GW_215

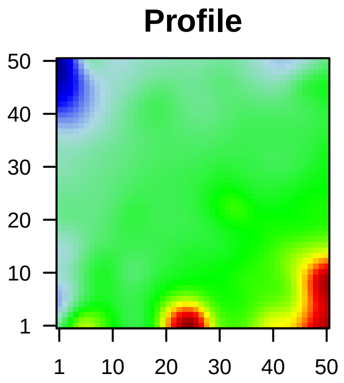
Global Summary

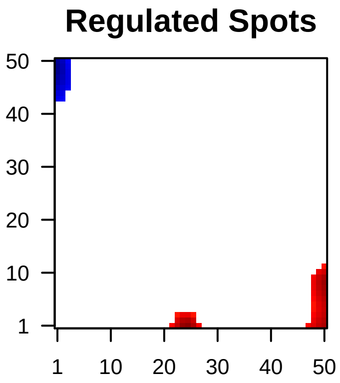
%DE = 0.15

genes with fdr < 0.2 = 1909 (1154 + / 755 −)
genes with fdr < 0.1 = 1619 (1010 + / 609 −)
genes with fdr < 0.05 = 1343 (849 + / 494 −)
genes with fdr < 0.01 = 1031 (683 + / 348 −)

genes in genesets = 16332

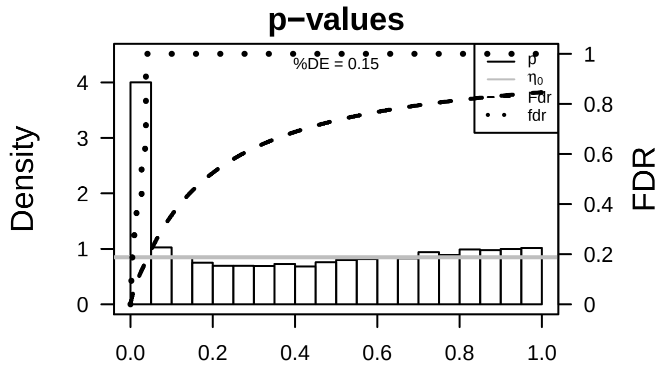
<FC> = 0
<shrinkage−t> = 0
<p−value> = 0.07
<fdr> = 0.85





Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	25890	1.59	2e−16	1e−14	50 x 4	ABI family, member 3 (NESH) binding protein [Source:HGNC
2	58	4.44	2e−16	1e−14	25 x 1	actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
3	70	2.46	2e−16	1e−14	25 x 1	actin, alpha, cardiac muscle 1 [Source:HGNC Symbol;Acc:14
4	72	1.82	2e−16	1e−14	4 x 1	actin, gamma 2, smooth muscle, enteric [Source:HGNC Sym
5	124	1.45	2e−16	1e−14	50 x 11	alcohol dehydrogenase 1A (class I), alpha polypeptide [Sour
6	131	−2.86	2e−16	1e−14	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
7	10551	2.89	2e−16	1e−14	50 x 10	anterior gradient 2 [Source:HGNC Symbol;Acc:328]
8	57016	−1.52	2e−16	1e−14	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductas
9	218	−2.32	2e−16	1e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
10	222	−1.59	2e−16	1e−14	1 x 49	aldehyde dehydrogenase 3 family, member B2 [Source:HGN
11	154796	1.74	2e−16	1e−14	50 x 12	angiomotin [Source:HGNC Symbol;Acc:17810]
12	270	1.51	2e−16	1e−14	50 x 7	adenosine monophosphate deaminase 1 [Source:HGNC Sy
13	65124	−1.68	2e−16	1e−14	1 x 45	sosondowah ankyrin repeat domain family member C [Sourc
14	10930	1.75	2e−16	1e−14	25 x 1	apolipoprotein B mRNA editing enzyme, catalytic polypeptide
15	341	2.21	2e−16	1e−14	50 x 1	apolipoprotein C−I [Source:HGNC Symbol;Acc:607]
16	347	3.19	2e−16	1e−14	50 x 7	apolipoprotein D [Source:HGNC Symbol;Acc:612]
17	348	1.84	2e−16	1e−14	50 x 1	apolipoprotein E [Source:HGNC Symbol;Acc:613]
18	445	1.86	2e−16	1e−14	50 x 47	argininosuccinate synthase 1 [Source:HGNC Symbol;Acc:75
19	563	1.45	2e−16	1e−14	50 x 10	alpha−2−glycoprotein 1, zinc−binding [Source:HGNC Symbol
20	80115	−1.46	2e−16	1e−14	1 x 43	BAI1−associated protein 2−like 2 [Source:HGNC Symbol;Acc



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	29.32	NULL	127	H.Tiss	WIRTH_Muscle
2	23.18	NULL	36	BP	muscle filament sliding
3	20.11	NULL	44	MF	structural constituent of muscle
4	18.68	NULL	16	H.Tiss	WIRTH_Hippocampus
5	18.56	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_F
6	16.46	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_D
7	15.1	NULL	375	Disease	GUDJ_psoriasis down
8	14.52	NULL	84	BP	muscle contraction
9	14.39	NULL	12	CC	myosin filament
10	13.85	NULL	13	CC	muscle myosin complex
11	12.6	NULL	37	CC	sarcomere
12	11.42	NULL	34	CC	myofibril
13	10.48	NULL	15	CC	MHC class II protein complex
14	9.85	NULL	88	CC	Z disc
15	9.81	NULL	16	CC	M band
16	9.77	NULL	20	CC	I band
17	9.36	NULL	12	BP	skeletal muscle contraction
18	9.3	NULL	18	BP	regulation of muscle contraction
19	9.24	NULL	10	GSEA C2	LUI_THYROID_CANCER_CLUSTER_5
20	9.09	NULL	5	GSEA C2	FERRARI_RESPONSE_TO_FENRETINIDE_DN
Underexpressed					
1	−20.28	NULL	135	H.Tiss	WIRTH_Mucosa
2	−17.99	NULL	572	Disease	GUDJ_psoriasis up
3	−12.98	NULL	21	CC	cornified envelope
4	−12.52	NULL	42	BP	keratinization
5	−12.16	NULL	53	BP	keratinocyte differentiation
6	−10.73	NULL	76	BP	epidermis development
7	−9.16	NULL	16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
8	−8.98	NULL	19	BP	peptide cross−linking
9	−7.87	NULL	15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
10	−7.61	NULL	16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
11	−6.82	NULL	530	Cancer	Lembcke_Normal vs Adenoma
12	−6.58	NULL	15	GSEA C2	BILD_HRAS_ONCOGENIC_SIGNATURE
13	−6.47	NULL	15	GSEA C2	CROMER_TUMORIGENESIS_UP
14	−6.34	NULL	1233	TF	KIM_MYC targets
15	−6.07	NULL	79	MF	serine−type endopeptidase inhibitor activity
16	−6.03	NULL	16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
17	−6.01	NULL	370	BP	mitotic cell cycle
18	−5.84	NULL	11	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_BONE_DN
19	−5.8	NULL	186	MF	structural molecule activity
20	−5.77	NULL	15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN

GW_215

Local Summary

%DE = 0.98

metagenes = 14

genes = 119

genes in genesets = 118

genes with fdr < 0.1 = 112 (112 + / 0 −)

genes with fdr < 0.05 = 112 (112 + / 0 −)

genes with fdr < 0.01 = 110 (110 + / 0 −)

<r> metagenes = 0.99

<r> genes = 0.61

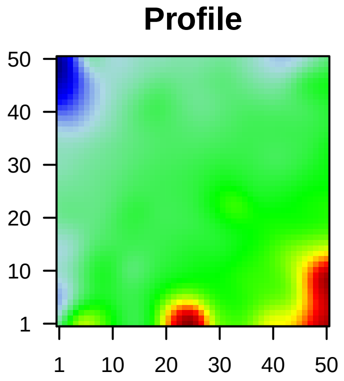
<FC> = 1.41

<shrinkage−t> = 49.38

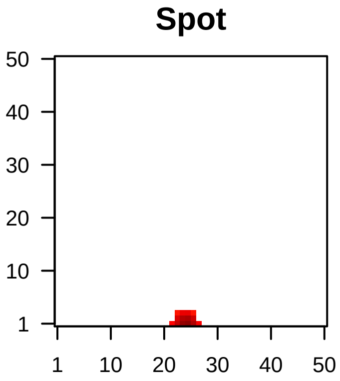
<p−value> = 0

<fdr> = 0.06

Profile



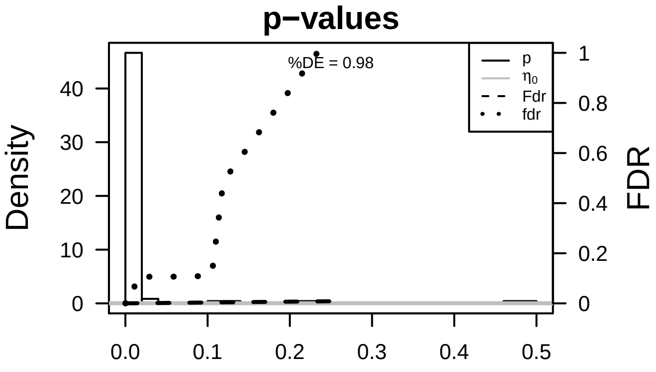
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	58	4.44	2e−16	1e−17	25 x 1	actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
2	70	2.46	2e−16	1e−17	25 x 1	actin, alpha, cardiac muscle 1 [Source:HGNC Symbol;Acc:14
3	10930	1.75	2e−16	1e−17	25 x 1	apolipoprotein B mRNA editing enzyme, catalytic polypeptide
4	1158	3.73	2e−16	1e−17	25 x 1	creatine kinase, muscle [Source:HGNC Symbol;Acc:1994]
5	1160	1.59	2e−16	1e−17	25 x 1	creatine kinase, mitochondrial 2 (sarcomeric) [Source:HGNC
6	202333	2.28	2e−16	1e−17	25 x 1	cardiomyopathy associated 5 [Source:HGNC Symbol;Acc:14
7	1346	2.12	2e−16	1e−17	25 x 1	cytochrome c oxidase subunit VIIa polypeptide 1 (muscle) [S
8	1410	1.95	2e−16	1e−17	25 x 1	crystallin, alpha B [Source:HGNC Symbol;Acc:2389]
9	115265	1.45	2e−16	1e−17	25 x 1	DNA−damage−inducible transcript 4−like [Source:HGNC Sy
10	1674	1.61	2e−16	1e−17	25 x 1	desmin [Source:HGNC Symbol;Acc:2770]
11	1917	2.69	2e−16	1e−17	25 x 1	eukaryotic translation elongation factor 1 alpha 2 [Source:HG
12	2027	2.39	2e−16	1e−17	25 x 1	enolase 3 (beta, muscle) [Source:HGNC Symbol;Acc:3354]
13	2273	2.48	2e−16	1e−17	25 x 1	four and a half LIM domains 1 [Source:HGNC Symbol;Acc:37
14	2318	2.46	2e−16	1e−17	25 x 1	filamin C, gamma [Source:HGNC Symbol;Acc:3756]
15	283120	1.91	2e−16	1e−17	25 x 1	H19, imprinted maternally expressed transcript (non−protein
16	126393	2.28	2e−16	1e−17	25 x 1	heat shock protein, alpha−crystallin−related, B6 [Source:HG
17	27129	1.53	2e−16	1e−17	25 x 1	heat shock 27kDa protein family, member 7 (cardiovascular) [
18	10324	2.84	2e−16	1e−17	25 x 1	kelch−like family member 41 [Source:HGNC Symbol;Acc:169
19	4151	3.18	2e−16	1e−17	25 x 1	myoglobin [Source:HGNC Symbol;Acc:6915]
20	4604	2.19	2e−16	1e−17	25 x 1	myosin binding protein C, slow type [Source:HGNC Symbol;A

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	66.31	NULL	60 / 127	H.Tiss	WIRTH_Muscle
2	62.5	NULL	23 / 36	BP	muscle filament sliding
3	51.47	NULL	11 / 16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_F
4	51.45	NULL	11 / 16	H.Tiss	WIRTH_Hippocampus
5	49.29	NULL	23 / 44	MF	structural constituent of muscle
6	41.29	NULL	10 / 12	CC	myosin filament
7	35.12	NULL	8 / 13	CC	muscle myosin complex
8	33.52	NULL	12 / 37	CC	sarcomere
9	32.3	NULL	23 / 84	BP	muscle contraction
10	30.83	NULL	15 / 34	CC	myofibril
11	30.6	NULL	8 / 14	CC	contractile fiber
12	28.72	NULL	6 / 12	BP	skeletal muscle contraction
13	28.05	NULL	9 / 16	CC	M band
14	26.29	NULL	22 / 88	CC	Z disc
15	25.43	NULL	10 / 20	CC	I band
16	22.83	NULL	6 / 18	BP	regulation of muscle contraction
17	22.45	NULL	7 / 12	MF	titin binding
18	22.39	NULL	9 / 37	BP	cardiac muscle contraction
19	20.27	NULL	5 / 11	BP	cardiac muscle tissue morphogenesis
20	19.79	NULL	7 / 15	GSEA C2	REACTOME_STRIATED_MUSCLE_CONTRACTION
21	19.34	NULL	5 / 11	CC	A band
22	19.12	NULL	7 / 15	BP	striated muscle contraction
23	18.96	NULL	2 / 6	GSEA C2	BIOCARTA_HSP27_PATHWAY
24	17.67	NULL	8 / 42	CC	myosin complex
25	17.26	NULL	4 / 14	BP	adult heart development
26	17.09	NULL	5 / 26	BP	ventricular cardiac muscle tissue morphogenesis
27	17.04	NULL	4 / 16	MF	microfilament motor activity
28	16.4	NULL	25 / 297	MF	actin binding
29	16.03	NULL	3 / 15	Cancer	BEN−PORATH_UP
30	14.22	NULL	2 / 10	BP	heart contraction
31	13.77	NULL	4 / 14	MF	tropomyosin binding
32	13.76	NULL	2 / 10	BP	creatine metabolic process
33	13.47	NULL	3 / 13	CC	pseudopodium
34	13.23	NULL	7 / 21	BP	sarcomere organization
35	12.99	NULL	4 / 18	CC	costamere
36	12.74	NULL	2 / 12	BP	muscle fiber development
37	12.65	NULL	2 / 16	GSEA C2	SASSON_RESPONSE_TO_GONADOTROPHINS_DN
38	12.65	NULL	2 / 16	GSEA C2	SASSON_RESPONSE_TO_FORSKOLIN_DN
39	12.28	NULL	6 / 36	CC	sarcoplasmic reticulum
40	12.21	NULL	1 / 9	GSEA C2	PENG_GLUCOSE_DEPRIVATION_UP

GW_215

Local Summary

%DE = 0.88

metagenes = 34

genes = 512

genes in genesets = 509

genes with fdr < 0.1 = 417 (411 + / 6 −)

genes with fdr < 0.05 = 399 (397 + / 2 −)

genes with fdr < 0.01 = 354 (353 + / 1 −)

<r> metagenes = 0.83

<r> genes = 0.33

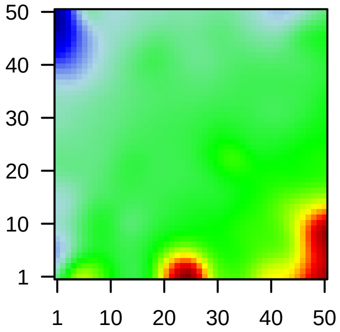
<FC> = 0.83

<shrinkage−t> = 28.91

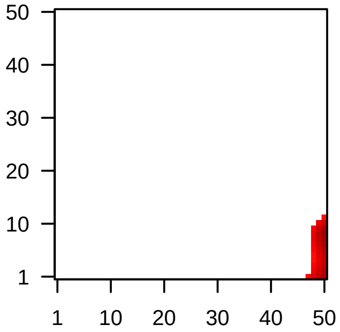
<p−value> = 0

<fdr> = 0.25

Profile



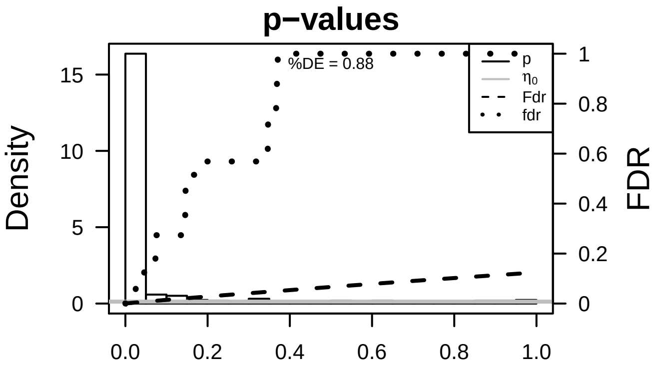
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	25890	1.59	2e−16	2e−16	50 x 4	ABI family, member 3 (NESH) binding protein [Source:HGNC
2	124	1.45	2e−16	2e−16	50 x 11	alcohol dehydrogenase 1A (class I), alpha polypeptide [Sourc
3	10551	2.89	2e−16	2e−16	50 x 10	anterior gradient 2 [Source:HGNC Symbol;Acc:328]
4	154796	1.74	2e−16	2e−16	50 x 12	angiomotin [Source:HGNC Symbol;Acc:17810]
5	270	1.51	2e−16	2e−16	50 x 7	adenosine monophosphate deaminase 1 [Source:HGNC Sym
6	341	2.21	2e−16	2e−16	50 x 1	apolipoprotein C−I [Source:HGNC Symbol;Acc:607]
7	347	3.19	2e−16	2e−16	50 x 7	apolipoprotein D [Source:HGNC Symbol;Acc:612]
8	348	1.84	2e−16	2e−16	50 x 1	apolipoprotein E [Source:HGNC Symbol;Acc:613]
9	563	1.45	2e−16	2e−16	50 x 10	alpha−2−glycoprotein 1, zinc−binding [Source:HGNC Symbol
10	80341	3.15	2e−16	2e−16	50 x 10	BPI fold containing family B, member 2 [Source:HGNC Symb
11	713	1.86	2e−16	2e−16	50 x 1	complement component 1, q subcomponent, B chain [Source
12	714	1.57	2e−16	2e−16	50 x 1	complement component 1, q subcomponent, C chain [Source
13	92747	4.26	2e−16	2e−16	50 x 10	BPI fold containing family B, member 1 [Source:HGNC Symb
14	260436	2.11	2e−16	2e−16	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symbo
15	6358	1.66	2e−16	2e−16	50 x 7	chemokine (C−C motif) ligand 14 [Source:HGNC Symbol;Acc
16	6352	1.63	2e−16	2e−16	48 x 1	chemokine (C−C motif) ligand 5 [Source:HGNC Symbol;Acc:
17	972	1.46	2e−16	2e−16	50 x 1	CD74 molecule, major histocompatibility complex, class II inv
18	1675	2.49	2e−16	2e−16	50 x 9	complement factor D (adipsin) [Source:HGNC Symbol;Acc:27
19	9071	1.49	2e−16	2e−16	50 x 12	claudin 10 [Source:HGNC Symbol;Acc:2033]
20	5010	1.73	2e−16	2e−16	50 x 7	claudin 11 [Source:HGNC Symbol;Acc:8514]

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	32.71	NULL	14 / 16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_D
2	24.42	NULL	12 / 15	CC	MHC class II protein complex
3	16.03	NULL	16 / 47	BP	antigen processing and presentation
4	15.33	NULL	57 / 312	BP	immune response
5	14.9	NULL	101 / 1182	CC	extracellular region
6	14.64	NULL	2 / 5	GSEA C2	FERRARI_RESPONSE_TO_FENRETINIDE_DN
7	14.16	NULL	4 / 7	GSEA C2	BIOCARTA_COMP_PATHWAY
8	14.1	NULL	3 / 5	GSEA C2	WONG_ENDOMETRIAL_CANCER_LATE
9	14.02	NULL	3 / 10	GSEA C2	LUI_THYROID_CANCER_CLUSTER_5
10	13.4	NULL	7 / 16	GSEA C2	BOQUEST_STEM_CELL_CULTURED_VS_FRESH_DN
11	13.24	NULL	4 / 7	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
12	13.12	NULL	4 / 8	GSEA C2	REACTOME_COMPLEMENT_CASCADE
13	13.12	NULL	4 / 8	GSEA C2	REACTOME_INITIAL_TRIGGERING_OF_COMPLEMENT
14	12.96	NULL	6 / 14	GSEA C2	WU_SILENCED_BY_METHYLATION_IN_BLADDER_CANCER
15	12.84	NULL	71 / 683	CC	extracellular space
16	12.52	NULL	7 / 21	CC	clathrin−coated endocytic vesicle membrane
17	12.52	NULL	9 / 28	CC	transport vesicle membrane
18	12.29	NULL	7 / 12	GSEA C2	ZHAN_MULTIPLE_MYELOMA_DN
19	12.22	NULL	4 / 8	GSEA C2	GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_DN
20	12.06	NULL	6 / 12	GSEA C2	BERTUCCI_INVASIVE_CARCINOMA_DUCTAL_VS_LOBULAR_
21	11.89	NULL	6 / 14	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_LUNG_DN
22	11.88	NULL	7 / 23	CC	integral to lumenal side of endoplasmic reticulum membrane
23	11.64	NULL	104 / 553	Cancer	Lembcke_Colonic Inflammation
24	11.55	NULL	83 / 417	H.Tiss	WIRTH_Immune system
25	11.45	NULL	3 / 6	GSEA C2	SANA_RESPONSE_TO_IFNG_UP
26	11.35	NULL	3 / 9	GSEA C2	GOUYER_TATI_TARGETS_UP
27	11.15	NULL	40 / 375	Disease	GUDJ_psoriasis down
28	10.93	NULL	8 / 20	BP	complement activation
29	10.62	NULL	6 / 11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
30	10.53	NULL	4 / 13	GSEA C2	NING_CHRONIC_OBSTRUCTIVE_PULMONARY_DISEASE_DN
31	10.51	NULL	9 / 35	CC	trans−Golgi network membrane
32	10.39	NULL	4 / 7	Glio	Donson−cytotoxic effectors−associated with LTS in HGA
33	10.28	NULL	2 / 3	GSEA C2	KEGG_VIRAL_MYOCARDITIS
34	10.16	NULL	14 / 60	BP	T cell costimulation
35	10.1	NULL	3 / 14	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_
36	9.97	NULL	2 / 4	GSEA C2	REACTOME_CLASSICAL_ANTIBODY_MEDIATED_COMPLEMEN
37	9.86	NULL	4 / 13	Cancer	GENTLES_modul17
38	9.84	NULL	48 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
39	9.84	NULL	48 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
40	9.84	NULL	48 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down

GW_215

Local Summary

%DE = 0.91

metagenes = 22

genes = 304

genes in genesets = 296

genes with fdr < 0.1 = 267 (30 + / 237 −)

genes with fdr < 0.05 = 250 (26 + / 224 −)

genes with fdr < 0.01 = 224 (20 + / 204 −)

<r> metagenes = 0.9

<r> genes = 0.38

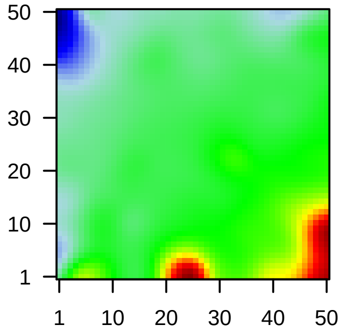
<FC> = −0.79

<shrinkage−t> = −27.92

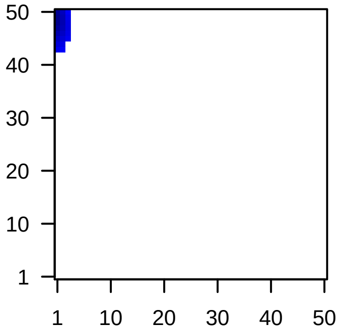
<p−value> = 0

<fdr> = 0.21

Profile



Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	131	−2.86	2e−16	9e−17	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	57016	−1.52	2e−16	9e−17	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
3	218	−2.32	2e−16	9e−17	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
4	222	−1.59	2e−16	9e−17	1 x 49	aldehyde dehydrogenase 3 family, member B2 [Source:HGN
5	65124	−1.68	2e−16	9e−17	1 x 45	sosondowah ankyrin repeat domain family member C [Source
6	80115	−1.46	2e−16	9e−17	1 x 43	BAI1−associated protein 2−like 2 [Source:HGNC Symbol;Acc
7	375791	−1.66	2e−16	9e−17	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Sym
8	1048	−1.48	2e−16	9e−17	2 x 50	carcinoembryonic antigen−related cell adhesion molecule 5 [
9	9022	−1.7	2e−16	9e−17	1 x 50	chloride intracellular channel 3 [Source:HGNC Symbol;Acc:2
10	84518	−2.15	2e−16	9e−17	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
11	49860	−2.35	2e−16	9e−17	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
12	1475	−2.19	2e−16	9e−17	1 x 50	cystatin A (stefin A) [Source:HGNC Symbol;Acc:2481]
13	92196	1.5	2e−16	9e−17	3 x 50	death associated protein−like 1 [Source:HGNC Symbol;Acc:2
14	414325	−1.92	2e−16	9e−17	1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
15	1673	−2.46	2e−16	9e−17	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
16	84985	−1.53	2e−16	9e−17	1 x 44	family with sequence similarity 83, member A [Source:HGNC
17	9982	−2.86	2e−16	9e−17	1 x 47	fibroblast growth factor binding protein 1 [Source:HGNC Sym
18	10804	−2.3	2e−16	9e−17	1 x 47	gap junction protein, beta 6, 30kDa [Source:HGNC Symbol;A
19	2877	−1.99	2e−16	9e−17	1 x 50	glutathione peroxidase 2 (gastrointestinal) [Source:HGNC Sy
20	1839	−1.82	2e−16	9e−17	1 x 45	heparin−binding EGF−like growth factor [Source:HGNC Sym

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−43.48	NULL	88 / 135	H.Tiss	WIRTH_Mucosa
2	−33.19	NULL	18 / 21	CC	cornified envelope
3	−29.05	NULL	20 / 42	BP	keratinization
4	−28.28	NULL	112 / 572	Disease	GUDJ_psoriasis up
5	−25.94	NULL	24 / 53	BP	keratinocyte differentiation
6	−24.25	NULL	27 / 76	BP	epidermis development
7	−23.78	NULL	10 / 19	BP	peptide cross−linking
8	−18.85	NULL	8 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
9	−17.78	NULL	8 / 15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
10	−17.01	NULL	6 / 13	BP	negative regulation of peptidase activity
11	−16.59	NULL	9 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
12	−16.09	NULL	30 / 186	MF	structural molecule activity
13	−15.38	NULL	4 / 15	GSEA C2	LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
14	−15.15	NULL	14 / 79	MF	serine−type endopeptidase inhibitor activity
15	−14.5	NULL	10 / 52	BP	negative regulation of endopeptidase activity
16	−14.47	NULL	21 / 82	CC	intermediate filament
17	−14.18	NULL	7 / 29	BP	regulation of proteolysis
18	−13.89	NULL	6 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
19	−13.32	NULL	4 / 16	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_LUNG_UP
20	−13.07	NULL	3 / 11	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_BONE_DN
21	−12.78	NULL	6 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
22	−12.45	NULL	13 / 44	CC	keratin filament
23	−12.38	NULL	7 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
24	−11.81	NULL	3 / 12	MF	retinol binding
25	−11.38	NULL	6 / 15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL
26	−11.31	NULL	3 / 13	GSEA C2	FARMER_BREAST_CANCER_APOCRINE VS LUMINAL
27	−11.28	NULL	3 / 13	BP	retinoic acid metabolic process
28	−11.14	NULL	3 / 10	GSEA C2	NIKOLSKY_BREAST_CANCER_20Q12_Q13_AMPLICON
29	−11.09	NULL	3 / 15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
30	−11.09	NULL	3 / 16	GSEA C2	AMIT_SERUM_RESPONSE_480_MCF10A
31	−11.02	NULL	2 / 11	GSEA C2	LEI_MYB_TARGETS
32	−10.99	NULL	2 / 8	GSEA C2	MCLACHLAN_DENTAL_CARIES_UP
33	−10.83	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
34	−10.67	NULL	5 / 16	GSEA C2	COLDREN_GEFITINIB_RESISTANCE_DN
35	−10.46	NULL	3 / 12	BP	cellular aldehyde metabolic process
36	−10.46	NULL	2 / 14	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_
37	−10.42	NULL	8 / 38	BP	epithelial cell differentiation
38	−10.26	NULL	2 / 9	GSEA C2	MCLACHLAN_DENTAL_CARIES_DN
39	−10.2	NULL	5 / 23	MF	peptidase inhibitor activity
40	−10.11	NULL	6 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN

p−values