GW_289

Global Summary

%DE = 0.14

genes with fdr < 0.2 = 1771 (952 + / 819 −)

genes with fdr < 0.1 = 1519 (818 + / 701 −)

genes with fdr < 0.05 = 1198 (641 + / 557 −)

genes with fdr < 0.01 = 758 (410 + / 348 −)

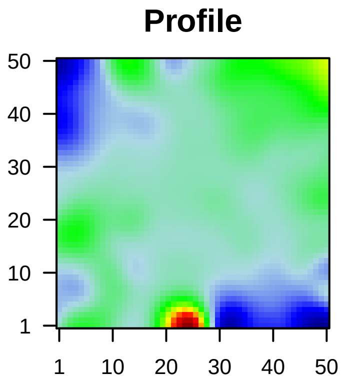
genes in genesets = 16332

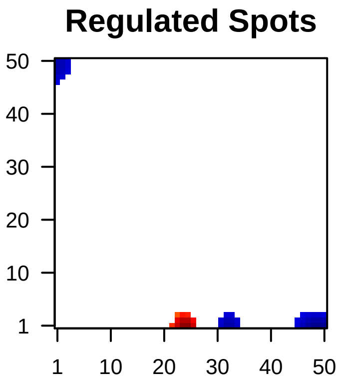
<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.1

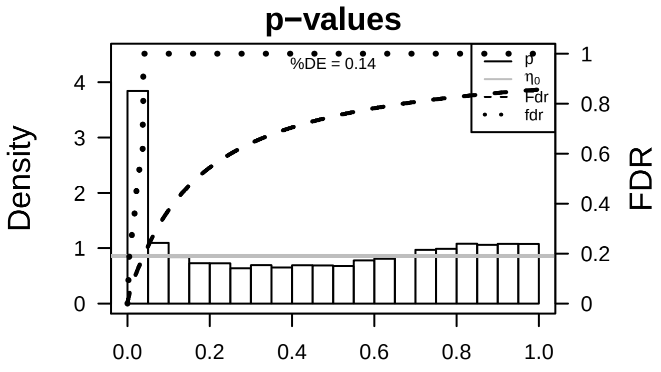
<fdr> = 0.86





Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	58	4.79	2e−16	3e−14	25 x 1	actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
2	70	3.45	2e−16	3e−14	25 x 1	actin, alpha, cardiac muscle 1 [Source:HGNC Symbol;Acc:14
3	131	−2.95	2e−16	3e−14	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
4	57016	1.82	2e−16	3e−14	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
5	1646	2.04	2e−16	3e−14	13 x 50	aldo−keto reductase family 1, member C2 [Source:HGNC Sy
6	8644	3.37	2e−16	3e−14	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
7	1109	3.73	2e−16	3e−14	13 x 50	aldo−keto reductase family 1, member C4 [Source:HGNC Sy
8	220	−2.26	2e−16	3e−14	4 x 46	aldehyde dehydrogenase 1 family, member A3 [Source:HGN
9	10930	1.99	2e−16	3e−14	25 x 1	apolipoprotein B mRNA editing enzyme, catalytic polypeptide
10	140458	1.86	2e−16	3e−14	25 x 1	ankyrin repeat and SOCS box containing 5 [Source:HGNC S
11	684	−1.69	2e−16	3e−14	32 x 1	bone marrow stromal cell antigen 2 [Source:HGNC Symbol;A
12	51806	−1.77	2e−16	3e−14	4 x 50	calmodulin−like 5 [Source:HGNC Symbol;Acc:18180]
13	845	1.8	2e−16	3e−14	25 x 1	calsequestrin 2 (cardiac muscle) [Source:HGNC Symbol;Acc:
14	6364	−3.08	2e−16	3e−14	46 x 1	chemokine (C−C motif) ligand 20 [Source:HGNC Symbol;Acc
15	894	2.15	2e−16	3e−14	50 x 4	cyclin D2 [Source:HGNC Symbol;Acc:1583]
16	4680	−1.86	2e−16	3e−14	1 x 50	carcinoembryonic antigen−related cell adhesion molecule 6 (
17	1114	1.74	2e−16	3e−14	25 x 1	chromogranin B (secretogranin 1) [Source:HGNC Symbol;Ac
18	1158	3.98	2e−16	3e−14	25 x 1	creatine kinase, muscle [Source:HGNC Symbol;Acc:1994]
19	1160	1.81	2e−16	3e−14	25 x 1	creatine kinase, mitochondrial 2 (sarcomeric) [Source:HGNC
20	9076	−2.07	2e−16	3e−14	49 x 50	claudin 1 [Source:HGNC Symbol;Acc:2032]



Global Geneset Analysis

Rank	GSZ	p−value	#all		Geneset
Overexpressed					
1	32.43	NULL	127	H.Tiss	WIRTH_Muscle
2	24.61	NULL	36	BP	muscle filament sliding
3	20.87	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_F
4	20.06	NULL	16	H.Tiss	WIRTH_Hippocampus
5	19.76	NULL	44	MF	structural constituent of muscle
6	16.07	NULL	84	BP	muscle contraction
7	15.51	NULL	12	CC	myosin filament
8	14.12	NULL	37	CC	sarcomere
9	13.06	NULL	13	CC	muscle myosin complex
10	12.8	NULL	88	CC	Z disc
11	12.63	NULL	34	CC	myofibril
12	11.93	NULL	20	CC	I band
13	11.92	NULL	14	CC	contractile fiber
14	10.96	NULL	16	CC	M band
15	10.52	NULL	12	BP	skeletal muscle contraction
16	10.03	NULL	37	BP	cardiac muscle contraction
17	9.38	NULL	92	BP	translational elongation
18	9.32	NULL	153	MF	structural constituent of ribosome
19	9.21	NULL	15	GSEA C2	REACTOME_STRIATED_MUSCLE_CONTRACTION
20	9.1	NULL	18	BP	regulation of muscle contraction
Underexpressed					
1	−21.44	NULL	572	Disease	GUDJ_psoriasis up
2	−14.78	NULL	553	Cancer	Lembcke_Colonic Inflammation
3	−14.56	NULL	312	BP	immune response
4	−13.67	NULL	51	BP	type I interferon signaling pathway
5	−13.03	NULL	417	H.Tiss	WIRTH_Immune system
6	−12.34	NULL	316	Cancer	SPANG_BCL6−index2
7	−12.2	NULL	135	H.Tiss	WIRTH_Mucosa
8	−11.71	NULL	204	BP	cytokine−mediated signaling pathway
9	−10.92	NULL	10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
10	−10.63	NULL	265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
11	−10.63	NULL	265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
12	−10.63	NULL	265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
13	−10.63	NULL	265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
14	−10.39	NULL	16	GSEA C2	MOSERLE_IFNA_RESPONSE
15	−10.29	NULL	274	Lymphoma	SPANG_IL21 DN
16	−10.17	NULL	123	BP	defense response to virus
17	−10.06	NULL	21	CC	cornified envelope
18	−10.03	NULL	16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
19	−10.02	NULL	16	GSEA C2	ZHANG_INTERFERON_RESPONSE
20	−10	NULL	60	BP	interferon−gamma−mediated signaling pathway

GW_289

Local Summary

%DE = 0.97

metagenes = 12

genes = 118

genes in genesets = 117

genes with fdr < 0.1 = 113 (113 + / 0 −)

genes with fdr < 0.05 = 113 (113 + / 0 −)

genes with fdr < 0.01 = 111 (111 + / 0 −)

<r> metagenes = 0.99

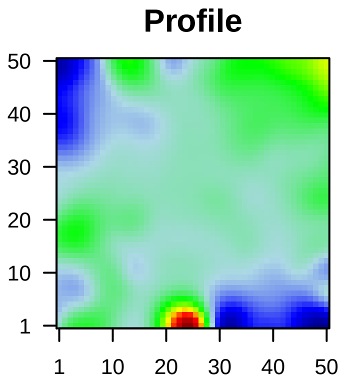
<r> genes = 0.62

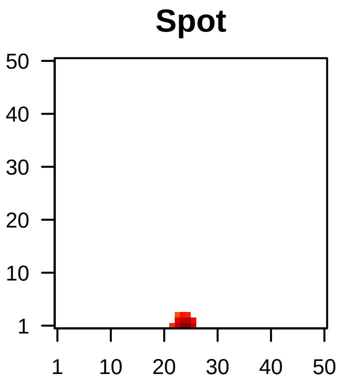
<FC> = 1.64

<shrinkage−t> = 57.4

<p−value> = 0

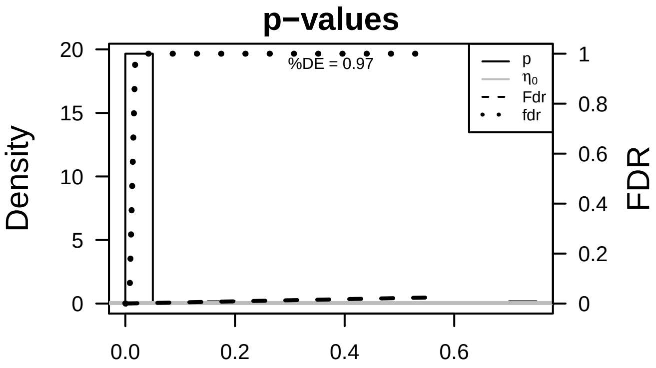
<fdr> = 0.04


Profile


Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	58	4.79	2e−16	2e−17	25 x 1	actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
2	70	3.45	2e−16	2e−17	25 x 1	actin, alpha, cardiac muscle 1 [Source:HGNC Symbol;Acc:14
3	10930	1.99	2e−16	2e−17	25 x 1	apolipoprotein B mRNA editing enzyme, catalytic polypeptide
4	140458	1.86	2e−16	2e−17	25 x 1	ankyrin repeat and SOCS box containing 5 [Source:HGNC Sy
5	845	1.8	2e−16	2e−17	25 x 1	calsequestrin 2 (cardiac muscle) [Source:HGNC Symbol;Acc:
6	1114	1.74	2e−16	2e−17	25 x 1	chromogranin B (secretogranin 1) [Source:HGNC Symbol;Acc
7	1158	3.98	2e−16	2e−17	25 x 1	creatine kinase, muscle [Source:HGNC Symbol;Acc:1994]
8	1160	1.81	2e−16	2e−17	25 x 1	creatine kinase, mitochondrial 2 (sarcomeric) [Source:HGNC
9	202333	2.36	2e−16	2e−17	25 x 1	cardiomyopathy associated 5 [Source:HGNC Symbol;Acc:14
10	1410	2.48	2e−16	2e−17	25 x 1	crystallin, alpha B [Source:HGNC Symbol;Acc:2389]
11	115265	2.47	2e−16	2e−17	25 x 1	DNA−damage−inducible transcript 4−like [Source:HGNC Syn
12	1674	1.86	2e−16	2e−17	25 x 1	desmin [Source:HGNC Symbol;Acc:2770]
13	1917	3.04	2e−16	2e−17	25 x 1	eukaryotic translation elongation factor 1 alpha 2 [Source:HG
14	2027	2.27	2e−16	2e−17	25 x 1	enolase 3 (beta, muscle) [Source:HGNC Symbol;Acc:3354]
15	2273	2.51	2e−16	2e−17	25 x 1	four and a half LIM domains 1 [Source:HGNC Symbol;Acc:37
16	2318	2.83	2e−16	2e−17	25 x 1	filamin C, gamma [Source:HGNC Symbol;Acc:3756]
17	283120	2.53	2e−16	2e−17	25 x 1	H19, imprinted maternally expressed transcript (non−protein
18	126393	2.04	2e−16	2e−17	25 x 1	heat shock protein, alpha−crystallin−related, B6 [Source:HGN
19	27129	1.86	2e−16	2e−17	25 x 1	heat shock 27kDa protein family, member 7 (cardiovascular) [
20	10324	3.18	2e−16	2e−17	25 x 1	kelch−like family member 41 [Source:HGNC Symbol;Acc:169


p−values

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	66.34	NULL	60 / 127	H.Tiss	WIRTH_Muscle
2	61.66	NULL	23 / 36	BP	muscle filament sliding
3	54.08	NULL	11 / 16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_F
4	52.21	NULL	11 / 16	H.Tiss	WIRTH_Hippocampus
5	47.57	NULL	22 / 44	MF	structural constituent of muscle
6	44.54	NULL	10 / 12	CC	myosin filament
7	35.51	NULL	8 / 13	CC	muscle myosin complex
8	33.44	NULL	8 / 14	CC	contractile fiber
9	32.81	NULL	12 / 37	CC	sarcomere
10	32.73	NULL	23 / 84	BP	muscle contraction
11	30	NULL	14 / 34	CC	myofibril
12	27.73	NULL	9 / 16	CC	M band
13	27.46	NULL	6 / 12	BP	skeletal muscle contraction
14	26.75	NULL	10 / 20	CC	I band
15	26.33	NULL	21 / 88	CC	Z disc
16	23.33	NULL	9 / 37	BP	cardiac muscle contraction
17	22.88	NULL	5 / 11	BP	cardiac muscle tissue morphogenesis
18	21.63	NULL	6 / 12	MF	titin binding
19	20.85	NULL	7 / 15	GSEA C2	REACTOME_STRIATED_MUSCLE_CONTRACTION
20	20.8	NULL	6 / 18	BP	regulation of muscle contraction
21	20.78	NULL	7 / 15	BP	striated muscle contraction
22	20.33	NULL	5 / 11	CC	A band
23	18.18	NULL	2 / 6	GSEA C2	BIOCARTA_HSP27_PATHWAY
24	17.99	NULL	8 / 42	CC	myosin complex
25	16.93	NULL	3 / 15	Cancer	BEN−PORATH_UP
26	16.92	NULL	4 / 16	MF	microfilament motor activity
27	16.56	NULL	25 / 297	MF	actin binding
28	16.06	NULL	4 / 14	BP	adult heart development
29	15.67	NULL	5 / 26	BP	ventricular cardiac muscle tissue morphogenesis
30	15.35	NULL	2 / 10	BP	heart contraction
31	13.71	NULL	3 / 13	CC	pseudopodium
32	13.51	NULL	4 / 15	GSEA C2	EBAUER_MYOGENIC_TARGETS_OF_PAX3_FOXO1_FUSION
33	13.43	NULL	4 / 14	MF	tropomyosin binding
34	13.33	NULL	2 / 10	BP	creatine metabolic process
35	13.22	NULL	6 / 21	BP	sarcomere organization
36	12.66	NULL	4 / 18	CC	costamere
37	12.6	NULL	2 / 20	MF	myosin binding
38	12.42	NULL	2 / 12	BP	muscle fiber development
39	12.4	NULL	7 / 56	MF	motor activity
40	12.29	NULL	1 / 5	GSEA C2	LIU_VAV3_PROSTATE_CARCINOGENESIS_UP

GW_289

Local Summary

%DE = 0.92

metagenes = 10

genes = 136

genes in genesets = 133

genes with fdr < 0.1 = 116 (1 + / 115 −)

genes with fdr < 0.05 = 110 (1 + / 109 −)

genes with fdr < 0.01 = 96 (1 + / 95 −)

<r> metagenes = 0.99

<r> genes = 0.43

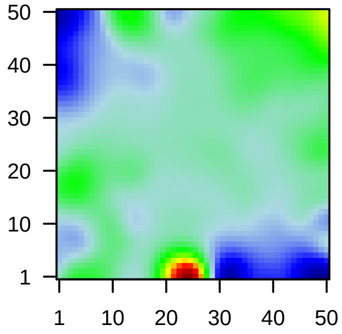
<FC> = −0.78

<shrinkage−t> = −27.57

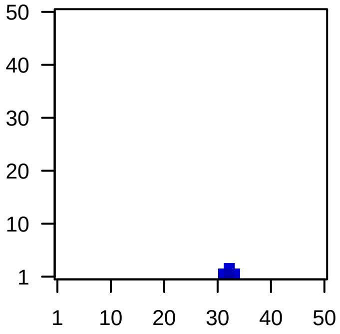
<p−value> = 0

<fdr> = 0.28

Profile



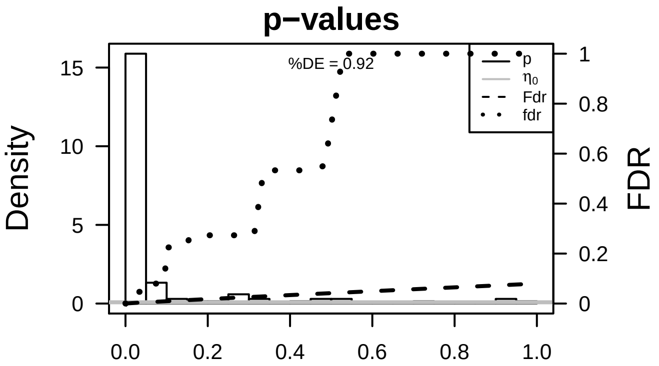
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	684	−1.69	2e−16	6e−16	32 x 1	bone marrow stromal cell antigen 2 [Source:HGNC Symbol;A
2	10866	−1.9	2e−16	6e−16	32 x 1	HLA complex P5 (non−protein coding) [Source:HGNC Symbo
3	3106	−1.9	2e−16	6e−16	32 x 1	major histocompatibility complex, class I, B [Source:HGNC Sy
4	3136	−2.07	2e−16	6e−16	32 x 1	
5	3627	−1.65	1e−15	1e−14	32 x 1	chemokine (C−X−C motif) ligand 10 [Source:HGNC Symbol;A
6	3134	−1.62	3e−15	1e−14	32 x 1	major histocompatibility complex, class I, F [Source:HGNC Sy
7	8743	−1.62	4e−15	3e−14	32 x 1	tumor necrosis factor (ligand) superfamily, member 10 [Sourc
8	6890	−1.6	7e−15	4e−14	32 x 1	transporter 1, ATP−binding cassette, sub−family B (MDR/TAP
9	115362	−1.59	1e−14	3e−12	32 x 1	guanylate binding protein 5 [Source:HGNC Symbol;Acc:1989
10	629	−1.5	3e−13	5e−12	32 x 1	complement factor B [Source:HGNC Symbol;Acc:1037]
11	4599	−1.35	8e−13	3e−11	32 x 1	myxovirus (influenza virus) resistance 1, interferon−inducible
12	85441	−1.43	4e−12	3e−11	32 x 1	helicase with zinc finger 2, transcriptional coactivator [Source
13	3133	−1.42	6e−12	5e−11	32 x 1	major histocompatibility complex, class I, E [Source:HGNC Sy
14	7453	−1.39	1e−11	5e−11	32 x 1	tryptophanyl−tRNA synthetase [Source:HGNC Symbol;Acc:1
15	4600	−1.39	2e−11	2e−10	32 x 1	myxovirus (influenza virus) resistance 2 (mouse) [Source:HG
16	94240	−1.37	3e−11	6e−10	32 x 1	epithelial stromal interaction 1 (breast) [Source:HGNC Symbo
17	10561	−1.32	1e−10	6e−10	32 x 1	interferon−induced protein 44 [Source:HGNC Symbol;Acc:16
18	10964	−1.31	2e−10	6e−10	32 x 1	interferon−induced protein 44−like [Source:HGNC Symbol;Ac
19	6772	−1.31	2e−10	6e−10	32 x 1	signal transducer and activator of transcription 1, 91kDa [Sou
20	10346	−1.3	3e−10	6e−10	32 x 1	tripartite motif containing 22 [Source:HGNC Symbol;Acc:163

p−values



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−51.73	NULL	29 / 51	BP	type I interferon signaling pathway
2	−46.84	NULL	6 / 6	Lymphoma	DAVE_MHCCII BL DN
3	−46.42	NULL	13 / 16	GSEA C2	MOSERLE_IFNA_RESPONSE
4	−40.78	NULL	11 / 16	GSEA C2	ZHANG_INTERFERON_RESPONSE
5	−39.83	NULL	7 / 10	CC	MHC class I protein complex
6	−37.66	NULL	9 / 10	GSEA C2	BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
7	−35.4	NULL	10 / 13	GSEA C2	BOWIE_RESPONSE_TO_TAMOXIFEN
8	−34.34	NULL	8 / 11	GSEA C2	BENNETT_SYSTEMIC_LUPUS_ERYTHEMATOSUS
9	−33.67	NULL	8 / 18	BP	positive regulation of T cell mediated cytotoxicity
10	−33.62	NULL	8 / 10	GSEA C2	GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
11	−33.47	NULL	11 / 16	GSEA C2	UROSEVIC_RESPONSE_TO_IMIQUIMOD
12	−32.55	NULL	31 / 123	BP	defense response to virus
13	−32.49	NULL	2 / 2	MMML CGS	MACIEJ_MMML 27
14	−32.44	NULL	11 / 16	GSEA C2	EINAV_INTERFERON_SIGNATURE_IN_CANCER
15	−29.95	NULL	7 / 18	MF	peptide antigen binding
16	−29.46	NULL	3 / 4	GSEA C2	KRASNOSELSKAYA_ILF3_TARGETS_UP
17	−29.26	NULL	6 / 8	GSEA C2	ROETH_TERT_TARGETS_UP
18	−28.64	NULL	27 / 109	BP	response to virus
19	−28.56	NULL	6 / 14	GSEA C2	RADAEVA_RESPONSE_TO_IFNA1_UP
20	−28.14	NULL	34 / 204	BP	cytokine−mediated signaling pathway
21	−28.02	NULL	13 / 31	BP	negative regulation of viral genome replication
22	−27.46	NULL	3 / 5	GSEA C2	KIM_LRRC3B_TARGETS
23	−27.05	NULL	16 / 60	BP	interferon−gamma−mediated signaling pathway
24	−25.21	NULL	7 / 16	GSEA C2	MAHADEVAN_RESPONSE_TO_MP470_UP
25	−23.3	NULL	7 / 14	Glio	Donson−immune cell intra signaling−associated with LTS in HGA
26	−22.63	NULL	6 / 12	GSEA C2	TSAI_DNAJB4_TARGETS_UP
27	−21.35	NULL	33 / 274	Lymphoma	SPANG_IL21 DN
28	−20.81	NULL	4 / 12	GSEA C2	ZHU_CMV_8_HR_UP
29	−20.6	NULL	48 / 572	Disease	GUDJ_psoriasis up
30	−20.53	NULL	5 / 23	CC	integral to lumenal side of endoplasmic reticulum membrane
31	−20.29	NULL	6 / 16	GSEA C2	XU_HGF_TARGETS_INDUCED_BY_AKT1_6HR
32	−20.13	NULL	6 / 16	GSEA C2	ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_UP
33	−19.85	NULL	13 / 70	BP	antigen processing and presentation of exogenous peptide antigen
34	−19.78	NULL	6 / 32	CC	ER to Golgi transport vesicle membrane
35	−19.24	NULL	13 / 74	BP	antigen processing and presentation of exogenous peptide antigen
36	−19.2	NULL	6 / 14	GSEA C2	XU_AKT1_TARGETS_6HR
37	−19.1	NULL	4 / 10	GSEA C2	DAUER_STAT3_TARGETS_DN
38	−18.73	NULL	5 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
39	−17.92	NULL	3 / 9	GSEA C2	DER_IFN_ALPHA_RESPONSE_UP
40	−17.92	NULL	3 / 9	GSEA C2	DER_IFN_GAMMA_RESPONSE_UP

GW_289

Local Summary

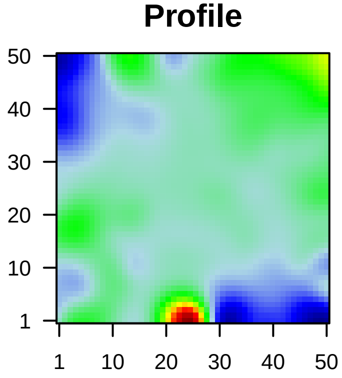
%DE = 0.87
metagenes = 17
genes = 278
genes in genesets = 275

genes with fdr < 0.1 = 232 (8 + / 224 −)
genes with fdr < 0.05 = 178 (4 + / 174 −)
genes with fdr < 0.01 = 118 (3 + / 115 −)

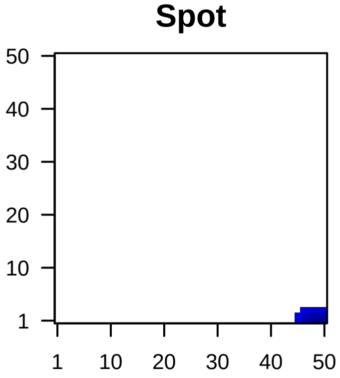
<r> metagenes = 0.99
<r> genes = 0.6

<FC> = −0.56
<shrinkage−t> = −19.71
<p−value> = 0
<fdr> = 0.45

Profile

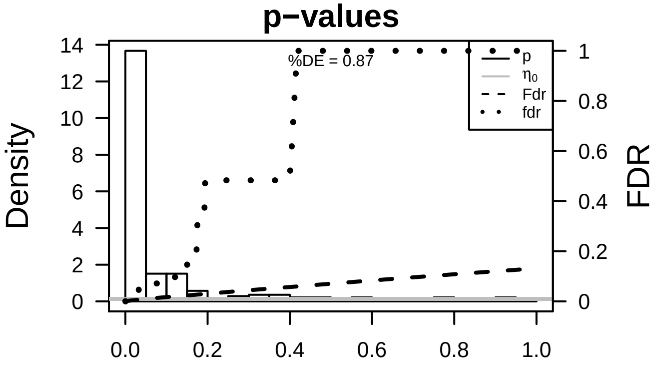


Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	6364	−3.08	2e−16	2e−15	46 x 1	chemokine (C−C motif) ligand 20 [Source:HGNC Symbol;Acc
2	3543	−1.54	2e−16	2e−15	49 x 1	immunoglobulin lambda−like polypeptide 1 [Source:HGNC Sy
3	3669	−1.71	2e−16	2e−15	48 x 1	interferon stimulated exonuclease gene 20kDa [Source:HGN
4	5880	−1.74	2e−16	2e−15	50 x 1	ras−related C3 botulinum toxin substrate 2 (rho family, small
5	10537	−1.86	2e−16	2e−15	50 x 1	ubiquitin D [Source:HGNC Symbol;Acc:18795]
6	260436	−1.61	5e−15	2e−13	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symbo
7	3002	−1.59	1e−14	3e−12	49 x 1	granzyme B (granzyme 2, cytotoxic T−lymphocyte−associate
8	3936	−1.51	2e−13	3e−12	50 x 1	lymphocyte cytosolic protein 1 (L−plastin) [Source:HGNC Syr
9	3128	−1.51	2e−13	3e−12	50 x 1	major histocompatibility complex, class II, DR beta 6 (pseudo
10	57172	−1.5	3e−13	1e−11	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
11	4283	−1.48	6e−13	6e−10	49 x 1	chemokine (C−X−C motif) ligand 9 [Source:HGNC Symbol;Ac
12	241	−1.37	3e−11	6e−10	50 x 1	arachidonate 5−lipoxygenase−activating protein [Source:HGN
13	3113	−1.36	3e−11	2e−09	50 x 1	major histocompatibility complex, class II, DP alpha 1 [Source
14	5996	−1.33	1e−10	3e−09	50 x 1	regulator of G−protein signaling 1 [Source:HGNC Symbol;Acc
15	6352	−1.29	3e−10	3e−09	48 x 1	chemokine (C−C motif) ligand 5 [Source:HGNC Symbol;Acc:
16	10563	−1.29	4e−10	3e−09	50 x 1	chemokine (C−X−C motif) ligand 13 [Source:HGNC Symbol;
17	3122	−1.2	4e−10	4e−09	50 x 1	major histocompatibility complex, class II, DR alpha [Source:
18	25849	−1.28	5e−10	8e−09	50 x 2	prostate androgen−regulated mucin−like protein 1 [Source:H
19	5341	−1.27	7e−10	1e−08	50 x 1	pleckstrin [Source:HGNC Symbol;Acc:9070]
20	4067	−1.26	1e−09	6e−08	46 x 2	v−yes−1 Yamaguchi sarcoma viral related oncogene homolog



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−31.12	NULL	98 / 417	H.Tiss	WIRTH_Immune system
2	−26.17	NULL	13 / 15	CC	MHC class II protein complex
3	−23.28	NULL	95 / 553	Cancer	Lembcke_Colonic Inflammation
4	−22.82	NULL	56 / 312	BP	immune response
5	−18.39	NULL	40 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
6	−18.39	NULL	40 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
7	−18.39	NULL	40 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
8	−18.39	NULL	40 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
9	−17.74	NULL	7 / 11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
10	−17.12	NULL	3 / 5	GSEA C2	WONG_ENDOMETRIAL_CANCER_LATE
11	−16.93	NULL	6 / 12	GSEA C2	BIOCARTA_CTL_PATHWAY
12	−16.39	NULL	15 / 47	BP	antigen processing and presentation
13	−16.25	NULL	7 / 11	GSEA C2	BIOCARTA_THELPER_PATHWAY
14	−16	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
15	−15.52	NULL	7 / 15	GSEA C2	FINAK_BREAST_CANCER_SDPP_SIGNATURE
16	−15.47	NULL	8 / 13	Cancer	GENTLES_modul18
17	−15.42	NULL	2 / 4	MMML CGS	MACIEJ_MMML 2
18	−15.15	NULL	18 / 60	BP	T cell costimulation
19	−15.02	NULL	4 / 7	Glio	Donson−cytotoxic effectors−associated with LTS in HGA
20	−14.42	NULL	5 / 13	GSEA C2	HAHTOLA_CTCL_PATHOGENESIS
21	−13.72	NULL	7 / 43	MF	chemokine activity
22	−13.66	NULL	17 / 74	BP	regulation of immune response
23	−13.57	NULL	4 / 8	GSEA C2	GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_DN
24	−13.55	NULL	3 / 6	GSEA C2	SANA_RESPONSE_TO_IFNG_UP
25	−13.2	NULL	28 / 162	CC	external side of plasma membrane
26	−13.04	NULL	6 / 13	GSEA C2	BIOCARTA_IL17_PATHWAY
27	−12.72	NULL	2 / 5	GSEA C2	WEST_ADRENOCORTICAL_CARCINOMA_VS_ADENOMA_DN
28	−12.56	NULL	6 / 14	GSEA C2	BIOCARTA_NO2IL12_PATHWAY
29	−12.33	NULL	5 / 15	Glio	Donson−chemokines/cytokines−associated with LTS in HGA
30	−12.25	NULL	8 / 21	CC	clathrin−coated endocytic vesicle membrane
31	−12.08	NULL	2 / 6	GSEA C2	BUDHU_LIVER_CANCER_METASTASIS_UP
32	−12.06	NULL	3 / 7	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
33	−12.01	NULL	31 / 316	Cancer	SPANG_BCL6−index2
34	−11.97	NULL	5 / 12	BP	immunoglobulin mediated immune response
35	−11.64	NULL	8 / 23	CC	integral to lumenal side of endoplasmic reticulum membrane
36	−11.45	NULL	2 / 6	GSEA C2	LUI_THYROID_CANCER_CLUSTER_4
37	−11.41	NULL	17 / 84	BP	T cell receptor signaling pathway
38	−11.16	NULL	26 / 204	BP	cell surface receptor signaling pathway
39	−11.09	NULL	4 / 8	GSEA C2	REACTOME_IMMUNOREGULATORY_INTERACTIONS_BETWEE
40	−10.99	NULL	4 / 10	GSEA C2	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_

GW_289

Local Summary

%DE = 0.86

metagenes = 12

genes = 187

genes in genesets = 182

genes with fdr < 0.1 = 141 (20 + / 121 −)

genes with fdr < 0.05 = 131 (19 + / 112 −)

genes with fdr < 0.01 = 113 (18 + / 95 −)

<r> metagenes = 0.97

<r> genes = 0.47

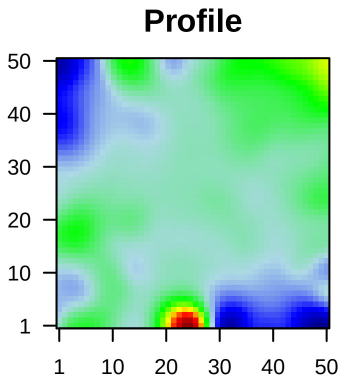
<FC> = −0.59

<shrinkage−t> = −20.8

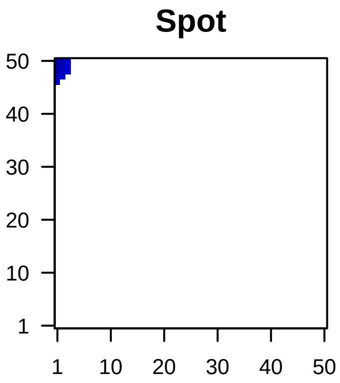
<p−value> = 0

<fdr> = 0.32

Profile

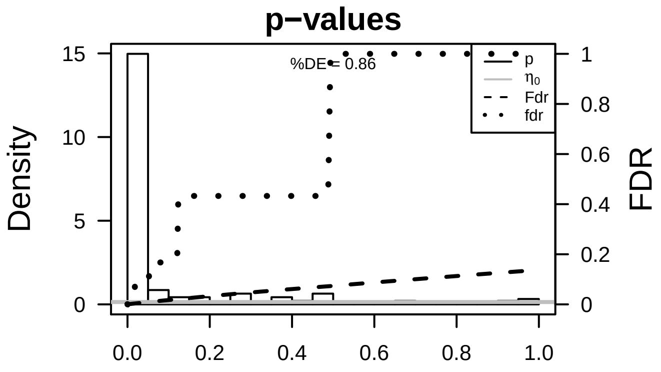


Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	131	−2.95	2e−16	2e−16	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	57016	1.82	2e−16	2e−16	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
3	8644	3.37	2e−16	2e−16	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
4	4680	−1.86	2e−16	2e−16	1 x 50	carcinoembryonic antigen−related cell adhesion molecule 6 (
5	1672	−2.13	2e−16	2e−16	1 x 50	defensin, beta 1 [Source:HGNC Symbol;Acc:2766]
6	414325	−1.75	2e−16	2e−16	1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
7	1673	−1.79	2e−16	2e−16	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
8	2877	2.25	2e−16	2e−16	1 x 50	glutathione peroxidase 2 (gastrointestinal) [Source:HGNC Sy
9	2941	2.69	2e−16	2e−16	3 x 50	glutathione S−transferase alpha 4 [Source:HGNC Symbol;Ac
10	56300	−3.35	2e−16	2e−16	1 x 47	interleukin 36, gamma [Source:HGNC Symbol;Acc:15741]
11	53833	−1.69	2e−16	2e−16	1 x 46	interleukin 20 receptor beta [Source:HGNC Symbol;Acc:6004
12	5653	−2.22	2e−16	2e−16	1 x 50	kallikrein−related peptidase 6 [Source:HGNC Symbol;Acc:63
13	388533	1.89	2e−16	2e−16	1 x 49	keratinocyte differentiation−associated protein [Source:HGNC
14	84648	−2.01	2e−16	2e−16	1 x 48	late cornified envelope 3D [Source:HGNC Symbol;Acc:16615
15	3934	−2.71	2e−16	2e−16	1 x 50	lipocalin 2 [Source:HGNC Symbol;Acc:6526]
16	84659	−1.95	2e−16	2e−16	1 x 48	ribonuclease, RNase A family, 7 [Source:HGNC Symbol;Acc:
17	6278	−3.95	2e−16	2e−16	1 x 49	S100 calcium binding protein A7 [Source:HGNC Symbol;Acc:
18	338324	−2.72	2e−16	2e−16	1 x 48	S100 calcium binding protein A7A [Source:HGNC Symbol;Ac
19	6286	−2.44	2e−16	2e−16	1 x 50	S100 calcium binding protein P [Source:HGNC Symbol;Acc:1
20	54809	−1.8	2e−16	2e−16	1 x 46	sterile alpha motif domain containing 9 [Source:HGNC Symb



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−32.97	NULL	18 / 21	CC	cornified envelope
2	−32.41	NULL	77 / 135	H.Tiss	WIRTH_Mucosa
3	−28.2	NULL	5 / 10	MF	RAGE receptor binding
4	−26.6	NULL	6 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
5	−26.38	NULL	3 / 10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
6	−25.43	NULL	85 / 572	Disease	GUDJ_psoriasis up
7	−22.73	NULL	19 / 42	BP	keratinization
8	−19.65	NULL	23 / 53	BP	keratinocyte differentiation
9	−19.51	NULL	22 / 76	BP	epidermis development
10	−16.03	NULL	4 / 27	BP	response to bacterium
11	−14.68	NULL	6 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
12	−14.44	NULL	3 / 16	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_DN
13	−14.22	NULL	6 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
14	−13.36	NULL	3 / 16	GSEA C2	CHEOK_RESPONSE_TO_MERCAPTOPURINE_AND_LD_MTX_
15	−12.83	NULL	3 / 15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
16	−12.44	NULL	6 / 13	BP	negative regulation of peptidase activity
17	−11.28	NULL	1 / 6	GSEA C2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_B_DN
18	−11.1	NULL	10 / 52	BP	negative regulation of endopeptidase activity
19	−10.79	NULL	4 / 15	GSEA C2	LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
20	−10.75	NULL	3 / 13	GSEA C2	FARMER_BREAST_CANCER_APOCRINE VS LUMINAL
21	−10.28	NULL	7 / 29	BP	regulation of proteolysis
22	−10.05	NULL	12 / 79	MF	serine−type endopeptidase inhibitor activity
23	−9.95	NULL	50 / 1182	CC	extracellular region
24	−9.92	NULL	7 / 73	BP	defense response to bacterium
25	−9.75	NULL	4 / 15	GSEA C2	CHANG_IMMORTALIZED_BY_HPV31_DN
26	−9.71	NULL	2 / 15	MF	interleukin−1 receptor binding
27	−9.68	NULL	6 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
28	−9.6	NULL	3 / 13	GSEA C2	HAN_SATB1_TARGETS_DN
29	−9.55	NULL	2 / 8	GSEA C2	MCLACHLAN_DENTAL_CARIES_UP
30	−9.54	NULL	3 / 16	GSEA C2	JAEGER_METASTASIS_DN
31	−9.34	NULL	1 / 16	BP	response to reactive oxygen species
32	−9.31	NULL	3 / 16	GSEA C2	LEE_LIVER_CANCER_ACOX1_UP
33	−9.19	NULL	2 / 12	GSEA C2	ZHAN_MULTIPLE_MYELOMA_DN
34	−8.9	NULL	2 / 9	GSEA C2	MCLACHLAN_DENTAL_CARIES_DN
35	−8.87	NULL	6 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
36	−8.86	NULL	1 / 9	GSEA C2	REACTOME_ETHANOL_OXIDATION
37	−8.8	NULL	3 / 18	BP	retinol metabolic process
38	−8.72	NULL	1 / 8	GSEA C2	MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_UP
39	−8.62	NULL	4 / 15	GSEA C2	LEE_LIVER_CANCER_MYC_E2F1_UP
40	−8.59	NULL	12 / 122	MF	serine−type endopeptidase activity