

Expression profiling of nemaline myopathy: Sanoudou et al.
Web supplement "ReINet 2". Relevance network analysis of 206 "reliably changed" probe sets
across 21 normal skeletal muscle specimens at CCC > 0.8.

Relevance Networks

by Atul Butte, MD <atul_butte@harvard.edu>

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Please cite Butte AJ, et al., Proceedings of the National Academy of Science USA 97(22):12182-6, 2000.

Analysis

Associations computed: 13:23 09/30/2002

Networks constructed: 13:44 09/30/2002

Dissimilarity measure: r

Minimum number of points needed for dissimilarity calculation: 5

Ignore negative and zero expression measures: FALSE

Set negative expression measures to zero: FALSE

Only use points with pairs of P calls in dissimilarity calculations: FALSE

Normalization: none

Parameters used

Keep associations greater than: 0.8

Keep associations less than: -0.8

General description

Number of networks: 19

Number of features (genes): 202

Number of features (genes) used: 59

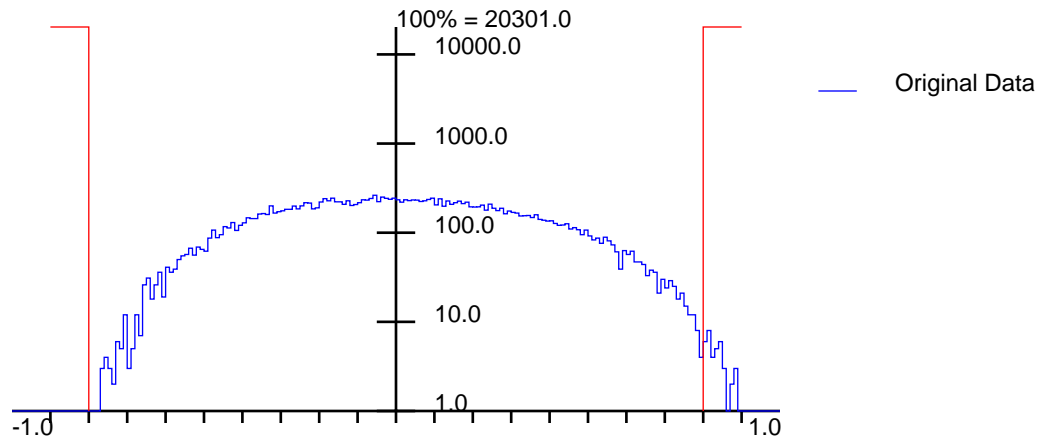
Total number of edges possible between 202 features (genes): 20301

Number of edges left after analysis: 43

Absolute value of strongest link from any of the 59 nodes used in this analysis: 0.9602087

Absolute value of weakest link from any of the 59 nodes used in this analysis: 0.8045203

Histogram



Data ranges from -0.81874144 to 0.9602087.

Samples Used (21 samples)

C:\Documents and Settings\Guest\Desktop\S+83Norm.Unnorm.txt_1

C:\Documents and Settings\Guest\Desktop\S+83Norm.Unnorm.txt_2

C:\Documents and Settings\Guest\Desktop\S+83Norm.Unnorm.txt_3

C:\Documents and Settings\Guest\Desktop\S+83Norm.Unnorm.txt_4

C:\Documents and Settings\Guest\Desktop\S+83Norm.Unnorm.txt_5

C:\Documents and Settings\Guest\Desktop\S+83Norm.Unnorm.txt_6

C:\Documents and Settings\Guest\Desktop\S+83Norm.Unnorm.txt_7

C:\Documents and Settings\Guest\Desktop\S+83Norm.Unnorm.txt_8

C:\Documents and Settings\Guest\Desktop\S+83Norm.Unnorm.txt_9

C:\Documents and Settings\Guest\Desktop\S+83Norm.Unnorm.txt_10

C:\Documents and Settings\Guest\Desktop\S+83Norm.Unnorm.txt_11

C:\Documents and Settings\Guest\Desktop\S+83Norm.Unnorm.txt_12

C:\Documents and Settings\Guest\Desktop\S+83Norm.Unnorm.txt_13

C:\Documents and Settings\Guest\Desktop\S+83Norm.Unnorm.txt_14

C:\Documents and Settings\Guest\Desktop\S+83Norm.Unnorm.txt_15

C:\Documents and Settings\Guest\Desktop\S+83Norm.Unnorm.txt_16

C:\Documents and Settings\Guest\Desktop\S+83Norm.Unnorm.txt_17

C:\Documents and Settings\Guest\Desktop\S+83Norm.Unnorm.txt_18

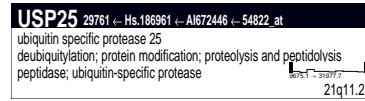
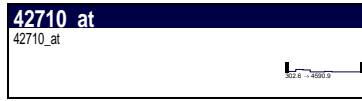
C:\Documents and Settings\Guest\Desktop\S+83Norm.Unnorm.txt_19

C:\Documents and Settings\Guest\Desktop\S+83Norm.Unnorm.txt_20

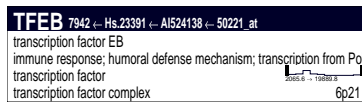
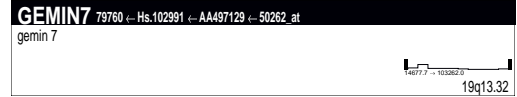
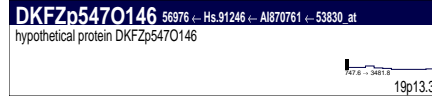
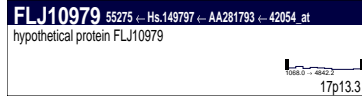
C:\Documents and Settings\Guest\Desktop\S+83Norm.Unnorm.txt_21

Network Table of Contents

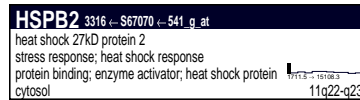
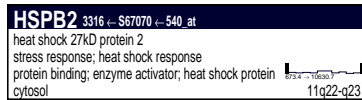
Network 1 (size 3)



Network 2 (size 5)



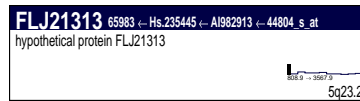
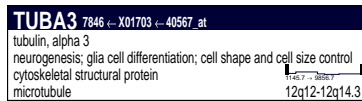
Network 3 (size 2)



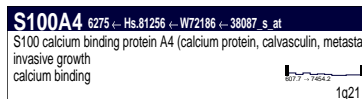
Network 4 (size 2)



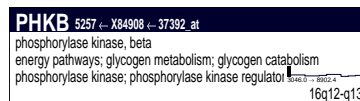
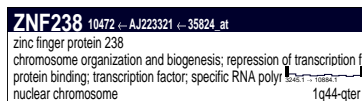
Network 5 (size 2)



Network 6 (size 2)




Network 7 (size 2)




Network 8 (size 2)

MAGED2 10916 ← Z38046 ← 34860_g_at
melanoma antigen, family D, 2



Xp11.4-p11.1

FLJ20811 54470 ← Hs.83530 ← AA015605 ← 38440_s_at
hypothetical protein FLJ20811




Xq21.33-q22.3

Network 9 (size 2)

LDHB 3945 ← X13794 ← 33819_at
lactate dehydrogenase B

L-lactate dehydrogenase




12p12.2-p12.1

43827_s_at
43827_s_at




Network 10 (size 2)

PEA15 8682 ← Hs.194673 ← X86809 ← 32260_at
phosphoprotein enriched in astrocytes 15
small molecule transport



1q21.1

AK3 205 ← Hs.274691 ← AW015546 ← 48822_s_at
adenylate kinase 3
nucleobase, nucleoside, nucleotide and nucleic acid metabolism




1

Network 11 (size 8)

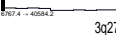
DAF 1604 ← M31516 ← 38895_at
decay accelerating factor for complement (CD55, Cromer blood group system)

soluble fraction; integral plasma membrane protein




1q32

BCL6 604 ← U00115 ← 40891_at
B-cell CLL/lymphoma 6 (zinc finger protein 51)
oncogenesis; inflammatory response; transcription regulation; positive control of cell proliferation; repression of transcription factor mediator complex



3q27

GLUL 2752 ← X59834 ← 40522_at
glutamate-ammonia ligase (glutamine synthase)
glutamine biosynthesis; neurotransmitter maintenance




1q31

48063_at
48063_at




45773_at
45773_at




46699_at
46699_at



50763_at
50763_at




KIAA1917 114804 ← Hs.294151 ← A1745248 ← 44600_at
KIAA1917 protein



17q25.3

Network 12 (size 3)

SH3GLB1 51100 ← AB007960 ← 39691_at
SH3-domain GRB2-like endophilin B1



1p22


USP24 23358 ← AB028980 ← 35847_at
ubiquitin specific protease 24



1p32.2

OPTN 10133 ← AF070533 ← 41744_at
optineurin
cell death; pathogenesis; signal transduction


cytoplasm



10p12.33

Network 13 (size 2)


FTHFD 10840 ← AF052732 ← 38316_at
formyltetrahydrofolate dehydrogenase
10-formyltetrahydrofolate catabolism
enzyme; electron transporter



3q21.3

RAF1 5894 ← X03484 ← 1917_at
v-raf-1 murine leukemia viral oncogene homolog 1
apoptosis; oncogenesis; cell proliferation; signal transduction; protein tyrosine kinase


mitochondrial outer membrane



3p25

Network 14 (size 3)

LSP1 4046 ← M33552 ← 36493_at
lymphocyte-specific protein 1
cell motility; cellular defense response; cell shape and cell size control
actin binding
actin cytoskeleton



11p15.5


54980_at
54980_at




55894_at
55894_at





Network 15 (size 2)


P7OV1 53635 ← Hs.19555 ← W25984 ← 32130_at
 prostate tumor over expressed gene 1


RERE 473 ← AB007927 ← 32253_at
 arginine-glutamic acid dipeptide (RE) repeats
 NLS-bearing substrate-nucleus import
 molecular_function unknown; poly-glutamine tract bind
 nucleus


Network 16 (size 4)


UBE2D1 7321 ← AF020761 ← 37826_at
 ubiquitin-conjugating enzyme E2D 1 (UBC4/5 homolog, yeast)
 ubiquitin-dependent protein degradation
 ubiquitin-protein ligase; ubiquitin conjugating enzyme



ZNF161 7716 ← D28118 ← 350_at
 zinc finger protein 161
 cellular defense response; transcription regulation from Pol II promoter
 specific RNA polymerase II transcription factor



ZNF161 7716 ← D28118 ← 32828_at
 zinc finger protein 161
 cellular defense response; transcription regulation from Pol II promoter
 specific RNA polymerase II transcription factor


55989 at
 55989_at


Network 17 (size 5)

UCP3 7352 ← U84763 ← 34420_at
 uncoupling protein 3 (mitochondrial, proton carrier)
 respiration; energy pathways; lipid metabolism; proton transport
 transporter; uncoupling protein
 mitochondrion; membrane fraction; mitochondrial inner membrane



UCP3 7352 ← U84763 ← 34421_g_at
 uncoupling protein 3 (mitochondrial, proton carrier)
 respiration; energy pathways; lipid metabolism; proton transport
 transporter; uncoupling protein
 mitochondrion; membrane fraction; mitochondrial inner membr.



UCP3 7352 ← U82818 ← 34422_r_at
 uncoupling protein 3 (mitochondrial, proton carrier)
 respiration; energy pathways; lipid metabolism; proton transport
 transporter; uncoupling protein
 mitochondrion; membrane fraction; mitochondrial inner membrane


54028 at
 54028_at


46671 at
 46671_at


Network 18 (size 5)

PFKFB1 5207 ← X52638 ← 33980_at
 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 1
 fructose 2,6-bisphosphate metabolism
 fructose-2,6-bisphosphate 2-phosphatase



FBP2 8789 ← Y10812 ← 40293_at
 fructose-1,6-bisphosphatase 2
 fructose metabolism
 fructose-bisphosphatase



50751 at
 50751_at



44112 at
 44112_at


PGM1 5236 ← M83088 ← 32210_at
 phosphoglucomutase 1


Network 19 (size 3)

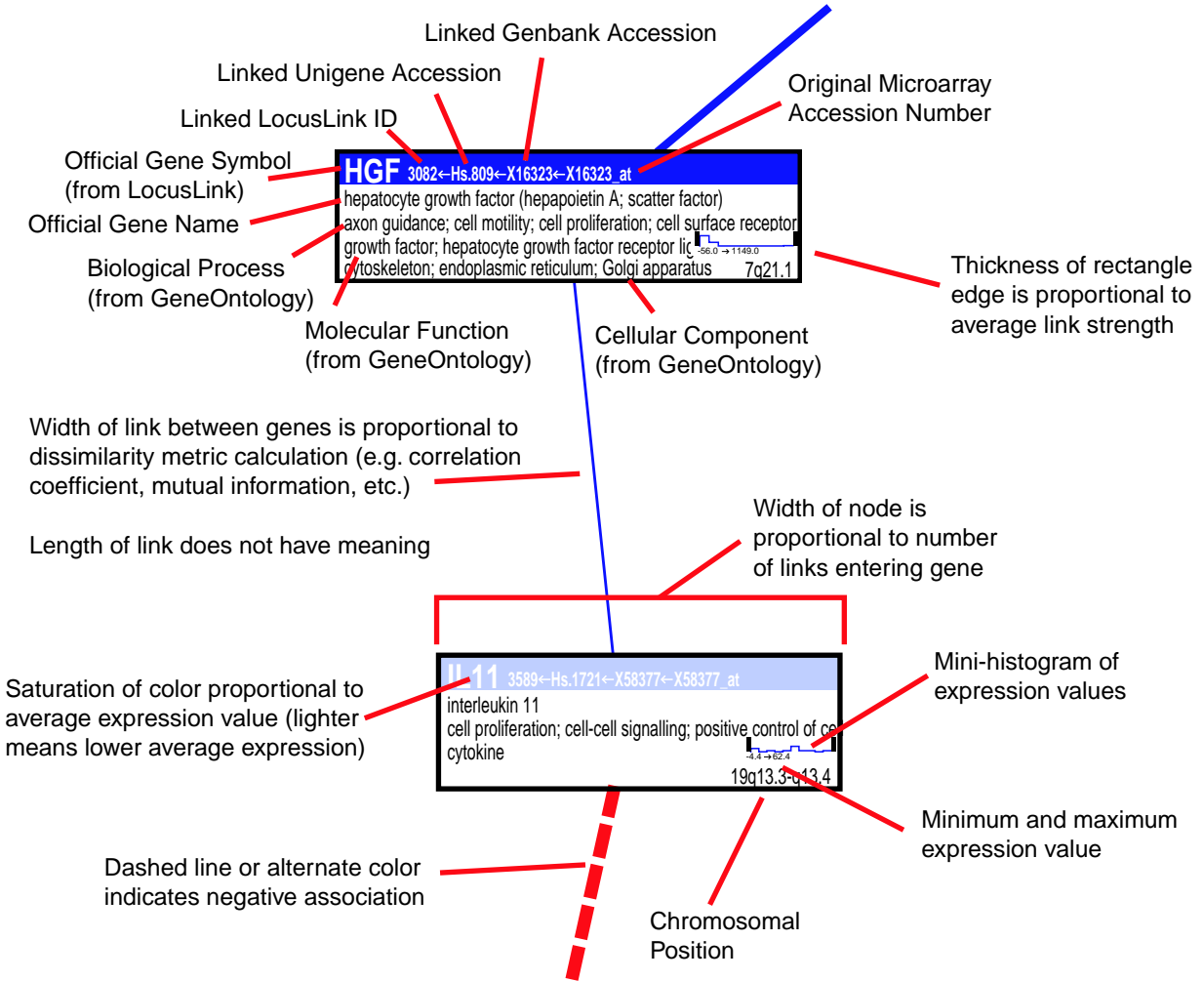
LKAP 9665 ← AB007890 ← 31936_s_at
 limkain b1


UBE4A 9354 ← D50916 ← 36579_at
 ubiquitination factor E4A (UFD2 homolog, yeast)
 ubiquitin-dependent protein degradation
 ubiquitin conjugating enzyme
 ubiquitin ligase complex


SIRT1 23411 ← Hs.31176 ← AI381553 ← 46399_at
 sirtuin silent mating type information regulation 2 homolog 1 (S. cerevis)
 chromatin silencing; protein ADP-ribosylation
 NAD(+) ADP-ribosyltransferase


End of Network Table of Contents

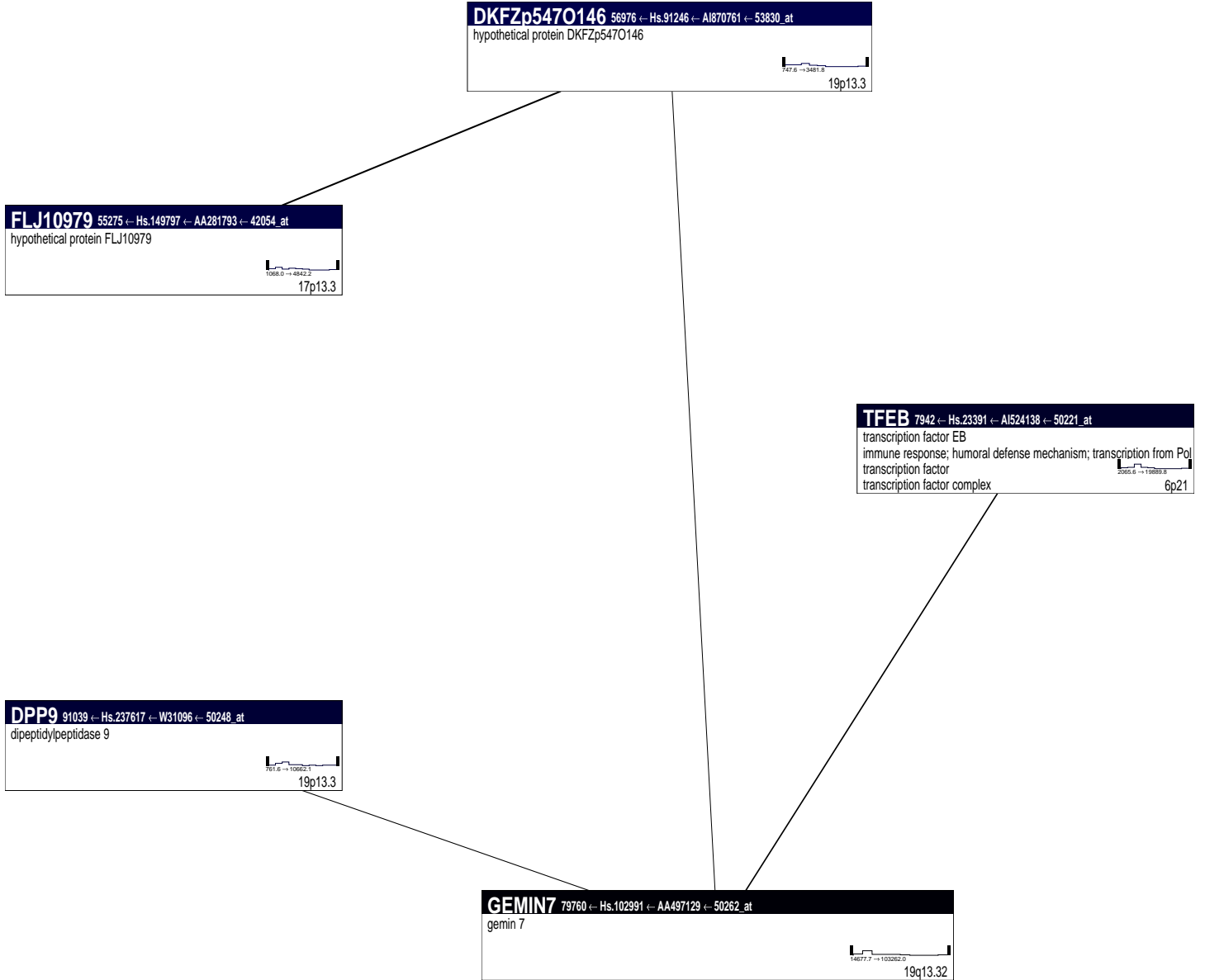
Relevance Networks Legend



USP25 29761 ← Hs.186961 ← AI672446 ← 54822_at
ubiquitin specific protease 25
deubiquitylation; protein modification; proteolysis and peptidolysis
peptidase; ubiquitin-specific protease
9675.1 → 31977.7
21q11.2

42711 g at
42711_g_at
2509.9 → 18028.3

42710 at
42710_at
302.6 → 4590.9



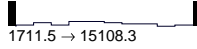
HSPB2 3316 ← S67070 ← 541_g_at

heat shock 27kD protein 2

stress response; heat shock response

protein binding; enzyme activator; heat shock protein

cytosol



11q22-q23

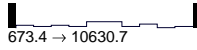
HSPB2 3316 ← S67070 ← 540_at

heat shock 27kD protein 2

stress response; heat shock response

protein binding; enzyme activator; heat shock protein

cytosol



11q22-q23

48287 at

48287_at



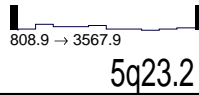
1164 at

1164_at



FLJ21313 65983 ← Hs.235445 ← AI982913 ← 44804_s_at

hypothetical protein FLJ21313



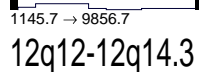
TUBA3 7846 ← X01703 ← 40567_at

tubulin, alpha 3

neurogenesis; glia cell differentiation; cell shape and cell size control

cytoskeletal structural protein

microtubule



45786 at

45786_at



S100A4 6275 ← Hs.81256 ← W72186 ← 38087_s_at

S100 calcium binding protein A4 (calcium protein, calvasculin, metastas
invasive growth
calcium binding



1q21

PHKB 5257 ← X84908 ← 37392_at

phosphorylase kinase, beta

energy pathways; glycogen metabolism; glycogen catabolism

phosphorylase kinase; phosphorylase kinase regulator

3046.0 → 8902.4

16q12-q13

ZNF238 10472 ← AJ223321 ← 35824_at

zinc finger protein 238

chromosome organization and biogenesis; repression of transcription fr

protein binding; transcription factor; specific RNA polyr

3245.1 → 10884.1

nuclear chromosome

1q44-qter

FLJ20811 54470 ← Hs.83530 ← AA015605 ← 38440_s_at

hypothetical protein FLJ20811

158.2 → 2165.4
Xq21.33-q22.3

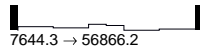
MAGED2 10916 ← Z98046 ← 34860_g_at

melanoma antigen, family D, 2

3675.3 → 18475.5
Xp11.4-p11.1

43827 s at

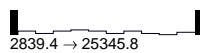
43827_s_at



LDHB 3945 ← X13794 ← 33819_at

lactate dehydrogenase B

L-lactate dehydrogenase



12p12.2-p12.1

AK3 205 ← Hs.274691 ← AW015546 ← 48822_s_at

adenylate kinase 3

nucleobase, nucleoside, nucleotide and nucleic acid metabolism

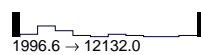


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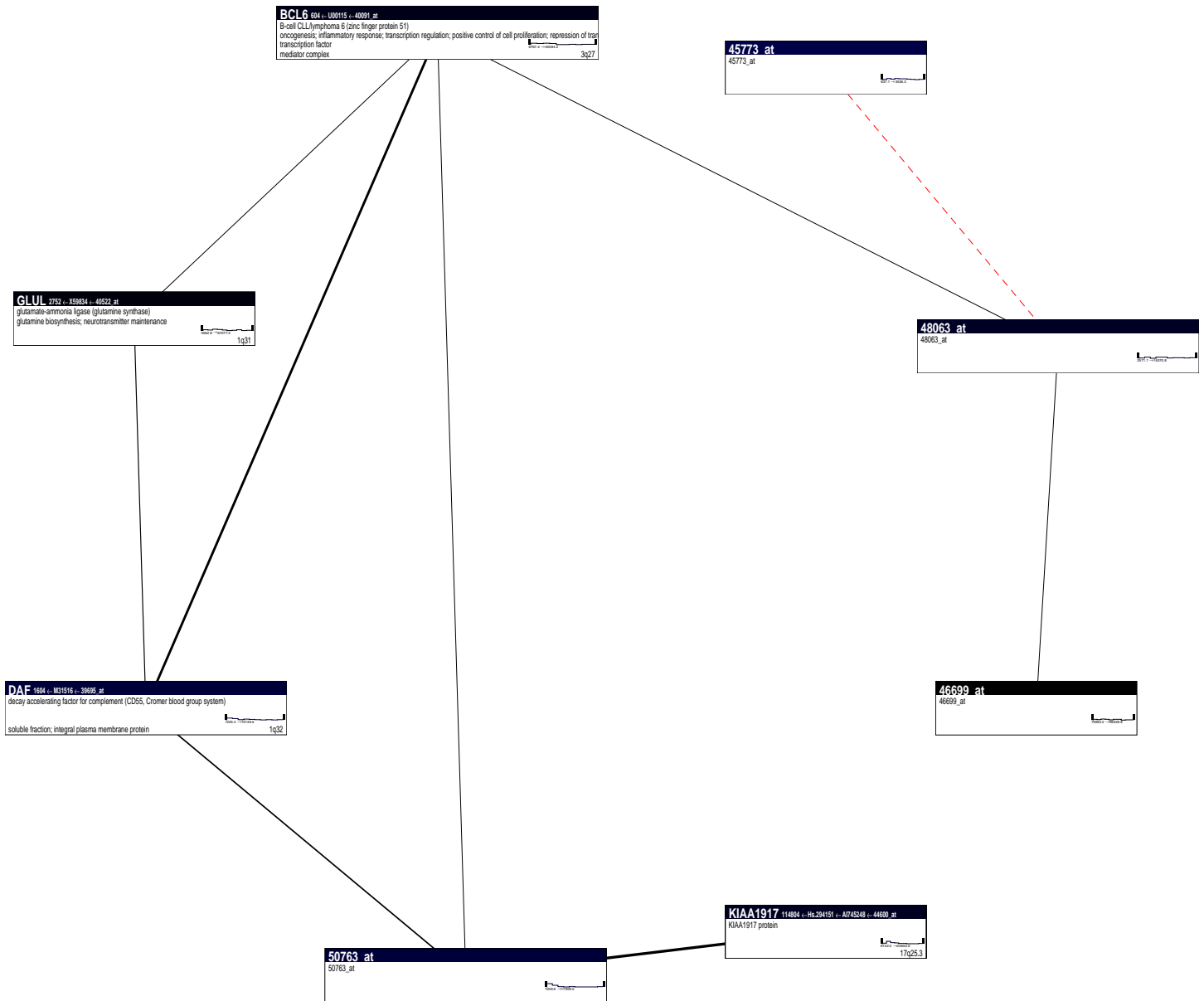
PEA15 8682 ← Hs.194673 ← X86809 ← 32260_at

phosphoprotein enriched in astrocytes 15

small molecule transport



1q21.1



SH3GLB1 51100 ← AB007960 ← 39691_at
SH3-domain GRB2-like endophilin B1
4701.2 → 16553.8
1p22

USP24 23358 ← AB028980 ← 35847_at
ubiquitin specific protease 24
2474.5 → 11267.6
1p32.2

OPTN 10133 ← AF070533 ← 41744_at
optineurin
cell death; pathogenesis; signal transduction
3321.1 → 19431.2
10p12.33

RAF1 5894 ← X03484 ← 1917_at

v-raf-1 murine leukemia viral oncogene homolog 1
apoptosis; oncogenesis; cell proliferation; signal transduction; protein p
protein kinase
mitochondrial outer membrane

1302.3 → 9729.3

3p25

FTHFD 10840 ← AF052732 ← 38316_at

formyltetrahydrofolate dehydrogenase
10-formyltetrahydrofolate catabolism
enzyme; electron transporter

702.0 → 4801.8

3q21.3

55894 at

55894_at



54980 at

54980_at



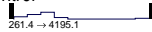
LSP1 4046 ← M33552 ← 36493_at

lymphocyte-specific protein 1

cell motility; cellular defense response; cell shape and cell size control

actin binding

actin cytoskeleton



11p15.5

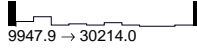
RERE 473 ← AB007927 ← 32253_at

arginine-glutamic acid dipeptide (RE) repeats

NLS-bearing substrate-nucleus import

molecular_function unknown; poly-glutamine tract bind

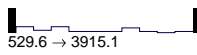
nucleus



1p36.1-p36.2

PTOV1 53635 ← Hs.19555 ← W25984 ← 32130_at

prostate tumor over expressed gene 1



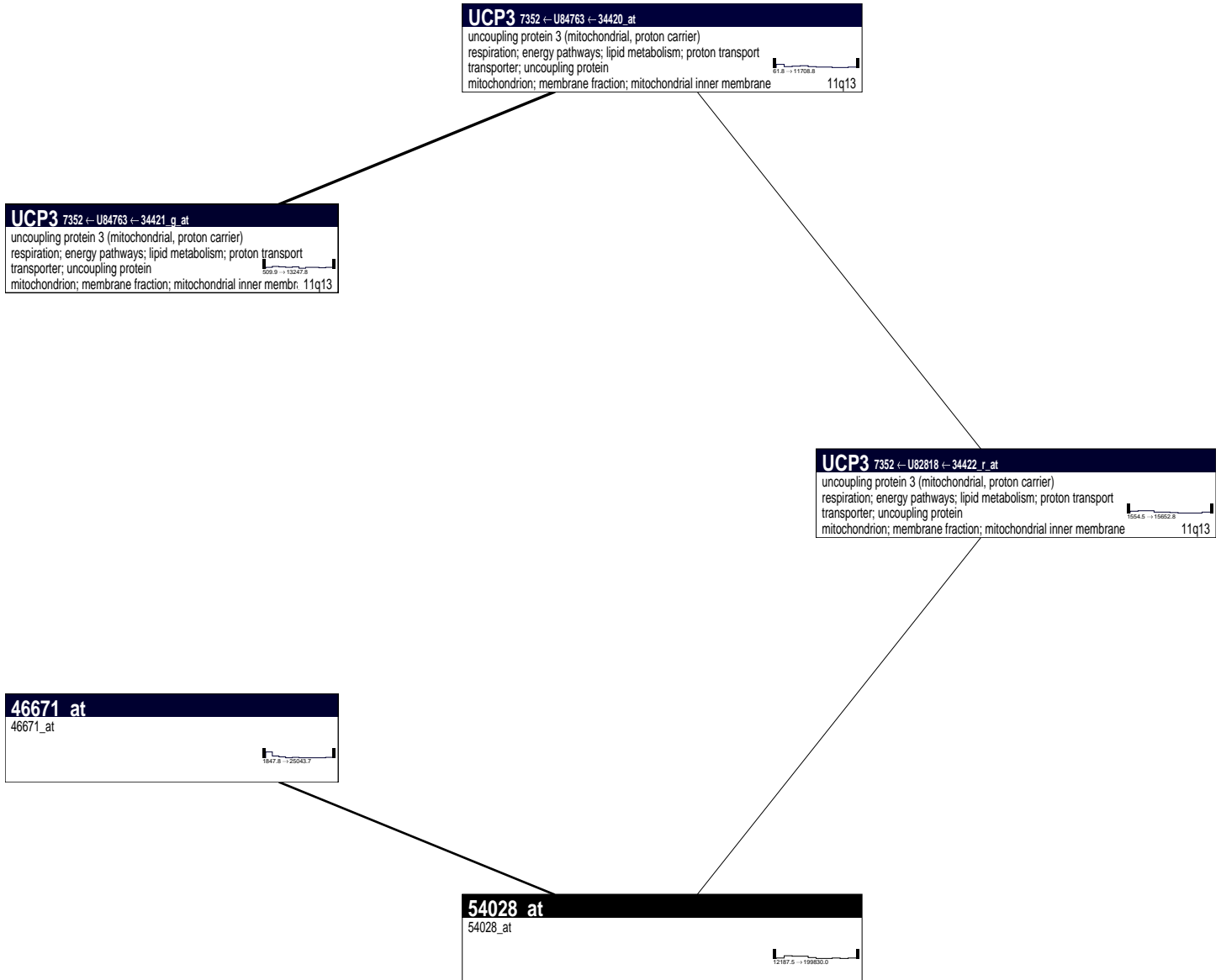
19q13.33

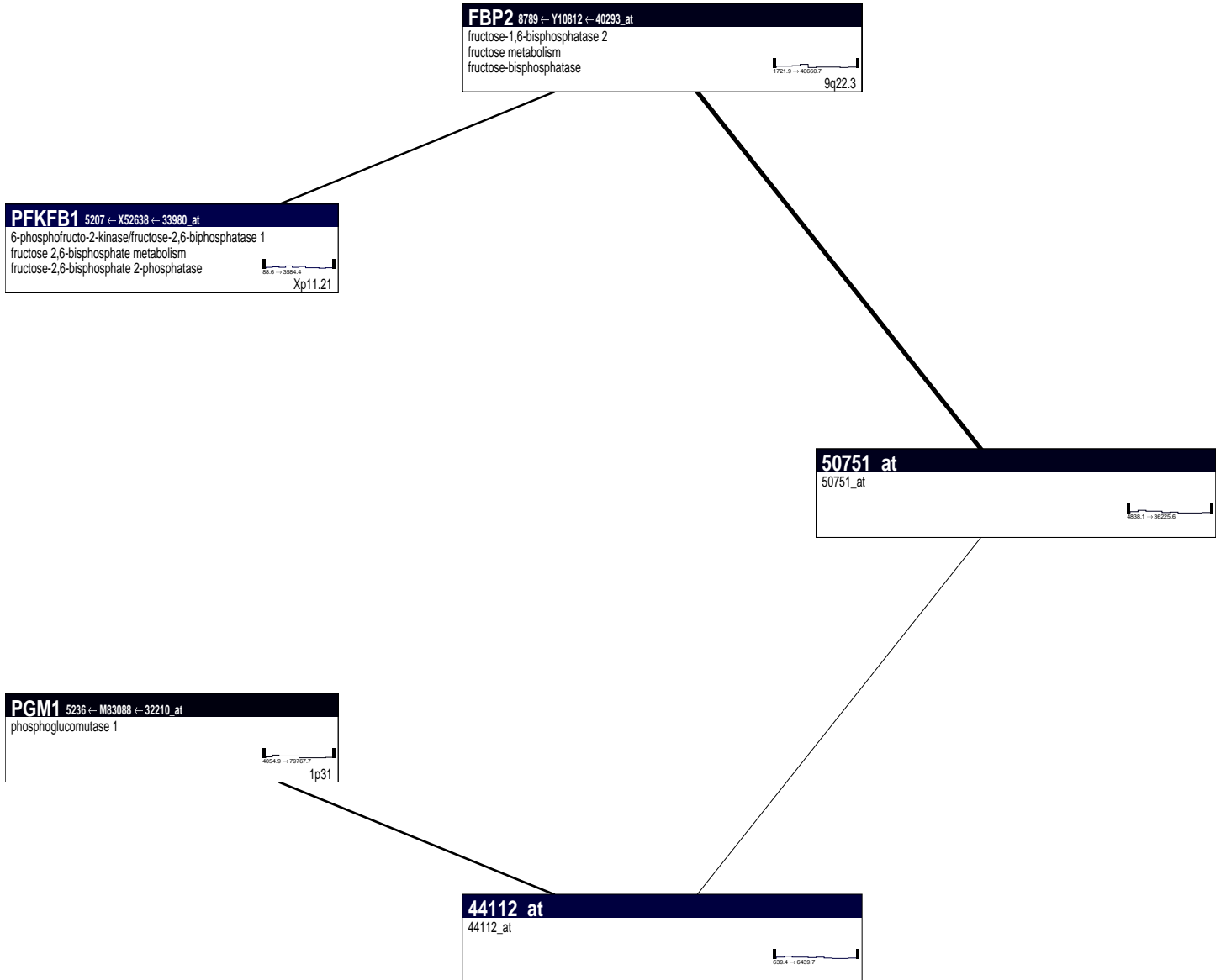
55989 at
55989_at
2093.7 → 7075.2

UBE2D1 7321 ← AF020761 ← 37826_at
ubiquitin-conjugating enzyme E2D 1 (UBC4/5 homolog, yeast)
ubiquitin-dependent protein degradation
ubiquitin--protein ligase; ubiquitin conjugating enzyme
4894.2 → 20814.0
10q11.2-q21

ZNF161 7716 ← D28118 ← 32628_at
zinc finger protein 161
cellular defense response; transcription regulation from Pol II promoter
specific RNA polymerase II transcription factor
1477.4 → 7979.6
17q23.3

ZNF161 7716 ← D28118 ← 350_at
zinc finger protein 161
cellular defense response; transcription regulation from Pol II promoter
specific RNA polymerase II transcription factor
715.3 → 3811.0
17q23.3





SIRT1 23411 ← Hs.31176 ← AI381553 ← 46399_at
sirtuin silent mating type information regulation 2 homolog 1 (S. cerevisiae)
chromatin silencing; protein ADP-ribosylation
NAD(+) ADP-ribosyltransferase
248.6 → 1538.8
10q22.2

UBE4A 9354 ← D50916 ← 36579_at
ubiquitination factor E4A (UFD2 homolog, yeast)
ubiquitin-dependent protein degradation
ubiquitin conjugating enzyme
ubiquitin ligase complex
1202.8 → 7298.6
11q23.3

LKAP 9665 ← AB007890 ← 31936_s_at
limkain b1
2222.3 → 7938.5
16p13.2