GW_246

Global Summary

%DE = 0.14

genes with fdr < 0.2 = 1787 (948 + / 839 −)

genes with fdr < 0.1 = 1408 (767 + / 641 −)

genes with fdr < 0.05 = 1248 (691 + / 557 −)

genes with fdr < 0.01 = 868 (498 + / 370 −)

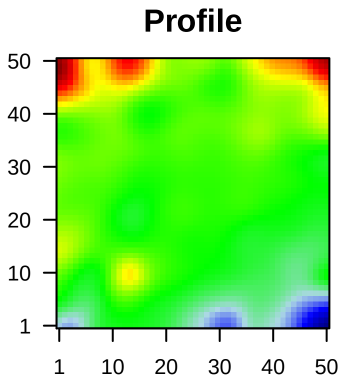
genes in genesets = 16332

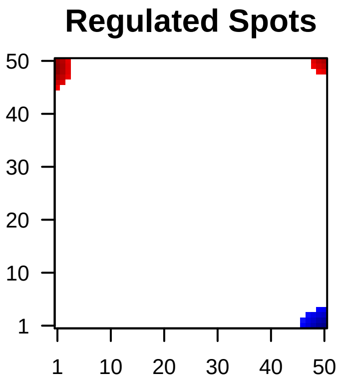
<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.1

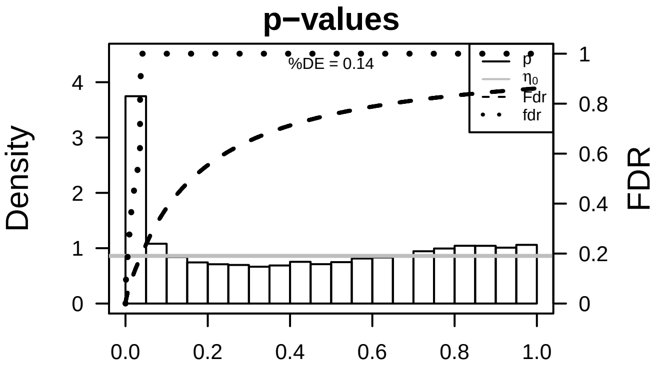
<fdr> = 0.86


Profile


Regulated Spots

Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	344752	1.43	2e−16	3e−14	11 x 50	arylacetamide deacetylase−like 2 [Source:HGNC Symbol;Acc
2	113146	2.01	2e−16	3e−14	1 x 44	AHNAK nucleoprotein 2 [Source:HGNC Symbol;Acc:20125]
3	57016	2.16	2e−16	3e−14	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
4	441282	1.81	2e−16	3e−14	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC S
5	8644	2.09	2e−16	3e−14	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
6	1109	1.94	2e−16	3e−14	13 x 50	aldo−keto reductase family 1, member C4 [Source:HGNC Sy
7	216	2.2	2e−16	3e−14	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGN
8	242	1.83	2e−16	3e−14	1 x 48	arachidonate 12−lipoxygenase, 12R type [Source:HGNC Syn
9	241	−1.61	2e−16	3e−14	50 x 1	arachidonate 5−lipoxygenase−activating protein [Source:HGN
10	401138	1.62	2e−16	3e−14	1 x 5	amelotin [Source:HGNC Symbol;Acc:33188]
11	383	1.43	2e−16	3e−14	7 x 45	arginase 1 [Source:HGNC Symbol;Acc:663]
12	151516	2.26	2e−16	3e−14	1 x 46	aspartic peptidase, retroviral−like 1 [Source:HGNC Symbol;A
13	479	2.01	2e−16	3e−14	7 x 50	ATPase, H+/K+ transporting, nongastric, alpha polypeptide [S
14	344905	1.69	2e−16	3e−14	50 x 50	ATPase type 13A5 [Source:HGNC Symbol;Acc:31789]
15	339512	1.71	2e−16	3e−14	50 x 50	chromosome 1 open reading frame 110 [Source:HGNC Symb
16	713	−1.55	2e−16	3e−14	50 x 1	complement component 1, q subcomponent, B chain [Source
17	92747	2.22	2e−16	3e−14	50 x 10	BPI fold containing family B, member 1 [Source:HGNC Symb
18	260436	−1.64	2e−16	3e−14	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symb
19	29113	1.59	2e−16	3e−14	2 x 47	chromosome 6 open reading frame 15 [Source:HGNC Symb
20	352999	1.99	2e−16	3e−14	50 x 10	chromosome 6 open reading frame 58 [Source:HGNC Symb


p−values

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	17.84	NULL	42	BP	keratinization
2	13.92	NULL	21	CC	cornified envelope
3	12.87	NULL	53	BP	keratinocyte differentiation
4	12.4	NULL	135	H.Tiss	WIRTH_Mucosa
5	9.91	NULL	572	Disease	GUDJ_psoriasis up
6	9.23	NULL	76	BP	epidermis development
7	8.46	NULL	19	BP	peptide cross−linking
8	8.4	NULL	1033	Chr	Chr 2
9	8.14	NULL	504	Chr	Chr 15
10	8.07	NULL	186	MF	structural molecule activity
11	7.43	NULL	8	GSEA C2	LIU_CDX2_TARGETS_DN
12	6.96	NULL	386	Chr	Chr 22
13	6.49	NULL	1253	BP	small molecule metabolic process
14	6.48	NULL	82	CC	intermediate filament
15	6.28	NULL	21	CC	gap junction
16	6.03	NULL	7	GSEA C2	MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
17	5.6	NULL	15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
18	5.57	NULL	13	BP	regulation of blood vessel size
19	5.53	NULL	142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
20	5.53	NULL	142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
Underexpressed					
1	−14.68	NULL	553	Cancer	Lembcke_Colonic Inflammation
2	−13.5	NULL	417	H.Tiss	WIRTH_Immune system
3	−12.27	NULL	265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
4	−12.27	NULL	265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
5	−12.27	NULL	265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
6	−12.27	NULL	265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
7	−12.24	NULL	312	BP	immune response
8	−10.22	NULL	250	Lymphoma	LENZ_Stromal signature 1
9	−9.77	NULL	15	CC	MHC class II protein complex
10	−9.63	NULL	51	BP	type I interferon signaling pathway
11	−9.47	NULL	316	Cancer	SPANG_BCL6−index2
12	−8.92	NULL	60	BP	interferon−gamma−mediated signaling pathway
13	−8.44	NULL	47	BP	antigen processing and presentation
14	−8.31	NULL	190	CC	extracellular matrix
15	−8	NULL	74	BP	regulation of immune response
16	−7.77	NULL	204	BP	cytokine−mediated signaling pathway
17	−7.53	NULL	52	Chr	Chr HSCHR6_MHC_QBL
18	−7.44	NULL	162	CC	external side of plasma membrane
19	−7.4	NULL	11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
20	−7.37	NULL	10	GSEA C2	GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3

GW_246

Local Summary

%DE = 0.79

metagenes = 15

genes = 222

genes in genesets = 216

genes with fdr < 0.1 = 158 (138 + / 20 −)

genes with fdr < 0.05 = 146 (129 + / 17 −)

genes with fdr < 0.01 = 126 (113 + / 13 −)

<r> metagenes = 0.95

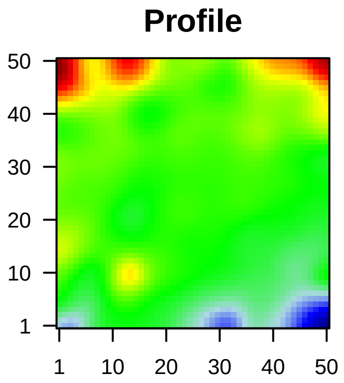
<r> genes = 0.45

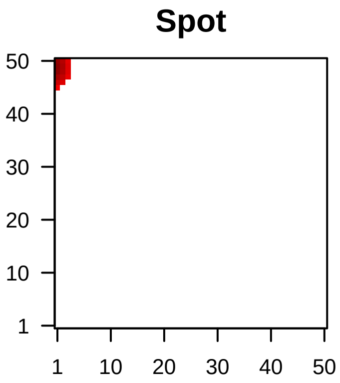
<FC> = 0.63

<shrinkage−t> = 22.09

<p−value> = 0

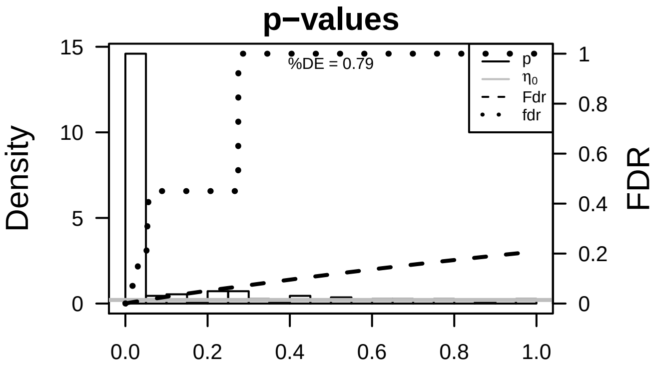
<fdr> = 0.33





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	57016	2.16	2e−16	3e−16	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
2	441282	1.81	2e−16	3e−16	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC Sy
3	8644	2.09	2e−16	3e−16	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Syı
4	242	1.83	2e−16	3e−16	1 x 48	arachidonate 12−lipoxygenase, 12R type [Source:HGNC Syn
5	151516	2.26	2e−16	3e−16	1 x 46	aspartic peptidase, retroviral−like 1 [Source:HGNC Symbol;A
6	29113	1.59	2e−16	3e−16	2 x 47	chromosome 6 open reading frame 15 [Source:HGNC Symbc
7	1475	1.49	2e−16	3e−16	1 x 50	cystatin A (stefin A) [Source:HGNC Symbol;Acc:2481]
8	9547	1.73	2e−16	3e−16	1 x 46	chemokine (C−X−C motif) ligand 14 [Source:HGNC Symbol;/
9	126410	1.93	2e−16	3e−16	1 x 49	cytochrome P450, family 4, subfamily F, polypeptide 22 [Sour
10	55894	2.1	2e−16	3e−16	1 x 47	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
11	414325	2.64	2e−16	3e−16	1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
12	1673	1.9	2e−16	3e−16	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
13	1823	1.89	2e−16	3e−16	1 x 45	desmocollin 1 [Source:HGNC Symbol;Acc:3035]
14	2312	2.1	2e−16	3e−16	1 x 49	filaggrin [Source:HGNC Symbol;Acc:3748]
15	10804	1.75	2e−16	3e−16	1 x 47	gap junction protein, beta 6, 30kDa [Source:HGNC Symbol;A
16	2877	1.76	2e−16	3e−16	1 x 50	glutathione peroxidase 2 (gastrointestinal) [Source:HGNC Syı
17	448834	1.93	2e−16	3e−16	1 x 48	keratinocyte proline−rich protein [Source:HGNC Symbol;Acc:
18	3848	2.09	2e−16	3e−16	1 x 47	keratin 1 [Source:HGNC Symbol;Acc:6412]
19	3858	2.43	2e−16	3e−16	1 x 47	keratin 10 [Source:HGNC Symbol;Acc:6413]
20	286887	1.32	2e−16	3e−16	1 x 47	keratin 6C [Source:HGNC Symbol;Acc:20406]



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	40.56	NULL	18 / 21	CC	cornified envelope
2	36.8	NULL	24 / 53	BP	keratinocyte differentiation
3	35.65	NULL	19 / 42	BP	keratinization
4	29.02	NULL	82 / 135	H.Tiss	WIRTH_Mucosa
5	25.43	NULL	10 / 19	BP	peptide cross−linking
6	22.16	NULL	93 / 572	Disease	GUDJ_psoriasis up
7	18.22	NULL	23 / 76	BP	epidermis development
8	16.57	NULL	12 / 21	CC	desmosome
9	14.57	NULL	23 / 186	MF	structural molecule activity
10	12.61	NULL	7 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
11	12.52	NULL	10 / 44	CC	keratin filament
12	12.51	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
13	12.33	NULL	16 / 82	CC	intermediate filament
14	12.08	NULL	3 / 12	BP	cellular aldehyde metabolic process
15	11.89	NULL	6 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
16	11.63	NULL	3 / 10	GSEA C2	SMID_BREAST_CANCER_ERBB2_UP
17	11.51	NULL	3 / 11	GSEA C2	MURAKAMI_UV_RESPONSE_24HR
18	11.37	NULL	3 / 10	GSEA C2	MURAKAMI_UV_RESPONSE_1HR_UP
19	11.2	NULL	3 / 16	GSEA C2	AMIT_SERUM_RESPONSE_480_MCF10A
20	10.76	NULL	2 / 10	GSEA C2	KEGG_LINOLEIC_ACID_METABOLISM
21	10.61	NULL	7 / 51	MF	protein binding, bridging
22	10.24	NULL	3 / 15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
23	10.15	NULL	3 / 10	GSEA C2	NIKOLSKY_BREAST_CANCER_20Q12_Q13_AMPLICON
24	10	NULL	2 / 6	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_UP
25	9.92	NULL	4 / 15	GSEA C2	CHANG_IMMORTALIZED_BY_HPV31_DN
26	9.76	NULL	6 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
27	9.44	NULL	3 / 11	GSEA C2	MURAKAMI_UV_RESPONSE_6HR_DN
28	9.35	NULL	3 / 21	CC	gap junction
29	9.23	NULL	5 / 15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL
30	9.11	NULL	4 / 15	MF	retinol dehydrogenase activity
31	9	NULL	4 / 10	GSEA C2	REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION_P
32	8.91	NULL	4 / 10	GSEA C2	FOURNIER_ACINAR_DEVELOPMENT_LATE_UP
33	8.77	NULL	8 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
34	8.16	NULL	3 / 13	GSEA C2	FARMER_BREAST_CANCER_APOCRINE VS LUMINAL
35	8.15	NULL	6 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
36	8.09	NULL	4 / 39	BP	retinoid metabolic process
37	7.76	NULL	2 / 12	GSEA C2	REACTOME_GAP_JUNCTION_ASSEMBLY
38	7.59	NULL	13 / 79	MF	serine−type endopeptidase inhibitor activity
39	7.41	NULL	3 / 13	GSEA C2	HAN_SATB1_TARGETS_DN
40	7.4	NULL	2 / 13	GSEA C2	REACTOME_GAP_JUNCTION_TRAFFICKING

GW_246

Local Summary

%DE = 0.76

metagenes = 8

genes = 145

genes in genesets = 144

genes with fdr < 0.1 = 101 (99 + / 2 −)

genes with fdr < 0.05 = 82 (81 + / 1 −)

genes with fdr < 0.01 = 75 (74 + / 1 −)

<r> metagenes = 0.98

<r> genes = 0.3

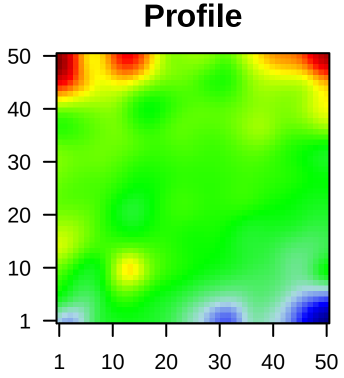
<FC> = 0.63

<shrinkage−t> = 22.08

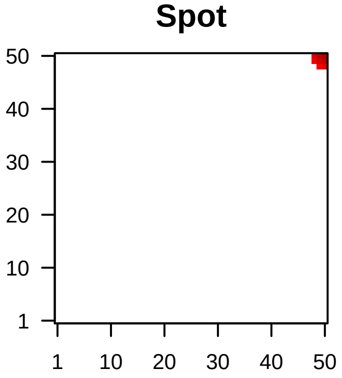
<p−value> = 0

<fdr> = 0.41

Profile



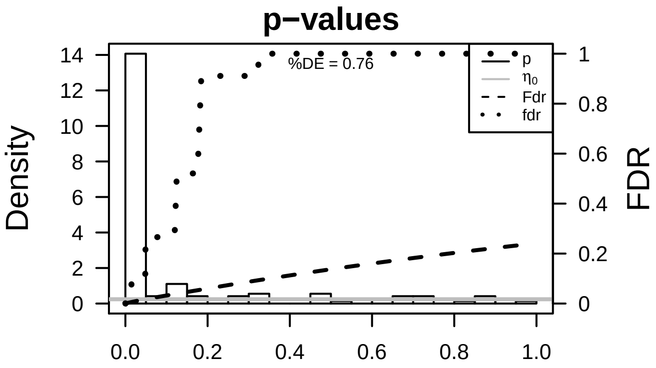
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	216	2.2	2e−16	6e−16	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGNC
2	344905	1.69	2e−16	6e−16	50 x 50	ATPase type 13A5 [Source:HGNC Symbol;Acc:31789]
3	339512	1.71	2e−16	6e−16	50 x 50	chromosome 1 open reading frame 110 [Source:HGNC Symb
4	4072	1.96	2e−16	6e−16	50 x 50	epithelial cell adhesion molecule [Source:HGNC Symbol;Acc:
5	83888	2.58	2e−16	6e−16	50 x 50	fibroblast growth factor binding protein 2 [Source:HGNC Sym
6	2938	1.66	2e−16	6e−16	50 x 50	glutathione S−transferase alpha 2 [Source:HGNC Symbol;Ac
7	2944	1.97	2e−16	6e−16	50 x 50	glutathione S−transferase mu 1 [Source:HGNC Symbol;Acc:4
8	4915	1.55	2e−16	6e−16	50 x 50	neurotrophic tyrosine kinase, receptor, type 2 [Source:HGNC
9	4922	3.26	2e−16	6e−16	50 x 50	neurotensin [Source:HGNC Symbol;Acc:8038]
10	4953	1.82	2e−16	6e−16	50 x 50	ornithine decarboxylase 1 [Source:HGNC Symbol;Acc:8109]
11	139728	1.86	2e−16	6e−16	49 x 49	pregnancy up−regulated nonubiquitous CaM kinase [Source:
12	6657	1.59	2e−16	6e−16	50 x 50	SRY (sex determining region Y)−box 2 [Source:HGNC Symb
13	11166	1.77	2e−16	6e−16	50 x 50	SRY (sex determining region Y)−box 21 [Source:HGNC Sym
14	7348	1.77	2e−16	6e−16	50 x 50	uroplakin 1B [Source:HGNC Symbol;Acc:12578]
15	1592	1.39	7e−16	2e−11	50 x 50	cytochrome P450, family 26, subfamily A, polypeptide 1 [Sou
16	256764	1.39	7e−16	2e−11	50 x 50	WD repeat domain 72 [Source:HGNC Symbol;Acc:26790]
17	56548	1.22	1e−12	2e−11	50 x 50	carbohydrate (N−acetylglucosamine 6−O) sulfotransferase 7
18	83959	1.21	2e−12	2e−11	50 x 50	solute carrier family 4, sodium borate transporter, member 11
19	2719	1.21	2e−12	2e−11	50 x 50	glypican 3 [Source:HGNC Symbol;Acc:4451]
20	3880	1.21	2e−12	6e−11	50 x 49	keratin 19 [Source:HGNC Symbol;Acc:6436]

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	26.56	NULL	2 / 7	GSEA C2	MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
2	22.67	NULL	5 / 15	GSEA C2	KEGG_GLUTATHIONE_METABOLISM
3	17.86	NULL	3 / 13	BP	regulation of blood vessel size
4	16.98	NULL	4 / 13	GSEA C2	KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_
5	16.67	NULL	8 / 34	BP	glutathione metabolic process
6	16.53	NULL	6 / 25	BP	glutathione derivative biosynthetic process
7	15.93	NULL	5 / 20	MF	glutathione transferase activity
8	15.67	NULL	4 / 15	GSEA C2	REACTOME_GLUTATHIONE_CONJUGATION
9	15.64	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
10	15.56	NULL	3 / 11	MF	glutathione binding
11	15.56	NULL	3 / 11	GSEA C2	KEGG_DRUG_METABOLISM_CYTOCHROME_P450
12	14.87	NULL	2 / 7	GSEA C2	FREDERICK_PRKCI_TARGETS
13	13.73	NULL	11 / 119	BP	xenobiotic metabolic process
14	13.59	NULL	1 / 11	Glio	neurons_glio
15	13.09	NULL	1 / 6	GSEA C2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_D_DN
16	13.09	NULL	1 / 6	GSEA C2	KAPOSI_LIVER_CANCER_POOR_SURVIVAL_DN
17	11.52	NULL	3 / 16	GSEA C2	BOYAULT_LIVER_CANCER_SUBCLASS_G1_DN
18	11.34	NULL	1 / 15	MF	neuropeptide hormone activity
19	11.25	NULL	3 / 12	GSEA C2	BROCKE_APOPTOSIS_REVERSED_BY_IL6
20	11.03	NULL	2 / 9	GSEA C2	REACTOME_METABOLISM_OF_AMINO_ACIDS
21	10.7	NULL	1 / 11	GSEA C2	YAMANAKA_GLIOBLASTOMA_SURVIVAL_UP
22	10.69	NULL	2 / 15	GSEA C2	LEE_LIVER_CANCER_MYC_UP
23	10.69	NULL	2 / 15	GSEA C2	LEE_LIVER_CANCER_E2F1_UP
24	10.23	NULL	1 / 9	GSEA C2	ABDULRAHMAN_KIDNEY_CANCER_VHL_DN
25	10.23	NULL	1 / 9	GSEA C2	REACTOME_ETHANOL_OXIDATION
26	9.9	NULL	2 / 15	GSEA C2	REACTOME_PHASE_II_CONJUGATION
27	9.82	NULL	1 / 7	GSEA C2	REACTOME_REGULATION_OF_ORNITHINE_DECARBOXYLASE
28	9.79	NULL	2 / 11	GSEA C2	SMID_BREAST_CANCER_BASAL_UP
29	9.61	NULL	1 / 10	GSEA C2	MAINA_VHL_TARGETS_UP
30	9.61	NULL	1 / 10	GSEA C2	FRIDMAN_SENESCENCE_DN
31	9.48	NULL	2 / 10	GSEA C2	CONRAD_STEM_CELL
32	9.37	NULL	4 / 15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
33	9.22	NULL	1 / 5	GSEA C2	KERLEY_RESPONSE_TO_CISPLATIN_DN
34	9.22	NULL	1 / 4	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_13
35	9.13	NULL	1 / 9	GSEA C2	GOERING_BLOOD_HDL_CHOLESTEROL_QTL_CIS
36	9.12	NULL	2 / 23	BP	stem cell differentiation
37	9.05	NULL	1 / 8	GSEA C2	PUJANA_CHEK2_PCC_NETWORK
38	8.78	NULL	2 / 10	GSEA C2	CERVERA_SDHB_TARGETS_1_DN
39	8.62	NULL	1 / 12	GSEA C2	MOROSETTI_FACIOSCAPULOHUMERAL_MUSCULAR_DISTRO
40	8.57	NULL	1 / 7	GSEA C2	REACTOME_G1_S_TRANSITION

GW_246

Local Summary

%DE = 0.92

metagenes = 16

genes = 268

genes in genesets = 266

genes with fdr < 0.1 = 235 (11 + / 224 −)

genes with fdr < 0.05 = 216 (7 + / 209 −)

genes with fdr < 0.01 = 205 (6 + / 199 −)

<r> metagenes = 0.99

<r> genes = 0.6

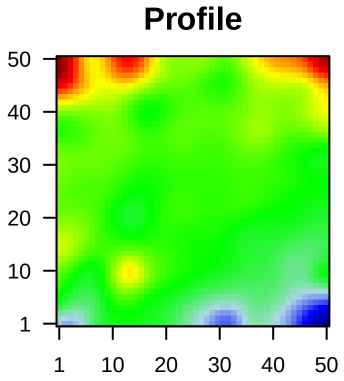
<FC> = −0.62

<shrinkage−t> = −21.78

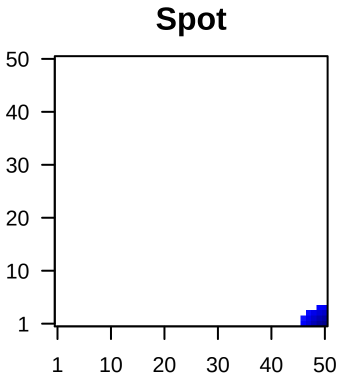
<p−value> = 0

<fdr> = 0.22

Profile



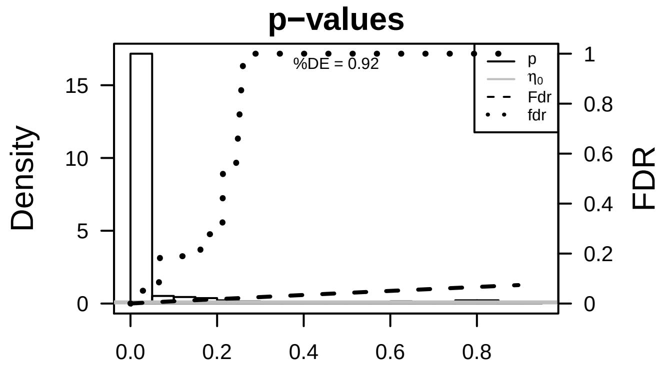
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	241	−1.61	2e−16	4e−16	50 x 1	arachidonate 5−lipoxygenase−activating protein [Source:HGN
2	713	−1.55	2e−16	4e−16	50 x 1	complement component 1, q subcomponent, B chain [Source
3	260436	−1.64	2e−16	4e−16	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symbo
4	972	−1.53	2e−16	4e−16	50 x 1	CD74 molecule, major histocompatibility complex, class II inva
5	4283	−1.42	2e−16	4e−16	49 x 1	chemokine (C−X−C motif) ligand 9 [Source:HGNC Symbol;Ac
6	2634	−1.44	2e−16	4e−16	47 x 1	guanylate binding protein 2, interferon−inducible [Source:HGN
7	3108	−1.45	2e−16	4e−16	50 x 1	major histocompatibility complex, class II, DM alpha [Source:I
8	3109	−1.64	2e−16	4e−16	50 x 1	major histocompatibility complex, class II, DM beta [Source:H
9	3113	−1.77	2e−16	4e−16	50 x 1	major histocompatibility complex, class II, DP alpha 1 [Source
10	3122	−1.71	2e−16	4e−16	50 x 1	major histocompatibility complex, class II, DR alpha [Source:H
11	3512	1.92	2e−16	4e−16	50 x 1	immunoglobulin J polypeptide, linker protein for immunoglobu
12	3936	−1.54	2e−16	4e−16	50 x 1	lymphocyte cytosolic protein 1 (L−plastin) [Source:HGNC Syr
13	5996	−1.43	2e−16	4e−16	50 x 1	regulator of G−protein signaling 1 [Source:HGNC Symbol;Acc
14	962	−1.34	6e−15	2e−13	50 x 1	CD48 molecule [Source:HGNC Symbol;Acc:1683]
15	4050	−1.32	2e−14	6e−13	50 x 1	lymphotoxin beta (TNF superfamily, member 3) [Source:HGN
16	915	−1.3	4e−14	1e−12	49 x 1	CD3d molecule, delta (CD3−TCR complex) [Source:HGNC S
17	3001	−1.28	1e−13	5e−12	48 x 1	granzyme A (granzyme 1, cytotoxic T−lymphocyte−associate
18	3689	−1.24	5e−13	5e−12	50 x 1	integrin, beta 2 (complement component 3 receptor 3 and 4 s
19	1436	−1.24	6e−13	7e−12	50 x 1	colony stimulating factor 1 receptor [Source:HGNC Symbol;A
20	7454	−1.22	1e−12	7e−12	50 x 1	Wiskott−Aldrich syndrome [Source:HGNC Symbol;Acc:12731

p−values



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−37.57	NULL	12 / 15	CC	MHC class II protein complex
2	−28.34	NULL	91 / 417	H.Tiss	WIRTH_Immune system
3	−23.71	NULL	15 / 47	BP	antigen processing and presentation
4	−22.92	NULL	94 / 553	Cancer	Lembcke_Colonic Inflammation
5	−21.56	NULL	52 / 312	BP	immune response
6	−20.87	NULL	7 / 11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
7	−20.35	NULL	7 / 21	CC	clathrin−coated endocytic vesicle membrane
8	−19.35	NULL	7 / 23	CC	integral to lumenal side of endoplasmic reticulum membrane
9	−18.97	NULL	16 / 60	BP	T cell costimulation
10	−18.48	NULL	2 / 3	GSEA C2	KEGG_VIRAL_MYOCARDITIS
11	−18.03	NULL	6 / 11	GSEA C2	BIOCARTA_THELPER_PATHWAY
12	−17.83	NULL	6 / 12	GSEA C2	BIOCARTA_CTL_PATHWAY
13	−17.56	NULL	43 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
14	−17.56	NULL	43 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
15	−17.56	NULL	43 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
16	−17.56	NULL	43 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
17	−17.34	NULL	7 / 28	CC	transport vesicle membrane
18	−16.65	NULL	7 / 15	GSEA C2	FINAK_BREAST_CANCER_SDPP_SIGNATURE
19	−16.48	NULL	8 / 35	CC	trans−Golgi network membrane
20	−16.2	NULL	4 / 7	Glio	Donson−cytotoxic effectors−associated with LTS in HGA
21	−16.09	NULL	7 / 32	CC	ER to Golgi transport vesicle membrane
22	−16.02	NULL	18 / 74	BP	regulation of immune response
23	−15.82	NULL	2 / 4	GSEA C2	REACTOME_CLASSICAL_ANTIBODY_MEDIATED_COMPLEMEN
24	−15.79	NULL	3 / 6	GSEA C2	SANA_RESPONSE_TO_IFNG_UP
25	−15.55	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
26	−15.52	NULL	2 / 4	GSEA C2	KEGG_LEISHMANIA_INFECTION
27	−15.39	NULL	16 / 84	BP	T cell receptor signaling pathway
28	−15.03	NULL	2 / 6	GSEA C2	LUI_THYROID_CANCER_CLUSTER_4
29	−14.96	NULL	7 / 13	Cancer	GENTLES_modul18
30	−14.6	NULL	5 / 10	GSEA C2	LEE_DIFFERENTIATING_T_LYMPHOCYTE
31	−14.59	NULL	6 / 8	Glio	Donson−migration tethering and rolling−associated with LTS in HG
32	−14.53	NULL	13 / 87	BP	antigen processing and presentation of exogenous peptide antigen
33	−14.36	NULL	2 / 5	GSEA C2	WEST_ADRENOCORTICAL_CARCINOMA_VS_ADENOMA_DN
34	−14.31	NULL	11 / 60	BP	interferon−gamma−mediated signaling pathway
35	−14.18	NULL	4 / 8	GSEA C2	REACTOME_IMMUNOREGULATORY_INTERACTIONS_BETWEE
36	−14.1	NULL	6 / 15	Glio	Donson−chemokines/cytokines−associated with LTS in HGA
37	−13.96	NULL	8 / 46	CC	endocytic vesicle membrane
38	−13.42	NULL	8 / 52	Chr	Chr HSCHR6_MHC_QBL
39	−13.32	NULL	5 / 13	GSEA C2	HAHTOLA_CTCL_PATHOGENESIS
40	−13.32	NULL	3 / 8	GSEA C2	LINDSTEDT_DENDRITIC_CELL_MATURATION_D