GW_257

Global Summary

%DE = 0.14

genes with fdr < 0.2 = 1841 (1015 + / 826 −)

genes with fdr < 0.1 = 1451 (807 + / 644 −)

genes with fdr < 0.05 = 1180 (663 + / 517 −)

genes with fdr < 0.01 = 872 (490 + / 382 −)

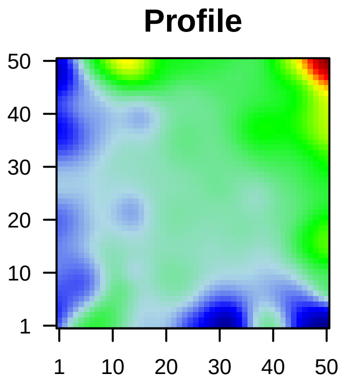
genes in genesets = 16332

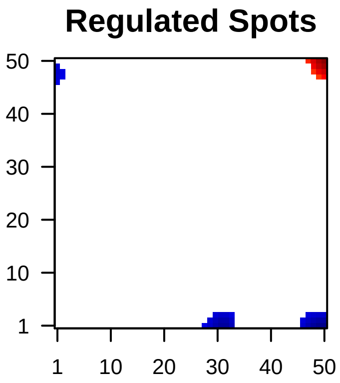
<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.1

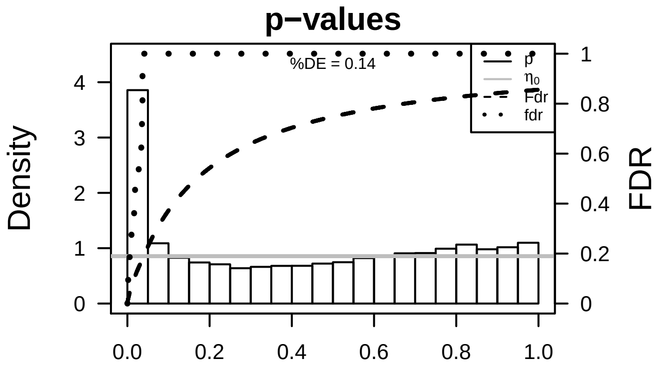
<fdr> = 0.86


Profile


Regulated Spots

Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	8745	1.81	2e−16	3e−14	50 x 50	ADAM metallopeptidase domain 23 [Source:HGNC Symbol;A
2	124	2.09	2e−16	3e−14	50 x 11	alcohol dehydrogenase 1A (class I), alpha polypeptide [Sourc
3	126	2.09	2e−16	3e−14	50 x 12	alcohol dehydrogenase 1C (class I), gamma polypeptide [Sou
4	57016	2.29	2e−16	3e−14	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
5	441282	2.14	2e−16	3e−14	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC S
6	1646	1.68	2e−16	3e−14	13 x 50	aldo−keto reductase family 1, member C2 [Source:HGNC Sy
7	8644	2.81	2e−16	3e−14	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
8	1109	2.91	2e−16	3e−14	13 x 50	aldo−keto reductase family 1, member C4 [Source:HGNC Sy
9	216	2.51	2e−16	3e−14	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGN
10	218	2.79	2e−16	3e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
11	501	−1.76	2e−16	3e−14	6 x 46	aldehyde dehydrogenase 7 family, member A1 [Source:HGN
12	84707	1.49	2e−16	3e−14	50 x 48	brain expressed X−linked 2 [Source:HGNC Symbol;Acc:3093
13	399948	2.29	2e−16	3e−14	50 x 15	colorectal cancer associated 1 [Source:HGNC Symbol;Acc:3
14	64073	−1.66	2e−16	3e−14	1 x 46	chromosome 19 open reading frame 33 [Source:HGNC Sym
15	339512	1.69	2e−16	3e−14	50 x 50	chromosome 1 open reading frame 110 [Source:HGNC Sym
16	205428	1.57	2e−16	3e−14	50 x 50	chromosome 3 open reading frame 58 [Source:HGNC Symb
17	29923	1.72	2e−16	3e−14	4 x 44	hypoxia inducible lipid droplet−associated [Source:HGNC Sy
18	375791	−1.47	2e−16	3e−14	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Sym
19	26256	1.62	2e−16	3e−14	50 x 50	calcium binding tyrosine−(Y)−phosphorylation regulated [Sou
20	1056	1.82	2e−16	3e−14	50 x 50	carboxyl ester lipase [Source:HGNC Symbol;Acc:1848]


p−values

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	9.43	NULL	519	Chr	Chr 14
2	9.13	NULL	914	Chr	Chr 3
3	8.83	NULL	8	GSEA C2	RUNNE_GENDER_EFFECT_UP
4	8.5	NULL	4640	CC	nucleus
5	8.45	NULL	386	Chr	Chr 22
6	8.24	NULL	1581	BP	regulation of transcription, DNA−dependent
7	8.19	NULL	7	MMML CGS	MACIEJ_MMML 5
8	8.17	NULL	1749	MF	DNA binding
9	7.46	NULL	1574	BP	transcription, DNA−templated
10	7.39	NULL	13	GSEA C2	SINGH_NFE2L2_TARGETS
11	7.11	NULL	940	MF	nucleic acid binding
12	6.99	NULL	436	miRNA target−starBase	hsa−miR−548n
13	6.99	NULL	34	BP	glutathione metabolic process
14	6.92	NULL	9	GSEA C2	REACTOME_ETHANOL_OXIDATION
15	6.92	NULL	235	miRNA target−starBase	hsa−miR−1252
16	6.89	NULL	603	miRNA target−starBase	hsa−miR−20a
17	6.85	NULL	34	Chr	Chr Y
18	6.76	NULL	463	miRNA target−starBase	hsa−miR−301a
19	6.67	NULL	7	GSEA C2	FREDERICK_PRKCI_TARGETS
20	6.58	NULL	315	miRNA target−starBase	hsa−miR−30e
Underexpressed					
1	−14.75	NULL	717	Chr	Chr 16
2	−13.03	NULL	312	BP	immune response
3	−11.84	NULL	572	Disease	GUDJ_psoriasis up
4	−11.35	NULL	21	CC	cornified envelope
5	−10.9	NULL	51	BP	type I interferon signaling pathway
6	−10.4	NULL	42	BP	keratinization
7	−10.04	NULL	553	Cancer	Lembcke_Colonic Inflammation
8	−9.4	NULL	1720	Chr	Chr 1
9	−9.04	NULL	135	H.Tiss	WIRTH_Mucosa
10	−8.48	NULL	10	BP	cellular response to zinc ion
11	−8.25	NULL	7	MMML CGS	MACIEJ_MMML 13
12	−7.99	NULL	47	BP	antigen processing and presentation
13	−7.83	NULL	15	GSEA C2	LIANG_SILENCED_BY_METHYLATION_2
14	−7.78	NULL	204	BP	cytokine−mediated signaling pathway
15	−7.76	NULL	60	BP	interferon−gamma−mediated signaling pathway
16	−7.65	NULL	417	H.Tiss	WIRTH_Immune system
17	−7.49	NULL	31	BP	negative regulation of viral genome replication
18	−7.45	NULL	13	GSEA C2	BOWIE_RESPONSE_TO_TAMOXIFEN
19	−7.42	NULL	16	GSEA C2	UROSEVIC_RESPONSE_TO_IMIQUIMOD
20	−7.36	NULL	43	MF	chemokine activity

GW_257

Local Summary

%DE = 0.85

metagenes = 12

genes = 192

genes in genesets = 190

genes with fdr < 0.1 = 132 (130 + / 2 −)

genes with fdr < 0.05 = 128 (126 + / 2 −)

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

<r> metagenes = 0.97

<r> genes = 0.28

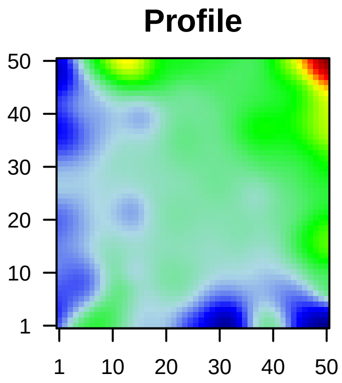
<FC> = 0.7

<shrinkage−t> = 24.46

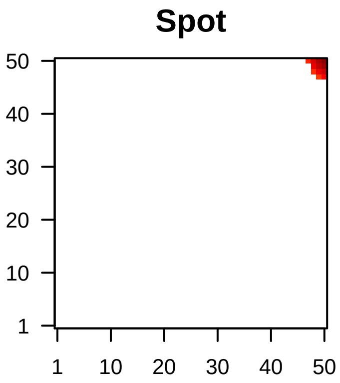
<p−value> = 0

<fdr> = 0.34

Profile



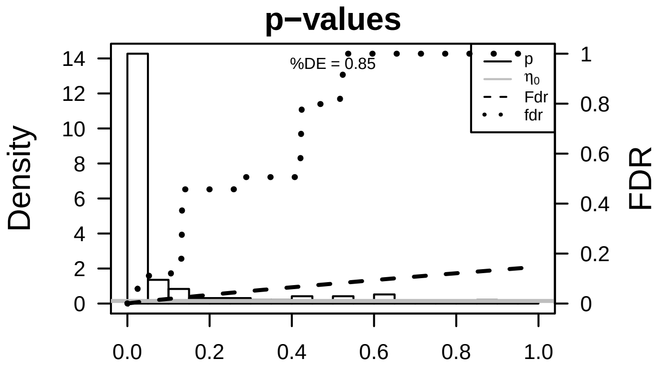
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	8745	1.81	2e−16	3e−16	50 x 50	ADAM metallopeptidase domain 23 [Source:HGNC Symbol;A
2	216	2.51	2e−16	3e−16	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGN
3	84707	1.49	2e−16	3e−16	50 x 48	brain expressed X−linked 2 [Source:HGNC Symbol;Acc:3093
4	339512	1.69	2e−16	3e−16	50 x 50	chromosome 1 open reading frame 110 [Source:HGNC Sym
5	205428	1.57	2e−16	3e−16	50 x 50	chromosome 3 open reading frame 58 [Source:HGNC Symb
6	26256	1.62	2e−16	3e−16	50 x 50	calcium binding tyrosine−(Y)−phosphorylation regulated [Sou
7	1056	1.82	2e−16	3e−16	50 x 50	carboxyl ester lipase [Source:HGNC Symbol;Acc:1848]
8	26047	2.11	2e−16	3e−16	50 x 50	contactin associated protein−like 2 [Source:HGNC Symbol;A
9	10655	1.47	2e−16	3e−16	50 x 50	doublesex and mab−3 related transcription factor 2 [Source:H
10	2938	2.87	2e−16	3e−16	50 x 50	glutathione S−transferase alpha 2 [Source:HGNC Symbol;Ac
11	3866	2.62	2e−16	3e−16	50 x 50	keratin 15 [Source:HGNC Symbol;Acc:6421]
12	3880	2.02	2e−16	3e−16	50 x 49	keratin 19 [Source:HGNC Symbol;Acc:6436]
13	3856	1.56	2e−16	3e−16	50 x 48	keratin 8 pseudogene 3 [Source:HGNC Symbol;Acc:31056]
14	80896	1.75	2e−16	3e−16	50 x 50	N−acetylneuraminate pyruvate lyase (dihydrodipicolinate synt
15	4915	1.61	2e−16	3e−16	50 x 50	neurotrophic tyrosine kinase, receptor, type 2 [Source:HGNC
16	4922	2.23	2e−16	3e−16	50 x 50	neurotensin [Source:HGNC Symbol;Acc:8038]
17	139728	1.73	2e−16	3e−16	49 x 49	pregnancy up−regulated nonubiquitous CaM kinase [Source:
18	11166	1.64	2e−16	3e−16	50 x 50	SRY (sex determining region Y)−box 21 [Source:HGNC Sym
19	7358	1.44	2e−16	3e−16	50 x 50	UDP−glucose 6−dehydrogenase [Source:HGNC Symbol;Acc
20	256764	1.81	2e−16	3e−16	50 x 50	WD repeat domain 72 [Source:HGNC Symbol;Acc:26790]

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	24.98	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
2	16.13	NULL	2 / 7	GSEA C2	MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
3	15.36	NULL	4 / 13	BP	regulation of blood vessel size
4	13.94	NULL	3 / 16	GSEA C2	BOYAULT_LIVER_CANCER_SUBCLASS_G1_DN
5	13.43	NULL	8 / 34	BP	glutathione metabolic process
6	12.98	NULL	4 / 15	GSEA C2	REACTOME_GLUTATHIONE_CONJUGATION
7	12.63	NULL	3 / 11	GSEA C2	ITO_PTTG1_TARGETS_UP
8	12.45	NULL	2 / 7	GSEA C2	FREDERICK_PRKCI_TARGETS
9	12.13	NULL	1 / 6	GSEA C2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_D_DN
10	12.13	NULL	1 / 6	GSEA C2	KAPOSI_LIVER_CANCER_POOR_SURVIVAL_DN
11	11.18	NULL	4 / 15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
12	11.06	NULL	3 / 9	GSEA C2	BROWNE_HCMV_INFECTION_8HR_UP
13	10.85	NULL	2 / 12	BP	cellular aldehyde metabolic process
14	10.85	NULL	3 / 12	GSEA C2	BROCKE_APOPTOSIS_REVERSED_BY_IL6
15	10.75	NULL	2 / 9	GSEA C2	REACTOME_GLUCURONIDATION
16	10.7	NULL	1 / 2	GSEA C2	KUROKAWA_LIVER_CANCER_EARLY_RECURRENCE_UP
17	10.45	NULL	2 / 10	GSEA C2	HANN_RESISTANCE_TO_BCL2_INHIBITOR_DN
18	10.26	NULL	6 / 25	BP	glutathione derivative biosynthetic process
19	10.15	NULL	11 / 119	BP	xenobiotic metabolic process
20	9.51	NULL	1 / 9	GSEA C2	ABDULRAHMAN_KIDNEY_CANCER_VHL_DN
21	9.51	NULL	1 / 9	GSEA C2	REACTOME_ETHANOL_OXIDATION
22	8.94	NULL	1 / 10	GSEA C2	MAINA_VHL_TARGETS_UP
23	8.94	NULL	1 / 10	GSEA C2	FRIDMAN_SENESCENCE_DN
24	8.92	NULL	2 / 10	GSEA C2	CERVERA_SDHB_TARGETS_1_DN
25	8.9	NULL	5 / 20	MF	glutathione transferase activity
26	8.56	NULL	2 / 18	MF	acyl−CoA dehydrogenase activity
27	8.16	NULL	2 / 10	GSEA C2	KEGG_ASCORBATE_AND_ALDARATE_METABOLISM
28	7.84	NULL	2 / 16	GSEA C2	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_
29	7.82	NULL	1 / 4	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_13
30	7.71	NULL	2 / 12	BP	glutamate metabolic process
31	7.61	NULL	2 / 6	GSEA C2	YAGUE_PRETUMOR_DRUG_RESISTANCE_UP
32	7.48	NULL	3 / 48	BP	cerebral cortex development
33	7.48	NULL	1 / 11	Glio	neurons_glio
34	7.39	NULL	1 / 10	GSEA C2	YAMASHITA_LIVER_CANCER_WITH_EPCAM_DN
35	7.35	NULL	2 / 13	GSEA C2	SINGH_NFE2L2_TARGETS
36	7.34	NULL	1 / 15	H.Tiss	WIRTH_Cerebellum
37	7.32	NULL	1 / 8	GSEA C2	KEGG_GLYCEROLIPID_METABOLISM
38	7.32	NULL	2 / 12	BP	response to arsenic−containing substance
39	7.31	NULL	1 / 14	MF	Ras GTPase activator activity
40	7.31	NULL	1 / 14	GSEA C2	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINE

GW_257

Local Summary

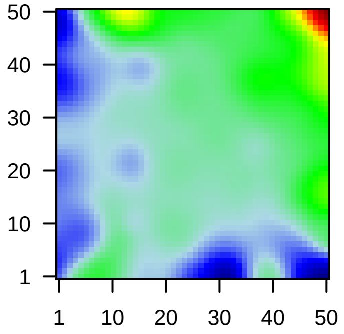
%DE = 0.9
metagenes = 15
genes = 160
genes in genesets = 157

genes with fdr < 0.1 = 126 (1 + / 125 −)
genes with fdr < 0.05 = 112 (1 + / 111 −)
genes with fdr < 0.01 = 94 (1 + / 93 −)

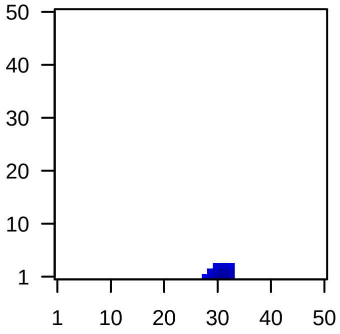
<r> metagenes = 0.94
<r> genes = 0.37

<FC> = −0.56
<shrinkage−t> = −19.62
<p−value> = 0
<fdr> = 0.37

Profile

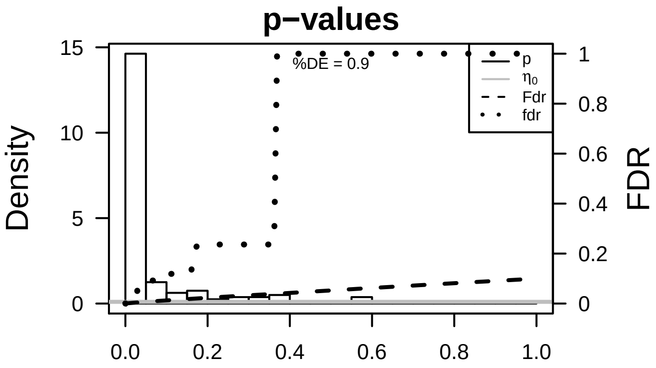


Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	3106	−1.57	2e−16	1e−15	32 x 1	major histocompatibility complex, class I, B [Source:HGNC Sy
2	9636	−1.67	2e−16	1e−15	32 x 1	ISG15 ubiquitin−like modifier [Source:HGNC Symbol;Acc:405
3	4599	−1.35	2e−16	1e−15	32 x 1	myxovirus (influenza virus) resistance 1, interferon−inducible
4	684	−1.4	4e−16	3e−13	32 x 1	bone marrow stromal cell antigen 2 [Source:HGNC Symbol;A
5	3136	−1.32	2e−14	1e−11	32 x 1	
6	629	−1.24	6e−13	3e−11	32 x 1	complement factor B [Source:HGNC Symbol;Acc:1037]
7	10866	−1.21	2e−12	3e−11	32 x 1	HLA complex P5 (non−protein coding) [Source:HGNC Symbo
8	10561	−1.2	4e−12	5e−11	32 x 1	interferon−induced protein 44 [Source:HGNC Symbol;Acc:16
9	2537	−1.18	7e−12	6e−10	32 x 1	interferon, alpha−inducible protein 6 [Source:HGNC Symbol;
10	3134	−1.14	5e−11	1e−09	32 x 1	major histocompatibility complex, class I, F [Source:HGNC Sy
11	10410	−1.01	2e−10	1e−09	32 x 1	interferon induced transmembrane protein 3 [Source:HGNC S
12	10581	−1	3e−10	1e−09	32 x 1	interferon induced transmembrane protein 2 [Source:HGNC S
13	9560	−1.09	3e−10	7e−09	32 x 1	chemokine (C−C motif) ligand 4−like 1 [Source:HGNC Symbo
14	51191	−1.05	1e−09	7e−09	32 x 1	HECT and RLD domain containing E3 ubiquitin protein ligase
15	94240	−1.04	1e−09	7e−09	32 x 1	epithelial stromal interaction 1 (breast) [Source:HGNC Symbo
16	6890	−1.04	2e−09	9e−09	32 x 1	transporter 1, ATP−binding cassette, sub−family B (MDR/TAP
17	8519	−1.03	2e−09	3e−08	32 x 1	interferon induced transmembrane protein 1 [Source:HGNC S
18	10964	−1.02	4e−09	7e−08	32 x 1	interferon−induced protein 44−like [Source:HGNC Symbol;Ac
19	85441	−0.99	1e−08	7e−08	32 x 1	helicase with zinc finger 2, transcriptional coactivator [Source
20	3665	−0.98	1e−08	7e−08	32 x 1	interferon regulatory factor 7 [Source:HGNC Symbol;Acc:612



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−50.95	NULL	29 / 51	BP	type I interferon signaling pathway
2	−43.55	NULL	9 / 10	GSEA C2	BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
3	−41.2	NULL	6 / 6	Lymphoma	DAVE_MHCCII BL DN
4	−38.95	NULL	10 / 13	GSEA C2	BOWIE_RESPONSE_TO_TAMOXIFEN
5	−36.93	NULL	13 / 16	GSEA C2	MOSERLE_IFNA_RESPONSE
6	−36.63	NULL	8 / 10	GSEA C2	GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
7	−36.09	NULL	11 / 16	GSEA C2	EINAV_INTERFERON_SIGNATURE_IN_CANCER
8	−36.08	NULL	11 / 16	GSEA C2	ZHANG_INTERFERON_RESPONSE
9	−35.71	NULL	6 / 8	GSEA C2	ROETH_TERT_TARGETS_UP
10	−35.47	NULL	7 / 10	CC	MHC class I protein complex
11	−34.64	NULL	11 / 16	GSEA C2	UROSEVIC_RESPONSE_TO_IMIQUIMOD
12	−34.25	NULL	14 / 31	BP	negative regulation of viral genome replication
13	−33.35	NULL	8 / 11	GSEA C2	BENNETT_SYSTEMIC_LUPUS_ERYTHEMATOSUS
14	−31.66	NULL	3 / 4	GSEA C2	KRASNOSELSKAYA_ILF3_TARGETS_UP
15	−31.44	NULL	3 / 5	GSEA C2	KIM_LRRC3B_TARGETS
16	−29.24	NULL	8 / 18	BP	positive regulation of T cell mediated cytotoxicity
17	−29.12	NULL	31 / 123	BP	defense response to virus
18	−28.37	NULL	27 / 109	BP	response to virus
19	−27.34	NULL	34 / 204	BP	cytokine−mediated signaling pathway
20	−26.29	NULL	2 / 2	MMML CGS	MACIEJ_MMML 27
21	−25.8	NULL	7 / 18	MF	peptide antigen binding
22	−23.93	NULL	6 / 16	GSEA C2	XU_HGF_TARGETS_INDUCED_BY_AKT1_6HR
23	−22.46	NULL	6 / 12	GSEA C2	TSAI_DNAJB4_TARGETS_UP
24	−22.4	NULL	16 / 60	BP	interferon−gamma−mediated signaling pathway
25	−22.2	NULL	6 / 14	GSEA C2	XU_AKT1_TARGETS_6HR
26	−22.19	NULL	5 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
27	−22.04	NULL	6 / 14	GSEA C2	RADAEVA_RESPONSE_TO_IFNA1_UP
28	−21.9	NULL	4 / 10	GSEA C2	DAUER_STAT3_TARGETS_DN
29	−20.94	NULL	3 / 4	MMML CGS	MACIEJ_MMML 47
30	−20.9	NULL	4 / 15	GSEA C2	BECKER_TAMOXIFEN_RESISTANCE_UP
31	−20.34	NULL	5 / 16	GSEA C2	ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_UP
32	−19.87	NULL	7 / 16	GSEA C2	MAHADEVAN_RESPONSE_TO_MP470_UP
33	−19.49	NULL	5 / 18	BP	response to interferon−gamma
34	−18.82	NULL	13 / 70	BP	antigen processing and presentation of exogenous peptide antigen
35	−18.5	NULL	4 / 14	GSEA C2	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_8D_UP
36	−18.26	NULL	5 / 23	CC	integral to lumenal side of endoplasmic reticulum membrane
37	−18.25	NULL	13 / 74	BP	antigen processing and presentation of exogenous peptide antigen
38	−18.01	NULL	33 / 274	Lymphoma	SPANG_IL21 DN
39	−17.72	NULL	6 / 32	CC	ER to Golgi transport vesicle membrane
40	−17.68	NULL	50 / 572	Disease	GUDJ_psoriasis up

GW_257

Local Summary

%DE = 0.88

metagenes = 14

genes = 247

genes in genesets = 245

genes with fdr < 0.1 = 202 (6 + / 196 −)

genes with fdr < 0.05 = 159 (5 + / 154 −)

genes with fdr < 0.01 = 100 (3 + / 97 −)

<r> metagenes = 0.99

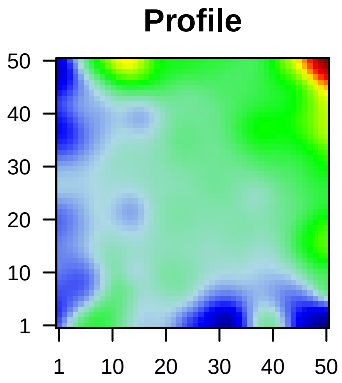
<r> genes = 0.62

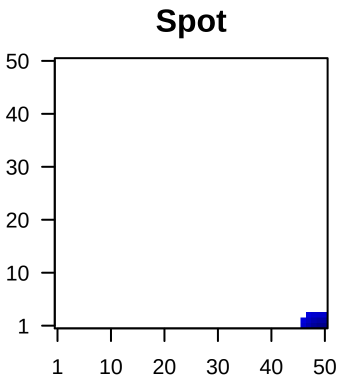
<FC> = −0.41

<shrinkage−t> = −14.32

<p−value> = 0

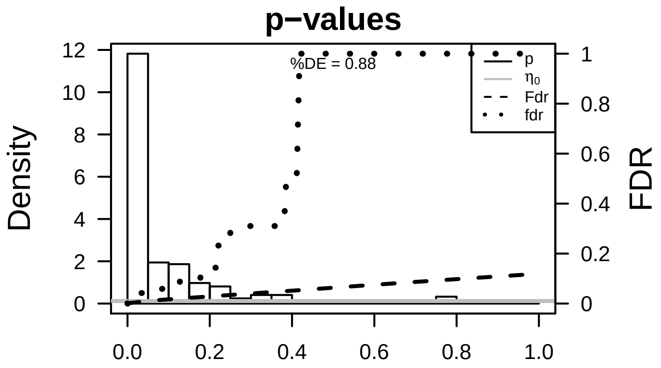
<fdr> = 0.53





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	3543	−1.57	2e−16	7e−15	49 x 1	immunoglobulin lambda−like polypeptide 1 [Source:HGNC Sy
2	3512	−1.38	1e−15	5e−12	50 x 1	immunoglobulin J polypeptide, linker protein for immunoglobu
3	57172	−1.26	3e−13	5e−12	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
4	260436	−1.26	4e−13	7e−11	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symbo
5	3059	1.21	3e−12	2e−09	50 x 1	hematopoietic cell−specific Lyn substrate 1 [Source:HGNC Sy
6	54855	−1.11	1e−10	2e−09	49 x 1	family with sequence similarity 46, member C [Source:HGNC
7	51755	−1.11	1e−10	2e−09	49 x 1	cyclin−dependent kinase 12 [Source:HGNC Symbol;Acc:242
8	5920	−1.1	2e−10	3e−08	48 x 1	retinoic acid receptor responder (tazarotene induced) 3 [Sour
9	3108	−1.05	1e−09	5e−08	50 x 1	major histocompatibility complex, class II, DM alpha [Source:
10	4067	1.01	4e−09	5e−08	46 x 2	v−yes−1 Yamaguchi sarcoma viral related oncogene homolo
11	10537	−1.01	4e−09	4e−07	50 x 1	ubiquitin D [Source:HGNC Symbol;Acc:18795]
12	972	−0.96	3e−08	4e−07	50 x 1	CD74 molecule, major histocompatibility complex, class II inv
13	9235	−0.95	3e−08	9e−07	46 x 1	interleukin 32 [Source:HGNC Symbol;Acc:16830]
14	6363	−0.92	9e−08	9e−07	50 x 1	chemokine (C−C motif) ligand 19 [Source:HGNC Symbol;Acc
15	3575	−0.92	9e−08	1e−06	50 x 2	interleukin 7 receptor [Source:HGNC Symbol;Acc:6024]
16	3002	−0.91	1e−07	2e−06	49 x 1	granzyme B (granzyme 2, cytotoxic T−lymphocyte−associate
17	3120	−0.89	3e−07	2e−06	47 x 1	major histocompatibility complex, class II, DQ beta 2 [Source:
18	3128	−0.88	3e−07	2e−06	50 x 1	major histocompatibility complex, class II, DR beta 6 (pseudo
19	3109	−0.88	3e−07	8e−06	50 x 1	major histocompatibility complex, class II, DM beta [Source:H
20	3113	−0.85	1e−06	8e−06	50 x 1	major histocompatibility complex, class II, DP alpha 1 [Source



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−36.74	NULL	12 / 15	CC	MHC class II protein complex
2	−26.76	NULL	89 / 417	H.Tiss	WIRTH_Immune system
3	−24.02	NULL	50 / 312	BP	immune response
4	−22.84	NULL	89 / 553	Cancer	Lembcke_Colonic Inflammation
5	−20.82	NULL	3 / 6	GSEA C2	SANA_RESPONSE_TO_IFNG_UP
6	−20.23	NULL	4 / 8	GSEA C2	GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_DN
7	−19.53	NULL	14 / 47	BP	antigen processing and presentation
8	−18.56	NULL	3 / 7	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
9	−18.36	NULL	2 / 4	MMML CGS	MACIEJ_MMML 2
10	−18.25	NULL	2 / 3	GSEA C2	KEGG_VIRAL_MYOCARDITIS
11	−18.24	NULL	7 / 21	CC	clathrin−coated endocytic vesicle membrane
12	−17.89	NULL	3 / 5	GSEA C2	WONG_ENDOMETRIAL_CANCER_LATE
13	−17.35	NULL	7 / 23	CC	integral to lumenal side of endoplasmic reticulum membrane
14	−15.85	NULL	5 / 12	BP	dendritic cell chemotaxis
15	−15.57	NULL	7 / 28	CC	transport vesicle membrane
16	−15.54	NULL	6 / 12	GSEA C2	BIOCARTA_CTL_PATHWAY
17	−15.47	NULL	2 / 4	GSEA C2	KEGG_LEISHMANIA_INFECTION
18	−15.46	NULL	39 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
19	−15.46	NULL	39 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
20	−15.46	NULL	39 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
21	−15.46	NULL	39 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
22	−15.43	NULL	16 / 60	BP	T cell costimulation
23	−14.94	NULL	5 / 12	BP	immunoglobulin mediated immune response
24	−14.7	NULL	13 / 87	BP	antigen processing and presentation of exogenous peptide antigen
25	−14.46	NULL	7 / 32	CC	ER to Golgi transport vesicle membrane
26	−14.16	NULL	7 / 11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
27	−13.96	NULL	5 / 17	BP	positive regulation of neutrophil chemotaxis
28	−13.76	NULL	7 / 35	CC	trans−Golgi network membrane
29	−13.68	NULL	5 / 15	Glio	Donson−chemokines/cytokines−associated with LTS in HGA
30	−13.67	NULL	8 / 52	Chr	Chr HSCHR6_MHC_QBL
31	−13.66	NULL	7 / 15	GSEA C2	FINAK_BREAST_CANCER_SDPP_SIGNATURE
32	−13.63	NULL	17 / 74	BP	regulation of immune response
33	−13.59	NULL	1 / 2	GSEA C2	KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUCT
34	−13.59	NULL	1 / 2	GSEA C2	KEGG_AUTOIMMUNE_THYROID_DISEASE
35	−13.59	NULL	1 / 2	GSEA C2	KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS
36	−13.58	NULL	15 / 84	BP	T cell receptor signaling pathway
37	−13.17	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
38	−13.08	NULL	3 / 8	GSEA C2	LINDSTEDT_DENDRITIC_CELL_MATURATION_D
39	−12.96	NULL	6 / 11	GSEA C2	BIOCARTA_THELPER_PATHWAY
40	−12.63	NULL	5 / 13	GSEA C2	HAHTOLA_CTCL_PATHOGENESIS

GW_257

Local Summary

%DE = 0.87

metagenes = 6

genes = 92

genes in genesets = 89

genes with fdr < 0.1 = 72 (9 + / 63 −)

genes with fdr < 0.05 = 72 (9 + / 63 −)

genes with fdr < 0.01 = 60 (6 + / 54 −)

<r> metagenes = 0.98

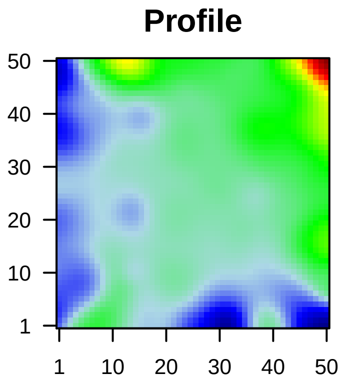
<r> genes = 0.52

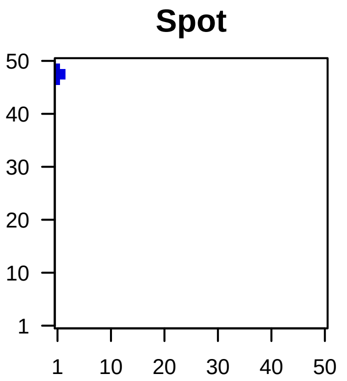
<FC> = −0.63

<shrinkage−t> = −22.08

<p−value> = 0

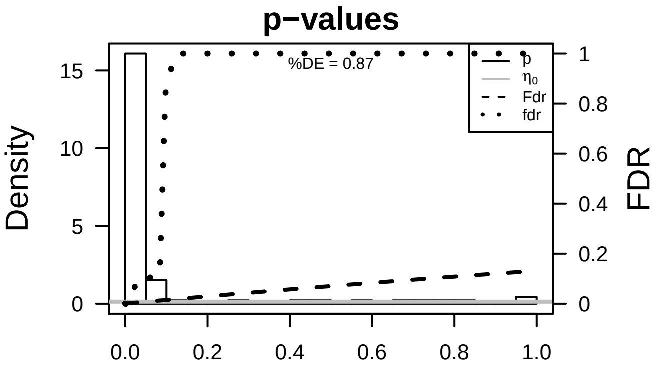
<fdr> = 0.25





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	441282	2.14	2e−16	2e−16	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC Sy
2	64073	−1.66	2e−16	2e−16	1 x 46	chromosome 19 open reading frame 33 [Source:HGNC Symb
3	414325	−1.51	2e−16	2e−16	1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
4	1673	−1.91	2e−16	2e−16	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
5	5650	−1.52	2e−16	2e−16	1 x 49	kallikrein−related peptidase 7 [Source:HGNC Symbol;Acc:63
6	84648	−1.86	2e−16	2e−16	1 x 48	late cornified envelope 3D [Source:HGNC Symbol;Acc:16615
7	5266	−1.36	2e−16	2e−16	1 x 49	peptidase inhibitor 3, skin−derived [Source:HGNC Symbol;Ac
8	6278	−2.67	2e−16	2e−16	1 x 49	S100 calcium binding protein A7 [Source:HGNC Symbol;Acc:
9	338324	−1.89	2e−16	2e−16	1 x 48	S100 calcium binding protein A7A [Source:HGNC Symbol;Ac
10	374897	−2.45	2e−16	2e−16	1 x 49	suprabasin [Source:HGNC Symbol;Acc:24950]
11	6590	−1.87	2e−16	2e−16	1 x 49	secretory leukocyte peptidase inhibitor [Source:HGNC Symb
12	6701	−1.45	2e−16	2e−16	1 x 49	small proline−rich protein 2B [Source:HGNC Symbol;Acc:112
13	6706	−2.11	2e−16	2e−16	1 x 48	small proline−rich protein 2G [Source:HGNC Symbol;Acc:112
14	1828	−1.34	7e−15	1e−12	1 x 48	desmoglein 1 [Source:HGNC Symbol;Acc:3048]
15	115572	−1.29	9e−14	6e−12	1 x 48	family with sequence similarity 46, member B [Source:HGNC
16	55894	−1.23	9e−13	6e−12	1 x 47	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
17	387695	−1.23	1e−12	1e−10	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Symb
18	84659	−1.16	2e−11	1e−10	1 x 48	ribonuclease, RNase A family, 7 [Source:HGNC Symbol;Acc:
19	3848	−1.16	2e−11	1e−10	1 x 47	keratin 1 [Source:HGNC Symbol;Acc:6412]
20	26525	−1.15	2e−11	5e−10	1 x 49	interleukin 36 receptor antagonist [Source:HGNC Symbol;Acc



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−24.85	NULL	8 / 21	CC	cornified envelope
2	−22.01	NULL	4 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
3	−21.26	NULL	3 / 15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
4	−20.07	NULL	8 / 42	BP	keratinization
5	−19.57	NULL	2 / 8	GSEA C2	MCLACHLAN_DENTAL_CARIES_UP
6	−19.3	NULL	12 / 76	BP	epidermis development
7	−19	NULL	29 / 135	H.Tiss	WIRTH_Mucosa
8	−18.62	NULL	3 / 16	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_DN
9	−18.18	NULL	2 / 9	GSEA C2	MCLACHLAN_DENTAL_CARIES_DN
10	−18.11	NULL	3 / 10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
11	−18.06	NULL	48 / 572	Disease	GUDJ_psoriasis up
12	−17.71	NULL	11 / 53	BP	keratinocyte differentiation
13	−17.03	NULL	2 / 10	GSEA C2	NIKOLSKY_BREAST_CANCER_20Q12_Q13_AMPLICON
14	−16.06	NULL	2 / 11	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_BONE_DN
15	−14.93	NULL	3 / 10	MF	RAGE receptor binding
16	−14.77	NULL	3 / 15	GSEA C2	LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
17	−14.52	NULL	2 / 13	GSEA C2	CHARAFE_BREAST_CANCER_LUMINAL_VS_BASAL_DN
18	−14.52	NULL	2 / 13	GSEA C2	HAN_SATB1_TARGETS_DN
19	−13.69	NULL	3 / 13	GSEA C2	FARMER_BREAST_CANCER_APOCRINE VS LUMINAL
20	−13.32	NULL	2 / 15	GSEA C2	SMID_BREAST_CANCER_LUMINAL_B_DN
21	−13.06	NULL	5 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
22	−12.09	NULL	3 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
23	−12.09	NULL	3 / 16	GSEA C2	JAEGER_METASTASIS_DN
24	−11.72	NULL	3 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_DN
25	−11.35	NULL	6 / 21	CC	desmosome
26	−11.1	NULL	1 / 16	BP	response to reactive oxygen species
27	−10.92	NULL	2 / 16	GSEA C2	DOANE_BREAST_CANCER_ESR1_DN
28	−10.92	NULL	2 / 16	GSEA C2	LEE_LIVER_CANCER_MYC_TGFA_UP
29	−10.92	NULL	2 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
30	−10.36	NULL	3 / 16	GSEA C2	HAHTOLA_MYCOSIS_FUNGOIDES_SKIN_DN
31	−10.36	NULL	2 / 23	MF	peptidase inhibitor activity
32	−10.03	NULL	1 / 19	BP	defense response to Gram−negative bacterium
33	−8.86	NULL	1 / 11	GSEA C2	MISSIAGLIA_REGULATED_BY_METHYLATION_UP
34	−8.66	NULL	2 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
35	−8.57	NULL	4 / 10	GSEA C2	REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION_P
36	−8.52	NULL	6 / 52	BP	negative regulation of endopeptidase activity
37	−8.43	NULL	2 / 10	GSEA C2	SMID_BREAST_CANCER_ERBB2_UP
38	−8.25	NULL	2 / 34	MF	endopeptidase inhibitor activity
39	−8.24	NULL	2 / 15	GSEA C2	KARAKAS_TGFB1_SIGNALING
40	−8.12	NULL	3 / 15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL