GW_146

Global Summary

%DE = 0.17

genes with fdr < 0.2 = 2492 (1456 + / 1036 −)

genes with fdr < 0.1 = 1954 (1184 + / 770 −)

genes with fdr < 0.05 = 1747 (1079 + / 668 −)

genes with fdr < 0.01 = 1329 (853 + / 476 −)

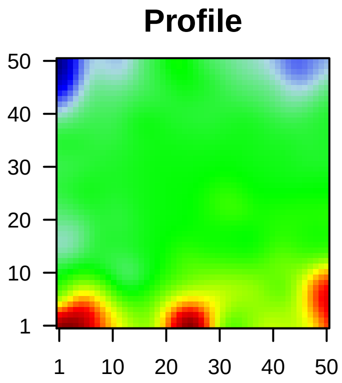
genes in genesets = 16332

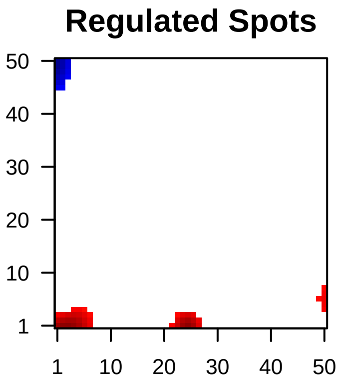
<FC> = 0

<shrinkage−t> = −0.01

<p−value> = 0.05

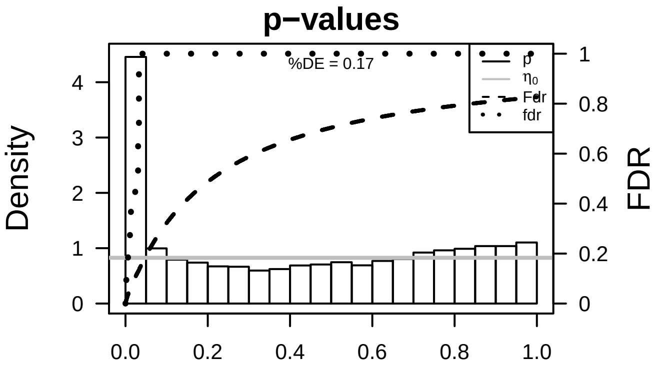
<fdr> = 0.83





Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	58	5.49	2e−16	1e−14	25 x 1	actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
2	59	1.68	2e−16	1e−14	3 x 1	actin, alpha 2, smooth muscle, aorta [Source:HGNC Symbol;
3	70	3.94	2e−16	1e−14	25 x 1	actin, alpha, cardiac muscle 1 [Source:HGNC Symbol;Acc:14
4	72	2.05	2e−16	1e−14	4 x 1	actin, gamma 2, smooth muscle, enteric [Source:HGNC Syml
5	131	−2.94	2e−16	1e−14	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
6	57016	−3.16	2e−16	1e−14	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
7	441282	−2.18	2e−16	1e−14	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC Sy
8	218	−3.62	2e−16	1e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
9	241	1.75	2e−16	1e−14	50 x 1	arachidonate 5−lipoxygenase−activating protein [Source:HGN
10	249	1.72	2e−16	1e−14	6 x 1	alkaline phosphatase, liver/bone/kidney [Source:HGNC Symb
11	23452	2.26	2e−16	1e−14	3 x 1	angiopoietin−like 2 [Source:HGNC Symbol;Acc:490]
12	65124	−1.79	2e−16	1e−14	1 x 45	sosondowah ankyrin repeat domain family member C [Source
13	244	−1.72	2e−16	1e−14	1 x 43	annexin A8−like 2 [Source:HGNC Symbol;Acc:23335]
14	10930	2.06	2e−16	1e−14	25 x 1	apolipoprotein B mRNA editing enzyme, catalytic polypeptide
15	347	2.23	2e−16	1e−14	50 x 7	apolipoprotein D [Source:HGNC Symbol;Acc:612]
16	366	2.62	2e−16	1e−14	1 x 1	aquaporin 9 [Source:HGNC Symbol;Acc:643]
17	140458	2.02	2e−16	1e−14	25 x 1	ankyrin repeat and SOCS box containing 5 [Source:HGNC Sy
18	64651	1.72	2e−16	1e−14	6 x 2	cysteine−serine−rich nuclear protein 1 [Source:HGNC Symbo
19	633	1.67	2e−16	1e−14	3 x 1	biglycan [Source:HGNC Symbol;Acc:1044]
20	274	1.94	2e−16	1e−14	26 x 1	bridging integrator 1 [Source:HGNC Symbol;Acc:1052]



Global Geneset Analysis

Rank	GSZ	p−value	#all		Geneset
Overexpressed					
1	26.24	NULL	127	H.Tiss	WIRTH_Muscle
2	22.11	NULL	36	BP	muscle filament sliding
3	20.78	NULL	553	Cancer	Lembcke_Colonic Inflammation
4	19.8	NULL	265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
5	19.8	NULL	265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
6	19.8	NULL	265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
7	19.8	NULL	265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
8	19.33	NULL	250	Lymphoma	LENZ_Stromal signature 1
9	19.18	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_F
10	18.58	NULL	44	MF	structural constituent of muscle
11	18.37	NULL	190	CC	extracellular matrix
12	17.03	NULL	16	H.Tiss	WIRTH_Hippocampus
13	16.37	NULL	683	CC	extracellular space
14	16.03	NULL	84	BP	muscle contraction
15	13.93	NULL	1182	CC	extracellular region
16	13.64	NULL	12	CC	myosin filament
17	13.24	NULL	242	BP	extracellular matrix organization
18	12.54	NULL	37	CC	sarcomere
19	12.41	NULL	269	BP	inflammatory response
20	12.17	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
Underexpressed					
1	−34.2	NULL	135	H.Tiss	WIRTH_Mucosa
2	−18.32	NULL	572	Disease	GUDJ_psoriasis up
3	−17.64	NULL	21	CC	cornified envelope
4	−16.07	NULL	76	BP	epidermis development
5	−15.53	NULL	42	BP	keratinization
6	−15.38	NULL	53	BP	keratinocyte differentiation
7	−13.74	NULL	142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
8	−13.74	NULL	142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
9	−11.18	NULL	370	BP	mitotic cell cycle
10	−9.51	NULL	530	Cancer	Lembcke_Normal vs Adenoma
11	−8.65	NULL	8	GSEA C2	LIU_CDX2_TARGETS_DN
12	−8.32	NULL	15	GSEA C2	AIGNER_ZEB1_TARGETS
13	−8.29	NULL	21	CC	desmosome
14	−8.28	NULL	44	CC	keratin filament
15	−8.24	NULL	82	CC	intermediate filament
16	−7.93	NULL	19	BP	peptide cross−linking
17	−7.92	NULL	1233	TF	KIM_MYC targets
18	−7.86	NULL	949	CC	nucleoplasm
19	−7.48	NULL	232	BP	mitosis
20	−6.81	NULL	649	BP	gene expression

GW_146

Local Summary

%DE = 0.96

metagenes = 24

genes = 344

genes in genesets = 340

genes with fdr < 0.1 = 322 (320 + / 2 −)

genes with fdr < 0.05 = 307 (305 + / 2 −)

genes with fdr < 0.01 = 307 (305 + / 2 −)

<r> metagenes = 0.96

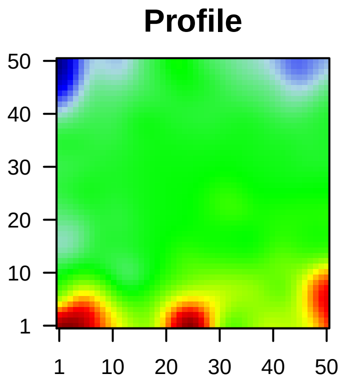
<r> genes = 0.39

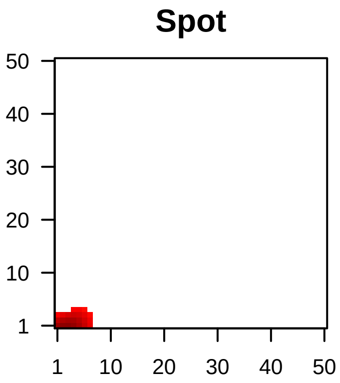
<FC> = 1.18

<shrinkage−t> = 41.42

<p−value> = 0

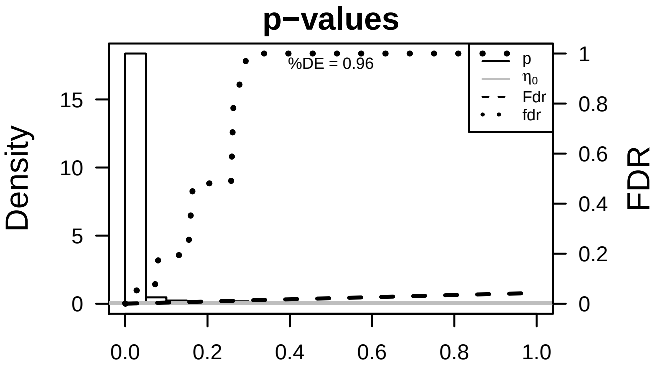
<fdr> = 0.12





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	59	1.68	2e−16	5e−17	3 x 1	actin, alpha 2, smooth muscle, aorta [Source:HGNC Symbol;
2	72	2.05	2e−16	5e−17	4 x 1	actin, gamma 2, smooth muscle, enteric [Source:HGNC Syml
3	249	1.72	2e−16	5e−17	6 x 1	alkaline phosphatase, liver/bone/kidney [Source:HGNC Symb
4	23452	2.26	2e−16	5e−17	3 x 1	angiopoietin−like 2 [Source:HGNC Symbol;Acc:490]
5	366	2.62	2e−16	5e−17	1 x 1	aquaporin 9 [Source:HGNC Symbol;Acc:643]
6	64651	1.72	2e−16	5e−17	6 x 2	cysteine−serine−rich nuclear protein 1 [Source:HGNC Symbc
7	633	1.67	2e−16	5e−17	3 x 1	biglycan [Source:HGNC Symbol;Acc:1044]
8	199675	1.68	2e−16	5e−17	5 x 4	chromosome 19 open reading frame 59 [Source:HGNC Symb
9	114902	1.83	2e−16	5e−17	4 x 1	C1q and tumor necrosis factor related protein 5 [Source:HGN
10	6348	2.28	2e−16	5e−17	4 x 4	chemokine (C−C motif) ligand 3 [Source:HGNC Symbol;Acc:
11	414062	2.98	2e−16	5e−17	1 x 1	chemokine (C−C motif) ligand 3−like 3 [Source:HGNC Symbc
12	57124	1.79	2e−16	5e−17	3 x 1	CD248 molecule, endosialin [Source:HGNC Symbol;Acc:182
13	22918	2.07	2e−16	5e−17	4 x 1	CD93 molecule [Source:HGNC Symbol;Acc:15855]
14	1306	2.21	2e−16	5e−17	4 x 1	collagen, type XV, alpha 1 [Source:HGNC Symbol;Acc:2192]
15	1277	2.2	2e−16	5e−17	2 x 1	collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
16	1278	2.2	2e−16	5e−17	2 x 1	collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198]
17	1281	2.09	2e−16	5e−17	2 x 1	collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]
18	1289	2.02	2e−16	5e−17	2 x 1	collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209]
19	1290	1.76	2e−16	5e−17	2 x 1	collagen, type V, alpha 2 [Source:HGNC Symbol;Acc:2210]
20	1291	1.99	2e−16	5e−17	2 x 1	collagen, type VI, alpha 1 [Source:HGNC Symbol;Acc:2211]



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	33.82	NULL	69 / 190	CC	extracellular matrix
2	33.45	NULL	84 / 250	Lymphoma	LENZ_Stromal signature 1
3	29.7	NULL	14 / 16	MMML CGS	GACIEJ_MMML 1
4	28.92	NULL	13 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
5	27.44	NULL	65 / 242	BP	extracellular matrix organization
6	26.09	NULL	32 / 69	BP	extracellular matrix disassembly
7	25.84	NULL	8 / 11	MF	platelet−derived growth factor binding
8	22.93	NULL	27 / 64	BP	collagen catabolic process
9	22.15	NULL	79 / 553	Cancer	Lembcke_Colonic Inflammation
10	22.1	NULL	89 / 683	CC	extracellular space
11	21.6	NULL	8 / 12	miRNA target	miR−29c
12	21.03	NULL	11 / 19	MF	extracellular matrix binding
13	20.95	NULL	21 / 57	MF	extracellular matrix structural constituent
14	20.9	NULL	119 / 1182	CC	extracellular region
15	19.62	NULL	7 / 15	GSEA C2	LEE_LIVER_CANCER_HEPATOBLAST
16	19.61	NULL	11 / 15	GSEA C2	CROMER_TUMORIGENESIS_UP
17	19.08	NULL	48 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
18	19.08	NULL	48 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
19	19.08	NULL	48 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
20	19.08	NULL	48 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
21	18.77	NULL	11 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_UP
22	18.47	NULL	40 / 183	CC	proteinaceous extracellular matrix
23	18.16	NULL	4 / 6	GSEA C2	AGARWAL_AKT_PATHWAY_TARGETS
24	15.93	NULL	5 / 10	GSEA C2	KEGG_ECM_RECEPTOR_INTERACTION
25	15.57	NULL	7 / 15	GSEA C2	MISHRA_CARCINOMA_ASSOCIATED_FIBROBLAST_UP
26	15.25	NULL	7 / 12	GSEA C2	LY_AGING_MIDDLE_UP
27	15.09	NULL	4 / 5	GSEA C2	COLLER_MYC_TARGETS_DN
28	15.01	NULL	4 / 8	GSEA C2	HAEGERSTRAND_RESPONSE_TO_IMATINIB
29	14.91	NULL	21 / 83	CC	basement membrane
30	14.83	NULL	10 / 40	BP	cellular response to amino acid stimulus
31	14.71	NULL	3 / 6	Glio	Martinez_Glio_hypometh
32	14.65	NULL	6 / 10	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C4
33	14.65	NULL	8 / 15	GSEA C2	DASU_IL6_SIGNALING_SCAR_DN
34	14.63	NULL	15 / 37	BP	collagen fibril organization
35	14.59	NULL	8 / 16	GSEA C2	ROZANOV_MMP14_TARGETS_SUBSET
36	14.47	NULL	6 / 10	GSEA C2	JEON_SMAD6_TARGETS_UP
37	14.44	NULL	8 / 43	MF	chemokine activity
38	14.36	NULL	8 / 16	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_
39	14.35	NULL	5 / 7	GSEA C2	TSUNODA_CISPLATIN_RESISTANCE_UP
40	14.33	NULL	11 / 36	BP	embryo implantation

GW_146

Local Summary

%DE = 0.98

metagenes = 15

genes = 120

genes in genesets = 119

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

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

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

<r> metagenes = 0.98

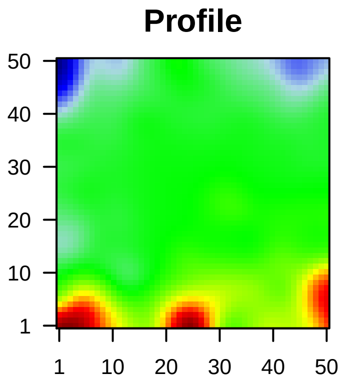
<r> genes = 0.61

<FC> = 1.72

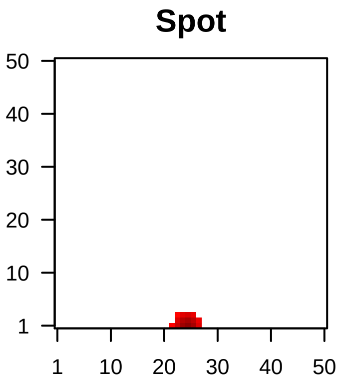
<shrinkage−t> = 60.08

<p−value> = 0

<fdr> = 0.03



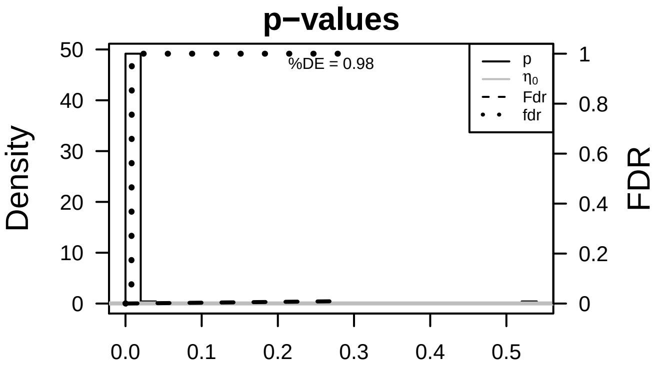
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	58	5.49	2e−16	9e−18	25 x 1	actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
2	70	3.94	2e−16	9e−18	25 x 1	actin, alpha, cardiac muscle 1 [Source:HGNC Symbol;Acc:14
3	10930	2.06	2e−16	9e−18	25 x 1	apolipoprotein B mRNA editing enzyme, catalytic polypeptide
4	140458	2.02	2e−16	9e−18	25 x 1	ankyrin repeat and SOCS box containing 5 [Source:HGNC Sy
5	274	1.94	2e−16	9e−18	26 x 1	bridging integrator 1 [Source:HGNC Symbol;Acc:1052]
6	1158	4.27	2e−16	9e−18	25 x 1	creatine kinase, muscle [Source:HGNC Symbol;Acc:1994]
7	1160	1.75	2e−16	9e−18	25 x 1	creatine kinase, mitochondrial 2 (sarcomeric) [Source:HGNC
8	202333	2.68	2e−16	9e−18	25 x 1	cardiomyopathy associated 5 [Source:HGNC Symbol;Acc:14
9	1346	2	2e−16	9e−18	25 x 1	cytochrome c oxidase subunit VIIa polypeptide 1 (muscle) [S
10	1410	2.13	2e−16	9e−18	25 x 1	crystallin, alpha B [Source:HGNC Symbol;Acc:2389]
11	8048	1.75	2e−16	9e−18	25 x 1	cysteine and glycine−rich protein 3 (cardiac LIM protein) [Sou
12	115265	1.97	2e−16	9e−18	25 x 1	DNA−damage−inducible transcript 4−like [Source:HGNC Sym
13	23109	2.03	2e−16	9e−18	25 x 1	dendrin [Source:HGNC Symbol;Acc:24458]
14	1674	2.27	2e−16	9e−18	25 x 1	desmin [Source:HGNC Symbol;Acc:2770]
15	1917	2.97	2e−16	9e−18	25 x 1	eukaryotic translation elongation factor 1 alpha 2 [Source:HG
16	2027	2.31	2e−16	9e−18	25 x 1	enolase 3 (beta, muscle) [Source:HGNC Symbol;Acc:3354]
17	2273	2.68	2e−16	9e−18	25 x 1	four and a half LIM domains 1 [Source:HGNC Symbol;Acc:37
18	2318	2.99	2e−16	9e−18	25 x 1	filamin C, gamma [Source:HGNC Symbol;Acc:3756]
19	283120	2.13	2e−16	9e−18	25 x 1	H19, imprinted maternally expressed transcript (non−protein
20	3270	1.89	2e−16	9e−18	25 x 1	histidine rich calcium binding protein [Source:HGNC Symbol;



p−values

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	64.45	NULL	60 / 127	H.Tiss	WIRTH_Muscle
2	60.07	NULL	23 / 36	BP	muscle filament sliding
3	53.51	NULL	11 / 16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_F
4	51.6	NULL	11 / 16	H.Tiss	WIRTH_Hippocampus
5	46.92	NULL	23 / 44	MF	structural constituent of muscle
6	42.65	NULL	10 / 12	CC	myosin filament
7	32.49	NULL	23 / 84	BP	muscle contraction
8	32.3	NULL	12 / 37	CC	sarcomere
9	31.5	NULL	8 / 13	CC	muscle myosin complex
10	31.25	NULL	8 / 14	CC	contractile fiber
11	29.49	NULL	9 / 16	CC	M band
12	27.62	NULL	6 / 12	BP	skeletal muscle contraction
13	27.5	NULL	15 / 34	CC	myofibril
14	26.41	NULL	22 / 88	CC	Z disc
15	25.35	NULL	10 / 20	CC	I band
16	23.34	NULL	5 / 11	BP	cardiac muscle tissue morphogenesis
17	22.71	NULL	7 / 12	MF	titin binding
18	22.7	NULL	9 / 37	BP	cardiac muscle contraction
19	21.32	NULL	5 / 11	CC	A band
20	20.96	NULL	6 / 18	BP	regulation of muscle contraction
21	19.61	NULL	2 / 6	GSEA C2	BIOCARTA_HSP27_PATHWAY
22	19.51	NULL	7 / 15	BP	striated muscle contraction
23	17.74	NULL	7 / 15	GSEA C2	REACTOME_STRIATED_MUSCLE_CONTRACTION
24	17.71	NULL	3 / 15	Cancer	BEN−PORATH_UP
25	16.01	NULL	25 / 297	MF	actin binding
26	15.69	NULL	8 / 42	CC	myosin complex
27	15.47	NULL	4 / 14	BP	adult heart development
28	15.42	NULL	2 / 10	BP	heart contraction
29	15.06	NULL	4 / 16	MF	microfilament motor activity
30	14.54	NULL	5 / 26	BP	ventricular cardiac muscle tissue morphogenesis
31	13.99	NULL	7 / 21	BP	sarcomere organization
32	13.94	NULL	4 / 14	MF	tropomyosin binding
33	13.62	NULL	2 / 20	MF	myosin binding
34	13.41	NULL	3 / 13	CC	pseudopodium
35	13.21	NULL	4 / 18	CC	costamere
36	13.19	NULL	1 / 5	GSEA C2	LIU_VAV3_PROSTATE_CARCINOGENESIS_UP
37	13.04	NULL	2 / 10	BP	creatine metabolic process
38	12.95	NULL	4 / 15	GSEA C2	EBAUER_MYOGENIC_TARGETS_OF_PAX3_FOXO1_FUSION
39	12.65	NULL	1 / 9	GSEA C2	PENG_GLUCOSE_DEPRIVATION_UP
40	12.65	NULL	1 / 9	GSEA C2	PENG_GLUCOSE_DEPRIVATION_DN

GW_146

Local Summary

%DE = 0.99

metagenes = 6

genes = 128

genes in genesets = 128

genes with fdr < 0.1 = 123 (122 + / 1 −)

genes with fdr < 0.05 = 123 (122 + / 1 −)

genes with fdr < 0.01 = 119 (118 + / 1 −)

<r> metagenes = 0.95

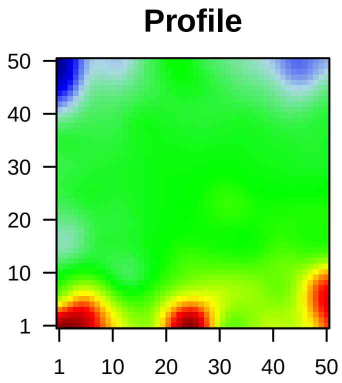
<r> genes = 0.39

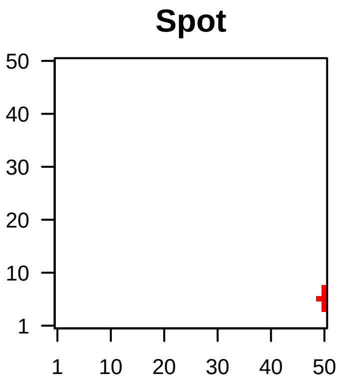
<FC> = 1.03

<shrinkage−t> = 35.95

<p−value> = 0

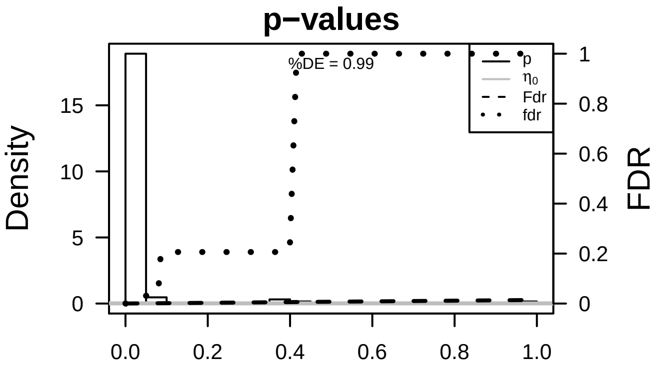
<fdr> = 0.1





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	347	2.23	2e−16	3e−17	50 x 7	apolipoprotein D [Source:HGNC Symbol;Acc:612]
2	6347	1.97	2e−16	3e−17	50 x 4	chemokine (C−C motif) ligand 2 [Source:HGNC Symbol;Acc:
3	1116	2.21	2e−16	3e−17	50 x 4	chitinase 3−like 1 (cartilage glycoprotein−39) [Source:HGNC
4	6387	1.88	2e−16	3e−17	50 x 6	chemokine (C−X−C motif) ligand 12 [Source:HGNC Symbol;
5	1545	1.73	2e−16	3e−17	50 x 4	cytochrome P450, family 1, subfamily B, polypeptide 1 [Sourc
6	1601	1.73	2e−16	3e−17	50 x 5	Dab, mitogen−responsive phosphoprotein, homolog 2 (Droso
7	2532	1.78	2e−16	3e−17	50 x 5	Duffy blood group, atypical chemokine receptor [Source:HGN
8	2219	1.91	2e−16	3e−17	50 x 5	ficolin (collagen/fibrinogen domain containing) 1 [Source:HGN
9	4239	1.79	2e−16	3e−17	50 x 6	microfibrillar−associated protein 4 [Source:HGNC Symbol;Ac
10	5142	1.81	2e−16	3e−17	50 x 4	phosphodiesterase 4B, cAMP−specific [Source:HGNC Symb
11	5175	1.77	2e−16	3e−17	50 x 4	platelet/endothelial cell adhesion molecule 1 [Source:HGNC
12	221476	1.67	2e−16	3e−17	50 x 7	peptidase inhibitor 16 [Source:HGNC Symbol;Acc:21245]
13	5320	1.87	2e−16	3e−17	50 x 8	phospholipase A2, group IIA (platelets, synovial fluid) [Source
14	338773	1.79	2e−16	3e−17	50 x 5	transmembrane protein 119 [Source:HGNC Symbol;Acc:278
15	347733	1.76	2e−16	3e−17	50 x 5	tubulin, beta 2B class IIb [Source:HGNC Symbol;Acc:30829]
16	270	1.64	4e−16	4e−16	50 x 7	adenosine monophosphate deaminase 1 [Source:HGNC Sym
17	8404	1.64	7e−16	6e−16	50 x 6	SPARC−like 1 (hevin) [Source:HGNC Symbol;Acc:11220]
18	388125	1.62	1e−15	6e−16	50 x 6	C2 calcium−dependent domain containing 4B [Source:HGNC
19	2	1.62	1e−15	8e−16	50 x 5	alpha−2−macroglobulin [Source:HGNC Symbol;Acc:7]
20	5166	1.61	2e−15	8e−16	50 x 7	pyruvate dehydrogenase kinase, isozyme 4 [Source:HGNC S



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	17.74	NULL	4 / 15	GSEA C2	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_10D_DN
2	17.13	NULL	4 / 12	GSEA C2	BERTUCCI_INVASIVE_CARCINOMA_DUCTAL_VS_LOBULAR_D
3	16.76	NULL	4 / 15	GSEA C2	NAKAJIMA_MAST_CELL
4	16.55	NULL	4 / 10	GSEA C2	LU_TUMOR_VASCULATURE_DN
5	15.81	NULL	3 / 8	Glio	Donson−migration tethering and rolling−associated with LTS in HG
6	15.79	NULL	4 / 15	Cancer	GENTLES_modul13
7	15.64	NULL	3 / 7	GSEA C2	LOPEZ_MESOTHELIOMA_SURVIVAL_WORST_VS_BEST_DN
8	14.5	NULL	4 / 13	Cancer	GENTLES_modul17
9	14.44	NULL	3 / 14	GSEA C2	FRASOR_RESPONSE_TO_ESTRADIOL_UP
10	14.2	NULL	2 / 4	GSEA C2	LU_TUMOR_ENDOTHELIAL_MARKERS_DN
11	12.99	NULL	3 / 14	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_LUNG_DN
12	12.9	NULL	3 / 21	BP	chemokine−mediated signaling pathway
13	12.75	NULL	3 / 12	GSEA C2	ZHAN_V1_LATE_DIFFERENTIATION_GENES_UP
14	12.29	NULL	14 / 190	CC	extracellular matrix
15	12.1	NULL	2 / 12	GSEA C2	BIOCARTA_CCR5_PATHWAY
16	12.1	NULL	2 / 12	GSEA C2	REACTOME_CHEMOKINE_RECEPTORS_BIND_CHEMOKINES
17	11.85	NULL	3 / 7	GSEA C2	LOPEZ_MESOTELIOMA_SURVIVAL_TIME_DN
18	11.8	NULL	2 / 5	GSEA C2	SMIRNOV_CIRCULATING_ENDOTHELIOCYTES_IN_CANCER_D
19	11.76	NULL	6 / 59	Lymphoma	LENZ_Stromal signature 2
20	11.27	NULL	3 / 10	BP	germ cell migration
21	11.06	NULL	27 / 683	CC	extracellular space
22	10.96	NULL	2 / 12	GSEA C2	ZHAN_MULTIPLE_MYELOMA_DN
23	10.8	NULL	2 / 9	GSEA C2	LEE_LIVER_CANCER
24	10.8	NULL	2 / 9	GSEA C2	LEE_LIVER_CANCER_TOP50
25	10.75	NULL	5 / 46	Glio	OL vs. OPC
26	10.25	NULL	2 / 15	GSEA C2	ABE_INNER_EAR
27	10.16	NULL	2 / 16	GSEA C2	COLIN_PILOCYTIC_ASTROCYTOMA_VS_GLIOBLASTOMA_DN
28	10.11	NULL	2 / 10	GSEA C2	REACTOME_INTRINSIC_PATHWAY
29	10.09	NULL	2 / 14	GSEA C2	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_8D_DN
30	10.02	NULL	2 / 16	GSEA C2	CHEN_LVAD_SUPPORT_OF_FAILING_HEART_DN
31	9.82	NULL	1 / 4	GSEA C2	REACTOME_INTEGRATION_OF_ENERGY_METABOLISM
32	9.8	NULL	2 / 13	BP	negative regulation of androgen receptor signaling pathway
33	9.78	NULL	3 / 27	BP	negative regulation of smooth muscle cell proliferation
34	9.74	NULL	9 / 112	MF	heparin binding
35	9.66	NULL	2 / 10	CC	paranode region of axon
36	9.62	NULL	2 / 12	BP	regulation of glucose metabolic process
37	9.58	NULL	2 / 7	GSEA C2	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINE
38	9.58	NULL	2 / 7	GSEA C2	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINE
39	9.56	NULL	10 / 183	CC	proteinaceous extracellular matrix
40	9.56	NULL	4 / 15	GSEA C2	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_GRANULO

GW_146

Local Summary

%DE = 0.92

metagenes = 16

genes = 230

genes in genesets = 224

genes with fdr < 0.1 = 205 (9 + / 196 −)

genes with fdr < 0.05 = 204 (9 + / 195 −)

genes with fdr < 0.01 = 192 (9 + / 183 −)

<r> metagenes = 0.94

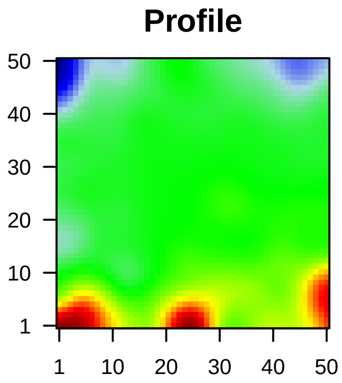
<r> genes = 0.44

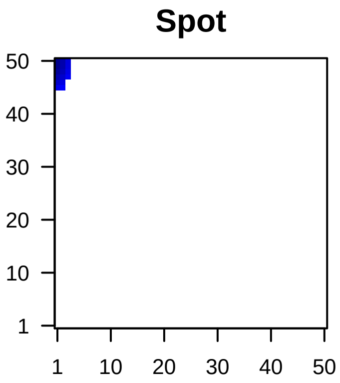
<FC> = −1.27

<shrinkage−t> = −44.91

<p−value> = 0

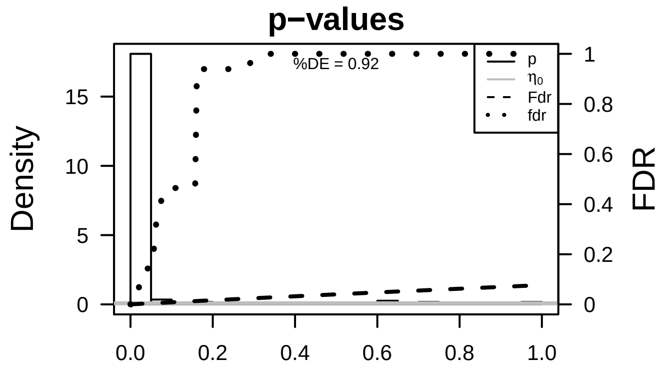
<fdr> = 0.13





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	131	−2.94	2e−16	5e−17	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	57016	−3.16	2e−16	5e−17	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
3	441282	−2.18	2e−16	5e−17	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC Sy
4	218	−3.62	2e−16	5e−17	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
5	65124	−1.79	2e−16	5e−17	1 x 45	sosondowah ankyrin repeat domain family member C [Source
6	387695	−2.5	2e−16	5e−17	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Sym
7	375791	−1.91	2e−16	5e−17	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Sym
8	810	−2.88	2e−16	5e−17	1 x 50	calmodulin−like 3 [Source:HGNC Symbol;Acc:1452]
9	84290	−1.93	2e−16	5e−17	1 x 50	calpain, small subunit 2 [Source:HGNC Symbol;Acc:16371]
10	9635	−3.34	2e−16	5e−17	1 x 46	chloride channel accessory 2 [Source:HGNC Symbol;Acc:20
11	22802	−2.4	2e−16	5e−17	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
12	84518	−2.97	2e−16	5e−17	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
13	49860	−2.4	2e−16	5e−17	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
14	1475	−2.13	2e−16	5e−17	1 x 50	cystatin A (stefin A) [Source:HGNC Symbol;Acc:2481]
15	9547	−1.77	2e−16	5e−17	1 x 46	chemokine (C−X−C motif) ligand 14 [Source:HGNC Symbol;
16	92196	−1.98	2e−16	5e−17	3 x 50	death associated protein−like 1 [Source:HGNC Symbol;Acc:2
17	1672	2.11	2e−16	5e−17	1 x 50	defensin, beta 1 [Source:HGNC Symbol;Acc:2766]
18	414325	−1.73	2e−16	5e−17	1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
19	1825	−1.72	2e−16	5e−17	1 x 45	desmocollin 3 [Source:HGNC Symbol;Acc:3037]
20	1830	−2.68	2e−16	5e−17	1 x 48	desmoglein 3 [Source:HGNC Symbol;Acc:3050]



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−67.73	NULL	83 / 135	H.Tiss	WIRTH_Mucosa
2	−46.58	NULL	18 / 21	CC	cornified envelope
3	−37.46	NULL	24 / 53	BP	keratinocyte differentiation
4	−36.07	NULL	19 / 42	BP	keratinization
5	−30.17	NULL	23 / 76	BP	epidermis development
6	−28.15	NULL	97 / 572	Disease	GUDJ_psoriasis up
7	−27.44	NULL	10 / 19	BP	peptide cross−linking
8	−22.72	NULL	12 / 21	CC	desmosome
9	−17.04	NULL	23 / 186	MF	structural molecule activity
10	−16.78	NULL	16 / 82	CC	intermediate filament
11	−16.58	NULL	10 / 44	CC	keratin filament
12	−15.17	NULL	7 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
13	−15.01	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
14	−14.44	NULL	5 / 15	GSEA C2	AIGNER_ZEB1_TARGETS
15	−14.35	NULL	4 / 10	GSEA C2	REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION_P
16	−13.64	NULL	6 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
17	−12.46	NULL	3 / 12	BP	cellular aldehyde metabolic process
18	−12.15	NULL	4 / 15	GSEA C2	CHANG_IMMORTALIZED_BY_HPV31_DN
19	−12.06	NULL	7 / 15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
20	−11.85	NULL	3 / 16	GSEA C2	AMIT_SERUM_RESPONSE_480_MCF10A
21	−11.72	NULL	3 / 10	GSEA C2	MURAKAMI_UV_RESPONSE_1HR_UP
22	−11.64	NULL	6 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
23	−11.37	NULL	3 / 11	GSEA C2	MURAKAMI_UV_RESPONSE_6HR_DN
24	−11.13	NULL	3 / 10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
25	−10.04	NULL	7 / 38	BP	epithelial cell differentiation
26	−9.9	NULL	7 / 51	MF	protein binding, bridging
27	−9.89	NULL	3 / 13	BP	intermediate filament cytoskeleton organization
28	−9.86	NULL	2 / 12	GSEA C2	REACTOME_GAP_JUNCTION_ASSEMBLY
29	−9.72	NULL	1 / 6	GSEA C2	SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_DN
30	−9.56	NULL	5 / 15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL
31	−9.41	NULL	2 / 13	GSEA C2	REACTOME_GAP_JUNCTION_TRAFFICKING
32	−8.72	NULL	2 / 9	GSEA C2	NIKOLSKY_BREAST_CANCER_17P11_AMPLICON
33	−8.72	NULL	2 / 8	GSEA C2	DORN_ADENOVIRUS_INFECTION_24HR_UP
34	−8.65	NULL	2 / 15	CC	connexon complex
35	−8.53	NULL	4 / 14	GSEA C2	CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U
36	−8.49	NULL	5 / 10	MF	RAGE receptor binding
37	−8.03	NULL	2 / 9	GSEA C2	WANG_RESPONSE_TO_PACLITAXEL_VIA_MAPK8_UP
38	−7.74	NULL	3 / 21	CC	gap junction
39	−7.66	NULL	4 / 15	GSEA C2	LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
40	−7.45	NULL	5 / 16	GSEA C2	COLDREN_GEFITINIB_RESISTANCE_DN