GW_158

Global Summary

%DE = 0.13

genes with fdr < 0.2 = 1646 (909 + / 737 −)

genes with fdr < 0.1 = 1303 (747 + / 556 −)

genes with fdr < 0.05 = 991 (591 + / 400 −)

genes with fdr < 0.01 = 689 (440 + / 249 −)

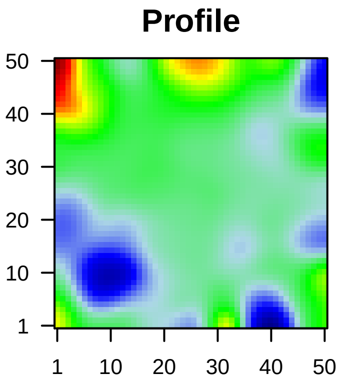
genes in genesets = 16332

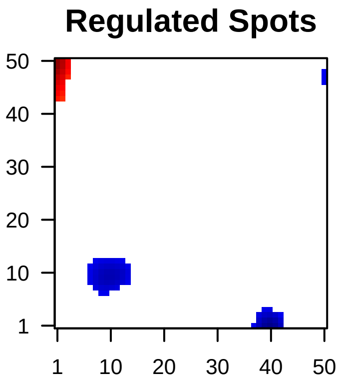
<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.12

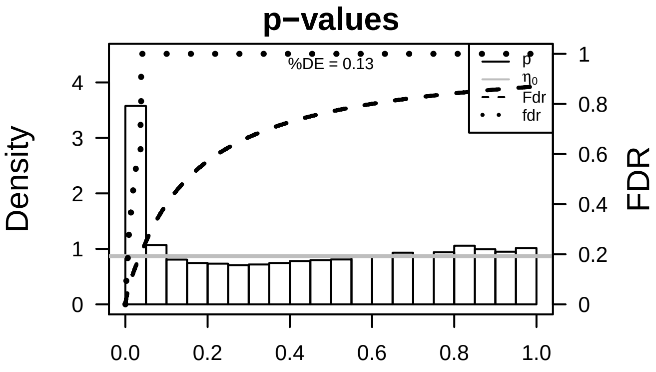
<fdr> = 0.87





Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	57016	1.31	2e−16	4e−14	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
2	218	1.21	2e−16	4e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
3	25805	1.15	2e−16	4e−14	8 x 1	BMP and activin membrane−bound inhibitor [Source:HGNC
4	768	1.13	2e−16	4e−14	1 x 6	carbonic anhydrase IX [Source:HGNC Symbol;Acc:1383]
5	57172	−1.56	2e−16	4e−14	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
6	857	1.63	2e−16	4e−14	1 x 4	caveolin 1, caveolae protein, 22kDa [Source:HGNC Symbol;
7	875	−1.22	2e−16	4e−14	49 x 47	cystathionine−beta−synthase [Source:HGNC Symbol;Acc:15
8	131076	−1.22	2e−16	4e−14	1 x 16	coiled−coil domain containing 58 [Source:HGNC Symbol;Acc
9	4680	1.24	2e−16	4e−14	1 x 50	carcinoembryonic antigen−related cell adhesion molecule 6 (
10	1675	1.22	2e−16	4e−14	50 x 9	complement factor D (adipsin) [Source:HGNC Symbol;Acc:27
11	91612	1.4	2e−16	4e−14	24 x 48	churchill domain containing 1 [Source:HGNC Symbol;Acc:20
12	22802	1.48	2e−16	4e−14	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
13	1308	1.38	2e−16	4e−14	1 x 43	collagen, type XVII, alpha 1 [Source:HGNC Symbol;Acc:2194
14	1281	1.07	2e−16	4e−14	2 x 1	collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]
15	49860	2.57	2e−16	4e−14	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
16	1514	1.35	2e−16	4e−14	1 x 2	cathepsin L [Source:HGNC Symbol;Acc:2537]
17	3627	1.72	2e−16	4e−14	32 x 1	chemokine (C−X−C motif) ligand 10 [Source:HGNC Symbol;
18	9547	1.36	2e−16	4e−14	1 x 46	chemokine (C−X−C motif) ligand 14 [Source:HGNC Symbol;
19	4283	1.55	2e−16	4e−14	49 x 1	chemokine (C−X−C motif) ligand 9 [Source:HGNC Symbol;A
20	84259	1.27	2e−16	4e−14	5 x 42	DCN1, defective in cullin neddylation 1, domain containing 5 [



Global Geneset Analysis

Rank	GSZ	p−value	#all		Geneset
Overexpressed					
1	20.59	NULL	572	Disease	GUDJ_psoriasis up
2	19.86	NULL	135	H.Tiss	WIRTH_Mucosa
3	14.52	NULL	16	GSEA C2	MOSERLE_IFNA_RESPONSE
4	11.82	NULL	15	CC	MHC class II protein complex
5	11.32	NULL	60	BP	interferon−gamma−mediated signaling pathway
6	11.26	NULL	204	BP	cytokine−mediated signaling pathway
7	11.04	NULL	1182	CC	extracellular region
8	10.63	NULL	47	BP	antigen processing and presentation
9	10.04	NULL	23	CC	integral to lumenal side of endoplasmic reticulum membrane
10	10.01	NULL	312	BP	immune response
11	9.98	NULL	123	BP	defense response to virus
12	9.67	NULL	633	Chr	Chr 9
13	9.49	NULL	16	GSEA C2	ZHANG_INTERFERON_RESPONSE
14	9.35	NULL	683	CC	extracellular space
15	9.31	NULL	21	CC	clathrin−coated endocytic vesicle membrane
16	9.09	NULL	51	BP	type I interferon signaling pathway
17	9.06	NULL	32	CC	ER to Golgi transport vesicle membrane
18	8.76	NULL	13	GSEA C2	BOWIE_RESPONSE_TO_TAMOXIFEN
19	8.39	NULL	190	CC	extracellular matrix
20	8.35	NULL	265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
Underexpressed					
1	−8.19	NULL	386	Chr	Chr 22
2	−5.21	NULL	504	Chr	Chr 15
3	−5.07	NULL	918	Chr	Chr 17
4	−4.98	NULL	1749	MF	DNA binding
5	−4.83	NULL	1581	BP	regulation of transcription, DNA−dependent
6	−4.78	NULL	1135	Chr	Chr 19
7	−4.77	NULL	1574	BP	transcription, DNA−templated
8	−4.67	NULL	127	H.Tiss	WIRTH_Muscle
9	−4.61	NULL	630	Chr	Chr X
10	−4.34	NULL	92	BP	anterior/posterior pattern specification
11	−4.18	NULL	400	H.Tiss	WIRTH_Nervous System
12	−4.15	NULL	261	miRNA 3UTR	CTCA−125B−−125A
13	−4.06	NULL	21	BP	feeding behavior
14	−4	NULL	914	Chr	Chr 3
15	−3.65	NULL	6	H.Tiss	WIRTH_Bone marrow
16	−3.64	NULL	64	BP	activation of signaling protein activity involved in unfolded protein re
17	−3.6	NULL	379	Glio	Down_a
18	−3.58	NULL	182	miRNA 3UTR	CTGA−24
19	−3.57	NULL	15	GSEA C2	KRIGE_AMINO_ACID_DEPRIVATION
20	−3.53	NULL	36	BP	muscle filament sliding

GW_158

Local Summary

%DE = 0.75

metagenes = 20

genes = 293

genes in genesets = 286

genes with fdr < 0.1 = 185 (168 + / 17 −)

genes with fdr < 0.05 = 168 (155 + / 13 −)

genes with fdr < 0.01 = 142 (133 + / 9 −)

<r> metagenes = 0.89

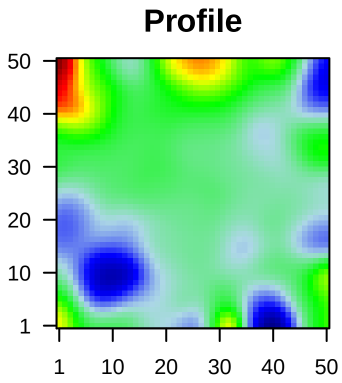
<r> genes = 0.38

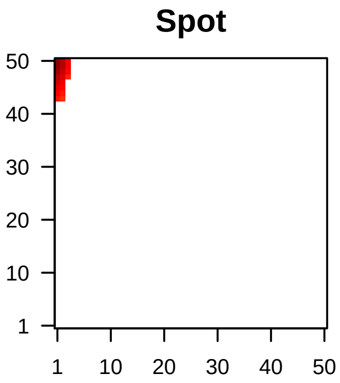
<FC> = 0.45

<shrinkage−t> = 15.77

<p−value> = 0

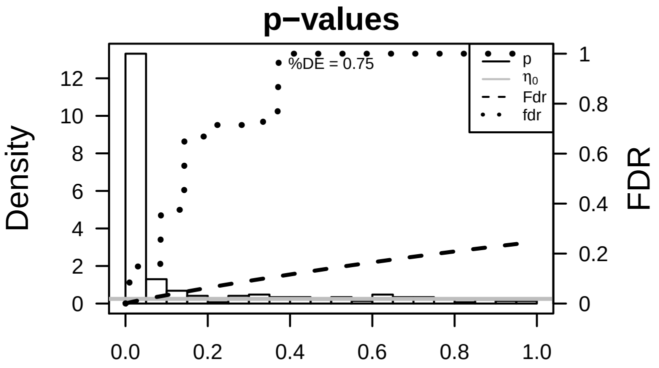
<fdr> = 0.41





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	57016	1.31	2e−16	5e−16	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
2	218	1.21	2e−16	5e−16	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
3	4680	1.24	2e−16	5e−16	1 x 50	carcinoembryonic antigen−related cell adhesion molecule 6 (
4	22802	1.48	2e−16	5e−16	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
5	1308	1.38	2e−16	5e−16	1 x 43	collagen, type XVII, alpha 1 [Source:HGNC Symbol;Acc:2194
6	49860	2.57	2e−16	5e−16	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
7	9547	1.36	2e−16	5e−16	1 x 46	chemokine (C−X−C motif) ligand 14 [Source:HGNC Symbol;
8	55894	1.74	2e−16	5e−16	1 x 47	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
9	414325	2.07	2e−16	5e−16	1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
10	1673	1.84	2e−16	5e−16	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
11	1828	1.18	2e−16	5e−16	1 x 48	desmoglein 1 [Source:HGNC Symbol;Acc:3048]
12	2150	1.31	2e−16	5e−16	1 x 44	coagulation factor II (thrombin) receptor−like 1 [Source:HGNC
13	9982	1.08	2e−16	5e−16	1 x 47	fibroblast growth factor binding protein 1 [Source:HGNC Sym
14	163351	1.54	2e−16	5e−16	1 x 50	guanylate binding protein family, member 6 [Source:HGNC Sy
15	3489	1.65	2e−16	5e−16	1 x 44	insulin−like growth factor binding protein 6 [Source:HGNC Sy
16	3860	1.38	2e−16	5e−16	1 x 50	keratin 13 [Source:HGNC Symbol;Acc:6415]
17	3851	2.67	2e−16	5e−16	1 x 50	keratin 4 [Source:HGNC Symbol;Acc:6441]
18	9119	1.39	2e−16	5e−16	1 x 44	keratin 75 [Source:HGNC Symbol;Acc:24431]
19	388533	1.58	2e−16	5e−16	1 x 49	keratinocyte differentiation−associated protein [Source:HGNC
20	4118	1.95	2e−16	5e−16	1 x 50	mal, T−cell differentiation protein [Source:HGNC Symbol;Acc



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	48.79	NULL	87 / 135	H.Tiss	WIRTH_Mucosa
2	22.76	NULL	110 / 572	Disease	GUDJ_psoriasis up
3	18.37	NULL	27 / 76	BP	epidermis development
4	16.6	NULL	18 / 21	CC	cornified envelope
5	16.56	NULL	3 / 6	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_UP
6	16.05	NULL	20 / 42	BP	keratinization
7	15.72	NULL	13 / 44	CC	keratin filament
8	15.04	NULL	24 / 53	BP	keratinocyte differentiation
9	13.97	NULL	6 / 13	BP	negative regulation of peptidase activity
10	13.35	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
11	13.08	NULL	6 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
12	12.69	NULL	7 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
13	12.43	NULL	8 / 15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
14	12.17	NULL	6 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
15	12.15	NULL	21 / 82	CC	intermediate filament
16	11.9	NULL	8 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
17	11.35	NULL	10 / 19	BP	peptide cross−linking
18	10.02	NULL	8 / 38	BP	epithelial cell differentiation
19	9.98	NULL	29 / 186	MF	structural molecule activity
20	9.87	NULL	12 / 21	CC	desmosome
21	9.86	NULL	7 / 29	BP	regulation of proteolysis
22	9.81	NULL	2 / 6	GSEA C2	SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_DN
23	9.71	NULL	3 / 10	GSEA C2	MURAKAMI_UV_RESPONSE_1HR_UP
24	9.68	NULL	2 / 7	GSEA C2	YE_METASTATIC_LIVER_CANCER
25	9.5	NULL	10 / 52	BP	negative regulation of endopeptidase activity
26	9.41	NULL	2 / 11	Glio	VERHAAK_Brain
27	9.3	NULL	4 / 12	H.Tiss	WIRTH_Prim. lymphoid organs
28	9.28	NULL	67 / 1182	CC	extracellular region
29	9.1	NULL	4 / 14	GSEA C2	CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U
30	9.07	NULL	3 / 15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
31	9.04	NULL	6 / 15	GSEA C2	AIGNER_ZEB1_TARGETS
32	9.02	NULL	3 / 12	BP	cellular aldehyde metabolic process
33	8.97	NULL	4 / 16	GSEA C2	LEE_LIVER_CANCER_MYC_TGFA_UP
34	8.96	NULL	3 / 10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
35	8.84	NULL	3 / 15	GSEA C2	ALONSO_METASTASIS_NEURAL_UP
36	8.8	NULL	1 / 5	GSEA C2	BUSA_SAM68_TARGETS_UP
37	8.53	NULL	3 / 12	BP	hemidesmosome assembly
38	8.36	NULL	4 / 15	GSEA C2	LEE_LIVER_CANCER_MYC_E2F1_UP
39	8.31	NULL	4 / 13	H.Tiss	WIRTH_Tonsil
40	8.19	NULL	4 / 10	GSEA C2	FOURNIER_ACINAR_DEVELOPMENT_LATE_UP

GW_158

Local Summary

%DE = 0.76

metagenes = 18

genes = 268

genes in genesets = 241

genes with fdr < 0.1 = 146 (0 + / 146 −)

genes with fdr < 0.05 = 128 (0 + / 128 −)

genes with fdr < 0.01 = 89 (0 + / 89 −)

<r> metagenes = 0.98

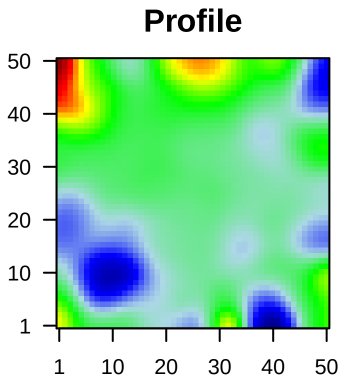
<r> genes = 0.46

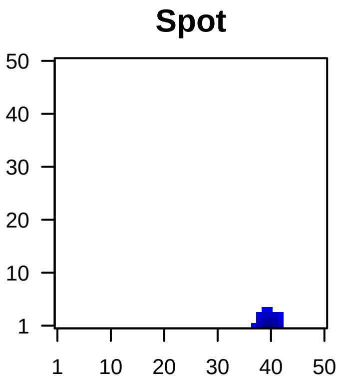
<FC> = −0.33

<shrinkage−t> = −11.51

<p−value> = 0.01

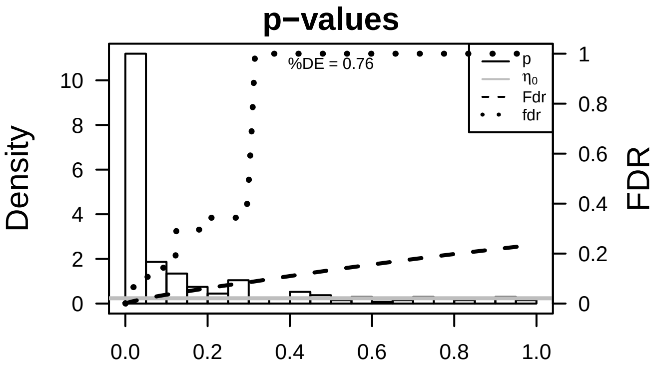
<fdr> = 0.54





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	100132406	−1.18	2e−16	7e−15	39 x 1	neuroblastoma breakpoint family, member 10 [Source:HGNC
2	400818	−1.48	2e−16	7e−15	40 x 1	Neuroblastoma breakpoint family member 1 [Source:UniProt
3	618	−0.98	1e−12	8e−10	39 x 1	brain cytoplasmic RNA 1 [Source:HGNC Symbol;Acc:1022]
4	641737	−0.87	2e−11	8e−10	40 x 1	
5	440275	−0.92	3e−11	6e−09	40 x 1	eukaryotic translation initiation factor 2 alpha kinase 4 [Sourc
6	136051	−0.89	1e−10	9e−08	40 x 1	zinc finger protein 786 [Source:HGNC Symbol;Acc:21806]
7	8566	−0.84	1e−09	3e−07	41 x 2	pyridoxal (pyridoxine, vitamin B6) kinase [Source:HGNC Sym
8	90639	−0.8	6e−09	3e−07	40 x 1	cytochrome c oxidase assembly homolog 19 (S. cerevisiae) [
9	255031	−0.79	1e−08	2e−06	40 x 1	long intergenic non−protein coding RNA 957 [Source:HGNC
10	55142	−0.76	4e−08	5e−06	40 x 1	HAUS augmin−like complex, subunit 2 [Source:HGNC Symb
11	57835	−0.73	1e−07	5e−06	40 x 1	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:E7
12	727956	−0.72	2e−07	7e−06	40 x 1	succinate dehydrogenase complex, subunit A, flavoprotein ps
13	84061	−0.71	3e−07	7e−06	39 x 1	magnesium transporter 1 [Source:HGNC Symbol;Acc:28880]
14	3586	−0.64	5e−07	7e−06	40 x 1	interleukin 10 [Source:HGNC Symbol;Acc:5962]
15	1375	−0.69	5e−07	8e−06	42 x 1	carnitine palmitoyltransferase 1B (muscle) [Source:HGNC Sy
16	152485	−0.69	7e−07	8e−06	41 x 1	zinc finger protein 827 [Source:HGNC Symbol;Acc:27193]
17	100134868	−0.68	8e−07	1e−05	40 x 1	
18	23015	−0.68	1e−06	2e−05	39 x 1	golgin A8 family, member A [Source:HGNC Symbol;Acc:3197
19	55333	−0.67	1e−06	2e−05	40 x 1	synaptojanin 2 binding protein [Source:HGNC Symbol;Acc:18
20	7707	−0.66	2e−06	2e−05	39 x 1	zinc finger protein 148 [Source:HGNC Symbol;Acc:12933]



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−11.58	NULL	2 / 4	GSEA C2	BIOCARTA_CYTOKINE_PATHWAY
2	−8.22	NULL	3 / 14	MMML CGS	MACIEJ_MMML 8
3	−7.67	NULL	3 / 13	GSEA C2	SPIRA_SMOKERS_LUNG_CANCER_DN
4	−7.18	NULL	3 / 16	GSEA C2	HAMAI_APOPTOSIS_VIA_TRAIL_UP
5	−6.96	NULL	2 / 15	GSEA C2	FIRESTEIN_PROLIFERATION
6	−6.85	NULL	1 / 5	GSEA C2	BIOCARTA_INFLAM_PATHWAY
7	−6.15	NULL	1 / 6	GSEA C2	BUDHU_LIVER_CANCER_METASTASIS_UP
8	−6.15	NULL	1 / 6	GSEA C2	SEIKE_LUNG_CANCER_POOR_SURVIVAL
9	−5.89	NULL	1 / 9	GSEA C2	TARTE_PLASMA_CELL_VS_B_LYMPHOCYTE_UP
10	−5.89	NULL	1 / 9	GSEA C2	DER_IFN_ALPHA_RESPONSE_UP
11	−5.82	NULL	3 / 24	BP	negative regulation of T cell proliferation
12	−5.81	NULL	1 / 11	GSEA C2	BIOCARTA_EIF2_PATHWAY
13	−5.73	NULL	3 / 15	GSEA C2	WANG_CLIM2_TARGETS_UP
14	−5.69	NULL	2 / 13	GSEA C2	GAZDA_DIAMOND_BLACKFAN_ANEMIA_ERYTHROID_DN
15	−5.67	NULL	2 / 14	BP	cellular response to estradiol stimulus
16	−5.37	NULL	2 / 15	Glio	Donson−chemokines/cytokines−associated with LTS in HGA
17	−5.28	NULL	2 / 23	BP	protein N−linked glycosylation
18	−5.28	NULL	2 / 16	GSEA C2	LUI_THYROID_CANCER_CLUSTER_1
19	−5.23	NULL	1 / 11	GSEA C2	DER_IFN_BETA_RESPONSE_UP
20	−5.19	NULL	1 / 8	GSEA C2	BIOCARTA_ASBCELL_PATHWAY
21	−5.12	NULL	2 / 14	BP	mitochondrion morphogenesis
22	−5.11	NULL	2 / 14	GSEA C2	MITSIADES_RESPONSE_TO_APLIDIN_DN
23	−5.02	NULL	3 / 39	miRNA target sites	hsa−miR−1258
24	−4.98	NULL	1 / 14	Cancer	LIU_COMMON_CANCER_GENES
25	−4.96	NULL	1 / 12	GSEA C2	DOANE_RESPONSE_TO_ANDROGEN_UP
26	−4.96	NULL	1 / 12	GSEA C2	IZADPANAH_STEM_CELL_ADIPOSE_VS_BONE_UP
27	−4.96	NULL	1 / 12	GSEA C2	WANG_CISPLATIN_RESPONSE_AND_XPC_UP
28	−4.82	NULL	2 / 15	GSEA C2	THUM_SYSTOLIC_HEART_FAILURE_DN
29	−4.77	NULL	2 / 15	GSEA C2	CAIRO_HEPATOBLASTOMA_UP
30	−4.73	NULL	1 / 13	GSEA C2	RUTELLA_RESPONSE_TO_CSF2RB_AND_IL4_DN
31	−4.73	NULL	1 / 13	GSEA C2	HAN_SATB1_TARGETS_DN
32	−4.63	NULL	1 / 10	CC	oligosaccharyltransferase complex
33	−4.58	NULL	1 / 8	GSEA C2	WILLIAMS_ESR2_TARGETS_DN
34	−4.55	NULL	2 / 22	CC	heterochromatin
35	−4.54	NULL	1 / 10	BP	negative regulation of nitric oxide biosynthetic process
36	−4.54	NULL	1 / 10	GSEA C2	BIOCARTA_IL10_PATHWAY
37	−4.52	NULL	1 / 14	GSEA C2	ACEVEDO_NORMAL_TISSUE_ADJACENT_TO_LIVER_TUMOR_
38	−4.47	NULL	2 / 17	BP	negative regulation of interleukin−6 production
39	−4.33	NULL	1 / 15	GSEA C2	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_HSC_DN
40	−4.33	NULL	1 / 15	GSEA C2	HAHTOLA_SEZARY_SYNDROM_UP

GW_158

Local Summary

%DE = 0.82

metagenes = 45

genes = 372

genes in genesets = 353

genes with fdr < 0.1 = 232 (1 + / 231 −)

genes with fdr < 0.05 = 191 (1 + / 190 −)

genes with fdr < 0.01 = 109 (1 + / 108 −)

<r> metagenes = 0.86

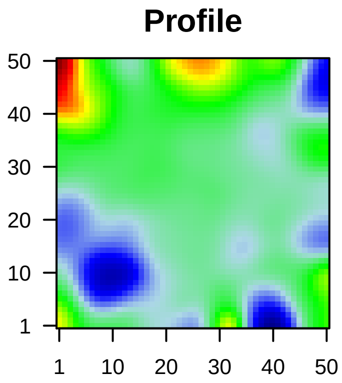
<r> genes = 0.22

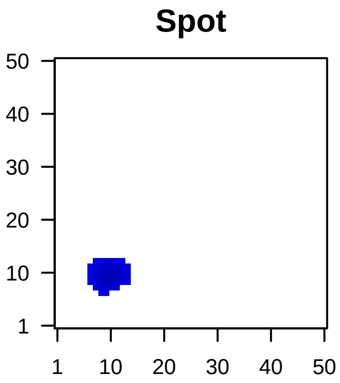
<FC> = −0.3

<shrinkage−t> = −10.42

<p−value> = 0.01

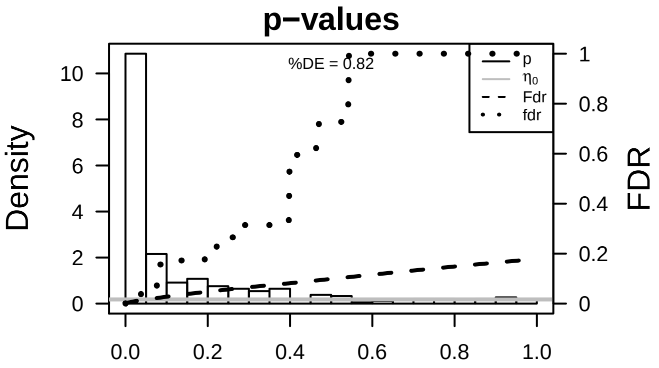
<fdr> = 0.59





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	2026	−0.91	5e−11	1e−06	10 x 10	enolase 2 (gamma, neuronal) [Source:HGNC Symbol;Acc:33
2	55506	−0.77	3e−08	1e−06	12 x 9	H2A histone family, member Y2 [Source:HGNC Symbol;Acc:1
3	1951	−0.76	3e−08	1e−06	9 x 13	cadherin, EGF LAG seven−pass G−type receptor 3 [Source:H
4	64847	−0.74	9e−08	1e−06	10 x 9	spermatogenesis associated 20 [Source:HGNC Symbol;Acc:
5	729442	−0.74	1e−07	1e−06	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
6	4037	−0.74	1e−07	1e−06	10 x 7	low density lipoprotein receptor−related protein 3 [Source:HG
7	3303	0.73	1e−07	3e−06	11 x 12	heat shock 70kDa protein 1A [Source:HGNC Symbol;Acc:52
8	401357	−0.72	2e−07	3e−06	11 x 13	
9	441520	−0.71	2e−07	3e−06	14 x 11	cancer/testis antigen family 45, member A2 [Source:HGNC S
10	645037	−0.71	2e−07	3e−06	14 x 11	G antigen 2C [Source:HGNC Symbol;Acc:31958]
11	729021	−0.71	3e−07	3e−06	11 x 13	
12	729422	−0.7	4e−07	3e−06	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
13	8408	−0.7	4e−07	3e−06	11 x 12	unc−51 like autophagy activating kinase 1 [Source:HGNC Sy
14	645073	−0.7	4e−07	3e−06	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
15	23532	−0.7	4e−07	5e−05	13 x 10	preferentially expressed antigen in melanoma [Source:HGNC
16	2576	−0.65	2e−06	5e−05	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
17	5446	−0.64	3e−06	5e−05	13 x 10	paraoxonase 3 [Source:HGNC Symbol;Acc:9206]
18	7466	−0.64	3e−06	5e−05	8 x 8	Wolfram syndrome 1 (wolframin) [Source:HGNC Symbol;Acc:
19	8497	−0.64	4e−06	5e−05	12 x 10	protein tyrosine phosphatase, receptor type, f polypeptide (P
20	9761	−0.63	4e−06	5e−05	11 x 8	malectin [Source:HGNC Symbol;Acc:28973]



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−9.51	NULL	3 / 10	CC	oligosaccharyltransferase complex
2	−7.29	NULL	1 / 4	GSEA C2	WEBER_METHYLATED_ICP_IN_SPERM_DN
3	−7.04	NULL	3 / 16	CC	photoreceptor inner segment
4	−6.62	NULL	5 / 24	BP	tissue development
5	−6.55	NULL	2 / 10	MF	K63−linked polyubiquitin binding
6	−5.93	NULL	2 / 14	GSEA C2	NUYTTEN_NIPP1_TARGETS_DN
7	−5.86	NULL	4 / 28	MF	ribosome binding
8	−5.83	NULL	3 / 14	GSEA C2	RIZKI_TUMOR_INVASIVENESS_2D_DN
9	−5.77	NULL	1 / 6	GSEA C2	NIELSEN_GIST_VS_SYNOVIAL_SARCOMA_UP
10	−5.7	NULL	3 / 23	Chr	Chr HSCHR6_MHC_DBB
11	−5.63	NULL	2 / 13	GSEA C2	ENK_UV_RESPONSE_KERATINOCYTE_UP
12	−5.56	NULL	2 / 10	BP	positive regulation of macroautophagy
13	−5.45	NULL	2 / 5	GSEA C2	NIKOLSKY_BREAST_CANCER_19Q13.4_AMPLICON
14	−5.39	NULL	28 / 630	Chr	Chr X
15	−5.36	NULL	2 / 8	GSEA C2	WEBER_METHYLATED_ICP_IN_FIBROBLAST
16	−5.34	NULL	2 / 16	GSEA C2	ELVIDGE_HIF1A_TARGETS_DN
17	−5.34	NULL	2 / 16	GSEA C2	ELVIDGE_HIF1A_AND_HIF2A_TARGETS_DN
18	−5.31	NULL	2 / 12	Glio	willscher_GBM_LTSmut_proteomics−B_UP
19	−5.31	NULL	2 / 12	Glio	willscher_GBM_STSwt_proteomics−B_DOWN
20	−5.27	NULL	1 / 7	GSEA C2	NIELSEN_SYNOVIAL_SARCOMA_UP
21	−5.06	NULL	2 / 13	GSEA C2	DOUGLAS_BMI1_TARGETS_UP
22	−5	NULL	2 / 16	GSEA C2	JIANG_HYPOXIA_VIA_VHL
23	−4.95	NULL	1 / 5	miRNA target	miR−196a
24	−4.85	NULL	57 / 1135	Chr	Chr 19
25	−4.84	NULL	2 / 13	GSEA C2	REACTOME_POST_TRANSLATIONAL_PROTEIN_MODIFICATIO
26	−4.84	NULL	1 / 13	GSEA C2	REACTOME_GLYCOLYSIS
27	−4.81	NULL	2 / 15	GSEA C2	SMIRNOV_CIRCULATING_ENDOTHELIOCYTES_IN_CANCER_
28	−4.76	NULL	2 / 15	GSEA C2	BIOCARTA_PROTEASOME_PATHWAY
29	−4.76	NULL	3 / 22	MF	polyubiquitin binding
30	−4.66	NULL	3 / 30	CC	rough endoplasmic reticulum
31	−4.64	NULL	2 / 14	Cancer	LIU_COMMON_CANCER_GENES
32	−4.63	NULL	8 / 96	BP	chromatin modification
33	−4.63	NULL	2 / 14	GSEA C2	KEGG_GLYCOSYLPHOSPHATIDYLINOSITOL_GPI_ANCHOR_B
34	−4.63	NULL	2 / 14	GSEA C2	REACTOME_SYNTHESIS_OF_GPI_ANCHORED_PROTEINS
35	−4.62	NULL	1 / 14	GSEA C2	TOMIDA_METASTASIS_DN
36	−4.61	NULL	2 / 13	BP	inner cell mass cell proliferation
37	−4.58	NULL	3 / 21	BP	chromatin organization
38	−4.56	NULL	1 / 9	GSEA C2	GOZGIT_ESR1_TARGETS_DN
39	−4.52	NULL	1 / 5	miRNA 3UTR	GTTCG−369−5P
40	−4.43	NULL	2 / 15	GSEA C2	REACTOME_SYNTHESIS_OF_GLYCOSYLPHOSPHATIDYLINOS

GW_158

Local Summary

%DE = 0.59

metagenes = 3

genes = 40

genes in genesets = 40

genes with fdr < 0.1 = 24 (2 + / 22 −)

genes with fdr < 0.05 = 15 (0 + / 15 −)

genes with fdr < 0.01 = 9 (0 + / 9 −)

<r> metagenes = 0.99

<r> genes = 0.27

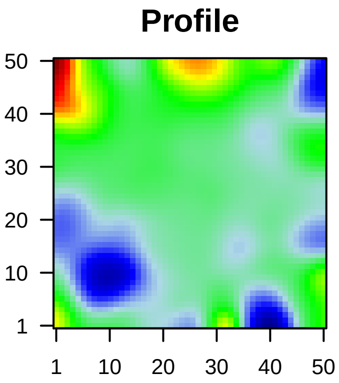
<FC> = −0.3

<shrinkage−t> = −10.47

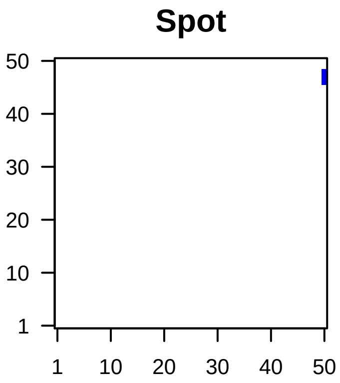
<p−value> = 0

<fdr> = 0.55

Profile



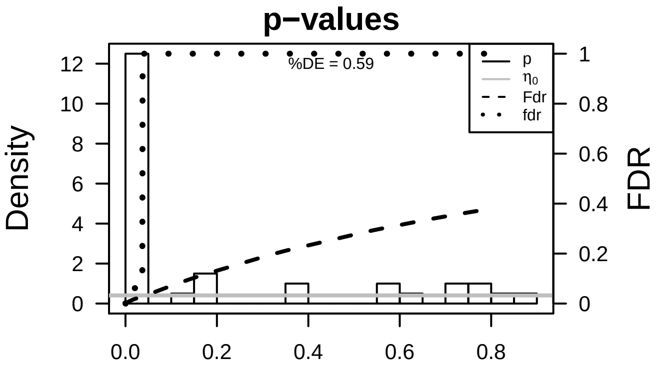
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	26227	−1.23	2e−16	4e−15	50 x 46	phosphoglycerate dehydrogenase [Source:HGNC Symbol;Ac
2	7345	−1.05	4e−14	7e−11	50 x 46	ubiquitin carboxyl−terminal esterase L1 (ubiquitin thiolesteras
3	84707	−0.96	4e−12	3e−08	50 x 48	brain expressed X−linked 2 [Source:HGNC Symbol;Acc:3093
4	3856	−0.83	2e−09	1e−05	50 x 48	keratin 8 pseudogene 3 [Source:HGNC Symbol;Acc:31056]
5	57216	−0.68	9e−07	3e−04	50 x 48	VANGL planar cell polarity protein 2 [Source:HGNC Symbol;A
6	440	−0.59	2e−05	3e−04	50 x 46	asparagine synthetase (glutamine−hydrolyzing) [Source:HGN
7	5625	−0.57	4e−05	3e−04	50 x 48	proline dehydrogenase (oxidase) 1 [Source:HGNC Symbol;Ac
8	56704	−0.56	5e−05	5e−03	50 x 47	junctophilin 1 [Source:HGNC Symbol;Acc:14201]
9	79190	−0.5	3e−04	6e−03	50 x 47	iroquois homeobox 6 [Source:HGNC Symbol;Acc:14675]
10	8492	−0.47	7e−04	2e−02	50 x 47	protease, serine, 12 (neurotrypsin, motopsin) [Source:HGNC
11	7419	−0.39	4e−03	2e−02	50 x 47	voltage−dependent anion channel 3 [Source:HGNC Symbol;A
12	54800	−0.4	4e−03	2e−02	50 x 48	kelch−like family member 24 [Source:HGNC Symbol;Acc:259
13	51804	−0.38	5e−03	2e−02	50 x 46	SIX homeobox 4 [Source:HGNC Symbol;Acc:10890]
14	1690	−0.38	6e−03	2e−02	50 x 47	cochlin [Source:HGNC Symbol;Acc:2180]
15	253782	−0.38	6e−03	2e−02	50 x 47	ceramide synthase 6 [Source:HGNC Symbol;Acc:23826]
16	1329	−0.37	7e−03	6e−02	50 x 48	cytochrome c oxidase subunit Vb [Source:HGNC Symbol;Acc
17	59271	0.34	1e−02	6e−02	50 x 48	eva−1 homolog C (C. elegans) [Source:HGNC Symbol;Acc:1
18	64395	−0.33	2e−02	6e−02	50 x 46	germ cell−less, spermatogenesis associated 1 [Source:HGN
19	9252	0.32	2e−02	6e−02	50 x 47	ribosomal protein S6 kinase, 90kDa, polypeptide 5 [Source:H
20	56475	−0.31	2e−02	6e−02	50 x 47	reprimo, TP53 dependent G2 arrest mediator candidate [Sou

p−values



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−23.91	NULL	2 / 16	GSEA C2	PACHER_TARGETS_OF_IGF1_AND_IGF2_UP
2	−23.91	NULL	2 / 16	GSEA C2	ZHAN_MULTIPLE_MYELOMA_CD1_VS_CD2_UP
3	−22.29	NULL	2 / 18	BP	glutamine metabolic process
4	−21.58	NULL	2 / 19	BP	cellular amino acid biosynthetic process
5	−21.09	NULL	1 / 8	GSEA C2	MUNSHI_MULTIPLE_MYELOMA_DN
6	−18.24	NULL	1 / 10	MF	omega peptidase activity
7	−17.46	NULL	1 / 14	GSEA C2	KEGG_GLYCINE_SERINE_AND_THREONINE_METABOLISM
8	−16.88	NULL	2 / 29	MF	cofactor binding
9	−16.74	NULL	1 / 15	BP	spinal cord development
10	−16.74	NULL	1 / 15	GSEA C2	VANHARANTA_UTERINE_FIBROID_WITH_7Q_DELETION_UP
11	−16.74	NULL	1 / 15	GSEA C2	ZHAN_MULTIPLE_MYELOMA_CD1_UP
12	−16.26	NULL	1 / 12	BP	muscle fiber development
13	−16.26	NULL	1 / 12	GSEA C2	CHANG_IMMORTALIZED_BY_HPV31_UP
14	−16.1	NULL	1 / 16	GSEA C2	HOSHIDA_LIVER_CANCER_LATE_RECURRENCE_DN
15	−15.48	NULL	1 / 13	BP	response to ischemia
16	−15.48	NULL	1 / 13	Lymphoma	BENTINK_mBL UP
17	−15.39	NULL	2 / 12	GSEA C2	ONDER_CDH1_TARGETS_1_UP
18	−14.18	NULL	1 / 15	GSEA C2	ABRAHAM_ALPC_VS_MULTIPLE_MYELOMA_DN
19	−13.64	NULL	1 / 16	BP	eating behavior
20	−13.01	NULL	1 / 7	GSEA C2	DASU_IL6_SIGNALING_DN
21	−12.3	NULL	1 / 19	BP	neuromuscular process
22	−11.81	NULL	1 / 10	BP	somatic stem cell division
23	−11.12	NULL	1 / 30	BP	neurogenesis
24	−11.11	NULL	1 / 11	BP	planar cell polarity pathway involved in neural tube closure
25	−11	NULL	1 / 9	GSEA C2	TIEN_INTESTINE_PROBIOTICS_24HR_DN
26	−11	NULL	1 / 9	GSEA C2	REACTOME_METABOLISM_OF_AMINO_ACIDS
27	−10.91	NULL	1 / 31	BP	neural tube development
28	−10.52	NULL	1 / 12	BP	Wnt signaling pathway, planar cell polarity pathway
29	−10.27	NULL	1 / 10	GSEA C2	AMUNDSON_RESPONSE_TO_ARSENITE
30	−10.27	NULL	1 / 10	GSEA C2	MOHANKUMAR_TLX1_TARGETS_DN
31	−10.27	NULL	1 / 10	GSEA C2	TARTE_PLASMA_CELL_VS_PLASMABLAST_DN
32	−10.27	NULL	1 / 10	GSEA C2	BROWNE_HCMV_INFECTION_12HR_UP
33	−10.01	NULL	1 / 13	GSEA C2	GUENTHER_GROWTH_SPHERICAL_VS_ADHERENT_UP
34	−9.79	NULL	1 / 28	BP	protein deubiquitination
35	−9.73	NULL	1 / 10	CC	junctional sarcoplasmic reticulum membrane
36	−9.67	NULL	1 / 11	GSEA C2	ODONNELL_TFRC_TARGETS_DN
37	−9.67	NULL	1 / 11	GSEA C2	ROSS_AML_WITH_PML_RARA_FUSION
38	−9.67	NULL	1 / 11	GSEA C2	SMITH_TERT_TARGETS_UP
39	−9.67	NULL	1 / 11	GSEA C2	CUI_GLUCOSE_DEPRIVATION
40	−9.67	NULL	1 / 11	GSEA C2	SATO_SILENCED_BY_METHYLATION_IN_PANCREATIC_CANC