GW_221

Global Summary

%DE = 0.13

genes with fdr < 0.2 = 1695 (925 + / 770 −)

genes with fdr < 0.1 = 1372 (759 + / 613 −)

genes with fdr < 0.05 = 1147 (641 + / 506 −)

genes with fdr < 0.01 = 778 (449 + / 329 −)

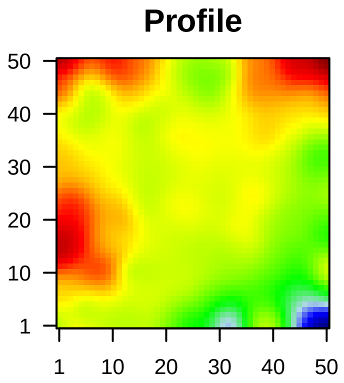
genes in genesets = 16332

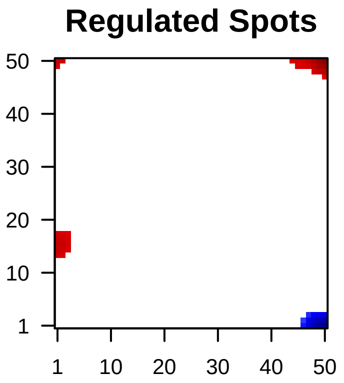
<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.11

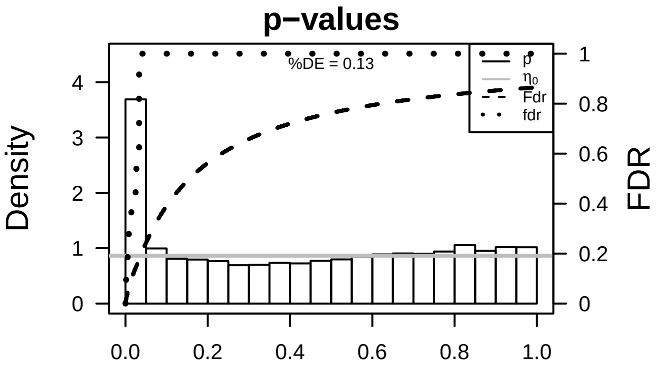
<fdr> = 0.87





Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	57016	1.85	2e−16	4e−14	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
2	441282	1.69	2e−16	4e−14	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC S
3	216	1.57	2e−16	4e−14	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGN
4	218	1.54	2e−16	4e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
5	239	1.65	2e−16	4e−14	5 x 49	arachidonate 12−lipoxygenase [Source:HGNC Symbol;Acc:4
6	401138	1.68	2e−16	4e−14	1 x 5	amelotin [Source:HGNC Symbol;Acc:33188]
7	55107	2.15	2e−16	4e−14	1 x 5	anoctamin 1, calcium activated chloride channel [Source:HG
8	8702	1.38	2e−16	4e−14	50 x 50	UDP−Gal:betaGlcNAc beta 1,4− galactosyltransferase, polyp
9	10409	−1.52	2e−16	4e−14	1 x 2	brain abundant, membrane attached signal protein 1 [Source:
10	590	1.37	2e−16	4e−14	16 x 50	butyrylcholinesterase [Source:HGNC Symbol;Acc:983]
11	655	1.55	2e−16	4e−14	50 x 50	bone morphogenetic protein 7 [Source:HGNC Symbol;Acc:1
12	684	−1.88	2e−16	4e−14	32 x 1	bone marrow stromal cell antigen 2 [Source:HGNC Symbol;A
13	339512	2.33	2e−16	4e−14	50 x 50	chromosome 1 open reading frame 110 [Source:HGNC Sym
14	149563	1.56	2e−16	4e−14	34 x 23	chromosome 1 open reading frame 64 [Source:HGNC Symb
15	84290	1.83	2e−16	4e−14	1 x 50	calpain, small subunit 2 [Source:HGNC Symbol;Acc:16371]
16	595	2.23	2e−16	4e−14	1 x 6	cyclin D1 [Source:HGNC Symbol;Acc:1582]
17	972	−1.31	2e−16	4e−14	50 x 1	CD74 molecule, major histocompatibility complex, class II inv
18	1048	1.97	2e−16	4e−14	2 x 50	carcinoembryonic antigen−related cell adhesion molecule 5 [
19	4680	1.35	2e−16	4e−14	1 x 50	carcinoembryonic antigen−related cell adhesion molecule 6 (
20	2017	1.4	2e−16	4e−14	1 x 14	cortactin [Source:HGNC Symbol;Acc:3338]



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	12.04	NULL	135	H.Tiss	WIRTH_Mucosa
2	11.04	NULL	142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
3	11.04	NULL	142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
4	10	NULL	530	Cancer	Lembcke_Normal vs Adenoma
5	9.52	NULL	714	Chr	Chr 6
6	8.37	NULL	918	Chr	Chr 17
7	8.17	NULL	370	BP	mitotic cell cycle
8	7.84	NULL	1135	Chr	Chr 19
9	7.76	NULL	16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
10	7.48	NULL	57	Glio	developing astrocytes
11	7.44	NULL	2	miRNA target	miR−16−1
12	7.37	NULL	717	Chr	Chr 16
13	6.84	NULL	16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
14	6.39	NULL	16	GSEA C2	SESTO_RESPONSE_TO_UV_C7
15	6.38	NULL	13	GSEA C2	CHIN_BREAST_CANCER_COPY_NUMBER_UP
16	6.19	NULL	15	GSEA C2	LY_AGING_MIDDLE_DN
17	6.16	NULL	534	Chr	Chr 8
18	6.05	NULL	16	GSEA C2	CROONQUIST_NRAS_VS_STROMAL_STIMULATION_DN
19	6.05	NULL	13	BP	regulation of blood vessel size
20	5.98	NULL	11	GSEA C2	REACTOME_UNWINDING_OF_DNA
Underexpressed					
1	−15.7	NULL	417	H.Tiss	WIRTH_Immune system
2	−13.59	NULL	312	BP	immune response
3	−12.07	NULL	630	Chr	Chr X
4	−12.06	NULL	15	CC	MHC class II protein complex
5	−11.57	NULL	553	Cancer	Lembcke_Colonic Inflammation
6	−11.12	NULL	60	BP	interferon−gamma−mediated signaling pathway
7	−10.76	NULL	23	CC	integral to lumenal side of endoplasmic reticulum membrane
8	−10.71	NULL	47	BP	antigen processing and presentation
9	−10.34	NULL	51	BP	type I interferon signaling pathway
10	−10.31	NULL	316	Cancer	SPANG_BCL6−index2
11	−10.02	NULL	699	Chr	Chr 5
12	−9.16	NULL	204	BP	cytokine−mediated signaling pathway
13	−9.08	NULL	32	CC	ER to Golgi transport vesicle membrane
14	−8.75	NULL	74	BP	regulation of immune response
15	−8.68	NULL	123	BP	defense response to virus
16	−8.43	NULL	52	Chr	Chr HSCHR6_MHC_QBL
17	−8.41	NULL	265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
18	−8.41	NULL	265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
19	−8.41	NULL	265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
20	−8.41	NULL	265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down

GW_221

Local Summary

%DE = 0.56

metagenes = 14

genes = 170

genes in genesets = 170

genes with fdr < 0.1 = 61 (55 + / 6 −)

genes with fdr < 0.05 = 61 (55 + / 6 −)

genes with fdr < 0.01 = 26 (24 + / 2 −)

<r> metagenes = 0.98

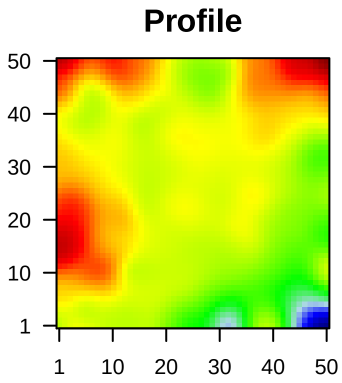
<r> genes = 0.31

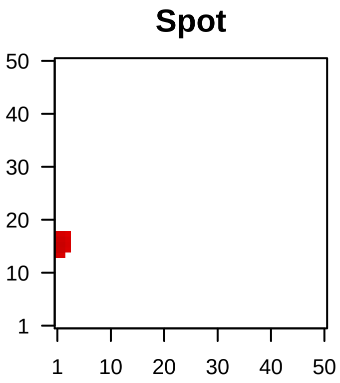
<FC> = 0.29

<shrinkage−t> = 10.3

<p−value> = 0.01

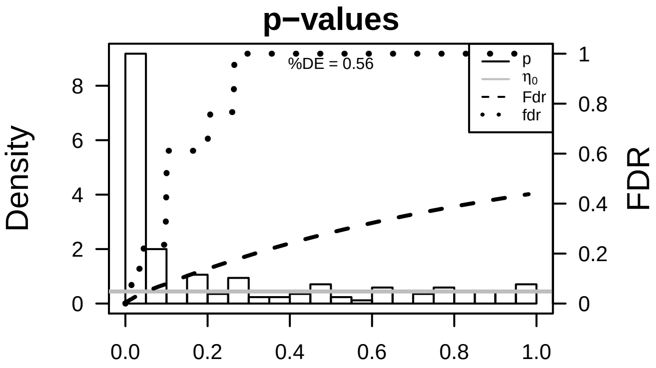
<fdr> = 0.65





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	2017	1.4	2e−16	3e−15	1 x 14	cortactin [Source:HGNC Symbol;Acc:3338]
2	8772	2.18	2e−16	3e−15	1 x 14	Fas (TNFRSF6)−associated via death domain [Source:HGNC
3	219927	1.84	2e−16	3e−15	1 x 15	mitochondrial ribosomal protein L21 [Source:HGNC Symbol;
4	283869	2.3	2e−16	3e−15	1 x 17	neuropeptide W [Source:HGNC Symbol;Acc:30509]
5	220064	2.45	2e−16	3e−15	1 x 14	oral cancer overexpressed 1 [Source:HGNC Symbol;Acc:175
6	219931	1.86	2e−16	3e−15	1 x 14	two pore segment channel 2 [Source:HGNC Symbol;Acc:208
7	51069	1.17	3e−14	7e−11	2 x 18	mitochondrial ribosomal protein L2 [Source:HGNC Symbol;A
8	3508	1.1	9e−13	9e−11	1 x 14	immunoglobulin mu binding protein 2 [Source:HGNC Symbol;
9	64928	1.08	2e−12	5e−09	1 x 18	mitochondrial ribosomal protein L14 [Source:HGNC Symbol;
10	3326	0.99	7e−11	4e−07	1 x 14	heat shock protein 90kDa alpha (cytosolic), class B member
11	9533	0.9	6e−09	2e−06	3 x 17	polymerase (RNA) I polypeptide C, 30kDa [Source:HGNC Sy
12	388581	0.85	3e−08	2e−06	1 x 15	family with sequence similarity 132, member A [Source:HGN
13	705	0.84	5e−08	2e−06	1 x 16	bystin−like [Source:HGNC Symbol;Acc:1157]
14	26873	0.83	7e−08	4e−06	1 x 17	5−oxoprolinase (ATP−hydrolysing) [Source:HGNC Symbol;Ac
15	2030	0.82	1e−07	2e−05	1 x 14	solute carrier family 29 (equilibrative nucleoside transporter),
16	10428	0.77	6e−07	2e−05	1 x 15	craniofacial development protein 1 [Source:HGNC Symbol;Ac
17	284085	0.77	6e−07	4e−05	3 x 18	keratin 18 pseudogene 55 [Source:HGNC Symbol;Acc:26874
18	131076	−0.75	1e−06	4e−05	1 x 16	coiled−coil domain containing 58 [Source:HGNC Symbol;Acc
19	4495	−0.74	2e−06	8e−05	1 x 16	metallothionein 1G [Source:HGNC Symbol;Acc:7399]
20	3217	0.72	3e−06	6e−04	1 x 15	homeobox B7 [Source:HGNC Symbol;Acc:5118]



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	18.19	NULL	1 / 6	GSEA C2	GALI_TP53_TARGETS_APOPTOTIC_DN
2	14.42	NULL	1 / 9	GSEA C2	BIOCARTA_RELA_PATHWAY
3	14.42	NULL	1 / 9	GSEA C2	BIOCARTA_NFKB_PATHWAY
4	14.42	NULL	1 / 9	GSEA C2	BIOCARTA_SODD_PATHWAY
5	14.42	NULL	1 / 9	GSEA C2	REACTOME_DEATH_RECEPTOR_SIGNALLING
6	13.94	NULL	2 / 13	GSEA C2	NADERI_BREAST_CANCER_PROGNOSIS_UP
7	13.58	NULL	1 / 10	MF	death receptor binding
8	13.58	NULL	1 / 10	BP	positive regulation of macrophage differentiation
9	12.87	NULL	1 / 11	BP	regulation of extrinsic apoptotic signaling pathway in absence of lig
10	12.87	NULL	1 / 11	GSEA C2	HOFMANN_CELL_LYMPHOMA_DN
11	12.87	NULL	1 / 11	GSEA C2	ST_TUMOR_NECROSIS_FACTOR_PATHWAY
12	12.25	NULL	1 / 12	GSEA C2	BIOCARTA_FAS_PATHWAY
13	11.71	NULL	1 / 13	BP	lymph node development
14	11.71	NULL	1 / 13	GSEA C2	BIOCARTA_TNFR1_PATHWAY
15	11.23	NULL	1 / 14	GSEA C2	GENTILE_UV_RESPONSE_CLUSTER_D5
16	11.23	NULL	1 / 14	GSEA C2	BIOCARTA_DEATH_PATHWAY
17	10.8	NULL	1 / 15	BP	positive regulation of extrinsic apoptotic signaling pathway via deat
18	10.42	NULL	1 / 16	BP	positive regulation of activated T cell proliferation
19	10.42	NULL	1 / 16	GSEA C2	LAU_APOPTOSIS_CDKN2A_UP
20	10.42	NULL	1 / 16	GSEA C2	BIOCARTA_CERAMIDE_PATHWAY
21	9.94	NULL	1 / 13	GSEA C2	CHIANG_LIVER_CANCER_SUBCLASS_UNANNOTATED_UP
22	9.78	NULL	2 / 23	BP	positive regulation of proteolysis
23	9.75	NULL	1 / 18	BP	positive regulation of T cell mediated cytotoxicity
24	9.51	NULL	2 / 26	MF	tumor necrosis factor receptor binding
25	9.19	NULL	1 / 20	BP	positive regulation of interleukin−8 production
26	8.29	NULL	1 / 24	BP	T cell homeostasis
27	8.19	NULL	1 / 27	MF	G−protein coupled receptor binding
28	7.83	NULL	3 / 14	Pathw Act	BENTINK_myc.1
29	7.75	NULL	1 / 27	BP	positive regulation of extrinsic apoptotic signaling pathway
30	7.74	NULL	2 / 21	BP	feeding behavior
31	7.72	NULL	2 / 34	BP	extrinsic apoptotic signaling pathway
32	7.6	NULL	1 / 28	BP	spleen development
33	7.45	NULL	2 / 30	BP	extrinsic apoptotic signaling pathway in absence of ligand
34	7.45	NULL	1 / 29	BP	positive regulation of interferon−gamma production
35	7.43	NULL	1 / 13	H.Tiss	WIRTH_Sec. lymphoid organs
36	7.27	NULL	2 / 15	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
37	7.22	NULL	14 / 153	MF	structural constituent of ribosome
38	7.17	NULL	1 / 31	BP	T cell differentiation in thymus
39	7.12	NULL	1 / 14	GSEA C2	CLIMENT_BREAST_CANCER_COPY_NUMBER_UP
40	7.04	NULL	1 / 32	BP	extrinsic apoptotic signaling pathway via death domain receptors

GW_221

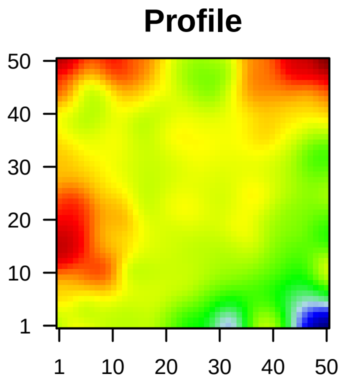
Local Summary

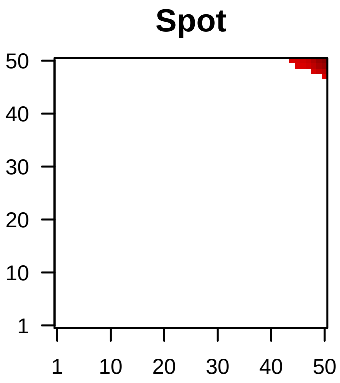
%DE = 0.7
metagenes = 17
genes = 276
genes in genesets = 275

genes with fdr < 0.1 = 125 (113 + / 12 −)
genes with fdr < 0.05 = 103 (93 + / 10 −)
genes with fdr < 0.01 = 88 (80 + / 8 −)

<r> metagenes = 0.9
<r> genes = 0.27

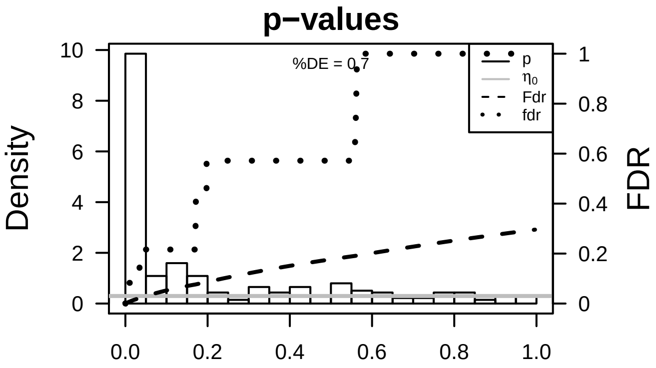
<FC> = 0.32
<shrinkage−t> = 11.33
<p−value> = 0
<fdr> = 0.59





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	216	1.57	2e−16	1e−15	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGNC
2	8702	1.38	2e−16	1e−15	50 x 50	UDP−Gal:betaGlcNAc beta 1,4− galactosyltransferase, polyp
3	655	1.55	2e−16	1e−15	50 x 50	bone morphogenetic protein 7 [Source:HGNC Symbol;Acc:10
4	339512	2.33	2e−16	1e−15	50 x 50	chromosome 1 open reading frame 110 [Source:HGNC Symb
5	1592	1.27	2e−16	1e−15	50 x 50	cytochrome P450, family 26, subfamily A, polypeptide 1 [Sour
6	2944	1.58	2e−16	1e−15	50 x 50	glutathione S−transferase mu 1 [Source:HGNC Symbol;Acc:4
7	3880	1.47	2e−16	1e−15	50 x 49	keratin 19 [Source:HGNC Symbol;Acc:6436]
8	4915	1.66	2e−16	1e−15	50 x 50	neurotrophic tyrosine kinase, receptor, type 2 [Source:HGNC
9	4922	3.27	2e−16	1e−15	50 x 50	neurotensin [Source:HGNC Symbol;Acc:8038]
10	4953	2.12	2e−16	1e−15	50 x 50	ornithine decarboxylase 1 [Source:HGNC Symbol;Acc:8109]
11	28978	1.35	2e−16	1e−15	49 x 50	transmembrane protein 14A [Source:HGNC Symbol;Acc:210
12	256764	1.67	2e−16	1e−15	50 x 50	WD repeat domain 72 [Source:HGNC Symbol;Acc:26790]
13	79844	1.52	2e−16	1e−15	50 x 50	zinc finger, DHHC−type containing 11 [Source:HGNC Symbo
14	1690	1.22	3e−15	2e−11	50 x 47	cochlin [Source:HGNC Symbol;Acc:2180]
15	51090	1.13	3e−13	2e−11	50 x 49	plasmolipin [Source:HGNC Symbol;Acc:18553]
16	56963	1.11	5e−13	9e−11	50 x 50	repulsive guidance molecule family member a [Source:HGNC
17	730101	1.08	2e−12	9e−11	50 x 49	
18	4072	1.08	3e−12	1e−10	50 x 50	epithelial cell adhesion molecule [Source:HGNC Symbol;Acc:
19	54578	1.07	5e−12	1e−10	50 x 50	UDP glucuronosyltransferase 1 family, polypeptide A6 [Sourc
20	387103	1.06	7e−12	1e−10	45 x 49	centromere protein W [Source:HGNC Symbol;Acc:21488]



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	20.52	NULL	2 / 7	GSEA C2	MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
2	18.97	NULL	5 / 15	GSEA C2	KEGG_GLUTATHIONE_METABOLISM
3	18.9	NULL	40 / 142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
4	18.9	NULL	40 / 142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
5	16.02	NULL	3 / 13	BP	regulation of blood vessel size
6	15.17	NULL	4 / 13	GSEA C2	KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_
7	14.67	NULL	4 / 16	GSEA C2	HORIUCHI_WTAP_TARGETS_DN
8	13.58	NULL	15 / 57	Glio	developing astrocytes
9	13.51	NULL	1 / 11	Glio	neurons_glio
10	13.01	NULL	3 / 11	MF	glutathione binding
11	13.01	NULL	3 / 11	GSEA C2	KEGG_DRUG_METABOLISM_CYTOCHROME_P450
12	12.48	NULL	6 / 15	GSEA C2	SMID_BREAST_CANCER_LUMINAL_A_DN
13	12.05	NULL	8 / 16	GSEA C2	FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
14	11.89	NULL	3 / 16	GSEA C2	SESTO_RESPONSE_TO_UV_C7
15	11.52	NULL	2 / 9	GSEA C2	REACTOME_METABOLISM_OF_AMINO_ACIDS
16	11.36	NULL	1 / 15	MF	neuropeptide hormone activity
17	11.22	NULL	1 / 7	GSEA C2	REACTOME_REGULATION_OF_ORNITHINE_DECARBOXYLASE
18	10.96	NULL	4 / 15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
19	10.92	NULL	7 / 15	GSEA C2	FINETTI_BREAST_CANCER_KINOME_RED
20	10.87	NULL	3 / 11	GSEA C2	ITO_PTTG1_TARGETS_UP
21	10.75	NULL	3 / 15	GSEA C2	WHITEFORD_PEDIATRIC_CANCER_MARKERS
22	10.63	NULL	3 / 13	GSEA C2	COLLER_MYC_TARGETS_UP
23	10.59	NULL	3 / 11	GSEA C2	REACTOME_UNWINDING_OF_DNA
24	10.4	NULL	1 / 8	GSEA C2	PUJANA_CHEK2_PCC_NETWORK
25	10.29	NULL	2 / 14	GSEA C2	RUIZ_TNC_TARGETS_DN
26	10.29	NULL	3 / 11	GSEA C2	DANG_MYC_TARGETS_UP
27	10.26	NULL	6 / 25	BP	glutathione derivative biosynthetic process
28	10.14	NULL	6 / 14	GSEA C2	AMUNDSON_GAMMA_RADIATION_RESPONSE
29	10.14	NULL	3 / 14	GSEA C2	KORKOLA_YOLK_SAC_TUMOR
30	10.07	NULL	6 / 14	MMML CGS	MACIEJ_MMML 4
31	9.9	NULL	3 / 8	GSEA C2	REACTOME_E2F_TRANSCRIPTIONAL_TARGETS_AT_G1_S
32	9.9	NULL	2 / 15	GSEA C2	LI_AMPLIFIED_IN_LUNG_CANCER
33	9.8	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
34	9.61	NULL	3 / 15	GSEA C2	YANG_BREAST_CANCER_ESR1_LASER_DN
35	9.55	NULL	2 / 16	GSEA C2	KOBAYASHI_EGFR_SIGNALING_24HR_DN
36	9.5	NULL	11 / 119	BP	xenobiotic metabolic process
37	9.49	NULL	4 / 15	GSEA C2	FOURNIER_ACINAR_DEVELOPMENT_LATE_DN
38	9.49	NULL	3 / 16	GSEA C2	CAIRO_HEPATOBLASTOMA_CLASSES_UP
39	9.43	NULL	2 / 14	GSEA C2	FOURNIER_ACINAR_DEVELOPMENT_LATE_2
40	9.16	NULL	1 / 10	GSEA C2	LUI_TARGETS_OF_PAX8_PPARG_FUSION

GW_221

Local Summary

%DE = 0.71

metagenes = 3

genes = 93

genes in genesets = 91

genes with fdr < 0.1 = 60 (45 + / 15 −)

genes with fdr < 0.05 = 56 (43 + / 13 −)

genes with fdr < 0.01 = 53 (41 + / 12 −)

<r> metagenes = 1

<r> genes = 0.56

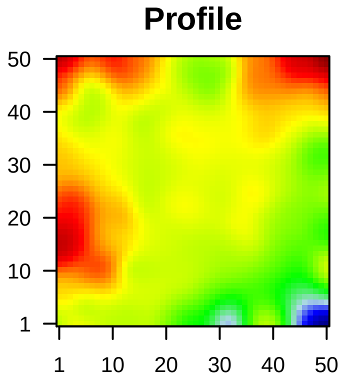
<FC> = 0.44

<shrinkage−t> = 15.57

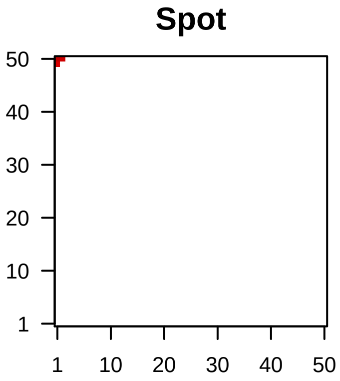
<p−value> = 0

<fdr> = 0.36

Profile



Spot



Local Genelist

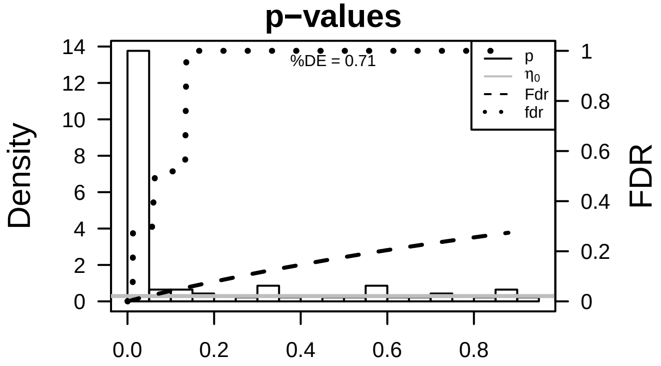
Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	57016	1.85	2e−16	4e−16	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
2	441282	1.69	2e−16	4e−16	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC Sy
3	218	1.54	2e−16	4e−16	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
4	84290	1.83	2e−16	4e−16	1 x 50	calpain, small subunit 2 [Source:HGNC Symbol;Acc:16371]
5	1048	1.97	2e−16	4e−16	2 x 50	carcinoembryonic antigen−related cell adhesion molecule 5 [S
6	4680	1.35	2e−16	4e−16	1 x 50	carcinoembryonic antigen−related cell adhesion molecule 6 (n
7	1562	1.42	2e−16	4e−16	1 x 50	cytochrome P450, family 2, subfamily C, polypeptide 18 [Sour
8	1672	1.84	2e−16	4e−16	1 x 50	defensin, beta 1 [Source:HGNC Symbol;Acc:2766]
9	2877	1.78	2e−16	4e−16	1 x 50	glutathione peroxidase 2 (gastrointestinal) [Source:HGNC Sy
10	192666	2.54	2e−16	4e−16	1 x 50	keratin 24 [Source:HGNC Symbol;Acc:18527]
11	3851	1.31	2e−16	4e−16	1 x 50	keratin 4 [Source:HGNC Symbol;Acc:6441]
12	5266	1.23	2e−16	4e−16	1 x 49	peptidase inhibitor 3, skin−derived [Source:HGNC Symbol;Ac
13	6947	2.01	2e−16	4e−16	2 x 50	transcobalamin I (vitamin B12 binding protein, R binder family
14	7053	1.77	2e−16	4e−16	1 x 50	transglutaminase 3 [Source:HGNC Symbol;Acc:11779]
15	9407	2.18	2e−16	4e−16	1 x 50	transmembrane protease, serine 11D [Source:HGNC Symbol
16	3860	1.14	1e−15	1e−13	1 x 50	keratin 13 [Source:HGNC Symbol;Acc:6415]
17	131	1.21	5e−15	2e−12	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
18	388533	1.15	8e−14	9e−11	1 x 49	keratinocyte differentiation−associated protein [Source:HGNC
19	6707	0.97	6e−12	9e−11	1 x 50	small proline−rich protein 3 [Source:HGNC Symbol;Acc:1126
20	43849	1.06	7e−12	1e−09	1 x 50	kallikrein−related peptidase 12 [Source:HGNC Symbol;Acc:6

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	28.2	NULL	45 / 135	H.Tiss	WIRTH_Mucosa
2	23.37	NULL	7 / 19	BP	peptide cross−linking
3	21.79	NULL	4 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
4	20.1	NULL	3 / 12	BP	cellular aldehyde metabolic process
5	19.54	NULL	3 / 10	GSEA C2	SMID_BREAST_CANCER_ERBB2_UP
6	16.17	NULL	16 / 53	BP	keratinocyte differentiation
7	15.97	NULL	5 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
8	15.86	NULL	13 / 42	BP	keratinization
9	14.85	NULL	12 / 21	CC	cornified envelope
10	14.83	NULL	2 / 8	GSEA C2	MCLACHLAN_DENTAL_CARIES_UP
11	14.29	NULL	3 / 13	GSEA C2	FARMER_BREAST_CANCER_APOCRINE VS LUMINAL
12	13.77	NULL	2 / 9	GSEA C2	MCLACHLAN_DENTAL_CARIES_DN
13	13.47	NULL	3 / 14	GSEA C2	CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U
14	12.9	NULL	2 / 10	GSEA C2	NIKOLSKY_BREAST_CANCER_20Q12_Q13_AMPLICON
15	12.78	NULL	3 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
16	12.63	NULL	3 / 16	GSEA C2	JAEGER_METASTASIS_DN
17	12.39	NULL	3 / 27	BP	response to bacterium
18	12.17	NULL	2 / 11	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_BONE_DN
19	11.56	NULL	2 / 12	H.Tiss	WIRTH_Prim. lymphoid organs
20	10.99	NULL	2 / 13	GSEA C2	CHARAFE_BREAST_CANCER_LUMINAL_VS_BASAL_DN
21	10.99	NULL	2 / 13	GSEA C2	HAN_SATB1_TARGETS_DN
22	10.77	NULL	1 / 9	GSEA C2	GOUYER_TUMOR_INVASIVENESS
23	10.09	NULL	2 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_DN
24	10.09	NULL	2 / 15	GSEA C2	SMID_BREAST_CANCER_LUMINAL_B_DN
25	10.08	NULL	1 / 10	GSEA C2	KEGG_LINOLEIC_ACID_METABOLISM
26	10	NULL	1 / 10	GSEA C2	BIOCARTA_P35ALZHEIMERS_PATHWAY
27	9.96	NULL	2 / 14	GSEA C2	KEGG_PHENYLALANINE_METABOLISM
28	9.88	NULL	5 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
29	9.88	NULL	2 / 16	BP	cobalamin metabolic process
30	9.45	NULL	43 / 572	Disease	GUDJ_psoriasis up
31	9.38	NULL	4 / 39	BP	retinoid metabolic process
32	9.33	NULL	1 / 6	GSEA C2	SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_DN
33	9.11	NULL	1 / 11	GSEA C2	ROME_INSULIN_TARGETS_IN_MUSCLE_DN
34	9.09	NULL	1 / 6	GSEA C2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_B_DN
35	9.04	NULL	2 / 13	H.Tiss	WIRTH_Tonsil
36	9.01	NULL	1 / 12	GSEA C2	ONDER_CDH1_TARGETS_1_UP
37	8.98	NULL	1 / 12	BP	acute inflammatory response
38	8.94	NULL	1 / 9	GSEA C2	NIKOLSKY_BREAST_CANCER_17P11_AMPLICON
39	8.72	NULL	13 / 76	BP	epidermis development
40	8.64	NULL	1 / 12	GSEA C2	ODONNELL_METASTASIS_DN

p−values



GW_221

Local Summary

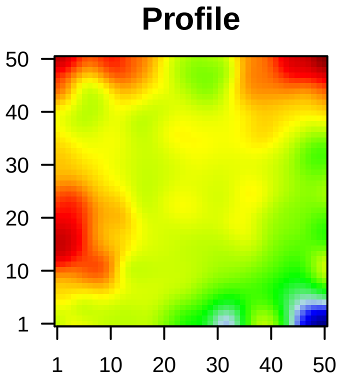
%DE = 0.99
metagenes = 14
genes = 247
genes in genesets = 245

genes with fdr < 0.1 = 240 (4 + / 236 −)
genes with fdr < 0.05 = 237 (4 + / 233 −)
genes with fdr < 0.01 = 229 (4 + / 225 −)

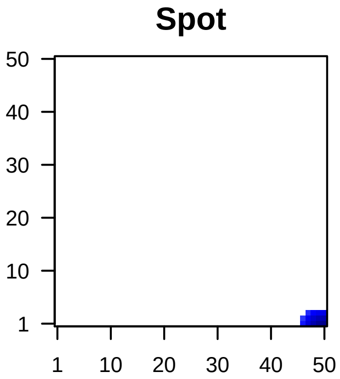
<r> metagenes = 0.99
<r> genes = 0.62

<FC> = −0.61
<shrinkage−t> = −21.21
<p−value> = 0
<fdr> = 0.21

Profile



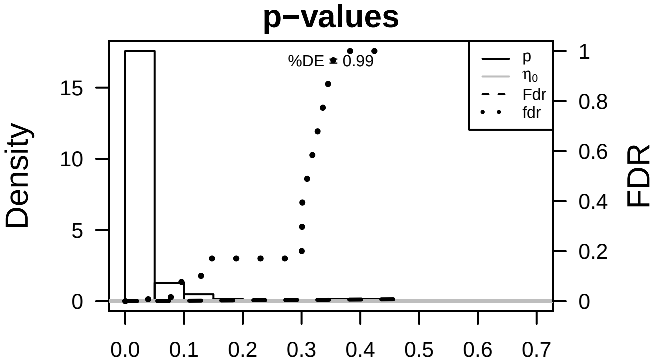
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	972	−1.31	2e−16	1e−16	50 x 1	CD74 molecule, major histocompatibility complex, class II inv
2	3108	−1.37	2e−16	1e−16	50 x 1	major histocompatibility complex, class II, DM alpha [Source:
3	3122	−1.35	2e−16	1e−16	50 x 1	major histocompatibility complex, class II, DR alpha [Source:
4	3128	−1.29	2e−16	1e−16	50 x 1	major histocompatibility complex, class II, DR beta 6 (pseudo
5	3936	−1.36	2e−16	1e−16	50 x 1	lymphocyte cytosolic protein 1 (L−plastin) [Source:HGNC Sy
6	10537	−1.36	2e−16	1e−16	50 x 1	ubiquitin D [Source:HGNC Symbol;Acc:18795]
7	260436	−1.25	7e−16	1e−15	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symb
8	3113	−1.24	1e−15	2e−15	50 x 1	major histocompatibility complex, class II, DP alpha 1 [Source
9	4283	−1.22	2e−15	2e−15	49 x 1	chemokine (C−X−C motif) ligand 9 [Source:HGNC Symbol;A
10	10563	−1.22	3e−15	2e−15	50 x 1	chemokine (C−X−C motif) ligand 13 [Source:HGNC Symbol;
11	5341	−1.21	3e−15	6e−15	50 x 1	pleckstrin [Source:HGNC Symbol;Acc:9070]
12	348	−1.2	7e−15	6e−15	50 x 1	apolipoprotein E [Source:HGNC Symbol;Acc:613]
13	3002	−1.2	8e−15	5e−14	49 x 1	granzyme B (granzyme 2, cytotoxic T−lymphocyte−associate
14	4050	−1.17	4e−14	5e−14	50 x 1	lymphotoxin beta (TNF superfamily, member 3) [Source:HGN
15	9806	−1.16	4e−14	2e−13	50 x 1	sparc/osteonectin, cwcv and kazal−like domains proteoglyca
16	5920	−1.14	1e−13	2e−13	48 x 1	retinoic acid receptor responder (tazarotene induced) 3 [Sour
17	241	−1.14	1e−13	2e−13	50 x 1	arachidonate 5−lipoxygenase−activating protein [Source:HG
18	962	−1.13	2e−13	2e−13	50 x 1	CD48 molecule [Source:HGNC Symbol;Acc:1683]
19	9404	−1.12	3e−13	3e−12	50 x 1	leupaxin [Source:HGNC Symbol;Acc:14061]
20	915	−1.09	1e−12	3e−12	49 x 1	CD3d molecule, delta (CD3−TCR complex) [Source:HGNC S

p−values



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−37.81	NULL	12 / 15	CC	MHC class II protein complex
2	−33.36	NULL	89 / 417	H.Tiss	WIRTH_Immune system
3	−26.1	NULL	89 / 553	Cancer	Lembcke_Colonic Inflammation
4	−22.18	NULL	50 / 312	BP	immune response
5	−21.86	NULL	14 / 47	BP	antigen processing and presentation
6	−21.48	NULL	7 / 11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
7	−21.32	NULL	7 / 15	GSEA C2	FINAK_BREAST_CANCER_SDPP_SIGNATURE
8	−20.48	NULL	3 / 6	GSEA C2	SANA_RESPONSE_TO_IFNG_UP
9	−20.16	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
10	−19.95	NULL	16 / 60	BP	T cell costimulation
11	−19.39	NULL	6 / 12	GSEA C2	BIOCARTA_CTL_PATHWAY
12	−19.35	NULL	2 / 3	GSEA C2	KEGG_VIRAL_MYOCARDITIS
13	−19.19	NULL	7 / 21	CC	clathrin−coated endocytic vesicle membrane
14	−19.07	NULL	6 / 11	GSEA C2	BIOCARTA_THELPER_PATHWAY
15	−18.24	NULL	7 / 23	CC	integral to lumenal side of endoplasmic reticulum membrane
16	−17.99	NULL	5 / 15	Glio	Donson−chemokines/cytokines−associated with LTS in HGA
17	−17.25	NULL	2 / 4	MMML CGS	MACIEJ_MMML 2
18	−16.91	NULL	39 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
19	−16.91	NULL	39 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
20	−16.91	NULL	39 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
21	−16.91	NULL	39 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
22	−16.33	NULL	7 / 28	CC	transport vesicle membrane
23	−16.23	NULL	2 / 4	GSEA C2	KEGG_LEISHMANIA_INFECTION
24	−15.94	NULL	5 / 12	BP	immunoglobulin mediated immune response
25	−15.74	NULL	17 / 74	BP	regulation of immune response
26	−15.66	NULL	5 / 12	BP	dendritic cell chemotaxis
27	−15.56	NULL	4 / 7	Glio	Donson−cytotoxic effectors−associated with LTS in HGA
28	−15.23	NULL	13 / 87	BP	antigen processing and presentation of exogenous peptide antigen
29	−15.17	NULL	7 / 13	Cancer	GENTLES_modul18
30	−15.15	NULL	25 / 162	CC	external side of plasma membrane
31	−15.14	NULL	7 / 32	CC	ER to Golgi transport vesicle membrane
32	−15.05	NULL	15 / 84	BP	T cell receptor signaling pathway
33	−14.96	NULL	5 / 17	BP	positive regulation of neutrophil chemotaxis
34	−14.51	NULL	1 / 2	GSEA C2	KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUC
35	−14.51	NULL	1 / 2	GSEA C2	KEGG_AUTOIMMUNE_THYROID_DISEASE
36	−14.51	NULL	1 / 2	GSEA C2	KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS
37	−14.44	NULL	5 / 13	GSEA C2	HAHTOLA_CTCL_PATHOGENESIS
38	−14.39	NULL	7 / 35	CC	trans−Golgi network membrane
39	−14.16	NULL	5 / 13	GSEA C2	BIOCARTA_IL17_PATHWAY
40	−14.01	NULL	4 / 8	Glio	Donson−migration tethering and rolling−associated with LTS in HG