMER_TUMORIGENESIS_UP
23	19.5	NULL	8 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_UP
24	19.4	NULL	5 / 13	GSEA C2	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
25	19.1	NULL	2 / 8	GSEA C2	OSAWA_TNF_TARGETS
26	18.97	NULL	19 / 153	CC	endoplasmic reticulum lumen
27	18.62	NULL	11 / 19	MF	extracellular matrix binding
28	18.58	NULL	1 / 3	GSEA C2	REN_MIF_TARGETS_DN
29	18.2	NULL	6 / 16	GSEA C2	CROONQUIST_STROMAL_STIMULATION_UP
30	17.61	NULL	4 / 15	GSEA C2	REACTOME_NCAM1_INTERACTIONS
31	17.53	NULL	5 / 15	GSEA C2	CHANG_POU5F1_TARGETS_UP
32	17.22	NULL	5 / 16	GSEA C2	REACTOME_SIGNALING_BY_PDGF
33	17.18	NULL	6 / 13	GSEA C2	TSAI_RESPONSE_TO_RADIATION_THERAPY
34	16.98	NULL	4 / 16	GSEA C2	REACTOME_AXON_GUIDANCE
35	16.98	NULL	4 / 16	GSEA C2	REACTOME_NCAM_SIGNALING_FOR_NEURITE_OUT_GROWT
36	16.94	NULL	2 / 11	GSEA C2	REACTOME_PLATELET_ADHESION_TO_EXPOSED_COLLAGE
37	16.92	NULL	4 / 14	GSEA C2	WILCOX_PRESPONSE_TO_ROGESTERONE_DN
38	16.81	NULL	20 / 119	Lymphoma	ROSOLOWSKI_green total
39	16.62	NULL	26 / 183	CC	proteinaceous extracellular matrix
40	16.55	NULL	7 / 16	GSEA C2	ROZANOV_MMP14_TARGETS_SUBSET

GW_028

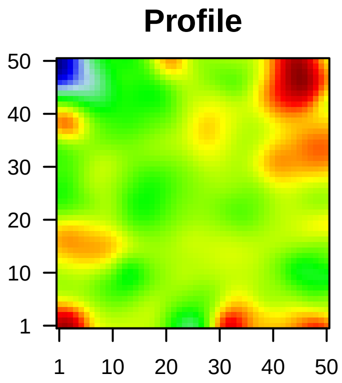
Local Summary

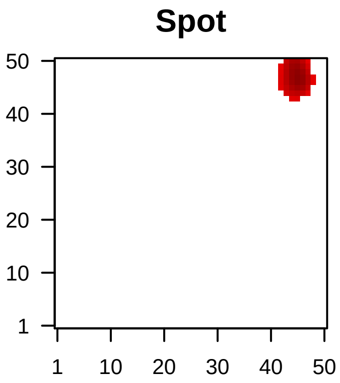
%DE = 0.62
metagenes = 44
genes = 456
genes in genesets = 453

genes with fdr < 0.1 = 185 (176 + / 9 −)
genes with fdr < 0.05 = 126 (119 + / 7 −)
genes with fdr < 0.01 = 67 (65 + / 2 −)

<r> metagenes = 0.92
<r> genes = 0.34

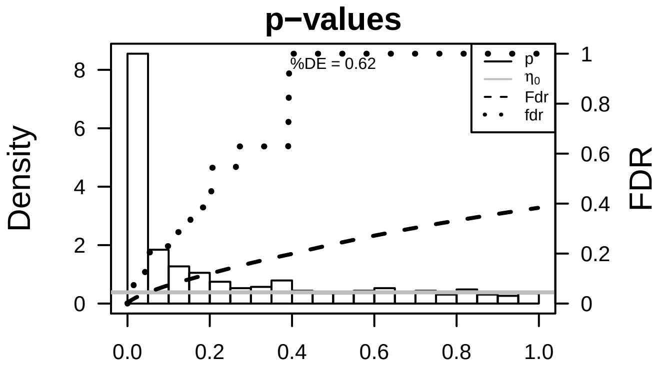
<FC> = 0.25
<shrinkage−t> = 8.76
<p−value> = 0.02
<fdr> = 0.68





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	3787	1.31	2e−16	2e−14	46 x 45	potassium voltage−gated channel, delayed−rectifier, subfamil
2	116832	−1.6	2e−16	2e−14	46 x 50	ribosomal protein L39−like [Source:HGNC Symbol;Acc:1709
3	51087	1.22	2e−14	6e−09	47 x 46	Y box binding protein 2 [Source:HGNC Symbol;Acc:17948]
4	10388	1.05	3e−11	2e−08	47 x 46	synaptonemal complex protein 2 [Source:HGNC Symbol;Acc:
5	51053	1.02	1e−10	6e−07	45 x 49	geminin, DNA replication inhibitor [Source:HGNC Symbol;Ac
6	10635	0.93	4e−09	6e−07	45 x 50	RAD51 associated protein 1 [Source:HGNC Symbol;Acc:169
7	3148	0.92	7e−09	6e−07	46 x 46	high mobility group box 2 [Source:HGNC Symbol;Acc:5000]
8	7083	0.91	1e−08	2e−06	45 x 49	thymidine kinase 1, soluble [Source:HGNC Symbol;Acc:1183
9	1029	0.87	4e−08	2e−06	45 x 45	cyclin−dependent kinase inhibitor 2A [Source:HGNC Symbol;
10	339535	0.87	5e−08	2e−06	48 x 46	long intergenic non−protein coding RNA 1139 [Source:HGNC
11	3833	0.87	5e−08	2e−06	45 x 48	kinesin family member C1 [Source:HGNC Symbol;Acc:6389]
12	9833	0.86	6e−08	8e−06	44 x 50	maternal embryonic leucine zipper kinase [Source:HGNC Sy
13	64105	0.85	1e−07	1e−05	45 x 48	centromere protein K [Source:HGNC Symbol;Acc:29479]
14	2189	0.83	2e−07	1e−05	45 x 45	Fanconi anemia, complementation group G [Source:HGNC S
15	55355	0.82	3e−07	1e−05	44 x 49	Holliday junction recognition protein [Source:HGNC Symbol;
16	26255	0.8	4e−07	1e−05	44 x 48	pituitary tumor−transforming 3, pseudogene [Source:HGNC
17	23642	0.8	5e−07	1e−05	44 x 45	small nucleolar RNA host gene 1 (non−protein coding) [Sour
18	10274	0.8	5e−07	1e−05	47 x 50	stromal antigen 1 [Source:HGNC Symbol;Acc:11354]
19	890	0.79	6e−07	1e−05	44 x 50	cyclin A2 [Source:HGNC Symbol;Acc:1578]
20	91057	0.79	6e−07	1e−05	46 x 47	coiled−coil domain containing 34 [Source:HGNC Symbol;Acc



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	38.94	NULL	98 / 142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
2	38.94	NULL	98 / 142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
3	30.29	NULL	16 / 16	GSEA C2	EGUCHI_CELL_CYCLE_RB1_TARGETS
4	24.31	NULL	113 / 370	BP	mitotic cell cycle
5	22.39	NULL	54 / 149	BP	DNA replication
6	19.29	NULL	13 / 14	MMML CGS	MACIEJ_MMML 4
7	18.36	NULL	8 / 11	GSEA C2	REACTOME_UNWINDING_OF_DNA
8	18.02	NULL	109 / 530	Cancer	Lembcke_Normal vs Adenoma
9	17.95	NULL	26 / 57	Glio	developing astrocytes
10	17.88	NULL	21 / 30	BP	DNA strand elongation involved in DNA replication
11	17.44	NULL	11 / 16	GSEA C2	GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
12	17.17	NULL	11 / 16	GSEA C2	SONG_TARGETS_OF_IE86_CMV_PROTEIN
13	16.69	NULL	122 / 949	CC	nucleoplasm
14	15.88	NULL	12 / 15	GSEA C2	CHANG_CYCLING_GENES
15	15.76	NULL	10 / 16	Cancer	WOLFER_overlap genes
16	15.58	NULL	8 / 11	GSEA C2	LIANG_SILENCED_BY_METHYLATION_DN
17	14.96	NULL	26 / 56	CC	chromosome, centromeric region
18	14.76	NULL	13 / 16	GSEA C2	FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
19	14.67	NULL	11 / 16	GSEA C2	FRASOR_RESPONSE_TO_SERM_OR_FULVESTRANT_DN
20	14.29	NULL	11 / 15	GSEA C2	WU_APOPTOSIS_BY_CDKN1A_VIA_TP53
21	14.23	NULL	57 / 298	BP	DNA repair
22	13.93	NULL	12 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_2
23	13.8	NULL	9 / 16	GSEA C2	REACTOME_G2_M_CHECKPOINTS
24	13.74	NULL	11 / 22	BP	CENP−A containing nucleosome assembly at centromere
25	13.72	NULL	8 / 16	GSEA C2	BIOCARTA_MCM_PATHWAY
26	13.59	NULL	12 / 15	GSEA C2	FINETTI_BREAST_CANCER_KINOME_RED
27	13.59	NULL	6 / 9	GSEA C2	KUMAMOTO_RESPONSE_TO_NUTLIN_3A_DN
28	13.55	NULL	7 / 16	GSEA C2	CROONQUIST_NRAS_VS_STROMAL_STIMULATION_DN
29	13.55	NULL	10 / 16	GSEA C2	VERNELL_RETINOBLASTOMA_PATHWAY_UP
30	13.48	NULL	9 / 11	GSEA C2	KALMA_E2F1_TARGETS
31	13.48	NULL	12 / 16	GSEA C2	REACTOME_DNA_STRAND_ELONGATION
32	13.15	NULL	12 / 16	GSEA C2	SCIAN_CELL_CYCLE_TARGETS_OF_TP53_AND_TP73_DN
33	13.1	NULL	5 / 8	GSEA C2	REACTOME_E2F_TRANSCRIPTIONAL_TARGETS_AT_G1_S
34	12.86	NULL	36 / 148	BP	G1/S transition of mitotic cell cycle
35	12.78	NULL	11 / 16	GSEA C2	CROONQUIST_NRAS_SIGNALING_DN
36	12.71	NULL	8 / 15	GSEA C2	KAUFFMANN_MELANOMA_RELAPSE_UP
37	12.49	NULL	14 / 22	BP	DNA replication initiation
38	12.47	NULL	6 / 14	GSEA C2	SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_UP
39	12.33	NULL	7 / 13	GSEA C2	SA_REG_CASCADE_OF_CYCLIN_EXPR
40	12.14	NULL	6 / 13	GSEA C2	SLEBOS_HEAD_AND_NECK_CANCER_WITH_HPV_UP

GW_028

Local Summary

%DE = 0.86

metagenes = 13

genes = 193

genes in genesets = 188

genes with fdr < 0.1 = 138 (32 + / 106 −)

genes with fdr < 0.05 = 133 (29 + / 104 −)

genes with fdr < 0.01 = 116 (25 + / 91 −)

<r> metagenes = 0.97

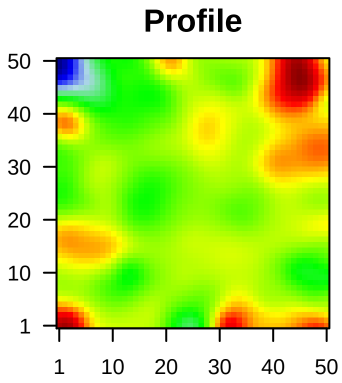
<r> genes = 0.47

<FC> = −0.44

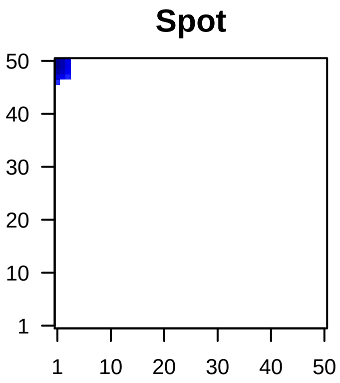
<shrinkage−t> = −15.43

<p−value> = 0

<fdr> = 0.33



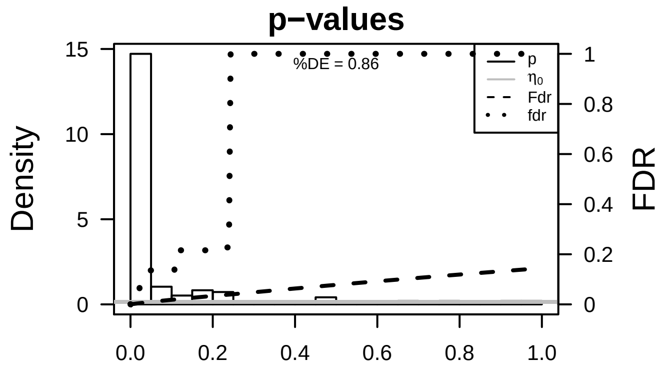
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	131	1.78	2e−16	2e−16	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	57016	−1.5	2e−16	2e−16	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
3	441282	−1.51	2e−16	2e−16	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC Sy
4	8644	−2.07	2e−16	2e−16	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
5	49860	−2.76	2e−16	2e−16	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
6	1475	1.95	2e−16	2e−16	1 x 50	cystatin A (stefin A) [Source:HGNC Symbol;Acc:2481]
7	9547	−1.54	2e−16	2e−16	1 x 46	chemokine (C−X−C motif) ligand 14 [Source:HGNC Symbol;
8	92196	−1.33	2e−16	2e−16	3 x 50	death associated protein−like 1 [Source:HGNC Symbol;Acc:2
9	414325	−1.5	2e−16	2e−16	1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
10	1673	−1.67	2e−16	2e−16	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
11	2941	−1.49	2e−16	2e−16	3 x 50	glutathione S−transferase alpha 4 [Source:HGNC Symbol;Ac
12	11012	−1.49	2e−16	2e−16	1 x 50	kallikrein−related peptidase 11 [Source:HGNC Symbol;Acc:6
13	43849	−1.35	2e−16	2e−16	1 x 50	kallikrein−related peptidase 12 [Source:HGNC Symbol;Acc:6
14	26085	−1.61	2e−16	2e−16	1 x 50	kallikrein−related peptidase 13 [Source:HGNC Symbol;Acc:6
15	5653	−2.2	2e−16	2e−16	1 x 50	kallikrein−related peptidase 6 [Source:HGNC Symbol;Acc:63
16	5650	−1.66	2e−16	2e−16	1 x 49	kallikrein−related peptidase 7 [Source:HGNC Symbol;Acc:63
17	192666	1.66	2e−16	2e−16	1 x 50	keratin 24 [Source:HGNC Symbol;Acc:18527]
18	3851	−2.61	2e−16	2e−16	1 x 50	keratin 4 [Source:HGNC Symbol;Acc:6441]
19	388533	−2.99	2e−16	2e−16	1 x 49	keratinocyte differentiation−associated protein [Source:HGNC
20	84648	−1.55	2e−16	2e−16	1 x 48	late cornified envelope 3D [Source:HGNC Symbol;Acc:16615



p−values

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−20.16	NULL	78 / 135	H.Tiss	WIRTH_Mucosa
2	−16.3	NULL	23 / 53	BP	keratinocyte differentiation
3	−15.2	NULL	19 / 42	BP	keratinization
4	−14.92	NULL	3 / 15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
5	−14.53	NULL	87 / 572	Disease	GUDJ_psoriasis up
6	−14.36	NULL	6 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
7	−13.61	NULL	7 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
8	−13.29	NULL	3 / 10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
9	−12.98	NULL	22 / 76	BP	epidermis development
10	−12.89	NULL	5 / 10	MF	RAGE receptor binding
11	−10.98	NULL	18 / 21	CC	cornified envelope
12	−10.25	NULL	1 / 16	BP	response to reactive oxygen species
13	−10.07	NULL	2 / 16	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_LUNG_UP
14	−9.9	NULL	12 / 122	MF	serine−type endopeptidase activity
15	−9.42	NULL	6 / 53	MF	serine−type peptidase activity
16	−9.29	NULL	1 / 19	BP	defense response to Gram−negative bacterium
17	−9.04	NULL	6 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
18	−8.8	NULL	2 / 15	GSEA C2	ALONSO_METASTASIS_NEURAL_UP
19	−8.74	NULL	2 / 17	Disease	BCHETNIA_EBM up
20	−8.59	NULL	1 / 11	Glio	VERHAAK_Brain
21	−8.33	NULL	2 / 11	GSEA C2	ROME_INSULIN_TARGETS_IN_MUSCLE_DN
22	−8.27	NULL	3 / 16	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_DN
23	−8.17	NULL	1 / 12	MF	channel activity
24	−8.14	NULL	3 / 12	BP	cellular aldehyde metabolic process
25	−7.83	NULL	2 / 38	BP	myelination
26	−7.8	NULL	1 / 13	GSEA C2	HASLINGER_B_CLL_WITH_MUTATED_VH_GENES
27	−7.28	NULL	6 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
28	−7.26	NULL	1 / 12	GSEA C2	ODONNELL_METASTASIS_DN
29	−7.26	NULL	1 / 12	GSEA C2	SYED_ESTRADIOL_RESPONSE
30	−7.18	NULL	1 / 15	BP	positive regulation of extrinsic apoptotic signaling pathway via deat
31	−7.18	NULL	1 / 15	GSEA C2	BIOCARTA_MAL_PATHWAY
32	−7.12	NULL	2 / 25	BP	protein tetramerization
33	−7	NULL	1 / 6	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_UP
34	−6.99	NULL	1 / 10	BP	positive regulation of endothelial cell apoptotic process
35	−6.99	NULL	1 / 10	BP	retinal metabolic process
36	−6.91	NULL	1 / 16	Cancer	GENTLES_modul11
37	−6.61	NULL	1 / 11	BP	prostaglandin metabolic process
38	−6.49	NULL	50 / 1182	CC	extracellular region
39	−6.33	NULL	2 / 55	Glio	OL vs. MOG− OL
40	−6.25	NULL	4 / 10	GSEA C2	REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION_P