GW_122

Global Summary

%DE = 0.14

genes with fdr < 0.2 = 1846 (1001 + / 845 −)

genes with fdr < 0.1 = 1423 (778 + / 645 −)

genes with fdr < 0.05 = 1169 (637 + / 532 −)

genes with fdr < 0.01 = 852 (456 + / 396 −)

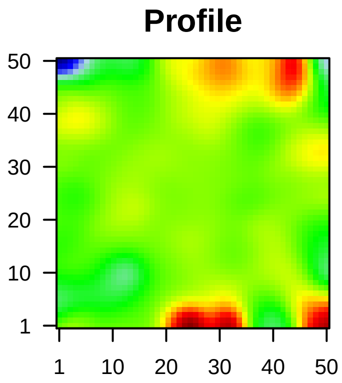
genes in genesets = 16332

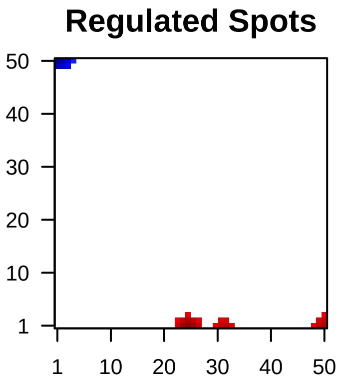
<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.1

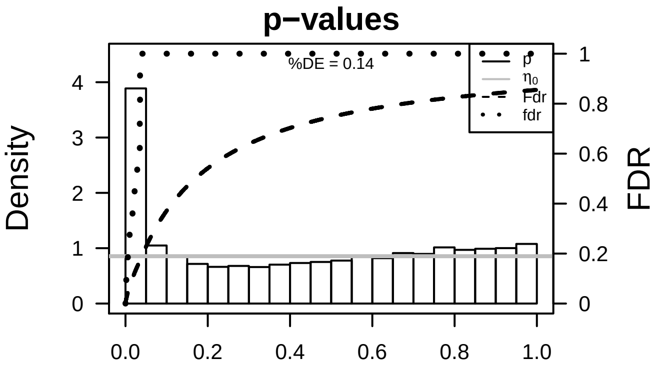
<fdr> = 0.86


Profile


Regulated Spots

Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	144568	−1.53	2e−16	3e−14	1 x 50	alpha−2−macroglobulin−like 1 [Source:HGNC Symbol;Acc:23
2	154664	−1.41	2e−16	3e−14	50 x 50	ATP−binding cassette, sub−family A (ABC1), member 13 [Sou
3	79852	−1.45	2e−16	3e−14	3 x 50	epoxide hydrolase 3 [Source:HGNC Symbol;Acc:23760]
4	58	4.75	2e−16	3e−14	25 x 1	actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
5	70	2.27	2e−16	3e−14	25 x 1	actin, alpha, cardiac muscle 1 [Source:HGNC Symbol;Acc:14
6	27299	1.38	2e−16	3e−14	49 x 1	ADAM−like, decysin 1 [Source:HGNC Symbol;Acc:16299]
7	131	−2.2	2e−16	3e−14	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
8	8644	−2.33	2e−16	3e−14	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
9	218	−1.53	2e−16	3e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
10	200315	1.38	2e−16	3e−14	1 x 40	apolipoprotein B mRNA editing enzyme, catalytic polypeptide
11	341	1.34	2e−16	3e−14	50 x 1	apolipoprotein C−I [Source:HGNC Symbol;Acc:607]
12	360	1.43	2e−16	3e−14	1 x 50	aquaporin 3 (Gill blood group) [Source:HGNC Symbol;Acc:63
13	115749	−1.32	2e−16	3e−14	50 x 50	chromosome 12 open reading frame 56 [Source:HGNC Symb
14	713	2.02	2e−16	3e−14	50 x 1	complement component 1, q subcomponent, B chain [Source
15	714	1.7	2e−16	3e−14	50 x 1	complement component 1, q subcomponent, C chain [Source
16	760	1.44	2e−16	3e−14	1 x 44	carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
17	51806	−1.47	2e−16	3e−14	4 x 50	calmodulin−like 5 [Source:HGNC Symbol;Acc:18180]
18	595	−1.76	2e−16	3e−14	1 x 6	cyclin D1 [Source:HGNC Symbol;Acc:1582]
19	1048	−1.9	2e−16	3e−14	2 x 50	carcinoembryonic antigen−related cell adhesion molecule 5 [
20	4680	−2.38	2e−16	3e−14	1 x 50	carcinoembryonic antigen−related cell adhesion molecule 6 (


p−values

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	18.52	NULL	36	BP	muscle filament sliding
2	18.52	NULL	127	H.Tiss	WIRTH_Muscle
3	17.03	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_F
4	15.46	NULL	16	H.Tiss	WIRTH_Hippocampus
5	14.91	NULL	16	GSEA C2	MOSERLE_IFNA_RESPONSE
6	13.61	NULL	44	MF	structural constituent of muscle
7	13.46	NULL	51	BP	type I interferon signaling pathway
8	12.64	NULL	142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
9	12.64	NULL	142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
10	11.54	NULL	37	CC	sarcomere
11	11.41	NULL	13	GSEA C2	BOWIE_RESPONSE_TO_TAMOXIFEN
12	11.22	NULL	16	GSEA C2	ZHANG_INTERFERON_RESPONSE
13	10.64	NULL	123	BP	defense response to virus
14	10.56	NULL	8	GSEA C2	ROETH_TERT_TARGETS_UP
15	10.36	NULL	10	GSEA C2	BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
16	10.33	NULL	16	GSEA C2	EINAV_INTERFERON_SIGNATURE_IN_CANCER
17	10.25	NULL	204	BP	cytokine−mediated signaling pathway
18	10.08	NULL	370	BP	mitotic cell cycle
19	9.84	NULL	10	GSEA C2	GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
20	9.29	NULL	417	H.Tiss	WIRTH_Immune system
Underexpressed					
1	−16.26	NULL	42	BP	keratinization
2	−15.69	NULL	135	H.Tiss	WIRTH_Mucosa
3	−14.39	NULL	21	CC	cornified envelope
4	−11.95	NULL	53	BP	keratinocyte differentiation
5	−9.01	NULL	19	BP	peptide cross−linking
6	−7.98	NULL	914	Chr	Chr 3
7	−7.76	NULL	1253	BP	small molecule metabolic process
8	−7.65	NULL	15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
9	−7.53	NULL	434	BP	oxidation−reduction process
10	−7.2	NULL	1033	Chr	Chr 2
11	−6.97	NULL	76	BP	epidermis development
12	−6.66	NULL	1146	TF	HEBENSTREIT_low expression TF
13	−6.29	NULL	16	GSEA C2	CROMER_TUMORIGENESIS_DN
14	−6.27	NULL	296	MF	oxidoreductase activity
15	−6.09	NULL	15	MF	interleukin−1 receptor binding
16	−6.09	NULL	717	Chr	Chr 16
17	−5.99	NULL	13	BP	negative regulation of peptidase activity
18	−5.93	NULL	390	BP	metabolic process
19	−5.9	NULL	63	MF	oxidoreductase activity, acting on paired donors, with incorporation
20	−5.87	NULL	2	miRNA target	miR−16−1

GW_122

Local Summary

%DE = 0.79

metagenes = 11

genes = 105

genes in genesets = 105

genes with fdr < 0.1 = 62 (61 + / 1 −)

genes with fdr < 0.05 = 59 (58 + / 1 −)

genes with fdr < 0.01 = 57 (56 + / 1 −)

<r> metagenes = 0.98

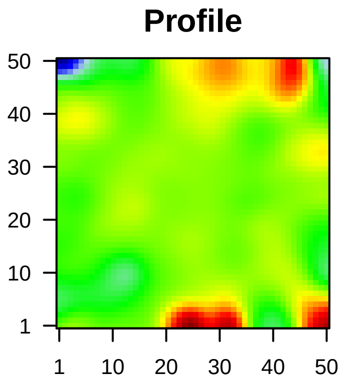
<r> genes = 0.64

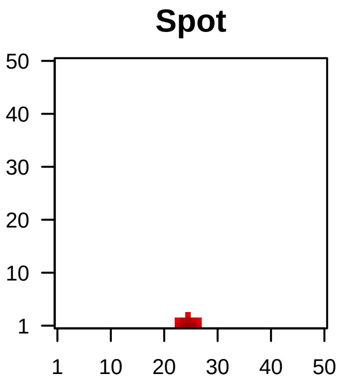
<FC> = 0.82

<shrinkage−t> = 28.75

<p−value> = 0

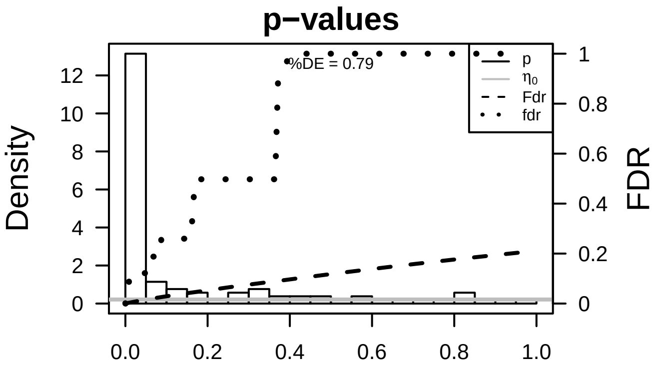
<fdr> = 0.4





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	58	4.75	2e−16	2e−16	25 x 1	actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
2	70	2.27	2e−16	2e−16	25 x 1	actin, alpha, cardiac muscle 1 [Source:HGNC Symbol;Acc:14
3	1158	3.12	2e−16	2e−16	25 x 1	creatine kinase, muscle [Source:HGNC Symbol;Acc:1994]
4	202333	1.7	2e−16	2e−16	25 x 1	cardiomyopathy associated 5 [Source:HGNC Symbol;Acc:14
5	2273	1.36	2e−16	2e−16	25 x 1	four and a half LIM domains 1 [Source:HGNC Symbol;Acc:37
6	2318	1.56	2e−16	2e−16	25 x 1	filamin C, gamma [Source:HGNC Symbol;Acc:3756]
7	10324	2.31	2e−16	2e−16	25 x 1	kelch−like family member 41 [Source:HGNC Symbol;Acc:169
8	4151	2.48	2e−16	2e−16	25 x 1	myoglobin [Source:HGNC Symbol;Acc:6915]
9	4604	1.48	2e−16	2e−16	25 x 1	myosin binding protein C, slow type [Source:HGNC Symbol;A
10	4606	1.33	2e−16	2e−16	25 x 1	myosin binding protein C, fast type [Source:HGNC Symbol;A
11	4620	3	2e−16	2e−16	25 x 1	myosin, heavy chain 2, skeletal muscle, adult [Source:HGNC
12	4625	2.7	2e−16	2e−16	25 x 1	myosin, heavy chain 7, cardiac muscle, beta [Source:HGNC
13	4632	1.48	2e−16	2e−16	25 x 1	myosin, light chain 1, alkali; skeletal, fast [Source:HGNC Sym
14	4633	2.39	2e−16	2e−16	25 x 1	myosin, light chain 2, regulatory, cardiac, slow [Source:HGNC
15	8736	1.7	2e−16	2e−16	25 x 1	myomesin 1 [Source:HGNC Symbol;Acc:7613]
16	9499	1.96	2e−16	2e−16	25 x 1	myotilin [Source:HGNC Symbol;Acc:12399]
17	4703	2.03	2e−16	2e−16	25 x 1	nebulin [Source:HGNC Symbol;Acc:7720]
18	6588	3.39	2e−16	2e−16	25 x 1	sarcolipin [Source:HGNC Symbol;Acc:11089]
19	8557	1.94	2e−16	2e−16	25 x 1	titin−cap [Source:HGNC Symbol;Acc:11610]
20	7060	1.9	2e−16	2e−16	25 x 1	thrombospondin 4 [Source:HGNC Symbol;Acc:11788]



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	64.47	NULL	23 / 36	BP	muscle filament sliding
2	60.54	NULL	57 / 127	H.Tiss	WIRTH_Muscle
3	57.95	NULL	11 / 16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_F
4	57.23	NULL	11 / 16	H.Tiss	WIRTH_Hippocampus
5	47.82	NULL	22 / 44	MF	structural constituent of muscle
6	40.23	NULL	12 / 37	CC	sarcomere
7	36.7	NULL	10 / 12	CC	myosin filament
8	32.66	NULL	8 / 13	CC	muscle myosin complex
9	31.66	NULL	23 / 84	BP	muscle contraction
10	27.35	NULL	15 / 34	CC	myofibril
11	27.13	NULL	8 / 16	CC	M band
12	26.09	NULL	2 / 6	GSEA C2	BIOCARTA_HSP27_PATHWAY
13	25.47	NULL	9 / 37	BP	cardiac muscle contraction
14	25.11	NULL	5 / 11	BP	cardiac muscle tissue morphogenesis
15	24.59	NULL	8 / 14	CC	contractile fiber
16	22.96	NULL	21 / 88	CC	Z disc
17	22.32	NULL	3 / 15	Cancer	BEN−PORATH_UP
18	20.48	NULL	6 / 12	BP	skeletal muscle contraction
19	20.25	NULL	7 / 12	MF	titin binding
20	19.8	NULL	4 / 14	BP	adult heart development
21	19.75	NULL	9 / 20	CC	I band
22	19.61	NULL	5 / 26	BP	ventricular cardiac muscle tissue morphogenesis
23	19.53	NULL	1 / 9	GSEA C2	PENG_GLUCOSE_DEPRIVATION_UP
24	19.53	NULL	1 / 9	GSEA C2	PENG_GLUCOSE_DEPRIVATION_DN
25	18.73	NULL	7 / 15	BP	striated muscle contraction
26	18.3	NULL	1 / 10	GSEA C2	BIOCARTA_EPHA4_PATHWAY
27	18.03	NULL	2 / 20	MF	myosin binding
28	17.93	NULL	2 / 10	BP	heart contraction
29	17.92	NULL	4 / 11	CC	A band
30	17.82	NULL	2 / 14	GSEA C2	BIOCARTA_UCALPAIN_PATHWAY
31	17.74	NULL	4 / 16	MF	microfilament motor activity
32	17.36	NULL	6 / 18	BP	regulation of muscle contraction
33	17.11	NULL	2 / 15	GSEA C2	BIOCARTA_INTEGRIN_PATHWAY
34	16.39	NULL	1 / 12	GSEA C2	BIOCARTA_NO1_PATHWAY
35	16.39	NULL	1 / 12	GSEA C2	BIOCARTA_RAB_PATHWAY
36	16.17	NULL	8 / 42	CC	myosin complex
37	16.05	NULL	2 / 16	GSEA C2	SASSON_RESPONSE_TO_GONADOTROPHINS_DN
38	16.05	NULL	2 / 16	GSEA C2	SASSON_RESPONSE_TO_FORSKOLIN_DN
39	15.77	NULL	2 / 10	BP	creatine metabolic process
40	15.62	NULL	1 / 13	GSEA C2	NING_CHRONIC_OBSTRUCTIVE_PULMONARY_DISEASE_UP

GW_122

Local Summary

%DE = 0.87

metagenes = 6

genes = 117

genes in genesets = 115

genes with fdr < 0.1 = 90 (88 + / 2 −)

genes with fdr < 0.05 = 88 (87 + / 1 −)

genes with fdr < 0.01 = 82 (81 + / 1 −)

<r> metagenes = 0.99

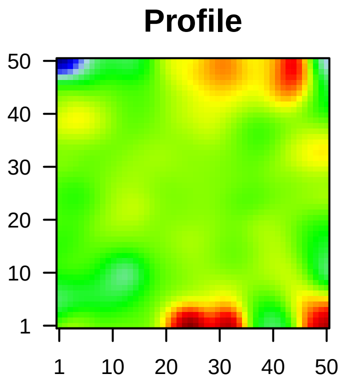
<r> genes = 0.46

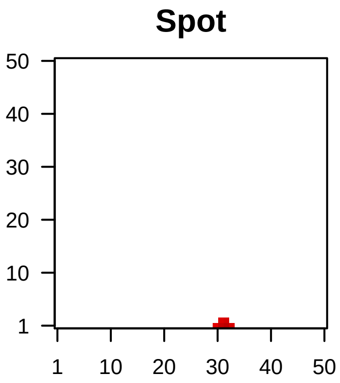
<FC> = 0.73

<shrinkage−t> = 25.57

<p−value> = 0

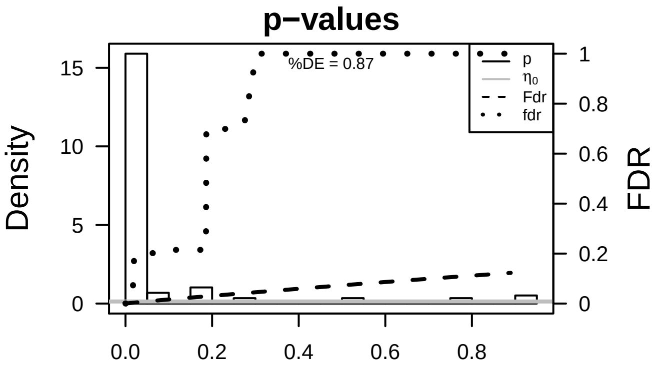
<fdr> = 0.25


Profile


Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	3627	1.71	2e−16	2e−16	32 x 1	chemokine (C−X−C motif) ligand 10 [Source:HGNC Symbol;A
2	94240	2.04	2e−16	2e−16	32 x 1	epithelial stromal interaction 1 (breast) [Source:HGNC Symbo
3	2633	1.82	2e−16	2e−16	32 x 1	guanylate binding protein 1, interferon−inducible [Source:HGN
4	115362	1.6	2e−16	2e−16	32 x 1	guanylate binding protein 5 [Source:HGNC Symbol;Acc:1989
5	10561	1.83	2e−16	2e−16	32 x 1	interferon−induced protein 44 [Source:HGNC Symbol;Acc:16
6	10964	2.46	2e−16	2e−16	32 x 1	interferon−induced protein 44−like [Source:HGNC Symbol;Ac
7	2537	1.64	2e−16	2e−16	32 x 1	interferon, alpha−inducible protein 6 [Source:HGNC Symbol;A
8	3433	1.87	2e−16	2e−16	32 x 1	interferon−induced protein with tetratricopeptide repeats 2 [So
9	9636	1.52	2e−16	2e−16	32 x 1	ISG15 ubiquitin−like modifier [Source:HGNC Symbol;Acc:405
10	400759	1.38	2e−16	2e−16	32 x 1	guanylate binding protein 1, interferon−inducible pseudogene
11	4321	1.43	2e−16	2e−16	32 x 1	matrix metallopeptidase 12 (macrophage elastase) [Source:H
12	4599	1.22	2e−16	2e−16	32 x 1	myxovirus (influenza virus) resistance 1, interferon−inducible
13	10346	1.4	2e−16	2e−16	32 x 1	tripartite motif containing 22 [Source:HGNC Symbol;Acc:1637
14	11274	1.42	2e−16	2e−16	32 x 1	ubiquitin specific peptidase 18 [Source:HGNC Symbol;Acc:12
15	7453	1.48	2e−16	2e−16	32 x 1	tryptophanyl−tRNA synthetase [Source:HGNC Symbol;Acc:1
16	8519	1.31	4e−16	7e−14	32 x 1	interferon induced transmembrane protein 1 [Source:HGNC S
17	51191	1.26	5e−15	8e−14	32 x 1	HECT and RLD domain containing E3 ubiquitin protein ligase
18	64135	1.25	1e−14	3e−13	32 x 1	interferon induced with helicase C domain 1 [Source:HGNC S
19	10410	1.12	4e−14	3e−13	32 x 1	interferon induced transmembrane protein 3 [Source:HGNC S
20	55008	1.21	6e−14	3e−13	32 x 1	HECT and RLD domain containing E3 ubiquitin protein ligase



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	62.21	NULL	12 / 16	GSEA C2	MOSERLE_IFNA_RESPONSE
2	52.92	NULL	29 / 51	BP	type I interferon signaling pathway
3	49.74	NULL	6 / 8	GSEA C2	ROETH_TERT_TARGETS_UP
4	47.85	NULL	9 / 10	GSEA C2	BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
5	46.92	NULL	11 / 16	GSEA C2	ZHANG_INTERFERON_RESPONSE
6	46.02	NULL	11 / 16	GSEA C2	EINAV_INTERFERON_SIGNATURE_IN_CANCER
7	43.72	NULL	10 / 13	GSEA C2	BOWIE_RESPONSE_TO_TAMOXIFEN
8	38.73	NULL	31 / 123	BP	defense response to virus
9	38.69	NULL	8 / 10	GSEA C2	GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
10	36.45	NULL	8 / 11	GSEA C2	BENNETT_SYSTEMIC_LUPUS_ERYTHEMATOSUS
11	33.92	NULL	3 / 4	MMML CGS	MACIEJ_MMML 47
12	33.91	NULL	27 / 109	BP	response to virus
13	32.28	NULL	13 / 31	BP	negative regulation of viral genome replication
14	32.09	NULL	7 / 16	GSEA C2	MAHADEVAN_RESPONSE_TO_MP470_UP
15	31.87	NULL	3 / 5	GSEA C2	KIM_LRRC3B_TARGETS
16	31.74	NULL	6 / 12	GSEA C2	TSAI_DNAJB4_TARGETS_UP
17	29.91	NULL	34 / 204	BP	cytokine−mediated signaling pathway
18	29.74	NULL	3 / 4	GSEA C2	KRASNOSELSKAYA_ILF3_TARGETS_UP
19	28.19	NULL	4 / 12	GSEA C2	ZHU_CMV_8_HR_UP
20	28.12	NULL	5 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
21	27.92	NULL	4 / 16	GSEA C2	SEITZ_NEOPLASTIC_TRANSFORMATION_BY_8P_DELETION_
22	27.14	NULL	10 / 16	GSEA C2	UROSEVIC_RESPONSE_TO_IMIQUIMOD
23	26.88	NULL	6 / 16	GSEA C2	XU_HGF_TARGETS_INDUCED_BY_AKT1_6HR
24	26.13	NULL	6 / 14	Glio	Donson−immune cell intra signaling−associated with LTS in HGA
25	26	NULL	31 / 274	Lymphoma	SPANG_IL21 DN
26	25.06	NULL	6 / 14	GSEA C2	XU_AKT1_TARGETS_6HR
27	23.53	NULL	6 / 6	Lymphoma	DAVE_MHCCII BL DN
28	23.07	NULL	4 / 14	GSEA C2	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_8D_UP
29	23.06	NULL	4 / 14	GSEA C2	SANA_TNF_SIGNALING_UP
30	22.77	NULL	16 / 60	BP	interferon−gamma−mediated signaling pathway
31	22.67	NULL	46 / 572	Disease	GUDJ_psoriasis up
32	22.1	NULL	4 / 10	GSEA C2	GRANDVAUX_IRF3_TARGETS_UP
33	22.04	NULL	3 / 9	GSEA C2	DER_IFN_ALPHA_RESPONSE_UP
34	22.04	NULL	3 / 9	GSEA C2	DER_IFN_GAMMA_RESPONSE_UP
35	21.65	NULL	5 / 16	GSEA C2	ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_UP
36	21.49	NULL	2 / 2	MMML CGS	MACIEJ_MMML 27
37	20.94	NULL	6 / 14	GSEA C2	RADAEVA_RESPONSE_TO_IFNA1_UP
38	20.26	NULL	4 / 10	GSEA C2	DAUER_STAT3_TARGETS_DN
39	19.4	NULL	7 / 10	CC	MHC class I protein complex
40	19.03	NULL	4 / 15	GSEA C2	BECKER_TAMOXIFEN_RESISTANCE_UP

GW_122

Local Summary

%DE = 0.64

metagenes = 6

genes = 182

genes in genesets = 180

genes with fdr < 0.1 = 95 (89 + / 6 −)

genes with fdr < 0.05 = 91 (85 + / 6 −)

genes with fdr < 0.01 = 73 (67 + / 6 −)

<r> metagenes = 1

<r> genes = 0.64

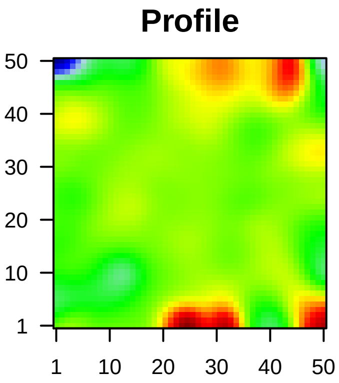
<FC> = 0.4

<shrinkage−t> = 14.07

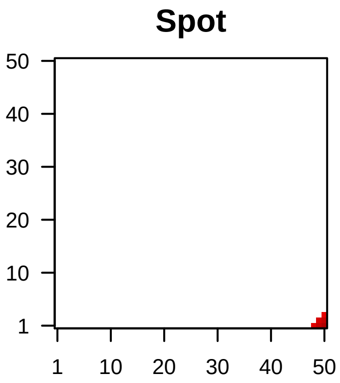
<p−value> = 0

<fdr> = 0.48

Profile



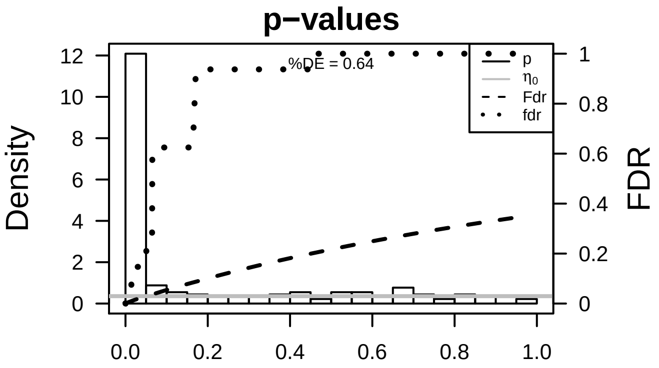
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	27299	1.38	2e−16	2e−15	49 x 1	ADAM−like, decysin 1 [Source:HGNC Symbol;Acc:16299]
2	341	1.34	2e−16	2e−15	50 x 1	apolipoprotein C−I [Source:HGNC Symbol;Acc:607]
3	713	2.02	2e−16	2e−15	50 x 1	complement component 1, q subcomponent, B chain [Source
4	714	1.7	2e−16	2e−15	50 x 1	complement component 1, q subcomponent, C chain [Source
5	115361	1.46	2e−16	2e−15	48 x 1	guanylate binding protein 4 [Source:HGNC Symbol;Acc:2048
6	3512	1.44	2e−16	2e−15	50 x 1	immunoglobulin J polypeptide, linker protein for immunoglobu
7	7305	1.36	2e−16	2e−15	50 x 1	TYRO protein tyrosine kinase binding protein [Source:HGNC
8	3122	1.23	4e−16	2e−13	50 x 1	major histocompatibility complex, class II, DR alpha [Source:
9	7941	1.31	4e−16	2e−13	50 x 3	phospholipase A2, group VII (platelet−activating factor acetyl
10	5996	1.32	4e−16	2e−13	50 x 1	regulator of G−protein signaling 1 [Source:HGNC Symbol;Ac
11	5552	1.28	3e−15	5e−13	50 x 1	serglycin [Source:HGNC Symbol;Acc:9361]
12	2207	1.25	1e−14	8e−13	50 x 1	Fc fragment of IgE, high affinity I, receptor for; gamma polype
13	5920	1.23	3e−14	8e−13	48 x 1	retinoic acid receptor responder (tazarotene induced) 3 [Sour
14	3109	1.22	4e−14	2e−12	50 x 1	major histocompatibility complex, class II, DM beta [Source:H
15	260436	−1.21	7e−14	2e−12	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symbo
16	64231	1.21	9e−14	4e−12	50 x 1	membrane−spanning 4−domains, subfamily A, member 6A [S
17	10875	1.19	1e−13	7e−12	50 x 1	fibrinogen−like 2 [Source:HGNC Symbol;Acc:3696]
18	3113	1.18	3e−13	7e−12	50 x 1	major histocompatibility complex, class II, DP alpha 1 [Source
19	84868	1.17	4e−13	3e−11	50 x 1	hepatitis A virus cellular receptor 2 [Source:HGNC Symbol;A
20	3126	1.15	9e−13	3e−11	50 x 1	major histocompatibility complex, class II, DR beta 4 [Source:

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	36.37	NULL	11 / 15	CC	MHC class II protein complex
2	32.64	NULL	2 / 4	GSEA C2	REACTOME_CLASSICAL_ANTIBODY_MEDIATED_COMPLEMEN
3	23.52	NULL	2 / 7	GSEA C2	BIOCARTA_COMP_PATHWAY
4	23.13	NULL	3 / 6	GSEA C2	SANA_RESPONSE_TO_IFNG_UP
5	21.79	NULL	2 / 8	GSEA C2	BIOCARTA_CLASSIC_PATHWAY
6	21.79	NULL	2 / 8	GSEA C2	REACTOME_COMPLEMENT_CASCADE
7	21.79	NULL	2 / 8	GSEA C2	REACTOME_INITIAL_TRIGGERING_OF_COMPLEMENT
8	21.23	NULL	4 / 8	GSEA C2	GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_DN
9	21.21	NULL	12 / 47	BP	antigen processing and presentation
10	19.45	NULL	41 / 312	BP	immune response
11	19.4	NULL	2 / 3	GSEA C2	KEGG_VIRAL_MYOCARDITIS
12	18.22	NULL	6 / 21	CC	clathrin−coated endocytic vesicle membrane
13	17.87	NULL	3 / 8	GSEA C2	LINDSTEDT_DENDRITIC_CELL_MATURATION_D
14	17.53	NULL	30 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
15	17.53	NULL	30 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
16	17.53	NULL	30 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
17	17.53	NULL	30 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
18	17.33	NULL	6 / 23	CC	integral to lumenal side of endoplasmic reticulum membrane
19	16.88	NULL	2 / 6	GSEA C2	BUDHU_LIVER_CANCER_METASTASIS_UP
20	16.62	NULL	6 / 11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
21	16.33	NULL	3 / 16	GSEA C2	KAAB_FAILED_HEART_VENTRICLE_DN
22	16.28	NULL	70 / 417	H.Tiss	WIRTH_Immune system
23	16.26	NULL	2 / 4	GSEA C2	KEGG_LEISHMANIA_INFECTION
24	16.02	NULL	3 / 5	GSEA C2	WONG_ENDOMETRIAL_CANCER_LATE
25	15.81	NULL	8 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
26	15.74	NULL	3 / 10	GSEA C2	HOSHIDA_LIVER_CANCER_SUBCLASS_S1
27	15.55	NULL	6 / 28	CC	transport vesicle membrane
28	14.7	NULL	5 / 12	BP	immunoglobulin mediated immune response
29	14.52	NULL	11 / 87	BP	antigen processing and presentation of exogenous peptide antigen
30	14.44	NULL	6 / 32	CC	ER to Golgi transport vesicle membrane
31	14.26	NULL	3 / 14	GSEA C2	WU_SILENCED_BY_METHYLATION_IN_BLADDER_CANCER
32	13.74	NULL	6 / 35	CC	trans−Golgi network membrane
33	13.68	NULL	2 / 10	GSEA C2	AMUNDSON_GAMMA_RADIATION_RESISTANCE
34	13.52	NULL	2 / 6	GSEA C2	LUI_THYROID_CANCER_CLUSTER_4
35	13.49	NULL	3 / 11	GSEA C2	KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY
36	13.02	NULL	2 / 20	BP	complement activation
37	12.98	NULL	5 / 11	GSEA C2	BIOCARTA_THELPER_PATHWAY
38	12.86	NULL	12 / 60	BP	T cell costimulation
39	12.69	NULL	1 / 2	GSEA C2	KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUC
40	12.69	NULL	1 / 2	GSEA C2	KEGG_AUTOIMMUNE_THYROID_DISEASE

GW_122

Local Summary

%DE = 0.94

metagenes = 7

genes = 135

genes in genesets = 132

genes with fdr < 0.1 = 117 (11 + / 106 −)

genes with fdr < 0.05 = 114 (10 + / 104 −)

genes with fdr < 0.01 = 108 (8 + / 100 −)

<r> metagenes = 0.99

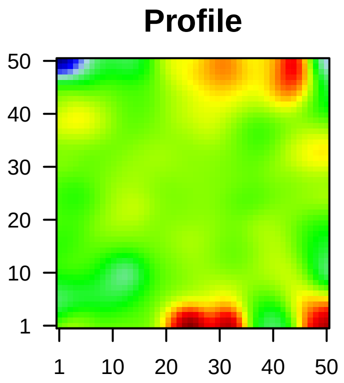
<r> genes = 0.51

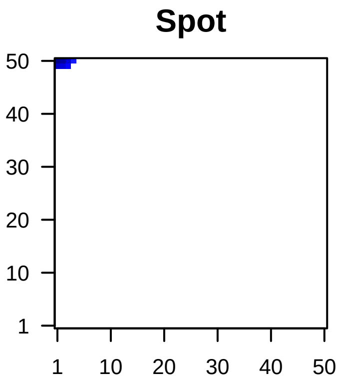
<FC> = −0.92

<shrinkage−t> = −32.73

<p−value> = 0

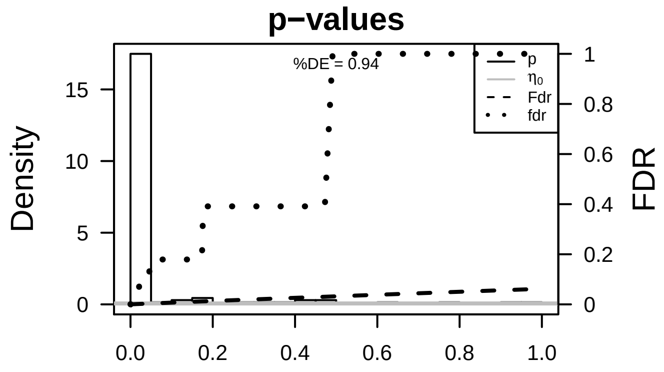
<fdr> = 0.17


Profile


Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	144568	−1.53	2e−16	4e−17	1 x 50	alpha−2−macroglobulin−like 1 [Source:HGNC Symbol;Acc:23
2	79852	−1.45	2e−16	4e−17	3 x 50	epoxide hydrolase 3 [Source:HGNC Symbol;Acc:23760]
3	131	−2.2	2e−16	4e−17	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
4	8644	−2.33	2e−16	4e−17	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
5	218	−1.53	2e−16	4e−17	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
6	360	1.43	2e−16	4e−17	1 x 50	aquaporin 3 (Gill blood group) [Source:HGNC Symbol;Acc:63
7	51806	−1.47	2e−16	4e−17	4 x 50	calmodulin−like 5 [Source:HGNC Symbol;Acc:18180]
8	1048	−1.9	2e−16	4e−17	2 x 50	carcinoembryonic antigen−related cell adhesion molecule 5 [
9	4680	−2.38	2e−16	4e−17	1 x 50	carcinoembryonic antigen−related cell adhesion molecule 6 (
10	22802	−2.09	2e−16	4e−17	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
11	84518	−1.73	2e−16	4e−17	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
12	49860	−2.34	2e−16	4e−17	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
13	1562	−1.53	2e−16	4e−17	1 x 50	cytochrome P450, family 2, subfamily C, polypeptide 18 [Sou
14	92196	−2.29	2e−16	4e−17	3 x 50	death associated protein−like 1 [Source:HGNC Symbol;Acc:2
15	1673	−1.81	2e−16	4e−17	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
16	131177	−1.42	2e−16	4e−17	3 x 50	family with sequence similarity 3, member D [Source:HGNC
17	9245	−1.62	2e−16	4e−17	4 x 50	glucosaminyl (N−acetyl) transferase 3, mucin type [Source:H
18	2877	−2.43	2e−16	4e−17	1 x 50	glutathione peroxidase 2 (gastrointestinal) [Source:HGNC Sy
19	26525	−1.58	2e−16	4e−17	1 x 49	interleukin 36 receptor antagonist [Source:HGNC Symbol;Acc
20	43849	−1.49	2e−16	4e−17	1 x 50	kallikrein−related peptidase 12 [Source:HGNC Symbol;Acc:6


p−values

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−45.08	NULL	57 / 135	H.Tiss	WIRTH_Mucosa
2	−40.93	NULL	12 / 21	CC	cornified envelope
3	−36.46	NULL	13 / 42	BP	keratinization
4	−32.79	NULL	16 / 53	BP	keratinocyte differentiation
5	−28.33	NULL	7 / 19	BP	peptide cross−linking
6	−23.15	NULL	6 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
7	−19.04	NULL	16 / 76	BP	epidermis development
8	−15.87	NULL	55 / 572	Disease	GUDJ_psoriasis up
9	−14.48	NULL	3 / 15	GSEA C2	CHANG_IMMORTALIZED_BY_HPV31_DN
10	−13.8	NULL	1 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
11	−13.71	NULL	5 / 13	BP	negative regulation of peptidase activity
12	−12.58	NULL	12 / 186	MF	structural molecule activity
13	−12.52	NULL	2 / 11	GSEA C2	ROME_INSULIN_TARGETS_IN_MUSCLE_DN
14	−12.03	NULL	3 / 16	GSEA C2	AMIT_SERUM_RESPONSE_480_MCF10A
15	−11.95	NULL	4 / 15	MF	retinol dehydrogenase activity
16	−10.16	NULL	6 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
17	−9.74	NULL	4 / 23	MF	peptidase inhibitor activity
18	−9.62	NULL	4 / 15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
19	−9.41	NULL	6 / 38	BP	epithelial cell differentiation
20	−9.08	NULL	1 / 6	GSEA C2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_B_DN
21	−8.98	NULL	3 / 15	GSEA C2	LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
22	−8.77	NULL	2 / 12	H.Tiss	WIRTH_Prim. lymphoid organs
23	−8.73	NULL	3 / 13	H.Tiss	WIRTH_Tonsil
24	−8.72	NULL	5 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
25	−8.43	NULL	1 / 6	GSEA C2	SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_DN
26	−8.04	NULL	2 / 8	GSEA C2	MCLACHLAN_DENTAL_CARIES_UP
27	−7.99	NULL	2 / 15	GSEA C2	ALONSO_METASTASIS_NEURAL_UP
28	−7.94	NULL	1 / 12	GSEA C2	ODONNELL_METASTASIS_DN
29	−7.94	NULL	1 / 12	GSEA C2	SYED_ESTRADIOL_RESPONSE
30	−7.86	NULL	6 / 82	CC	intermediate filament
31	−7.62	NULL	3 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
32	−7.55	NULL	4 / 34	MF	endopeptidase inhibitor activity
33	−7.47	NULL	2 / 9	GSEA C2	MCLACHLAN_DENTAL_CARIES_DN
34	−7.42	NULL	9 / 79	MF	serine−type endopeptidase inhibitor activity
35	−7.27	NULL	4 / 44	CC	keratin filament
36	−7.02	NULL	1 / 9	GSEA C2	REACTOME_ETHANOL_OXIDATION
37	−7	NULL	2 / 10	GSEA C2	NIKOLSKY_BREAST_CANCER_20Q12_Q13_AMPLICON
38	−6.99	NULL	1 / 11	Glio	VERHAAK_Brain
39	−6.97	NULL	1 / 10	BP	positive regulation of endothelial cell apoptotic process
40	−6.97	NULL	1 / 10	BP	retinal metabolic process