GW_089

Global Summary

%DE = 0.12

genes with fdr < 0.2 = 1401 (776 + / 625 −)
genes with fdr < 0.1 = 1034 (606 + / 428 −)
genes with fdr < 0.05 = 848 (519 + / 329 −)
genes with fdr < 0.01 = 643 (414 + / 229 −)

genes in genesets = 16332

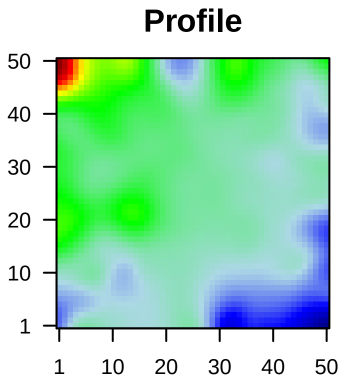
<FC> = 0
<shrinkage−t> = 0
<p−value> = 0.13
<fdr> = 0.88

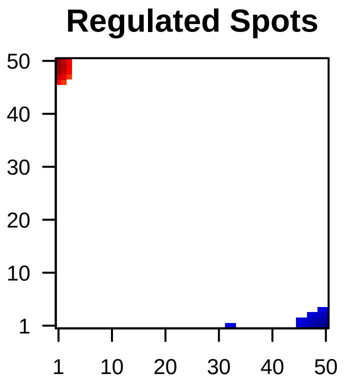
Global Genelist

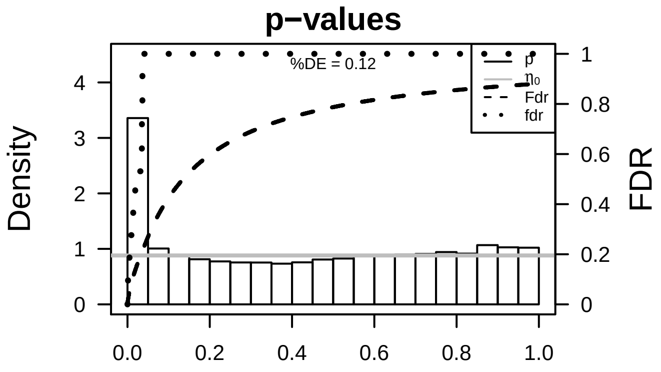
Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	57016	1.79	2e−16	4e−14	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
2	441282	1.87	2e−16	4e−14	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC Sy
3	8644	2.03	2e−16	4e−14	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Syı
4	1109	2.05	2e−16	4e−14	13 x 50	aldo−keto reductase family 1, member C4 [Source:HGNC Syı
5	218	1.29	2e−16	4e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
6	11199	1.35	2e−16	4e−14	15 x 50	annexin A10 [Source:HGNC Symbol;Acc:534]
7	339512	1.97	2e−16	4e−14	50 x 50	chromosome 1 open reading frame 110 [Source:HGNC Symb
8	29923	1.36	2e−16	4e−14	4 x 44	hypoxia inducible lipid droplet−associated [Source:HGNC Syr
9	83648	1.26	2e−16	4e−14	11 x 36	family with sequence similarity 167, member A [Source:HGNC
10	131076	1.31	2e−16	4e−14	1 x 16	coiled−coil domain containing 58 [Source:HGNC Symbol;Acc
11	414062	−1.33	2e−16	4e−14	1 x 1	chemokine (C−C motif) ligand 3−like 3 [Source:HGNC Symbo
12	8900	1.32	2e−16	4e−14	1 x 42	cyclin A1 [Source:HGNC Symbol;Acc:1577]
13	952	1.25	2e−16	4e−14	45 x 5	CD38 molecule [Source:HGNC Symbol;Acc:1667]
14	9076	−1.72	2e−16	4e−14	49 x 50	claudin 1 [Source:HGNC Symbol;Acc:2032]
15	49860	1.56	2e−16	4e−14	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
16	57834	2.07	2e−16	4e−14	13 x 50	cytochrome P450, family 4, subfamily F, polypeptide 11 [Sour
17	1672	1.95	2e−16	4e−14	1 x 50	defensin, beta 1 [Source:HGNC Symbol;Acc:2766]
18	55894	1.48	2e−16	4e−14	1 x 47	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
19	414325	1.76	2e−16	4e−14	1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
20	1673	1.44	2e−16	4e−14	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	16.05	NULL	135	H.Tiss	WIRTH_Mucosa
2	11.52	NULL	42	BP	keratinization
3	11.36	NULL	53	BP	keratinocyte differentiation
4	11.21	NULL	21	CC	cornified envelope
5	8.65	NULL	1720	Chr	Chr 1
6	8.18	NULL	20	MF	glutathione transferase activity
7	8.17	NULL	572	Disease	GUDJ_psoriasis up
8	7.59	NULL	34	BP	glutathione metabolic process
9	7.27	NULL	534	Chr	Chr 8
10	7.25	NULL	15	GSEA C2	REACTOME_GLUTATHIONE_CONJUGATION
11	7.07	NULL	13	GSEA C2	SINGH_NFE2L2_TARGETS
12	7	NULL	25	BP	glutathione derivative biosynthetic process
13	6.79	NULL	4	MMML CGS	MACIEJ_MMML 23
14	6.76	NULL	76	BP	epidermis development
15	6.56	NULL	630	Chr	Chr X
16	6.52	NULL	10	MF	RAGE receptor binding
17	6.34	NULL	11	MF	glutathione binding
18	6.27	NULL	11	GSEA C2	KEGG_DRUG_METABOLISM_CYTOCHROME_P450
19	6.21	NULL	79	MF	electron carrier activity
20	6.15	NULL	1253	BP	small molecule metabolic process
Underexpressed					
1	−10.59	NULL	312	BP	immune response
2	−10.01	NULL	417	H.Tiss	WIRTH_Immune system
3	−9.5	NULL	386	Chr	Chr 22
4	−9.13	NULL	204	BP	cytokine−mediated signaling pathway
5	−8.66	NULL	60	BP	interferon−gamma−mediated signaling pathway
6	−8.59	NULL	51	BP	type I interferon signaling pathway
7	−8.51	NULL	15	CC	MHC class II protein complex
8	−8.22	NULL	553	Cancer	Lembcke_Colonic Inflammation
9	−7.94	NULL	274	Lymphoma	SPANG_IL21 DN
10	−7.74	NULL	316	Cancer	SPANG_BCL6−index2
11	−7.58	NULL	866	Chr	Chr 12
12	−7.42	NULL	15	GSEA C2	LEE_LIVER_CANCER_HEPATOBLAST
13	−7.35	NULL	265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
14	−7.35	NULL	265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
15	−7.35	NULL	265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
16	−7.35	NULL	265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
17	−7.33	NULL	123	BP	defense response to virus
18	−7.08	NULL	2659	CC	plasma membrane
19	−7.06	NULL	185	Cancer	SPANG_LPS−index2
20	−6.7	NULL	16	GSEA C2	MOSERLE_IFNA_RESPONSE


Profile


Regulated Spots


p−values

GW_089

Local Summary

%DE = 0.83

metagenes = 14

genes = 200

genes in genesets = 194

genes with fdr < 0.1 = 155 (144 + / 11 −)

genes with fdr < 0.05 = 143 (133 + / 10 −)

genes with fdr < 0.01 = 119 (114 + / 5 −)

<r> metagenes = 0.97

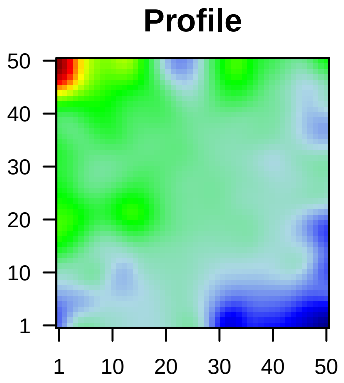
<r> genes = 0.47

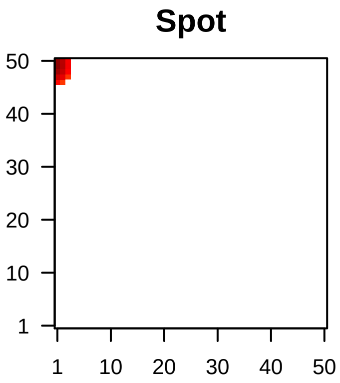
<FC> = 0.63

<shrinkage−t> = 22.32

<p−value> = 0

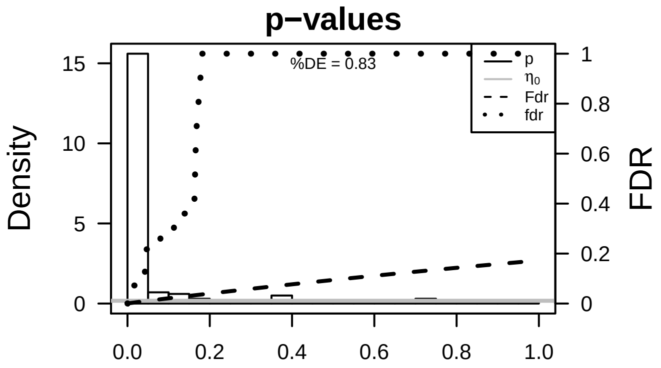
<fdr> = 0.3





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	57016	1.79	2e−16	2e−16	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
2	441282	1.87	2e−16	2e−16	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC S
3	8644	2.03	2e−16	2e−16	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
4	218	1.29	2e−16	2e−16	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
5	49860	1.56	2e−16	2e−16	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
6	1672	1.95	2e−16	2e−16	1 x 50	defensin, beta 1 [Source:HGNC Symbol;Acc:2766]
7	55894	1.48	2e−16	2e−16	1 x 47	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
8	414325	1.76	2e−16	2e−16	1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
9	1673	1.44	2e−16	2e−16	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
10	1828	1.39	2e−16	2e−16	1 x 48	desmoglein 1 [Source:HGNC Symbol;Acc:3048]
11	2877	2.01	2e−16	2e−16	1 x 50	glutathione peroxidase 2 (gastrointestinal) [Source:HGNC Sy
12	56300	1.29	2e−16	2e−16	1 x 47	interleukin 36, gamma [Source:HGNC Symbol;Acc:15741]
13	5650	1.67	2e−16	2e−16	1 x 49	kallikrein−related peptidase 7 [Source:HGNC Symbol;Acc:63
14	388533	2.01	2e−16	2e−16	1 x 49	keratinocyte differentiation−associated protein [Source:HGNC
15	353142	1.37	2e−16	2e−16	1 x 47	late cornified envelope 3A [Source:HGNC Symbol;Acc:29461
16	84648	1.49	2e−16	2e−16	1 x 48	late cornified envelope 3D [Source:HGNC Symbol;Acc:16615
17	3934	1.37	2e−16	2e−16	1 x 50	lipocalin 2 [Source:HGNC Symbol;Acc:6526]
18	3963	1.57	2e−16	2e−16	1 x 47	lectin, galactoside−binding, soluble, 7 [Source:HGNC Symbol
19	653499	1.51	2e−16	2e−16	1 x 47	lectin, galactoside−binding, soluble, 7 [Source:HGNC Symbol
20	643479	1.23	2e−16	2e−16	1 x 49	



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	39.07	NULL	79 / 135	H.Tiss	WIRTH_Mucosa
2	32.2	NULL	18 / 21	CC	cornified envelope
3	32.08	NULL	19 / 42	BP	keratinization
4	30.59	NULL	23 / 53	BP	keratinocyte differentiation
5	27.68	NULL	87 / 572	Disease	GUDJ_psoriasis up
6	22.72	NULL	22 / 76	BP	epidermis development
7	22.04	NULL	5 / 10	MF	RAGE receptor binding
8	17.65	NULL	3 / 10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
9	17.59	NULL	7 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
10	17.02	NULL	10 / 19	BP	peptide cross−linking
11	15.44	NULL	3 / 15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
12	14.24	NULL	4 / 15	MF	retinol dehydrogenase activity
13	13.85	NULL	6 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
14	13.58	NULL	6 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
15	12.65	NULL	6 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
16	12.6	NULL	6 / 13	BP	negative regulation of peptidase activity
17	12.43	NULL	7 / 15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
18	12.37	NULL	2 / 6	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_UP
19	12.29	NULL	3 / 12	BP	cellular aldehyde metabolic process
20	12.13	NULL	3 / 10	GSEA C2	SMID_BREAST_CANCER_ERBB2_UP
21	10.84	NULL	3 / 16	GSEA C2	AMIT_SERUM_RESPONSE_480_MCF10A
22	10.54	NULL	3 / 16	GSEA C2	CHEOK_RESPONSE_TO_MERCAPTOPURINE_AND_LD_MTX_
23	10.38	NULL	4 / 39	BP	retinoid metabolic process
24	10.02	NULL	2 / 10	GSEA C2	KEGG_LINOLEIC_ACID_METABOLISM
25	9.89	NULL	4 / 27	BP	response to bacterium
26	9.4	NULL	3 / 16	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_DN
27	9.18	NULL	51 / 1182	CC	extracellular region
28	9.09	NULL	7 / 73	BP	defense response to bacterium
29	9.04	NULL	4 / 15	GSEA C2	LEE_LIVER_CANCER_MYC_E2F1_UP
30	8.92	NULL	4 / 15	GSEA C2	CHANG_IMMORTALIZED_BY_HPV31_DN
31	8.89	NULL	3 / 14	GSEA C2	CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U
32	8.69	NULL	6 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
33	8.37	NULL	2 / 17	Disease	BCHETNIA_EBM up
34	8.36	NULL	3 / 15	GSEA C2	LEE_LIVER_CANCER_MYC_UP
35	8.24	NULL	4 / 16	GSEA C2	HAHTOLA_MYCOSIS_FUNGOIDES_SKIN_DN
36	8.18	NULL	9 / 21	CC	desmosome
37	8.08	NULL	3 / 16	GSEA C2	LEE_LIVER_CANCER_ACOX1_UP
38	8.03	NULL	2 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
39	7.92	NULL	3 / 13	GSEA C2	HAN_SATB1_TARGETS_DN
40	7.83	NULL	20 / 186	MF	structural molecule activity

GW_089

Local Summary

%DE = 0.79

metagenes = 2

genes = 102

genes in genesets = 100

genes with fdr < 0.1 = 59 (0 + / 59 −)

genes with fdr < 0.05 = 59 (0 + / 59 −)

genes with fdr < 0.01 = 40 (0 + / 40 −)

<r> metagenes = 1

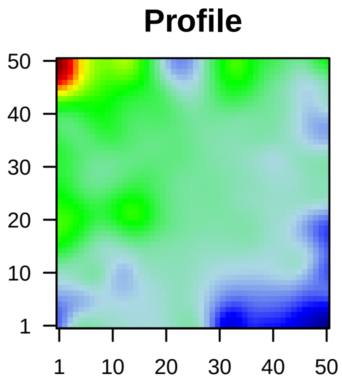
<r> genes = 0.5

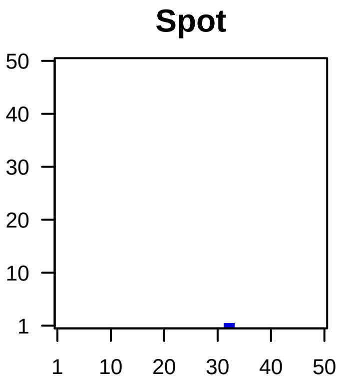
<FC> = −0.38

<shrinkage−t> = −13.45

<p−value> = 0

<fdr> = 0.51





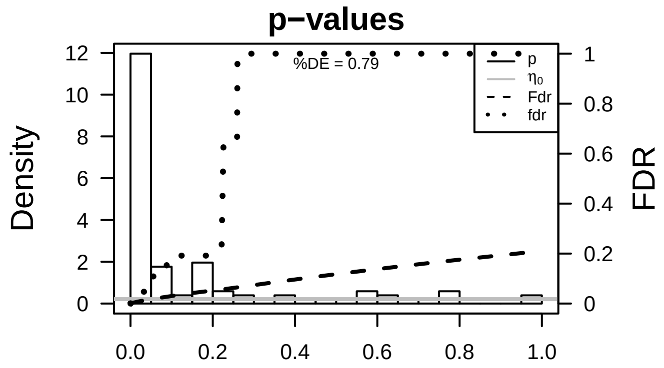
Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	9997	−1.18	4e−15	2e−12	32 x 1	SCO2 cytochrome c oxidase assembly protein [Source:HGN
2	10410	−1.02	1e−13	6e−11	32 x 1	interferon induced transmembrane protein 3 [Source:HGNC
3	27074	−1.04	3e−12	4e−10	32 x 1	lysosomal−associated membrane protein 3 [Source:HGNC S
4	10346	−0.99	3e−11	4e−10	32 x 1	tripartite motif containing 22 [Source:HGNC Symbol;Acc:163
5	629	−0.99	4e−11	5e−09	32 x 1	complement factor B [Source:HGNC Symbol;Acc:1037]
6	4321	−0.94	3e−10	8e−08	32 x 1	matrix metallopeptidase 12 (macrophage elastase) [Source:H
7	9560	−0.88	4e−09	4e−06	32 x 1	chemokine (C−C motif) ligand 4−like 1 [Source:HGNC Symb
8	10581	−0.72	2e−07	8e−06	32 x 1	interferon induced transmembrane protein 2 [Source:HGNC
9	3433	−0.75	6e−07	1e−05	32 x 1	interferon−induced protein with tetratricopeptide repeats 2 [S
10	8743	−0.73	1e−06	1e−05	32 x 1	tumor necrosis factor (ligand) superfamily, member 10 [Sourc
11	83666	−0.72	2e−06	1e−05	32 x 1	poly (ADP−ribose) polymerase family, member 9 [Source:HG
12	1890	−0.71	2e−06	1e−05	32 x 1	thymidine phosphorylase [Source:HGNC Symbol;Acc:3148]
13	8519	−0.7	3e−06	9e−05	32 x 1	interferon induced transmembrane protein 1 [Source:HGNC
14	10561	−0.67	7e−06	1e−04	32 x 1	interferon−induced protein 44 [Source:HGNC Symbol;Acc:16
15	6773	−0.65	1e−05	1e−04	32 x 1	signal transducer and activator of transcription 2, 113kDa [So
16	3430	−0.64	2e−05	1e−04	32 x 1	interferon−induced protein 35 [Source:HGNC Symbol;Acc:53
17	10964	−0.64	2e−05	1e−04	32 x 1	interferon−induced protein 44−like [Source:HGNC Symbol;Ac
18	4940	−0.63	3e−05	3e−04	32 x 1	2'−5'−oligoadenylate synthetase 3, 100kDa [Source:HGNC S
19	3628	−0.61	4e−05	3e−04	33 x 1	inositol polyphosphate−1−phosphatase [Source:HGNC Symb
20	2633	−0.59	7e−05	3e−04	32 x 1	guanylate binding protein 1, interferon−inducible [Source:HG

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−50.79	NULL	12 / 16	GSEA C2	MOSERLE_IFNA_RESPONSE
2	−49.77	NULL	29 / 51	BP	type I interferon signaling pathway
3	−41.18	NULL	8 / 10	GSEA C2	GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
4	−39.18	NULL	11 / 16	GSEA C2	ZHANG_INTERFERON_RESPONSE
5	−38.48	NULL	9 / 10	GSEA C2	BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
6	−37.37	NULL	10 / 13	GSEA C2	BOWIE_RESPONSE_TO_TAMOXIFEN
7	−35.4	NULL	31 / 123	BP	defense response to virus
8	−34.51	NULL	27 / 109	BP	response to virus
9	−31.28	NULL	6 / 8	GSEA C2	ROETH_TERT_TARGETS_UP
10	−31.24	NULL	10 / 16	GSEA C2	UROSEVIC_RESPONSE_TO_IMIQUIMOD
11	−30.41	NULL	8 / 11	GSEA C2	BENNETT_SYSTEMIC_LUPUS_ERYTHEMATOSUS
12	−30.08	NULL	13 / 31	BP	negative regulation of viral genome replication
13	−28.27	NULL	11 / 16	GSEA C2	EINAV_INTERFERON_SIGNATURE_IN_CANCER
14	−27.22	NULL	34 / 204	BP	cytokine−mediated signaling pathway
15	−26.68	NULL	6 / 14	Glio	Donson−immune cell intra signaling−associated with LTS in HGA
16	−24.68	NULL	3 / 4	MMML CGS	MACIEJ_MMML 47
17	−24.6	NULL	6 / 12	GSEA C2	TSAI_DNAJB4_TARGETS_UP
18	−24.16	NULL	31 / 274	Lymphoma	SPANG_IL21 DN
19	−23.99	NULL	5 / 16	GSEA C2	ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_UP
20	−22.89	NULL	7 / 16	GSEA C2	MAHADEVAN_RESPONSE_TO_MP470_UP
21	−21.67	NULL	45 / 572	Disease	GUDJ_psoriasis up
22	−20.9	NULL	3 / 4	GSEA C2	KRASNOSELSKAYA_ILF3_TARGETS_UP
23	−20.65	NULL	16 / 60	BP	interferon−gamma−mediated signaling pathway
24	−19.88	NULL	6 / 14	GSEA C2	XU_AKT1_TARGETS_6HR
25	−19.53	NULL	3 / 5	GSEA C2	KIM_LRRC3B_TARGETS
26	−19.28	NULL	4 / 10	GSEA C2	DAUER_STAT3_TARGETS_DN
27	−18.77	NULL	6 / 14	GSEA C2	RADAEVA_RESPONSE_TO_IFNA1_UP
28	−18.4	NULL	5 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
29	−18.3	NULL	4 / 10	GSEA C2	GRANDVAUX_IRF3_TARGETS_UP
30	−18.13	NULL	6 / 10	CC	MHC class I protein complex
31	−18.08	NULL	8 / 18	BP	positive regulation of T cell mediated cytotoxicity
32	−17.48	NULL	5 / 6	Lymphoma	DAVE_MHCCII BL DN
33	−17.46	NULL	5 / 18	BP	response to interferon−gamma
34	−16.96	NULL	3 / 6	GSEA C2	ISHIKAWA_STING_SIGNALING
35	−16.37	NULL	25 / 312	BP	immune response
36	−15.83	NULL	4 / 14	GSEA C2	SANA_TNF_SIGNALING_UP
37	−15.46	NULL	4 / 16	GSEA C2	SEITZ_NEOPLASTIC_TRANSFORMATION_BY_8P_DELETION_
38	−15.29	NULL	3 / 14	GSEA C2	XU_RESPONSE_TO_TRETINOIN_AND_NSC682994_UP
39	−15.14	NULL	6 / 16	GSEA C2	XU_HGF_TARGETS_INDUCED_BY_AKT1_6HR
40	−14.85	NULL	3 / 15	GSEA C2	LIANG_SILENCED_BY_METHYLATION_2



GW_089

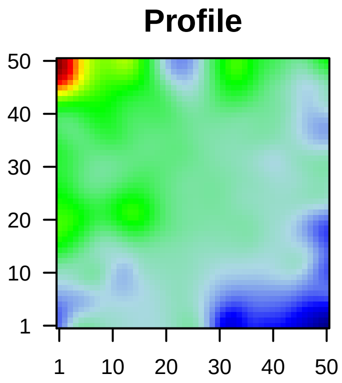
Local Summary

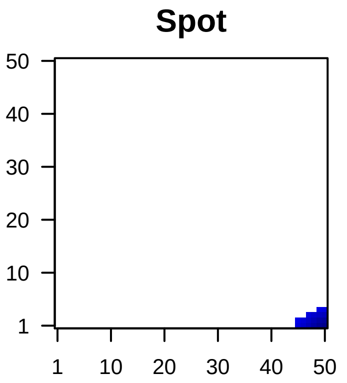
%DE = 0.87
metagenes = 18
genes = 292
genes in genesets = 289

genes with fdr < 0.1 = 201 (10 + / 191 −)
genes with fdr < 0.05 = 186 (10 + / 176 −)
genes with fdr < 0.01 = 115 (7 + / 108 −)

<r> metagenes = 0.99
<r> genes = 0.58

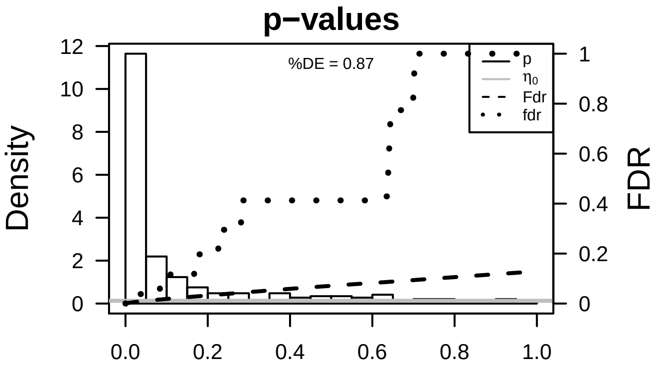
<FC> = −0.32
<shrinkage−t> = −11.27
<p−value> = 0.01
<fdr> = 0.55


Profile


Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	5341	−1.08	6e−13	2e−11	50 x 1	pleckstrin [Source:HGNC Symbol;Acc:9070]
2	348	−1.06	1e−12	1e−10	50 x 1	apolipoprotein E [Source:HGNC Symbol;Acc:613]
3	3123	−1.04	4e−12	3e−10	45 x 1	major histocompatibility complex, class II, DR beta 1 [Source:
4	5552	−1.01	1e−11	1e−09	50 x 1	serglycin [Source:HGNC Symbol;Acc:9361]
5	3689	−0.99	4e−11	3e−09	50 x 1	integrin, beta 2 (complement component 3 receptor 3 and 4 s
6	10537	−0.96	2e−10	3e−09	50 x 1	ubiquitin D [Source:HGNC Symbol;Acc:18795]
7	3543	0.87	2e−10	2e−08	49 x 1	immunoglobulin lambda−like polypeptide 1 [Source:HGNC Sy
8	972	−0.92	8e−10	6e−08	50 x 1	CD74 molecule, major histocompatibility complex, class II inva
9	3122	−0.83	2e−09	3e−07	50 x 1	major histocompatibility complex, class II, DR alpha [Source:H
10	894	−0.85	1e−08	3e−07	50 x 4	cyclin D2 [Source:HGNC Symbol;Acc:1583]
11	255231	−0.84	2e−08	3e−07	49 x 1	mucolipin 2 [Source:HGNC Symbol;Acc:13357]
12	3059	−0.83	3e−08	3e−07	50 x 1	hematopoietic cell−specific Lyn substrate 1 [Source:HGNC Sy
13	3936	−0.82	4e−08	1e−06	50 x 1	lymphocyte cytosolic protein 1 (L−plastin) [Source:HGNC Syr
14	1545	−0.8	7e−08	4e−06	50 x 4	cytochrome P450, family 1, subfamily B, polypeptide 1 [Sourc
15	969	−0.77	2e−07	4e−06	50 x 1	CD69 molecule [Source:HGNC Symbol;Acc:1694]
16	5880	−0.77	3e−07	8e−06	50 x 1	ras−related C3 botulinum toxin substrate 2 (rho family, small (
17	5142	−0.75	6e−07	8e−06	50 x 4	phosphodiesterase 4B, cAMP−specific [Source:HGNC Symbo
18	64759	−0.74	7e−07	3e−05	50 x 4	tensin 3 [Source:HGNC Symbol;Acc:21616]
19	3126	−0.72	2e−06	3e−05	50 x 1	major histocompatibility complex, class II, DR beta 4 [Source:
20	7454	−0.7	3e−06	3e−05	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	−35.78	NULL	13 / 15	CC	MHC class II protein complex
2	−28.65	NULL	96 / 417	H.Tiss	WIRTH_Immune system
3	−22.48	NULL	8 / 21	CC	clathrin−coated endocytic vesicle membrane
4	−22.39	NULL	98 / 553	Cancer	Lembcke_Colonic Inflammation
5	−22.06	NULL	3 / 3	MMML CGS	MACIEJ_MMML 7
6	−21.4	NULL	8 / 23	CC	integral to lumenal side of endoplasmic reticulum membrane
7	−20.94	NULL	16 / 47	BP	antigen processing and presentation
8	−20.34	NULL	56 / 312	BP	immune response
9	−19.22	NULL	8 / 28	CC	transport vesicle membrane
10	−17.91	NULL	2 / 3	GSEA C2	KEGG_VIRAL_MYOCARDITIS
11	−17.86	NULL	8 / 32	CC	ER to Golgi transport vesicle membrane
12	−17.4	NULL	43 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
13	−17.4	NULL	43 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
14	−17.4	NULL	43 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
15	−17.4	NULL	43 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
16	−16.45	NULL	5 / 12	GSEA C2	ZHAN_MULTIPLE_MYELOMA_DN
17	−16.26	NULL	9 / 35	CC	trans−Golgi network membrane
18	−16.21	NULL	9 / 46	CC	endocytic vesicle membrane
19	−15.52	NULL	17 / 84	BP	T cell receptor signaling pathway
20	−15.44	NULL	7 / 15	GSEA C2	FINAK_BREAST_CANCER_SDPP_SIGNATURE
21	−15.18	NULL	2 / 4	GSEA C2	KEGG_LEISHMANIA_INFECTION
22	−15.07	NULL	7 / 11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
23	−14.93	NULL	5 / 13	MMML CGS	MACIEJ_MMML 6
24	−14.92	NULL	14 / 87	BP	antigen processing and presentation of exogenous peptide antigen
25	−14.86	NULL	17 / 60	BP	T cell costimulation
26	−14.75	NULL	9 / 52	Chr	Chr HSCHR6_MHC_QBL
27	−14.15	NULL	12 / 60	BP	interferon−gamma−mediated signaling pathway
28	−14.07	NULL	18 / 74	BP	regulation of immune response
29	−13.78	NULL	5 / 12	BP	immunoglobulin mediated immune response
30	−13.62	NULL	6 / 11	GSEA C2	BIOCARTA_THELPER_PATHWAY
31	−13.53	NULL	5 / 10	GSEA C2	LEE_DIFFERENTIATING_T_LYMPHOCYTE
32	−13.49	NULL	6 / 8	Glio	Donson−migration tethering and rolling−associated with LTS in HG
33	−13.26	NULL	5 / 16	GSEA C2	FERRANDO_TAL1_NEIGHBORS
34	−13.02	NULL	4 / 11	GSEA C2	APPEL_IMATINIB_RESPONSE
35	−13.01	NULL	2 / 6	GSEA C2	BUDHU_LIVER_CANCER_METASTASIS_UP
36	−13	NULL	6 / 12	GSEA C2	BIOCARTA_CTL_PATHWAY
37	−12.99	NULL	26 / 162	CC	external side of plasma membrane
38	−12.97	NULL	3 / 8	GSEA C2	LINDSTEDT_DENDRITIC_CELL_MATURATION_D
39	−12.96	NULL	6 / 15	Glio	Donson−chemokines/cytokines−associated with LTS in HGA
40	−12.78	NULL	31 / 316	Cancer	SPANG_BCL6−index2