GW_112

Global Summary

%DE = 0.15

genes with fdr < 0.2 = 1997 (1100 + / 897 −)

genes with fdr < 0.1 = 1511 (864 + / 647 −)

genes with fdr < 0.05 = 1432 (822 + / 610 −)

genes with fdr < 0.01 = 974 (604 + / 370 −)

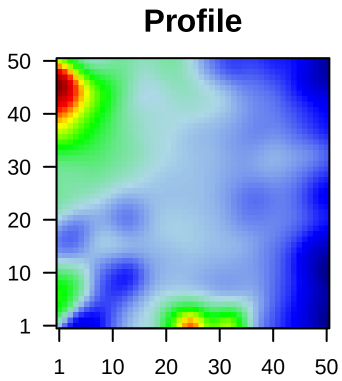
genes in genesets = 16332

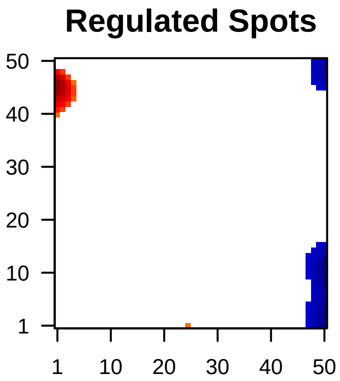
<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.08

<fdr> = 0.85



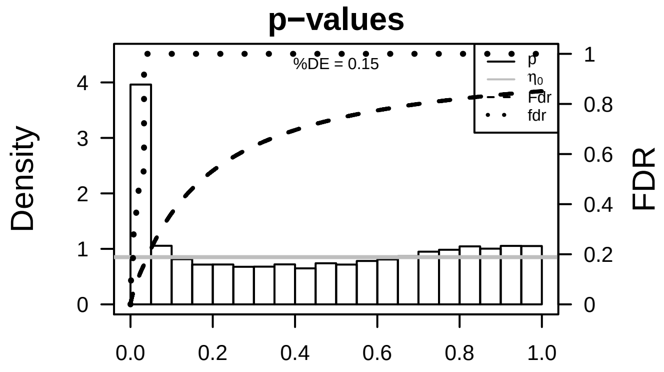


Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	58	2.41	2e−16	2e−14	25 x 1	actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
2	70	3.45	2e−16	2e−14	25 x 1	actin, alpha, cardiac muscle 1 [Source:HGNC Symbol;Acc:14
3	131	−2.32	2e−16	2e−14	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
4	113146	1.35	2e−16	2e−14	1 x 44	AHNAK nucleoprotein 2 [Source:HGNC Symbol;Acc:20125]
5	216	−1.63	2e−16	2e−14	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGN
6	218	−1.3	2e−16	2e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
7	27063	1.52	2e−16	2e−14	25 x 1	ankyrin repeat domain 1 (cardiac muscle) [Source:HGNC Sy
8	348	−1.31	2e−16	2e−14	50 x 1	apolipoprotein E [Source:HGNC Symbol;Acc:613]
9	140458	1.48	2e−16	2e−14	25 x 1	ankyrin repeat and SOCS box containing 5 [Source:HGNC S
10	151516	1.7	2e−16	2e−14	1 x 46	aspartic peptidase, retroviral−like 1 [Source:HGNC Symbol;A
11	25805	−1.49	2e−16	2e−14	8 x 1	BMP and activin membrane−bound inhibitor [Source:HGNC
12	8424	1.61	2e−16	2e−14	3 x 48	butyrobetaine (gamma), 2−oxoglutarate dioxygenase (gamm
13	84707	−1.45	2e−16	2e−14	50 x 48	brain expressed X−linked 2 [Source:HGNC Symbol;Acc:3093
14	387695	1.4	2e−16	2e−14	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Sym
15	375791	1.34	2e−16	2e−14	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Sym
16	760	1.37	2e−16	2e−14	1 x 44	carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
17	59082	1.35	2e−16	2e−14	6 x 44	caspase recruitment domain family, member 18 [Source:HGN
18	845	1.56	2e−16	2e−14	25 x 1	calsequestrin 2 (cardiac muscle) [Source:HGNC Symbol;Acc:
19	8900	1.81	2e−16	2e−14	1 x 42	cyclin A1 [Source:HGNC Symbol;Acc:1577]
20	1001	1.64	2e−16	2e−14	1 x 43	cadherin 3, type 1, P−cadherin (placental) [Source:HGNC Sy

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	20.16	NULL	572	Disease	GUDJ_psoriasis up
2	18.69	NULL	127	H.Tiss	WIRTH_Muscle
3	15.21	NULL	36	BP	muscle filament sliding
4	14.77	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_F
5	12.83	NULL	135	H.Tiss	WIRTH_Mucosa
6	12.77	NULL	16	H.Tiss	WIRTH_Hippocampus
7	12.59	NULL	76	BP	epidermis development
8	12.56	NULL	21	CC	cornified envelope
9	12.22	NULL	12	CC	myosin filament
10	11.39	NULL	44	MF	structural constituent of muscle
11	11.22	NULL	42	BP	keratinization
12	10.93	NULL	51	BP	type I interferon signaling pathway
13	10.05	NULL	14	CC	contractile fiber
14	10.04	NULL	15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
15	9.9	NULL	84	BP	muscle contraction
16	9.64	NULL	16	GSEA C2	MOSERLE_IFNA_RESPONSE
17	9.42	NULL	13	GSEA C2	BOWIE_RESPONSE_TO_TAMOXIFEN
18	9.01	NULL	16	GSEA C2	EINAV_INTERFERON_SIGNATURE_IN_CANCER
19	8.84	NULL	21	CC	desmosome
20	8.81	NULL	31	BP	negative regulation of viral genome replication
Underexpressed					
1	−7.03	NULL	4	MMML CGS	MACIEJ_MMML 23
2	−6.17	NULL	109	BP	SRP−dependent cotranslational protein targeting to membrane
3	−6	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_D
4	−5.94	NULL	81	BP	viral transcription
5	−5.87	NULL	87	BP	translational termination
6	−5.68	NULL	92	BP	translational elongation
7	−5.68	NULL	14	MF	glutathione peroxidase activity
8	−5.41	NULL	553	Cancer	Lembcke_Colonic Inflammation
9	−5.41	NULL	43	MF	chemokine activity
10	−5.37	NULL	128	BP	translational initiation
11	−5.36	NULL	19	BP	hydrogen peroxide catabolic process
12	−5.31	NULL	29	BP	positive regulation of cell death
13	−5.23	NULL	153	MF	structural constituent of ribosome
14	−5.22	NULL	6	GSEA C2	KAPOSI_LIVER_CANCER_POOR_SURVIVAL_DN
15	−5.07	NULL	15	GSEA C2	MISHRA_CARCINOMA_ASSOCIATED_FIBROBLAST_UP
16	−4.97	NULL	167	CC	ribosome
17	−4.95	NULL	11	MF	platelet−derived growth factor binding
18	−4.93	NULL	253	BP	translation
19	−4.9	NULL	92	BP	viral life cycle
20	−4.86	NULL	9	GSEA C2	REACTOME_ETHANOL_OXIDATION



GW_112

Local Summary

%DE = 0.98

metagenes = 1

genes = 64

genes in genesets = 64

genes with fdr < 0.1 = 62 (62 + / 0 −)

genes with fdr < 0.05 = 62 (62 + / 0 −)

genes with fdr < 0.01 = 60 (60 + / 0 −)

<r> metagenes = NA

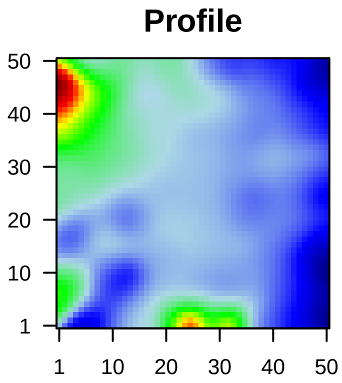
<r> genes = 0.71

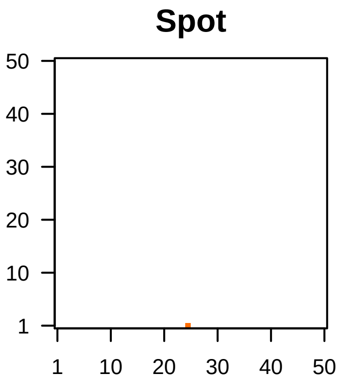
<FC> = 1.33

<shrinkage−t> = 46.38

<p−value> = 0

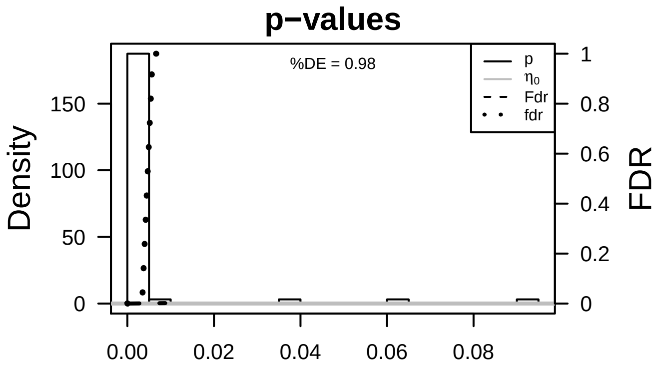
<fdr> = 0.05





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	58	2.41	2e−16	8e−18	25 x 1	actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
2	70	3.45	2e−16	8e−18	25 x 1	actin, alpha, cardiac muscle 1 [Source:HGNC Symbol;Acc:14
3	27063	1.52	2e−16	8e−18	25 x 1	ankyrin repeat domain 1 (cardiac muscle) [Source:HGNC Syr
4	140458	1.48	2e−16	8e−18	25 x 1	ankyrin repeat and SOCS box containing 5 [Source:HGNC Sy
5	845	1.56	2e−16	8e−18	25 x 1	calsequestrin 2 (cardiac muscle) [Source:HGNC Symbol;Acc:
6	1114	1.78	2e−16	8e−18	25 x 1	chromogranin B (secretogranin 1) [Source:HGNC Symbol;Ac
7	1158	2.05	2e−16	8e−18	25 x 1	creatine kinase, muscle [Source:HGNC Symbol;Acc:1994]
8	202333	1.41	2e−16	8e−18	25 x 1	cardiomyopathy associated 5 [Source:HGNC Symbol;Acc:14
9	115265	1.93	2e−16	8e−18	25 x 1	DNA−damage−inducible transcript 4−like [Source:HGNC Syn
10	1674	1.61	2e−16	8e−18	25 x 1	desmin [Source:HGNC Symbol;Acc:2770]
11	2318	1.68	2e−16	8e−18	25 x 1	filamin C, gamma [Source:HGNC Symbol;Acc:3756]
12	27129	1.39	2e−16	8e−18	25 x 1	heat shock 27kDa protein family, member 7 (cardiovascular) [
13	10324	1.93	2e−16	8e−18	25 x 1	kelch−like family member 41 [Source:HGNC Symbol;Acc:169
14	4151	1.9	2e−16	8e−18	25 x 1	myoglobin [Source:HGNC Symbol;Acc:6915]
15	389125	1.32	2e−16	8e−18	25 x 1	musculoskeletal, embryonic nuclear protein 1 [Source:HGNC
16	4606	1.75	2e−16	8e−18	25 x 1	myosin binding protein C, fast type [Source:HGNC Symbol;Ac
17	4608	2.82	2e−16	8e−18	25 x 1	myosin binding protein H [Source:HGNC Symbol;Acc:7552]
18	4619	2.23	2e−16	8e−18	25 x 1	myosin, heavy chain 1, skeletal muscle, adult [Source:HGNC
19	4620	2.37	2e−16	8e−18	25 x 1	myosin, heavy chain 2, skeletal muscle, adult [Source:HGNC
20	4621	1.31	2e−16	8e−18	25 x 1	myosin, heavy chain 3, skeletal muscle, embryonic [Source:H



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	62.66	NULL	11 / 16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_F
2	58.22	NULL	19 / 36	BP	muscle filament sliding
3	52.8	NULL	38 / 127	H.Tiss	WIRTH_Muscle
4	51.57	NULL	9 / 16	H.Tiss	WIRTH_Hippocampus
5	48.62	NULL	7 / 12	CC	myosin filament
6	41.14	NULL	17 / 44	MF	structural constituent of muscle
7	34.62	NULL	7 / 14	CC	contractile fiber
8	31.91	NULL	5 / 11	BP	cardiac muscle tissue morphogenesis
9	29.11	NULL	6 / 12	BP	skeletal muscle contraction
10	29.01	NULL	9 / 37	CC	sarcomere
11	28.47	NULL	5 / 13	CC	muscle myosin complex
12	28.1	NULL	16 / 84	BP	muscle contraction
13	25.42	NULL	6 / 16	CC	M band
14	24.66	NULL	8 / 37	BP	cardiac muscle contraction
15	24.4	NULL	1 / 5	GSEA C2	LIU_VAV3_PROSTATE_CARCINOGENESIS_UP
16	23.32	NULL	5 / 20	CC	I band
17	22.48	NULL	8 / 34	CC	myofibril
18	21.87	NULL	16 / 88	CC	Z disc
19	21.46	NULL	2 / 10	BP	heart contraction
20	21.23	NULL	3 / 11	CC	A band
21	19.69	NULL	4 / 12	MF	titin binding
22	19.59	NULL	2 / 15	Cancer	BEN−PORATH_UP
23	17.97	NULL	4 / 15	BP	striated muscle contraction
24	17.65	NULL	5 / 18	BP	regulation of muscle contraction
25	17.09	NULL	3 / 15	GSEA C2	EBAUER_MYOGENIC_TARGETS_OF_PAX3_FOXO1_FUSION
26	16.42	NULL	2 / 20	MF	myosin binding
27	15.85	NULL	2 / 15	BP	actin filament−based movement
28	15.32	NULL	4 / 15	GSEA C2	REACTOME_STRIATED_MUSCLE_CONTRACTION
29	15.08	NULL	5 / 42	CC	myosin complex
30	14.8	NULL	1 / 6	GSEA C2	BIOCARTA_HSP27_PATHWAY
31	14.57	NULL	3 / 16	MF	microfilament motor activity
32	14.56	NULL	17 / 297	MF	actin binding
33	13.42	NULL	3 / 13	CC	pseudopodium
34	13.36	NULL	2 / 16	GSEA C2	DAVICIONI_TARGETS_OF_PAX_FOXO1_FUSIONS_DN
35	13.17	NULL	1 / 12	GSEA C2	KEGG_CARDIAC_MUSCLE_CONTRACTION
36	12.96	NULL	3 / 37	CC	actin filament
37	12.95	NULL	3 / 18	CC	costamere
38	12.89	NULL	2 / 10	BP	creatine metabolic process
39	12.73	NULL	3 / 29	CC	sarcoplasmic reticulum membrane
40	12.28	NULL	3 / 14	MF	tropomyosin binding

GW_112

Local Summary

%DE = 0.96

metagenes = 27

genes = 320

genes in genesets = 314

genes with fdr < 0.1 = 299 (288 + / 11 −)

genes with fdr < 0.05 = 280 (272 + / 8 −)

genes with fdr < 0.01 = 254 (246 + / 8 −)

<r> metagenes = 0.91

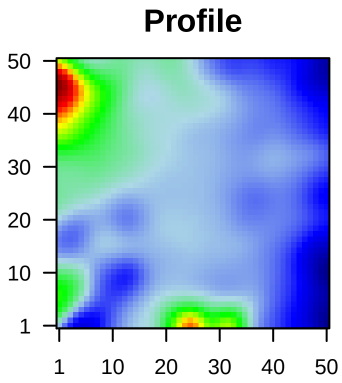
<r> genes = 0.36

<FC> = 0.78

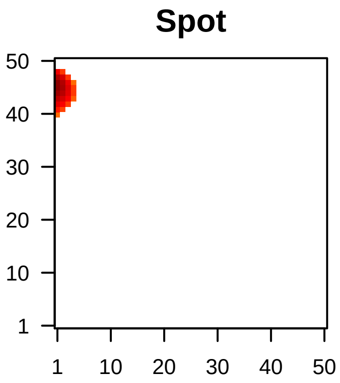
<shrinkage−t> = 27.25

<p−value> = 0

<fdr> = 0.21



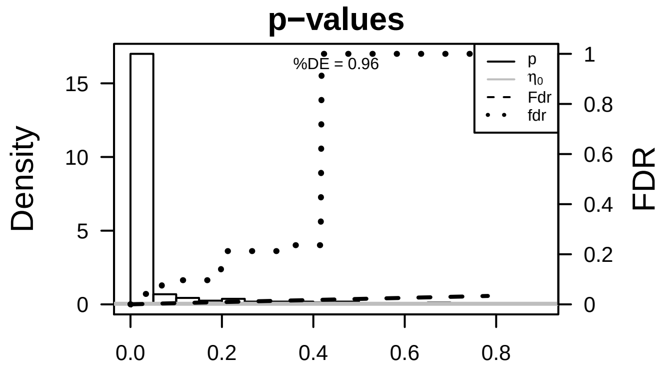
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	113146	1.35	2e−16	5e−17	1 x 44	AHNAK nucleoprotein 2 [Source:HGNC Symbol;Acc:20125]
2	151516	1.7	2e−16	5e−17	1 x 46	aspartic peptidase, retroviral−like 1 [Source:HGNC Symbol;A
3	760	1.37	2e−16	5e−17	1 x 44	carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
4	8900	1.81	2e−16	5e−17	1 x 42	cyclin A1 [Source:HGNC Symbol;Acc:1577]
5	1001	1.64	2e−16	5e−17	1 x 43	cadherin 3, type 1, P−cadherin (placental) [Source:HGNC Sy
6	1041	2.54	2e−16	5e−17	1 x 46	corneodesmosin [Source:HGNC Symbol;Acc:1802]
7	1212	1.31	2e−16	5e−17	3 x 45	clathrin, light chain B [Source:HGNC Symbol;Acc:2091]
8	1308	1.89	2e−16	5e−17	1 x 43	collagen, type XVII, alpha 1 [Source:HGNC Symbol;Acc:2194
9	51200	2.46	2e−16	5e−17	1 x 44	carboxypeptidase A4 [Source:HGNC Symbol;Acc:15740]
10	1474	1.9	2e−16	5e−17	1 x 47	cystatin E/M [Source:HGNC Symbol;Acc:2478]
11	1515	2.23	2e−16	5e−17	1 x 44	cathepsin V [Source:HGNC Symbol;Acc:2538]
12	55894	1.89	2e−16	5e−17	1 x 47	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
13	414325	1.72	2e−16	5e−17	1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
14	93099	1.36	2e−16	5e−17	1 x 47	dermokine [Source:HGNC Symbol;Acc:25063]
15	1823	1.98	2e−16	5e−17	1 x 45	desmocollin 1 [Source:HGNC Symbol;Acc:3035]
16	1828	2.04	2e−16	5e−17	1 x 48	desmoglein 1 [Source:HGNC Symbol;Acc:3048]
17	90527	1.31	2e−16	5e−17	1 x 48	dual oxidase maturation factor 1 [Source:HGNC Symbol;Acc:
18	2171	1.31	2e−16	5e−17	1 x 46	fatty acid binding protein 5 (psoriasis−associated) [Source:HC
19	644054	1.67	2e−16	5e−17	2 x 46	family with sequence similarity 25, member C [Source:HGNC
20	100133093	1.74	2e−16	5e−17	2 x 46	family with sequence similarity 25, member C [Source:HGNC



p−values

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	22.17	NULL	86 / 572	Disease	GUDJ_psoriasis up
2	21.93	NULL	39 / 135	H.Tiss	WIRTH_Mucosa
3	21.12	NULL	11 / 21	CC	desmosome
4	16.92	NULL	17 / 76	BP	epidermis development
5	14.59	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
6	13.8	NULL	6 / 15	GSEA C2	AIGNER_ZEB1_TARGETS
7	12.85	NULL	4 / 13	GSEA C2	REACTOME_GAP_JUNCTION_TRAFFICKING
8	12.35	NULL	17 / 82	CC	intermediate filament
9	12.35	NULL	6 / 21	CC	cornified envelope
10	12.01	NULL	6 / 15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL
11	11.57	NULL	4 / 15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
12	11.56	NULL	9 / 44	CC	keratin filament
13	11.19	NULL	4 / 10	GSEA C2	REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION_P
14	11.04	NULL	4 / 12	BP	hemidesmosome assembly
15	11.03	NULL	4 / 12	GSEA C2	REACTOME_GAP_JUNCTION_ASSEMBLY
16	10.91	NULL	4 / 15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_DN
17	10.88	NULL	4 / 21	CC	gap junction
18	9.76	NULL	4 / 16	GSEA C2	COLDREN_GEFITINIB_RESISTANCE_DN
19	9.69	NULL	4 / 15	CC	connexon complex
20	9.62	NULL	10 / 53	BP	keratinocyte differentiation
21	9.59	NULL	3 / 10	BP	negative regulation of interleukin−2 production
22	9.22	NULL	7 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
23	9.17	NULL	3 / 6	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_UP
24	8.98	NULL	3 / 13	BP	intermediate filament cytoskeleton organization
25	8.92	NULL	2 / 14	GSEA C2	KIM_RESPONSE_TO_TSA_AND_DECITABINE_UP
26	8.14	NULL	2 / 8	GSEA C2	DORN_ADENOVIRUS_INFECTION_24HR_UP
27	8.11	NULL	3 / 10	GSEA C2	DAZARD_UV_RESPONSE_CLUSTER_G3
28	8.01	NULL	9 / 85	Glio	laffaire_hypermeth_LGG_vs_control
29	7.79	NULL	20 / 186	MF	structural molecule activity
30	7.79	NULL	2 / 2	miRNA target	miR−199a*
31	7.52	NULL	3 / 25	BP	response to zinc ion
32	7.47	NULL	11 / 112	Glio	Christensen_hypermethylated_in_grade2_oligoastrocytoma
33	7.24	NULL	3 / 16	GSEA C2	LANDEMAINE_LUNG_METASTASIS
34	7.17	NULL	3 / 11	GSEA C2	MURAKAMI_UV_RESPONSE_24HR
35	7.13	NULL	3 / 12	BP	keratinocyte proliferation
36	7.04	NULL	8 / 44	BP	skin development
37	7.01	NULL	12 / 132	Glio	Christensen_hypermethylated_in_grade3_oligoastrocytoma
38	6.99	NULL	9 / 99	BP	homophilic cell adhesion
39	6.73	NULL	7 / 42	BP	keratinization
40	6.68	NULL	9 / 115	CC	cell−cell junction

GW_112

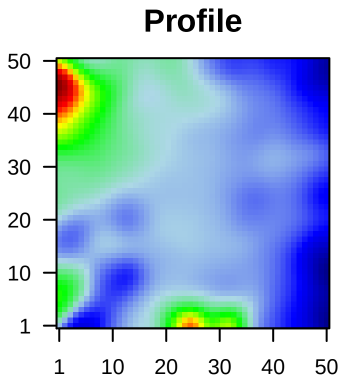
Local Summary

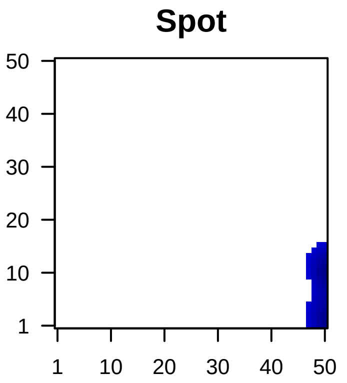
%DE = 0.76
metagenes = 57
genes = 719
genes in genesets = 713

genes with fdr < 0.1 = 393 (35 + / 358 −)
genes with fdr < 0.05 = 339 (33 + / 306 −)
genes with fdr < 0.01 = 265 (25 + / 240 −)

<r> metagenes = 0.77
<r> genes = 0.28

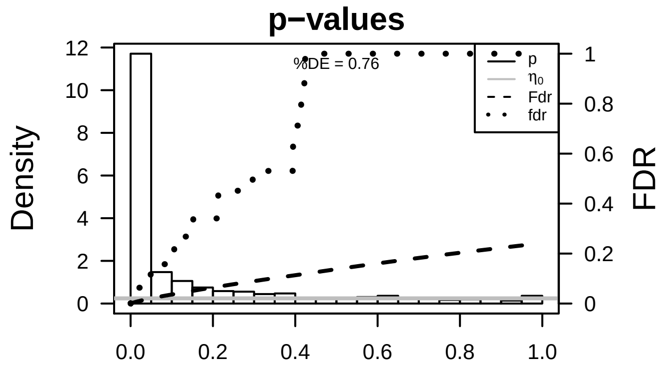
<FC> = −0.32
<shrinkage−t> = −11.13
<p−value> = 0
<fdr> = 0.52





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	348	−1.31	2e−16	8e−15	50 x 1	apolipoprotein E [Source:HGNC Symbol;Acc:613]
2	79901	−1.35	2e−16	8e−15	50 x 7	cytochrome b reductase 1 [Source:HGNC Symbol;Acc:20797
3	3512	−2.15	2e−16	8e−15	50 x 1	immunoglobulin J polypeptide, linker protein for immunoglobu
4	8284	1.48	2e−16	8e−15	48 x 8	lysine (K)−specific demethylase 5D [Source:HGNC Symbol;A
5	6192	1.51	2e−16	8e−15	50 x 9	ribosomal protein S4, Y−linked 1 [Source:HGNC Symbol;Acc
6	1512	−1.3	4e−16	4e−14	47 x 1	cathepsin H [Source:HGNC Symbol;Acc:2535]
7	1116	1.29	7e−16	4e−13	50 x 4	chitinase 3−like 1 (cartilage glycoprotein−39) [Source:HGNC
8	10232	−1.26	4e−15	4e−13	50 x 11	mesothelin [Source:HGNC Symbol;Acc:7371]
9	7033	−1.24	7e−15	4e−13	50 x 10	trefoil factor 3 (intestinal) [Source:HGNC Symbol;Acc:11757]
10	5552	−1.24	7e−15	7e−13	50 x 1	serglycin [Source:HGNC Symbol;Acc:9361]
11	3169	−1.23	1e−14	7e−13	50 x 12	forkhead box A1 [Source:HGNC Symbol;Acc:5021]
12	4239	−1.23	2e−14	3e−12	50 x 6	microfibrillar−associated protein 4 [Source:HGNC Symbol;Ac
13	3620	1.21	4e−14	2e−11	48 x 1	indoleamine 2,3−dioxygenase 1 [Source:HGNC Symbol;Acc:
14	7305	−1.18	2e−13	2e−11	50 x 1	TYRO protein tyrosine kinase binding protein [Source:HGNC
15	148170	−1.16	3e−13	2e−11	50 x 9	CDC42 effector protein (Rho GTPase binding) 5 [Source:HG
16	3126	1.16	4e−13	3e−11	50 x 1	major histocompatibility complex, class II, DR beta 4 [Source:
17	7018	−1.15	7e−13	3e−11	50 x 10	transferrin [Source:HGNC Symbol;Acc:11740]
18	1396	−1.14	9e−13	3e−11	50 x 5	cysteine−rich protein 1 (intestinal) [Source:HGNC Symbol;Ac
19	115361	1.14	1e−12	3e−11	48 x 1	guanylate binding protein 4 [Source:HGNC Symbol;Acc:2048
20	894	1.14	1e−12	1e−10	50 x 4	cyclin D2 [Source:HGNC Symbol;Acc:1583]



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−16.72	NULL	14 / 16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_D
2	−13.42	NULL	7 / 12	GSEA C2	ZHAN_MULTIPLE_MYELOMA_DN
3	−13.32	NULL	60 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
4	−13.32	NULL	60 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
5	−13.32	NULL	60 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
6	−13.32	NULL	60 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
7	−12.35	NULL	4 / 7	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
8	−11.71	NULL	125 / 553	Cancer	Lembcke_Colonic Inflammation
9	−11.22	NULL	3 / 5	GSEA C2	WONG_ENDOMETRIAL_CANCER_LATE
10	−10.46	NULL	4 / 11	GSEA C2	APPEL_IMATINIB_RESPONSE
11	−10.4	NULL	7 / 16	GSEA C2	BOQUEST_STEM_CELL_CULTURED_VS_FRESH_DN
12	−10.02	NULL	98 / 417	H.Tiss	WIRTH_Immune system
13	−9.87	NULL	5 / 12	GSEA C2	ZHAN_V1_LATE_DIFFERENTIATION_GENES_UP
14	−9.75	NULL	7 / 14	GSEA C2	WU_SILENCED_BY_METHYLATION_IN_BLADDER_CANCER
15	−9.27	NULL	4 / 10	BP	negative regulation of blood coagulation
16	−9.22	NULL	7 / 27	MF	antigen binding
17	−9.19	NULL	4 / 7	GSEA C2	BIOCARTA_COMP_PATHWAY
18	−9.1	NULL	4 / 11	GSEA C2	GUTIERREZ_CHRONIC_LYMPHOCYTIC_LEUKEMIA_UP
19	−9.04	NULL	7 / 8	Glio	Donson−migration tethering and rolling−associated with LTS in HG
20	−9.01	NULL	4 / 13	GSEA C2	NING_CHRONIC_OBSTRUCTIVE_PULMONARY_DISEASE_DN
21	−8.61	NULL	5 / 14	GSEA C2	CHEOK_RESPONSE_TO_HD_MTX_UP
22	−8.52	NULL	4 / 8	GSEA C2	REACTOME_COMPLEMENT_CASCADE
23	−8.52	NULL	4 / 8	GSEA C2	REACTOME_INITIAL_TRIGGERING_OF_COMPLEMENT
24	−8.5	NULL	4 / 14	Lymphoma	WRIGHT_GCB UP
25	−8.39	NULL	6 / 15	GSEA C2	FINAK_BREAST_CANCER_SDPP_SIGNATURE
26	−8.32	NULL	7 / 15	GSEA C2	NAKAJIMA_MAST_CELL
27	−8	NULL	6 / 16	GSEA C2	FERRANDO_TAL1_NEIGHBORS
28	−7.98	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
29	−7.97	NULL	9 / 16	GSEA C2	SU_THYMUS
30	−7.97	NULL	5 / 7	GSEA C2	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINE
31	−7.88	NULL	5 / 14	BP	ruffle organization
32	−7.87	NULL	4 / 10	BP	cellular response to antibiotic
33	−7.78	NULL	2 / 4	GSEA C2	REACTOME_CLASSICAL_ANTIBODY_MEDIATED_COMPLEME
34	−7.71	NULL	3 / 14	GSEA C2	WANG_BARRETTS_ESOPHAGUS_UP
35	−7.67	NULL	4 / 13	MMML CGS	MACIEJ_MMML 6
36	−7.66	NULL	4 / 12	GSEA C2	HADDAD_T_LYMPHOCYTE_AND_NK_PROGENITOR_DN
37	−7.55	NULL	2 / 4	Lymphoma	WRIGHT_custom GCB−DLBCL UP
38	−7.52	NULL	6 / 10	GSEA C2	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_
39	−7.49	NULL	108 / 1182	CC	extracellular region
40	−7.49	NULL	3 / 9	GSEA C2	GOUYER_TATI_TARGETS_UP

GW_112

Local Summary

%DE = 0.68

metagenes = 17

genes = 224

genes in genesets = 223

genes with fdr < 0.1 = 111 (9 + / 102 −)

genes with fdr < 0.05 = 91 (7 + / 84 −)

genes with fdr < 0.01 = 57 (5 + / 52 −)

<r> metagenes = 0.96

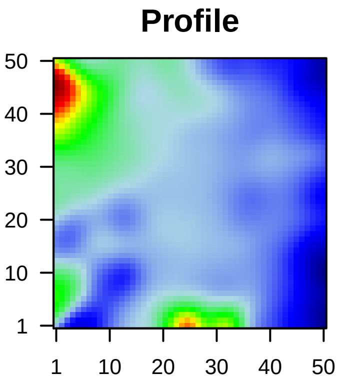
<r> genes = 0.26

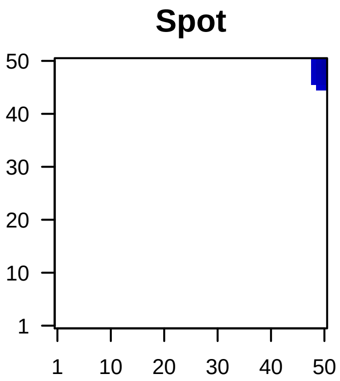
<FC> = −0.32

<shrinkage−t> = −11.11

<p−value> = 0

<fdr> = 0.57





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	216	−1.63	2e−16	2e−15	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGN
2	84707	−1.45	2e−16	2e−15	50 x 48	brain expressed X−linked 2 [Source:HGNC Symbol;Acc:3093
3	3304	−1.27	2e−16	2e−15	49 x 49	heat shock 70kDa protein 1A [Source:HGNC Symbol;Acc:52
4	3866	1.44	2e−16	2e−15	50 x 50	keratin 15 [Source:HGNC Symbol;Acc:6421]
5	3856	−1.59	2e−16	2e−15	50 x 48	keratin 8 pseudogene 3 [Source:HGNC Symbol;Acc:31056]
6	4922	−1.56	2e−16	2e−15	50 x 50	neurotensin [Source:HGNC Symbol;Acc:8038]
7	26227	−1.34	2e−16	2e−15	50 x 46	phosphoglycerate dehydrogenase [Source:HGNC Symbol;Ac
8	139728	−1.61	2e−16	2e−15	49 x 49	pregnancy up−regulated nonubiquitous CaM kinase [Source:
9	339512	−1.21	4e−14	9e−12	50 x 50	chromosome 1 open reading frame 110 [Source:HGNC Sym
10	4072	−1.18	2e−13	7e−09	50 x 50	epithelial cell adhesion molecule [Source:HGNC Symbol;Acc:
11	3880	−1.03	1e−10	9e−08	50 x 49	keratin 19 [Source:HGNC Symbol;Acc:6436]
12	1974	−0.89	1e−09	6e−07	49 x 47	eukaryotic translation initiation factor 4A2 [Source:HGNC Sy
13	6657	−0.91	1e−08	6e−07	50 x 50	SRY (sex determining region Y)−box 2 [Source:HGNC Symb
14	5635	−0.9	2e−08	6e−07	50 x 50	phosphoribosyl pyrophosphate synthetase−associated protei
15	445	0.89	2e−08	1e−06	50 x 47	argininosuccinate synthase 1 [Source:HGNC Symbol;Acc:75
16	5584	0.88	4e−08	5e−06	48 x 50	protein kinase C, iota [Source:HGNC Symbol;Acc:9404]
17	6659	−0.85	1e−07	5e−06	50 x 45	SRY (sex determining region Y)−box 4 [Source:HGNC Symb
18	11166	−0.82	2e−07	5e−06	50 x 50	SRY (sex determining region Y)−box 21 [Source:HGNC Sym
19	205428	−0.82	3e−07	5e−06	50 x 50	chromosome 3 open reading frame 58 [Source:HGNC Symb
20	256764	−0.82	3e−07	1e−05	50 x 50	WD repeat domain 72 [Source:HGNC Symbol;Acc:26790]

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−16.93	NULL	2 / 7	GSEA C2	MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
2	−16.46	NULL	2 / 6	GSEA C2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_D_DN
3	−14.55	NULL	1 / 2	GSEA C2	KUROKAWA_LIVER_CANCER_EARLY_RECURRENCE_UP
4	−13.61	NULL	4 / 15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
5	−12.16	NULL	4 / 13	BP	regulation of blood vessel size
6	−12.1	NULL	1 / 6	GSEA C2	KAPOSI_LIVER_CANCER_POOR_SURVIVAL_DN
7	−11.81	NULL	1 / 2	miRNA target	miR−129
8	−11.58	NULL	2 / 14	GSEA C2	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINE
9	−10.96	NULL	2 / 10	GSEA C2	CERVERA_SDHB_TARGETS_1_DN
10	−10.47	NULL	3 / 12	GSEA C2	HELLER_SILENCED_BY_METHYLATION_DN
11	−10.46	NULL	3 / 12	GSEA C2	BROCKE_APOPTOSIS_REVERSED_BY_IL6
12	−9.8	NULL	2 / 15	BP	spinal cord development
13	−9.64	NULL	1 / 9	GSEA C2	ABDULRAHMAN_KIDNEY_CANCER_VHL_DN
14	−9.64	NULL	1 / 9	GSEA C2	REACTOME_ETHANOL_OXIDATION
15	−9.38	NULL	2 / 10	GSEA C2	HANN_RESISTANCE_TO_BCL2_INHIBITOR_DN
16	−9.09	NULL	1 / 10	GSEA C2	MAINA_VHL_TARGETS_UP
17	−9.09	NULL	1 / 10	GSEA C2	FRIDMAN_SENESCENCE_DN
18	−8.86	NULL	2 / 14	MF	calmodulin−dependent protein kinase activity
19	−8.76	NULL	2 / 12	BP	cellular aldehyde metabolic process
20	−8.67	NULL	3 / 16	GSEA C2	BOYAULT_LIVER_CANCER_SUBCLASS_G1_DN
21	−8.65	NULL	3 / 11	GSEA C2	ITO_PTTG1_TARGETS_UP
22	−8.59	NULL	2 / 11	GSEA C2	CONCANNON_APOPTOSIS_BY_EPOXOMICIN_UP
23	−8.52	NULL	1 / 5	GSEA C2	DASU_IL6_SIGNALING_UP
24	−8.45	NULL	2 / 14	GSEA C2	KEGG_GLYCINE_SERINE_AND_THREONINE_METABOLISM
25	−8.37	NULL	2 / 8	GSEA C2	SATO_SILENCED_EPIGENETICALLY_IN_PANCREATIC_CANCE
26	−8.34	NULL	3 / 16	GSEA C2	KAN_RESPONSE_TO_ARSENIC_TRIOXIDE
27	−8.22	NULL	1 / 11	Glio	neurons_glio
28	−8.1	NULL	2 / 11	GSEA C2	WOOD_EBV_EBNA1_TARGETS_UP
29	−8.07	NULL	2 / 16	GSEA C2	PACHER_TARGETS_OF_IGF1_AND_IGF2_UP
30	−8.07	NULL	2 / 16	GSEA C2	ZHAN_MULTIPLE_MYELOMA_CD1_VS_CD2_UP
31	−7.68	NULL	1 / 6	GSEA C2	SESTO_RESPONSE_TO_UV_C0
32	−7.68	NULL	1 / 6	GSEA C2	BIOCARTA_TID_PATHWAY
33	−7.55	NULL	2 / 18	BP	glutamine metabolic process
34	−7.52	NULL	1 / 14	MF	Ras GTPase activator activity
35	−7.52	NULL	1 / 14	GSEA C2	MAHADEVAN_IMATINIB_RESISTANCE_UP
36	−7.23	NULL	1 / 15	GSEA C2	DORSAM_HOXA9_TARGETS_UP
37	−7.03	NULL	1 / 7	GSEA C2	WEINMANN_ADAPTATION_TO_HYPOXIA_UP
38	−6.97	NULL	2 / 18	MF	acyl−CoA dehydrogenase activity
39	−6.89	NULL	1 / 15	MF	neuropeptide hormone activity
40	−6.76	NULL	5 / 60	miRNA 3UTR	ACGG−328