GW_063

Global Summary

%DE = 0.13

genes with fdr < 0.2 = 1580 (968 + / 612 −)

genes with fdr < 0.1 = 1141 (744 + / 397 −)

genes with fdr < 0.05 = 919 (637 + / 282 −)

genes with fdr < 0.01 = 661 (489 + / 172 −)

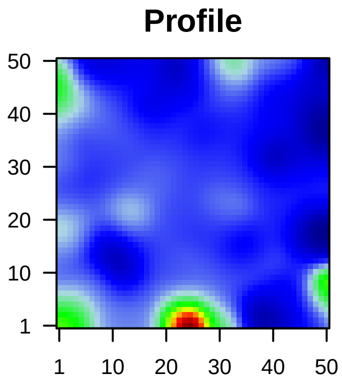
genes in genesets = 16332

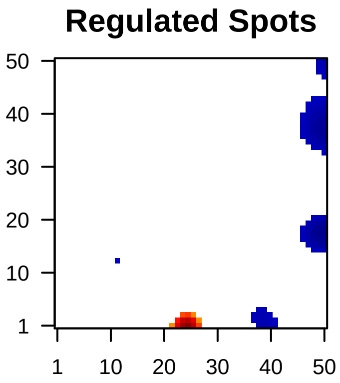
<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.12

<fdr> = 0.87



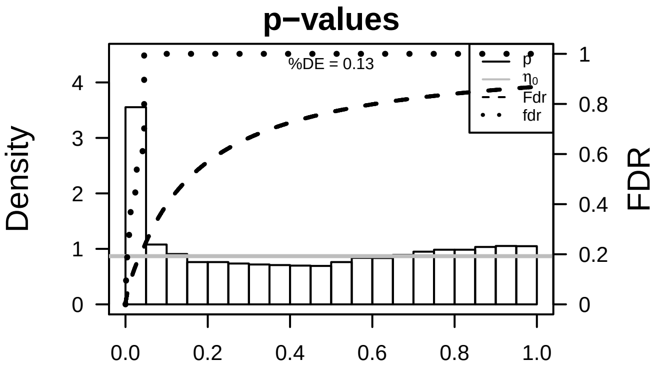


Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	58	5.35	2e−16	2e−14	25 x 1	actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
2	70	3.49	2e−16	2e−14	25 x 1	actin, alpha, cardiac muscle 1 [Source:HGNC Symbol;Acc:14
3	10551	2.19	2e−16	2e−14	50 x 10	anterior gradient 2 [Source:HGNC Symbol;Acc:328]
4	501	−1.69	2e−16	2e−14	6 x 46	aldehyde dehydrogenase 7 family, member A1 [Source:HGNC
5	270	1.62	2e−16	2e−14	50 x 7	adenosine monophosphate deaminase 1 [Source:HGNC Sym
6	27063	1.48	2e−16	2e−14	25 x 1	ankyrin repeat domain 1 (cardiac muscle) [Source:HGNC Syr
7	10930	1.95	2e−16	2e−14	25 x 1	apolipoprotein B mRNA editing enzyme, catalytic polypeptide
8	347	3.05	2e−16	2e−14	50 x 7	apolipoprotein D [Source:HGNC Symbol;Acc:612]
9	140458	2.05	2e−16	2e−14	25 x 1	ankyrin repeat and SOCS box containing 5 [Source:HGNC Sy
10	618	1.5	2e−16	2e−14	39 x 1	brain cytoplasmic RNA 1 [Source:HGNC Symbol;Acc:1022]
11	80341	1.88	2e−16	2e−14	50 x 10	BPI fold containing family B, member 2 [Source:HGNC Symb
12	64073	1.58	2e−16	2e−14	1 x 46	chromosome 19 open reading frame 33 [Source:HGNC Symb
13	92747	4.32	2e−16	2e−14	50 x 10	BPI fold containing family B, member 1 [Source:HGNC Symb
14	352999	2.82	2e−16	2e−14	50 x 10	chromosome 6 open reading frame 58 [Source:HGNC Symbo
15	23589	1.53	2e−16	2e−14	1 x 46	calcium regulated heat stable protein 1, 24kDa [Source:HGNC
16	845	1.6	2e−16	2e−14	25 x 1	calsequestrin 2 (cardiac muscle) [Source:HGNC Symbol;Acc:
17	1675	2.16	2e−16	2e−14	50 x 9	complement factor D (adipsin) [Source:HGNC Symbol;Acc:27
18	1158	4.09	2e−16	2e−14	25 x 1	creatine kinase, muscle [Source:HGNC Symbol;Acc:1994]
19	1160	1.54	2e−16	2e−14	25 x 1	creatine kinase, mitochondrial 2 (sarcomeric) [Source:HGNC
20	202333	2.15	2e−16	2e−14	25 x 1	cardiomyopathy associated 5 [Source:HGNC Symbol;Acc:143

Global Geneset Analysis

Rank	GSZ	p−value	#all		Geneset
Overexpressed					
1	33.54	NULL	127	H.Tiss	WIRTH_Muscle
2	25.24	NULL	36	BP	muscle filament sliding
3	24.81	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_F
4	22.69	NULL	16	H.Tiss	WIRTH_Hippocampus
5	19.75	NULL	44	MF	structural constituent of muscle
6	16.16	NULL	84	BP	muscle contraction
7	15.38	NULL	12	CC	myosin filament
8	15.1	NULL	1182	CC	extracellular region
9	14.32	NULL	683	CC	extracellular space
10	14.15	NULL	572	Disease	GUDJ_psoriasis up
11	13.2	NULL	37	CC	sarcomere
12	12.56	NULL	14	CC	contractile fiber
13	12.53	NULL	88	CC	Z disc
14	12.48	NULL	34	CC	myofibril
15	12.19	NULL	16	CC	M band
16	12.03	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_D
17	11.36	NULL	13	CC	muscle myosin complex
18	11.14	NULL	20	CC	I band
19	10.8	NULL	12	BP	skeletal muscle contraction
20	9.9	NULL	15	GSEA C2	REACTOME_STRIATED_MUSCLE_CONTRACTION
Underexpressed					
1	−11.2	NULL	1749	MF	DNA binding
2	−10.07	NULL	1581	BP	regulation of transcription, DNA−dependent
3	−9.81	NULL	1574	BP	transcription, DNA−templated
4	−8.48	NULL	504	Chr	Chr 15
5	−7.94	NULL	4640	CC	nucleus
6	−7.91	NULL	823	MF	sequence−specific DNA binding transcription factor activity
7	−7.1	NULL	940	MF	nucleic acid binding
8	−6.67	NULL	10	GSEA C2	CHASSOT_SKIN_WOUND
9	−6.3	NULL	318	MF	chromatin binding
10	−6.25	NULL	280	Chr	Chr 13
11	−6.18	NULL	500	MF	sequence−specific DNA binding
12	−5.72	NULL	24	TF Tissue	VAQUERIZAS_Trachea
13	−5.63	NULL	368	miRNA target−starBase	hsa−miR−144
14	−5.59	NULL	1820	MF	metal ion binding
15	−5.47	NULL	314	miRNA 3UTR	TTGC−130A−−301−−130B
16	−5.36	NULL	391	miRNA 3UTR	TGAA−181A−−181B−−181C−−181D
17	−5.31	NULL	319	miRNA target−starBase	hsa−miR−367
18	−5.27	NULL	186	miRNA target−starBase	hsa−miR−382
19	−5.22	NULL	300	miRNA target−starBase	hsa−miR−548c−3p
20	−5.19	NULL	381	miRNA target−starBase	hsa−let−7c



GW_063

Local Summary

%DE = 0.99

metagenes = 14

genes = 116

genes in genesets = 116

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

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

genes with fdr < 0.01 = 112 (112 + / 0 −)

<r> metagenes = 0.98

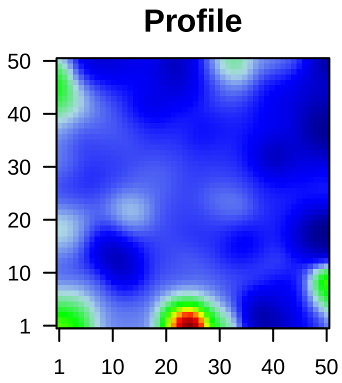
<r> genes = 0.62

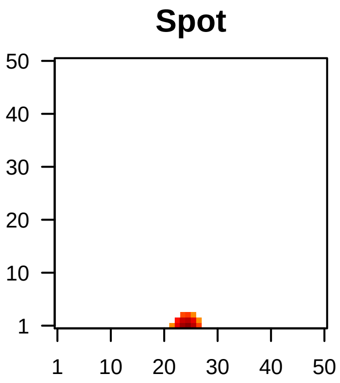
<FC> = 1.57

<shrinkage−t> = 55.06

<p−value> = 0

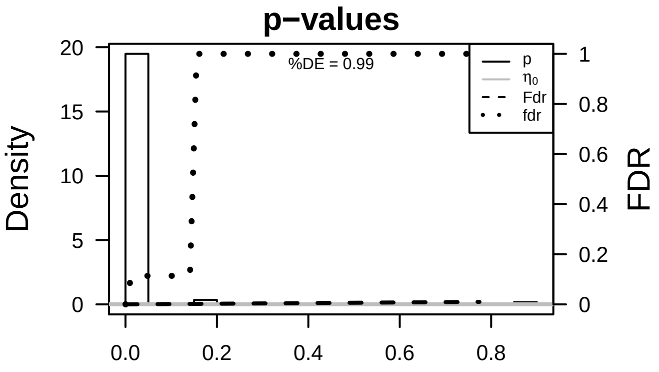
<fdr> = 0.04





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	58	5.35	2e−16	6e−18	25 x 1	actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:1
2	70	3.49	2e−16	6e−18	25 x 1	actin, alpha, cardiac muscle 1 [Source:HGNC Symbol;Acc:14
3	27063	1.48	2e−16	6e−18	25 x 1	ankyrin repeat domain 1 (cardiac muscle) [Source:HGNC Sy
4	10930	1.95	2e−16	6e−18	25 x 1	apolipoprotein B mRNA editing enzyme, catalytic polypeptide
5	140458	2.05	2e−16	6e−18	25 x 1	ankyrin repeat and SOCS box containing 5 [Source:HGNC S
6	845	1.6	2e−16	6e−18	25 x 1	calsequestrin 2 (cardiac muscle) [Source:HGNC Symbol;Acc:
7	1158	4.09	2e−16	6e−18	25 x 1	creatine kinase, muscle [Source:HGNC Symbol;Acc:1994]
8	1160	1.54	2e−16	6e−18	25 x 1	creatine kinase, mitochondrial 2 (sarcomeric) [Source:HGNC
9	202333	2.15	2e−16	6e−18	25 x 1	cardiomyopathy associated 5 [Source:HGNC Symbol;Acc:14
10	1346	1.95	2e−16	6e−18	25 x 1	cytochrome c oxidase subunit VIIa polypeptide 1 (muscle) [S
11	1410	1.82	2e−16	6e−18	25 x 1	crystallin, alpha B [Source:HGNC Symbol;Acc:2389]
12	8048	1.66	2e−16	6e−18	25 x 1	cysteine and glycine−rich protein 3 (cardiac LIM protein) [Sou
13	115265	2.02	2e−16	6e−18	25 x 1	DNA−damage−inducible transcript 4−like [Source:HGNC Sy
14	23109	1.62	2e−16	6e−18	25 x 1	dendrin [Source:HGNC Symbol;Acc:24458]
15	1674	1.9	2e−16	6e−18	25 x 1	desmin [Source:HGNC Symbol;Acc:2770]
16	1917	2.34	2e−16	6e−18	25 x 1	eukaryotic translation elongation factor 1 alpha 2 [Source:HG
17	2027	2.23	2e−16	6e−18	25 x 1	enolase 3 (beta, muscle) [Source:HGNC Symbol;Acc:3354]
18	2273	2.64	2e−16	6e−18	25 x 1	four and a half LIM domains 1 [Source:HGNC Symbol;Acc:37
19	2318	2.68	2e−16	6e−18	25 x 1	filamin C, gamma [Source:HGNC Symbol;Acc:3756]
20	283120	1.54	2e−16	6e−18	25 x 1	H19, imprinted maternally expressed transcript (non−protein



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	64.21	NULL	60 / 127	H.Tiss	WIRTH_Muscle
2	57.42	NULL	11 / 16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_F
3	56.69	NULL	23 / 36	BP	muscle filament sliding
4	53.78	NULL	11 / 16	H.Tiss	WIRTH_Hippocampus
5	43.59	NULL	23 / 44	MF	structural constituent of muscle
6	41.36	NULL	10 / 12	CC	myosin filament
7	32.9	NULL	8 / 14	CC	contractile fiber
8	31.63	NULL	23 / 84	BP	muscle contraction
9	28.1	NULL	8 / 13	CC	muscle myosin complex
10	27.73	NULL	12 / 37	CC	sarcomere
11	26.8	NULL	6 / 12	BP	skeletal muscle contraction
12	26.57	NULL	8 / 16	CC	M band
13	26.51	NULL	15 / 34	CC	myofibril
14	24.13	NULL	21 / 88	CC	Z disc
15	23.08	NULL	5 / 11	BP	cardiac muscle tissue morphogenesis
16	23.08	NULL	9 / 20	CC	I band
17	23.04	NULL	7 / 12	MF	titin binding
18	21.07	NULL	2 / 6	GSEA C2	BIOCARTA_HSP27_PATHWAY
19	19.94	NULL	7 / 15	GSEA C2	REACTOME_STRIATED_MUSCLE_CONTRACTION
20	19.69	NULL	6 / 18	BP	regulation of muscle contraction
21	19.55	NULL	9 / 37	BP	cardiac muscle contraction
22	18.76	NULL	3 / 15	Cancer	BEN−PORATH_UP
23	18.68	NULL	7 / 15	BP	striated muscle contraction
24	16.6	NULL	4 / 11	CC	A band
25	16.23	NULL	25 / 297	MF	actin binding
26	14.33	NULL	4 / 15	GSEA C2	EBAUER_MYOGENIC_TARGETS_OF_PAX3_FOXO1_FUSION
27	14.26	NULL	3 / 13	CC	pseudopodium
28	14.12	NULL	2 / 20	MF	myosin binding
29	13.68	NULL	1 / 9	GSEA C2	PENG_GLUCOSE_DEPRIVATION_UP
30	13.68	NULL	1 / 9	GSEA C2	PENG_GLUCOSE_DEPRIVATION_DN
31	13.49	NULL	2 / 10	BP	creatine metabolic process
32	13.47	NULL	2 / 16	GSEA C2	SASSON_RESPONSE_TO_GONADOTROPHINS_DN
33	13.47	NULL	2 / 16	GSEA C2	SASSON_RESPONSE_TO_FORSKOLIN_DN
34	13.31	NULL	2 / 14	GSEA C2	BIOCARTA_UCALPAIN_PATHWAY
35	12.98	NULL	1 / 5	GSEA C2	LIU_VAV3_PROSTATE_CARCINOGENESIS_UP
36	12.96	NULL	4 / 16	MF	microfilament motor activity
37	12.82	NULL	1 / 10	GSEA C2	BIOCARTA_EPHA4_PATHWAY
38	12.78	NULL	4 / 14	MF	tropomyosin binding
39	12.77	NULL	2 / 15	GSEA C2	BIOCARTA_INTEGRIN_PATHWAY
40	12.25	NULL	5 / 36	CC	sarcoplasmic reticulum

GW_063

Local Summary

%DE = 0.57

metagenes = 15

genes = 240

genes in genesets = 214

genes with fdr < 0.1 = 62 (4 + / 58 −)

genes with fdr < 0.05 = 59 (4 + / 55 −)

genes with fdr < 0.01 = 38 (3 + / 35 −)

<r> metagenes = 0.99

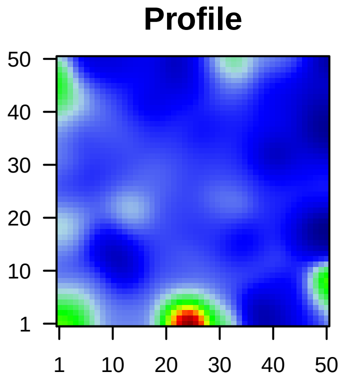
<r> genes = 0.5

<FC> = −0.22

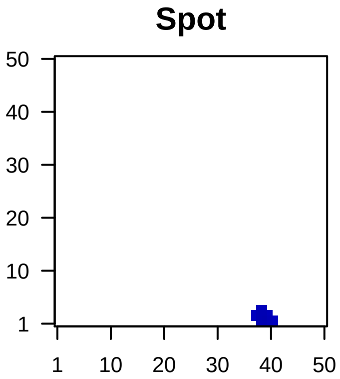
<shrinkage−t> = −7.62

<p−value> = 0.03

<fdr> = 0.71



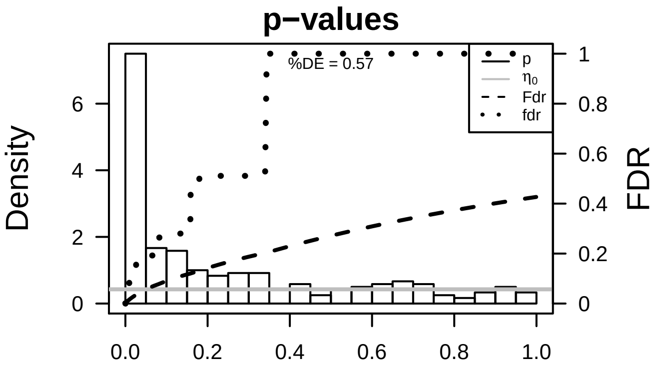
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	618	1.5	2e−16	1e−14	39 x 1	brain cytoplasmic RNA 1 [Source:HGNC Symbol;Acc:1022]
2	125050	1.98	2e−16	1e−14	40 x 1	RNA, 7SK small nuclear [Source:HGNC Symbol;Acc:10037]
3	100132406	−1.06	4e−09	3e−06	39 x 1	neuroblastoma breakpoint family, member 10 [Source:HGNC
4	440353	−1	3e−08	2e−05	40 x 1	
5	100132247	−0.94	2e−07	1e−04	39 x 3	nuclear pore complex interacting protein family, member B5 [
6	727866	−0.87	1e−06	6e−04	38 x 3	family with sequence similarity 156, member B [Source:HGN
7	728404	−0.8	9e−06	6e−04	39 x 2	ArfGAP with GTPase domain, ankyrin repeat and PH domain
8	155060	−0.78	2e−05	6e−04	39 x 4	
9	613037	−0.77	2e−05	6e−04	40 x 2	nuclear pore complex interacting protein family, member B5 [
10	400818	−0.75	3e−05	6e−04	40 x 1	Neuroblastoma breakpoint family member 1 [Source:UniProt
11	114785	−0.75	3e−05	6e−04	39 x 1	methyl−CpG binding domain protein 6 [Source:HGNC Symbo
12	440348	−0.75	4e−05	6e−04	39 x 3	nuclear pore complex interacting protein family, member B15
13	9905	−0.74	4e−05	9e−04	40 x 2	small G protein signaling modulator 2 [Source:HGNC Symbol
14	100128288	−0.73	5e−05	1e−03	39 x 1	
15	158399	−0.72	7e−05	1e−03	39 x 1	zinc finger protein 483 [Source:HGNC Symbol;Acc:23384]
16	115703	−0.71	8e−05	1e−03	41 x 1	Rho GTPase activating protein 33 [Source:HGNC Symbol;Ac
17	91368	−0.65	8e−05	2e−03	39 x 1	CDKN2A interacting protein N−terminal like [Source:HGNC S
18	81033	−0.64	1e−04	2e−03	39 x 1	potassium voltage−gated channel, subfamily H (eag−related),
19	728903	−0.69	1e−04	4e−03	39 x 1	
20	401261	0.67	2e−04	4e−03	41 x 1	



p−values

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−7.1	NULL	2 / 11	GSEA C2	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_
2	−6.49	NULL	2 / 12	GSEA C2	CAFFAREL_RESPONSE_TO_THC_8HR_5_UP
3	−5.73	NULL	2 / 19	MF	mitogen−activated protein kinase kinase kinase binding
4	−5.56	NULL	3 / 16	GSEA C2	HAMAI_APOPTOSIS_VIA_TRAIL_UP
5	−5.43	NULL	2 / 12	GSEA C2	NIKOLSKY_BREAST_CANCER_12Q24_AMPLICON
6	−4.91	NULL	1 / 7	GSEA C2	LIU_CMYB_TARGETS_DN
7	−4.91	NULL	1 / 7	GSEA C2	KEGG_STEROID_HORMONE_BIOSYNTHESIS
8	−4.83	NULL	1 / 7	GSEA C2	GENTILE_UV_LOW_DOSE_DN
9	−4.83	NULL	1 / 7	GSEA C2	GENTILE_UV_LOW_DOSE_UP
10	−4.81	NULL	1 / 11	GSEA C2	GARCIA_TARGETS_OF_FLI1_AND_DAX1_UP
11	−4.75	NULL	2 / 16	BP	cognition
12	−4.62	NULL	1 / 12	miRNA target set	hsa−miR−1249
13	−4.56	NULL	1 / 10	CC	oligosaccharyltransferase complex
14	−4.54	NULL	2 / 19	BP	sprouting angiogenesis
15	−4.51	NULL	2 / 29	BP	positive regulation of JUN kinase activity
16	−4.49	NULL	1 / 8	GSEA C2	BARRIER_CANCER_RELAPSE_NORMAL_SAMPLE_DN
17	−4.47	NULL	2 / 20	MF	ligand−dependent nuclear receptor binding
18	−4.38	NULL	1 / 12	MF	Rac GTPase activator activity
19	−4.38	NULL	1 / 12	GSEA C2	BARRIER_COLON_CANCER_RECURRENCE_DN
20	−4.38	NULL	1 / 12	GSEA C2	MCCABE_HOXC6_TARGETS_CANCER_UP
21	−4.21	NULL	1 / 11	GSEA C2	KIM_GASTRIC_CANCER_CHEMOSENSITIVITY
22	−4.18	NULL	2 / 15	GSEA C2	ZHOU_INFLAMMATORY_RESPONSE_LIVE_DN
23	−4.18	NULL	2 / 15	GSEA C2	ZHOU_INFLAMMATORY_RESPONSE_LPS_DN
24	−4.12	NULL	1 / 10	BP	lung morphogenesis
25	−4.11	NULL	1 / 11	BP	negative regulation of intracellular estrogen receptor signaling path
26	−4.03	NULL	1 / 10	GSEA C2	REACTOME_TRANSFORMATION_OF_LANOSTEROL_TO_CHO
27	−3.97	NULL	2 / 15	GSEA C2	THUM_SYSTOLIC_HEART_FAILURE_DN
28	−3.94	NULL	1 / 13	MF	magnesium ion transmembrane transporter activity
29	−3.92	NULL	1 / 8	GSEA C2	IIZUKA_LIVER_CANCER_PROGRESSION_L1_G1_DN
30	−3.92	NULL	1 / 8	GSEA C2	KAYO_CALORIE_RESTRICTION_MUSCLE_DN
31	−3.92	NULL	1 / 6	GSEA C2	TURJANSKI_MAPK8_AND_MAPK9_TARGETS
32	−3.9	NULL	1 / 11	CC	axolemma
33	−3.86	NULL	1 / 15	GSEA C2	ODONNELL_METASTASIS_UP
34	−3.83	NULL	1 / 13	GSEA C2	LUI_THYROID_CANCER_PAX8_PPARG_UP
35	−3.82	NULL	1 / 11	MF	C2H2 zinc finger domain binding
36	−3.82	NULL	1 / 10	BP	negative regulation of JUN kinase activity
37	−3.82	NULL	2 / 11	GSEA C2	STEIN_ESRRA_TARGETS_DN
38	−3.78	NULL	1 / 14	BP	magnesium ion transport
39	−3.78	NULL	1 / 12	CC	integrator complex
40	−3.78	NULL	1 / 12	BP	snRNA processing

GW_063

Local Summary

%DE = 0.46

metagenes = 1

genes = 5

genes in genesets = 5

genes with fdr < 0.1 = 1 (0 + / 1 −)

genes with fdr < 0.05 = 1 (0 + / 1 −)

genes with fdr < 0.01 = 0 (0 + / 0 −)

<r> metagenes = NA

<r> genes = 0.34

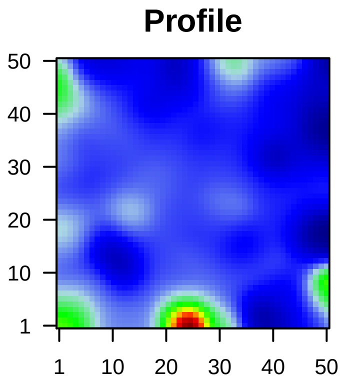
<FC> = −0.4

<shrinkage−t> = −13.85

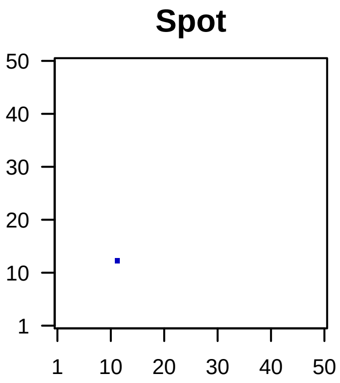
<p−value> = 0.01

<fdr> = 0.59

Profile



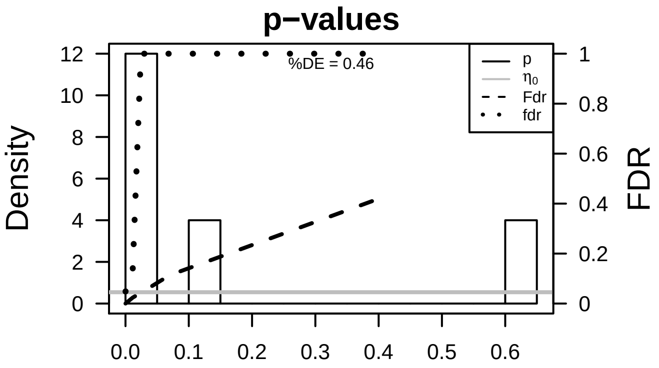
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	4088	−0.8	1e−05	0.05	12 x 13	SMAD family member 3 [Source:HGNC Symbol;Acc:6769]
2	54963	−0.43	2e−02	0.14	12 x 13	uridine−cytidine kinase 1−like 1 [Source:HGNC Symbol;Acc:1
3	26523	−0.38	4e−02	1.00	12 x 13	argonaute RISC catalytic component 1 [Source:HGNC Symb
4	154197	−0.29	1e−01	1.00	12 x 13	poly(A)−specific ribonuclease (PARN)−like domain containing
5	284339	−0.09	6e−01	1.00	12 x 13	transmembrane protein 145 [Source:HGNC Symbol;Acc:2691

p−values



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−45.41	NULL	1 / 8	GSEA C2	YEMELYANOV_GR_TARGETS_DN
2	−42.8	NULL	1 / 9	GSEA C2	BIOCARTA_NTHI_PATHWAY
3	−40.6	NULL	1 / 10	MF	co−SMAD binding
4	−40.6	NULL	1 / 10	BP	positive regulation of transcription factor import into nucleus
5	−40.6	NULL	1 / 10	GSEA C2	OUELLET_OVARIAN_CANCER_INVASIVE_VS_LMP_DN
6	−38.71	NULL	1 / 11	BP	positive regulation of catenin import into nucleus
7	−38.71	NULL	1 / 11	BP	positive regulation of positive chemotaxis
8	−38.71	NULL	1 / 11	BP	regulation of epithelial cell proliferation
9	−38.71	NULL	1 / 11	MF	transforming growth factor beta receptor binding
10	−38.71	NULL	1 / 11	GSEA C2	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_
11	−38.71	NULL	1 / 11	GSEA C2	TURJANSKI_MAPK1_AND_MAPK2_TARGETS
12	−37.05	NULL	1 / 12	GSEA C2	REACTOME_SIGNALING_BY_TGF_BETA
13	−35.59	NULL	1 / 13	MF	core promoter proximal region sequence−specific DNA binding
14	−35.59	NULL	1 / 13	BP	regulation of transforming growth factor beta receptor signaling pat
15	−35.59	NULL	1 / 13	GSEA C2	LAMB_CCND1_TARGETS
16	−35.59	NULL	1 / 13	GSEA C2	TSAI_RESPONSE_TO_RADIATION_THERAPY
17	−34.29	NULL	1 / 14	BP	positive regulation of chondrocyte differentiation
18	−34.29	NULL	1 / 14	BP	positive regulation of focal adhesion assembly
19	−34.29	NULL	1 / 14	GSEA C2	BIOCARTA_G1_PATHWAY
20	−34.29	NULL	1 / 14	GSEA C2	BIOCARTA_TOB1_PATHWAY
21	−33.13	NULL	1 / 15	BP	signal transduction involved in regulation of gene expression
22	−33.13	NULL	1 / 15	GSEA C2	ZIRN_TRETINOIN_RESPONSE_WT1_UP
23	−33.13	NULL	1 / 15	GSEA C2	BROWNE_HCMV_INFECTION_8HR_DN
24	−33.13	NULL	1 / 15	GSEA C2	MARTINEZ_RESPONSE_TO_TRABECTEDIN
25	−33.13	NULL	1 / 15	GSEA C2	GENTILE_UV_RESPONSE_CLUSTER_D6
26	−33.13	NULL	1 / 15	GSEA C2	BIOCARTA_TGFB_PATHWAY
27	−32.07	NULL	1 / 16	BP	negative regulation of mitotic cell cycle
28	−32.07	NULL	1 / 16	GSEA C2	FRASOR_RESPONSE_TO_ESTRADIOL_DN
29	−31.11	NULL	1 / 17	BP	embryonic pattern specification
30	−31.11	NULL	1 / 17	BP	osteoblast development
31	−31.11	NULL	1 / 17	BP	thyroid gland development
32	−29.41	NULL	1 / 19	BP	positive regulation of epithelial to mesenchymal transition
33	−29.41	NULL	1 / 19	MF	R−SMAD binding
34	−27.75	NULL	1 / 21	BP	negative regulation of protein catabolic process
35	−26.91	NULL	1 / 22	BP	release of cytochrome c from mitochondria
36	−26.13	NULL	1 / 23	MF	chromatin DNA binding
37	−25.42	NULL	1 / 24	BP	endoderm development
38	−25.42	NULL	1 / 24	TF Tissue	VAQUERIZAS_Trachea
39	−24.76	NULL	1 / 25	BP	gastrulation
40	−24.14	NULL	1 / 26	BP	negative regulation of osteoblast differentiation

GW_063

Local Summary

%DE = 0.63

metagenes = 29

genes = 274

genes in genesets = 269

genes with fdr < 0.1 = 90 (5 + / 85 −)

genes with fdr < 0.05 = 68 (5 + / 63 −)

genes with fdr < 0.01 = 36 (4 + / 32 −)

<r> metagenes = 0.97

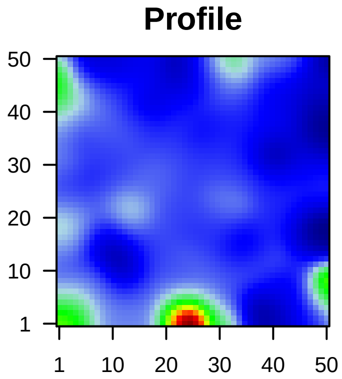
<r> genes = 0.31

<FC> = −0.27

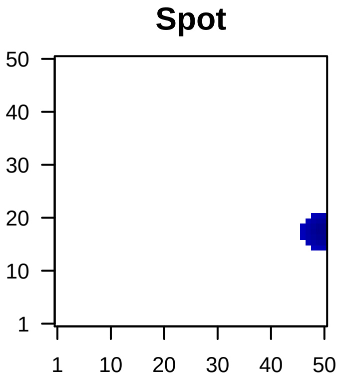
<shrinkage−t> = −9.47

<p−value> = 0.03

<fdr> = 0.71



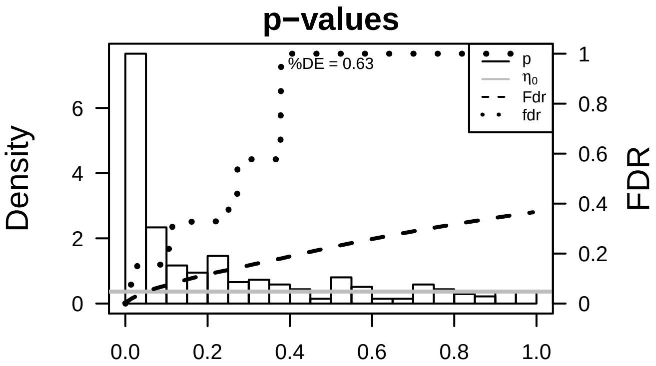
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	54959	1.18	6e−11	2e−08	50 x 17	odontogenic, ameloblast asssociated [Source:HGNC Symbol
2	26002	−1.15	2e−10	7e−08	50 x 16	monooxygenase, DBH−like 1 [Source:HGNC Symbol;Acc:21
3	1959	−1.11	9e−10	1e−05	50 x 19	early growth response 2 [Source:HGNC Symbol;Acc:3239]
4	56997	0.95	2e−07	1e−05	50 x 16	aarF domain containing kinase 3 [Source:HGNC Symbol;Acc
5	130872	−0.93	2e−07	2e−05	50 x 19	AHA1, activator of heat shock 90kDa protein ATPase homolo
6	5569	0.91	5e−07	3e−04	50 x 16	protein kinase (cAMP−dependent, catalytic) inhibitor alpha [S
7	55082	−0.83	4e−06	3e−04	50 x 18	arginine and glutamate rich 1 [Source:HGNC Symbol;Acc:25
8	835	−0.81	8e−06	3e−04	49 x 18	caspase 2, apoptosis−related cysteine peptidase [Source:HG
9	3670	0.79	1e−05	3e−04	50 x 17	ISL LIM homeobox 1 [Source:HGNC Symbol;Acc:6132]
10	84532	−0.78	1e−05	3e−04	50 x 17	acyl−CoA synthetase short−chain family member 1 [Source:
11	8543	−0.78	2e−05	4e−04	50 x 15	LIM domain only 4 [Source:HGNC Symbol;Acc:6644]
12	23360	−0.77	2e−05	4e−04	50 x 20	formin binding protein 4 [Source:HGNC Symbol;Acc:19752]
13	63917	−0.75	3e−05	4e−04	50 x 16	UDP−N−acetyl−alpha−D−galactosamine:polypeptide N−acet
14	200030	−0.75	3e−05	4e−04	50 x 20	neuroblastoma breakpoint family, member 1 [Source:HGNC
15	648	−0.74	4e−05	4e−04	50 x 17	COMMD3−BMI1 readthrough [Source:HGNC Symbol;Acc:48
16	9847	−0.74	4e−05	4e−04	50 x 16	C2 calcium−dependent domain containing 5 [Source:HGNC
17	57189	−0.74	4e−05	8e−04	50 x 15	KIAA1147 [Source:HGNC Symbol;Acc:29472]
18	728715	−0.73	5e−05	8e−04	50 x 18	
19	694	−0.67	6e−05	8e−04	50 x 18	B−cell translocation gene 1, anti−proliferative [Source:HGNC
20	23608	−0.72	6e−05	4e−03	47 x 16	makorin ring finger protein 1 [Source:HGNC Symbol;Acc:711



p−values

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−9.9	NULL	3 / 5	Lymphoma	MASCQUE_mBL UP
2	−9.79	NULL	1 / 5	GSEA C2	STAEGE_EWING_FAMILY_TUMOR
3	−9.29	NULL	3 / 15	GSEA C2	FAELT_B_CLL_WITH_VH3_21_DN
4	−8.39	NULL	1 / 3	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_30
5	−7.7	NULL	2 / 13	GSEA C2	BROWNE_HCMV_INFECTION_48HR_DN
6	−7.58	NULL	3 / 13	BP	histone H4−K16 acetylation
7	−7.43	NULL	10 / 81	miRNA target starBase	hsa−miR−188−5p
8	−7.41	NULL	2 / 11	MF	poly(A)−specific ribonuclease activity
9	−7.4	NULL	1 / 9	GSEA C2	RODWELL_AGING_KIDNEY_UP
10	−7.36	NULL	3 / 10	CC	nBAF complex
11	−7.24	NULL	6 / 53	miRNA 3UTR	UGCAA−502
12	−7.13	NULL	1 / 9	GSEA C2	ABE_VEGFA_TARGETS_30MIN
13	−7.01	NULL	3 / 15	BP	histone H4−K5 acetylation
14	−7.01	NULL	3 / 15	BP	histone H4−K8 acetylation
15	−6.98	NULL	3 / 11	CC	npBAF complex
16	−6.98	NULL	1 / 10	GSEA C2	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_
17	−6.98	NULL	2 / 14	BP	regulation of cysteine−type endopeptidase activity involved in apop
18	−6.87	NULL	2 / 16	GSEA C2	DAVICIONI_TARGETS_OF_PAX_FOXO1_FUSIONS_DN
19	−6.73	NULL	1 / 10	BP	cellular response to gonadotropin stimulus
20	−6.73	NULL	1 / 10	BP	regulation of ossification
21	−6.73	NULL	1 / 10	GSEA C2	CHASSOT_SKIN_WOUND
22	−6.73	NULL	1 / 10	GSEA C2	ABE_VEGFA_TARGETS
23	−6.71	NULL	2 / 9	GSEA C2	REACTOME_ETHANOL_OXIDATION
24	−6.66	NULL	3 / 12	CC	SWI/SNF complex
25	−6.62	NULL	1 / 11	GSEA C2	NUYTTEN_EZH2_TARGETS_UP
26	−6.62	NULL	1 / 11	GSEA C2	RIGGI_EWING_SARCOMA_PROGENITOR_DN
27	−6.59	NULL	4 / 40	miRNA target starBase	hsa−miR−758
28	−6.36	NULL	4 / 15	GSEA C2	GOLUB_ALL_VS_AML_UP
29	−6.33	NULL	2 / 16	GSEA C2	AMUNDSON_DNA_DAMAGE_RESPONSE_TP53
30	−6.32	NULL	3 / 18	CC	histone acetyltransferase complex
31	−6.31	NULL	1 / 12	GSEA C2	PEREZ_TP53_TARGETS
32	−6.31	NULL	1 / 12	GSEA C2	BOHN_PRIMARY_IMMUNODEFICIENCY_SYNDROM_DN
33	−6.31	NULL	1 / 12	GSEA C2	CHIANG_LIVER_CANCER_SUBCLASS_INTERFERON_UP
34	−6.24	NULL	2 / 26	BP	protein sumoylation
35	−6.23	NULL	2 / 16	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL
36	−6.14	NULL	3 / 21	TF Tissue	VAQUERIZAS_Tonsil
37	−6.13	NULL	2 / 10	GSEA C2	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_L
38	−6.08	NULL	1 / 12	GSEA C2	BIOCARTA_VIP_PATHWAY
39	−6.08	NULL	2 / 16	GSEA C2	MANN_RESPONSE_TO_AMIFOSTINE_UP
40	−6.05	NULL	3 / 32	miRNA target starBase	hsa−miR−17

GW_063

Local Summary

%DE = 0.54

metagenes = 44

genes = 504

genes in genesets = 499

genes with fdr < 0.1 = 115 (4 + / 111 −)

genes with fdr < 0.05 = 53 (3 + / 50 −)

genes with fdr < 0.01 = 10 (2 + / 8 −)

<r> metagenes = 0.87

<r> genes = 0.22

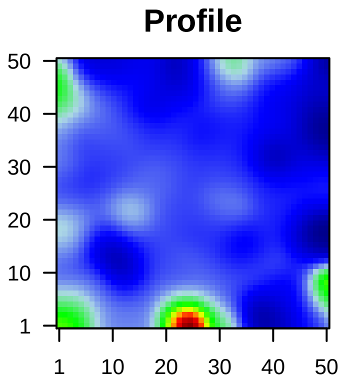
<FC> = −0.24

<shrinkage−t> = −8.3

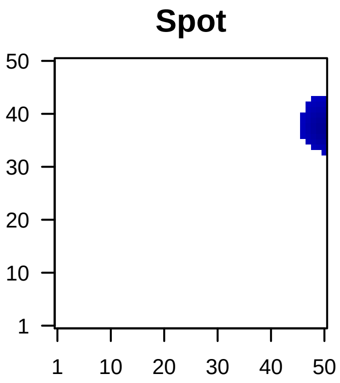
<p−value> = 0.09

<fdr> = 0.81

Profile

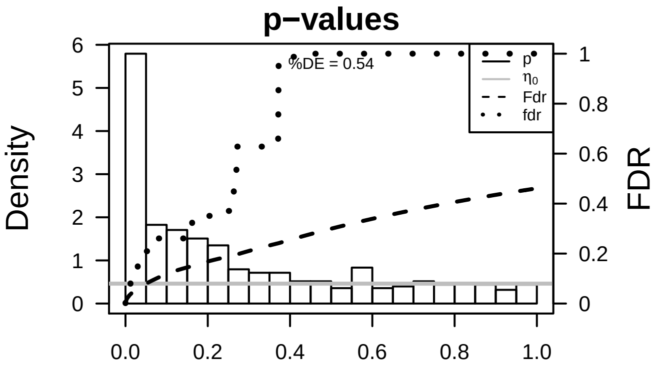


Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	5612	0.88	1e−06	0.002	50 x 34	protein−kinase, interferon−inducible double stranded RNA de
2	23151	−0.81	8e−06	0.003	50 x 38	GRAM domain containing 4 [Source:HGNC Symbol;Acc:2911
3	80208	−0.76	3e−05	0.003	50 x 35	spastic paraplegia 11 (autosomal recessive) [Source:HGNC
4	29123	−0.74	4e−05	0.003	50 x 39	ankyrin repeat domain 11 [Source:HGNC Symbol;Acc:21316]
5	56947	−0.72	6e−05	0.003	50 x 33	mitochondrial fission factor [Source:HGNC Symbol;Acc:2485
6	51497	−0.71	8e−05	0.003	48 x 42	negative elongation factor complex member C/D [Source:HG
7	91355	−0.7	1e−04	0.003	50 x 40	low density lipoprotein receptor−related protein 5−like [Sourc
8	22889	−0.7	1e−04	0.003	50 x 37	KIAA0907 [Source:HGNC Symbol;Acc:29145]
9	26577	0.69	1e−04	0.003	50 x 43	procollagen C−endopeptidase enhancer 2 [Source:HGNC Sy
10	23318	−0.69	1e−04	0.003	50 x 37	zinc finger, CCHC domain containing 11 [Source:HGNC Sym
11	25942	−0.69	1e−04	0.012	47 x 42	SIN3 transcription regulator family member A [Source:HGNC
12	4856	0.67	2e−04	0.012	50 x 40	nephroblastoma overexpressed [Source:HGNC Symbol;Acc:
13	7342	−0.66	2e−04	0.012	50 x 35	upstream binding protein 1 (LBP−1a) [Source:HGNC Symbol
14	85460	−0.64	4e−04	0.012	50 x 39	zinc finger protein 518B [Source:HGNC Symbol;Acc:29365]
15	57645	−0.64	4e−04	0.012	49 x 43	pogo transposable element with KRAB domain [Source:HGN
16	9698	−0.64	4e−04	0.012	48 x 38	pumilio RNA−binding family member 1 [Source:HGNC Symb
17	6599	−0.64	4e−04	0.014	50 x 36	SWI/SNF related, matrix associated, actin dependent regulat
18	9061	−0.62	6e−04	0.014	50 x 34	3'−phosphoadenosine 5'−phosphosulfate synthase 1 [Source
19	83759	−0.6	9e−04	0.014	47 x 42	RNA binding motif protein 4B [Source:HGNC Symbol;Acc:28
20	80209	−0.6	9e−04	0.014	50 x 36	proline and serine rich 1 [Source:HGNC Symbol;Acc:20291]



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset
1	−8.59	NULL	15 / 100	miRNA target starBase hsa−miR−544
2	−8.16	NULL	5 / 27	MF nucleotidyltransferase activity
3	−8.02	NULL	16 / 114	miRNA target starBase hsa−miR−217
4	−7.73	NULL	9 / 50	miRNA 3'UTR TACA−508
5	−7.44	NULL	12 / 80	miRNA target starBase hsa−miR−30a*
6	−6.79	NULL	16 / 119	miRNA target starBase hsa−miR−579
7	−6.79	NULL	20 / 153	miRNA target starBase hsa−miR−450b−5p
8	−6.69	NULL	18 / 113	miRNA target starBase hsa−miR−507
9	−6.67	NULL	4 / 15	GSEA C2 GENTILE_UV_RESPONSE_CLUSTER_D2
10	−6.56	NULL	10 / 41	BP mRNA 3'−end processing
11	−6.31	NULL	6 / 14	GSEA C2 REACTOME_MRNA_3_END_PROCESSING
12	−6.28	NULL	10 / 44	BP termination of RNA polymerase II transcription
13	−6.25	NULL	22 / 180	miRNA target starBase hsa−miR−374a
14	−6.23	NULL	17 / 121	miRNA target starBase hsa−miR−543
15	−6.23	NULL	24 / 171	miRNA target starBase hsa−miR−369−3p
16	−6.17	NULL	28 / 281	miRNA target starBase hsa−miR−570
17	−6.17	NULL	9 / 54	miRNA target starBase hsa−miR−409−5p
18	−6.16	NULL	12 / 100	miRNA target starBase hsa−miR−377
19	−6.1	NULL	19 / 146	miRNA target starBase hsa−miR−922
20	−6.1	NULL	4 / 19	MF Wnt−activated receptor activity
21	−6.08	NULL	21 / 174	BP mRNA processing
22	−6.06	NULL	15 / 149	miRNA target starBase hsa−miR−655
23	−6.02	NULL	26 / 319	miRNA target starBase hsa−miR−367
24	−5.98	NULL	10 / 58	miRNA target starBase hsa−miR−455−5p
25	−5.97	NULL	11 / 76	CC catalytic step 2 spliceosome
26	−5.96	NULL	9 / 70	miRNA target starBase hsa−miR−622
27	−5.89	NULL	9 / 69	miRNA target starBase hsa−miR−299−5p
28	−5.87	NULL	12 / 107	miRNA 3'UTR ATCA−409−3P
29	−5.82	NULL	8 / 45	miRNA target starBase hsa−miR−411
30	−5.8	NULL	53 / 595	MF RNA binding
31	−5.73	NULL	13 / 108	miRNA target starBase hsa−miR−449b
32	−5.71	NULL	3 / 16	GSEA C2 GAZDA_DIAMOND_BLACKFAN_ANEMIA_MYELOID_UP
33	−5.66	NULL	16 / 134	miRNA target starBase hsa−miR−656
34	−5.61	NULL	16 / 158	miRNA 3'UTR ATAT−448
35	−5.6	NULL	20 / 243	miRNA 3'UTR ATGT−493
36	−5.5	NULL	2 / 6	GSEA C2 MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_7
37	−5.49	NULL	22 / 197	miRNA target starBase hsa−miR−448
38	−5.49	NULL	39 / 421	miRNA target starBase hsa−let−7b
39	−5.48	NULL	21 / 163	BP mRNA splicing, via spliceosome
40	−5.43	NULL	10 / 100	miRNA target starBase hsa−miR−1299

GW_063

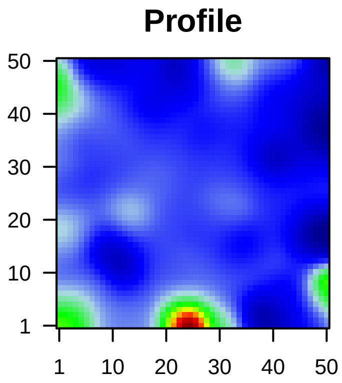
Local Summary

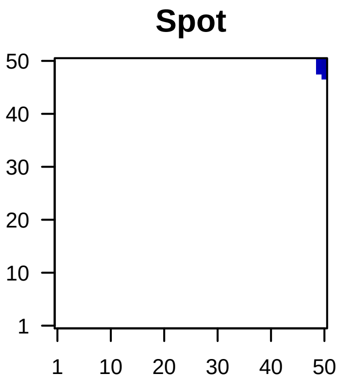
%DE = 0.75
metagenes = 7
genes = 134
genes in genesets = 133

genes with fdr < 0.1 = 71 (8 + / 63 −)
genes with fdr < 0.05 = 54 (5 + / 49 −)
genes with fdr < 0.01 = 35 (4 + / 31 −)

<r> metagenes = 0.99
<r> genes = 0.3

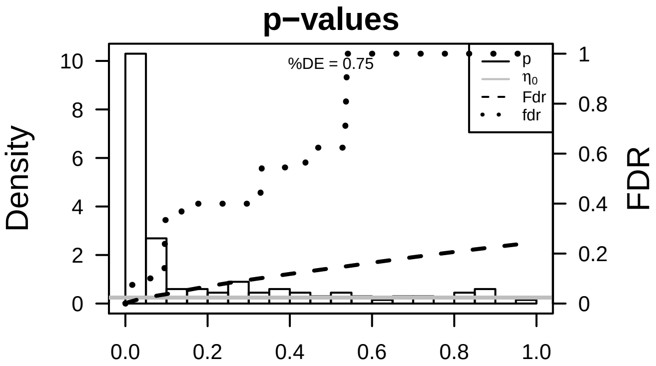
<FC> = −0.29
<shrinkage−t> = −10.29
<p−value> = 0.01
<fdr> = 0.6





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	3866	−1.6	2e−16	7e−15	50 x 50	keratin 15 [Source:HGNC Symbol;Acc:6421]
2	11166	−1.4	8e−15	1e−12	50 x 50	SRY (sex determining region Y)−box 21 [Source:HGNC Symb
3	26047	−1.36	5e−14	9e−12	50 x 50	contactin associated protein−like 2 [Source:HGNC Symbol;A
4	3304	−1.21	3e−13	1e−09	49 x 49	heat shock 70kDa protein 1A [Source:HGNC Symbol;Acc:52
5	2719	1.2	3e−11	1e−09	50 x 50	glypican 3 [Source:HGNC Symbol;Acc:4451]
6	94234	−1.18	6e−11	3e−07	50 x 50	forkhead box Q1 [Source:HGNC Symbol;Acc:20951]
7	4922	−1.04	1e−08	5e−05	50 x 50	neurotensin [Source:HGNC Symbol;Acc:8038]
8	6657	−0.87	1e−06	7e−05	50 x 50	SRY (sex determining region Y)−box 2 [Source:HGNC Symb
9	6446	−0.76	4e−06	7e−05	50 x 50	serum/glucocorticoid regulated kinase 1 [Source:HGNC Sym
10	5625	−0.81	7e−06	7e−05	50 x 48	proline dehydrogenase (oxidase) 1 [Source:HGNC Symbol;A
11	3856	−0.8	1e−05	7e−05	50 x 48	keratin 8 pseudogene 3 [Source:HGNC Symbol;Acc:31056]
12	1056	−0.8	1e−05	1e−04	50 x 50	carboxyl ester lipase [Source:HGNC Symbol;Acc:1848]
13	2944	−0.79	1e−05	2e−04	50 x 50	glutathione S−transferase mu 1 [Source:HGNC Symbol;Acc:
14	154664	−0.77	2e−05	1e−03	50 x 50	ATP−binding cassette, sub−family A (ABC1), member 13 [So
15	10966	−0.72	6e−05	1e−03	50 x 50	RAB40B, member RAS oncogene family [Source:HGNC Sym
16	4953	0.71	8e−05	1e−03	50 x 50	ornithine decarboxylase 1 [Source:HGNC Symbol;Acc:8109]
17	57216	−0.7	1e−04	1e−03	50 x 48	VANGL planar cell polarity protein 2 [Source:HGNC Symbol;
18	2222	−0.69	1e−04	1e−03	50 x 50	farnesyl−diphosphate farnesyltransferase 1 [Source:HGNC S
19	3880	−0.68	2e−04	4e−03	50 x 49	keratin 19 [Source:HGNC Symbol;Acc:6436]
20	120	−0.65	4e−04	4e−03	50 x 50	adducin 3 (gamma) [Source:HGNC Symbol;Acc:245]



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−26.62	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
2	−17.85	NULL	3 / 12	GSEA C2	BROCKE_APOPTOSIS_REVERSED_BY_IL6
3	−17.66	NULL	1 / 2	GSEA C2	KUROKAWA_LIVER_CANCER_EARLY_RECURRENCE_UP
4	−17.26	NULL	2 / 7	GSEA C2	MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
5	−13.48	NULL	2 / 10	GSEA C2	CERVERA_SDHB_TARGETS_1_DN
6	−12.94	NULL	2 / 10	GSEA C2	HANN_RESISTANCE_TO_BCL2_INHIBITOR_DN
7	−11.37	NULL	2 / 9	GSEA C2	BROWNE_HCMV_INFECTION_8HR_UP
8	−11.24	NULL	3 / 13	BP	regulation of blood vessel size
9	−10.72	NULL	2 / 23	BP	stem cell differentiation
10	−10.28	NULL	1 / 5	GSEA C2	DASU_IL6_SIGNALING_UP
11	−10.25	NULL	6 / 25	BP	glutathione derivative biosynthetic process
12	−10.12	NULL	2 / 10	GSEA C2	CONRAD_STEM_CELL
13	−10.08	NULL	8 / 34	BP	glutathione metabolic process
14	−9.82	NULL	2 / 10	GSEA C2	XU_GH1_AUTOCRINE_TARGETS_DN
15	−9.54	NULL	1 / 11	CC	axolemma
16	−9.49	NULL	1 / 15	H.Tiss	WIRTH_Cerebellum
17	−9.26	NULL	1 / 6	GSEA C2	SESTO_RESPONSE_TO_UV_C0
18	−9.26	NULL	1 / 6	GSEA C2	BIOCARTA_TID_PATHWAY
19	−9.21	NULL	2 / 13	GSEA C2	BROWNE_HCMV_INFECTION_6HR_DN
20	−9.18	NULL	3 / 11	MF	glutathione binding
21	−9.18	NULL	3 / 11	GSEA C2	KEGG_DRUG_METABOLISM_CYTOCHROME_P450
22	−9.16	NULL	1 / 16	GSEA C2	ROY_WOUND_BLOOD_VESSEL_DN
23	−9.15	NULL	3 / 33	BP	regulation of sequence−specific DNA binding transcription factor a
24	−8.49	NULL	1 / 7	GSEA C2	WEINMANN_ADAPTATION_TO_HYPOXIA_UP
25	−8.48	NULL	2 / 16	GSEA C2	KEGG_STEROID_BIOSYNTHESIS
26	−8.39	NULL	2 / 14	GSEA C2	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_8D_DN
27	−8.34	NULL	1 / 14	BP	transmission of nerve impulse
28	−8.34	NULL	1 / 14	GSEA C2	SILIGAN_TARGETS_OF_EWS_FLI1_FUSION_DN
29	−8.34	NULL	1 / 14	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_B
30	−8.26	NULL	2 / 15	GSEA C2	LEE_LIVER_CANCER_MYC_UP
31	−8.26	NULL	2 / 15	GSEA C2	LEE_LIVER_CANCER_E2F1_UP
32	−8.16	NULL	4 / 13	GSEA C2	KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_
33	−8.15	NULL	4 / 15	GSEA C2	REACTOME_GLUTATHIONE_CONJUGATION
34	−8.09	NULL	1 / 20	MF	scaffold protein binding
35	−8.03	NULL	5 / 20	MF	glutathione transferase activity
36	−7.92	NULL	1 / 3	GSEA C2	RUNNE_GENDER_EFFECT_DN
37	−7.87	NULL	1 / 8	GSEA C2	BARRIER_CANCER_RELAPSE_NORMAL_SAMPLE_DN
38	−7.87	NULL	1 / 8	GSEA C2	ADDYA_ERYTHROID_DIFFERENTIATION_BY_HEMIN
39	−7.87	NULL	1 / 8	GSEA C2	CHANDRAN_METASTASIS_UP
40	−7.87	NULL	1 / 8	GSEA C2	WU_APOPTOSIS_BY_CDKN1A_NOT_VIA_TP53