GW_131

Global Summary

%DE = 0.15

genes with fdr < 0.2 = 1846 (928 + / 918 −)

genes with fdr < 0.1 = 1556 (766 + / 790 −)

genes with fdr < 0.05 = 1199 (584 + / 615 −)

genes with fdr < 0.01 = 830 (388 + / 442 −)

genes in genesets = 16332

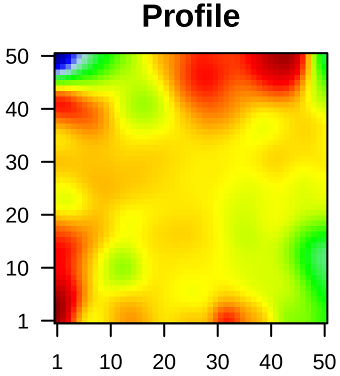
<FC> = 0

<shrinkage−t> = 0

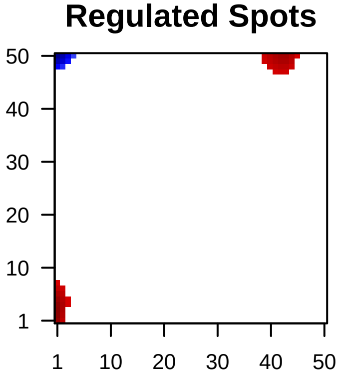
<p−value> = 0.1

<fdr> = 0.85

Profile



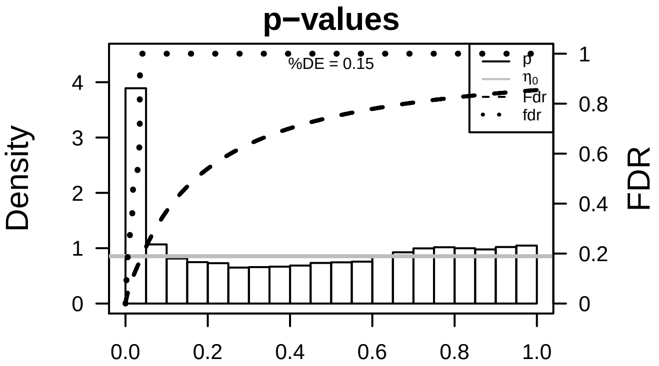
Regulated Spots



Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	70	1.45	2e−16	3e−14	25 x 1	actin, alpha, cardiac muscle 1 [Source:HGNC Symbol;Acc:14
2	131	−2.64	2e−16	3e−14	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
3	57016	−2.56	2e−16	3e−14	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
4	441282	−1.79	2e−16	3e−14	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC S
5	8644	−1.94	2e−16	3e−14	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
6	1109	−1.97	2e−16	3e−14	13 x 50	aldo−keto reductase family 1, member C4 [Source:HGNC Sy
7	216	−1.57	2e−16	3e−14	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGN
8	217	−1.52	2e−16	3e−14	50 x 15	aldehyde dehydrogenase 2 family (mitochondrial) [Source:HG
9	218	−2.97	2e−16	3e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
10	222	−1.92	2e−16	3e−14	1 x 49	aldehyde dehydrogenase 3 family, member B2 [Source:HGN
11	55107	2.47	2e−16	3e−14	1 x 5	anoctamin 1, calcium activated chloride channel [Source:HG
12	306	1.6	2e−16	3e−14	4 x 42	annexin A3 [Source:HGNC Symbol;Acc:541]
13	330	2.02	2e−16	3e−14	47 x 1	baculoviral IAP repeat containing 3 [Source:HGNC Symbol;A
14	655	−1.45	2e−16	3e−14	50 x 50	bone morphogenetic protein 7 [Source:HGNC Symbol;Acc:1
15	387695	−2.03	2e−16	3e−14	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Sym
16	375791	−1.65	2e−16	3e−14	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Sym
17	810	−2.03	2e−16	3e−14	1 x 50	calmodulin−like 3 [Source:HGNC Symbol;Acc:1452]
18	51806	−1.96	2e−16	3e−14	4 x 50	calmodulin−like 5 [Source:HGNC Symbol;Acc:18180]
19	857	1.51	2e−16	3e−14	1 x 4	caveolin 1, caveolae protein, 22kDa [Source:HGNC Symbol;
20	6364	1.94	2e−16	3e−14	46 x 1	chemokine (C−C motif) ligand 20 [Source:HGNC Symbol;Acc

p−values



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	14.67	NULL	142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
2	14.67	NULL	142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
3	12.4	NULL	370	BP	mitotic cell cycle
4	9.4	NULL	530	Cancer	Lembcke_Normal vs Adenoma
5	9.3	NULL	16	GSEA C2	MOSERLE_IFNA_RESPONSE
6	8.95	NULL	15	GSEA C2	CROMER_TUMORIGENESIS_UP
7	8.86	NULL	949	CC	nucleoplasm
8	8.66	NULL	232	BP	mitosis
9	8.56	NULL	1233	TF	KIM_MYC targets
10	8.46	NULL	16	GSEA C2	XU_HGF_TARGETS_INDUCED_BY_AKT1_6HR
11	8.41	NULL	13	GSEA C2	FRIDMAN_SENESCENCE_UP
12	7.65	NULL	123	BP	defense response to virus
13	7.54	NULL	12	BP	hemidesmosome assembly
14	7.31	NULL	699	Chr	Chr 5
15	7.27	NULL	51	BP	type I interferon signaling pathway
16	7.12	NULL	13	GSEA C2	WANG_METHYLATED_IN_BREAST_CANCER
17	7.12	NULL	68	Glio	cultured astroglia vs. in vivo astrocytes
18	6.91	NULL	15	GSEA C2	LY_AGING_MIDDLE_DN
19	6.82	NULL	16	GSEA C2	FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
20	6.8	NULL	96	BP	rRNA processing
Underexpressed					
1	−26.9	NULL	135	H.Tiss	WIRTH_Mucosa
2	−17.47	NULL	21	CC	cornified envelope
3	−15.9	NULL	42	BP	keratinization
4	−14.36	NULL	53	BP	keratinocyte differentiation
5	−12.63	NULL	8	GSEA C2	LIU_CDX2_TARGETS_DN
6	−12.12	NULL	76	BP	epidermis development
7	−10.29	NULL	16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
8	−8.74	NULL	12	BP	cellular aldehyde metabolic process
9	−8.4	NULL	15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
10	−8.35	NULL	15	CC	MHC class II protein complex
11	−8.23	NULL	10	MF	RAGE receptor binding
12	−8	NULL	19	BP	peptide cross−linking
13	−7.95	NULL	15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
14	−7.79	NULL	10	GSEA C2	FOURNIER_ACINAR_DEVELOPMENT_LATE_UP
15	−7.47	NULL	16	GSEA C2	CROMER_TUMORIGENESIS_DN
16	−7.34	NULL	9	GSEA C2	REACTOME_ETHANOL_OXIDATION
17	−7.24	NULL	16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
18	−7.16	NULL	119	BP	xenobiotic metabolic process
19	−7.06	NULL	16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
20	−6.88	NULL	16	GSEA C2	JAEGER_METASTASIS_DN

GW_131

Local Summary

%DE = 0.83

metagenes = 17

genes = 300

genes in genesets = 297

genes with fdr < 0.1 = 200 (185 + / 15 −)

genes with fdr < 0.05 = 196 (181 + / 15 −)

genes with fdr < 0.01 = 160 (152 + / 8 −)

<r> metagenes = 0.94

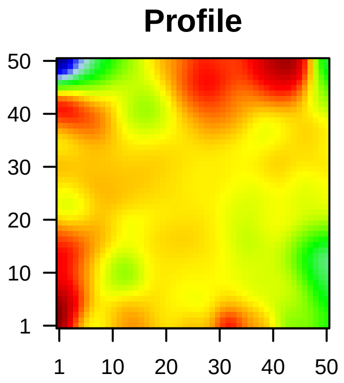
<r> genes = 0.33

<FC> = 0.55

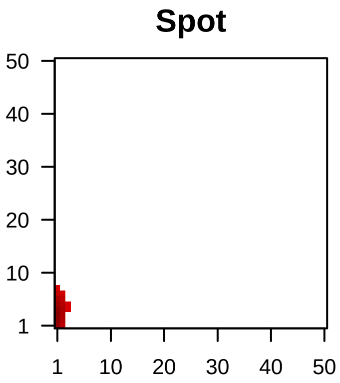
<shrinkage−t> = 19.28

<p−value> = 0

<fdr> = 0.39



Profile



Spot

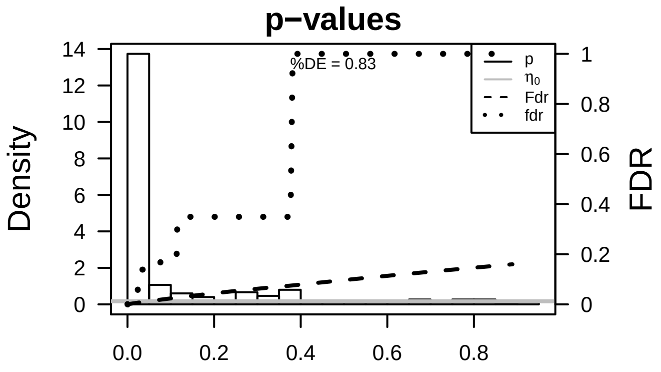
Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	55107	2.47	2e−16	5e−16	1 x 5	anoctamin 1, calcium activated chloride channel [Source:HGN
2	857	1.51	2e−16	5e−16	1 x 4	caveolin 1, caveolae protein, 22kDa [Source:HGNC Symbol;A
3	1437	1.84	2e−16	5e−16	1 x 4	colony stimulating factor 2 (granulocyte−macrophage) [Sourc
4	2920	2.01	2e−16	5e−16	1 x 1	chemokine (C−X−C motif) ligand 2 [Source:HGNC Symbol;Ac
5	1687	1.61	2e−16	5e−16	1 x 4	deafness, autosomal dominant 5 [Source:HGNC Symbol;Acc
6	10272	1.51	2e−16	5e−16	1 x 4	follistatin−like 3 (secreted glycoprotein) [Source:HGNC Symb
7	11009	2.06	2e−16	5e−16	1 x 3	interleukin 24 [Source:HGNC Symbol;Acc:11346]
8	3909	1.61	2e−16	5e−16	1 x 5	laminin, alpha 3 [Source:HGNC Symbol;Acc:6483]
9	3918	1.72	2e−16	5e−16	1 x 4	laminin, gamma 2 [Source:HGNC Symbol;Acc:6493]
10	3956	1.44	2e−16	5e−16	1 x 1	lectin, galactoside−binding, soluble, 1 [Source:HGNC Symbol
11	4314	1.73	2e−16	5e−16	1 x 1	matrix metallopeptidase 3 (stromelysin 1, progelatinase) [Sou
12	4318	1.69	2e−16	5e−16	1 x 1	matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 9
13	4489	1.61	2e−16	5e−16	1 x 4	metallothionein 1A [Source:HGNC Symbol;Acc:7393]
14	4502	2.1	2e−16	5e−16	1 x 3	metallothionein 2A [Source:HGNC Symbol;Acc:7406]
15	4907	1.8	2e−16	5e−16	1 x 3	5'−nucleotidase, ecto (CD73) [Source:HGNC Symbol;Acc:80
16	4973	1.73	2e−16	5e−16	1 x 1	oxidized low density lipoprotein (lectin−like) receptor 1 [Sourc
17	5743	1.58	2e−16	5e−16	1 x 1	prostaglandin−endoperoxide synthase 2 (prostaglandin G/H s
18	12	−1.44	2e−16	5e−16	1 x 1	
19	5054	1.79	2e−16	5e−16	1 x 2	serpin peptidase inhibitor, clade E (nexin, plasminogen activa
20	6695	1.5	2e−16	5e−16	1 x 2	sparc/osteonectin, cwcv and kazal−like domains proteoglycar

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	25.09	NULL	10 / 15	GSEA C2	CROMER_TUMORIGENESIS_UP
2	18.16	NULL	57 / 242	BP	extracellular matrix organization
3	17.44	NULL	6 / 10	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C4
4	17.23	NULL	5 / 14	GSEA C2	SIMBULAN_UV_RESPONSE_IMMORTALIZED_DN
5	16.37	NULL	6 / 15	GSEA C2	LEE_LIVER_CANCER_HEPATOBLAST
6	16.07	NULL	5 / 13	GSEA C2	FRIDMAN_SENESCENCE_UP
7	15.83	NULL	39 / 250	Lymphoma	LENZ_Stromal signature 1
8	15.77	NULL	7 / 15	GSEA C2	ONDER_CDH1_SIGNALING_VIA_CTNNB1
9	15.69	NULL	6 / 12	BP	hemidesmosome assembly
10	15.03	NULL	5 / 16	GSEA C2	KIM_WT1_TARGETS_UP
11	14.84	NULL	4 / 9	GSEA C2	ZERBINI_RESPONSE_TO_SULINDAC_UP
12	14.7	NULL	5 / 16	GSEA C2	AMIT_EGF_RESPONSE_60_HELA
13	14.52	NULL	6 / 16	MF	fibronectin binding
14	14.38	NULL	4 / 16	GSEA C2	KEGG_BLADDER_CANCER
15	14.38	NULL	8 / 16	GSEA C2	BEGUM_TARGETS_OF_PAX3_FOXO1_FUSION_DN
16	14.19	NULL	4 / 15	GSEA C2	DASU_IL6_SIGNALING_SCAR_DN
17	14.18	NULL	3 / 10	BP	cellular response to zinc ion
18	14.1	NULL	17 / 83	CC	basement membrane
19	14.06	NULL	4 / 13	GSEA C2	CHIN_BREAST_CANCER_COPY_NUMBER_UP
20	13.85	NULL	2 / 8	GSEA C2	NAKAYAMA_SOFT_TISSUE_TUMORS_PCA1_UP
21	13.8	NULL	52 / 403	BP	cell adhesion
22	13.74	NULL	5 / 8	GSEA C2	SASAKI_TARGETS_OF_TP73_AND_TP63
23	13.67	NULL	4 / 16	GSEA C2	LI_PROSTATE_CANCER_EPIGENETIC
24	13.56	NULL	5 / 10	GSEA C2	KEGG_ECM_RECEPTOR_INTERACTION
25	13.54	NULL	4 / 13	GSEA C2	TSAI_RESPONSE_TO_RADIATION_THERAPY
26	13.5	NULL	5 / 11	GSEA C2	BIOCARTA_PLATELETAPP_PATHWAY
27	13.47	NULL	5 / 16	GSEA C2	FERRARI_RESPONSE_TO_FENRETINIDE_UP
28	13.36	NULL	2 / 5	GSEA C2	VERNELL_RETINOBLASTOMA_PATHWAY_DN
29	13.31	NULL	5 / 16	GSEA C2	AMIT_SERUM_RESPONSE_60_MCF10A
30	13.19	NULL	14 / 85	MF	integrin binding
31	13.11	NULL	4 / 15	GSEA C2	SAGIV_CD24_TARGETS_DN
32	12.98	NULL	10 / 35	Glio	Colman_survival_associated
33	12.92	NULL	5 / 16	GSEA C2	URS_ADIPOCYTE_DIFFERENTIATION_DN
34	12.89	NULL	4 / 11	GSEA C2	LIU_SOX4_TARGETS_UP
35	12.83	NULL	93 / 1182	CC	extracellular region
36	12.71	NULL	61 / 683	CC	extracellular space
37	12.57	NULL	4 / 16	GSEA C2	XU_HGF_TARGETS_INDUCED_BY_AKT1_6HR
38	12.51	NULL	2 / 6	Glio	Martinez_Glio_hypometh
39	12.37	NULL	3 / 11	GSEA C2	BIOCARTA_STEM_PATHWAY
40	12.37	NULL	34 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up



p−values

GW_131

Local Summary

%DE = 0.91

metagenes = 21

genes = 318

genes in genesets = 316

genes with fdr < 0.1 = 259 (254 + / 5 −)

genes with fdr < 0.05 = 226 (225 + / 1 −)

genes with fdr < 0.01 = 174 (174 + / 0 −)

<r> metagenes = 0.96

<r> genes = 0.36

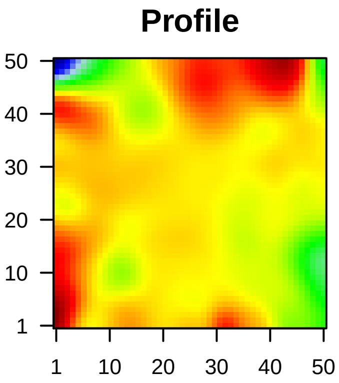
<FC> = 0.44

<shrinkage−t> = 15.59

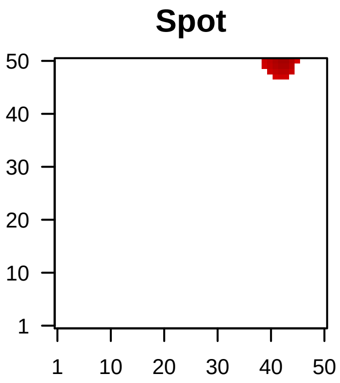
<p−value> = 0

<fdr> = 0.47

Profile



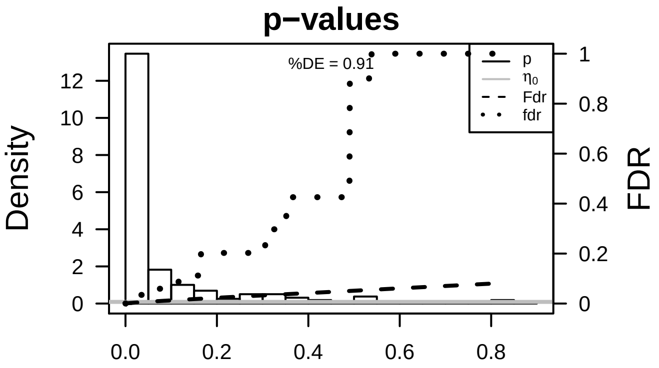
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	8500	1.51	2e−16	6e−15	42 x 50	protein tyrosine phosphatase, receptor type, f polypeptide (PT
2	54443	1.31	1e−13	3e−10	43 x 50	anillin, actin binding protein [Source:HGNC Symbol;Acc:1408
3	1829	1.2	1e−11	2e−08	44 x 50	desmoglein 2 [Source:HGNC Symbol;Acc:3049]
4	220042	1.08	8e−10	5e−08	42 x 50	chromosome 11 open reading frame 82 [Source:HGNC Symb
5	55839	1.05	3e−09	6e−08	44 x 50	centromere protein N [Source:HGNC Symbol;Acc:30873]
6	55646	1.03	6e−09	6e−08	40 x 50	Ly1 antibody reactive [Source:HGNC Symbol;Acc:26021]
7	9833	1.02	7e−09	5e−07	44 x 50	maternal embryonic leucine zipper kinase [Source:HGNC Sy
8	55127	0.97	4e−08	5e−07	40 x 50	HEAT repeat containing 1 [Source:HGNC Symbol;Acc:25517]
9	4173	0.97	4e−08	9e−07	44 x 50	minichromosome maintenance complex component 4 [Source
10	144455	0.95	7e−08	3e−06	45 x 50	E2F transcription factor 7 [Source:HGNC Symbol;Acc:23820]
11	55165	0.91	3e−07	3e−06	44 x 50	centrosomal protein 55kDa [Source:HGNC Symbol;Acc:1161
12	890	0.9	3e−07	4e−06	44 x 50	cyclin A2 [Source:HGNC Symbol;Acc:1578]
13	6611	0.88	6e−07	4e−06	42 x 50	spermine synthase [Source:HGNC Symbol;Acc:11123]
14	93081	0.88	6e−07	4e−06	43 x 49	testis expressed 30 [Source:HGNC Symbol;Acc:25188]
15	55536	0.87	7e−07	4e−06	42 x 50	cell division cycle associated 7−like [Source:HGNC Symbol;A
16	29028	0.87	8e−07	6e−06	44 x 50	ATPase family, AAA domain containing 2 [Source:HGNC Sym
17	64151	0.86	1e−06	6e−06	44 x 48	non−SMC condensin I complex, subunit G [Source:HGNC Sy
18	22974	0.86	1e−06	3e−05	44 x 50	TPX2, microtubule−associated [Source:HGNC Symbol;Acc:1
19	10733	0.83	2e−06	3e−05	44 x 50	polo−like kinase 4 [Source:HGNC Symbol;Acc:11397]
20	9319	0.82	3e−06	3e−05	43 x 50	thyroid hormone receptor interactor 13 [Source:HGNC Symbo

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	38.16	NULL	54 / 142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
2	38.16	NULL	54 / 142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
3	23.71	NULL	11 / 16	GSEA C2	FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
4	21.79	NULL	10 / 15	GSEA C2	FINETTI_BREAST_CANCER_KINOME_RED
5	21.23	NULL	63 / 370	BP	mitotic cell cycle
6	20.28	NULL	8 / 15	GSEA C2	FOURNIER_ACINAR_DEVELOPMENT_LATE_DN
7	20.16	NULL	8 / 14	MMML CGS	MACIEJ_MMML 4
8	20.02	NULL	64 / 530	Cancer	Lembcke_Normal vs Adenoma
9	18.7	NULL	8 / 13	GSEA C2	CROONQUIST_IL6_DEPRIVATION_DN
10	18.53	NULL	10 / 18	BP	spindle organization
11	17.78	NULL	6 / 15	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
12	17.72	NULL	14 / 57	Glio	developing astrocytes
13	17.12	NULL	8 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_2
14	16.6	NULL	5 / 10	GSEA C2	MONTERO_THYROID_CANCER_POOR_SURVIVAL_UP
15	15.56	NULL	32 / 232	BP	mitosis
16	15.43	NULL	17 / 56	CC	chromosome, centromeric region
17	15.4	NULL	7 / 13	GSEA C2	WINNEPENNINCKX_MELANOMA_METASTASIS_UP
18	15.38	NULL	5 / 9	GSEA C2	BIOCARTA_RANMS_PATHWAY
19	15.23	NULL	7 / 16	GSEA C2	KANG_DOXORUBICIN_RESISTANCE_UP
20	15.19	NULL	7 / 14	GSEA C2	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
21	14.64	NULL	51 / 572	Disease	GUDJ_psoriasis up
22	14.55	NULL	6 / 16	GSEA C2	EGUCHI_CELL_CYCLE_RB1_TARGETS
23	13.86	NULL	7 / 11	BP	mitotic metaphase plate congression
24	13.84	NULL	7 / 16	Cancer	RHODES_UNDIFFERENTIATED_CANCER
25	13.81	NULL	6 / 15	GSEA C2	LEE_EARLY_T_LYMPHOCYTE_UP
26	13.79	NULL	6 / 15	GSEA C2	LY_AGING_MIDDLE_DN
27	13.68	NULL	6 / 16	GSEA C2	SCIAN_CELL_CYCLE_TARGETS_OF_TP53_AND_TP73_DN
28	13.56	NULL	7 / 15	GSEA C2	SMID_BREAST_CANCER_LUMINAL_A_DN
29	13.52	NULL	6 / 16	Cancer	WOLFER_overlap genes
30	13.5	NULL	6 / 15	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
31	12.73	NULL	14 / 66	CC	condensed chromosome kinetochore
32	11.84	NULL	4 / 14	GSEA C2	LOPEZ_MESOTELIOMA_SURVIVAL_TIME_UP
33	11.68	NULL	5 / 14	GSEA C2	AMUNDSON_GAMMA_RADIATION_RESPONSE
34	11.6	NULL	5 / 14	GSEA C2	XU_HGF_TARGETS_INDUCED_BY_AKT1_48HR_DN
35	11.55	NULL	4 / 9	GSEA C2	KUMAMOTO_RESPONSE_TO_NUTLIN_3A_DN
36	11.53	NULL	5 / 14	GSEA C2	ZHAN_MULTIPLE_MYELOMA_PR_UP
37	11.42	NULL	10 / 35	BP	mitotic nuclear envelope disassembly
38	11.25	NULL	12 / 59	CC	nuclear pore
39	11.25	NULL	4 / 11	GSEA C2	ODONNELL_TFRC_TARGETS_DN
40	11.23	NULL	11 / 68	Cancer	SHAUGHNESSY_MM high risk

GW_131

Local Summary

%DE = 0.97

metagenes = 9

genes = 159

genes in genesets = 156

genes with fdr < 0.1 = 152 (1 + / 151 −)

genes with fdr < 0.05 = 148 (1 + / 147 −)

genes with fdr < 0.01 = 146 (1 + / 145 −)

<r> metagenes = 0.99

<r> genes = 0.5

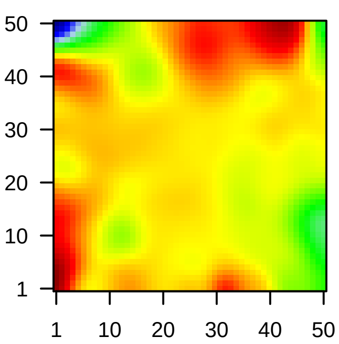
<FC> = −1.27

<shrinkage−t> = −44.9

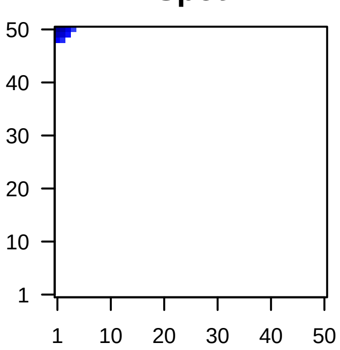
<p−value> = 0

<fdr> = 0.08

Profile



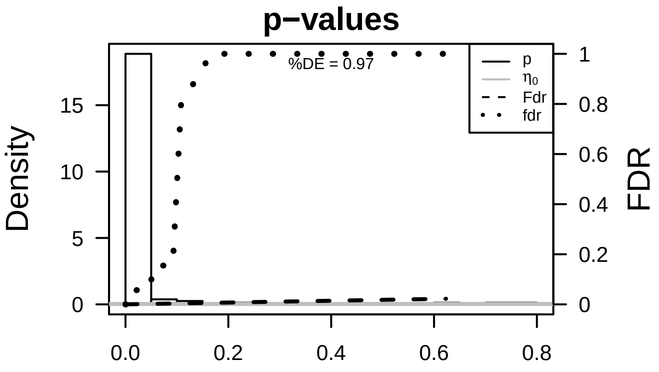
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	131	−2.64	2e−16	2e−17	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	57016	−2.56	2e−16	2e−17	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
3	441282	−1.79	2e−16	2e−17	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC S
4	8644	−1.94	2e−16	2e−17	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
5	218	−2.97	2e−16	2e−17	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
6	222	−1.92	2e−16	2e−17	1 x 49	aldehyde dehydrogenase 3 family, member B2 [Source:HGN
7	387695	−2.03	2e−16	2e−17	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Sym
8	375791	−1.65	2e−16	2e−17	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Sym
9	810	−2.03	2e−16	2e−17	1 x 50	calmodulin−like 3 [Source:HGNC Symbol;Acc:1452]
10	51806	−1.96	2e−16	2e−17	4 x 50	calmodulin−like 5 [Source:HGNC Symbol;Acc:18180]
11	4680	−2.18	2e−16	2e−17	1 x 50	carcinoembryonic antigen−related cell adhesion molecule 6 (
12	22802	−2.12	2e−16	2e−17	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
13	9022	−1.45	2e−16	2e−17	1 x 50	chloride intracellular channel 3 [Source:HGNC Symbol;Acc:2
14	84518	−2.83	2e−16	2e−17	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
15	49860	−2.33	2e−16	2e−17	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
16	1476	−1.57	2e−16	2e−17	1 x 50	cystatin B (stefin B) [Source:HGNC Symbol;Acc:2482]
17	92196	−1.65	2e−16	2e−17	3 x 50	death associated protein−like 1 [Source:HGNC Symbol;Acc:2
18	1672	−1.92	2e−16	2e−17	1 x 50	defensin, beta 1 [Source:HGNC Symbol;Acc:2766]
19	414325	−1.52	2e−16	2e−17	1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
20	1673	−2.1	2e−16	2e−17	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]

p−values



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−57.39	NULL	67 / 135	H.Tiss	WIRTH_Mucosa
2	−42.25	NULL	14 / 21	CC	cornified envelope
3	−36.16	NULL	16 / 42	BP	keratinization
4	−34.87	NULL	19 / 53	BP	keratinocyte differentiation
5	−28.49	NULL	18 / 76	BP	epidermis development
6	−26.42	NULL	70 / 572	Disease	GUDJ_psoriasis up
7	−26.35	NULL	8 / 19	BP	peptide cross−linking
8	−19.3	NULL	5 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
9	−18.77	NULL	4 / 10	MF	RAGE receptor binding
10	−17.91	NULL	5 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
11	−16.58	NULL	6 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
12	−16.18	NULL	3 / 12	BP	cellular aldehyde metabolic process
13	−15.28	NULL	4 / 10	GSEA C2	SMID_BREAST_CANCER_ERBB2_UP
14	−15.14	NULL	6 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
15	−14.82	NULL	6 / 13	BP	negative regulation of peptidase activity
16	−14.63	NULL	6 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
17	−14.31	NULL	3 / 15	GSEA C2	CHANG_IMMORTALIZED_BY_HPV31_DN
18	−13.9	NULL	4 / 15	GSEA C2	LEE_LIVER_CANCER_MYC_E2F1_UP
19	−13.56	NULL	3 / 16	GSEA C2	AMIT_SERUM_RESPONSE_480_MCF10A
20	−12.56	NULL	6 / 15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
21	−12.29	NULL	13 / 186	MF	structural molecule activity
22	−12.11	NULL	2 / 10	GSEA C2	MURAKAMI_UV_RESPONSE_1HR_UP
23	−11.81	NULL	1 / 6	GSEA C2	SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_DN
24	−11.33	NULL	3 / 15	GSEA C2	LEE_LIVER_CANCER_MYC_UP
25	−11.3	NULL	4 / 16	GSEA C2	LEE_LIVER_CANCER_MYC_TGFA_UP
26	−11.16	NULL	4 / 15	MF	retinol dehydrogenase activity
27	−11.03	NULL	1 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
28	−11.02	NULL	3 / 15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
29	−10.49	NULL	3 / 16	GSEA C2	CHEOK_RESPONSE_TO_MERCAPTOPURINE_AND_LD_MTX_
30	−10.45	NULL	2 / 10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
31	−10.42	NULL	4 / 16	GSEA C2	JAEGER_METASTASIS_DN
32	−9.98	NULL	3 / 10	GSEA C2	KEGG_LINOLEIC_ACID_METABOLISM
33	−9.73	NULL	3 / 14	GSEA C2	CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U
34	−9.66	NULL	44 / 1182	CC	extracellular region
35	−9.62	NULL	3 / 13	GSEA C2	FARMER_BREAST_CANCER_APOCRINE VS LUMINAL
36	−9.62	NULL	2 / 11	GSEA C2	MURAKAMI_UV_RESPONSE_6HR_DN
37	−9.58	NULL	4 / 13	H.Tiss	WIRTH_Tonsil
38	−9.57	NULL	2 / 14	GSEA C2	KEGG_PHENYLALANINE_METABOLISM
39	−9.43	NULL	3 / 16	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_DN
40	−9.15	NULL	4 / 27	BP	response to bacterium