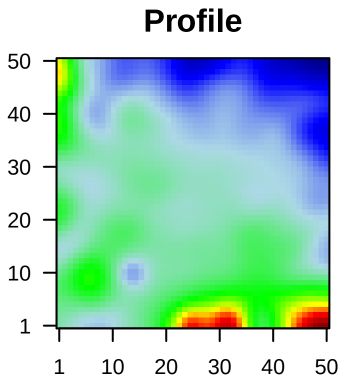
GW_156

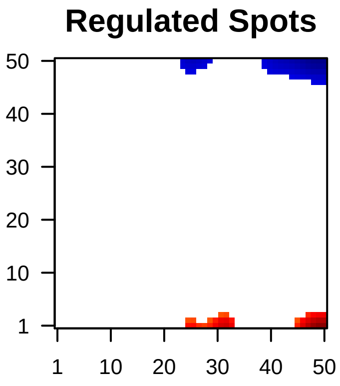
Global Summary

%DE = 0.14
genes with fdr < 0.2 = 1825 (1069 + / 756 −)
genes with fdr < 0.1 = 1397 (875 + / 522 −)
genes with fdr < 0.05 = 1135 (742 + / 393 −)
genes with fdr < 0.01 = 803 (580 + / 223 −)

genes in genesets = 16332

<FC> = 0
<shrinkage−t> = 0
<p−value> = 0.11
<fdr> = 0.86



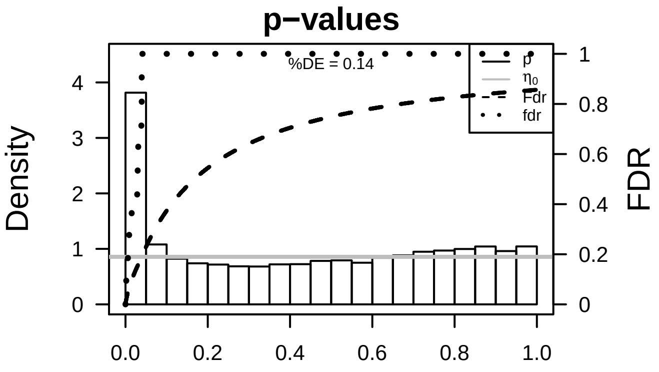


Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	58	2.92	2e−16	5e−14	25 x 1	actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
2	70	2.55	2e−16	5e−14	25 x 1	actin, alpha, cardiac muscle 1 [Source:HGNC Symbol;Acc:14
3	1109	−1.57	2e−16	5e−14	13 x 50	aldo−keto reductase family 1, member C4 [Source:HGNC Sy
4	401138	2.2	2e−16	5e−14	1 x 5	amelotin [Source:HGNC Symbol;Acc:33188]
5	341	1.48	2e−16	5e−14	50 x 1	apolipoprotein C−I [Source:HGNC Symbol;Acc:607]
6	348	1.52	2e−16	5e−14	50 x 1	apolipoprotein E [Source:HGNC Symbol;Acc:613]
7	387695	1.74	2e−16	5e−14	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Symb
8	6366	1.46	2e−16	5e−14	50 x 2	chemokine (C−C motif) ligand 21 [Source:HGNC Symbol;Acc
9	915	1.56	2e−16	5e−14	49 x 1	CD3d molecule, delta (CD3−TCR complex) [Source:HGNC S
10	629	1.91	2e−16	5e−14	32 x 1	complement factor B [Source:HGNC Symbol;Acc:1037]
11	1158	1.97	2e−16	5e−14	25 x 1	creatine kinase, muscle [Source:HGNC Symbol;Acc:1994]
12	1258	1.47	2e−16	5e−14	1 x 7	cyclic nucleotide gated channel beta 1 [Source:HGNC Symbo
13	49860	2.18	2e−16	5e−14	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
14	1410	1.76	2e−16	5e−14	25 x 1	crystallin, alpha B [Source:HGNC Symbol;Acc:2389]
15	6376	1.53	2e−16	5e−14	44 x 1	chemokine (C−X3−C motif) ligand 1 [Source:HGNC Symbol;
16	3627	1.57	2e−16	5e−14	32 x 1	chemokine (C−X−C motif) ligand 10 [Source:HGNC Symbol;
17	6373	1.65	2e−16	5e−14	32 x 1	chemokine (C−X−C motif) ligand 11 [Source:HGNC Symbol;
18	9547	1.96	2e−16	5e−14	1 x 46	chemokine (C−X−C motif) ligand 14 [Source:HGNC Symbol;
19	4283	1.45	2e−16	5e−14	49 x 1	chemokine (C−X−C motif) ligand 9 [Source:HGNC Symbol;Ac
20	1673	1.68	2e−16	5e−14	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	15.36	NULL	127	H.Tiss	WIRTH_Muscle
2	14.49	NULL	36	BP	muscle filament sliding
3	14.28	NULL	16	H.Tiss	WIRTH_Hippocampus
4	13.72	NULL	51	BP	type I interferon signaling pathway
5	13.15	NULL	312	BP	immune response
6	12.9	NULL	572	Disease	GUDJ_psoriasis up
7	12.79	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_F
8	12.59	NULL	16	GSEA C2	UROSEVIC_RESPONSE_TO_IMIQUIMOD
9	11.45	NULL	553	Cancer	Lembcke_Colonic Inflammation
10	11.03	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
11	11.02	NULL	15	CC	MHC class II protein complex
12	11.01	NULL	417	H.Tiss	WIRTH_Immune system
13	10.79	NULL	44	MF	structural constituent of muscle
14	10.79	NULL	204	BP	cytokine−mediated signaling pathway
15	10.77	NULL	16	GSEA C2	ZHANG_INTERFERON_RESPONSE
16	10.71	NULL	60	BP	interferon−gamma−mediated signaling pathway
17	10.71	NULL	47	BP	antigen processing and presentation
18	10.61	NULL	123	BP	defense response to virus
19	10.57	NULL	16	GSEA C2	MOSERLE_IFNA_RESPONSE
20	10.54	NULL	13	GSEA C2	BOWIE_RESPONSE_TO_TAMOXIFEN
Underexpressed					
1	−9.26	NULL	914	Chr	Chr 3
2	−8.87	NULL	436	miRNA target−starBase	hsa−miR−548n
3	−8.47	NULL	315	miRNA target−starBase	hsa−miR−30e
4	−7.74	NULL	264	miRNA target−starBase	hsa−miR−30a
5	−7.57	NULL	268	miRNA target−starBase	hsa−miR−30d
6	−7.29	NULL	268	miRNA target−starBase	hsa−miR−30b
7	−7.24	NULL	336	miRNA target−starBase	hsa−miR−548d−5p
8	−7.08	NULL	307	miRNA target−starBase	hsa−miR−548c−5p
9	−7.01	NULL	336	miRNA target−starBase	hsa−miR−548b−5p
10	−6.94	NULL	278	miRNA target−starBase	hsa−miR−30c
11	−6.93	NULL	310	miRNA target−starBase	hsa−miR−340
12	−6.86	NULL	158	miRNA target−starBase	hsa−miR−141
13	−6.85	NULL	649	BP	gene expression
14	−6.84	NULL	313	miRNA target−starBase	hsa−miR−559
15	−6.84	NULL	217	miRNA target−starBase	hsa−miR−548m
16	−6.84	NULL	335	miRNA target−starBase	hsa−miR−142−5p
17	−6.81	NULL	368	miRNA target−starBase	hsa−miR−144
18	−6.76	NULL	215	miRNA target−starBase	hsa−miR−203
19	−6.7	NULL	321	miRNA target−starBase	hsa−miR−548a−5p
20	−6.66	NULL	288	miRNA target−starBase	hsa−miR−548j



GW_156

Local Summary

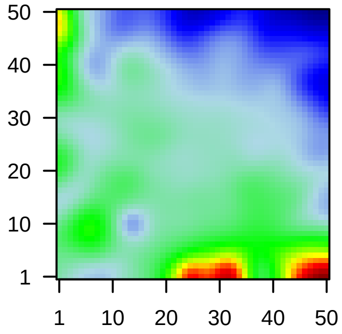
%DE = 0.93
metagenes = 18
genes = 222
genes in genesets = 219

genes with fdr < 0.1 = 194 (192 + / 2 −)
genes with fdr < 0.05 = 183 (181 + / 2 −)
genes with fdr < 0.01 = 173 (171 + / 2 −)

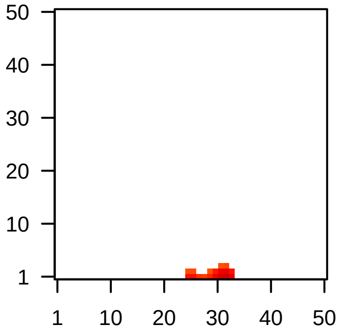
<r> metagenes = 0.73
<r> genes = 0.26

<FC> = 0.84
<shrinkage−t> = 29.35
<p−value> = 0
<fdr> = 0.19

Profile



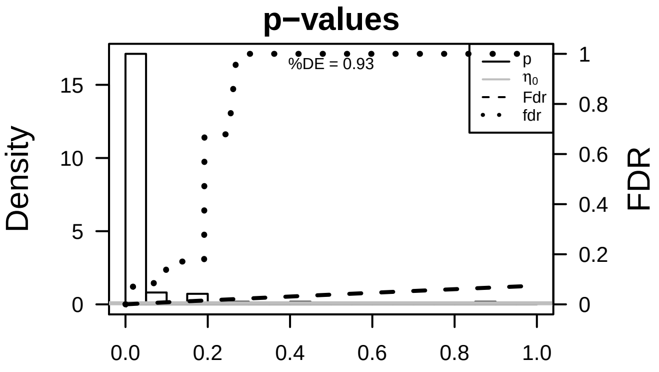
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	58	2.92	2e−16	2e−16	25 x 1	actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
2	70	2.55	2e−16	2e−16	25 x 1	actin, alpha, cardiac muscle 1 [Source:HGNC Symbol;Acc:14
3	629	1.91	2e−16	2e−16	32 x 1	complement factor B [Source:HGNC Symbol;Acc:1037]
4	1158	1.97	2e−16	2e−16	25 x 1	creatine kinase, muscle [Source:HGNC Symbol;Acc:1994]
5	1410	1.76	2e−16	2e−16	25 x 1	crystallin, alpha B [Source:HGNC Symbol;Acc:2389]
6	3627	1.57	2e−16	2e−16	32 x 1	chemokine (C−X−C motif) ligand 10 [Source:HGNC Symbol;
7	6373	1.65	2e−16	2e−16	32 x 1	chemokine (C−X−C motif) ligand 11 [Source:HGNC Symbol;
8	1917	1.51	2e−16	2e−16	25 x 1	eukaryotic translation elongation factor 1 alpha 2 [Source:HG
9	55008	1.51	2e−16	2e−16	32 x 1	HECT and RLD domain containing E3 ubiquitin protein ligase
10	9636	1.77	2e−16	2e−16	32 x 1	ISG15 ubiquitin−like modifier [Source:HGNC Symbol;Acc:40
11	4151	2.24	2e−16	2e−16	25 x 1	myoglobin [Source:HGNC Symbol;Acc:6915]
12	4600	1.75	2e−16	2e−16	32 x 1	myxovirus (influenza virus) resistance 2 (mouse) [Source:HG
13	4606	1.56	2e−16	2e−16	25 x 1	myosin binding protein C, fast type [Source:HGNC Symbol;A
14	4608	2.16	2e−16	2e−16	25 x 1	myosin binding protein H [Source:HGNC Symbol;Acc:7552]
15	4620	2.94	2e−16	2e−16	25 x 1	myosin, heavy chain 2, skeletal muscle, adult [Source:HGNC
16	4633	1.69	2e−16	2e−16	25 x 1	myosin, light chain 2, regulatory, cardiac, slow [Source:HGNC
17	4703	1.43	2e−16	2e−16	25 x 1	nebulin [Source:HGNC Symbol;Acc:7720]
18	6288	1.5	2e−16	2e−16	31 x 1	serum amyloid A1 [Source:HGNC Symbol;Acc:10513]
19	6588	3.42	2e−16	2e−16	25 x 1	sarcolipin [Source:HGNC Symbol;Acc:11089]
20	8557	1.86	2e−16	2e−16	25 x 1	titin−cap [Source:HGNC Symbol;Acc:11610]

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	39.11	NULL	19 / 36	BP	muscle filament sliding
2	38.81	NULL	11 / 16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_F
3	38.13	NULL	9 / 16	H.Tiss	WIRTH_Hippocampus
4	36.79	NULL	38 / 127	H.Tiss	WIRTH_Muscle
5	31.39	NULL	29 / 51	BP	type I interferon signaling pathway
6	30.06	NULL	18 / 44	MF	structural constituent of muscle
7	29.09	NULL	7 / 12	CC	myosin filament
8	29.09	NULL	13 / 16	GSEA C2	MOSERLE_IFNA_RESPONSE
9	28.49	NULL	11 / 16	GSEA C2	UROSEVIC_RESPONSE_TO_IMIQUIMOD
10	27.89	NULL	9 / 10	GSEA C2	BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
11	25.57	NULL	11 / 16	GSEA C2	ZHANG_INTERFERON_RESPONSE
12	25.03	NULL	10 / 13	GSEA C2	BOWIE_RESPONSE_TO_TAMOXIFEN
13	24.16	NULL	11 / 16	GSEA C2	EINAV_INTERFERON_SIGNATURE_IN_CANCER
14	24.13	NULL	8 / 10	GSEA C2	GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
15	22.49	NULL	31 / 123	BP	defense response to virus
16	21.73	NULL	27 / 109	BP	response to virus
17	21.3	NULL	9 / 37	CC	sarcomere
18	21.22	NULL	6 / 8	GSEA C2	ROETH_TERT_TARGETS_UP
19	20.78	NULL	3 / 4	GSEA C2	KRASNOSELSKAYA_ILF3_TARGETS_UP
20	20.27	NULL	5 / 13	CC	muscle myosin complex
21	20.08	NULL	13 / 31	BP	negative regulation of viral genome replication
22	20.01	NULL	7 / 14	CC	contractile fiber
23	19.45	NULL	7 / 16	GSEA C2	MAHADEVAN_RESPONSE_TO_MP470_UP
24	19.3	NULL	5 / 15	GSEA C2	BECKER_TAMOXIFEN_RESISTANCE_UP
25	18.62	NULL	16 / 84	BP	muscle contraction
26	18.53	NULL	10 / 34	CC	myofibril
27	18.5	NULL	8 / 11	GSEA C2	BENNETT_SYSTEMIC_LUPUS_ERYTHEMATOSUS
28	18.13	NULL	5 / 11	BP	cardiac muscle tissue morphogenesis
29	17.79	NULL	3 / 5	GSEA C2	KIM_LRRC3B_TARGETS
30	17.17	NULL	6 / 12	BP	skeletal muscle contraction
31	16.94	NULL	34 / 204	BP	cytokine−mediated signaling pathway
32	15.78	NULL	4 / 12	GSEA C2	ZHU_CMV_8_HR_UP
33	15.74	NULL	5 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
34	15.48	NULL	5 / 20	CC	I band
35	15.44	NULL	6 / 12	GSEA C2	TSAI_DNAJB4_TARGETS_UP
36	15.18	NULL	17 / 88	CC	Z disc
37	15.15	NULL	4 / 10	GSEA C2	DAUER_STAT3_TARGETS_DN
38	15.06	NULL	6 / 14	GSEA C2	RADAEVA_RESPONSE_TO_IFNA1_UP
39	15.04	NULL	6 / 16	CC	M band
40	14.84	NULL	8 / 37	BP	cardiac muscle contraction

GW_156

Local Summary

%DE = 0.81

metagenes = 16

genes = 271

genes in genesets = 268

genes with fdr < 0.1 = 202 (199 + / 3 −)

genes with fdr < 0.05 = 183 (180 + / 3 −)

genes with fdr < 0.01 = 162 (162 + / 0 −)

<r> metagenes = 0.99

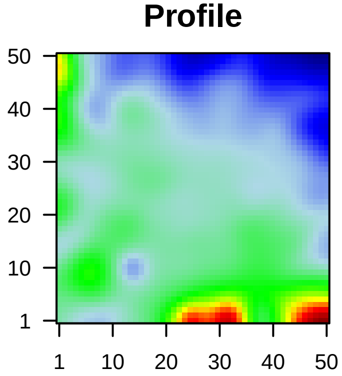
<r> genes = 0.6

<FC> = 0.6

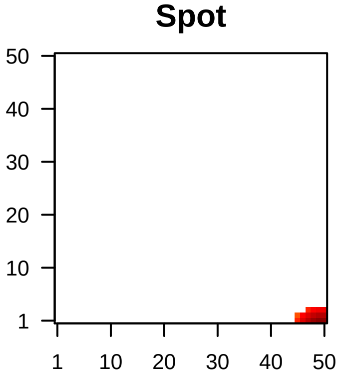
<shrinkage−t> = 21.18

<p−value> = 0

<fdr> = 0.32



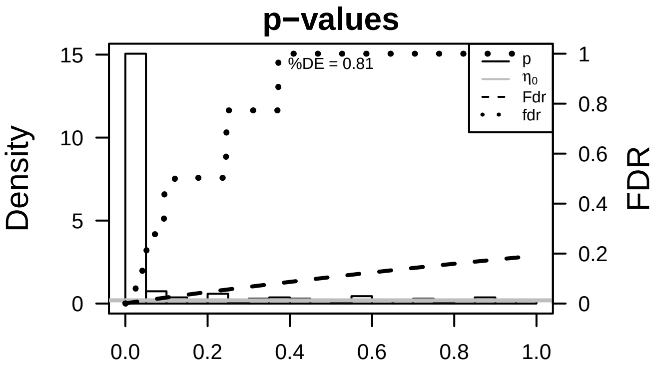
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	341	1.48	2e−16	9e−16	50 x 1	apolipoprotein C−I [Source:HGNC Symbol;Acc:607]
2	348	1.52	2e−16	9e−16	50 x 1	apolipoprotein E [Source:HGNC Symbol;Acc:613]
3	6366	1.46	2e−16	9e−16	50 x 2	chemokine (C−C motif) ligand 21 [Source:HGNC Symbol;Acc
4	915	1.56	2e−16	9e−16	49 x 1	CD3d molecule, delta (CD3−TCR complex) [Source:HGNC S
5	4283	1.45	2e−16	9e−16	49 x 1	chemokine (C−X−C motif) ligand 9 [Source:HGNC Symbol;A
6	3001	1.81	2e−16	9e−16	48 x 1	granzyme A (granzyme 1, cytotoxic T−lymphocyte−associate
7	3002	1.56	2e−16	9e−16	49 x 1	granzyme B (granzyme 2, cytotoxic T−lymphocyte−associate
8	2999	1.7	2e−16	9e−16	47 x 1	granzyme H (cathepsin G−like 2, protein h−CCPX) [Source:H
9	3120	1.67	2e−16	9e−16	47 x 1	major histocompatibility complex, class II, DQ beta 2 [Source:
10	3123	2.73	2e−16	9e−16	45 x 1	major histocompatibility complex, class II, DR beta 1 [Source:
11	3128	1.47	2e−16	9e−16	50 x 1	major histocompatibility complex, class II, DR beta 6 (pseudo
12	4818	1.51	2e−16	9e−16	49 x 1	natural killer cell group 7 sequence [Source:HGNC Symbol;A
13	5920	2.02	2e−16	9e−16	48 x 1	retinoic acid receptor responder (tazarotene induced) 3 [Sour
14	713	1.33	9e−15	6e−13	50 x 1	complement component 1, q subcomponent, B chain [Source
15	10673	1.31	3e−14	6e−13	50 x 1	tumor necrosis factor (ligand) superfamily, member 13b [Sour
16	914	1.31	3e−14	1e−12	49 x 1	CD2 molecule [Source:HGNC Symbol;Acc:1639]
17	3115	1.29	6e−14	1e−12	49 x 1	major histocompatibility complex, class II, DP beta 1 [Source:
18	256236	1.29	8e−14	1e−12	50 x 1	napsin B aspartic peptidase, pseudogene [Source:HGNC Syr
19	924	1.28	1e−13	4e−12	49 x 1	CD7 molecule [Source:HGNC Symbol;Acc:1695]
20	7351	1.26	3e−13	4e−12	50 x 1	uncoupling protein 2 (mitochondrial, proton carrier) [Source:H



p−values

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	39.92	NULL	13 / 15	CC	MHC class II protein complex
2	30.22	NULL	94 / 417	H.Tiss	WIRTH_Immune system
3	29.67	NULL	3 / 3	MMML CGS	MACIEJ_MMML 7
4	25.93	NULL	7 / 11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
5	25.15	NULL	4 / 7	Glio	Donson−cytotoxic effectors−associated with LTS in HGA
6	24.68	NULL	15 / 47	BP	antigen processing and presentation
7	24.57	NULL	17 / 60	BP	T cell costimulation
8	24.37	NULL	8 / 21	CC	clathrin−coated endocytic vesicle membrane
9	23.17	NULL	8 / 23	CC	integral to lumenal side of endoplasmic reticulum membrane
10	23.05	NULL	54 / 312	BP	immune response
11	22.23	NULL	6 / 11	GSEA C2	BIOCARTA_THELPER_PATHWAY
12	21.98	NULL	6 / 12	GSEA C2	BIOCARTA_CTL_PATHWAY
13	20.79	NULL	8 / 28	CC	transport vesicle membrane
14	19.43	NULL	93 / 553	Cancer	Lembcke_Colonic Inflammation
15	19.31	NULL	8 / 32	CC	ER to Golgi transport vesicle membrane
16	19.24	NULL	3 / 6	GSEA C2	SANA_RESPONSE_TO_IFNG_UP
17	18.49	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
18	18.37	NULL	8 / 35	CC	trans−Golgi network membrane
19	18.14	NULL	16 / 84	BP	T cell receptor signaling pathway
20	17.31	NULL	7 / 13	Cancer	GENTLES_modul18
21	17.14	NULL	5 / 13	GSEA C2	BIOCARTA_IL17_PATHWAY
22	16.75	NULL	4 / 8	GSEA C2	NIELSEN_SYNOVIAL_SARCOMA_DN
23	16.55	NULL	17 / 74	BP	regulation of immune response
24	16.49	NULL	12 / 60	BP	interferon−gamma−mediated signaling pathway
25	16.23	NULL	14 / 87	BP	antigen processing and presentation of exogenous peptide antigen
26	16.01	NULL	2 / 3	GSEA C2	KEGG_VIRAL_MYOCARDITIS
27	15.86	NULL	4 / 8	GSEA C2	REACTOME_IMMUNOREGULATORY_INTERACTIONS_BETWEE
28	15.76	NULL	8 / 46	CC	endocytic vesicle membrane
29	15.64	NULL	2 / 4	MMML CGS	MACIEJ_MMML 2
30	15.04	NULL	9 / 52	Chr	Chr HSCHR6_MHC_QBL
31	14.64	NULL	5 / 14	GSEA C2	BIOCARTA_NO2IL12_PATHWAY
32	14.48	NULL	5 / 13	MMML CGS	MACIEJ_MMML 6
33	14.28	NULL	5 / 12	BP	immunoglobulin mediated immune response
34	14.23	NULL	4 / 10	GSEA C2	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_
35	13.91	NULL	4 / 8	Glio	Donson−migration tethering and rolling−associated with LTS in HG
36	13.74	NULL	4 / 12	CC	T cell receptor complex
37	13.72	NULL	2 / 4	GSEA C2	REACTOME_CLASSICAL_ANTIBODY_MEDIATED_COMPLEMEN
38	13.72	NULL	4 / 10	GSEA C2	LEE_DIFFERENTIATING_T_LYMPHOCYTE
39	13.63	NULL	4 / 16	BP	cytolysis
40	13.44	NULL	2 / 4	GSEA C2	KEGG_LEISHMANIA_INFECTION

GW_156

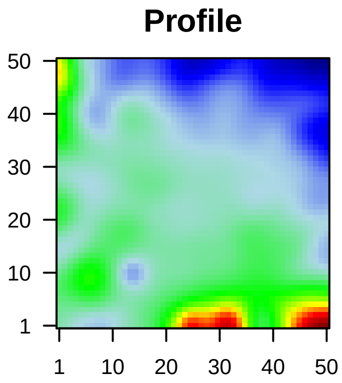
Local Summary

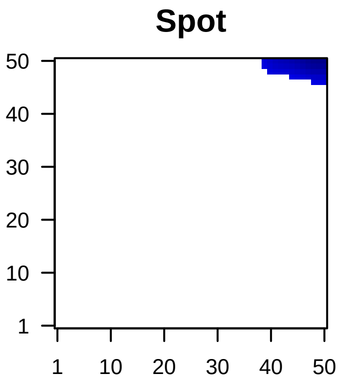
%DE = 0.7
metagenes = 45
genes = 632
genes in genesets = 627

genes with fdr < 0.1 = 298 (15 + / 283 −)
genes with fdr < 0.05 = 217 (13 + / 204 −)
genes with fdr < 0.01 = 105 (10 + / 95 −)

<r> metagenes = 0.82
<r> genes = 0.25

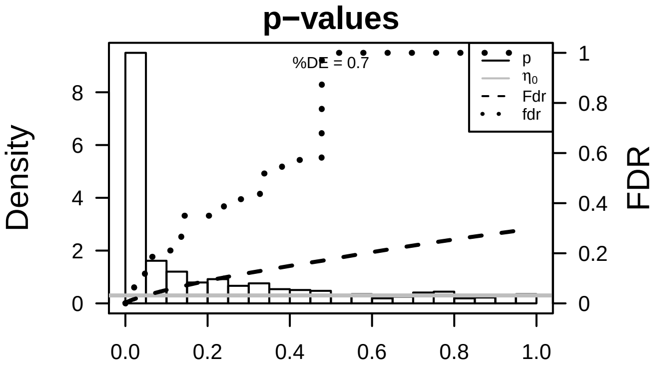
<FC> = −0.3
<shrinkage−t> = −10.6
<p−value> = 0.01
<fdr> = 0.64


Profile


Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	4072	−1.59	2e−16	2e−14	50 x 50	epithelial cell adhesion molecule [Source:HGNC Symbol;Acc:
2	256764	−2.51	2e−16	2e−14	50 x 50	WD repeat domain 72 [Source:HGNC Symbol;Acc:26790]
3	3304	−1.28	4e−16	8e−12	49 x 49	heat shock 70kDa protein 1A [Source:HGNC Symbol;Acc:52
4	875	−1.3	4e−14	9e−12	49 x 47	cystathionine−beta−synthase [Source:HGNC Symbol;Acc:15
5	55832	1.28	9e−14	2e−11	47 x 50	cullin−associated and neddylation−dissociated 1 [Source:HG
6	10576	1.26	2e−13	2e−11	41 x 50	chaperonin containing TCP1, subunit 2 (beta) [Source:HGNC
7	214	−1.25	3e−13	4e−10	50 x 50	activated leukocyte cell adhesion molecule [Source:HGNC S
8	26872	−1.2	2e−12	5e−10	40 x 50	six transmembrane epithelial antigen of the prostate 1 [Sourc
9	139728	−1.18	6e−12	5e−10	49 x 49	pregnancy up−regulated nonubiquitous CaM kinase [Source:
10	4922	−1.18	8e−12	2e−09	50 x 50	neurotensin [Source:HGNC Symbol;Acc:8038]
11	445	1.15	2e−11	2e−09	50 x 47	argininosuccinate synthase 1 [Source:HGNC Symbol;Acc:75
12	116028	−1.15	3e−11	7e−09	46 x 47	RecQ mediated genome instability 2 [Source:HGNC Symbol;
13	8833	−1.12	6e−11	3e−08	45 x 50	guanine monphosphate synthase [Source:HGNC Symbol;Ac
14	10643	−1.09	2e−10	8e−08	48 x 50	insulin−like growth factor 2 mRNA binding protein 3 [Source:
15	57122	1.06	6e−10	1e−07	45 x 49	nucleoporin 107kDa [Source:HGNC Symbol;Acc:29914]
16	339512	−1.04	1e−09	5e−07	50 x 50	chromosome 1 open reading frame 110 [Source:HGNC Sym
17	7345	−1.01	4e−09	7e−07	50 x 46	ubiquitin carboxyl−terminal esterase L1 (ubiquitin thiolesteras
18	2222	−0.99	7e−09	9e−07	50 x 50	farnesyl−diphosphate farnesyltransferase 1 [Source:HGNC S
19	26047	−0.98	1e−08	9e−07	50 x 50	contactin associated protein−like 2 [Source:HGNC Symbol;A
20	57291	−0.97	2e−08	9e−07	50 x 50	differentiation antagonizing non−protein coding RNA [Source:


p−values

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−16.01	NULL	87 / 142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
2	−16.01	NULL	87 / 142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
3	−14.44	NULL	11 / 16	Cancer	WOLFER_overlap genes
4	−12.71	NULL	95 / 370	BP	mitotic cell cycle
5	−12.67	NULL	15 / 16	GSEA C2	FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
6	−12.19	NULL	14 / 15	GSEA C2	FINETTI_BREAST_CANCER_KINOME_RED
7	−11.71	NULL	4 / 12	GSEA C2	HELLER_SILENCED_BY_METHYLATION_DN
8	−11.2	NULL	4 / 13	BP	regulation of blood vessel size
9	−11.07	NULL	12 / 16	GSEA C2	EGUCHI_CELL_CYCLE_RB1_TARGETS
10	−10.92	NULL	13 / 30	BP	DNA strand elongation involved in DNA replication
11	−10.85	NULL	8 / 11	GSEA C2	ODONNELL_TFRC_TARGETS_DN
12	−10.48	NULL	5 / 11	GSEA C2	REACTOME_PURINE_RIBONUCLEOSIDE_MONOPHOSPHATE_
13	−10.26	NULL	88 / 914	Chr	Chr 3
14	−10.12	NULL	5 / 8	GSEA C2	REACTOME_E2F_TRANSCRIPTIONAL_TARGETS_AT_G1_S
15	−9.62	NULL	6 / 11	GSEA C2	REACTOME_UNWINDING_OF_DNA
16	−9.48	NULL	1 / 2	GSEA C2	KUROKAWA_LIVER_CANCER_EARLY_RECURRENCE_UP
17	−9.47	NULL	6 / 11	GSEA C2	REACTOME_E2F_MEDIATED_REGULATION_OF_DNA_REPLIC
18	−9.14	NULL	5 / 14	BP	purine ribonucleoside monophosphate biosynthetic process
19	−9.09	NULL	2 / 15	GSEA C2	SABATES_COLORECTAL_ADENOMA_UP
20	−8.95	NULL	4 / 16	GSEA C2	KAN_RESPONSE_TO_ARSENIC_TRIOXIDE
21	−8.94	NULL	95 / 530	Cancer	Lembcke_Normal vs Adenoma
22	−8.94	NULL	23 / 57	Glio	developing astrocytes
23	−8.57	NULL	6 / 15	GSEA C2	KEGG_GLUTATHIONE_METABOLISM
24	−8.5	NULL	8 / 22	BP	DNA replication initiation
25	−8.38	NULL	2 / 7	GSEA C2	MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
26	−8.3	NULL	7 / 15	GSEA C2	REACTOME_NEP_NS2_INTERACTS_WITH_THE_CELLULAR_E
27	−8.26	NULL	5 / 15	Cancer	BEN−PORATH_UP
28	−8.22	NULL	37 / 149	BP	DNA replication
29	−8.21	NULL	34 / 148	BP	G1/S transition of mitotic cell cycle
30	−8.19	NULL	11 / 15	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
31	−8.03	NULL	7 / 11	GSEA C2	KALMA_E2F1_TARGETS
32	−8	NULL	10 / 16	GSEA C2	KANG_DOXORUBICIN_RESISTANCE_UP
33	−7.99	NULL	106 / 949	CC	nucleoplasm
34	−7.99	NULL	7 / 16	GSEA C2	REACTOME_DNA_STRAND_ELONGATION
35	−7.96	NULL	8 / 15	GSEA C2	ODONNELL_TARGETS_OF_MYC_AND_TFRC_DN
36	−7.9	NULL	7 / 15	GSEA C2	MMS_MOUSE_LYMPH_HIGH_4HRS_UP
37	−7.82	NULL	8 / 12	GSEA C2	LI_WILMS_TUMOR_VS_FETAL_KIDNEY_1_DN
38	−7.74	NULL	2 / 4	MMML CGS	MACIEJ_MMML 41
39	−7.72	NULL	5 / 13	GSEA C2	SLEBOS_HEAD_AND_NECK_CANCER_WITH_HPV_UP
40	−7.68	NULL	3 / 11	GSEA C2	ITO_PTTG1_TARGETS_UP

GW_156

Local Summary

%DE = 0.67

metagenes = 13

genes = 239

genes in genesets = 236

genes with fdr < 0.1 = 106 (2 + / 104 −)

genes with fdr < 0.05 = 88 (2 + / 86 −)

genes with fdr < 0.01 = 50 (0 + / 50 −)

<r> metagenes = 0.96

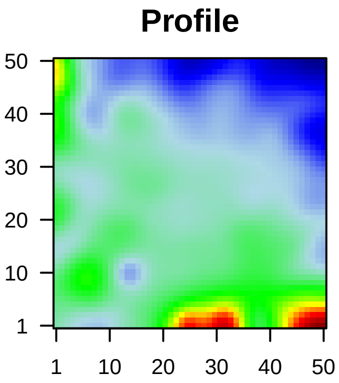
<r> genes = 0.33

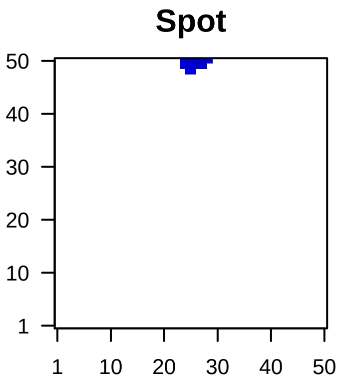
<FC> = −0.33

<shrinkage−t> = −11.53

<p−value> = 0.02

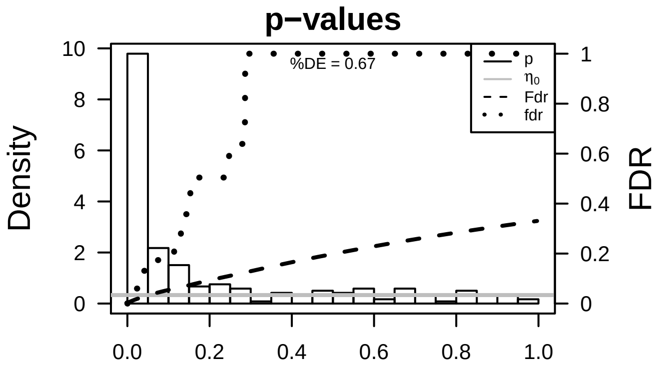
<fdr> = 0.62





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	71	−1.05	2e−11	7e−08	24 x 50	actin, gamma 1 [Source:HGNC Symbol;Acc:144]
2	10787	−1.06	8e−10	7e−06	25 x 50	NCK−associated protein 1 [Source:HGNC Symbol;Acc:7666]
3	10972	−0.92	9e−08	5e−05	25 x 50	transmembrane emp24−like trafficking protein 10 (yeast) [Sou
4	3716	−0.85	7e−07	8e−05	25 x 49	Janus kinase 1 [Source:HGNC Symbol;Acc:6190]
5	51377	−0.81	3e−06	8e−05	28 x 50	ubiquitin carboxyl−terminal hydrolase L5 [Source:HGNC Sym
6	1738	−0.79	4e−06	8e−05	28 x 50	dihydrolipoamide dehydrogenase [Source:HGNC Symbol;Acc
7	3799	−0.79	4e−06	8e−05	25 x 50	kinesin family member 5B [Source:HGNC Symbol;Acc:6324]
8	1499	−0.79	4e−06	1e−04	24 x 50	catenin (cadherin−associated protein), beta 1, 88kDa [Source
9	55970	−0.78	6e−06	6e−04	25 x 50	guanine nucleotide binding protein (G protein), gamma 12 [So
10	163126	−0.75	1e−05	6e−04	25 x 49	EP300 interacting inhibitor of differentiation 2 [Source:HGNC
11	201595	−0.71	3e−05	6e−04	26 x 50	STT3B, subunit of the oligosaccharyltransferase complex (cat
12	1176	−0.71	3e−05	6e−04	26 x 50	adaptor−related protein complex 3, sigma 1 subunit [Source:H
13	9960	−0.7	5e−05	6e−04	24 x 49	ubiquitin specific peptidase 3 [Source:HGNC Symbol;Acc:126
14	91137	−0.7	5e−05	6e−04	28 x 50	solute carrier family 25, member 46 [Source:HGNC Symbol;A
15	10175	−0.7	5e−05	1e−03	28 x 50	cornichon family AMPA receptor auxiliary protein 1 [Source:H
16	51014	−0.67	9e−05	1e−03	26 x 50	transmembrane emp24 protein transport domain containing 7
17	9652	−0.67	1e−04	1e−03	26 x 50	tetratricopeptide repeat domain 37 [Source:HGNC Symbol;Ac
18	201158	−0.67	1e−04	1e−03	26 x 50	trans−golgi network vesicle protein 23 homolog C (S. cerevisi
19	10730	−0.65	1e−04	1e−03	27 x 50	YME1−like 1 ATPase [Source:HGNC Symbol;Acc:12843]
20	55854	−0.65	2e−04	1e−03	28 x 50	zinc finger CCCH−type containing 15 [Source:HGNC Symbol



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−16.07	NULL	5 / 8	MMML CGS	MACIEJ_MMML 50
2	−10.94	NULL	3 / 10	MF	lamin binding
3	−10.78	NULL	5 / 15	BP	COPII vesicle coating
4	−10.22	NULL	2 / 14	BP	embryonic heart tube development
5	−9.71	NULL	3 / 11	GSEA C2	FINETTI_BREAST_CANCERS_KINOME_GRAY
6	−9.61	NULL	27 / 269	miRNA target−starBase	hsa−miR−124
7	−9.58	NULL	4 / 25	miRNA target−starBase	hsa−miR−1273
8	−9.49	NULL	2 / 4	GSEA C2	KUROKAWA_LIVER_CANCER_EARLY_RECURRENCE_DN
9	−9.34	NULL	25 / 324	miRNA target−starBase	hsa−miR−19a
10	−9.34	NULL	4 / 24	CC	endoplasmic reticulum−Golgi intermediate compartment membran
11	−9.12	NULL	16 / 184	miRNA target−starBase	hsa−miR−586
12	−8.7	NULL	14 / 134	miRNA target−starBase	hsa−miR−656
13	−8.62	NULL	3 / 16	GSEA C2	JI_RESPONSE_TO_FSH_DN
14	−8.51	NULL	2 / 13	BP	COPI coating of Golgi vesicle
15	−8.43	NULL	24 / 318	miRNA target−starBase	hsa−miR−590−3p
16	−8.4	NULL	3 / 14	GSEA C2	CHNG_MULTIPLE_MYELOMA_HYPERPLOID_DN
17	−8.4	NULL	5 / 49	Glio	Vishal_subnetwork signature of survival in GBM
18	−8.22	NULL	3 / 11	GSEA C2	REACTOME_BETACATENIN_PHOSPHORYLATION_CASCADE
19	−8.21	NULL	19 / 198	miRNA target−starBase	hsa−miR−33a
20	−8.11	NULL	16 / 241	miRNA target−starBase	hsa−miR−122
21	−7.99	NULL	1 / 3	miRNA target	miR−223
22	−7.72	NULL	22 / 310	miRNA target−starBase	hsa−miR−340
23	−7.72	NULL	30 / 436	miRNA target−starBase	hsa−miR−548n
24	−7.54	NULL	10 / 89	miRNA target−starBase	hsa−miR−216b
25	−7.54	NULL	1 / 5	miRNA target	miR−200a
26	−7.46	NULL	8 / 49	BP	ER to Golgi vesicle−mediated transport
27	−7.45	NULL	13 / 146	miRNA target−starBase	hsa−miR−494
28	−7.42	NULL	2 / 16	CC	lamellipodium membrane
29	−7.4	NULL	9 / 67	miRNA target−starBase	hsa−miR−1246
30	−7.39	NULL	15 / 155	miRNA target−starBase	hsa−miR−802
31	−7.39	NULL	1 / 6	GSEA C2	ST_INTERLEUKIN_13_PATHWAY
32	−7.39	NULL	1 / 6	GSEA C2	ST_IL_13_PATHWAY
33	−7.36	NULL	25 / 399	miRNA target−starBase	hsa−miR−519c−3p
34	−7.35	NULL	2 / 10	BP	notochord development
35	−7.35	NULL	2 / 10	BP	paraxial mesoderm development
36	−7.34	NULL	10 / 114	miRNA target−starBase	hsa−miR−498
37	−7.29	NULL	23 / 387	miRNA target−starBase	hsa−miR−519a
38	−7.28	NULL	22 / 364	miRNA target−starBase	hsa−miR−519b−3p
39	−7.25	NULL	2 / 14	BP	myoblast differentiation
40	−7.25	NULL	2 / 11	CC	trans−Golgi network transport vesicle