GW_196

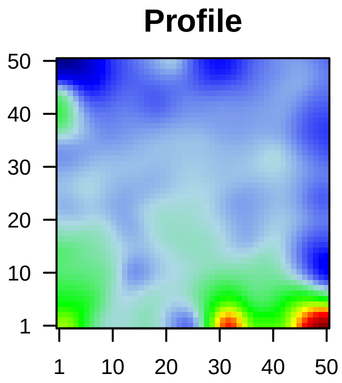
Global Summary

%DE = 0.13

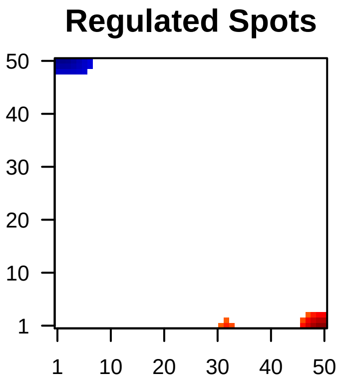
genes with fdr < 0.2 = 1609 (1004 + / 605 −)
genes with fdr < 0.1 = 1307 (855 + / 452 −)
genes with fdr < 0.05 = 1141 (767 + / 374 −)
genes with fdr < 0.01 = 770 (559 + / 211 −)

genes in genesets = 16332

<FC> = 0
<shrinkage−t> = 0
<p−value> = 0.1
<fdr> = 0.87



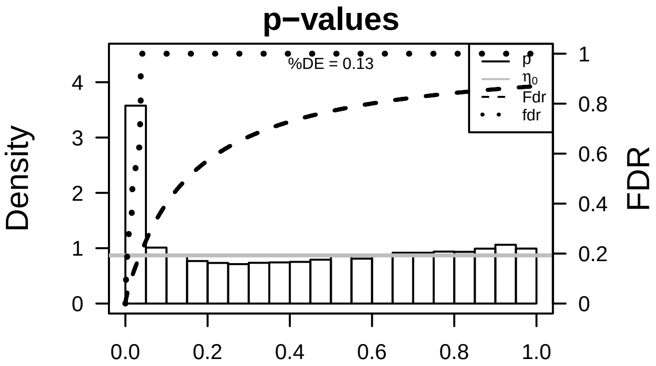
Profile



Regulated Spots

Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	1109	−1.38	2e−16	3e−14	13 x 50	aldo−keto reductase family 1, member C4 [Source:HGNC Sy
2	55107	1.62	2e−16	3e−14	1 x 5	anoctamin 1, calcium activated chloride channel [Source:HG
3	341	1.37	2e−16	3e−14	50 x 1	apolipoprotein C−I [Source:HGNC Symbol;Acc:607]
4	713	2.11	2e−16	3e−14	50 x 1	complement component 1, q subcomponent, B chain [Source
5	714	1.58	2e−16	3e−14	50 x 1	complement component 1, q subcomponent, C chain [Source
6	9560	1.24	2e−16	3e−14	32 x 1	chemokine (C−C motif) ligand 4−like 1 [Source:HGNC Symb
7	388372	1.22	2e−16	3e−14	32 x 1	chemokine (C−C motif) ligand 4−like 1 [Source:HGNC Symb
8	6352	1.62	2e−16	3e−14	48 x 1	chemokine (C−C motif) ligand 5 [Source:HGNC Symbol;Acc:
9	924	1.24	2e−16	3e−14	49 x 1	CD7 molecule [Source:HGNC Symbol;Acc:1695]
10	925	1.25	2e−16	3e−14	48 x 1	CD8a molecule [Source:HGNC Symbol;Acc:1706]
11	9076	−1.28	2e−16	3e−14	49 x 50	claudin 1 [Source:HGNC Symbol;Acc:2032]
12	3627	2.22	2e−16	3e−14	32 x 1	chemokine (C−X−C motif) ligand 10 [Source:HGNC Symbol;
13	6373	1.96	2e−16	3e−14	32 x 1	chemokine (C−X−C motif) ligand 11 [Source:HGNC Symbol;
14	4283	2.28	2e−16	3e−14	49 x 1	chemokine (C−X−C motif) ligand 9 [Source:HGNC Symbol;A
15	57007	1.5	2e−16	3e−14	14 x 50	atypical chemokine receptor 3 [Source:HGNC Symbol;Acc:23
16	3491	1.39	2e−16	3e−14	2 x 1	cysteine−rich, angiogenic inducer, 61 [Source:HGNC Symbol
17	1672	−1.58	2e−16	3e−14	1 x 50	defensin, beta 1 [Source:HGNC Symbol;Acc:2766]
18	414325	−1.33	2e−16	3e−14	1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
19	8632	1.24	2e−16	3e−14	1 x 8	dynein, axonemal, heavy chain 17 [Source:HGNC Symbol;A
20	1828	−1.69	2e−16	3e−14	1 x 48	desmoglein 1 [Source:HGNC Symbol;Acc:3048]



p−values

Global Geneset Analysis

Rank	GSZ	p−value	#all		Geneset
Overexpressed					
1	18.6	NULL	553	Cancer	Lembcke_Colonic Inflammation
2	17.09	NULL	265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
3	17.09	NULL	265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
4	17.09	NULL	265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
5	17.09	NULL	265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
6	17.06	NULL	51	BP	type I interferon signaling pathway
7	16.99	NULL	417	H.Tiss	WIRTH_Immune system
8	16.42	NULL	16	GSEA C2	MOSERLE_IFNA_RESPONSE
9	15.94	NULL	16	GSEA C2	UROSEVIC_RESPONSE_TO_IMIQUIMOD
10	15.92	NULL	312	BP	immune response
11	15.75	NULL	123	BP	defense response to virus
12	14.04	NULL	13	GSEA C2	BOWIE_RESPONSE_TO_TAMOXIFEN
13	13.44	NULL	204	BP	cytokine−mediated signaling pathway
14	13.31	NULL	16	GSEA C2	ZHANG_INTERFERON_RESPONSE
15	12.74	NULL	109	BP	response to virus
16	12.45	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
17	12.19	NULL	10	GSEA C2	BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
18	11.92	NULL	316	Cancer	SPANG_BCL6−index2
19	11.85	NULL	16	GSEA C2	EINAV_INTERFERON_SIGNATURE_IN_CANCER
20	11.78	NULL	14	Glio	Donson−immune cell intra signaling−associated with LTS in HGA
Underexpressed					
1	−6.64	NULL	714	Chr	Chr 6
2	−6.43	NULL	618	Chr	Chr 4
3	−6.3	NULL	135	H.Tiss	WIRTH_Mucosa
4	−5.43	NULL	630	Chr	Chr X
5	−5.27	NULL	92	BP	translational elongation
6	−5.22	NULL	19	BP	cellular amino acid biosynthetic process
7	−5.06	NULL	87	BP	translational termination
8	−5.05	NULL	1253	BP	small molecule metabolic process
9	−5	NULL	488	miRNA target starBase	hsa−miR−16
10	−4.95	NULL	81	BP	viral transcription
11	−4.91	NULL	456	miRNA target starBase	hsa−miR−130a
12	−4.9	NULL	11	GSEA C2	KEGG_DRUG_METABOLISM_CYTOCHROME_P450
13	−4.82	NULL	324	miRNA target starBase	hsa−miR−18a
14	−4.79	NULL	449	miRNA target starBase	hsa−miR−130b
15	−4.74	NULL	115	BP	nuclear−transcribed mRNA catabolic process, nonsense−mediated
16	−4.69	NULL	109	BP	SRP−dependent cotranslational protein targeting to membrane
17	−4.67	NULL	128	BP	translational initiation
18	−4.66	NULL	313	Glio	willscher_GBM_Verhaak−CL_expression_D_up
19	−4.66	NULL	313	Glio	willscher_GBM_Verhaak−MES_expression_D_down
20	−4.66	NULL	313	Glio	willscher_GBM_Verhaak−PNwt_expression_D_up

GW_196

Local Summary

%DE = 0.95

metagenes = 4

genes = 109

genes in genesets = 107

genes with fdr < 0.1 = 102 (102 + / 0 −)

genes with fdr < 0.05 = 102 (102 + / 0 −)

genes with fdr < 0.01 = 94 (94 + / 0 −)

<r> metagenes = 1

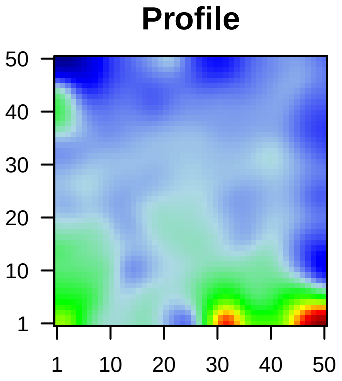
<r> genes = 0.49

<FC> = 0.89

<shrinkage−t> = 31.11

<p−value> = 0

<fdr> = 0.11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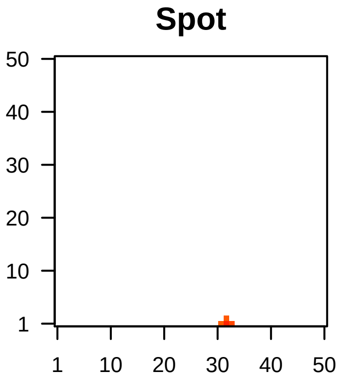
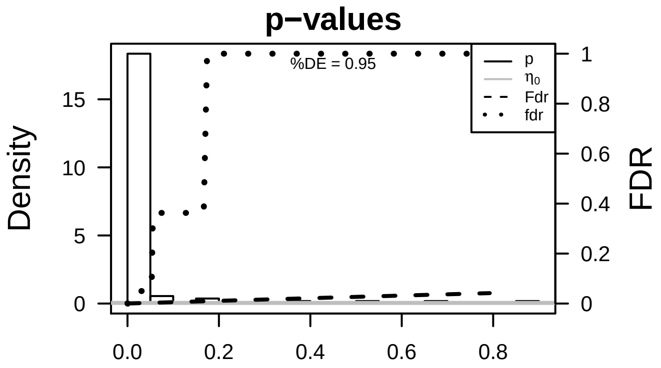

Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	9560	1.24	2e−16	5e−17	32 x 1	chemokine (C−C motif) ligand 4−like 1 [Source:HGNC Symbo
2	388372	1.22	2e−16	5e−17	32 x 1	chemokine (C−C motif) ligand 4−like 1 [Source:HGNC Symbo
3	3627	2.22	2e−16	5e−17	32 x 1	chemokine (C−X−C motif) ligand 10 [Source:HGNC Symbol;
4	6373	1.96	2e−16	5e−17	32 x 1	chemokine (C−X−C motif) ligand 11 [Source:HGNC Symbol;
5	94240	1.38	2e−16	5e−17	32 x 1	epithelial stromal interaction 1 (breast) [Source:HGNC Symbo
6	2633	1.45	2e−16	5e−17	32 x 1	guanylate binding protein 1, interferon−inducible [Source:HG
7	115362	1.73	2e−16	5e−17	32 x 1	guanylate binding protein 5 [Source:HGNC Symbol;Acc:1989
8	3430	1.34	2e−16	5e−17	32 x 1	interferon−induced protein 35 [Source:HGNC Symbol;Acc:53
9	10964	1.55	2e−16	5e−17	32 x 1	interferon−induced protein 44−like [Source:HGNC Symbol;Ac
10	2537	1.5	2e−16	5e−17	32 x 1	interferon, alpha−inducible protein 6 [Source:HGNC Symbol;
11	64135	1.33	2e−16	5e−17	32 x 1	interferon induced with helicase C domain 1 [Source:HGNC
12	3433	1.48	2e−16	5e−17	32 x 1	interferon−induced protein with tetratricopeptide repeats 2 [S
13	3437	1.23	2e−16	5e−17	32 x 1	interferon−induced protein with tetratricopeptide repeats 3 [S
14	3458	1.36	2e−16	5e−17	32 x 1	interferon, gamma [Source:HGNC Symbol;Acc:5438]
15	9636	1.57	2e−16	5e−17	32 x 1	ISG15 ubiquitin−like modifier [Source:HGNC Symbol;Acc:405
16	27074	1.34	2e−16	5e−17	32 x 1	lysosomal−associated membrane protein 3 [Source:HGNC S
17	4321	1.42	2e−16	5e−17	32 x 1	matrix metallopeptidase 12 (macrophage elastase) [Source:H
18	91543	1.48	2e−16	5e−17	32 x 1	radical S−adenosyl methionine domain containing 2 [Source:
19	51296	1.46	2e−16	5e−17	32 x 1	solute carrier family 15 (oligopeptide transporter), member 3 [
20	7453	1.5	2e−16	5e−17	32 x 1	tryptophanyl−tRNA synthetase [Source:HGNC Symbol;Acc:1


p−values

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	55.73	NULL	12 / 16	GSEA C2	MOSERLE_IFNA_RESPONSE
2	51.54	NULL	29 / 51	BP	type I interferon signaling pathway
3	47.8	NULL	9 / 10	GSEA C2	BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
4	43.64	NULL	10 / 13	GSEA C2	BOWIE_RESPONSE_TO_TAMOXIFEN
5	43.19	NULL	11 / 16	GSEA C2	EINAV_INTERFERON_SIGNATURE_IN_CANCER
6	41.83	NULL	11 / 16	GSEA C2	ZHANG_INTERFERON_RESPONSE
7	41.24	NULL	10 / 16	GSEA C2	UROSEVIC_RESPONSE_TO_IMIQUIMOD
8	40.63	NULL	8 / 11	GSEA C2	BENNETT_SYSTEMIC_LUPUS_ERYTHEMATOSUS
9	40.29	NULL	8 / 10	GSEA C2	GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
10	38.72	NULL	31 / 123	BP	defense response to virus
11	37.05	NULL	6 / 8	GSEA C2	ROETH_TERT_TARGETS_UP
12	35.1	NULL	27 / 109	BP	response to virus
13	33.56	NULL	6 / 14	GSEA C2	RADAEVA_RESPONSE_TO_IFNA1_UP
14	33.35	NULL	7 / 16	GSEA C2	MAHADEVAN_RESPONSE_TO_MP470_UP
15	33.2	NULL	13 / 31	BP	negative regulation of viral genome replication
16	33.05	NULL	3 / 4	GSEA C2	KRASNOSELSKAYA_ILF3_TARGETS_UP
17	28.93	NULL	34 / 204	BP	cytokine−mediated signaling pathway
18	28.59	NULL	6 / 14	Glio	Donson−immune cell intra signaling−associated with LTS in HGA
19	28.53	NULL	6 / 12	GSEA C2	TSAI_DNAJB4_TARGETS_UP
20	28.24	NULL	4 / 12	GSEA C2	ZHU_CMV_8_HR_UP
21	25.52	NULL	3 / 4	MMML CGS	MACIEJ_MMML 47
22	25.24	NULL	3 / 5	GSEA C2	KIM_LRRC3B_TARGETS
23	24.78	NULL	46 / 572	Disease	GUDJ_psoriasis up
24	24.76	NULL	6 / 14	GSEA C2	XU_AKT1_TARGETS_6HR
25	24.49	NULL	5 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
26	24.31	NULL	6 / 16	GSEA C2	XU_HGF_TARGETS_INDUCED_BY_AKT1_6HR
27	23.87	NULL	31 / 274	Lymphoma	SPANG_IL21 DN
28	23.73	NULL	6 / 6	Lymphoma	DAVE_MHCCII BL DN
29	23.47	NULL	16 / 60	BP	interferon−gamma−mediated signaling pathway
30	22.81	NULL	4 / 14	GSEA C2	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_8D_UP
31	22.16	NULL	4 / 10	GSEA C2	DAUER_STAT3_TARGETS_DN
32	20.06	NULL	5 / 16	GSEA C2	ZHAN_MULTIPLE_MYELOMA_LB_DN
33	19.83	NULL	3 / 9	GSEA C2	DER_IFN_ALPHA_RESPONSE_UP
34	19.83	NULL	3 / 9	GSEA C2	DER_IFN_GAMMA_RESPONSE_UP
35	19.69	NULL	7 / 10	CC	MHC class I protein complex
36	19.62	NULL	4 / 10	GSEA C2	GRANDVAUX_IRF3_TARGETS_UP
37	19.54	NULL	4 / 14	GSEA C2	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_3D_UP
38	19.47	NULL	4 / 16	GSEA C2	SEITZ_NEOPLASTIC_TRANSFORMATION_BY_8P_DELETION_
39	19.41	NULL	2 / 10	BP	positive regulation of cAMP−mediated signaling
40	18.88	NULL	4 / 14	GSEA C2	SANA_TNF_SIGNALING_UP

GW_196

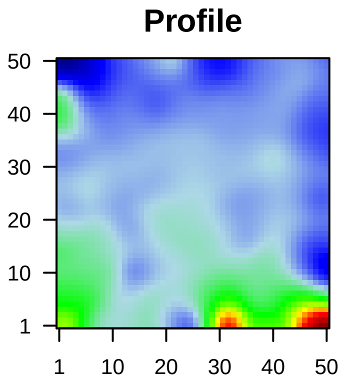
Local Summary

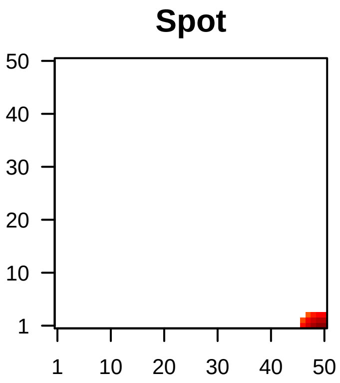
%DE = 0.91
metagenes = 14
genes = 247
genes in genesets = 245

genes with fdr < 0.1 = 205 (202 + / 3 −)
genes with fdr < 0.05 = 203 (200 + / 3 −)
genes with fdr < 0.01 = 183 (181 + / 2 −)

<r> metagenes = 0.99
<r> genes = 0.62

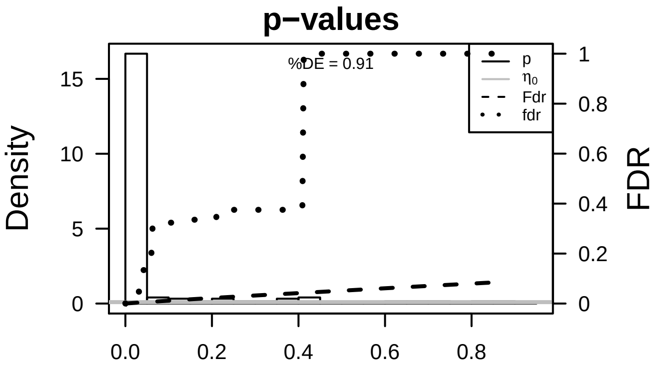
<FC> = 0.69
<shrinkage−t> = 24.3
<p−value> = 0
<fdr> = 0.22





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	341	1.37	2e−16	2e−16	50 x 1	apolipoprotein C−I [Source:HGNC Symbol;Acc:607]
2	713	2.11	2e−16	2e−16	50 x 1	complement component 1, q subcomponent, B chain [Source
3	714	1.58	2e−16	2e−16	50 x 1	complement component 1, q subcomponent, C chain [Source
4	6352	1.62	2e−16	2e−16	48 x 1	chemokine (C−C motif) ligand 5 [Source:HGNC Symbol;Acc:
5	924	1.24	2e−16	2e−16	49 x 1	CD7 molecule [Source:HGNC Symbol;Acc:1695]
6	925	1.25	2e−16	2e−16	48 x 1	CD8a molecule [Source:HGNC Symbol;Acc:1706]
7	4283	2.28	2e−16	2e−16	49 x 1	chemokine (C−X−C motif) ligand 9 [Source:HGNC Symbol;A
8	2207	1.27	2e−16	2e−16	50 x 1	Fc fragment of IgE, high affinity I, receptor for; gamma polype
9	10875	1.23	2e−16	2e−16	50 x 1	fibrinogen−like 2 [Source:HGNC Symbol;Acc:3696]
10	115361	1.32	2e−16	2e−16	48 x 1	guanylate binding protein 4 [Source:HGNC Symbol;Acc:2048
11	3001	1.57	2e−16	2e−16	48 x 1	granzyme A (granzyme 1, cytotoxic T−lymphocyte−associate
12	3002	1.92	2e−16	2e−16	49 x 1	granzyme B (granzyme 2, cytotoxic T−lymphocyte−associate
13	2999	1.46	2e−16	2e−16	47 x 1	granzyme H (cathepsin G−like 2, protein h−CCPX) [Source:H
14	84868	1.34	2e−16	2e−16	50 x 1	hepatitis A virus cellular receptor 2 [Source:HGNC Symbol;A
15	3109	1.46	2e−16	2e−16	50 x 1	major histocompatibility complex, class II, DM beta [Source:H
16	3113	1.4	2e−16	2e−16	50 x 1	major histocompatibility complex, class II, DP alpha 1 [Source
17	3620	2.29	2e−16	2e−16	48 x 1	indoleamine 2,3−dioxygenase 1 [Source:HGNC Symbol;Acc:
18	3543	1.18	2e−16	2e−16	49 x 1	immunoglobulin lambda−like polypeptide 1 [Source:HGNC Sy
19	3669	1.22	2e−16	2e−16	48 x 1	interferon stimulated exonuclease gene 20kDa [Source:HGN
20	3689	1.44	2e−16	2e−16	50 x 1	integrin, beta 2 (complement component 3 receptor 3 and 4 s



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	31.63	NULL	89 / 417	H.Tiss	WIRTH_Immune system
2	25.23	NULL	12 / 15	CC	MHC class II protein complex
3	24.67	NULL	7 / 11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
4	23.71	NULL	4 / 7	Glio	Donson−cytotoxic effectors−associated with LTS in HGA
5	23.05	NULL	89 / 553	Cancer	Lembcke_Colonic Inflammation
6	22.28	NULL	6 / 12	GSEA C2	BIOCARTA_CTL_PATHWAY
7	21.09	NULL	2 / 4	GSEA C2	REACTOME_CLASSICAL_ANTIBODY_MEDIATED_COMPLEMEN
8	20.96	NULL	50 / 312	BP	immune response
9	20.64	NULL	6 / 11	GSEA C2	BIOCARTA_THELPER_PATHWAY
10	19.48	NULL	3 / 5	GSEA C2	WONG_ENDOMETRIAL_CANCER_LATE
11	18.3	NULL	4 / 8	GSEA C2	GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_DN
12	18.19	NULL	39 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
13	18.19	NULL	39 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
14	18.19	NULL	39 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
15	18.19	NULL	39 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
16	17.51	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
17	17.44	NULL	7 / 13	Cancer	GENTLES_modul18
18	16.94	NULL	7 / 15	GSEA C2	FINAK_BREAST_CANCER_SDPP_SIGNATURE
19	16.62	NULL	17 / 74	BP	regulation of immune response
20	16.53	NULL	4 / 8	GSEA C2	NIELSEN_SYNOVIAL_SARCOMA_DN
21	16.44	NULL	14 / 47	BP	antigen processing and presentation
22	16.24	NULL	5 / 13	GSEA C2	HAHTOLA_CTCL_PATHOGENESIS
23	16.22	NULL	3 / 6	GSEA C2	SANA_RESPONSE_TO_IFNG_UP
24	16.03	NULL	4 / 16	BP	cytolysis
25	15.89	NULL	2 / 3	GSEA C2	KEGG_VIRAL_MYOCARDITIS
26	15.24	NULL	5 / 13	GSEA C2	BIOCARTA_IL17_PATHWAY
27	15.22	NULL	4 / 8	Glio	Donson−migration tethering and rolling−associated with LTS in HG
28	15.18	NULL	5 / 15	Glio	Donson−chemokines/cytokines−associated with LTS in HGA
29	15.1	NULL	2 / 7	GSEA C2	BIOCARTA_COMP_PATHWAY
30	14.81	NULL	4 / 10	GSEA C2	LEE_DIFFERENTIATING_T_LYMPHOCYTE
31	14.54	NULL	6 / 24	CC	immunological synapse
32	13.96	NULL	2 / 8	GSEA C2	BIOCARTA_CLASSIC_PATHWAY
33	13.96	NULL	2 / 8	GSEA C2	REACTOME_COMPLEMENT_CASCADE
34	13.96	NULL	2 / 8	GSEA C2	REACTOME_INITIAL_TRIGGERING_OF_COMPLEMENT
35	13.95	NULL	4 / 10	GSEA C2	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_
36	13.89	NULL	5 / 12	GSEA C2	ZHAN_MULTIPLE_MYELOMA_DN
37	13.65	NULL	16 / 60	BP	T cell costimulation
38	13.6	NULL	3 / 15	GSEA C2	HAHTOLA_SEZARY_SYNDROM_DN
39	13.49	NULL	5 / 12	BP	immunoglobulin mediated immune response
40	13.47	NULL	3 / 8	GSEA C2	LINDSTEDT_DENDRITIC_CELL_MATURATION_D

GW_196

Local Summary

%DE = 0.76

metagenes = 20

genes = 306

genes in genesets = 301

genes with fdr < 0.1 = 198 (27 + / 171 −)

genes with fdr < 0.05 = 174 (23 + / 151 −)

genes with fdr < 0.01 = 142 (18 + / 124 −)

<r> metagenes = 0.97

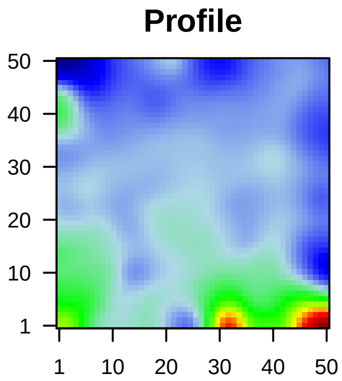
<r> genes = 0.41

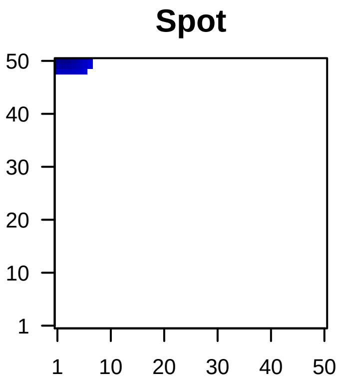
<FC> = −0.33

<shrinkage−t> = −11.61

<p−value> = 0

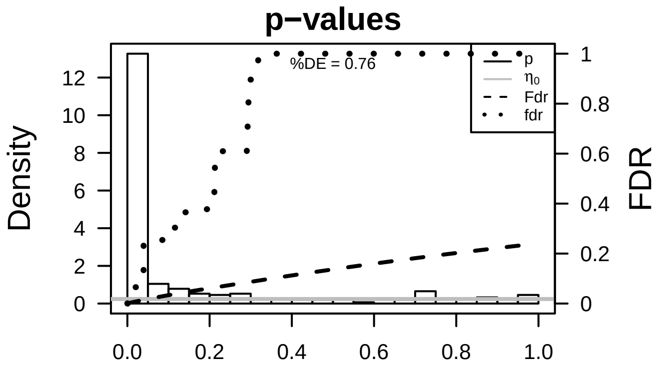
<fdr> = 0.42


Profile


Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	1672	−1.58	2e−16	2e−15	1 x 50	defensin, beta 1 [Source:HGNC Symbol;Acc:2766]
2	414325	−1.33	2e−16	2e−15	1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
3	1828	−1.69	2e−16	2e−15	1 x 48	desmoglein 1 [Source:HGNC Symbol;Acc:3048]
4	192666	−1.57	2e−16	2e−15	1 x 50	keratin 24 [Source:HGNC Symbol;Acc:18527]
5	5507	−1.38	2e−16	2e−15	3 x 50	protein phosphatase 1, regulatory subunit 3C [Source:HGNC
6	6286	−1.73	2e−16	2e−15	1 x 50	S100 calcium binding protein P [Source:HGNC Symbol;Acc:1
7	6947	−1.61	2e−16	2e−15	2 x 50	transcobalamin I (vitamin B12 binding protein, R binder family
8	7739	−1.39	2e−16	2e−15	1 x 50	zinc finger protein 185 (LIM domain) [Source:HGNC Symbol;
9	119391	−1.21	7e−16	2e−13	5 x 48	glutathione S−transferase omega 2 [Source:HGNC Symbol;A
10	144568	−1.17	4e−15	5e−12	1 x 50	alpha−2−macroglobulin−like 1 [Source:HGNC Symbol;Acc:23
11	144501	−1.11	1e−13	5e−12	1 x 49	keratin 80 [Source:HGNC Symbol;Acc:27056]
12	6337	−1.1	1e−13	5e−12	3 x 50	sodium channel, non−voltage−gated 1 alpha subunit [Source:
13	66004	−1.1	2e−13	2e−11	1 x 50	Ly6/neurotoxin 1 [Source:HGNC Symbol;Acc:29604]
14	2877	−1.08	4e−13	2e−11	1 x 50	glutathione peroxidase 2 (gastrointestinal) [Source:HGNC Sy
15	8644	−1.07	7e−13	1e−10	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
16	84648	−1.05	2e−12	2e−10	1 x 48	late cornified envelope 3D [Source:HGNC Symbol;Acc:16615
17	128876	−1.03	5e−12	3e−10	1 x 48	family with sequence similarity 83, member C [Source:HGNC
18	79852	−1.02	8e−12	2e−08	3 x 50	epoxide hydrolase 3 [Source:HGNC Symbol;Acc:23760]
19	5055	−0.95	2e−10	2e−08	1 x 50	serpin peptidase inhibitor, clade B (ovalbumin), member 2 [Sc
20	137797	−0.93	5e−10	2e−08	1 x 50	LY6/PLAUR domain containing 2 [Source:HGNC Symbol;Acc


p−values

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−24.07	NULL	82 / 135	H.Tiss	WIRTH_Mucosa
2	−12.22	NULL	6 / 13	BP	negative regulation of peptidase activity
3	−12.09	NULL	7 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
4	−11.86	NULL	15 / 21	CC	cornified envelope
5	−11.21	NULL	89 / 572	Disease	GUDJ_psoriasis up
6	−9.83	NULL	7 / 16	GSEA C2	JAEGER_METASTASIS_DN
7	−9.77	NULL	3 / 10	GSEA C2	REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION_
8	−9.71	NULL	5 / 10	GSEA C2	KEGG_LINOLEIC_ACID_METABOLISM
9	−9.21	NULL	3 / 16	CC	microvillus membrane
10	−9.11	NULL	6 / 15	GSEA C2	LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
11	−9.1	NULL	4 / 10	GSEA C2	SMID_BREAST_CANCER_ERBB2_UP
12	−9.02	NULL	2 / 11	MF	gamma−catenin binding
13	−8.89	NULL	4 / 13	GSEA C2	CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_
14	−8.82	NULL	1 / 5	GSEA C2	FERRARI_RESPONSE_TO_FENRETINIDE_DN
15	−8.77	NULL	4 / 14	GSEA C2	KIM_RESPONSE_TO_TSA_AND_DECITABINE_UP
16	−8.56	NULL	16 / 42	BP	keratinization
17	−8.42	NULL	5 / 21	CC	desmosome
18	−8.2	NULL	11 / 52	BP	negative regulation of endopeptidase activity
19	−8.2	NULL	3 / 11	GSEA C2	KEGG_DRUG_METABOLISM_CYTOCHROME_P450
20	−8.08	NULL	11 / 79	MF	serine−type endopeptidase inhibitor activity
21	−7.95	NULL	2 / 16	BP	cobalamin metabolic process
22	−7.8	NULL	20 / 53	BP	keratinocyte differentiation
23	−7.72	NULL	8 / 63	CC	Golgi lumen
24	−7.45	NULL	4 / 16	GSEA C2	COLDREN_GEFITINIB_RESISTANCE_DN
25	−7.45	NULL	3 / 13	GSEA C2	KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_
26	−7.34	NULL	4 / 16	GSEA C2	DAZARD_UV_RESPONSE_CLUSTER_G24
27	−7.25	NULL	1 / 7	GSEA C2	DASU_IL6_SIGNALING_DN
28	−7.11	NULL	4 / 23	MF	peptidase inhibitor activity
29	−6.98	NULL	2 / 22	BP	endothelial cell migration
30	−6.97	NULL	3 / 15	GSEA C2	VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_DN
31	−6.92	NULL	2 / 15	GSEA C2	STOSSI_RESPONSE_TO_ESTRADIOL
32	−6.89	NULL	5 / 34	MF	endopeptidase inhibitor activity
33	−6.88	NULL	1 / 11	GSEA C2	MURAKAMI_UV_RESPONSE_24HR
34	−6.78	NULL	3 / 14	GSEA C2	KOYAMA_SEMA3B_TARGETS_UP
35	−6.7	NULL	3 / 15	GSEA C2	MULLIGHAN_MLL_SIGNATURE_1_DN
36	−6.65	NULL	2 / 15	GSEA C2	LUI_THYROID_CANCER_CLUSTER_2
37	−6.6	NULL	2 / 15	BP	glycogen biosynthetic process
38	−6.54	NULL	2 / 12	MF	sodium channel activity
39	−6.4	NULL	1 / 13	GSEA C2	HAHTOLA_CTCL_PATHOGENESIS
40	−6.4	NULL	5 / 30	BP	excretion