GW_227

Global Summary

%DE = 0.12

genes with fdr < 0.2 = 1423 (820 + / 603 −)

genes with fdr < 0.1 = 1143 (697 + / 446 −)

genes with fdr < 0.05 = 916 (592 + / 324 −)

genes with fdr < 0.01 = 570 (399 + / 171 −)

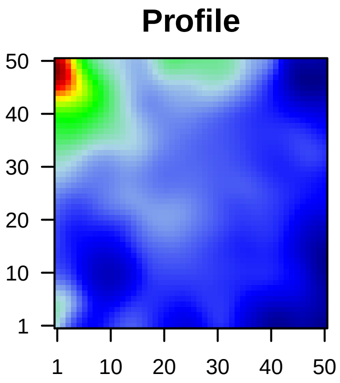
genes in genesets = 16332

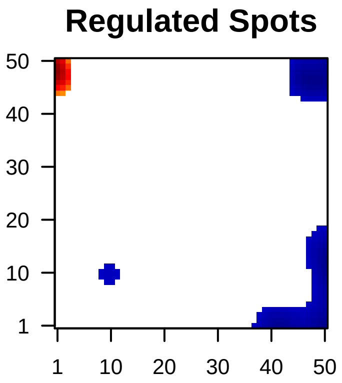
<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.13

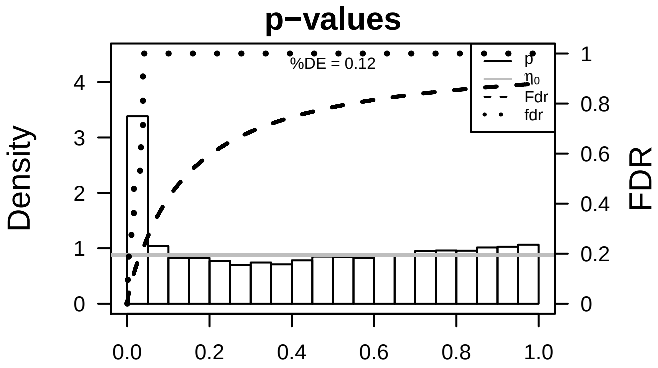
<fdr> = 0.88





Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	131	−1.7	2e−16	4e−14	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	242	2.61	2e−16	4e−14	1 x 48	arachidonate 12−lipoxygenase, 12R type [Source:HGNC Syn
3	59344	1.51	2e−16	4e−14	2 x 45	arachidonate lipoxygenase 3 [Source:HGNC Symbol;Acc:137
4	118932	1.54	2e−16	4e−14	4 x 50	ankyrin repeat domain 22 [Source:HGNC Symbol;Acc:28321]
5	8424	1.54	2e−16	4e−14	3 x 48	butyrobetaine (gamma), 2−oxoglutarate dioxygenase (gamma
6	387695	2.09	2e−16	4e−14	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Symb
7	375791	1.83	2e−16	4e−14	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Symb
8	760	1.87	2e−16	4e−14	1 x 44	carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
9	59082	1.63	2e−16	4e−14	6 x 44	caspase recruitment domain family, member 18 [Source:HGN
10	1041	2.22	2e−16	4e−14	1 x 46	corneodesmosin [Source:HGNC Symbol;Acc:1802]
11	1117	1.52	2e−16	4e−14	48 x 4	chitinase 3−like 2 [Source:HGNC Symbol;Acc:1933]
12	548596	−1.61	2e−16	4e−14	4 x 50	creatine kinase, mitochondrial 1B [Source:HGNC Symbol;Acc
13	9022	1.75	2e−16	4e−14	1 x 50	chloride intracellular channel 3 [Source:HGNC Symbol;Acc:2
14	84518	1.72	2e−16	4e−14	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
15	51200	1.5	2e−16	4e−14	1 x 44	carboxypeptidase A4 [Source:HGNC Symbol;Acc:15740]
16	1396	−1.51	2e−16	4e−14	50 x 5	cysteine−rich protein 1 (intestinal) [Source:HGNC Symbol;Ac
17	9547	1.62	2e−16	4e−14	1 x 46	chemokine (C−X−C motif) ligand 14 [Source:HGNC Symbol;
18	1672	1.86	2e−16	4e−14	1 x 50	defensin, beta 1 [Source:HGNC Symbol;Acc:2766]
19	55894	2.09	2e−16	4e−14	1 x 47	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
20	414325	2.56	2e−16	4e−14	1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	23.19	NULL	572	Disease	GUDJ_psoriasis up
2	21.48	NULL	135	H.Tiss	WIRTH_Mucosa
3	21.38	NULL	42	BP	keratinization
4	18.83	NULL	21	CC	cornified envelope
5	16.43	NULL	76	BP	epidermis development
6	15.16	NULL	53	BP	keratinocyte differentiation
7	11.61	NULL	534	Chr	Chr 8
8	7.81	NULL	10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
9	7.53	NULL	10	GSEA C2	NIKOLSKY_BREAST_CANCER_20Q12_Q13_AMPLICON
10	7.35	NULL	9	GSEA C2	ZERBINI_RESPONSE_TO_SULINDAC_UP
11	7.21	NULL	1182	CC	extracellular region
12	7.17	NULL	15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL
13	7.16	NULL	21	CC	desmosome
14	7.13	NULL	16	GSEA C2	JAEGER_METASTASIS_DN
15	7.06	NULL	16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
16	7.04	NULL	16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
17	6.89	NULL	29	BP	regulation of proteolysis
18	6.84	NULL	12	BP	keratinocyte proliferation
19	6.75	NULL	16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
20	6.62	NULL	79	MF	serine−type endopeptidase inhibitor activity
Underexpressed					
1	−12.1	NULL	142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
2	−12.1	NULL	142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
3	−11.65	NULL	504	Chr	Chr 15
4	−7.59	NULL	386	Chr	Chr 22
5	−6.93	NULL	149	BP	DNA replication
6	−6.69	NULL	57	Glio	developing astrocytes
7	−6.52	NULL	417	H.Tiss	WIRTH_Immune system
8	−6	NULL	8	GSEA C2	RUNNE_GENDER_EFFECT_UP
9	−5.95	NULL	370	BP	mitotic cell cycle
10	−5.91	NULL	7	MMML CGS	MACIEJ_MMML 5
11	−5.85	NULL	1749	MF	DNA binding
12	−5.74	NULL	4640	CC	nucleus
13	−5.59	NULL	1574	BP	transcription, DNA−templated
14	−5.57	NULL	16	GSEA C2	EGUCHI_CELL_CYCLE_RB1_TARGETS
15	−5.49	NULL	14	GSEA C2	ZHAN_MULTIPLE_MYELOMA_PR_UP
16	−5.45	NULL	232	BP	mitosis
17	−5.39	NULL	30	BP	DNA strand elongation involved in DNA replication
18	−5.31	NULL	14	MMML CGS	MACIEJ_MMML 4
19	−5.23	NULL	10	GSEA C2	MONTERO_THYROID_CANCER_POOR_SURVIVAL_UP
20	−5.12	NULL	16	GSEA C2	KANG_DOXORUBICIN_RESISTANCE_UP

GW_227

Local Summary

%DE = 0.91

metagenes = 20

genes = 271

genes in genesets = 264

genes with fdr < 0.1 = 220 (206 + / 14 −)

genes with fdr < 0.05 = 216 (202 + / 14 −)

genes with fdr < 0.01 = 193 (182 + / 11 −)

<r> metagenes = 0.92

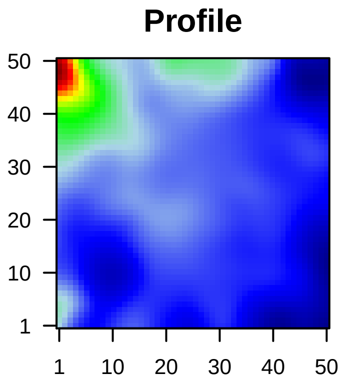
<r> genes = 0.41

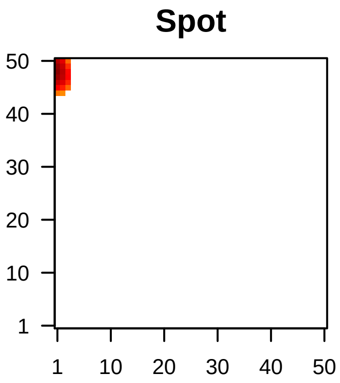
<FC> = 0.96

<shrinkage−t> = 33.83

<p−value> = 0

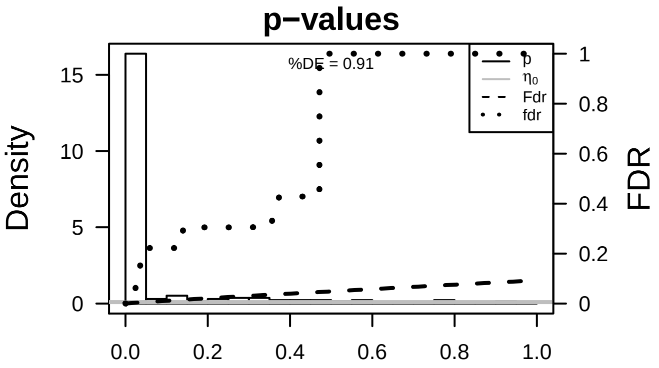
<fdr> = 0.23





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	131	−1.7	2e−16	8e−17	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	242	2.61	2e−16	8e−17	1 x 48	arachidonate 12−lipoxygenase, 12R type [Source:HGNC Syn
3	59344	1.51	2e−16	8e−17	2 x 45	arachidonate lipoxygenase 3 [Source:HGNC Symbol;Acc:137
4	8424	1.54	2e−16	8e−17	3 x 48	butyrobetaine (gamma), 2−oxoglutarate dioxygenase (gamma
5	387695	2.09	2e−16	8e−17	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Symb
6	375791	1.83	2e−16	8e−17	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Symb
7	760	1.87	2e−16	8e−17	1 x 44	carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
8	1041	2.22	2e−16	8e−17	1 x 46	corneodesmosin [Source:HGNC Symbol;Acc:1802]
9	9022	1.75	2e−16	8e−17	1 x 50	chloride intracellular channel 3 [Source:HGNC Symbol;Acc:2
10	84518	1.72	2e−16	8e−17	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
11	51200	1.5	2e−16	8e−17	1 x 44	carboxypeptidase A4 [Source:HGNC Symbol;Acc:15740]
12	9547	1.62	2e−16	8e−17	1 x 46	chemokine (C−X−C motif) ligand 14 [Source:HGNC Symbol;
13	1672	1.86	2e−16	8e−17	1 x 50	defensin, beta 1 [Source:HGNC Symbol;Acc:2766]
14	55894	2.09	2e−16	8e−17	1 x 47	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
15	414325	2.56	2e−16	8e−17	1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
16	1673	2.55	2e−16	8e−17	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
17	93099	1.76	2e−16	8e−17	1 x 47	dermokine [Source:HGNC Symbol;Acc:25063]
18	1823	1.65	2e−16	8e−17	1 x 45	desmocollin 1 [Source:HGNC Symbol;Acc:3035]
19	1828	2.23	2e−16	8e−17	1 x 48	desmoglein 1 [Source:HGNC Symbol;Acc:3048]
20	2171	1.6	2e−16	8e−17	1 x 46	fatty acid binding protein 5 (psoriasis−associated) [Source:H



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	38.02	NULL	18 / 21	CC	cornified envelope
2	34.21	NULL	87 / 135	H.Tiss	WIRTH_Mucosa
3	28.56	NULL	104 / 572	Disease	GUDJ_psoriasis up
4	27.48	NULL	19 / 42	BP	keratinization
5	26.17	NULL	24 / 53	BP	keratinocyte differentiation
6	24.12	NULL	24 / 76	BP	epidermis development
7	16.48	NULL	8 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
8	15.85	NULL	12 / 21	CC	desmosome
9	15.35	NULL	5 / 10	MF	RAGE receptor binding
10	14.02	NULL	3 / 15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
11	13.82	NULL	6 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
12	13.73	NULL	3 / 10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
13	13.49	NULL	13 / 79	MF	serine−type endopeptidase inhibitor activity
14	12.97	NULL	10 / 52	BP	negative regulation of endopeptidase activity
15	12.91	NULL	6 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
16	12.9	NULL	6 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
17	12.88	NULL	9 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
18	12.74	NULL	7 / 29	BP	regulation of proteolysis
19	12.67	NULL	6 / 13	BP	negative regulation of peptidase activity
20	11.84	NULL	4 / 10	GSEA C2	FOURNIER_ACINAR_DEVELOPMENT_LATE_UP
21	10.75	NULL	4 / 15	GSEA C2	CHANG_IMMORTALIZED_BY_HPV31_DN
22	10.67	NULL	3 / 10	GSEA C2	NIKOLSKY_BREAST_CANCER_20Q12_Q13_AMPLICON
23	10.47	NULL	6 / 15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL
24	10.41	NULL	62 / 1182	CC	extracellular region
25	10.32	NULL	10 / 19	BP	peptide cross−linking
26	10.24	NULL	3 / 16	GSEA C2	CHEOK_RESPONSE_TO_MERCAPTOPURINE_AND_LD_MTX_
27	10.19	NULL	5 / 23	MF	peptidase inhibitor activity
28	10.13	NULL	3 / 11	GSEA C2	MURAKAMI_UV_RESPONSE_24HR
29	9.94	NULL	8 / 15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
30	9.9	NULL	3 / 10	GSEA C2	SMID_BREAST_CANCER_ERBB2_UP
31	9.72	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
32	9.67	NULL	5 / 16	GSEA C2	JAEGER_METASTASIS_DN
33	9.61	NULL	4 / 15	GSEA C2	LEE_LIVER_CANCER_MYC_E2F1_UP
34	9.07	NULL	3 / 16	GSEA C2	AMIT_SERUM_RESPONSE_480_MCF10A
35	8.98	NULL	3 / 6	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_UP
36	8.9	NULL	3 / 13	GSEA C2	HAN_SATB1_TARGETS_DN
37	8.72	NULL	4 / 16	GSEA C2	LEE_LIVER_CANCER_MYC_TGFA_UP
38	8.59	NULL	3 / 16	GSEA C2	LEE_LIVER_CANCER_ACOX1_UP
39	8.57	NULL	4 / 12	H.Tiss	WIRTH_Prim. lymphoid organs
40	8.53	NULL	4 / 14	GSEA C2	CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U

GW_227

Local Summary

%DE = 0.61

metagenes = 103

genes = 1293

genes in genesets = 1258

genes with fdr < 0.1 = 393 (34 + / 359 −)

genes with fdr < 0.05 = 309 (27 + / 282 −)

genes with fdr < 0.01 = 155 (19 + / 136 −)

<r> metagenes = 0.7

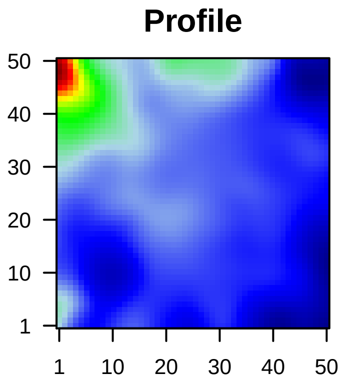
<r> genes = 0.25

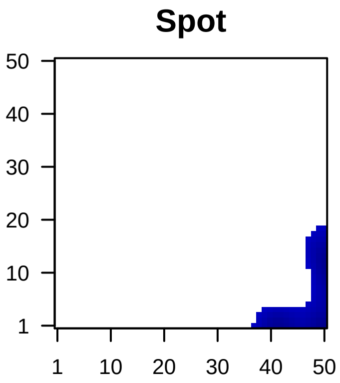
<FC> = −0.25

<shrinkage−t> = −8.94

<p−value> = 0.03

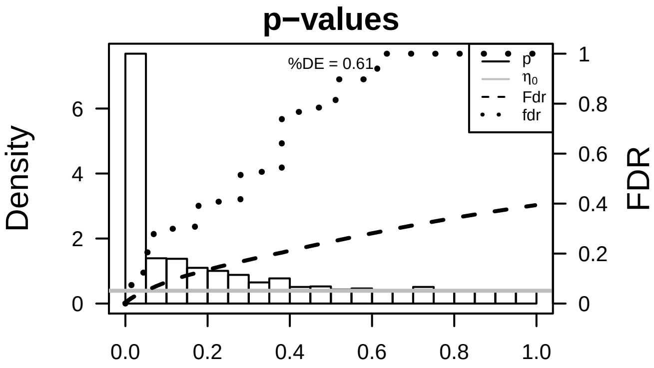
<fdr> = 0.72





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	1117	1.52	2e−16	2e−14	48 x 4	chitinase 3−like 2 [Source:HGNC Symbol;Acc:1933]
2	1396	−1.51	2e−16	2e−14	50 x 5	cysteine−rich protein 1 (intestinal) [Source:HGNC Symbol;Ac
3	3123	1.6	2e−16	2e−14	45 x 1	major histocompatibility complex, class II, DR beta 1 [Source:
4	3127	2.03	2e−16	2e−14	43 x 1	major histocompatibility complex, class II, DR beta 5 [Source:
5	6192	−2.08	2e−16	2e−14	50 x 9	ribosomal protein S4, Y−linked 1 [Source:HGNC Symbol;Acc:
6	10628	−1.49	2e−16	2e−14	48 x 1	thioredoxin interacting protein [Source:HGNC Symbol;Acc:16
7	5730	−1.29	1e−12	6e−10	50 x 1	prostaglandin D2 synthase 21kDa (brain) [Source:HGNC Syn
8	55268	−1.27	3e−12	6e−10	50 x 14	enoyl CoA hydratase domain containing 2 [Source:HGNC Syr
9	51316	−1.26	4e−12	6e−10	50 x 13	placenta−specific 8 [Source:HGNC Symbol;Acc:19254]
10	84952	−1.26	5e−12	7e−09	50 x 10	cingulin−like 1 [Source:HGNC Symbol;Acc:25931]
11	2878	−1.22	2e−11	7e−09	50 x 9	glutathione peroxidase 3 (plasma) [Source:HGNC Symbol;Ac
12	347	−1.21	4e−11	7e−09	50 x 7	apolipoprotein D [Source:HGNC Symbol;Acc:612]
13	57523	−1.2	5e−11	3e−08	50 x 12	NYN domain and retroviral integrase containing [Source:HGN
14	2	−1.17	1e−10	7e−08	50 x 5	alpha−2−macroglobulin [Source:HGNC Symbol;Acc:7]
15	79762	−1.15	2e−10	1e−07	50 x 15	chromosome 1 open reading frame 115 [Source:HGNC Symb
16	3169	−1.14	5e−10	1e−07	50 x 12	forkhead box A1 [Source:HGNC Symbol;Acc:5021]
17	3128	1.12	7e−10	2e−07	50 x 1	major histocompatibility complex, class II, DR beta 6 (pseudo
18	4239	−1.11	1e−09	6e−07	50 x 6	microfibrillar−associated protein 4 [Source:HGNC Symbol;Ac
19	58480	−1.08	3e−09	6e−07	50 x 8	ras homolog family member U [Source:HGNC Symbol;Acc:17
20	10439	−1.07	4e−09	6e−07	50 x 17	olfactomedin 1 [Source:HGNC Symbol;Acc:17187]



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−13.82	NULL	138 / 417	H.Tiss	WIRTH_Immune system
2	−12.92	NULL	3 / 7	MMML CGS	MACIEJ_MMML 5
3	−12	NULL	3 / 8	GSEA C2	RUNNE_GENDER_EFFECT_UP
4	−10.97	NULL	6 / 11	GSEA C2	TARTE_PLASMA_CELL_VS_B_LYMPHOCYTE_DN
5	−10.26	NULL	7 / 12	GSEA C2	ZHAN_MULTIPLE_MYELOMA_DN
6	−10.18	NULL	4 / 15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
7	−10.13	NULL	14 / 16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_D
8	−9.66	NULL	153 / 553	Cancer	Lembcke_Colonic Inflammation
9	−8.92	NULL	7 / 14	GSEA C2	WU_SILENCED_BY_METHYLATION_IN_BLADDER_CANCER
10	−8.62	NULL	4 / 13	GSEA C2	KANG_IMMORTALIZED_BY_TERT_UP
11	−7.95	NULL	5 / 10	BP	positive regulation of chemotaxis
12	−7.93	NULL	5 / 9	GSEA C2	MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN
13	−7.89	NULL	2 / 7	GSEA C2	LEE_NAIVE_T_LYMPHOCYTE
14	−7.68	NULL	6 / 16	GSEA C2	FERRANDO_TAL1_NEIGHBORS
15	−7.59	NULL	4 / 16	GSEA C2	YANG_BREAST_CANCER_ESR1_BULK_UP
16	−7.48	NULL	4 / 20	Lymphoma	ROSOLOWSKI_red UP
17	−7.06	NULL	4 / 14	GSEA C2	WINNEPENNINCKX_MELANOMA_METASTASIS_DN
18	−6.91	NULL	8 / 11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
19	−6.81	NULL	8 / 11	GSEA C2	BIOCARTA_THELPER_PATHWAY
20	−6.58	NULL	7 / 16	GSEA C2	KORKOLA_TERATOMA_UP
21	−6.55	NULL	8 / 15	GSEA C2	SHIPP_DLBCL_VS_FOLLICULAR_LYMPHOMA_DN
22	−6.46	NULL	2 / 9	GSEA C2	REACTOME_REGULATION_OF_BETA_CELL_DEVELOPMENT
23	−6.46	NULL	4 / 8	GSEA C2	BOQUEST_STEM_CELL_DN
24	−6.44	NULL	4 / 15	GSEA C2	FERRANDO_T_ALL_WITH_MLL_ENL_FUSION_DN
25	−6.4	NULL	4 / 34	Chr	Chr Y
26	−6.4	NULL	23 / 74	BP	regulation of immune response
27	−6.36	NULL	2 / 16	GSEA C2	CROONQUIST_STROMAL_STIMULATION_UP
28	−6.29	NULL	5 / 10	GSEA C2	BIOCARTA_LYM_PATHWAY
29	−6.18	NULL	7 / 15	GSEA C2	FINAK_BREAST_CANCER_SDPP_SIGNATURE
30	−6.13	NULL	1 / 8	GSEA C2	REACTOME_REGULATION_OF_GENE_EXPRESSION_IN_BETA
31	−6.12	NULL	23 / 152	BP	regulation of small GTPase mediated signal transduction
32	−6.07	NULL	6 / 14	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_D
33	−5.96	NULL	6 / 14	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_LUNG_DN
34	−5.95	NULL	4 / 10	GSEA C2	YAMASHITA_LIVER_CANCER_WITH_EPCAM_DN
35	−5.95	NULL	5 / 15	GSEA C2	DOANE_BREAST_CANCER_CLASSES_UP
36	−5.92	NULL	67 / 327	Lymphoma	SPANG_CD40 6hrs UP
37	−5.9	NULL	63 / 375	Disease	GUDJ_psoriasis down
38	−5.8	NULL	4 / 7	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
39	−5.79	NULL	3 / 14	BP	negative regulation of epithelial to mesenchymal transition
40	−5.76	NULL	6 / 16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_A

GW_227

Local Summary

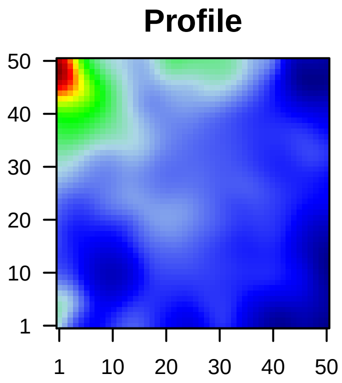
%DE = 0.71
metagenes = 12
genes = 89
genes in genesets = 88

genes with fdr < 0.1 = 36 (1 + / 35 −)
genes with fdr < 0.05 = 20 (1 + / 19 −)
genes with fdr < 0.01 = 10 (1 + / 9 −)

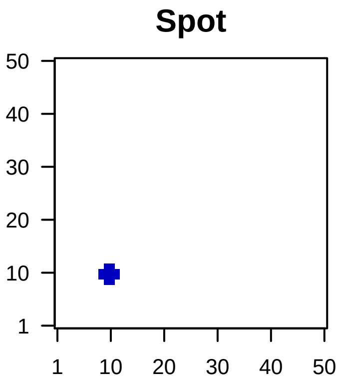
<r> metagenes = 0.96
<r> genes = 0.29

<FC> = −0.27
<shrinkage−t> = −9.56
<p−value> = 0.05
<fdr> = 0.75

Profile



Spot



Local Genelist

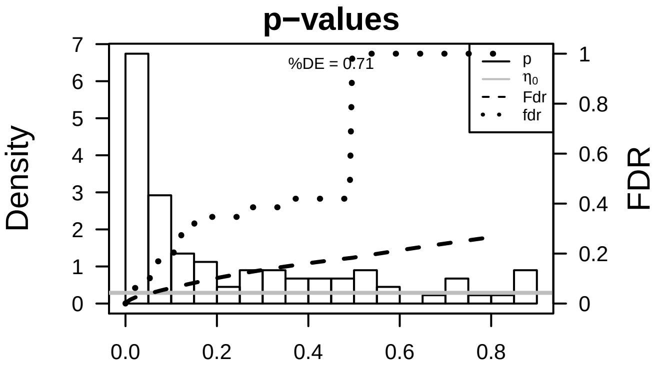
Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	29937	−0.88	1e−06	4e−05	11 x 9	neudesin neurotrophic factor [Source:HGNC Symbol;Acc:303
2	404217	0.84	4e−06	4e−05	10 x 9	cortexin 1 [Source:HGNC Symbol;Acc:31108]
3	25894	−0.83	5e−06	4e−04	12 x 11	pleckstrin homology domain containing, family G (with RhoGe
4	55258	−0.78	2e−05	7e−04	11 x 9	threonine synthase−like 2 (S. cerevisiae) [Source:HGNC Sym
5	100128927	−0.74	5e−05	1e−03	11 x 11	zinc finger and BTB domain containing 42 [Source:HGNC Sy
6	64847	−0.69	2e−04	1e−03	10 x 9	spermatogenesis associated 20 [Source:HGNC Symbol;Acc:
7	64710	−0.68	2e−04	1e−03	9 x 11	nuclear casein kinase and cyclin−dependent kinase substrate
8	51593	−0.68	2e−04	2e−03	10 x 12	serrate RNA effector molecule homolog (Arabidopsis) [Source
9	3911	−0.64	3e−04	5e−03	12 x 11	laminin, alpha 5 [Source:HGNC Symbol;Acc:6485]
10	100101267	−0.64	5e−04	5e−03	11 x 11	POM121 transmembrane nucleoporin C [Source:HGNC Syml
11	84939	−0.62	6e−04	2e−02	10 x 11	melanoma associated antigen (mutated) 1 [Source:HGNC Sy
12	11000	−0.58	1e−03	2e−02	9 x 11	solute carrier family 27 (fatty acid transporter), member 3 [So
13	23338	−0.57	2e−03	2e−02	10 x 12	jade family PHD finger 2 [Source:HGNC Symbol;Acc:22984]
14	26470	−0.54	3e−03	2e−02	10 x 9	seizure related 6 homolog (mouse)−like 2 [Source:HGNC Sy
15	55000	−0.51	3e−03	5e−02	10 x 10	taurine up−regulated 1 (non−protein coding) [Source:HGNC
16	8237	−0.49	7e−03	5e−02	10 x 9	ubiquitin specific peptidase 11 [Source:HGNC Symbol;Acc:1
17	56996	−0.48	9e−03	5e−02	10 x 11	solute carrier family 12, member 9 [Source:HGNC Symbol;Ac
18	55624	−0.48	9e−03	5e−02	10 x 9	protein O−linked mannose N−acetylglucosaminyltransferase
19	55810	−0.47	1e−02	5e−02	9 x 10	forkhead box J2 [Source:HGNC Symbol;Acc:24818]
20	50512	−0.45	1e−02	5e−02	12 x 11	podocalyxin−like 2 [Source:HGNC Symbol;Acc:17936]

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−8.51	NULL	2 / 15	GSEA C2	OLSSON_E2F3_TARGETS_DN
2	−7.98	NULL	1 / 16	GSEA C2	AIYAR_COBRA1_TARGETS_UP
3	−7.88	NULL	1 / 10	GSEA C2	KIM_WT1_TARGETS_8HR_DN
4	−7.74	NULL	1 / 10	BP	branching involved in salivary gland morphogenesis
5	−7.55	NULL	1 / 16	GSEA C2	LANDEMAINE_LUNG_METASTASIS
6	−7.48	NULL	1 / 11	BP	neuronal stem cell maintenance
7	−7.13	NULL	1 / 12	BP	response to arsenic−containing substance
8	−7.13	NULL	1 / 12	MMML CGS	MACIEJ_MMML 24
9	−7.13	NULL	1 / 12	GSEA C2	YAGI_AML_WITH_T_9_11_TRANSLOCATION
10	−7	NULL	1 / 12	BP	regulation of embryonic development
11	−6.89	NULL	1 / 13	GSEA C2	ZHONG_RESPONSE_TO_AZACITIDINE_AND_TSA_DN
12	−6.89	NULL	1 / 13	GSEA C2	SPIRA_SMOKERS_LUNG_CANCER_DN
13	−6.83	NULL	1 / 13	GSEA C2	COLDREN_GEFITINIB_RESISTANCE_UP
14	−6.83	NULL	1 / 13	GSEA C2	PENG_GLUTAMINE_DEPRIVATION_DN
15	−6.83	NULL	1 / 13	GSEA C2	BONOME_OVARIAN_CANCER_POOR_SURVIVAL_DN
16	−6.83	NULL	1 / 13	GSEA C2	WALLACE_JAK2_TARGETS_UP
17	−6.82	NULL	1 / 5	GSEA C2	NIKOLSKY_BREAST_CANCER_20P13_AMPLICON
18	−6.7	NULL	1 / 13	BP	morphogenesis of embryonic epithelium
19	−6.46	NULL	2 / 35	miRNA target starBase	hsa−miR−127−3p
20	−6.37	NULL	1 / 15	Pathw Act	BENTINK_ras.6
21	−6.31	NULL	1 / 15	GSEA C2	DIRMEIER_LMP1_RESPONSE_LATE_UP
22	−6.09	NULL	1 / 16	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_MODERATELY_VS_POO
23	−6.09	NULL	1 / 16	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_MODERATELY_VS_POO
24	−5.98	NULL	1 / 11	BP	cerebellar Purkinje cell layer development
25	−5.94	NULL	2 / 21	BP	chromatin organization
26	−5.9	NULL	1 / 5	GSEA C2	NGUYEN_NOTCH1_TARGETS_DN
27	−5.81	NULL	1 / 8	GSEA C2	NIKOLSKY_BREAST_CANCER_5P15_AMPLICON
28	−5.78	NULL	1 / 17	CC	basal lamina
29	−5.62	NULL	3 / 40	BP	histone H3 acetylation
30	−5.6	NULL	1 / 18	BP	focal adhesion assembly
31	−5.43	NULL	3 / 45	Glio	willscher_GBM_Verhaak−PNwt_expression_J_up
32	−5.39	NULL	1 / 8	GSEA C2	BIOCARTA_STRESS_PATHWAY
33	−5.37	NULL	1 / 26	MF	lyase activity
34	−5.33	NULL	1 / 6	GSEA C2	LOPEZ_MBD_TARGETS
35	−5.26	NULL	1 / 15	BP	histone H4−K5 acetylation
36	−5.26	NULL	1 / 15	BP	histone H4−K8 acetylation
37	−5.26	NULL	1 / 15	GSEA C2	HU_ANGIOGENESIS_UP
38	−5.23	NULL	1 / 10	BP	leukocyte tethering or rolling
39	−5.04	NULL	2 / 50	miRNA target starBase	hsa−miR−571
40	−4.93	NULL	1 / 38	miRNA target starBase	hsa−miR−517*

p−values



GW_227

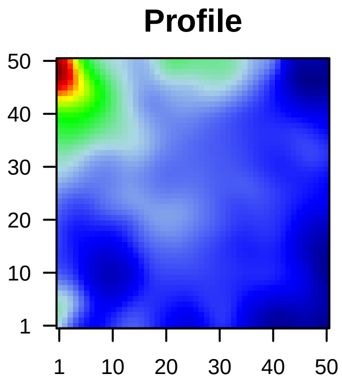
Local Summary

%DE = 0.64
metagenes = 54
genes = 614
genes in genesets = 609

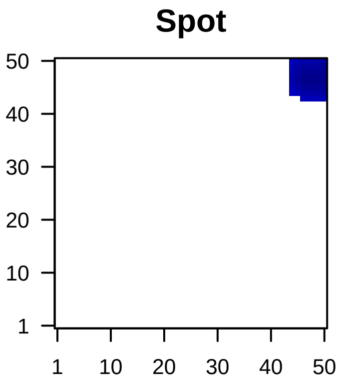
genes with fdr < 0.1 = 255 (20 + / 235 −)
genes with fdr < 0.05 = 144 (11 + / 133 −)
genes with fdr < 0.01 = 96 (6 + / 90 −)

<r> metagenes = 0.88
<r> genes = 0.24

<FC> = −0.28
<shrinkage−t> = −9.97
<p−value> = 0.02
<fdr> = 0.7



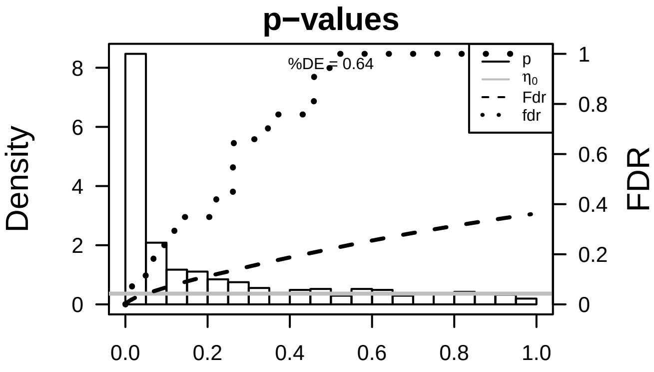
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	2944	−1.57	2e−16	1e−14	50 x 50	glutathione S−transferase mu 1 [Source:HGNC Symbol;Acc:4
2	3880	−2.09	2e−16	1e−14	50 x 49	keratin 19 [Source:HGNC Symbol;Acc:6436]
3	3856	−1.6	2e−16	1e−14	50 x 48	keratin 8 pseudogene 3 [Source:HGNC Symbol;Acc:31056]
4	26227	−1.81	2e−16	1e−14	50 x 46	phosphoglycerate dehydrogenase [Source:HGNC Symbol;Ac
5	84707	−1.37	5e−14	2e−11	50 x 48	brain expressed X−linked 2 [Source:HGNC Symbol;Acc:3093
6	2946	−1.35	1e−13	6e−10	50 x 50	glutathione S−transferase mu 2 (muscle) [Source:HGNC Sym
7	4072	−1.27	3e−12	1e−09	50 x 50	epithelial cell adhesion molecule [Source:HGNC Symbol;Acc:
8	256764	−1.24	8e−12	3e−09	50 x 50	WD repeat domain 72 [Source:HGNC Symbol;Acc:26790]
9	1056	−1.22	2e−11	8e−09	50 x 50	carboxyl ester lipase [Source:HGNC Symbol;Acc:1848]
10	9055	−1.19	6e−11	8e−09	45 x 49	protein regulator of cytokinesis 1 [Source:HGNC Symbol;Acc:
11	216	−1.17	1e−10	8e−09	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGNC
12	4922	−1.17	1e−10	5e−08	50 x 50	neurotensin [Source:HGNC Symbol;Acc:8038]
13	94234	1.14	4e−10	1e−07	50 x 50	forkhead box Q1 [Source:HGNC Symbol;Acc:20951]
14	116832	−1.11	9e−10	3e−06	46 x 50	ribosomal protein L39−like [Source:HGNC Symbol;Acc:17094
15	7345	−1.03	1e−08	1e−05	50 x 46	ubiquitin carboxyl−terminal esterase L1 (ubiquitin thiolesteras
16	9133	−0.98	7e−08	3e−05	45 x 49	cyclin B2 [Source:HGNC Symbol;Acc:1580]
17	139728	−0.95	2e−07	3e−05	49 x 49	pregnancy up−regulated nonubiquitous CaM kinase [Source:I
18	4175	−0.91	6e−07	3e−05	46 x 47	minichromosome maintenance complex component 6 [Source
19	51203	−0.91	7e−07	3e−05	45 x 48	nucleolar and spindle associated protein 1 [Source:HGNC Sy
20	5050	−0.9	7e−07	3e−05	47 x 45	platelet−activating factor acetylhydrolase 1b, catalytic subunit



p−values

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−35.3	NULL	81 / 142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
2	−35.3	NULL	81 / 142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
3	−20.61	NULL	15 / 16	GSEA C2	EGUCHI_CELL_CYCLE_RB1_TARGETS
4	−20.35	NULL	25 / 57	Glio	developing astrocytes
5	−19.76	NULL	12 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_2
6	−18.76	NULL	9 / 11	GSEA C2	KALMA_E2F1_TARGETS
7	−18.52	NULL	10 / 14	GSEA C2	ZHAN_MULTIPLE_MYELOMA_PR_UP
8	−18	NULL	45 / 149	BP	DNA replication
9	−17.94	NULL	8 / 11	GSEA C2	REACTOME_UNWINDING_OF_DNA
10	−17.31	NULL	18 / 30	BP	DNA strand elongation involved in DNA replication
11	−16.74	NULL	12 / 15	GSEA C2	CHANG_CYCLING_GENES
12	−16.69	NULL	89 / 370	BP	mitotic cell cycle
13	−16.65	NULL	6 / 10	GSEA C2	MONTERO_THYROID_CANCER_POOR_SURVIVAL_UP
14	−15.63	NULL	10 / 14	MMML CGS	MACIEJ_MMML 4
15	−15.42	NULL	11 / 16	GSEA C2	CROONQUIST_NRAS_SIGNALING_DN
16	−15.22	NULL	96 / 530	Cancer	Lembcke_Normal vs Adenoma
17	−15.07	NULL	9 / 13	GSEA C2	CROONQUIST_IL6_DEPRIVATION_DN
18	−14.84	NULL	10 / 16	GSEA C2	GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
19	−14.56	NULL	11 / 16	GSEA C2	FRASOR_RESPONSE_TO_SERM_OR_FULVESTRANT_DN
20	−14.23	NULL	10 / 16	GSEA C2	KANG_DOXORUBICIN_RESISTANCE_UP
21	−14.13	NULL	8 / 15	GSEA C2	WU_APOPTOSIS_BY_CDKN1A_VIA_TP53
22	−14.09	NULL	13 / 22	BP	DNA replication initiation
23	−14.03	NULL	5 / 8	GSEA C2	REACTOME_E2F_TRANSCRIPTIONAL_TARGETS_AT_G1_S
24	−14	NULL	8 / 11	GSEA C2	LIANG_SILENCED_BY_METHYLATION_DN
25	−13.95	NULL	11 / 16	GSEA C2	REACTOME_DNA_STRAND_ELONGATION
26	−13.79	NULL	10 / 16	GSEA C2	SONG_TARGETS_OF_IE86_CMV_PROTEIN
27	−13.45	NULL	6 / 11	GSEA C2	REACTOME_E2F_MEDIATED_REGULATION_OF_DNA_REPLICA
28	−13.42	NULL	47 / 232	BP	mitosis
29	−13.32	NULL	12 / 16	GSEA C2	FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
30	−13.17	NULL	11 / 15	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
31	−12.22	NULL	8 / 16	GSEA C2	CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_UP
32	−12.18	NULL	9 / 16	GSEA C2	REACTOME_G2_M_CHECKPOINTS
33	−12.05	NULL	6 / 9	GSEA C2	REACTOME_CELL_CYCLE_CHECKPOINTS
34	−11.97	NULL	8 / 15	GSEA C2	LEE_EARLY_T_LYMPHOCYTE_UP
35	−11.91	NULL	7 / 16	GSEA C2	CROONQUIST_NRAS_VS_STROMAL_STIMULATION_DN
36	−11.9	NULL	9 / 15	GSEA C2	BOYAULT_LIVER_CANCER_SUBCLASS_G23_UP
37	−11.87	NULL	8 / 14	GSEA C2	AMUNDSON_GAMMA_RADIATION_RESPONSE
38	−11.86	NULL	11 / 15	GSEA C2	FINETTI_BREAST_CANCER_KINOME_RED
39	−11.86	NULL	4 / 13	GSEA C2	KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_
40	−11.81	NULL	7 / 16	GSEA C2	LY_AGING_PREMATURE_DN