GW_216

Global Summary

%DE = 0.15

genes with fdr < 0.2 = 1875 (934 + / 941 −)

genes with fdr < 0.1 = 1449 (696 + / 753 −)

genes with fdr < 0.05 = 1191 (569 + / 622 −)

genes with fdr < 0.01 = 837 (408 + / 429 −)

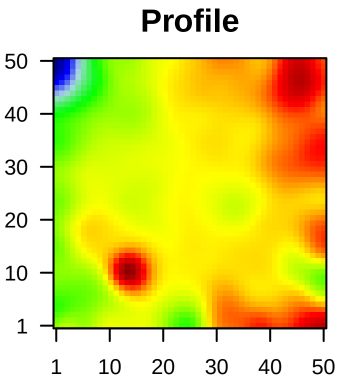
genes in genesets = 16332

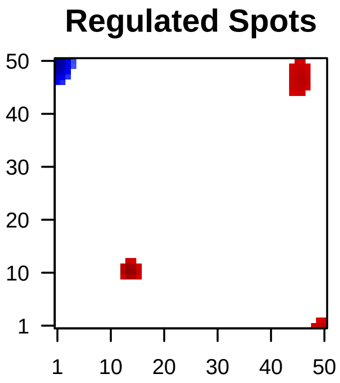
<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.1

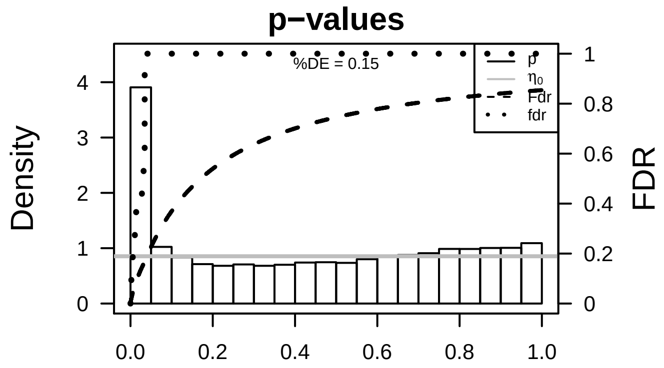
<fdr> = 0.85





Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	154664	2.78	2e−16	3e−14	50 x 50	ATP−binding cassette, sub−family A (ABC1), member 13 [Sou
2	113146	−1.75	2e−16	3e−14	1 x 44	AHNAK nucleoprotein 2 [Source:HGNC Symbol;Acc:20125]
3	57016	2.02	2e−16	3e−14	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
4	348	1.65	2e−16	3e−14	50 x 1	apolipoprotein E [Source:HGNC Symbol;Acc:613]
5	387695	−1.56	2e−16	3e−14	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Symb
6	64073	−1.78	2e−16	3e−14	1 x 46	chromosome 19 open reading frame 33 [Source:HGNC Symb
7	713	1.52	2e−16	3e−14	50 x 1	complement component 1, q subcomponent, B chain [Source
8	714	1.45	2e−16	3e−14	50 x 1	complement component 1, q subcomponent, C chain [Source
9	260436	3.5	2e−16	3e−14	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symbo
10	375791	−1.49	2e−16	3e−14	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Symb
11	768	1.71	2e−16	3e−14	1 x 6	carbonic anhydrase IX [Source:HGNC Symbol;Acc:1383]
12	51806	−1.88	2e−16	3e−14	4 x 50	calmodulin−like 5 [Source:HGNC Symbol;Acc:18180]
13	84290	−1.78	2e−16	3e−14	1 x 50	calpain, small subunit 2 [Source:HGNC Symbol;Acc:16371]
14	100133941	−1.49	2e−16	3e−14	3 x 50	CD24 molecule [Source:HGNC Symbol;Acc:1645]
15	629	1.47	2e−16	3e−14	32 x 1	complement factor B [Source:HGNC Symbol;Acc:1037]
16	56994	1.6	2e−16	3e−14	50 x 16	choline phosphotransferase 1 [Source:HGNC Symbol;Acc:17
17	163732	−1.53	2e−16	3e−14	1 x 43	Cbp/p300−interacting transactivator, with Glu/Asp−rich carbo
18	9635	−2.37	2e−16	3e−14	1 x 46	chloride channel accessory 2 [Source:HGNC Symbol;Acc:20
19	9022	−1.85	2e−16	3e−14	1 x 50	chloride intracellular channel 3 [Source:HGNC Symbol;Acc:2
20	84518	−2.41	2e−16	3e−14	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	9.01	NULL	142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
2	9.01	NULL	142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
3	8.01	NULL	149	BP	DNA replication
4	7.23	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
5	7.15	NULL	370	BP	mitotic cell cycle
6	6.79	NULL	13	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
7	6.51	NULL	417	H.Tiss	WIRTH_Immune system
8	5.9	NULL	12	GSEA C2	ZHAN_MULTIPLE_MYELOMA_DN
9	5.73	NULL	4	GSEA C2	REACTOME_CLASSICAL_ANTIBODY_MEDIATED_COMPLEMEN
10	5.69	NULL	37	BP	collagen fibril organization
11	5.68	NULL	630	Chr	Chr X
12	5.66	NULL	30	BP	DNA strand elongation involved in DNA replication
13	5.53	NULL	83	BP	respiratory electron transport chain
14	5.38	NULL	13	GSEA C2	SLEBOS_HEAD_AND_NECK_CANCER_WITH_HPV_UP
15	5.34	NULL	21	BP	telomere maintenance via semi−conservative replication
16	5.25	NULL	24	BP	telomere maintenance via recombination
17	5.24	NULL	918	Chr	Chr 17
18	5.22	NULL	298	BP	DNA repair
19	5.2	NULL	11	GSEA C2	KALMA_E2F1_TARGETS
20	5.14	NULL	6	GSEA C2	NIELSEN_LEIOMYOSARCOMA_UP
Underexpressed					
1	−22.16	NULL	135	H.Tiss	WIRTH_Mucosa
2	−18.22	NULL	21	CC	cornified envelope
3	−14.76	NULL	42	BP	keratinization
4	−14.1	NULL	53	BP	keratinocyte differentiation
5	−11.92	NULL	76	BP	epidermis development
6	−10.57	NULL	386	Chr	Chr 22
7	−9.59	NULL	714	Chr	Chr 6
8	−9.39	NULL	19	BP	peptide cross−linking
9	−8.19	NULL	4	MMML CGS	MACIEJ_MMML 23
10	−7.61	NULL	572	Disease	GUDJ_psoriasis up
11	−7.28	NULL	21	CC	desmosome
12	−7.09	NULL	186	MF	structural molecule activity
13	−6.66	NULL	13	GSEA C2	REACTOME_GAP_JUNCTION_TRAFFICKING
14	−6.64	NULL	21	CC	gap junction
15	−6.49	NULL	12	GSEA C2	REACTOME_GAP_JUNCTION_ASSEMBLY
16	−6.44	NULL	1033	Chr	Chr 2
17	−6.4	NULL	1146	TF	HEBENSTREIT_low expression TF
18	−6.38	NULL	15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
19	−6.35	NULL	16	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_LUNG_UP
20	−6.03	NULL	11	MF	oxygen transporter activity

GW_216

Local Summary

%DE = 0.77

metagenes = 5

genes = 154

genes in genesets = 152

genes with fdr < 0.1 = 92 (81 + / 11 −)

genes with fdr < 0.05 = 67 (63 + / 4 −)

genes with fdr < 0.01 = 46 (45 + / 1 −)

<r> metagenes = 1

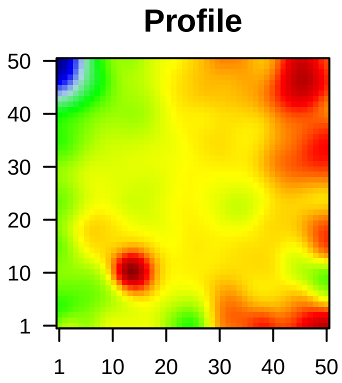
<r> genes = 0.66

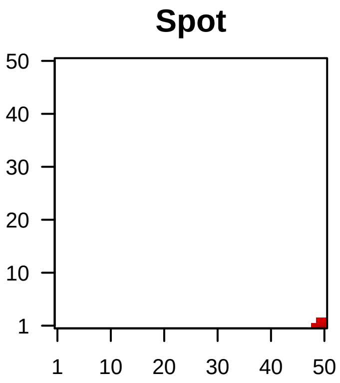
<FC> = 0.41

<shrinkage−t> = 14.22

<p−value> = 0

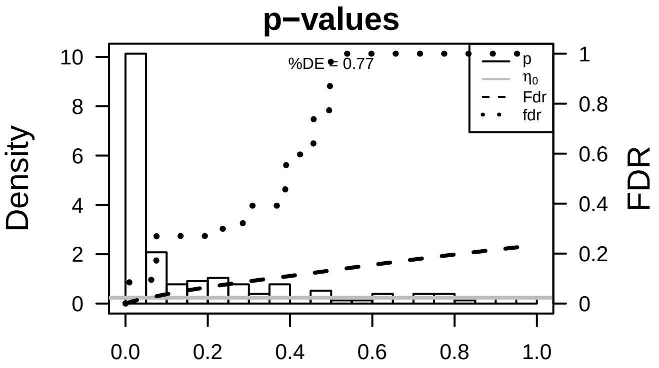
<fdr> = 0.56





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	348	1.65	2e−16	1e−15	50 x 1	apolipoprotein E [Source:HGNC Symbol;Acc:613]
2	713	1.52	2e−16	1e−15	50 x 1	complement component 1, q subcomponent, B chain [Source
3	714	1.45	2e−16	1e−15	50 x 1	complement component 1, q subcomponent, C chain [Source
4	260436	3.5	2e−16	1e−15	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symbo
5	4283	2.09	2e−16	1e−15	49 x 1	chemokine (C−X−C motif) ligand 9 [Source:HGNC Symbol;Ac
6	115361	1.49	2e−16	1e−15	48 x 1	guanylate binding protein 4 [Source:HGNC Symbol;Acc:2048
7	3620	2.15	2e−16	1e−15	48 x 1	indoleamine 2,3−dioxygenase 1 [Source:HGNC Symbol;Acc:
8	10537	1.49	2e−16	1e−15	50 x 1	ubiquitin D [Source:HGNC Symbol;Acc:18795]
9	341	1.37	6e−15	7e−10	50 x 1	apolipoprotein C−I [Source:HGNC Symbol;Acc:607]
10	27299	1.18	2e−11	2e−09	49 x 1	ADAM−like, decysin 1 [Source:HGNC Symbol;Acc:16299]
11	2207	1.15	7e−11	4e−09	50 x 1	Fc fragment of IgE, high affinity I, receptor for; gamma polype
12	3543	1.03	2e−10	2e−08	49 x 1	immunoglobulin lambda−like polypeptide 1 [Source:HGNC Sy
13	6363	1.08	8e−10	8e−08	50 x 1	chemokine (C−C motif) ligand 19 [Source:HGNC Symbol;Acc
14	4069	1.04	3e−09	8e−08	50 x 2	lysozyme [Source:HGNC Symbol;Acc:6740]
15	84868	1.02	6e−09	8e−08	50 x 1	hepatitis A virus cellular receptor 2 [Source:HGNC Symbol;Ac
16	3002	1.02	7e−09	2e−06	49 x 1	granzyme B (granzyme 2, cytotoxic T−lymphocyte−associate
17	3936	0.93	1e−07	2e−06	50 x 1	lymphocyte cytosolic protein 1 (L−plastin) [Source:HGNC Syr
18	6352	0.92	2e−07	2e−06	48 x 1	chemokine (C−C motif) ligand 5 [Source:HGNC Symbol;Acc:
19	5552	0.92	2e−07	2e−06	50 x 1	serglycin [Source:HGNC Symbol;Acc:9361]
20	7305	0.91	2e−07	4e−06	50 x 1	TYRO protein tyrosine kinase binding protein [Source:HGNC



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	26.74	NULL	2 / 4	GSEA C2	REACTOME_CLASSICAL_ANTIBODY_MEDIATED_COMPLEMEN
2	22.28	NULL	3 / 5	GSEA C2	WONG_ENDOMETRIAL_CANCER_LATE
3	20.59	NULL	2 / 4	MMML CGS	MACIEJ_MMML 2
4	19.15	NULL	2 / 7	GSEA C2	BIOCARTA_COMP_PATHWAY
5	19.13	NULL	6 / 11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
6	18.31	NULL	4 / 15	Glio	Donson−chemokines/cytokines−associated with LTS in HGA
7	17.87	NULL	11 / 15	CC	MHC class II protein complex
8	17.72	NULL	2 / 8	GSEA C2	BIOCARTA_CLASSIC_PATHWAY
9	17.72	NULL	2 / 8	GSEA C2	REACTOME_COMPLEMENT_CASCADE
10	17.72	NULL	2 / 8	GSEA C2	REACTOME_INITIAL_TRIGGERING_OF_COMPLEMENT
11	15.6	NULL	66 / 417	H.Tiss	WIRTH_Immune system
12	15.59	NULL	4 / 8	Glio	Donson−migration tethering and rolling−associated with LTS in HG
13	15.59	NULL	4 / 12	GSEA C2	ZHAN_MULTIPLE_MYELOMA_DN
14	15.45	NULL	5 / 12	GSEA C2	BIOCARTA_CTL_PATHWAY
15	15.2	NULL	5 / 11	GSEA C2	BIOCARTA_THELPER_PATHWAY
16	15.07	NULL	38 / 312	BP	immune response
17	15.04	NULL	2 / 11	BP	high−density lipoprotein particle remodeling
18	15.04	NULL	2 / 11	GSEA C2	APPEL_IMATINIB_RESPONSE
19	14.71	NULL	1 / 6	GSEA C2	NIELSEN_LEIOMYOSARCOMA_UP
20	13.19	NULL	4 / 10	GSEA C2	LEE_DIFFERENTIATING_T_LYMPHOCYTE
21	13.11	NULL	2 / 14	CC	very−low−density lipoprotein particle
22	13.01	NULL	3 / 7	Glio	Donson−cytotoxic effectors−associated with LTS in HGA
23	12.62	NULL	5 / 13	Cancer	GENTLES_modul18
24	12.61	NULL	2 / 15	BP	cholesterol efflux
25	12.61	NULL	2 / 15	CC	high−density lipoprotein particle
26	12.4	NULL	4 / 13	GSEA C2	BIOCARTA_IL17_PATHWAY
27	12.3	NULL	4 / 22	BP	positive regulation of interleukin−12 production
28	12.21	NULL	26 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
29	12.21	NULL	26 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
30	12.21	NULL	26 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
31	12.21	NULL	26 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
32	12.17	NULL	61 / 553	Cancer	Lembcke_Colonic Inflammation
33	12.11	NULL	3 / 6	GSEA C2	SANA_RESPONSE_TO_IFNG_UP
34	11.99	NULL	4 / 10	GSEA C2	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_
35	11.75	NULL	8 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
36	11.7	NULL	5 / 12	BP	immunoglobulin mediated immune response
37	11.56	NULL	3 / 15	GSEA C2	HAHTOLA_SEZARY_SYNDROM_DN
38	11.53	NULL	5 / 13	GSEA C2	HAHTOLA_CTCL_PATHOGENESIS
39	11.53	NULL	2 / 11	GSEA C2	ABE_VEGFA_TARGETS_2HR
40	11.48	NULL	2 / 6	GSEA C2	BUDHU_LIVER_CANCER_METASTASIS_UP

GW_216

Local Summary

%DE = 0.5

metagenes = 14

genes = 77

genes in genesets = 54

genes with fdr < 0.1 = 33 (31 + / 2 −)

genes with fdr < 0.05 = 32 (31 + / 1 −)

genes with fdr < 0.01 = 32 (31 + / 1 −)

<r> metagenes = 0.99

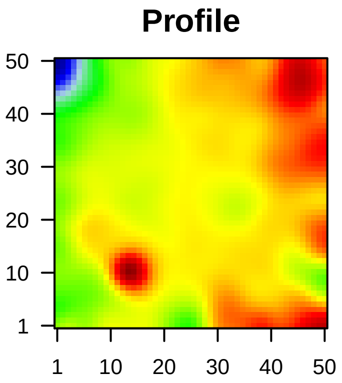
<r> genes = 0.35

<FC> = 1.06

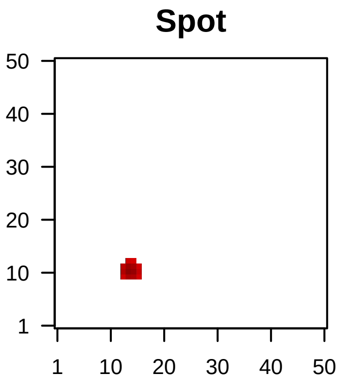
<shrinkage−t> = 37.1

<p−value> = 0

<fdr> = 0.53



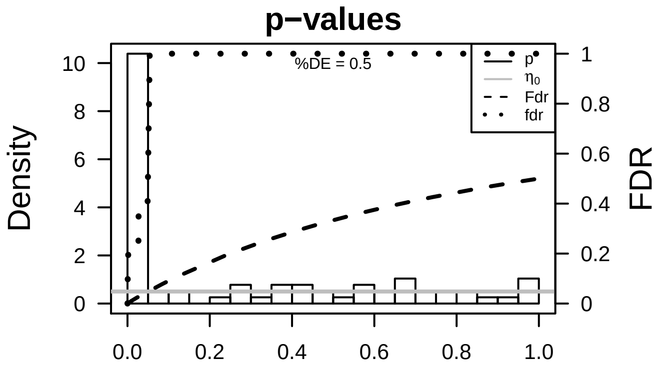
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	729428	4.58	2e−16	4e−16	14 x 11	G antigen 12C [Source:HGNC Symbol;Acc:28402]
2	729422	4.91	2e−16	4e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
3	100132399	2.32	2e−16	4e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
4	729431	2	2e−16	4e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
5	100008586	4.37	2e−16	4e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
6	645073	4.39	2e−16	4e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
7	729442	4.7	2e−16	4e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
8	26748	4.55	2e−16	4e−16	14 x 11	G antigen 12I [Source:HGNC Symbol;Acc:4105]
9	729396	3.52	2e−16	4e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
10	729447	3.7	2e−16	4e−16	14 x 11	G antigen 2A [Source:HGNC Symbol;Acc:4099]
11	645037	4.91	2e−16	4e−16	14 x 11	G antigen 2C [Source:HGNC Symbol;Acc:31958]
12	26749	3.77	2e−16	4e−16	14 x 11	G antigen 2E [Source:HGNC Symbol;Acc:31960]
13	2576	4.56	2e−16	4e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
14	2577	4.65	2e−16	4e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
15	2578	2.59	2e−16	4e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
16	2579	3.8	2e−16	4e−16	14 x 11	G antigen 12I [Source:HGNC Symbol;Acc:4105]
17	100101629	3.04	2e−16	4e−16	14 x 11	G antigen 2E [Source:HGNC Symbol;Acc:31960]
18	728403	1.62	2e−16	4e−16	16 x 11	testis specific protein, Y−linked 8 [Source:HGNC Symbol;Acc
19	4100	2.59	2e−16	4e−16	14 x 11	melanoma antigen family A, 1 (directs expression of antigen
20	64591	2.21	2e−16	4e−16	15 x 11	testis specific protein, Y−linked 2 [Source:HGNC Symbol;Acc



p−values

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	18.34	NULL	1 / 12	GSEA C2	RAY_TARGETS_OF_P210_BCR_ABL_FUSION_UP
2	13.87	NULL	30 / 630	Chr	Chr X
3	11.16	NULL	1 / 6	GSEA C2	NIELSEN_LEIOMYOSARCOMA_UP
4	10.92	NULL	1 / 10	GSEA C2	CONRAD_GERMLINE_STEM_CELL
5	9.67	NULL	1 / 12	GSEA C2	ACEVEDO_LIVER_CANCER_WITH_H3K27ME3_DN
6	8.89	NULL	2 / 34	Chr	Chr Y
7	7.97	NULL	1 / 21	BP	negative regulation of Notch signaling pathway
8	6.37	NULL	3 / 15	GSEA C2	MATTIOLI_MULTIPLE_MYELOMA_SUBGROUPS
9	6.03	NULL	1 / 5	GSEA C2	CHOI_ATL_ACUTE_STAGE
10	5.19	NULL	2 / 86	BP	nucleosome assembly
11	4.49	NULL	1 / 13	GSEA C2	PIEPOLI_LGI1_TARGETS_DN
12	4.46	NULL	8 / 481	BP	biological_process
13	4.24	NULL	6 / 419	CC	cellular_component
14	4.09	NULL	9 / 549	MF	molecular_function
15	3.96	NULL	1 / 68	MF	histone deacetylase binding
16	3.57	NULL	1 / 10	GSEA C2	TSUNODA_CISPLATIN_RESISTANCE_DN
17	3.28	NULL	1 / 15	GSEA C2	REACTOME_ADHERENS_JUNCTIONS_INTERACTIONS
18	2.96	NULL	1 / 16	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_DN
19	2.88	NULL	2 / 48	Cancer	KUIPER_MM poor survival
20	2.71	NULL	1 / 15	GSEA C2	LOPEZ_MBD_TARGETS_IMPRINTED_AND_X_LINKED
21	2.71	NULL	1 / 15	GSEA C2	ALONSO_METASTASIS_NEURAL_UP
22	2.6	NULL	1 / 16	GSEA C2	JAEGER_METASTASIS_UP
23	2.59	NULL	1 / 10	GSEA C2	XU_RESPONSE_TO_TRETINOIN_DN
24	2.22	NULL	7 / 259	BP	spermatogenesis
25	2.18	NULL	1 / 7	GSEA C2	REACTOME_AMINE_LIGAND_BINDING_RECEPTORS
26	2.01	NULL	1 / 32	BP	adherens junction organization
27	1.77	NULL	6 / 346	BP	cell differentiation
28	1.38	NULL	1 / 13	BP	positive regulation of smooth muscle contraction
29	1.37	NULL	1 / 57	BP	cell−cell junction organization
30	1.35	NULL	1 / 26	MF	cyclin−dependent protein serine/threonine kinase activity
31	1.27	NULL	9 / 120	H.Tiss	WIRTH_Testis
32	1.25	NULL	1 / 15	GSEA C2	REACTOME_REGULATION_OF_INSULIN_SECRETION_BY_ACE
33	1.19	NULL	1 / 16	GSEA C2	LANDEMAINE_LUNG_METASTASIS
34	1.19	NULL	1 / 70	BP	cell junction assembly
35	1.1	NULL	1 / 18	BP	smooth muscle contraction
36	1.06	NULL	1 / 19	BP	regulation of vasoconstriction
37	1	NULL	2 / 89	Glio	WIRTH_Normal Brain
38	0.9	NULL	2 / 504	BP	negative regulation of transcription from RNA polymerase II promo
39	0.84	NULL	1 / 26	MF	phosphatidylinositol phospholipase C activity
40	0.79	NULL	2 / 118	Glio	willscher_GBM_Verhaak−CL_expression_K_down

GW_216

Local Summary

%DE = 0.78

metagenes = 25

genes = 262

genes in genesets = 260

genes with fdr < 0.1 = 162 (153 + / 9 −)

genes with fdr < 0.05 = 149 (141 + / 8 −)

genes with fdr < 0.01 = 97 (94 + / 3 −)

<r> metagenes = 0.95

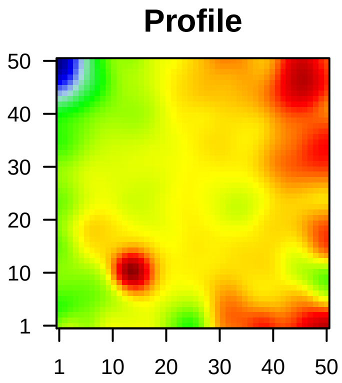
<r> genes = 0.37

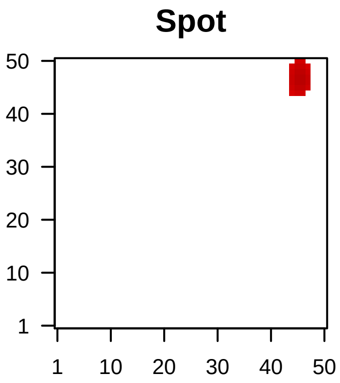
<FC> = 0.39

<shrinkage−t> = 13.85

<p−value> = 0

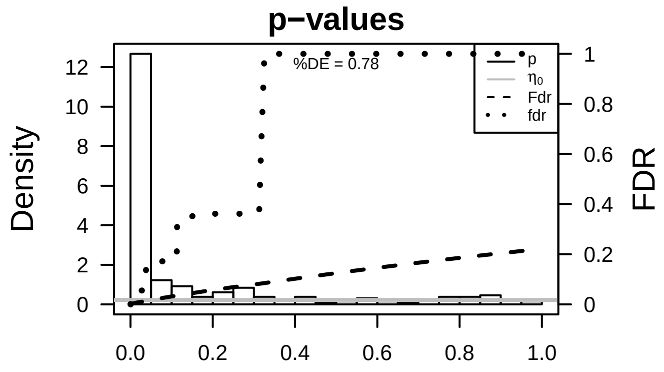
<fdr> = 0.5





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	84223	1.69	2e−16	6e−15	47 x 46	IQ motif containing G [Source:HGNC Symbol;Acc:25251]
2	3787	1.48	2e−16	6e−15	46 x 45	potassium voltage−gated channel, delayed−rectifier, subfamil
3	7298	1.27	5e−13	7e−11	46 x 48	thymidylate synthetase [Source:HGNC Symbol;Acc:12441]
4	246777	1.24	2e−12	7e−10	45 x 45	sperm equatorial segment protein 1 [Source:HGNC Symbol;
5	283212	1.19	1e−11	1e−08	46 x 44	kelch−like family member 35 [Source:HGNC Symbol;Acc:265
6	8317	1.1	4e−10	1e−08	45 x 47	cell division cycle 7 [Source:HGNC Symbol;Acc:1745]
7	54457	1.1	4e−10	3e−08	46 x 44	TAF7−like RNA polymerase II, TATA box binding protein (TBP
8	2189	1.08	9e−10	5e−08	45 x 45	Fanconi anemia, complementation group G [Source:HGNC S
9	1029	1.05	2e−09	5e−08	45 x 45	cyclin−dependent kinase inhibitor 2A [Source:HGNC Symbol;
10	84215	1.05	3e−09	1e−07	46 x 45	zinc finger protein 541 [Source:HGNC Symbol;Acc:25294]
11	10388	1.03	4e−09	2e−07	47 x 46	synaptonemal complex protein 2 [Source:HGNC Symbol;Acc:
12	116028	1.01	8e−09	2e−07	46 x 47	RecQ mediated genome instability 2 [Source:HGNC Symbol;
13	113802	1	1e−08	6e−07	46 x 46	HEN1 methyltransferase homolog 1 (Arabidopsis) [Source:H
14	4744	0.97	3e−08	6e−07	45 x 44	neurofilament, heavy polypeptide [Source:HGNC Symbol;Acc
15	4171	0.97	3e−08	9e−07	46 x 48	minichromosome maintenance complex component 2 [Source
16	51203	0.96	5e−08	1e−06	45 x 48	nucleolar and spindle associated protein 1 [Source:HGNC Sy
17	144455	0.94	9e−08	1e−06	45 x 50	E2F transcription factor 7 [Source:HGNC Symbol;Acc:23820]
18	5984	0.93	1e−07	1e−06	46 x 50	replication factor C (activator 1) 4, 37kDa [Source:HGNC Sym
19	9355	0.93	1e−07	2e−06	47 x 47	LIM homeobox 2 [Source:HGNC Symbol;Acc:6594]
20	57570	0.92	2e−07	2e−06	46 x 45	tRNA methyltransferase 5 [Source:HGNC Symbol;Acc:23141]



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	27.05	NULL	9 / 11	GSEA C2	KALMA_E2F1_TARGETS
2	25.47	NULL	58 / 142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
3	25.47	NULL	58 / 142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
4	23.3	NULL	6 / 13	GSEA C2	SLEBOS_HEAD_AND_NECK_CANCER_WITH_HPV_UP
5	20.55	NULL	12 / 21	BP	telomere maintenance via semi−conservative replication
6	20.32	NULL	42 / 149	BP	DNA replication
7	19.55	NULL	69 / 370	BP	mitotic cell cycle
8	19.17	NULL	9 / 16	GSEA C2	SONG_TARGETS_OF_IE86_CMV_PROTEIN
9	19.11	NULL	12 / 24	BP	telomere maintenance via recombination
10	18.37	NULL	6 / 14	GSEA C2	SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_UP
11	18.11	NULL	10 / 16	GSEA C2	REACTOME_DNA_STRAND_ELONGATION
12	17.97	NULL	13 / 16	GSEA C2	EGUCHI_CELL_CYCLE_RB1_TARGETS
13	17.36	NULL	7 / 14	GSEA C2	REACTOME_POLYMERASE_SWITCHING
14	17.33	NULL	8 / 16	GSEA C2	REACTOME_LAGGING_STRAND_SYNTHESIS
15	17.08	NULL	16 / 30	BP	DNA strand elongation involved in DNA replication
16	16.87	NULL	7 / 16	GSEA C2	PUJANA_BREAST_CANCER_WITH_BRCA1_MUTATED_UP
17	16.79	NULL	10 / 16	GSEA C2	REACTOME_ACTIVATION_OF_THE_PRE_REPLICATIVE_COMP
18	16.57	NULL	6 / 11	GSEA C2	LIANG_SILENCED_BY_METHYLATION_DN
19	16.26	NULL	5 / 15	GSEA C2	WU_APOPTOSIS_BY_CDKN1A_VIA_TP53
20	15.53	NULL	9 / 15	GSEA C2	KEGG_DNA_REPLICATION
21	15.42	NULL	8 / 14	GSEA C2	ZHAN_MULTIPLE_MYELOMA_PR_UP
22	14.93	NULL	6 / 15	GSEA C2	LEE_EARLY_T_LYMPHOCYTE_UP
23	14.93	NULL	6 / 13	GSEA C2	NADERI_BREAST_CANCER_PROGNOSIS_UP
24	14.65	NULL	8 / 18	BP	nucleotide−excision repair, DNA gap filling
25	14.49	NULL	16 / 49	BP	telomere maintenance
26	14.28	NULL	7 / 14	GSEA C2	REACTOME_REMOVAL_OF_THE_FLAP_INTERMEDIATE
27	14.22	NULL	7 / 15	GSEA C2	REACTOME_REPAIR_SYNTHESIS_OF_PATCH_27_30_BASES_
28	14.02	NULL	5 / 12	GSEA C2	LI_WILMS_TUMOR_VS_FETAL_KIDNEY_1_DN
29	13.77	NULL	10 / 16	GSEA C2	GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
30	13.69	NULL	6 / 15	GSEA C2	BOYAULT_LIVER_CANCER_SUBCLASS_G23_UP
31	13.25	NULL	8 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_2
32	13.24	NULL	42 / 298	BP	DNA repair
33	13.24	NULL	6 / 15	GSEA C2	KAUFFMANN_DNA_REPLICATION_GENES
34	13.2	NULL	7 / 16	GSEA C2	CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_UP
35	13.11	NULL	68 / 530	Cancer	Lembcke_Normal vs Adenoma
36	12.48	NULL	6 / 16	GSEA C2	KEGG_MISMATCH_REPAIR
37	12.38	NULL	2 / 5	Glio	Phillips Prolif up vs PN & MES
38	12.26	NULL	4 / 10	GSEA C2	MONTERO_THYROID_CANCER_POOR_SURVIVAL_UP
39	12.19	NULL	6 / 16	GSEA C2	FUJII_YBX1_TARGETS_DN
40	12.19	NULL	16 / 57	Glio	developing astrocytes

GW_216

Local Summary

%DE = 0.93

metagenes = 16

genes = 227

genes in genesets = 221

genes with fdr < 0.1 = 196 (19 + / 177 −)

genes with fdr < 0.05 = 194 (19 + / 175 −)

genes with fdr < 0.01 = 179 (17 + / 162 −)

<r> metagenes = 0.96

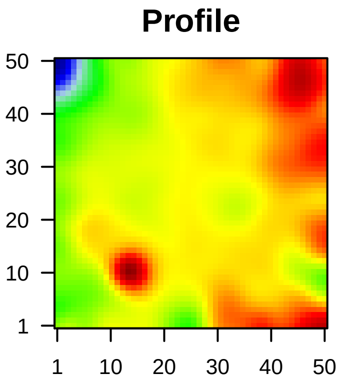
<r> genes = 0.45

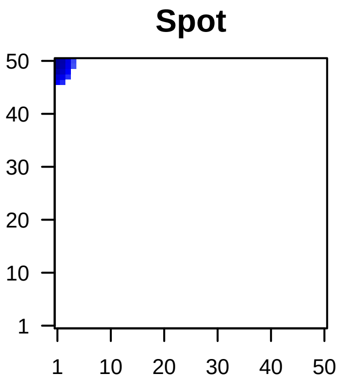
<FC> = −0.87

<shrinkage−t> = −30.62

<p−value> = 0

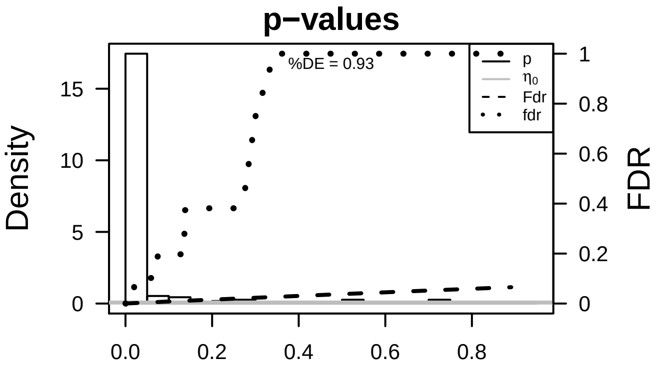
<fdr> = 0.18





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	57016	2.02	2e−16	6e−17	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
2	387695	−1.56	2e−16	6e−17	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Symb
3	64073	−1.78	2e−16	6e−17	1 x 46	chromosome 19 open reading frame 33 [Source:HGNC Symb
4	375791	−1.49	2e−16	6e−17	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Symb
5	51806	−1.88	2e−16	6e−17	4 x 50	calmodulin−like 5 [Source:HGNC Symbol;Acc:18180]
6	84290	−1.78	2e−16	6e−17	1 x 50	calpain, small subunit 2 [Source:HGNC Symbol;Acc:16371]
7	100133941	−1.49	2e−16	6e−17	3 x 50	CD24 molecule [Source:HGNC Symbol;Acc:1645]
8	9635	−2.37	2e−16	6e−17	1 x 46	chloride channel accessory 2 [Source:HGNC Symbol;Acc:20
9	9022	−1.85	2e−16	6e−17	1 x 50	chloride intracellular channel 3 [Source:HGNC Symbol;Acc:2
10	84518	−2.41	2e−16	6e−17	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
11	54544	−1.57	2e−16	6e−17	1 x 50	cysteine−rich C−terminal 1 [Source:HGNC Symbol;Acc:2987
12	49860	−2.28	2e−16	6e−17	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
13	92196	−1.62	2e−16	6e−17	3 x 50	death associated protein−like 1 [Source:HGNC Symbol;Acc:2
14	1672	−1.7	2e−16	6e−17	1 x 50	defensin, beta 1 [Source:HGNC Symbol;Acc:2766]
15	414325	−1.91	2e−16	6e−17	1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
16	93099	−1.73	2e−16	6e−17	1 x 47	dermokine [Source:HGNC Symbol;Acc:25063]
17	1824	−1.79	2e−16	6e−17	1 x 48	desmocollin 2 [Source:HGNC Symbol;Acc:3036]
18	2012	−1.44	2e−16	6e−17	3 x 50	epithelial membrane protein 1 [Source:HGNC Symbol;Acc:33
19	9982	−1.8	2e−16	6e−17	1 x 47	fibroblast growth factor binding protein 1 [Source:HGNC Sym
20	2706	−2.54	2e−16	6e−17	1 x 47	gap junction protein, beta 2, 26kDa [Source:HGNC Symbol;A



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−52.31	NULL	86 / 135	H.Tiss	WIRTH_Mucosa
2	−45.51	NULL	18 / 21	CC	cornified envelope
3	−34.5	NULL	19 / 42	BP	keratinization
4	−32.36	NULL	23 / 53	BP	keratinocyte differentiation
5	−29.79	NULL	24 / 76	BP	epidermis development
6	−23.37	NULL	93 / 572	Disease	GUDJ_psoriasis up
7	−23.32	NULL	10 / 19	BP	peptide cross−linking
8	−15.67	NULL	9 / 21	CC	desmosome
9	−12.79	NULL	5 / 10	MF	RAGE receptor binding
10	−12.63	NULL	6 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
11	−12.62	NULL	2 / 12	GSEA C2	REACTOME_GAP_JUNCTION_ASSEMBLY
12	−12.48	NULL	7 / 15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
13	−12.05	NULL	2 / 13	GSEA C2	REACTOME_GAP_JUNCTION_TRAFFICKING
14	−11.65	NULL	4 / 15	GSEA C2	AIGNER_ZEB1_TARGETS
15	−11.6	NULL	4 / 15	GSEA C2	CHANG_IMMORTALIZED_BY_HPV31_DN
16	−11.56	NULL	3 / 16	GSEA C2	AMIT_SERUM_RESPONSE_480_MCF10A
17	−11.24	NULL	6 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
18	−11.14	NULL	3 / 10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
19	−11.09	NULL	2 / 15	CC	connexon complex
20	−10.44	NULL	3 / 15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
21	−10.07	NULL	4 / 16	GSEA C2	HAHTOLA_MYCOSIS_FUNGOIDES_SKIN_DN
22	−9.9	NULL	20 / 186	MF	structural molecule activity
23	−9.26	NULL	4 / 10	GSEA C2	REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION_P
24	−9.25	NULL	6 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
25	−9.13	NULL	2 / 21	CC	gap junction
26	−8.9	NULL	1 / 7	GSEA C2	KONDO_PROSTATE_CANCER_WITH_H3K27ME3
27	−8.86	NULL	2 / 9	GSEA C2	WANG_RESPONSE_TO_PACLITAXEL_VIA_MAPK8_UP
28	−8.62	NULL	6 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
29	−8.61	NULL	12 / 122	MF	serine−type endopeptidase activity
30	−8.51	NULL	2 / 15	GSEA C2	ALONSO_METASTASIS_NEURAL_UP
31	−8.19	NULL	5 / 15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL
32	−8.14	NULL	3 / 16	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_LUNG_UP
33	−8.06	NULL	7 / 51	MF	protein binding, bridging
34	−8.05	NULL	2 / 11	GSEA C2	ROME_INSULIN_TARGETS_IN_MUSCLE_DN
35	−7.61	NULL	2 / 6	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_UP
36	−7.51	NULL	13 / 82	CC	intermediate filament
37	−7.21	NULL	6 / 53	MF	serine−type peptidase activity
38	−7.14	NULL	55 / 1182	CC	extracellular region
39	−7.07	NULL	7 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
40	−6.97	NULL	9 / 44	CC	keratin filament