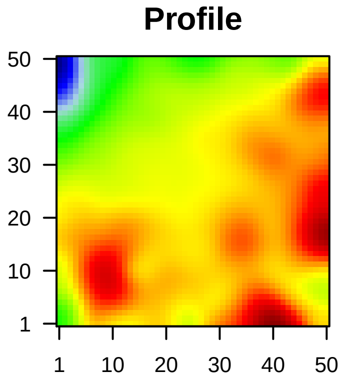
GW_136

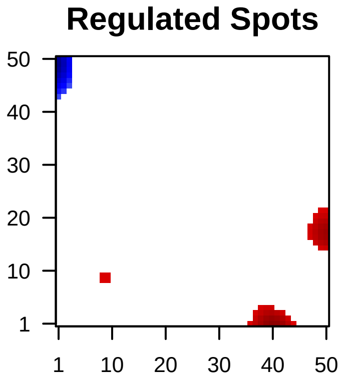
Global Summary

%DE = 0.14
genes with fdr < 0.2 = 1698 (901 + / 797 −)
genes with fdr < 0.1 = 1250 (649 + / 601 −)
genes with fdr < 0.05 = 1043 (517 + / 526 −)
genes with fdr < 0.01 = 681 (313 + / 368 −)

genes in genesets = 16332

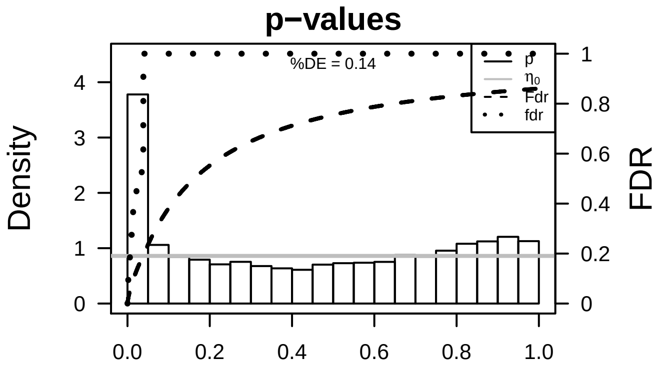
<FC> = 0
<shrinkage−t> = −0.01
<p−value> = 0.12
<fdr> = 0.86





Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	131	−2.59	2e−16	5e−14	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	133	−2.1	2e−16	5e−14	1 x 42	adrenomedullin [Source:HGNC Symbol;Acc:259]
3	113146	−2.09	2e−16	5e−14	1 x 44	AHNAK nucleoprotein 2 [Source:HGNC Symbol;Acc:20125]
4	57016	−2.59	2e−16	5e−14	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductas
5	8644	−2.55	2e−16	5e−14	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
6	218	−2.26	2e−16	5e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
7	347	2.15	2e−16	5e−14	50 x 7	apolipoprotein D [Source:HGNC Symbol;Acc:612]
8	387695	−2.2	2e−16	5e−14	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Sym
9	260436	4.41	2e−16	5e−14	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symb
10	810	−2.32	2e−16	5e−14	1 x 50	calmodulin−like 3 [Source:HGNC Symbol;Acc:1452]
11	169044	2.43	2e−16	5e−14	45 x 1	collagen, type XXII, alpha 1 [Source:HGNC Symbol;Acc:229
12	1281	−2.07	2e−16	5e−14	2 x 1	collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]
13	1464	2.2	2e−16	5e−14	1 x 3	chondroitin sulfate proteoglycan 4 [Source:HGNC Symbol;Ac
14	92196	2.1	2e−16	5e−14	3 x 50	death associated protein−like 1 [Source:HGNC Symbol;Acc:2
15	1672	−2.15	2e−16	5e−14	1 x 50	defensin, beta 1 [Source:HGNC Symbol;Acc:2766]
16	1673	−2.53	2e−16	5e−14	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
17	1830	−2.6	2e−16	5e−14	1 x 48	desmoglein 3 [Source:HGNC Symbol;Acc:3050]
18	2171	−2.41	2e−16	5e−14	1 x 46	fatty acid binding protein 5 (psoriasis−associated) [Source:H
19	8857	2.85	2e−16	5e−14	50 x 13	Fc fragment of IgG binding protein [Source:HGNC Symbol;Ac
20	9982	−3.24	2e−16	5e−14	1 x 47	fibroblast growth factor binding protein 1 [Source:HGNC Sym



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	9.11	NULL	15	CC	MHC class II protein complex
2	8.86	NULL	1749	MF	DNA binding
3	8.13	NULL	1135	Chr	Chr 19
4	8.1	NULL	1574	BP	transcription, DNA−templated
5	7.63	NULL	1581	BP	regulation of transcription, DNA−dependent
6	7.33	NULL	940	MF	nucleic acid binding
7	6.55	NULL	187	Chr	Chr 21
8	6.33	NULL	595	MF	RNA binding
9	6.32	NULL	23	CC	integral to lumenal side of endoplasmic reticulum membrane
10	5.79	NULL	52	Chr	Chr HSCHR6_MHC_QBL
11	5.6	NULL	115	BP	nuclear−transcribed mRNA catabolic process, nonsense−mediated
12	5.42	NULL	87	BP	translational termination
13	5.38	NULL	21	CC	clathrin−coated endocytic vesicle membrane
14	5.34	NULL	81	BP	viral transcription
15	5.3	NULL	92	BP	translational elongation
16	5.14	NULL	28	CC	transport vesicle membrane
17	5.14	NULL	92	BP	viral life cycle
18	5.12	NULL	128	BP	translational initiation
19	5.12	NULL	4640	CC	nucleus
20	5.05	NULL	16	GSEA C2	EINAV_INTERFERON_SIGNATURE_IN_CANCER
Underexpressed					
1	−30.04	NULL	135	H.Tiss	WIRTH_Mucosa
2	−26.13	NULL	572	Disease	GUDJ_psoriasis up
3	−15.99	NULL	21	CC	cornified envelope
4	−15.13	NULL	76	BP	epidermis development
5	−14.85	NULL	53	BP	keratinocyte differentiation
6	−12.83	NULL	42	BP	keratinization
7	−11.37	NULL	19	BP	peptide cross−linking
8	−11.29	NULL	16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
9	−11.14	NULL	618	Chr	Chr 4
10	−10.85	NULL	1182	CC	extracellular region
11	−9.63	NULL	633	Chr	Chr 9
12	−9.04	NULL	553	Cancer	Lembcke_Colonic Inflammation
13	−8.91	NULL	16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
14	−8.9	NULL	717	Chr	Chr 16
15	−8.84	NULL	683	CC	extracellular space
16	−8.71	NULL	10	MF	RAGE receptor binding
17	−8.32	NULL	186	MF	structural molecule activity
18	−8.21	NULL	15	GSEA C2	AIGNER_ZEB1_TARGETS
19	−7.85	NULL	265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
20	−7.85	NULL	265	Glio	willscher_GBM_Verhaak−MES_expression_B_up

GW_136

Local Summary

%DE = 0.87

metagenes = 25

genes = 354

genes in genesets = 326

genes with fdr < 0.1 = 268 (266 + / 2 −)

genes with fdr < 0.05 = 216 (214 + / 2 −)

genes with fdr < 0.01 = 139 (137 + / 2 −)

<r> metagenes = 0.95

<r> genes = 0.42

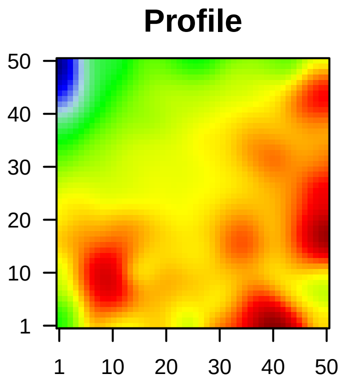
<FC> = 0.61

<shrinkage−t> = 21.36

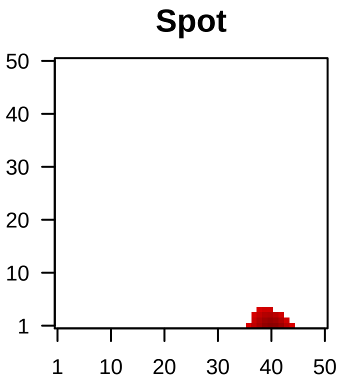
<p−value> = 0.01

<fdr> = 0.5

Profile



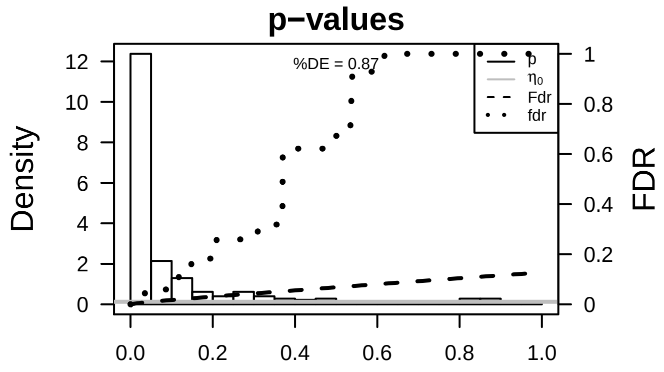
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	3127	2.55	2e−16	1e−14	43 x 1	major histocompatibility complex, class II, DR beta 5 [Source:
2	22809	1.7	2e−11	1e−08	44 x 1	activating transcription factor 5 [Source:HGNC Symbol;Acc:7
3	6376	1.59	3e−10	5e−07	44 x 1	chemokine (C−X3−C motif) ligand 1 [Source:HGNC Symbol;
4	9181	1.41	2e−08	5e−07	44 x 1	Rho/Rac guanine nucleotide exchange factor (GEF) 2 [Sourc
5	2120	1.41	2e−08	2e−06	44 x 1	ets variant 6 [Source:HGNC Symbol;Acc:3495]
6	28996	1.34	9e−08	2e−06	40 x 1	homeodomain interacting protein kinase 2 [Source:HGNC Sy
7	29944	1.34	1e−07	5e−06	42 x 1	paraneoplastic Ma antigen 3 [Source:HGNC Symbol;Acc:187
8	442578	1.3	3e−07	5e−06	39 x 1	
9	727956	1.27	4e−07	5e−06	40 x 1	succinate dehydrogenase complex, subunit A, flavoprotein ps
10	5152	1.26	6e−07	5e−06	40 x 3	phosphodiesterase 9A [Source:HGNC Symbol;Acc:8795]
11	374882	1.25	7e−07	5e−06	42 x 1	transmembrane protein 205 [Source:HGNC Symbol;Acc:296
12	8722	1.25	7e−07	2e−05	42 x 1	cathepsin F [Source:HGNC Symbol;Acc:2531]
13	1375	1.22	1e−06	2e−05	42 x 1	carnitine palmitoyltransferase 1B (muscle) [Source:HGNC Sy
14	84446	1.2	2e−06	2e−05	43 x 1	BR serine/threonine kinase 1 [Source:HGNC Symbol;Acc:18
15	7297	1.2	2e−06	2e−05	44 x 1	tyrosine kinase 2 [Source:HGNC Symbol;Acc:12440]
16	27148	1.19	2e−06	3e−05	41 x 1	serine/threonine kinase 36 [Source:HGNC Symbol;Acc:1720
17	65108	1.18	3e−06	4e−05	44 x 1	MARCKS−like 1 [Source:HGNC Symbol;Acc:7142]
18	84061	1.16	4e−06	4e−05	39 x 1	magnesium transporter 1 [Source:HGNC Symbol;Acc:28880]
19	25862	1.15	5e−06	4e−05	40 x 1	ubiquitin specific peptidase 49 [Source:HGNC Symbol;Acc:2
20	441268	1.14	6e−06	4e−05	41 x 1	

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset
1	9.86	NULL	2 / 9	GSEA C2 GOERING_BLOOD_HDL_CHOLESTEROL_QTL_CIS
2	9.43	NULL	3 / 16	BP negative regulation of neurogenesis
3	8.18	NULL	2 / 4	GSEA C2 BIOCARTA_CYTOKINE_PATHWAY
4	7.62	NULL	3 / 16	GSEA C2 HAMAI_APOPTOSIS_VIA_TRAIL_UP
5	7.04	NULL	1 / 2	miRNA target miR−193a
6	6.82	NULL	4 / 13	GSEA C2 SPIRA_SMOKERS_LUNG_CANCER_DN
7	6.65	NULL	4 / 14	MMML CGS MACIEJ_MMML 8
8	6.55	NULL	1 / 15	CC MHC class II protein complex
9	6.27	NULL	2 / 10	GSEA C2 MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_12
10	6.18	NULL	3 / 13	GSEA C2 BONOME_OVARIAN_CANCER_POOR_SURVIVAL_DN
11	6.16	NULL	51 / 1135	Chr Chr 19
12	6.11	NULL	2 / 15	GSEA C2 FIRESTEIN_PROLIFERATION
13	5.9	NULL	2 / 28	CC transport vesicle membrane
14	5.85	NULL	2 / 13	GSEA C2 ST_GAQ_PATHWAY
15	5.85	NULL	2 / 13	GSEA C2 ST_GA13_PATHWAY
16	5.73	NULL	1 / 9	GSEA C2 PENG_GLUCOSE_DEPRIVATION_UP
17	5.73	NULL	1 / 9	GSEA C2 PENG_GLUCOSE_DEPRIVATION_DN
18	5.73	NULL	2 / 11	GSEA C2 KIM_GASTRIC_CANCER_CHEMOSENSITIVITY
19	5.72	NULL	1 / 8	GSEA C2 BOQUEST_STEM_CELL_DN
20	5.64	NULL	2 / 8	GSEA C2 OSAWA_TNF_TARGETS
21	5.57	NULL	1 / 4	GSEA C2 MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_5
22	5.33	NULL	1 / 21	CC clathrin−coated endocytic vesicle membrane
23	5.18	NULL	3 / 23	BP G2 DNA damage checkpoint
24	5.08	NULL	1 / 11	GSEA C2 TRACEY_RESISTANCE_TO_IFNA2_DN
25	5.04	NULL	2 / 19	BP negative regulation of extrinsic apoptotic signaling pathway via dea
26	5.03	NULL	1 / 23	CC integral to lumenal side of endoplasmic reticulum membrane
27	5.03	NULL	1 / 6	GSEA C2 PENG_GLUTAMINE_DEPRIVATION_UP
28	5.03	NULL	1 / 6	GSEA C2 ST_INTERLEUKIN_13_PATHWAY
29	5.03	NULL	1 / 6	GSEA C2 ST_IL_13_PATHWAY
30	4.9	NULL	2 / 16	GSEA C2 KEGG_DORSO_VENTRAL_AXIS_FORMATION
31	4.81	NULL	1 / 12	GSEA C2 PENG_LEUCINE_DEPRIVATION_UP
32	4.79	NULL	2 / 14	GSEA C2 CAIRO_HEPATOBLASTOMA_CLASSES_DN
33	4.73	NULL	2 / 14	GSEA C2 MITSIADES_RESPONSE_TO_APLIDIN_DN
34	4.73	NULL	2 / 14	GSEA C2 BIOCARTA_IL12_PATHWAY
35	4.58	NULL	1 / 13	GSEA C2 GAUSSMANN_MLL_AF4_FUSION_TARGETS_F_DN
36	4.55	NULL	2 / 16	GSEA C2 LUI_THYROID_CANCER_CLUSTER_1
37	4.47	NULL	4 / 60	BP T cell costimulation
38	4.45	NULL	1 / 9	GSEA C2 BROWNE_HCMV_INFECTION_1HR_DN
39	4.43	NULL	1 / 8	GSEA C2 CHANG_CORE_SERUM_RESPONSE_DN
40	4.37	NULL	1 / 14	GSEA C2 LINDSTEDT_DENDRITIC_CELL_MATURATION_A

GW_136

Local Summary

%DE = 0.83

metagenes = 4

genes = 37

genes in genesets = 37

genes with fdr < 0.1 = 24 (24 + / 0 −)

genes with fdr < 0.05 = 17 (17 + / 0 −)

genes with fdr < 0.01 = 16 (16 + / 0 −)

<r> metagenes = 0.99

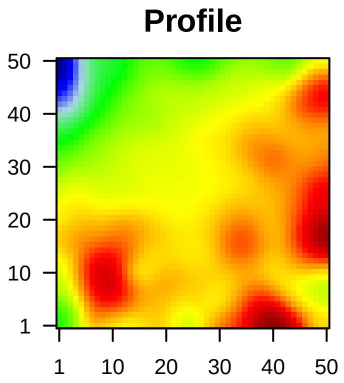
<r> genes = 0.31

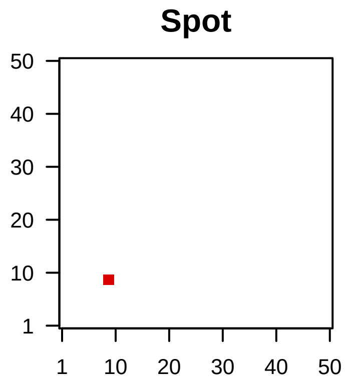
<FC> = 0.52

<shrinkage−t> = 18.31

<p−value> = 0.02

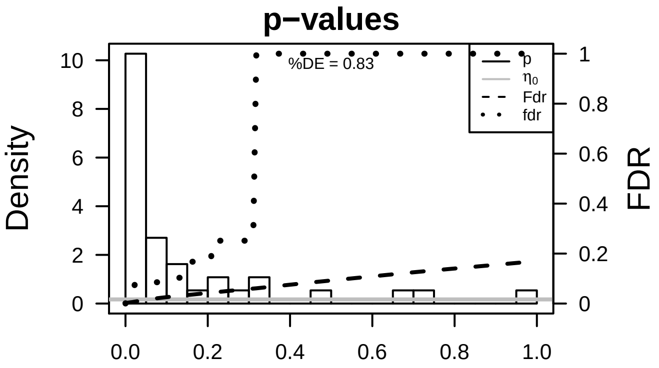
<fdr> = 0.58





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	51477	1.28	4e−07	2e−04	10 x 10	inositol−3−phosphate synthase 1 [Source:HGNC Symbol;Acc
2	26470	1.04	4e−05	2e−04	10 x 9	seizure related 6 homolog (mouse)−like 2 [Source:HGNC Sy
3	140465	1.01	6e−05	6e−04	9 x 9	myosin, light chain 6B, alkali, smooth muscle and non−muscl
4	55624	0.95	2e−04	2e−03	10 x 9	protein O−linked mannose N−acetylglucosaminyltransferase
5	64847	0.88	5e−04	2e−03	10 x 9	spermatogenesis associated 20 [Source:HGNC Symbol;Acc:
6	84033	0.83	1e−03	2e−03	10 x 10	obscurin, cytoskeletal calmodulin and titin−interacting RhoGE
7	151313	0.82	1e−03	5e−03	10 x 9	fumarylacetoacetate hydrolase domain containing 2B [Source
8	29927	0.76	3e−03	5e−03	9 x 10	Sec61 alpha 1 subunit (S. cerevisiae) [Source:HGNC Symbol
9	64132	0.74	3e−03	5e−03	10 x 9	xylosyltransferase II [Source:HGNC Symbol;Acc:15517]
10	8237	0.73	4e−03	1e−02	10 x 9	ubiquitin specific peptidase 11 [Source:HGNC Symbol;Acc:12
11	65980	0.68	7e−03	1e−02	9 x 10	bromodomain containing 9 [Source:HGNC Symbol;Acc:2581
12	83862	0.65	9e−03	1e−02	9 x 9	transmembrane protein 120A [Source:HGNC Symbol;Acc:21
13	57106	0.64	1e−02	1e−02	10 x 9	N−acetyltransferase 14 (GCN5−related, putative) [Source:HG
14	404217	0.64	1e−02	1e−02	10 x 9	cortexin 1 [Source:HGNC Symbol;Acc:31108]
15	8703	0.63	1e−02	1e−02	9 x 10	UDP−Gal:betaGlcNAc beta 1,4− galactosyltransferase, polyp
16	2026	0.62	1e−02	1e−02	10 x 10	enolase 2 (gamma, neuronal) [Source:HGNC Symbol;Acc:33
17	57414	0.61	1e−02	1e−02	9 x 10	rhomboid domain containing 2 [Source:HGNC Symbol;Acc:2
18	55000	0.57	2e−02	5e−02	10 x 10	taurine up−regulated 1 (non−protein coding) [Source:HGNC
19	53635	0.56	2e−02	9e−02	9 x 9	prostate tumor overexpressed 1 [Source:HGNC Symbol;Acc:
20	163033	0.49	5e−02	9e−02	9 x 9	zinc finger protein 579 [Source:HGNC Symbol;Acc:26646]



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	16.47	NULL	2 / 15	MF	acetylglucosaminyltransferase activity
2	12.62	NULL	1 / 6	GSEA C2	CAFFAREL_RESPONSE_TO_THC_24HR_3_UP
3	12.39	NULL	1 / 15	GSEA C2	KEGG_INOSITOL_PHOSPHATE_METABOLISM
4	12.06	NULL	1 / 11	BP	cerebellar Purkinje cell layer development
5	10.66	NULL	1 / 13	CC	muscle myosin complex
6	10.66	NULL	1 / 13	GSEA C2	REACTOME_SMOOTH_MUSCLE_CONTRACTION
7	10.21	NULL	1 / 14	GSEA C2	REACTOME_MUSCLE_CONTRACTION
8	9.83	NULL	2 / 44	MF	structural constituent of muscle
9	9.81	NULL	1 / 15	GSEA C2	GOLUB_ALL_VS_AML_UP
10	9.49	NULL	1 / 8	GSEA C2	NIKOLSKY_BREAST_CANCER_5P15_AMPLICON
11	9.12	NULL	1 / 12	MF	titin binding
12	8.51	NULL	1 / 29	BP	phospholipid biosynthetic process
13	8.33	NULL	1 / 14	MF	ankyrin binding
14	8.32	NULL	1 / 12	GSEA C2	THUM_SYSTOLIC_HEART_FAILURE_UP
15	8.32	NULL	1 / 12	GSEA C2	KEGG_VIBRIO_CHOLERAE_INFECTION
16	8.32	NULL	1 / 12	GSEA C2	REACTOME_INSULIN_SYNTHESIS_AND_SECRETION
17	8.11	NULL	1 / 12	BP	heparan sulfate proteoglycan biosynthetic process
18	8	NULL	1 / 15	GSEA C2	REACTOME_NRAGE_SIGNALS_DEATH_THROUGH_JNK
19	7.93	NULL	1 / 13	GSEA C2	CHIANG_LIVER_CANCER_SUBCLASS_UNANNOTATED_DN
20	7.71	NULL	1 / 16	CC	M band
21	7.71	NULL	1 / 16	GSEA C2	REACTOME_CELL_DEATH_SIGNALLING_VIA_NRAGE_NRIF_A
22	7.71	NULL	1 / 16	GSEA C2	REACTOME_G_ALPHA_12_13_SIGNALLING_EVENTS
23	7.71	NULL	1 / 16	GSEA C2	REACTOME_P75_NTR_RECEPTOR_MEDIATED_SIGNALLING
24	7.71	NULL	1 / 16	GSEA C2	REACTOME_RHO_GTPASE_CYCLE
25	7.6	NULL	1 / 14	GSEA C2	NUYTTEN_NIPP1_TARGETS_DN
26	7.6	NULL	1 / 14	GSEA C2	RIGGINS_TAMOXIFEN_RESISTANCE_UP
27	7.31	NULL	1 / 14	GSEA C2	MAYBURD_RESPONSE_TO_L663536_UP
28	7.3	NULL	1 / 15	GSEA C2	GAZDA_DIAMOND_BLACKFAN_ANEMIA_PROGENITOR_DN
29	7.3	NULL	1 / 15	GSEA C2	SENESE_HDAC1_TARGETS_UP
30	7.3	NULL	1 / 15	GSEA C2	DAIRKEE_CANCER_PRONE_RESPONSE_BPA_E2
31	7.11	NULL	1 / 15	GSEA C2	KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_CHONDROIT
32	7.03	NULL	1 / 16	GSEA C2	SENESE_HDAC1_AND_HDAC2_TARGETS_UP
33	7.03	NULL	1 / 16	GSEA C2	SENESE_HDAC3_TARGETS_UP
34	7.03	NULL	1 / 16	GSEA C2	FALVELLA_SMOKERS_WITH_LUNG_CANCER
35	7.03	NULL	1 / 16	GSEA C2	KEGG_PROTEIN_EXPORT
36	7.02	NULL	1 / 15	GSEA C2	REACTOME_ASSOCIATION_OF_TRIC_CCT_WITH_TARGET_P
37	7	NULL	1 / 24	BP	protein O−linked glycosylation
38	6.89	NULL	1 / 42	BP	inositol phosphate metabolic process
39	6.58	NULL	1 / 21	BP	sarcomere organization
40	6.56	NULL	1 / 18	BP	response to interferon−gamma

GW_136

Local Summary

%DE = 0.85

metagenes = 25

genes = 255

genes in genesets = 250

genes with fdr < 0.1 = 176 (174 + / 2 −)

genes with fdr < 0.05 = 145 (144 + / 1 −)

genes with fdr < 0.01 = 115 (114 + / 1 −)

<r> metagenes = 0.97

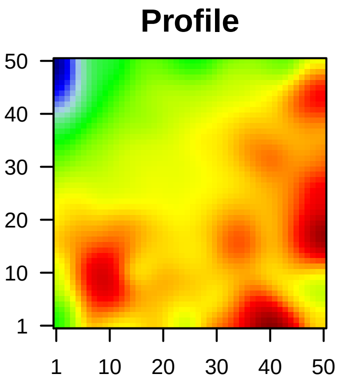
<r> genes = 0.32

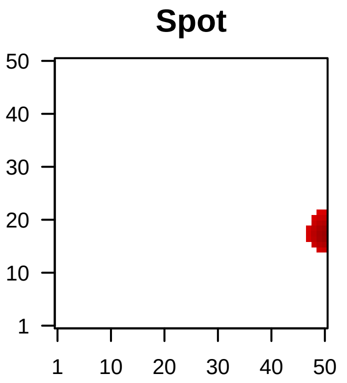
<FC> = 0.64

<shrinkage−t> = 22.4

<p−value> = 0

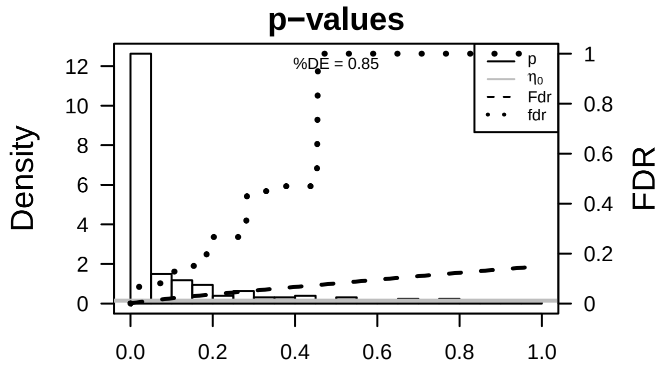
<fdr> = 0.47





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	4602	2.73	2e−16	8e−15	50 x 16	v−myb avian myeloblastosis viral oncogene homolog [Source
2	2248	2.04	7e−16	1e−14	50 x 19	fibroblast growth factor 3 [Source:HGNC Symbol;Acc:3681]
3	1298	2.03	9e−16	6e−13	50 x 17	collagen, type IX, alpha 2 [Source:HGNC Symbol;Acc:2218]
4	494470	1.93	2e−14	9e−13	50 x 17	ring finger protein 165 [Source:HGNC Symbol;Acc:31696]
5	9915	1.9	4e−14	5e−12	50 x 17	aryl−hydrocarbon receptor nuclear translocator 2 [Source:HG
6	9603	1.84	3e−13	5e−12	50 x 18	nuclear factor, erythroid 2−like 3 [Source:HGNC Symbol;Acc:
7	8543	1.83	3e−13	9e−12	50 x 15	LIM domain only 4 [Source:HGNC Symbol;Acc:6644]
8	728715	1.81	6e−13	3e−11	50 x 18	
9	1959	1.78	1e−12	1e−09	50 x 19	early growth response 2 [Source:HGNC Symbol;Acc:3239]
10	30812	1.68	3e−11	3e−08	50 x 18	SRY (sex determining region Y)−box 8 [Source:HGNC Symbo
11	84532	1.54	9e−10	4e−08	50 x 17	acyl−CoA synthetase short−chain family member 1 [Source:
12	83988	1.51	2e−09	9e−08	50 x 17	neurocalcin delta [Source:HGNC Symbol;Acc:7655]
13	55691	1.48	4e−09	3e−07	50 x 18	FERM domain containing 4A [Source:HGNC Symbol;Acc:254
14	57556	1.42	2e−08	3e−07	50 x 17	sema domain, transmembrane domain (TM), and cytoplasmic
15	909	1.4	3e−08	3e−07	50 x 16	CD1a molecule [Source:HGNC Symbol;Acc:1634]
16	79924	1.39	3e−08	3e−07	50 x 18	adrenomedullin 2 [Source:HGNC Symbol;Acc:28898]
17	221061	1.39	4e−08	8e−07	50 x 16	family with sequence similarity 171, member A1 [Source:HGN
18	51768	1.37	6e−08	7e−06	50 x 16	transmembrane 7 superfamily member 3 [Source:HGNC Sym
19	9686	1.29	3e−07	7e−06	50 x 19	vestigial like 4 (Drosophila) [Source:HGNC Symbol;Acc:2896
20	57189	1.27	4e−07	7e−06	50 x 15	KIAA1147 [Source:HGNC Symbol;Acc:29472]



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	15.18	NULL	6 / 16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_A
2	13.28	NULL	4 / 34	BP	thymus development
3	12.72	NULL	2 / 10	BP	positive regulation of histone H3−K4 methylation
4	12.38	NULL	3 / 15	GSEA C2	MASSARWEH_RESPONSE_TO_ESTRADIOL
5	11.94	NULL	2 / 16	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL
6	11.73	NULL	3 / 16	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_UP
7	10.79	NULL	2 / 12	GSEA C2	PROVENZANI_METASTASIS_UP
8	10.43	NULL	1 / 8	GSEA C2	ADDYA_ERYTHROID_DIFFERENTIATION_BY_HEMIN
9	10.41	NULL	2 / 7	GSEA C2	KANG_CISPLATIN_RESISTANCE_DN
10	10.22	NULL	2 / 16	GSEA C2	SASAKI_ADULT_T_CELL_LEUKEMIA
11	9.77	NULL	2 / 14	GSEA C2	CONCANNON_APOPTOSIS_BY_EPOXOMICIN_DN
12	9.74	NULL	1 / 9	GSEA C2	BASSO_CD40_SIGNALING_UP
13	9.74	NULL	1 / 9	GSEA C2	GUTIERREZ_WALDENSTROEMS_MACROGLOBULINEMIA_2
14	8.83	NULL	1 / 5	GSEA C2	STAEGE_EWING_FAMILY_TUMOR
15	8.75	NULL	2 / 13	GSEA C2	RAY_TARGETS_OF_P210_BCR_ABL_FUSION_DN
16	8.68	NULL	1 / 11	BP	homeostasis of number of cells
17	8.68	NULL	1 / 11	Pathw Act	BENTINK_e2f3.2
18	8.68	NULL	1 / 11	GSEA C2	DOANE_BREAST_CANCER_ESR1_UP
19	8.68	NULL	1 / 11	GSEA C2	TURJANSKI_MAPK1_AND_MAPK2_TARGETS
20	8.56	NULL	3 / 5	Lymphoma	MASCQUE_mBL UP
21	8.55	NULL	1 / 2	miRNA target	miR−153
22	8.49	NULL	2 / 15	GSEA C2	DORSAM_HOXA9_TARGETS_UP
23	8.27	NULL	4 / 42	BP	B cell differentiation
24	8.26	NULL	1 / 12	GSEA C2	DING_LUNG_CANCER_BY_MUTATION_RATE
25	8.1	NULL	5 / 40	TF Tissue	VAQUERIZAS_Fetal brain
26	8.06	NULL	2 / 15	GSEA C2	KYNG_DNA_DAMAGE_DN
27	8.05	NULL	2 / 16	GSEA C2	WU_HBX_TARGETS_3_UP
28	7.88	NULL	1 / 13	GSEA C2	OSADA_ASCL1_TARGETS_UP
29	7.88	NULL	1 / 13	GSEA C2	ALONSO_METASTASIS_UP
30	7.83	NULL	2 / 9	GSEA C2	GOZGIT_ESR1_TARGETS_DN
31	7.78	NULL	2 / 15	BP	embryonic digestive tract development
32	7.64	NULL	4 / 41	TF Tissue	VAQUERIZAS_Thymus
33	7.61	NULL	2 / 12	MF	fibroblast growth factor receptor binding
34	7.55	NULL	1 / 14	GSEA C2	LIEN_BREAST_CARCINOMA_METAPLASTIC_VS_DUCTAL_DN
35	7.55	NULL	1 / 14	GSEA C2	GOTTWEIN_TARGETS_OF_KSHV_MIR_K12_11
36	7.55	NULL	1 / 14	GSEA C2	TENEDINI_MEGAKARYOCYTE_MARKERS
37	7.55	NULL	1 / 14	GSEA C2	SMID_BREAST_CANCER_LUMINAL_A_UP
38	7.55	NULL	1 / 14	GSEA C2	VANTVEER_BREAST_CANCER_ESR1_UP
39	7.25	NULL	1 / 15	GSEA C2	LINDGREN_BLADDER_CANCER_CLUSTER_3_DN
40	7.25	NULL	1 / 15	GSEA C2	RUGO_RESPONSE_TO_GAMMA_RADIATION

GW_136

Local Summary

%DE = 0.94

metagenes = 21

genes = 300

genes in genesets = 292

genes with fdr < 0.1 = 280 (9 + / 271 −)

genes with fdr < 0.05 = 261 (9 + / 252 −)

genes with fdr < 0.01 = 249 (9 + / 240 −)

<r> metagenes = 0.91

<r> genes = 0.38

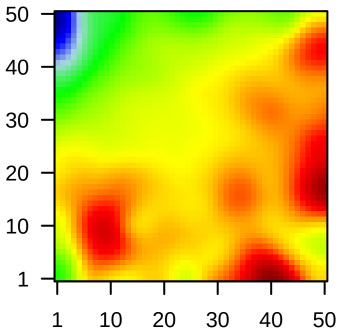
<FC> = −1.23

<shrinkage−t> = −43.68

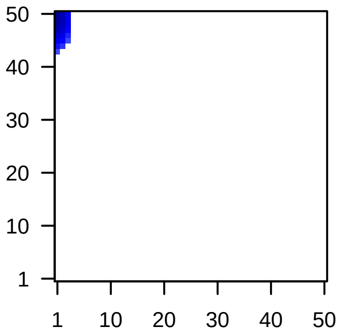
<p−value> = 0

<fdr> = 0.16

Profile



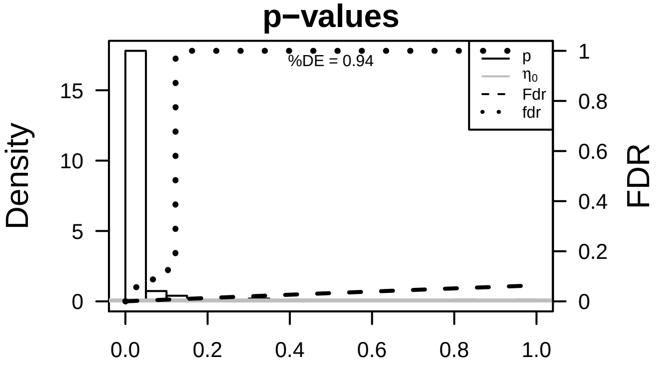
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	131	−2.59	2e−16	9e−17	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	113146	−2.09	2e−16	9e−17	1 x 44	AHNAK nucleoprotein 2 [Source:HGNC Symbol;Acc:20125]
3	57016	−2.59	2e−16	9e−17	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
4	8644	−2.55	2e−16	9e−17	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
5	218	−2.26	2e−16	9e−17	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
6	387695	−2.2	2e−16	9e−17	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Sym
7	810	−2.32	2e−16	9e−17	1 x 50	calmodulin−like 3 [Source:HGNC Symbol;Acc:1452]
8	92196	2.1	2e−16	9e−17	3 x 50	death associated protein−like 1 [Source:HGNC Symbol;Acc:2
9	1672	−2.15	2e−16	9e−17	1 x 50	defensin, beta 1 [Source:HGNC Symbol;Acc:2766]
10	1673	−2.53	2e−16	9e−17	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
11	1830	−2.6	2e−16	9e−17	1 x 48	desmoglein 3 [Source:HGNC Symbol;Acc:3050]
12	2171	−2.41	2e−16	9e−17	1 x 46	fatty acid binding protein 5 (psoriasis−associated) [Source:H
13	9982	−3.24	2e−16	9e−17	1 x 47	fibroblast growth factor binding protein 1 [Source:HGNC Sym
14	2706	−3.65	2e−16	9e−17	1 x 47	gap junction protein, beta 2, 26kDa [Source:HGNC Symbol;A
15	10804	−3.03	2e−16	9e−17	1 x 47	gap junction protein, beta 6, 30kDa [Source:HGNC Symbol;A
16	56300	−2.42	2e−16	9e−17	1 x 47	interleukin 36, gamma [Source:HGNC Symbol;Acc:15741]
17	3861	−2.25	2e−16	9e−17	1 x 45	keratin 14 [Source:HGNC Symbol;Acc:6416]
18	3868	−2.44	2e−16	9e−17	1 x 46	keratin 16 [Source:HGNC Symbol;Acc:6423]
19	3852	−2.11	2e−16	9e−17	1 x 44	keratin 5 [Source:HGNC Symbol;Acc:6442]
20	3853	−2.57	2e−16	9e−17	1 x 43	keratin 6A [Source:HGNC Symbol;Acc:6443]

p−values



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−57.85	NULL	88 / 135	H.Tiss	WIRTH_Mucosa
2	−35.66	NULL	18 / 21	CC	cornified envelope
3	−32.93	NULL	111 / 572	Disease	GUDJ_psoriasis up
4	−30.33	NULL	24 / 53	BP	keratinocyte differentiation
5	−29.18	NULL	27 / 76	BP	epidermis development
6	−27.28	NULL	20 / 42	BP	keratinization
7	−20.32	NULL	5 / 10	MF	RAGE receptor binding
8	−19.45	NULL	10 / 19	BP	peptide cross−linking
9	−18.84	NULL	13 / 44	CC	keratin filament
10	−18.79	NULL	8 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
11	−17.22	NULL	21 / 82	CC	intermediate filament
12	−17.12	NULL	9 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
13	−16.93	NULL	12 / 21	CC	desmosome
14	−16.49	NULL	6 / 15	GSEA C2	AIGNER_ZEB1_TARGETS
15	−16.32	NULL	8 / 15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
16	−15.92	NULL	6 / 15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL
17	−15.89	NULL	30 / 186	MF	structural molecule activity
18	−15.52	NULL	5 / 16	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_DN
19	−14.59	NULL	7 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
20	−14.02	NULL	10 / 52	BP	negative regulation of endopeptidase activity
21	−13.4	NULL	4 / 15	GSEA C2	CHANG_IMMORTALIZED_BY_HPV31_DN
22	−13.38	NULL	4 / 13	GSEA C2	REACTOME_GAP_JUNCTION_TRAFFICKING
23	−13.32	NULL	14 / 79	MF	serine−type endopeptidase inhibitor activity
24	−13.17	NULL	3 / 10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
25	−13.05	NULL	3 / 12	GSEA C2	REACTOME_GAP_JUNCTION_ASSEMBLY
26	−12.81	NULL	6 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
27	−12.63	NULL	7 / 29	BP	regulation of proteolysis
28	−12.55	NULL	6 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
29	−12.43	NULL	5 / 16	GSEA C2	JAEGER_METASTASIS_DN
30	−12.1	NULL	2 / 5	miRNA target	miR−196a
31	−11.97	NULL	6 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
32	−11.79	NULL	2 / 8	GSEA C2	MCLACHLAN_DENTAL_CARIES_UP
33	−11.52	NULL	3 / 10	GSEA C2	NIKOLSKY_BREAST_CANCER_20Q12_Q13_AMPLICON
34	−11.47	NULL	3 / 15	CC	connexon complex
35	−11.44	NULL	6 / 13	BP	negative regulation of peptidase activity
36	−11.38	NULL	3 / 11	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_BONE_DN
37	−11.21	NULL	3 / 10	BP	chronic inflammatory response
38	−11.17	NULL	4 / 14	GSEA C2	CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U
39	−11.03	NULL	4 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_DN
40	−11.02	NULL	4 / 12	H.Tiss	WIRTH_Prim. lymphoid organs