

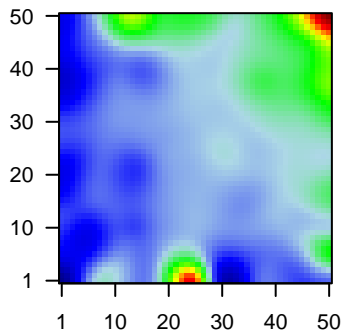
# GW\_171

## Global Summary

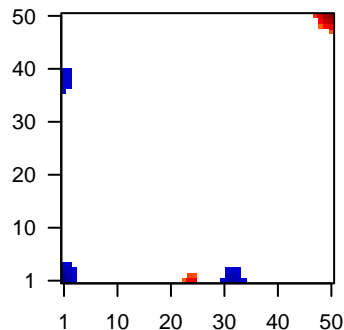
%DE = 0.16  
 # genes with  $fdr < 0.2$  = 2035 ( 1141 + / 894 - )  
 # genes with  $fdr < 0.1$  = 1637 ( 941 + / 696 - )  
 # genes with  $fdr < 0.05$  = 1473 ( 860 + / 613 - )  
 # genes with  $fdr < 0.01$  = 1026 ( 614 + / 412 - )  
 # genes in genesets = 16332

<FC> = 0  
 <shrinkage-t> = 0  
 <p-value> = 0.08  
 <fdr> = 0.84

Profile



Regulated Spots



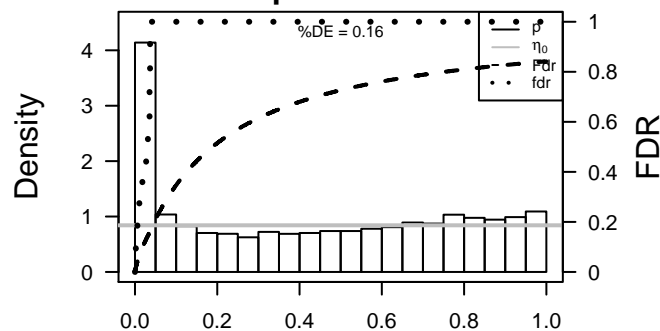
## Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	154664	1.42	2e-16	2e-14	50 x 50 ATP-binding cassette, sub-family A (ABC1), member 13 [Source:HGNC Symbol;Acc:1141]
2	10057	1.37	2e-16	2e-14	50 x 50 ATP-binding cassette, sub-family C (CFTR/MRP), member 5 [Source:HGNC Symbol;Acc:894]
3	58	5.03	2e-16	2e-14	25 x 1 actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12]
4	70	3.29	2e-16	2e-14	25 x 1 actin, alpha, cardiac muscle 1 [Source:HGNC Symbol;Acc:14]
5	8745	1.9	2e-16	2e-14	50 x 50 ADAM metallopeptidase domain 23 [Source:HGNC Symbol;Acc:1141]
6	131	2.4	2e-16	2e-14	1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide [Source:HGNC Symbol;Acc:1141]
7	1646	1.59	2e-16	2e-14	13 x 50 aldo-keto reductase family 1, member C2 [Source:HGNC Symbol;Acc:1141]
8	8644	2.55	2e-16	2e-14	1 x 50 aldo-keto reductase family 1, member C3 [Source:HGNC Symbol;Acc:1141]
9	1109	2.89	2e-16	2e-14	13 x 50 aldo-keto reductase family 1, member C4 [Source:HGNC Symbol;Acc:1141]
10	216	2.99	2e-16	2e-14	50 x 50 aldehyde dehydrogenase 1 family, member A1 [Source:HGNC Symbol;Acc:1141]
11	218	1.94	2e-16	2e-14	1 x 50 aldehyde dehydrogenase 3 family, member A1 [Source:HGNC Symbol;Acc:1141]
12	55107	1.54	2e-16	2e-14	1 x 5 anoctamin 1, calcium activated chloride channel [Source:HGNC Symbol;Acc:1141]
13	360	-1.53	2e-16	2e-14	1 x 50 aquaporin 3 (Gill blood group) [Source:HGNC Symbol;Acc:63]
14	140458	1.4	2e-16	2e-14	25 x 1 ankyrin repeat and SOCS box containing 5 [Source:HGNC Symbol;Acc:1141]
15	590	1.35	2e-16	2e-14	16 x 50 butyrylcholinesterase [Source:HGNC Symbol;Acc:983]
16	684	-1.82	2e-16	2e-14	32 x 1 bone marrow stromal cell antigen 2 [Source:HGNC Symbol;Acc:1141]
17	25758	1.55	2e-16	2e-14	9 x 3 KIAA1549-like [Source:HGNC Symbol;Acc:24836]
18	64073	-1.67	2e-16	2e-14	1 x 46 chromosome 19 open reading frame 33 [Source:HGNC Symbol;Acc:1141]
19	339512	1.79	2e-16	2e-14	50 x 50 chromosome 1 open reading frame 110 [Source:HGNC Symbol;Acc:1141]
20	205428	1.46	2e-16	2e-14	50 x 50 chromosome 3 open reading frame 58 [Source:HGNC Symbol;Acc:1141]

## Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	27.55	NULL	127	H.Tiss WIRTH_Muscle
2	21.8	NULL	36	BP muscle filament sliding
3	20.34	NULL	16	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_F
4	19.39	NULL	16	H.Tiss WIRTH_Hippocampus
5	17.56	NULL	44	MF structural constituent of muscle
6	13.81	NULL	37	CC sarcomere
7	11.72	NULL	12	CC myosin filament
8	11.13	NULL	13	CC muscle myosin complex
9	10.88	NULL	84	BP muscle contraction
10	9.57	NULL	34	CC myofibril
11	9.56	NULL	14	CC contractile fiber
12	9.48	NULL	88	CC Z disc
13	9.05	NULL	37	BP cardiac muscle contraction
14	8.83	NULL	15	GSEA C2KEGG_GLUTATHIONE_METABOLISM
15	8.82	NULL	16	CC M band
16	8.82	NULL	12	BP skeletal muscle contraction
17	8.43	NULL	20	CC I band
18	8.35	NULL	15	Cancer BEN-PORATH_UP
19	7.8	NULL	375	Disease GUDJ_poriasis down
20	7.56	NULL	34	BP glutathione metabolic process
<i>Underexpressed</i>				
1	-12.24	NULL	1135	Chr Chr 19
2	-10.1	NULL	572	Disease GUDJ_poriasis up
3	-10.04	NULL	265	Glio wilscher_GBM_Verhaak-CL_expression_B_up
4	-10.04	NULL	265	Glio wilscher_GBM_Verhaak-MES_expression_B_up
5	-10.04	NULL	265	Glio wilscher_GBM_Verhaak-PNwt_expression_B_down
6	-10.04	NULL	265	Glio wilscher_GBM_Verhaak-PNmut_expression_B_down
7	-9.25	NULL	64	BP collagen catabolic process
8	-8.94	NULL	69	BP extracellular matrix disassembly
9	-8.22	NULL	553	Cancer Lembecke_Colonc Inflammation
10	-7.96	NULL	519	Chr Chr 14
11	-7.59	NULL	16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_5
12	-7.56	NULL	957	Chr Chr 11
13	-7.37	NULL	190	CC extracellular matrix
14	-7.37	NULL	11	MF platelet-derived growth factor binding
15	-7.18	NULL	250	LymphomaLENS_Stromal signature 1
16	-7.12	NULL	242	BP extracellular matrix organization
17	-7.04	NULL	1182	CC extracellular region
18	-7	NULL	15	GSEA C2PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
19	-6.97	NULL	135	H.Tiss WIRTH_Mucosa
20	-6.91	NULL	51	BP type I interferon signaling pathway

p-values



# GW\_171

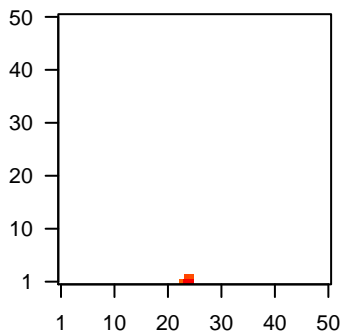
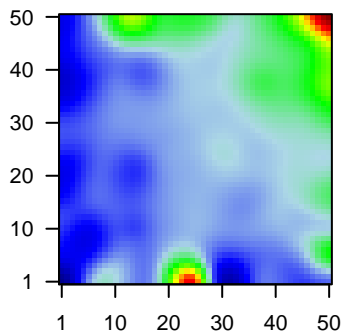
## Local Summary

%DE = 0.96  
 # metagenes = 5  
 # genes = 96  
 # genes in genesets = 96  
 # genes with  $fdr < 0.1 = 85$  ( 84 + / 1 - )  
 # genes with  $fdr < 0.05 = 85$  ( 84 + / 1 - )  
 # genes with  $fdr < 0.01 = 79$  ( 78 + / 1 - )

<r> metagenes = 1  
 <r> genes = 0.67  
 <FC> = 1.26  
 <shrinkage-t> = 44.03  
 <p-value> = 0  
 <fdr> = 0.16

Profile

Spot



## Local Genelist

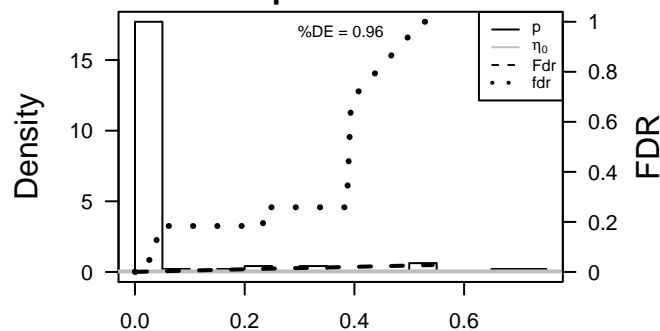
Rank	ID	log(FC)	fdr	p-value	Description
1	58	5.03	2e-16	3e-17	25 x 1 actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
2	70	3.29	2e-16	3e-17	25 x 1 actin, alpha, cardiac muscle 1 [Source:HGNC Symbol;Acc:14
3	140458	1.4	2e-16	3e-17	25 x 1 ankyrin repeat and SOCS box containing 5 [Source:HGNC S
4	845	1.34	2e-16	3e-17	25 x 1 calsequestrin 2 (cardiac muscle) [Source:HGNC Symbol;Acc:
5	1158	4.01	2e-16	3e-17	25 x 1 creatine kinase, muscle [Source:HGNC Symbol;Acc:1994]
6	1160	1.58	2e-16	3e-17	25 x 1 creatine kinase, mitochondrial 2 (sarcomeric) [Source:HGNC
7	202333	2.09	2e-16	3e-17	25 x 1 cardiomyopathy associated 5 [Source:HGNC Symbol;Acc:14:
8	1346	1.43	2e-16	3e-17	25 x 1 cytochrome c oxidase subunit VIIa polypeptide 1 (muscle) [Sc
9	1917	1.7	2e-16	3e-17	25 x 1 eukaryotic translation elongation factor 1 alpha 2 [Source:HG
10	2027	2.14	2e-16	3e-17	25 x 1 enolase 3 (beta, muscle) [Source:HGNC Symbol;Acc:3354]
11	2273	2.06	2e-16	3e-17	25 x 1 four and a half LIM domains 1 [Source:HGNC Symbol;Acc:37
12	2318	1.86	2e-16	3e-17	25 x 1 filamin C, gamma [Source:HGNC Symbol;Acc:3756]
13	126393	1.4	2e-16	3e-17	25 x 1 heat shock protein, alpha-crystallin-related, B6 [Source:HG
14	10324	2.87	2e-16	3e-17	25 x 1 kelch-like family member 41 [Source:HGNC Symbol;Acc:169
15	4151	3.38	2e-16	3e-17	25 x 1 myoglobin [Source:HGNC Symbol;Acc:6915]
16	4604	2.13	2e-16	3e-17	25 x 1 myosin binding protein C, slow type [Source:HGNC Symbol;A
17	4620	3.51	2e-16	3e-17	25 x 1 myosin, heavy chain 2, skeletal muscle, adult [Source:HGNC
18	4625	3.12	2e-16	3e-17	25 x 1 myosin, heavy chain 7, cardiac muscle, beta [Source:HGNC
19	4632	2.09	2e-16	3e-17	25 x 1 myosin, light chain 1, alkali; skeletal, fast [Source:HGNC Sym
20	4633	2.66	2e-16	3e-17	25 x 1 myosin, light chain 2, regulatory, cardiac, slow [Source:HGNC

## Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	65.16	NULL	55 / 127	H.Tiss WIRTH_Muscle
2	63.86	NULL	23 / 36	BP muscle filament sliding
3	58.28	NULL	11 / 16	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_F
4	57.06	NULL	11 / 16	H.Tiss WIRTH_Hippocampus
5	46.46	NULL	21 / 44	MF structural constituent of muscle
6	39.67	NULL	12 / 37	CC sarcomere
7	35.06	NULL	8 / 13	CC muscle myosin complex
8	34.97	NULL	10 / 12	CC myosin filament
9	32.69	NULL	23 / 84	BP muscle contraction
10	28.7	NULL	8 / 14	CC contractile fiber
11	28.42	NULL	14 / 34	CC myofibril
12	27	NULL	8 / 16	CC M band
13	25.6	NULL	9 / 37	BP cardiac muscle contraction
14	24.47	NULL	20 / 88	CC Z disc
15	24.19	NULL	9 / 20	CC I band
16	23.67	NULL	5 / 11	BP cardiac muscle tissue morphogenesis
17	23.37	NULL	6 / 12	BP skeletal muscle contraction
18	23.26	NULL	2 / 6	GSEA C2BIOCARTA_HSP27_PATHWAY
19	22.08	NULL	3 / 15	Cancer BEN-PORATH_UP
20	21.96	NULL	7 / 15	BP striated muscle contraction
21	20.43	NULL	6 / 12	MF titin binding
22	19.48	NULL	4 / 14	BP adult heart development
23	18.66	NULL	6 / 18	BP regulation of muscle contraction
24	18.64	NULL	4 / 11	CC A band
25	18.18	NULL	5 / 26	BP ventricular cardiac muscle tissue morphogenesis
26	18.12	NULL	2 / 10	BP heart contraction
27	17.53	NULL	4 / 16	MF microfilament motor activity
28	17.03	NULL	2 / 10	BP creatine metabolic process
29	16.78	NULL	2 / 20	MF myosin binding
30	16.57	NULL	8 / 42	CC myosin complex
31	16.35	NULL	1 / 9	GSEA C2PENG_GLUCCOSE_DEPRIVATION_UP
32	16.35	NULL	1 / 9	GSEA C2PENG_GLUCCOSE_DEPRIVATION_DN
33	15.72	NULL	1 / 5	GSEA C2LIU_VAV3_PROSTATE_CARCINOGENESIS_UP
34	15.53	NULL	2 / 14	GSEA C2BIOCARTA_UCALPAIN_PATHWAY
35	15.44	NULL	3 / 13	CC pseudopodium
36	15.3	NULL	1 / 10	GSEA C2BIOCARTA_EPHA4_PATHWAY
37	15.06	NULL	25 / 297	MF actin binding
38	14.89	NULL	2 / 15	GSEA C2BIOCARTA_INTEGRIN_PATHWAY
39	14.36	NULL	7 / 15	GSEA C2REACTOME_STRIATED_MUSCLE_CONTRACTION
40	13.67	NULL	1 / 12	GSEA C2BIOCARTA_NO1_PATHWAY

p-values



# GW\_171

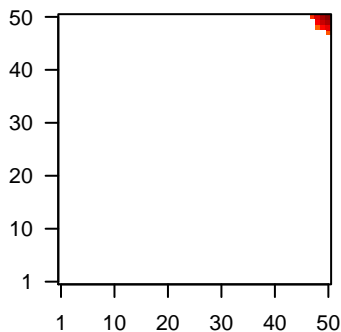
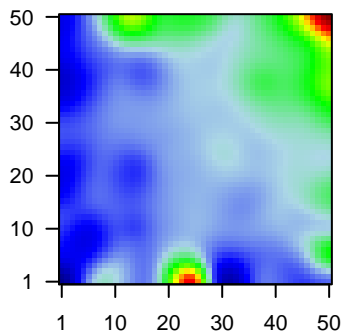
## Local Summary

%DE = 0.94  
 # metagenes = 11  
 # genes = 185  
 # genes in genesets = 184  
 # genes with  $fdr < 0.1 = 158$  ( 156 + / 2 - )  
 # genes with  $fdr < 0.05 = 154$  ( 152 + / 2 - )  
 # genes with  $fdr < 0.01 = 141$  ( 139 + / 2 - )

<r> metagenes = 0.97  
 <r> genes = 0.28  
 <FC> = 0.81  
 <shrinkage-t> = 28.4  
 <p-value> = 0  
 <fdr> = 0.21

Profile

Spot



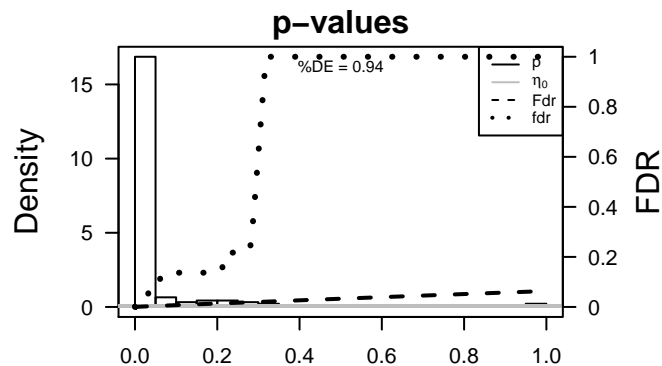
## Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	154664	1.42	2e-16	9e-17	50 x 50 ATP-binding cassette, sub-family A (ABC1), member 13 [Soi
2	10057	1.37	2e-16	9e-17	50 x 50 ATP-binding cassette, sub-family C (CFTR/MRP), member 5
3	8745	1.9	2e-16	9e-17	50 x 50 ADAM metallopeptidase domain 23 [Source:HGNC Symbol;A
4	216	2.99	2e-16	9e-17	50 x 50 aldehyde dehydrogenase 1 family, member A1 [Source:HGNC
5	339512	1.79	2e-16	9e-17	50 x 50 chromosome 1 open reading frame 110 [Source:HGNC Synt
6	205428	1.46	2e-16	9e-17	50 x 50 chromosome 3 open reading frame 58 [Source:HGNC Symbc
7	56548	1.41	2e-16	9e-17	50 x 50 carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 7
8	10655	1.56	2e-16	9e-17	50 x 50 doublesex and mab-3 related transcription factor 2 [Source:H
9	4072	2.09	2e-16	9e-17	50 x 50 epithelial cell adhesion molecule [Source:HGNC Symbol;Acc:
10	83888	2.98	2e-16	9e-17	50 x 50 fibroblast growth factor binding protein 2 [Source:HGNC Syml
11	2938	2.3	2e-16	9e-17	50 x 50 glutathione S-transferase alpha 2 [Source:HGNC Symbol;Ao
12	2944	2.69	2e-16	9e-17	50 x 50 glutathione S-transferase mu 1 [Source:HGNC Symbol;Acc:4
13	2946	1.95	2e-16	9e-17	50 x 50 glutathione S-transferase mu 2 (muscle) [Source:HGNC Syrr
14	2947	2.4	2e-16	9e-17	50 x 50 glutathione S-transferase mu 3 (brain) [Source:HGNC Symbx
15	10643	1.37	2e-16	9e-17	48 x 50 insulin-like growth factor 2 mRNA binding protein 3 [Source:t
16	3866	1.89	2e-16	9e-17	50 x 50 keratin 15 [Source:HGNC Symbol;Acc:6421]
17	3880	1.94	2e-16	9e-17	50 x 49 keratin 19 [Source:HGNC Symbol;Acc:6436]
18	4915	2.14	2e-16	9e-17	50 x 50 neurotrophic tyrosine kinase, receptor, type 2 [Source:HGNC
19	4922	2.14	2e-16	9e-17	50 x 50 neurotensin [Source:HGNC Symbol;Acc:8038]
20	4953	1.42	2e-16	9e-17	50 x 50 ornithine decarboxylase 1 [Source:HGNC Symbol;Acc:8109]

## Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	25.57	NULL	5 / 15	GSEA C2KEGG_GLUTATHIONE_METABOLISM
2	21.86	NULL	3 / 11	MF glutathione binding
3	21.86	NULL	3 / 11	GSEA C2KEGG_DRUG_METABOLISM_CYTOCHROME_P450
4	21.47	NULL	6 / 25	BP glutathione derivative biosynthetic process
5	21.45	NULL	4 / 13	GSEA C2KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_P
6	21.4	NULL	3 / 8	GSEA C2LIU_CDX2_TARGETS_DN
7	20.94	NULL	5 / 20	MF glutathione transferase activity
8	20.91	NULL	8 / 34	BP glutathione metabolic process
9	16.58	NULL	4 / 15	GSEA C2REACTOME_GLUTATHIONE_CONJUGATION
10	16.28	NULL	2 / 7	GSEA C2MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
11	15.1	NULL	11 / 119	BP xenobiotic metabolic process
12	13.49	NULL	2 / 7	GSEA C2FREDERICK_PRKCI_TARGETS
13	13.1	NULL	1 / 6	GSEA C2GAUSSMANN_MLL_AF4_FUSION_TARGETS_D_DN
14	13.1	NULL	1 / 6	GSEA C2KAPOSI_LIVER_CANCER_POOR_SURVIVAL_DN
15	12.7	NULL	3 / 16	GSEA C2BOYAUULT_LIVER_CANCER_SUBCLASS_G1_DN
16	12.28	NULL	3 / 13	BP regulation of blood vessel size
17	11.94	NULL	2 / 15	GSEA C2LEE_LIVER_CANCER_MYC_UP
18	11.94	NULL	2 / 15	GSEA C2LEE_LIVER_CANCER_E2F1_UP
19	11.73	NULL	3 / 6	GSEA C2MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_7
20	10.99	NULL	4 / 15	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_E
21	10.95	NULL	3 / 11	GSEA C2TO_PTTG1_TARGETS_UP
22	10.68	NULL	2 / 12	BP cellular aldehyde metabolic process
23	10.63	NULL	3 / 9	GSEA C2BROWNE_HCMV_INFECTION_8HR_UP
24	10.41	NULL	2 / 12	GSEA C2LEE_METASTASIS_AND_ALTERNATIVE_SPLICING_DN
25	10.27	NULL	2 / 15	GSEA C2REACTOME_PHASE_II_CONJUGATION
26	10.26	NULL	1 / 9	GSEA C2ABDULRAHMAN_KIDNEY_CANCER_VHL_DN
27	10.26	NULL	1 / 9	GSEA C2REACTOME_ETHANOL_OXIDATION
28	10.08	NULL	2 / 9	GSEA C2REACTOME_GLUCURONIDATION
29	9.64	NULL	1 / 10	GSEA C2MAINA_VHL_TARGETS_UP
30	9.64	NULL	1 / 10	GSEA C2FRIDMAN_SENESCENCE_DN
31	9.31	NULL	3 / 15	BP lipid glycosylation
32	9.19	NULL	1 / 9	GSEA C2GOERING_BLOOD_HDL_CHOLESTEROL_QTL_CIS
33	9.18	NULL	3 / 12	GSEA C2BROCKE_APOPTOSIS_REVERSED_BY_IL6
34	9.05	NULL	1 / 11	GSEA C2YAMANAKA_GLIOMASTOMA_SURVIVAL_UP
35	8.61	NULL	2 / 11	GSEA C2DANG_MYC_TARGETS_UP
36	8.42	NULL	2 / 18	MF acyl-CoA dehydrogenase activity
37	8.39	NULL	2 / 10	GSEA C2ONRAD_STEM_CELL
38	8.36	NULL	3 / 16	GSEA C2SANA_RESPONSE_TO_IFNG_DN
39	8.25	NULL	2 / 16	GSEA C2LEE_LIVER_CANCER_MYC_TGFA_UP
40	7.89	NULL	1 / 14	MF Ras GTPase activator activity



# GW\_171

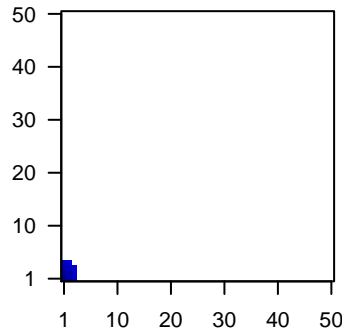
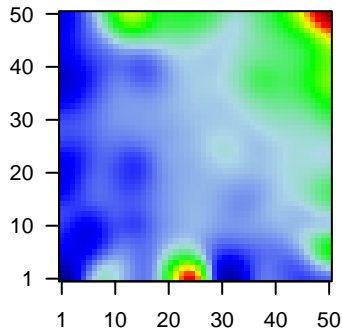
## Local Summary

%DE = 0.74  
 # metagenes = 11  
 # genes = 176  
 # genes in genesets = 176  
 # genes with  $fdr < 0.1 = 116$  ( 11 + / 105 - )  
 # genes with  $fdr < 0.05 = 109$  ( 10 + / 99 - )  
 # genes with  $fdr < 0.01 = 96$  ( 8 + / 88 - )

<r> metagenes = 0.98  
 <r> genes = 0.42  
 <FC> = -0.47  
 <shrinkage-t> = -16.4  
 <p-value> = 0  
 <fdr> = 0.37

Profile

Spot



## Local Genelist

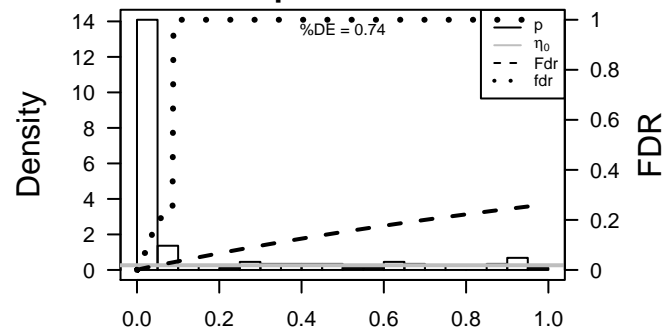
Rank	ID	log(FC)	fdr	p-value	Description
1	1277	-1.89	2e-16	9e-16	2 x 1 collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
2	1278	-1.49	2e-16	9e-16	2 x 1 collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198]
3	1281	-1.23	2e-16	9e-16	2 x 1 collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]
4	1289	-1.5	2e-16	9e-16	2 x 1 collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209]
5	1291	-1.67	2e-16	9e-16	2 x 1 collagen, type VI, alpha 1 [Source:HGNC Symbol;Acc:2211]
6	54541	-1.67	2e-16	9e-16	1 x 4 DNA-damage-inducible transcript 4 [Source:HGNC Symbol;Acc:54541]
7	4312	-1.5	2e-16	9e-16	1 x 1 matrix metalloproteinase 1 (interstitial collagenase) [Source:HGNC Symbol;Acc:4312]
8	4319	-1.75	2e-16	9e-16	1 x 3 matrix metalloproteinase 10 (stromelysin 2) [Source:HGNC Symbol;Acc:4319]
9	4316	-1.66	2e-16	9e-16	2 x 1 matrix metalloproteinase 7 (matrilysin, uterine) [Source:HGNC Symbol;Acc:4316]
10	4318	-1.81	2e-16	9e-16	1 x 1 matrix metalloproteinase 9 (gelatinase B, 92kDa gelatinase, 92kDa gelatinase with thrombospondin type 1 motifs) [Source:HGNC Symbol;Acc:4318]
11	4489	-1.27	2e-16	9e-16	1 x 4 metallothionein 1A [Source:HGNC Symbol;Acc:7393]
12	4502	-1.35	2e-16	9e-16	1 x 3 metallothionein 2A [Source:HGNC Symbol;Acc:7406]
13	1290	-1.32	1e-15	4e-13	2 x 1 collagen, type V, alpha 2 [Source:HGNC Symbol;Acc:2210]
14	7045	-1.16	1e-14	4e-13	1 x 2 transforming growth factor, beta-induced, 68kDa [Source:HGNC Symbol;Acc:7045]
15	10409	-1.26	2e-14	3e-11	1 x 2 brain abundant, membrane attached signal protein 1 [Source:HGNC Symbol;Acc:10409]
16	8406	1.17	1e-12	3e-11	2 x 1 sushi-repeat containing protein, X-linked [Source:HGNC Symbol;Acc:8406]
17	3956	-1.16	1e-12	1e-10	1 x 1 lectin, galactoside-binding, soluble, 1 [Source:HGNC Symbol;Acc:3956]
18	5270	1.13	6e-12	1e-10	1 x 3 serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1) member 1 [Source:HGNC Symbol;Acc:5270]
19	10631	-1.13	7e-12	5e-10	2 x 1 periostin, osteoblast specific factor [Source:HGNC Symbol;Acc:10631]
20	10630	-1.09	3e-11	5e-10	1 x 2 podoplanin [Source:HGNC Symbol;Acc:29602]

## Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-39.35	NULL	7 / 11	MF platelet-derived growth factor binding
2	-38.16	NULL	22 / 64	BP collagen catabolic process
3	-36.3	NULL	10 / 15	GSEA C2CROMER_TUMORIGENESIS_UP
4	-35.97	NULL	23 / 69	BP extracellular matrix disassembly
5	-33.57	NULL	9 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_5
6	-31.41	NULL	43 / 190	CC extracellular matrix
7	-29.26	NULL	5 / 10	GSEA C2KEGG_ECM_RECEPTOR_INTERACTION
8	-28.71	NULL	47 / 242	BP extracellular matrix organization
9	-26.87	NULL	4 / 10	BP protein heterotrimerization
10	-26.02	NULL	52 / 250	Lymphocyte-stromal interaction
11	-23.98	NULL	5 / 16	GSEA C2URS_ADIPOCYTE_DIFFERENTIATION_DN
12	-23.72	NULL	14 / 16	MMML C2CIEJ_MMML_1
13	-22.74	NULL	7 / 12	miRNA target-29c
14	-22.5	NULL	5 / 16	GSEA C2REACTOME_SIGNALING_BY_PDGF
15	-21.85	NULL	10 / 40	BP cellular response to amino acid stimulus
16	-21.37	NULL	12 / 37	BP collagen fibril organization
17	-20.57	NULL	7 / 15	GSEA C2ONDER_CDH1_TARGETS_2_UP
18	-20.5	NULL	6 / 10	GSEA C2VERRECCHIA_RESPONSE_TO_TGFB1_C4
19	-19.94	NULL	4 / 15	GSEA C2REACTOME_NCAM1_INTERACTIONS
20	-19.69	NULL	27 / 183	CC proteinaceous extracellular matrix
21	-19.35	NULL	8 / 16	GSEA C2ROZANOV_MMP14_TARGETS_SUBSET
22	-19.25	NULL	4 / 10	GSEA C2JEON_SMAD6_TARGETS_UP
23	-19.23	NULL	4 / 16	GSEA C2REACTOME_AXON_GUIDANCE
24	-19.23	NULL	4 / 16	GSEA C2REACTOME_NCAM_SIGNALING_FOR_NEURITE_OUT_GROWTH
25	-19.07	NULL	4 / 12	GSEA C2Y_AGING_MIDDLE_UP
26	-19.06	NULL	14 / 57	MF extracellular matrix structural constituent
27	-18.87	NULL	4 / 13	GSEA C2PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
28	-18.76	NULL	3 / 12	GSEA C2VERRECCHIA_RESPONSE_TO_TGFB1_C2
29	-18.32	NULL	3 / 8	GSEA C2HAEGERSTRAND_RESPONSE_TO_IMATINIB
30	-18.28	NULL	11 / 35	Glio Colman_survival_associated
31	-18.07	NULL	3 / 10	GSEA C2KEGG_FOCAL_ADHESION
32	-17.89	NULL	4 / 7	GSEA C2WANG_ESOPHAGUS_CANCER_PROGRESSION_UP
33	-17.83	NULL	2 / 6	Glio Martinez_Glio_hypometh
34	-17.61	NULL	2 / 5	GSEA C2DASU_IL6_SIGNALING_UP
35	-17.61	NULL	32 / 265	Glio wilscher_GBM_Verhaak-CL_expression_B_up
36	-17.61	NULL	32 / 265	Glio wilscher_GBM_Verhaak-MES_expression_B_up
37	-17.61	NULL	32 / 265	Glio wilscher_GBM_Verhaak-PNwt_expression_B_down
38	-17.61	NULL	32 / 265	Glio wilscher_GBM_Verhaak-PNmut_expression_B_down
39	-17.33	NULL	3 / 6	GSEA C2AGARWAL_AKT_PATHWAY_TARGETS
40	-17.32	NULL	4 / 11	BP dermatan sulfate biosynthetic process

p-values



# GW\_171

## Local Summary

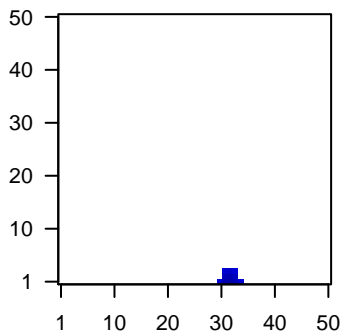
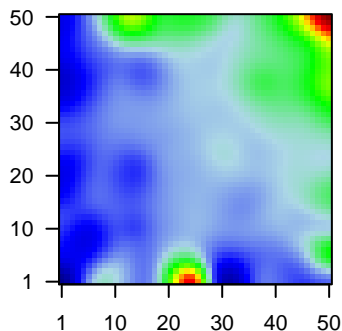
%DE = 0.77  
 # metagenes = 11  
 # genes = 140  
 # genes in genesets = 137  
 # genes with fdr < 0.1 = 91 ( 3 + / 88 - )  
 # genes with fdr < 0.05 = 85 ( 3 + / 82 - )  
 # genes with fdr < 0.01 = 58 ( 1 + / 57 - )

<r> metagenes = 0.99  
 <r> genes = 0.41

<FC> = -0.43  
 <shrinkage-t> = -15.16  
 <p-value> = 0  
 <fdr> = 0.43

Profile

Spot



## Local Genelist

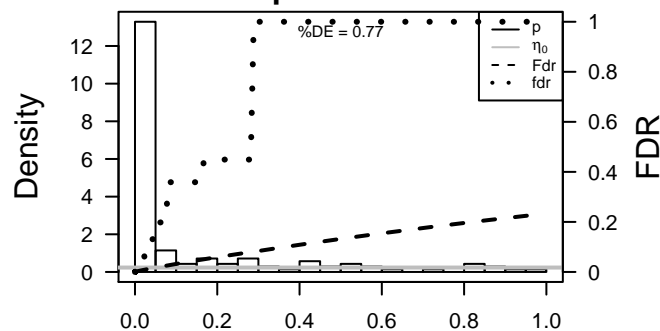
Rank	ID	log(FC)	fdr	p-value	Description
1	684	-1.82	2e-16	4e-15	32 x 1 bone marrow stromal cell antigen 2 [Source:HGNC Symbol;A
2	94240	-1.42	2e-16	4e-15	32 x 1 epithelial stromal interaction 1 (breast) [Source:HGNC Symbc
3	4061	-1.33	4e-16	2e-10	32 x 1 lymphocyte antigen 6 complex, locus E [Source:HGNC Symb
4	3627	-1.13	5e-12	5e-10	32 x 1 chemokine (C-X-C motif) ligand 10 [Source:HGNC Symbol;#
5	79156	-1.1	2e-11	2e-08	31 x 1 pleckstrin homology domain containing, family F (with FYVE c
6	8519	-1.02	6e-10	4e-08	32 x 1 interferon induced transmembrane protein 1 [Source:HGNC S
7	1591	-0.99	2e-09	7e-07	33 x 2 cytochrome P450, family 24, subfamily A, polypeptide 1 [Sou
8	54739	-0.91	3e-08	7e-07	32 x 1 XIAP associated factor 1 [Source:HGNC Symbol;Acc:30932]
9	51296	-0.9	4e-08	1e-06	32 x 1 solute carrier family 15 (oligopeptide transporter), member 3
10	5721	-0.88	1e-07	1e-06	32 x 1 proteasome (prosome, macropain) activator subunit 2 (PA28 I
11	9536	-0.86	2e-07	1e-06	31 x 2 prostaglandin E synthase [Source:HGNC Symbol;Acc:9599]
12	3665	-0.86	2e-07	1e-06	32 x 1 interferon regulatory factor 7 [Source:HGNC Symbol;Acc:612
13	10410	-0.79	2e-07	1e-06	32 x 1 interferon induced transmembrane protein 3 [Source:HGNC S
14	9560	-0.85	2e-07	2e-06	32 x 1 chemokine (C-C motif) ligand 4-like 1 [Source:HGNC Symbc
15	54922	-0.85	3e-07	6e-06	30 x 1 Ras interacting protein 1 [Source:HGNC Symbol;Acc:24716]
16	10561	-0.83	4e-07	1e-05	32 x 1 interferon-induced protein 44 [Source:HGNC Symbol;Acc:16:
17	219285	-0.81	1e-06	1e-05	32 x 1 sterile alpha motif domain containing 9-like [Source:HGNC S
18	83666	-0.8	1e-06	1e-05	32 x 1 poly (ADP-ribose) polymerase family, member 9 [Source:HGI
19	10964	-0.79	1e-06	2e-05	32 x 1 interferon-induced protein 44-like [Source:HGNC Symbol;Ac
20	54436	-0.77	3e-06	2e-05	33 x 3 SH3 domain and tetratricopeptide repeats 1 [Source:HGNC S

## Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-40.4	NULL	29 / 51	BP type I interferon signaling pathway
2	-34.73	NULL	8 / 10	GSEA C2GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
3	-33.03	NULL	11 / 16	GSEA C2UROSEVIC_RESPONSE_TO_IMIQUMOD
4	-32.54	NULL	9 / 10	GSEA C2BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
5	-30.57	NULL	11 / 16	GSEA C2EINAV_INTERFERON_SIGNATURE_IN_CANCER
6	-30.35	NULL	10 / 13	GSEA C2BOWIE_RESPONSE_TO_TAMOXIFEN
7	-29.42	NULL	11 / 16	GSEA C2ZHANG_INTERFERON_RESPONSE
8	-29.4	NULL	13 / 16	GSEA C2MOSELERLE_IFNA_RESPONSE
9	-28.73	NULL	6 / 6	LymphomA15_MHCCII_BL_DN
10	-26.29	NULL	27 / 109	BP response to virus
11	-24.02	NULL	6 / 8	GSEA C2ROETH_TERT_TARGETS_UP
12	-23.73	NULL	13 / 31	BP negative regulation of viral genome replication
13	-23.7	NULL	7 / 16	GSEA C2MAHADEVAN_RESPONSE_TO_MP470_UP
14	-23.32	NULL	31 / 123	BP defense response to virus
15	-23.13	NULL	5 / 18	BP response to interferon-gamma
16	-22.06	NULL	6 / 14	GSEA C2RADAIEVA_RESPONSE_TO_IFNA1_UP
17	-21.67	NULL	7 / 10	CC MHC class I protein complex
18	-20.4	NULL	34 / 204	BP cytokine-mediated signaling pathway
19	-20.1	NULL	5 / 16	GSEA C2ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_UP
20	-20	NULL	33 / 274	LymphomA15_PANG_IL21_DN
21	-18.78	NULL	3 / 16	GSEA C2NOJIMA_SFRP2_TARGETS_DN
22	-18.5	NULL	5 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_1
23	-18.02	NULL	4 / 15	GSEA C2BECKER_TAMOXIFEN_RESISTANCE_UP
24	-17.68	NULL	3 / 4	GSEA C2KRASNOSELSKAYA_ILF3_TARGETS_UP
25	-17.53	NULL	16 / 60	BP interferon-gamma-mediated signaling pathway
26	-16.68	NULL	2 / 15	GSEA C2CHOW_RASSF1_TARGETS_DN
27	-16.57	NULL	6 / 12	GSEA C2TSAI_DNAJB4_TARGETS_UP
28	-16.55	NULL	3 / 11	GSEA C2WHITESIDE_CISPLATIN_RESISTANCE_UP
29	-16.35	NULL	48 / 572	Disease GUDJ_psooriasis_up
30	-16.08	NULL	6 / 14	Glio Donson-immune cell intra signaling-associated with LTS in HGA
31	-16.03	NULL	5 / 16	GSEA C2ZHAN_MULTIPLE_MYELOMA_LB_DN
32	-15.43	NULL	2 / 2	MMML C6SCIEJ_MMML_27
33	-15.29	NULL	8 / 18	BP positive regulation of T cell mediated cytotoxicity
34	-15.28	NULL	4 / 14	GSEA C2TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_8D_UP
35	-15.16	NULL	7 / 18	MF peptide antigen binding
36	-14.89	NULL	3 / 13	GSEA C2TSAI_RESPONSE_TO_RADIATION_THERAPY
37	-14.69	NULL	3 / 5	GSEA C2KIM_LRRC3B_TARGETS
38	-14.26	NULL	3 / 6	GSEA C2SHIKAWA_STING_SIGNALING
39	-13.9	NULL	28 / 312	BP immune response
40	-13.79	NULL	3 / 9	GSEA C2FURUKAWA_DUSP6_TARGETS_PC135_UP

p-values



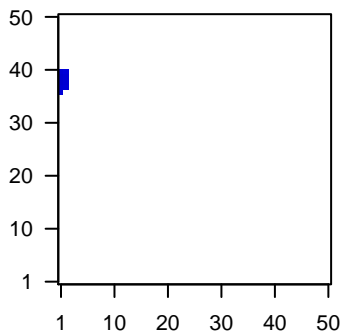
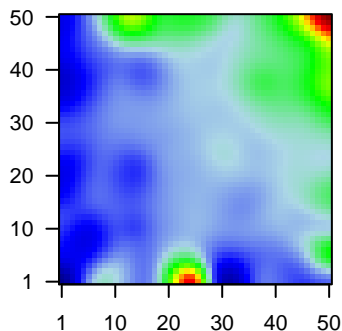
# GW\_171

## Local Summary

%DE = 0.7  
 # metagenes = 9  
 # genes = 133  
 # genes in genesets = 130  
  
 # genes with  $fdr < 0.1$  = 46 ( 0 + / 46 - )  
 # genes with  $fdr < 0.05$  = 46 ( 0 + / 46 - )  
 # genes with  $fdr < 0.01$  = 35 ( 0 + / 35 - )  
  
 $\langle r \rangle$  metagenes = 0.98  
 $\langle r \rangle$  genes = 0.27  
  
 $\langle FC \rangle = -0.31$   
 $\langle \text{shrinkage-t} \rangle = -10.9$   
 $\langle p\text{-value} \rangle = 0.01$   
 $\langle fdr \rangle = 0.64$

Profile

Spot



## Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	780854	-1.21	2e-13	2e-10	2 x 39 small nucleolar RNA, C/D box 3D [Source:HGNC Symbol;Acc:6467]
2	2760	-1.13	6e-12	3e-10	1 x 40 GM2 ganglioside activator [Source:HGNC Symbol;Acc:4367]
3	8942	-1.11	1e-11	5e-07	1 x 40 kynureninase [Source:HGNC Symbol;Acc:6469]
4	1984	-0.94	1e-08	3e-05	1 x 37 eukaryotic translation initiation factor 5A [Source:HGNC Syml
5	2196	-0.81	8e-07	1e-04	1 x 40 FAT atypical cadherin 2 [Source:HGNC Symbol;Acc:3596]
6	80326	-0.76	4e-06	1e-04	1 x 40 wingless-type MMTV integration site family, member 10A [So
7	780851	-0.74	7e-06	1e-04	2 x 39 small nucleolar RNA, C/D box 3A [Source:HGNC Symbol;Acc
8	2731	-0.73	9e-06	1e-04	1 x 38 glycine dehydrogenase (decarboxylating) [Source:HGNC Syn
9	645	-0.72	1e-05	2e-04	1 x 36 biliverdin reductase B (flavin reductase (NADPH)) [Source:HC
10	112399	-0.71	2e-05	5e-04	1 x 40 egl-9 family hypoxia-inducible factor 3 [Source:HGNC Symb
11	780853	-0.69	3e-05	5e-04	2 x 39 small nucleolar RNA, C/D box 3C [Source:HGNC Symbol;Acc
12	135398	-0.67	4e-05	6e-04	1 x 40 chromosome 6 open reading frame 141 [Source:HGNC Synt
13	54795	-0.65	8e-05	6e-04	1 x 36 transient receptor potential cation channel, subfamily M, merr
14	79148	-0.65	8e-05	6e-04	1 x 39 matrix metalloproteinase 28 [Source:HGNC Symbol;Acc:1436
15	80117	-0.64	9e-05	7e-04	2 x 40 ADP-ribosylation factor-like 14 [Source:HGNC Symbol;Acc:2
16	80256	-0.63	1e-04	7e-04	1 x 37 family with sequence similarity 214, member B [Source:HGNC
17	9052	-0.63	1e-04	2e-03	1 x 40 G protein-coupled receptor, family C, group 5, member A [So
18	83442	-0.61	2e-04	2e-03	1 x 36 SH3 domain binding glutamic acid-rich protein like 3 [Source
19	26027	-0.59	3e-04	2e-03	1 x 37 acyl-CoA thioesterase 11 [Source:HGNC Symbol;Acc:18156
20	27242	-0.58	4e-04	2e-03	1 x 40 tumor necrosis factor receptor superfamily, member 21 [Sour

## Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	C21CIEJ_MMML	-19.65	1 / 2	MMML C21CIEJ_MMML_43
2	C21E1_MYB_TARGETS	-13.47	2 / 11	GSEA C21E1_MYB_TARGETS
3	C25MID_BREAST_CANCER_RELAPSE_IN_LIVER_UP	-12.7	1 / 6	GSEA C25MID_BREAST_CANCER_RELAPSE_IN_LIVER_UP
4	target-mir-6468	-10.24	2 / 5	miRNA target-mir-6468
5	target-mir-659	-9.76	1 / 2	miRNA target-mir-659
6	BP	-9.74	1 / 10	BP neurological system process
7	BP	-9.6	1 / 10	BP tryptophan catabolic process
8	C25ESTO_RESPONSE_TO_UV_C3	-8.93	3 / 12	GSEA C25ESTO_RESPONSE_TO_UV_C3
9	BP	-8.31	1 / 13	BP NAD biosynthetic process
10	MF	-8.1	1 / 14	MF lipid transporter activity
11	C27FARMER_BREAST_CANCER_CLUSTER_3	-7.67	1 / 15	GSEA C27FARMER_BREAST_CANCER_CLUSTER_3
12	C27FARMER_BREAST_CANCER_CLUSTER_4	-7.4	1 / 16	GSEA C27FARMER_BREAST_CANCER_CLUSTER_4
13	C27EGG_AMINO_SUGAR_AND_NUCLEOTIDE_SUGAR_METABOL	-7.27	3 / 15	GSEA C27EGG_AMINO_SUGAR_AND_NUCLEOTIDE_SUGAR_METABOL
14	BP	-7.27	1 / 17	BP lipid storage
15	C21_LUNG_CANCER	-7.26	1 / 12	GSEA C21_LUNG_CANCER
16	target-mir-639	-7.26	1 / 12	miRNA target-mir-639
17	BP	-7.2	2 / 10	BP positive regulation of keratinocyte differentiation
18	C2DAZARD_UV_RESPONSE_CLUSTER_G2	-7.15	2 / 14	GSEA C2DAZARD_UV_RESPONSE_CLUSTER_G2
19	C25MID_BREAST_CANCER_NORMAL_LIKE_DN	-7.11	1 / 6	GSEA C25MID_BREAST_CANCER_NORMAL_LIKE_DN
20	C2AMUNDSON_DNA_DAMAGE_RESPONSE_TP53	-7.09	3 / 16	GSEA C2AMUNDSON_DNA_DAMAGE_RESPONSE_TP53
21	BP	-7.08	2 / 36	BP learning or memory
22	C2COLLER_MYC_TARGETS_UP	-6.94	1 / 13	GSEA C2COLLER_MYC_TARGETS_UP
23	C27REACTOME_POST_TRANSLATIONAL_PROTEIN_MODIFICATIO	-6.94	1 / 13	GSEA C27REACTOME_POST_TRANSLATIONAL_PROTEIN_MODIFICATIO
24	BP	-6.93	1 / 18	BP response to interferon-gamma
25	C2NIELSEN_LEIOMYOSARCOMA_UP	-6.86	1 / 6	GSEA C2NIELSEN_LEIOMYOSARCOMA_UP
26	MF	-6.76	2 / 48	MF pyridoxal phosphate binding
27	MF	-6.68	4 / 79	MF electron carrier activity
28	C2WATANABE_COLON_CANCER_MSI_VS_MSS_UP	-6.66	1 / 14	GSEA C2WATANABE_COLON_CANCER_MSI_VS_MSS_UP
29	C2RADAEVA_RESPONSE_TO_IFNA1_DN	-6.43	1 / 5	GSEA C2RADAEVA_RESPONSE_TO_IFNA1_DN
30	C2TIEN_INTESTINE_PROBIOTICS_6HR_UP	-6.41	1 / 15	GSEA C2TIEN_INTESTINE_PROBIOTICS_6HR_UP
31	C2FRASOR_TAMOXIFEN_RESPONSE_DN	-6.19	2 / 10	GSEA C2FRASOR_TAMOXIFEN_RESPONSE_DN
32	C2TIEN_INTESTINE_PROBIOTICS_2HR_UP	-6.18	1 / 16	GSEA C2TIEN_INTESTINE_PROBIOTICS_2HR_UP
33	C2ELVIDGE_HIF1A_AND_HIF2A_TARGETS_DN	-6.18	1 / 16	GSEA C2ELVIDGE_HIF1A_AND_HIF2A_TARGETS_DN
34	C2LIN_APC_TARGETS	-6.18	1 / 16	GSEA C2LIN_APC_TARGETS
35	MF	-6.15	1 / 10	MF 3-beta-hydroxy-delta5-steroid dehydrogenase activity
36	C2LUI_THYROID_CANCER_CLUSTER_5	-6.15	1 / 10	GSEA C2LUI_THYROID_CANCER_CLUSTER_5
37	C2BIOCARTA_IL10_PATHWAY	-6.15	1 / 10	GSEA C2BIOCARTA_IL10_PATHWAY
38	C2AMIT_EGF_RESPONSE_120_MCF10A	-6.03	2 / 16	GSEA C2AMIT_EGF_RESPONSE_120_MCF10A
39	target-mir-635	-5.97	4 / 27	miRNA target-mir-635
40	Disease	-5.78	14 / 572	Disease GUDJ_pсориазис up

p-values

