GW_182

Global Summary

%DE = 0.18

genes with fdr < 0.2 = 2506 (1474 + / 1032 −)

genes with fdr < 0.1 = 2106 (1256 + / 850 −)

genes with fdr < 0.05 = 1803 (1095 + / 708 −)

genes with fdr < 0.01 = 1469 (895 + / 574 −)

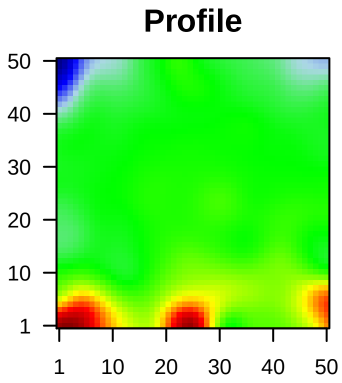
genes in genesets = 16332

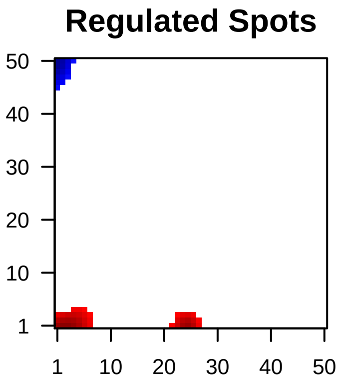
<FC> = 0

<shrinkage−t> = −0.01

<p−value> = 0.04

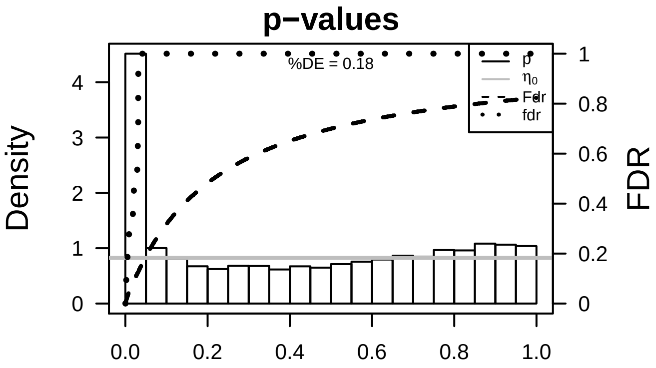
<fdr> = 0.82


Profile


Regulated Spots

Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	25890	1.79	2e−16	1e−14	50 x 4	ABI family, member 3 (NESH) binding protein [Source:HGNC
2	84448	1.87	2e−16	1e−14	25 x 1	actin binding LIM protein family, member 2 [Source:HGNC Sy
3	2180	1.83	2e−16	1e−14	7 x 46	acyl−CoA synthetase long−chain family member 1 [Source:H
4	58	4.38	2e−16	1e−14	25 x 1	actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
5	70	3.79	2e−16	1e−14	25 x 1	actin, alpha, cardiac muscle 1 [Source:HGNC Symbol;Acc:14
6	101	1.81	2e−16	1e−14	32 x 3	ADAM metallopeptidase domain 8 [Source:HGNC Symbol;Ac
7	131	−2.61	2e−16	1e−14	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
8	133	1.82	2e−16	1e−14	1 x 42	adrenomedullin [Source:HGNC Symbol;Acc:259]
9	57016	−2.21	2e−16	1e−14	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
10	218	−3.1	2e−16	1e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
11	222	−1.71	2e−16	1e−14	1 x 49	aldehyde dehydrogenase 3 family, member B2 [Source:HGN
12	241	2.4	2e−16	1e−14	50 x 1	arachidonate 5−lipoxygenase−activating protein [Source:HGN
13	249	1.93	2e−16	1e−14	6 x 1	alkaline phosphatase, liver/bone/kidney [Source:HGNC Symb
14	23452	1.82	2e−16	1e−14	3 x 1	angiopoietin−like 2 [Source:HGNC Symbol;Acc:490]
15	10930	1.9	2e−16	1e−14	25 x 1	apolipoprotein B mRNA editing enzyme, catalytic polypeptide
16	347	2.2	2e−16	1e−14	50 x 7	apolipoprotein D [Source:HGNC Symbol;Acc:612]
17	366	2.79	2e−16	1e−14	1 x 1	aquaporin 9 [Source:HGNC Symbol;Acc:643]
18	445328	−1.76	2e−16	1e−14	4 x 46	Rho guanine nucleotide exchange factor (GEF) 35 [Source:H
19	140458	1.99	2e−16	1e−14	25 x 1	ankyrin repeat and SOCS box containing 5 [Source:HGNC Sy
20	55971	−1.68	2e−16	1e−14	13 x 50	BAI1−associated protein 2−like 1 [Source:HGNC Symbol;Acc


p−values

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	26.73	NULL	127	H.Tiss	WIRTH_Muscle
2	21.06	NULL	36	BP	muscle filament sliding
3	20.92	NULL	265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
4	20.92	NULL	265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
5	20.92	NULL	265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
6	20.92	NULL	265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
7	18.7	NULL	553	Cancer	Lembcke_Colonic Inflammation
8	18.68	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_F
9	17.65	NULL	250	Lymphoma	LENZ_Stromal signature 1
10	17.09	NULL	44	MF	structural constituent of muscle
11	16.74	NULL	190	CC	extracellular matrix
12	15.53	NULL	16	H.Tiss	WIRTH_Hippocampus
13	15.26	NULL	84	BP	muscle contraction
14	13.3	NULL	12	CC	myosin filament
15	12.89	NULL	37	CC	sarcomere
16	12.86	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
17	12.85	NULL	16	MMML CGS	MACIEJ_MMML 1
18	11.35	NULL	269	BP	inflammatory response
19	11.29	NULL	683	CC	extracellular space
20	11.17	NULL	242	BP	extracellular matrix organization
Underexpressed					
1	−35.64	NULL	135	H.Tiss	WIRTH_Mucosa
2	−19.79	NULL	572	Disease	GUDJ_psoriasis up
3	−16.7	NULL	76	BP	epidermis development
4	−16.5	NULL	21	CC	cornified envelope
5	−14.79	NULL	42	BP	keratinization
6	−14.21	NULL	53	BP	keratinocyte differentiation
7	−11.99	NULL	15	GSEA C2	AIGNER_ZEB1_TARGETS
8	−11.58	NULL	8	GSEA C2	LIU_CDX2_TARGETS_DN
9	−9.82	NULL	82	CC	intermediate filament
10	−9.35	NULL	44	CC	keratin filament
11	−9.1	NULL	21	CC	desmosome
12	−8.78	NULL	186	MF	structural molecule activity
13	−8.77	NULL	13	H.Tiss	WIRTH_Tonsil
14	−8.57	NULL	530	Cancer	Lembcke_Normal vs Adenoma
15	−8.55	NULL	142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
16	−8.55	NULL	142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
17	−7.78	NULL	370	BP	mitotic cell cycle
18	−7.65	NULL	16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
19	−7.38	NULL	10	GSEA C2	REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION_P
20	−7.34	NULL	12	BP	hemidesmosome assembly

GW_182

Local Summary

%DE = 0.96

metagenes = 24

genes = 344

genes in genesets = 340

genes with fdr < 0.1 = 318 (313 + / 5 −)

genes with fdr < 0.05 = 316 (311 + / 5 −)

genes with fdr < 0.01 = 312 (307 + / 5 −)

<r> metagenes = 0.96

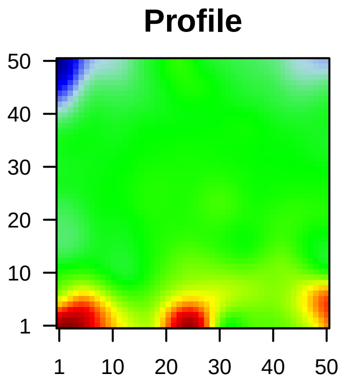
<r> genes = 0.39

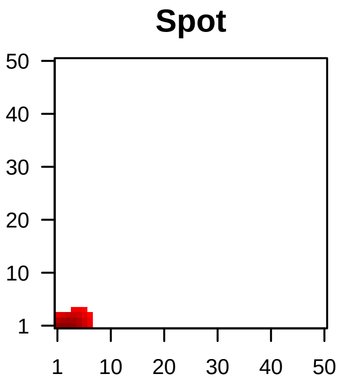
<FC> = 1.2

<shrinkage−t> = 41.97

<p−value> = 0

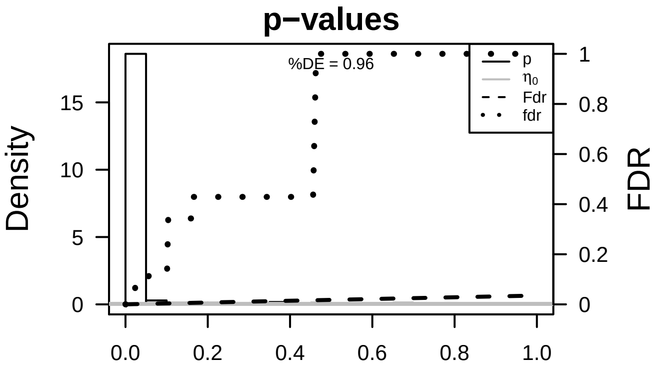
<fdr> = 0.09





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	249	1.93	2e−16	3e−17	6 x 1	alkaline phosphatase, liver/bone/kidney [Source:HGNC Symb
2	23452	1.82	2e−16	3e−17	3 x 1	angiopoietin−like 2 [Source:HGNC Symbol;Acc:490]
3	366	2.79	2e−16	3e−17	1 x 1	aquaporin 9 [Source:HGNC Symbol;Acc:643]
4	633	1.8	2e−16	3e−17	3 x 1	biglycan [Source:HGNC Symbol;Acc:1044]
5	6348	1.93	2e−16	3e−17	4 x 4	chemokine (C−C motif) ligand 3 [Source:HGNC Symbol;Acc:
6	414062	2.62	2e−16	3e−17	1 x 1	chemokine (C−C motif) ligand 3−like 3 [Source:HGNC Symbo
7	57124	1.94	2e−16	3e−17	3 x 1	CD248 molecule, endosialin [Source:HGNC Symbol;Acc:182
8	22918	1.89	2e−16	3e−17	4 x 1	CD93 molecule [Source:HGNC Symbol;Acc:15855]
9	1009	1.76	2e−16	3e−17	3 x 1	cadherin 11, type 2, OB−cadherin (osteoblast) [Source:HGN
10	1306	1.87	2e−16	3e−17	4 x 1	collagen, type XV, alpha 1 [Source:HGNC Symbol;Acc:2192]
11	1277	2.83	2e−16	3e−17	2 x 1	collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
12	1278	2.53	2e−16	3e−17	2 x 1	collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198]
13	1281	2.17	2e−16	3e−17	2 x 1	collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]
14	1289	2.82	2e−16	3e−17	2 x 1	collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209]
15	1290	1.85	2e−16	3e−17	2 x 1	collagen, type V, alpha 2 [Source:HGNC Symbol;Acc:2210]
16	1291	2.26	2e−16	3e−17	2 x 1	collagen, type VI, alpha 1 [Source:HGNC Symbol;Acc:2211]
17	1293	2.12	2e−16	3e−17	2 x 1	collagen, type VI, alpha 3 [Source:HGNC Symbol;Acc:2213]
18	81035	1.71	2e−16	3e−17	5 x 1	collectin sub−family member 12 [Source:HGNC Symbol;Acc:
19	83716	1.75	2e−16	3e−17	2 x 1	cysteine−rich secretory protein LCCL domain containing 2 [S
20	1441	1.88	2e−16	3e−17	5 x 4	colony stimulating factor 3 receptor (granulocyte) [Source:HG



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	33.07	NULL	84 / 250	Lymphoma	LENZ_Stromal signature 1
2	32.87	NULL	69 / 190	CC	extracellular matrix
3	32.3	NULL	14 / 16	MMML CGS	MACIEJ_MMML 1
4	30.27	NULL	13 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
5	28.4	NULL	8 / 11	MF	platelet−derived growth factor binding
6	27.19	NULL	65 / 242	BP	extracellular matrix organization
7	23.81	NULL	11 / 19	MF	extracellular matrix binding
8	23.1	NULL	11 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_UP
9	22.61	NULL	8 / 12	miRNA target	miR−29c
10	22.56	NULL	21 / 57	MF	extracellular matrix structural constituent
11	22.54	NULL	32 / 69	BP	extracellular matrix disassembly
12	21.41	NULL	79 / 553	Cancer	Lembcke_Colonic Inflammation
13	21.32	NULL	48 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
14	21.32	NULL	48 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
15	21.32	NULL	48 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
16	21.32	NULL	48 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
17	20.69	NULL	11 / 15	GSEA C2	CROMER_TUMORIGENESIS_UP
18	20.34	NULL	89 / 683	CC	extracellular space
19	20.27	NULL	119 / 1182	CC	extracellular region
20	19.35	NULL	27 / 64	BP	collagen catabolic process
21	19.31	NULL	5 / 10	GSEA C2	KEGG_ECM_RECEPTOR_INTERACTION
22	19.06	NULL	8 / 15	GSEA C2	DASU_IL6_SIGNALING_SCAR_DN
23	17.77	NULL	6 / 13	GSEA C2	TSAI_RESPONSE_TO_RADIATION_THERAPY
24	17.77	NULL	8 / 16	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_
25	17.73	NULL	15 / 37	BP	collagen fibril organization
26	17.65	NULL	7 / 16	GSEA C2	CROONQUIST_STROMAL_STIMULATION_UP
27	16.95	NULL	4 / 5	GSEA C2	COLLER_MYC_TARGETS_DN
28	16.71	NULL	7 / 16	GSEA C2	ZHU_CMV_ALL_DN
29	16.7	NULL	6 / 13	GSEA C2	FRIDMAN_SENESCENCE_UP
30	16.49	NULL	12 / 35	Glio	Colman_survival_associated
31	16.38	NULL	7 / 15	GSEA C2	LEE_LIVER_CANCER_HEPATOBLAST
32	16.11	NULL	18 / 68	CC	collagen
33	16.03	NULL	40 / 183	CC	proteinaceous extracellular matrix
34	15.97	NULL	6 / 13	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
35	15.95	NULL	5 / 10	BP	protein heterotrimerization
36	15.87	NULL	7 / 11	Glio	Phillips MES up vs Prolif & PN
37	15.51	NULL	8 / 15	GSEA C2	ONDER_CDH1_SIGNALING_VIA_CTNNB1
38	15.31	NULL	8 / 16	GSEA C2	ROZANOV_MMP14_TARGETS_SUBSET
39	15.28	NULL	21 / 83	CC	basement membrane
40	15.23	NULL	5 / 10	GSEA C2	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP

GW_182

Local Summary

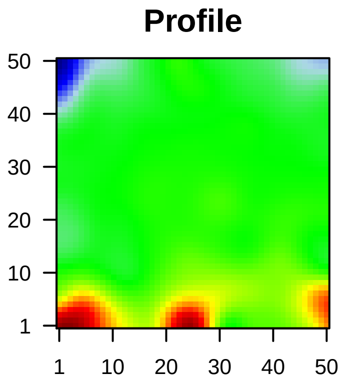
%DE = 0.99
metagenes = 15
genes = 120
genes in genesets = 119

genes with fdr < 0.1 = 118 (118 + / 0 −)
genes with fdr < 0.05 = 118 (118 + / 0 −)
genes with fdr < 0.01 = 117 (117 + / 0 −)

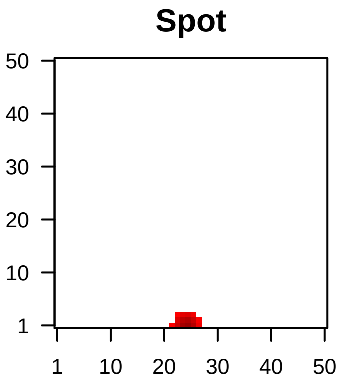
<r> metagenes = 0.98
<r> genes = 0.61

<FC> = 1.72
<shrinkage−t> = 60.34
<p−value> = 0
<fdr> = 0.02

Profile



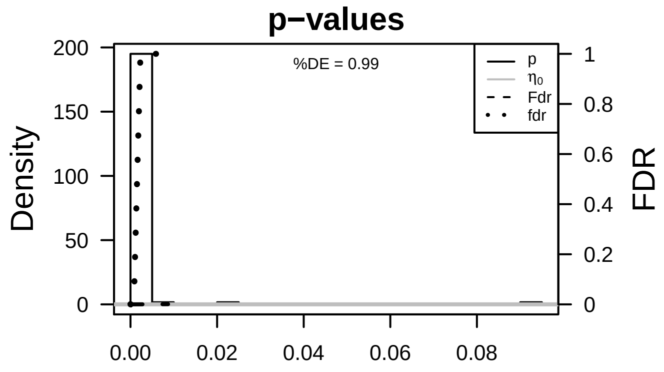
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	84448	1.87	2e−16	4e−18	25 x 1	actin binding LIM protein family, member 2 [Source:HGNC Sy
2	58	4.38	2e−16	4e−18	25 x 1	actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
3	70	3.79	2e−16	4e−18	25 x 1	actin, alpha, cardiac muscle 1 [Source:HGNC Symbol;Acc:14
4	10930	1.9	2e−16	4e−18	25 x 1	apolipoprotein B mRNA editing enzyme, catalytic polypeptide
5	140458	1.99	2e−16	4e−18	25 x 1	ankyrin repeat and SOCS box containing 5 [Source:HGNC Sy
6	10486	1.85	2e−16	4e−18	24 x 1	CAP, adenylate cyclase−associated protein, 2 (yeast) [Source
7	845	2	2e−16	4e−18	25 x 1	calsequestrin 2 (cardiac muscle) [Source:HGNC Symbol;Acc:
8	1114	2.36	2e−16	4e−18	25 x 1	chromogranin B (secretogranin 1) [Source:HGNC Symbol;Acc
9	1158	3.69	2e−16	4e−18	25 x 1	creatine kinase, muscle [Source:HGNC Symbol;Acc:1994]
10	1160	1.75	2e−16	4e−18	25 x 1	creatine kinase, mitochondrial 2 (sarcomeric) [Source:HGNC
11	202333	2.35	2e−16	4e−18	25 x 1	cardiomyopathy associated 5 [Source:HGNC Symbol;Acc:14
12	84940	1.67	2e−16	4e−18	25 x 1	coronin 6 [Source:HGNC Symbol;Acc:21356]
13	1346	2.02	2e−16	4e−18	25 x 1	cytochrome c oxidase subunit VIIa polypeptide 1 (muscle) [So
14	1410	1.95	2e−16	4e−18	25 x 1	crystallin, alpha B [Source:HGNC Symbol;Acc:2389]
15	115265	2.53	2e−16	4e−18	25 x 1	DNA−damage−inducible transcript 4−like [Source:HGNC Sym
16	23109	1.74	2e−16	4e−18	25 x 1	dendrin [Source:HGNC Symbol;Acc:24458]
17	1674	2.04	2e−16	4e−18	25 x 1	desmin [Source:HGNC Symbol;Acc:2770]
18	1917	3.01	2e−16	4e−18	25 x 1	eukaryotic translation elongation factor 1 alpha 2 [Source:HG
19	2027	1.92	2e−16	4e−18	25 x 1	enolase 3 (beta, muscle) [Source:HGNC Symbol;Acc:3354]
20	2273	2.66	2e−16	4e−18	25 x 1	four and a half LIM domains 1 [Source:HGNC Symbol;Acc:37

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all		Geneset
1	63.11	NULL	60 / 127	H.Tiss	WIRTH_Muscle
2	58.67	NULL	23 / 36	BP	muscle filament sliding
3	50.8	NULL	11 / 16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_F
4	47.6	NULL	11 / 16	H.Tiss	WIRTH_Hippocampus
5	46.84	NULL	23 / 44	MF	structural constituent of muscle
6	43.68	NULL	10 / 12	CC	myosin filament
7	32.84	NULL	8 / 14	CC	contractile fiber
8	32.02	NULL	8 / 13	CC	muscle myosin complex
9	31.42	NULL	23 / 84	BP	muscle contraction
10	31.25	NULL	12 / 37	CC	sarcomere
11	29.84	NULL	15 / 34	CC	myofibril
12	28.83	NULL	9 / 16	CC	M band
13	26.9	NULL	22 / 88	CC	Z disc
14	26.09	NULL	6 / 12	BP	skeletal muscle contraction
15	25.6	NULL	10 / 20	CC	I band
16	22.89	NULL	5 / 11	BP	cardiac muscle tissue morphogenesis
17	22.69	NULL	9 / 37	BP	cardiac muscle contraction
18	22.1	NULL	7 / 12	MF	titin binding
19	20.79	NULL	7 / 15	BP	striated muscle contraction
20	20.41	NULL	5 / 11	CC	A band
21	19.75	NULL	6 / 18	BP	regulation of muscle contraction
22	19.06	NULL	7 / 15	GSEA C2	REACTOME_STRIATED_MUSCLE_CONTRACTION
23	16.77	NULL	2 / 6	GSEA C2	BIOCARTA_HSP27_PATHWAY
24	16.75	NULL	25 / 297	MF	actin binding
25	16.68	NULL	8 / 42	CC	myosin complex
26	16.41	NULL	4 / 16	MF	microfilament motor activity
27	16.28	NULL	3 / 15	Cancer	BEN−PORATH_UP
28	15.28	NULL	4 / 14	BP	adult heart development
29	15.22	NULL	2 / 10	BP	heart contraction
30	15.05	NULL	5 / 26	BP	ventricular cardiac muscle tissue morphogenesis
31	14.01	NULL	4 / 14	MF	tropomyosin binding
32	13.91	NULL	7 / 21	BP	sarcomere organization
33	13.55	NULL	4 / 15	GSEA C2	EBAUER_MYOGENIC_TARGETS_OF_PAX3_FOXO1_FUSION
34	13.14	NULL	4 / 18	CC	costamere
35	13	NULL	1 / 5	GSEA C2	LIU_VAV3_PROSTATE_CARCINOGENESIS_UP
36	12.98	NULL	3 / 13	CC	pseudopodium
37	12.41	NULL	6 / 36	CC	sarcoplasmic reticulum
38	12.07	NULL	2 / 20	MF	myosin binding
39	12.06	NULL	2 / 10	BP	creatine metabolic process
40	12.02	NULL	2 / 12	BP	muscle fiber development

GW_182

Local Summary

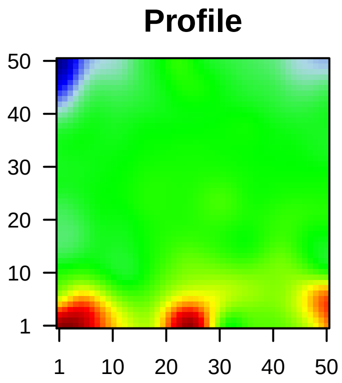
%DE = 0.93
metagenes = 16
genes = 244
genes in genesets = 238

genes with fdr < 0.1 = 220 (6 + / 214 −)
genes with fdr < 0.05 = 218 (6 + / 212 −)
genes with fdr < 0.01 = 211 (4 + / 207 −)

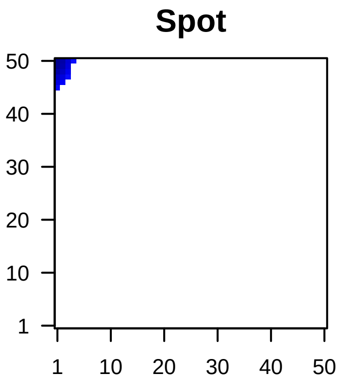
<r> metagenes = 0.95
<r> genes = 0.44

<FC> = −1.32
<shrinkage−t> = −46.69
<p−value> = 0
<fdr> = 0.11

Profile



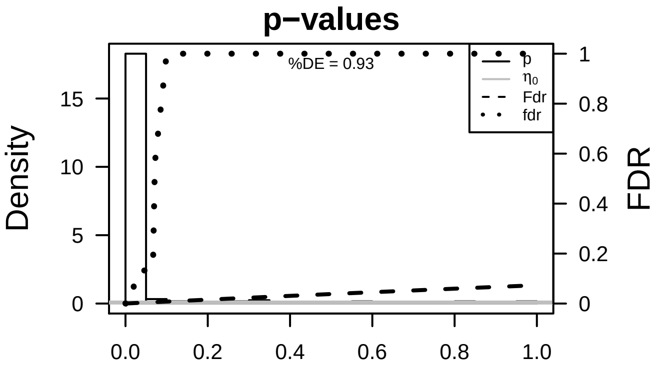
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	131	−2.61	2e−16	5e−17	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	57016	−2.21	2e−16	5e−17	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
3	218	−3.1	2e−16	5e−17	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
4	222	−1.71	2e−16	5e−17	1 x 49	aldehyde dehydrogenase 3 family, member B2 [Source:HGN
5	387695	−1.99	2e−16	5e−17	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Symb
6	64073	−1.66	2e−16	5e−17	1 x 46	chromosome 19 open reading frame 33 [Source:HGNC Symb
7	375791	−2.02	2e−16	5e−17	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Symb
8	810	−2.35	2e−16	5e−17	1 x 50	calmodulin−like 3 [Source:HGNC Symbol;Acc:1452]
9	51806	−1.76	2e−16	5e−17	4 x 50	calmodulin−like 5 [Source:HGNC Symbol;Acc:18180]
10	84290	−1.66	2e−16	5e−17	1 x 50	calpain, small subunit 2 [Source:HGNC Symbol;Acc:16371]
11	100133941	−1.98	2e−16	5e−17	3 x 50	CD24 molecule [Source:HGNC Symbol;Acc:1645]
12	4680	−2.44	2e−16	5e−17	1 x 50	carcinoembryonic antigen−related cell adhesion molecule 6 (
13	548596	−1.66	2e−16	5e−17	4 x 50	creatine kinase, mitochondrial 1B [Source:HGNC Symbol;Ac
14	9635	−2.53	2e−16	5e−17	1 x 46	chloride channel accessory 2 [Source:HGNC Symbol;Acc:20
15	22802	−2.25	2e−16	5e−17	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
16	84518	−2.83	2e−16	5e−17	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
17	49860	−2.16	2e−16	5e−17	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
18	1475	−2.25	2e−16	5e−17	1 x 50	cystatin A (stefin A) [Source:HGNC Symbol;Acc:2481]
19	1476	−1.63	2e−16	5e−17	1 x 50	cystatin B (stefin B) [Source:HGNC Symbol;Acc:2482]
20	92196	−1.85	2e−16	5e−17	3 x 50	death associated protein−like 1 [Source:HGNC Symbol;Acc:2

p−values



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−71.6	NULL	86 / 135	H.Tiss	WIRTH_Mucosa
2	−43.56	NULL	18 / 21	CC	cornified envelope
3	−34.76	NULL	24 / 53	BP	keratinocyte differentiation
4	−33.73	NULL	19 / 42	BP	keratinization
5	−30.01	NULL	25 / 76	BP	epidermis development
6	−29.95	NULL	98 / 572	Disease	GUDJ_psoriasis up
7	−26.58	NULL	10 / 19	BP	peptide cross−linking
8	−22.96	NULL	12 / 21	CC	desmosome
9	−17.52	NULL	10 / 44	CC	keratin filament
10	−17.49	NULL	16 / 82	CC	intermediate filament
11	−17.4	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
12	−17.22	NULL	8 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
13	−17.21	NULL	23 / 186	MF	structural molecule activity
14	−16.87	NULL	7 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
15	−16.54	NULL	6 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
16	−14.67	NULL	5 / 15	GSEA C2	AIGNER_ZEB1_TARGETS
17	−13.97	NULL	4 / 15	GSEA C2	CHANG_IMMORTALIZED_BY_HPV31_DN
18	−13.93	NULL	6 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
19	−13.54	NULL	4 / 10	GSEA C2	REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION_
20	−13.37	NULL	6 / 13	BP	negative regulation of peptidase activity
21	−12.92	NULL	9 / 38	BP	epithelial cell differentiation
22	−11.95	NULL	4 / 10	GSEA C2	SMID_BREAST_CANCER_ERBB2_UP
23	−11.6	NULL	7 / 15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
24	−11.56	NULL	3 / 13	BP	intermediate filament cytoskeleton organization
25	−11.23	NULL	3 / 12	BP	cellular aldehyde metabolic process
26	−11.22	NULL	4 / 15	GSEA C2	LEE_LIVER_CANCER_MYC_E2F1_UP
27	−11.06	NULL	2 / 8	GSEA C2	DORN_ADENOVIRUS_INFECTION_24HR_UP
28	−11.03	NULL	5 / 15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL
29	−11.01	NULL	4 / 16	GSEA C2	ROY_WOUND_BLOOD_VESSEL_DN
30	−10.95	NULL	6 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
31	−10.79	NULL	3 / 10	GSEA C2	MURAKAMI_UV_RESPONSE_1HR_UP
32	−10.64	NULL	3 / 16	GSEA C2	AMIT_SERUM_RESPONSE_480_MCF10A
33	−10.22	NULL	3 / 11	GSEA C2	MURAKAMI_UV_RESPONSE_6HR_DN
34	−10.2	NULL	6 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
35	−9.97	NULL	10 / 52	BP	negative regulation of endopeptidase activity
36	−9.81	NULL	4 / 14	GSEA C2	CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U
37	−9.65	NULL	13 / 79	MF	serine−type endopeptidase inhibitor activity
38	−9.47	NULL	3 / 10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
39	−9.46	NULL	4 / 16	GSEA C2	LEE_LIVER_CANCER_MYC_TGFA_UP
40	−9.41	NULL	7 / 51	MF	protein binding, bridging