Expression profiling of nemaline myopathy: Sanoudou et al.
Web supplement "RelNet 1". Relevance network analysis of 206 "reliably changed" probe sets across 13 NM skeletal muscle specimens at CCC > 0.8.

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

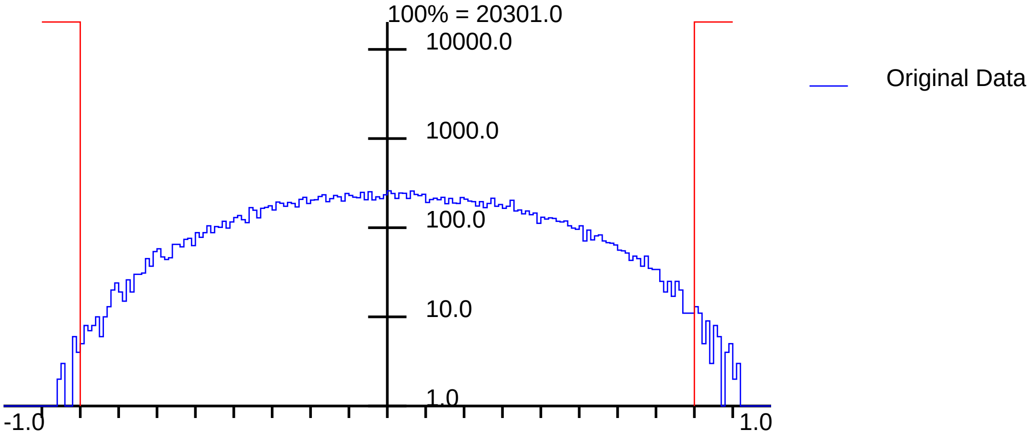
Please cite Butte AJ, et al., Proceedings of the National Academy of Science USA 97(22):12182-6, 2000.

Analysis
Associations computed: 13:36 09/30/2002
Networks constructed: 13:41 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: 18
Number of features (genes): 202
Number of features (genes) used: 86
Total number of edges possible between 202 features (genes): 20301
Number of edges left after analysis: 90
Absolute value of strongest link from any of the 86 nodes used in this analysis: 0.9684996
Absolute value of weakest link from any of the 86 nodes used in this analysis: 0.8005866

Histogram



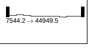
Data ranges from -0.8860942 to 0.9684996.

Samples Used (13 samples)
C:Documents and SettingsGuestDesktopS+83Nem.Unnorm.txt_1
C:Documents and SettingsGuestDesktopS+83Nem.Unnorm.txt_2
C:Documents and SettingsGuestDesktopS+83Nem.Unnorm.txt_3
C:Documents and SettingsGuestDesktopS+83Nem.Unnorm.txt_4
C:Documents and SettingsGuestDesktopS+83Nem.Unnorm.txt_5
C:Documents and SettingsGuestDesktopS+83Nem.Unnorm.txt_6
C:Documents and SettingsGuestDesktopS+83Nem.Unnorm.txt_7
C:Documents and SettingsGuestDesktopS+83Nem.Unnorm.txt_8
C:Documents and SettingsGuestDesktopS+83Nem.Unnorm.txt_9
C:Documents and SettingsGuestDesktopS+83Nem.Unnorm.txt_10
C:Documents and SettingsGuestDesktopS+83Nem.Unnorm.txt_11
C:Documents and SettingsGuestDesktopS+83Nem.Unnorm.txt_12
C:Documents and SettingsGuestDesktopS+83Nem.Unnorm.txt_13

Network Table of Contents

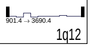
46699_at

46699_at



PDE4DIP 9659 ← Hs.265848 ← AI821791 ← 49961_at

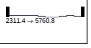
phosphodiesterase 4D interacting protein (myomegalin)



1q12

53149_at

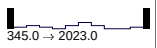
53149_at



Network 2 (size 3)

MRPS25 64432 ← Hs.23450 ← AA527138 ← 44538_at

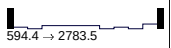
mitochondrial ribosomal protein S25



3p25

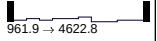
48091_at

48091_at



AK3 205 ← Hs.274691 ← AW015546 ← 48822_s_at

adenylate kinase 3
nucleobase, nucleoside, nucleotide and nucleic acid metabolism

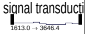


1

Network 3 (size 2)

DOK1 1796 ← U70987 ← 816_g_at

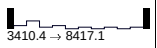
docking protein 1, 62kD (downstream of tyrosine kinase 1)
signal transduction; cell surface receptor linked signal transducti
protein binding



2p13

PANK4 55229 ← Hs.26156 ← AA630975 ← 43960_at

pantothenate kinase 4

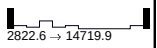


1p36.32

Network 4 (size 2)

S100A4 6275 ← Hs.81256 ← W72186 ← 38087_s_at

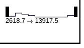
S100 calcium binding protein A4 (calcium protein, calvasculin, m
invasive growth
calcium binding



1q21

45786_at

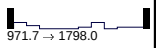
45786_at



Network 5 (size 2)

DDA3 84722 ← Hs.77550 ← AA926959 ← 37347_at

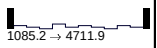
p53-regulated DDA3



1p13.1

LPIN1 23175 ← D80010 ← 38098_at

lipin 1

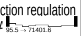


2p25.1

Network 6 (size 2)

ATP2A1 487 ← U96781 ← 41769_at

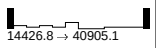
ATPase, Ca++ transporting, cardiac muscle, fast twitch 1
small molecule transport; striated muscle contraction regulation
adenosinetriphosphatase; calcium-transporting A
smooth endoplasmic reticulum



16p12.1

PFKM 5213 ← U24183 ← 36196_at

phosphofructokinase, muscle
glucose metabolism; glycolysis regulation
phosphofructokinase

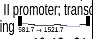


12q13.3

Network 7 (size 2)

NFATC3 4775 ← L41067 ← 40822_at

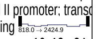
nuclear factor of activated T-cells, cytoplasmic, calcineurin-depe
inflammatory response; transcription from Pol II promoter; transc
transcription co-activator; transcription activating



16q13-q24

NFATC3 4775 ← L41067 ← 250_at

nuclear factor of activated T-cells, cytoplasmic, calcineurin-depe
inflammatory response; transcription from Pol II promoter; transc
transcription co-activator; transcription activating

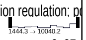


16q13-q24

Network 8 (size 2)

BCL6 604 ← U00115 ← 40091_at

B-cell CLL/lymphoma 6 (zinc finger protein 51)
oncogenesis; inflammatory response; transcription regulation; p
transcription factor
mediator complex

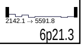


3q27

TUBB 7280 ← J00314 ← 709_at

tubulin, beta polypeptide

cytoskeletal structural protein
cytoskeleton



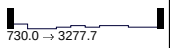
6p21.3

Network 9 (size 10)

PPP6C 5537 ← X92972 ← 37581_at
protein phosphatase 6, catalytic subunit
cell shape control; mitotic G1/S transition; protein dephosphorylation
protein serine/threonine phosphatase

9q34.11

SFRS2IP 9169 ← AF030234 ← 35258_f_at
splicing factor, arginine/serine-rich 2, interacting protein
mRNA splicing; mRNA processing
pre-mRNA splicing factor
nucleus; DNA-directed RNA polymerase II

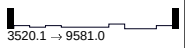


12p11.21

E2-EPF 27338 ← M91670 ← 40619_at
ubiquitin carrier protein
protein modification

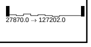
19q13.43

DMPK 1760 ← L08835 ← 37996_s_at
dystrophia myotonica-protein kinase
muscle contraction; protein modification
protein kinase



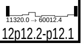
19q13.3

43827_s_at
43827_s_at



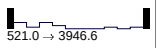
LDHB 3945 ← X13794 ← 33819_at
lactate dehydrogenase B

L-lactate dehydrogenase

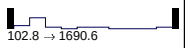


12p12.2-p12.1

50287_at
50287_at



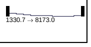
42710_at
42710_at



TUBG1 7283 ← M61764 ← 33346_r_at
tubulin, gamma 1
microtubule cytoskeleton organization and biogenesis
cytoskeletal structural protein
centrosome; microtubule; spindle pole body

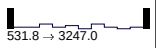
17q21

42711_g_at
42711_g_at



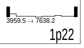
Network 10 (size 2)

ART3 419 ← U47054 ← 35134_at
ADP-ribosyltransferase 3
protein ADP-ribosylation
NAD(+) ADP-ribosyltransferase
integral plasma membrane protein



4p15.1-p14

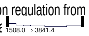
SH3GLB1 51100 ← AB007960 ← 39691_at
SH3-domain GRB2-like endophilin B1



1p22

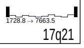
Network 11 (size 4)

CHD3 1107 ← U91543 ← 34707_at
chromodomain helicase DNA binding protein 3
chromosome organization and biogenesis; transcription regulation from
DNA binding; zinc binding; ATP dependent DNA helica



17p13.1

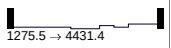
DUSP3 1845 ← Hs.181046 ← AL049417 ← 41225_at
dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-
protein dephosphorylation
protein tyrosine phosphatase



17q21

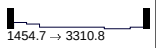
ANXA7 310 ← J04543 ← 37670_at
annexin A7

phospholipid binding; voltage-sensitive calcium channe



10q21.1-q21.2

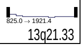
FDPS 2224 ← D14697 ← 37325_at
farnesyl diphosphate synthase (farnesyl pyrophosphate syntheta
cholesterol biosynthesis



1q21.2

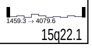
Network 12 (size 3)

TBC1D4 9882 ← AB011175 ← 34672_at
TBC1 domain family, member 4



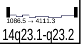
13q21.33

OAZ2 4947 ← AF057297 ← 36146_at
ornithine decarboxylase antizyme 2
polyamine metabolism
ornithine decarboxylase inhibitor



15q22.1

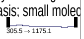
SYNE-2 23224 ← AL080133 ← 41815_at
synaptic nuclei expressed gene 2



14q23.1-q23.2

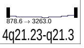
Network 13 (size 2)

NEDD4 4734 ← D42055 ← 32078_at
neural precursor cell expressed, developmentally down-regulate
developmental processes; sodium ion homeostasis; small molec
ubiquitin--protein ligase
cytoplasm



15q

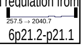
DKFZP564B1162 83478 ← Hs.93589 ← AA166703 ←
hypothetical protein DKFZp564B1162



4q21.23-q21.3

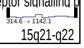
Network 14 (size 2)

PPARD 5467 ← L07592 ← 37152_at
peroxisome proliferative activated receptor, delta
energy pathways; lipid metabolism; transcription regulation from
transcription factor; steroid hormone receptor
nucleus



6p21.2-p21.1

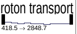
MADH3 4088 ← U68019 ← 38944_at
MAD, mothers against decapentaplegic homolog 3 (Drosophila)
transcription from Pol II promoter; TGFbeta receptor signalling p
tumor suppressor; transcription factor



15q21-q22

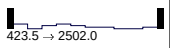
Network 15 (size 3)

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



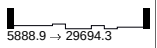
11q13

MAN2A2 4122 ← D55649 ← 41766_at
mannosidase, alpha, class 2A, member 2



15q25

GEMIN7 79760 ← Hs.102991 ← AA497129 ← 50262_at
gemin 7



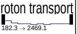
19q13.32

Network 16 (size 2)

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

11q13

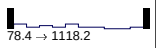
UCP3 7352 ← U84763 ← 34421_g_at
uncoupling protein 3 (mitochondrial, proton carrier)
respiration; energy pathways; lipid metabolism; proton transport
transporter; uncoupling protein
mitochondrion; membrane fraction; mitochondrial inner



11q13

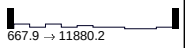
Network 17 (size 36)

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



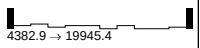
Xp11.21

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



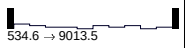
9q22.3

PGM1 5236 ← M83088 ← 32210_at
phosphoglucomutase 1



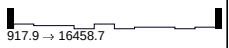
1p31

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



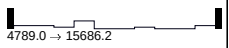
cytoplasm
10p12.33

OPTN 10133 ← AF061034 ← 41742_s_at
optineurin
cell death; pathogenesis; signal transduction



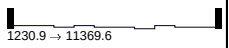
cytoplasm
10p12.33

PHYH 5264 ← AF023462 ← 32724_at
phytanoyl-CoA hydroxylase (Refsum disease)
neurogenesis; lipid metabolism
enzyme; electron transporter
peroxisome



10pter-p11.2

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



10q11.2-q21

34194_at
34194_at

FADS1 3992 ← Hs.132898 ← AF009767 ← 41720_r_at
fatty acid desaturase 1
fatty acid desaturation
C-5 sterol desaturase
integral membrane protein

11q12.2-q13.1

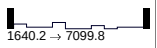
PPP1R2 5504 ← U68111 ← 33180_at
protein phosphatase 1, regulatory (inhibitor) subunit 2
energy pathways
type 1 serine/threonine specific protein phosphatase inhibitor

3q29

IMPA2 3613 ← AF014398 ← 36496_at
inositol(myo)-1(or 4)-monophosphatase 2
signal transduction; phosphate metabolism
myo-inositol-1(or 4)-monophosphatase

18p11.2

MN1 4330 ← X82209 ← 37283_at
meningioma (disrupted in balanced translocation) 1

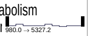


22q12.1

PPP1R2 5504 ← U68111 ← 812_at
protein phosphatase 1, regulatory (inhibitor) subunit 2
energy pathways
type 1 serine/threonine specific protein phosphatase inhibitor

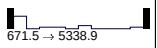
3q29

PHKB 5257 ← X84908 ← 37392_at
phosphorylase kinase, beta
energy pathways; glycogen metabolism; glycogen catabolism
phosphorylase kinase; phosphorylase kinase regulator

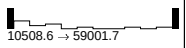


16q12-q13

1164_at
1164_at

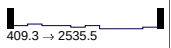


FHL3 2275 ← Hs.57687 ← AI375210 ← 53162_at
four and a half LIM domains 3
muscle development



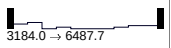
1p34

DAF 1604 ← M31516 ← 39695_at
decay accelerating factor for complement (CD55, Cromer blood group s



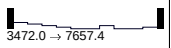
soluble fraction; integral plasma membrane protein
1q32

FLJ20739 55673 ← Hs.46679 ← AI620923 ← 52145_at
hypothetical protein FLJ20739



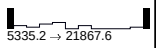
17q23.3

KIAA1917 114804 ← Hs.294151 ← AI745248 ← 44600_at
KIAA1917 protein

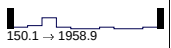


17q25.3

53198_at
53198_at

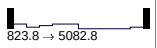


KUB3 91419 ← Hs.61188 ← AI525818 ← 53933_at
Ku70-binding protein 3

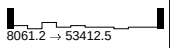


12q13.11

55989_at
55989_at

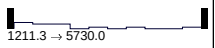


MAGED2 10916 ← Z98046 ← 34860_g_at
melanoma antigen, family D, 2



Xp11.4-p11.1

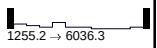
FLJ20811 54470 ← Hs.83530 ← AA015605 ← 38440_s_at
hypothetical protein FLJ20811



Xq21.33-q22.3

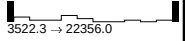
TUBB 7280 ← Hs.336780 ← AF035316 ← 39332_at
tubulin, beta polypeptide

cytoskeletal structural protein
cytoskeleton



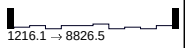
6p21.3

TUBA3 7846 ← X01703 ← 40567_at
tubulin, alpha 3
neurogenesis; glia cell differentiation; cell shape and cell size control
cytoskeletal structural protein
microtubule

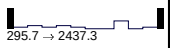


12q12-12q14.3

45773 at
45773_at

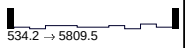


MAN2A2 4122 ← L28821 ← 38188_s_at
mannosidase, alpha, class 2A, member 2



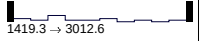
15q25

FLJ12168 79735 ← Hs.325860 ← AI361002 ← 57547_at
hypothetical protein FLJ12168



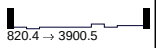
19q13.33

CDK4 1019 ← U37022 ← 1942_s_at
cyclin-dependent kinase 4
oncogenesis; cell cycle control; cell proliferation; mitotic G1/S transition
cyclin-dependent protein kinase



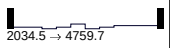
12q14

ADCY9 115 ← AF036927 ← 33800_at
adenylate cyclase 9
signal transduction
adenylate cyclase
integral plasma membrane protein



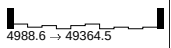
16p13.3

KIAA0469 9903 ← AB007938 ← 37230_at
KIAA0469 gene product

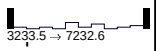


1p36.23

54028 at
54028_at

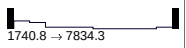


RXRA 6256 ← U66306 ← 32800_at
retinoid X receptor, alpha
vitamin metabolism; signal transduction
DNA binding; retinoid-X receptor; retinoic acid re
nucleus



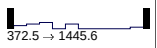
9q34.3

CARM1 10498 ← AF055027 ← 40182_s_at
coactivator-associated arginine methyltransferase-1



19p13.2

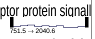
PTOV1 53635 ← Hs.19555 ← W25984 ← 32130_at
prostate tumor over expressed gene 1



19q13.33

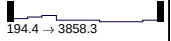
Network 18 (size 4)

TBXA2R 6915; 58509; 126326 ← [3 genes] ← 32914_f_at ← 32914_f_a
thromboxane A2 receptor
respiration; muscle contraction; G-protein linked receptor protein signall
thromboxane A2 receptor
plasma membrane; integral plasma membrane protein



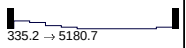
19p13.3

PHKA1 5255 ← X73874 ← 39291_at
phosphorylase kinase, alpha 1 (muscle)
energy pathways; glycogen metabolism; glycogen catabolism
phosphorylase kinase; phosphorylase kinase regulatoı

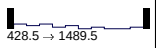


Xq12-q13

51756 at
51756_at



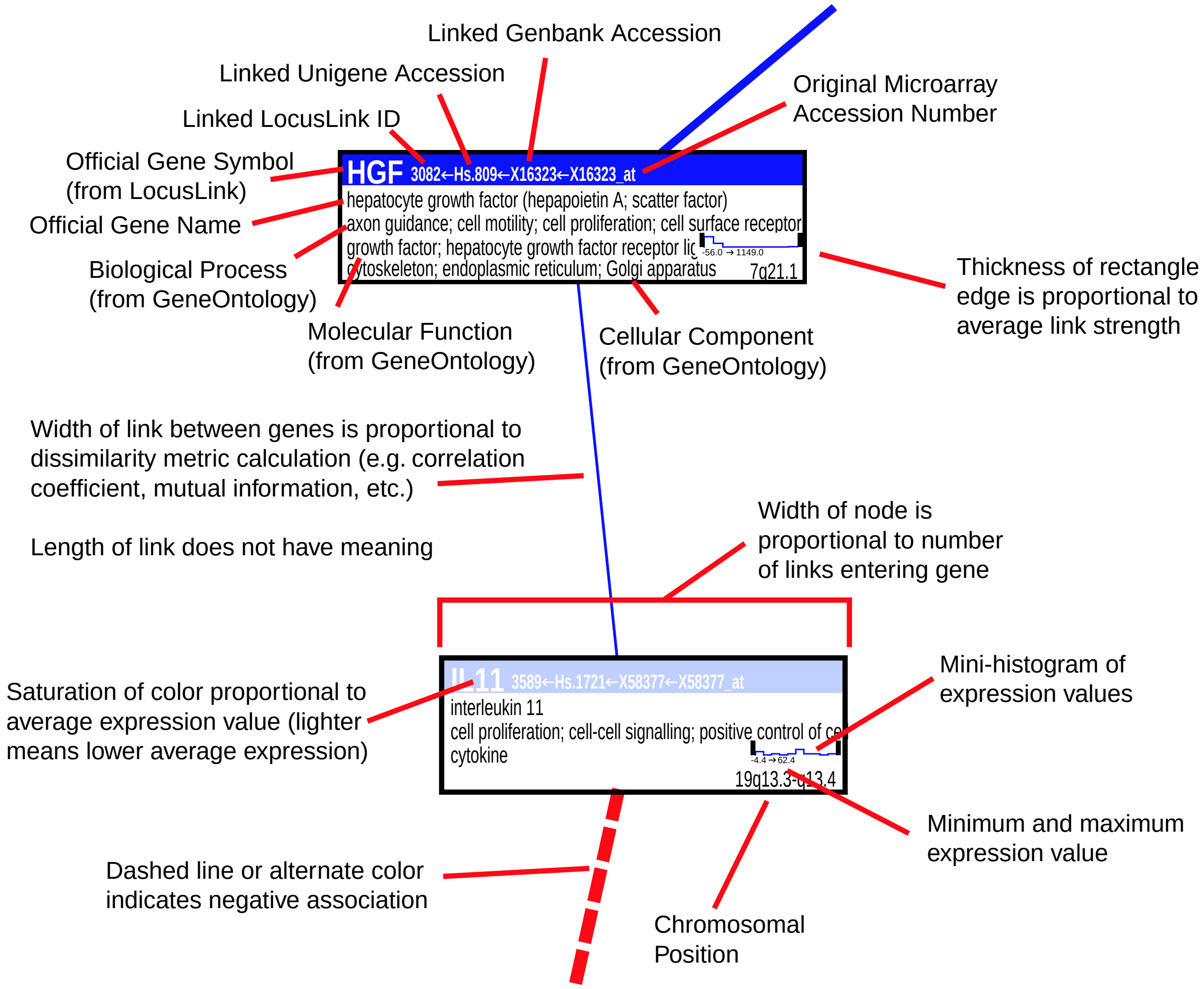
KIAA0399 23140 ← AB007859 ← 38626_at
KIAA0399 protein



17p13.3

End of Network Table of Contents

Relevance Networks Legend



Linked Genbank Accession

Linked Unigene Accession

Linked LocusLink ID

Original Microarray Accession Number

Official Gene Symbol (from LocusLink)

Official Gene Name

Biological Process (from GeneOntology)

Thickness of rectangle edge is proportional to average link strength

Molecular Function (from GeneOntology)

Cellular Component (from GeneOntology)

Width of link between genes is proportional to dissimilarity metric calculation (e.g. correlation coefficient, mutual information, etc.)

Length of link does not have meaning

Width of node is proportional to number of links entering gene

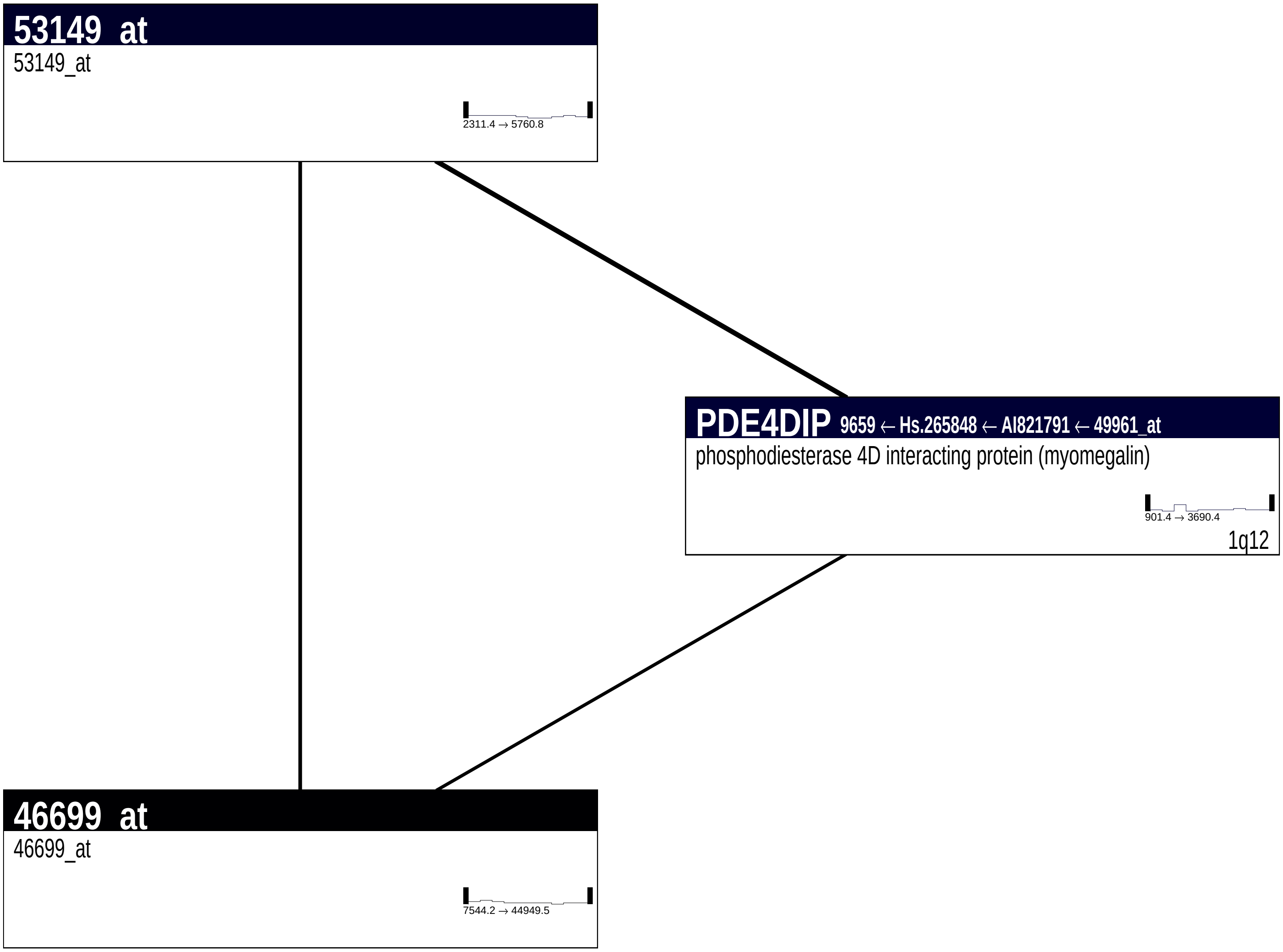
Saturation of color proportional to average expression value (lighter means lower average expression)

Mini-histogram of expression values

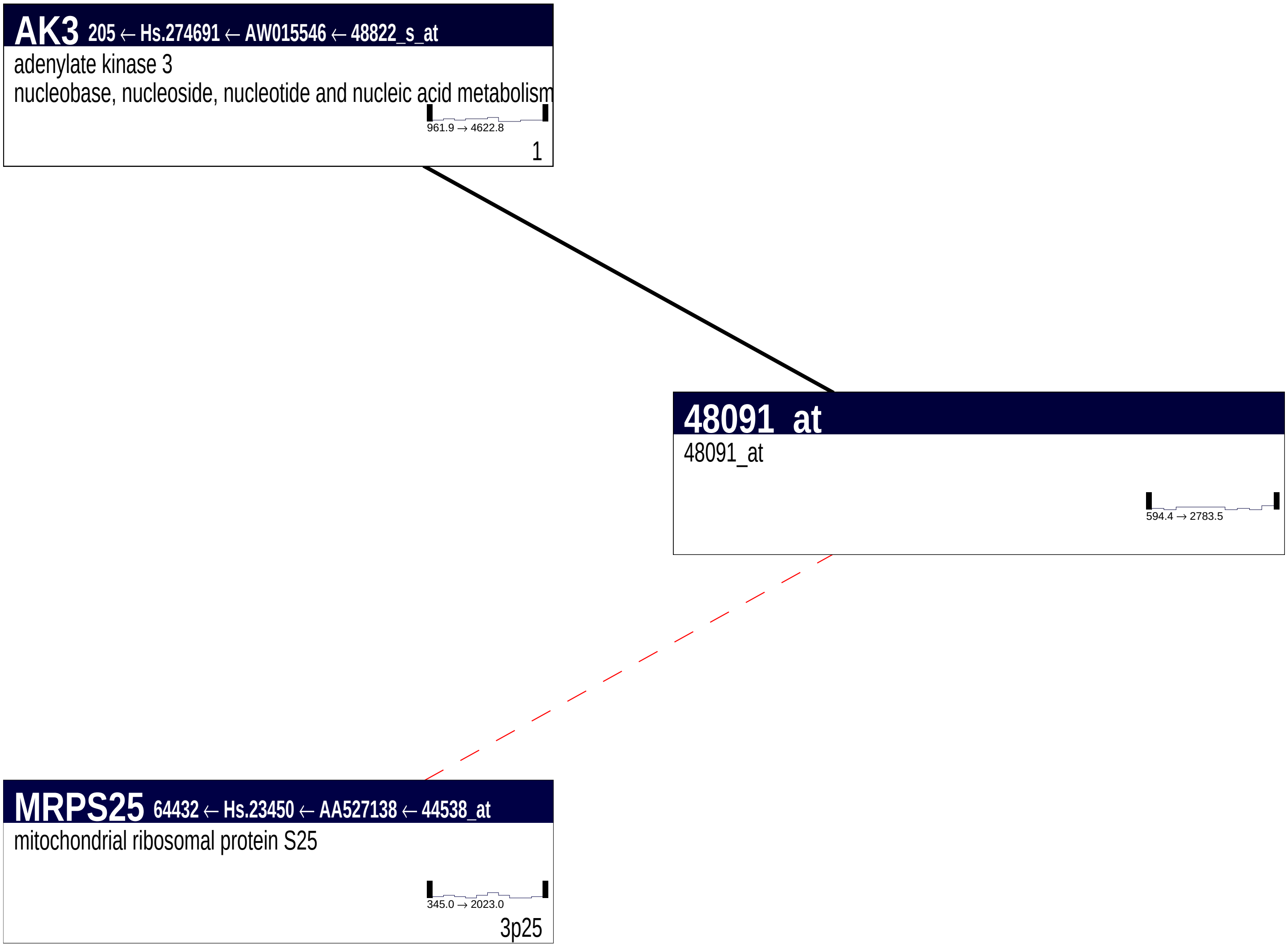
Minimum and maximum expression value

Dashed line or alternate color indicates negative association

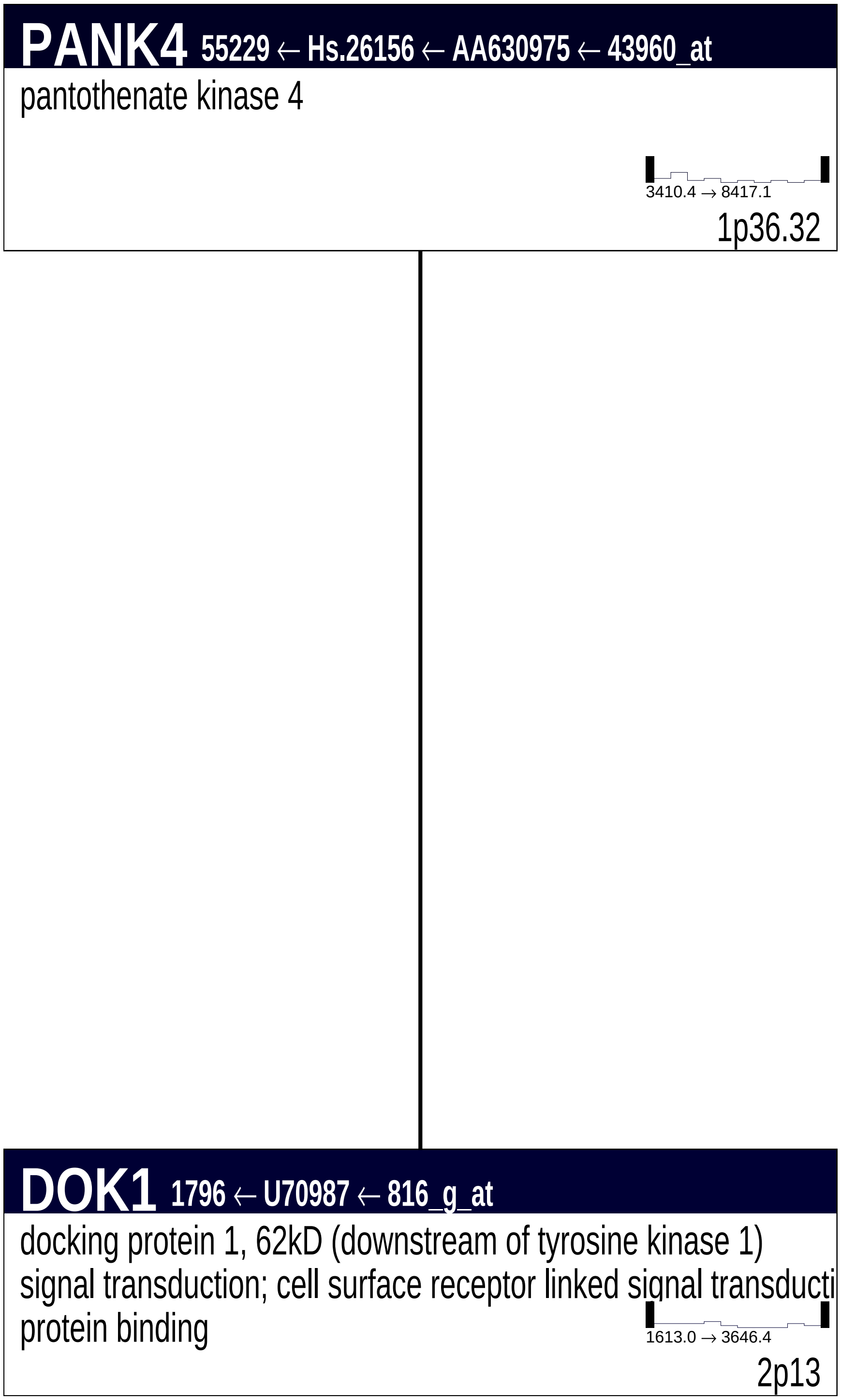
Chromosomal Position



Network: 1 **Networks constructed: 13:41 09/30/2002**



Network: 2 Networks constructed: 13:41 09/30/2002



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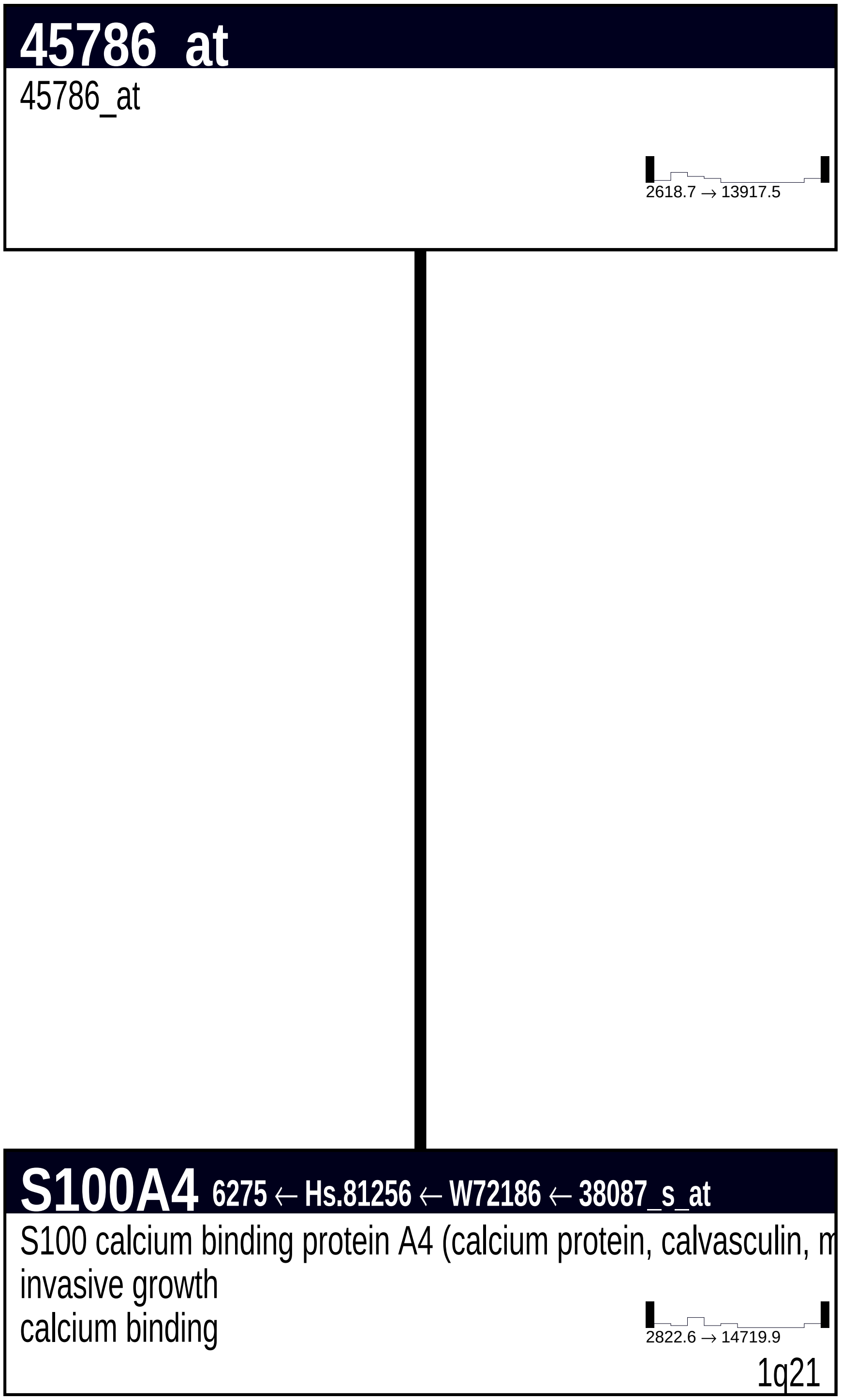
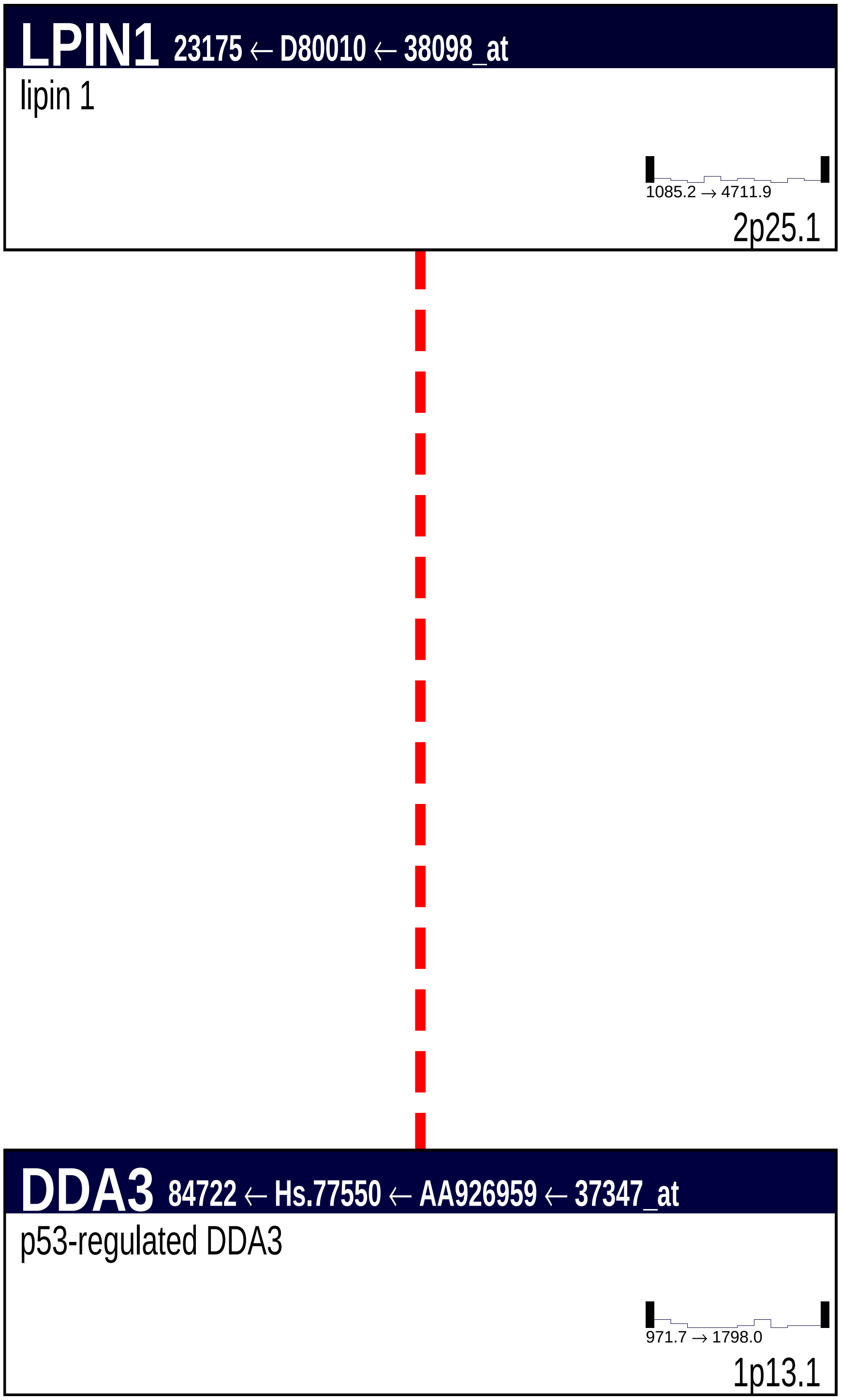
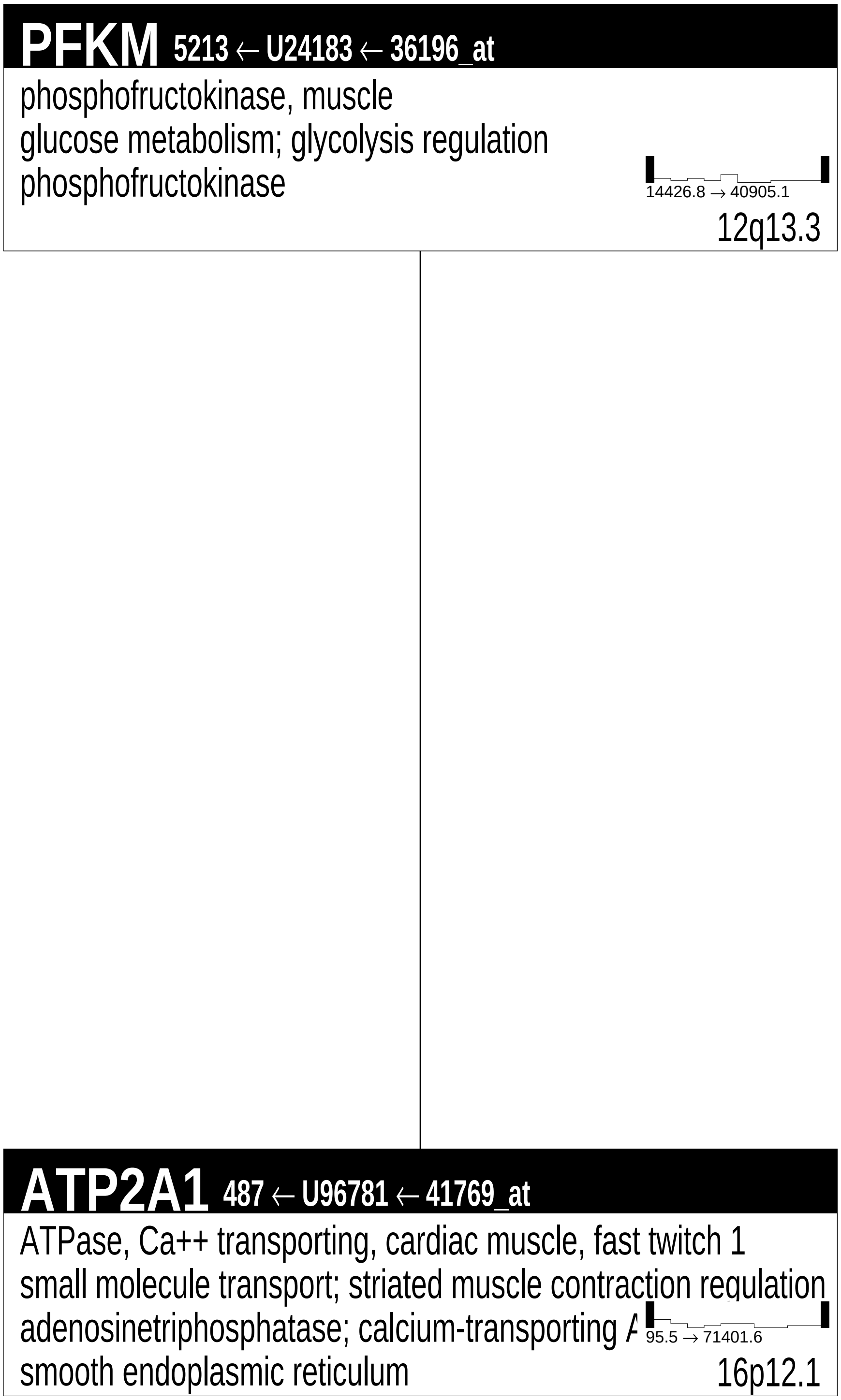


Network: 4 **Networks constructed: 13:41 09/30/2002**

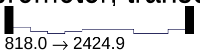


Network: 5 **Networks constructed: 13:41 09/30/2002**


PFKM 5213 ← U24183 ← 36196_at
phosphofructokinase, muscle
glucose metabolism; glycolysis regulation
phosphofructokinase
14426.8 → 40905.1
12q13.3
ATP2A1 487 ← U96781 ← 41769_at
ATPase, Ca++ transporting, cardiac muscle, fast twitch 1
small molecule transport; striated muscle contraction regulation
adenosinetriphosphatase; calcium-transporting A
95.5 → 71401.6
smooth endoplasmic reticulum
16p12.1

NFATC3 4775 ← L41067 ← 250_at

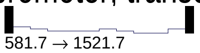
nuclear factor of activated T-cells, cytoplasmic, calcineurin-depe
inflammatory response; transcription from Pol II promoter; transc
transcription co-activator; transcription activating



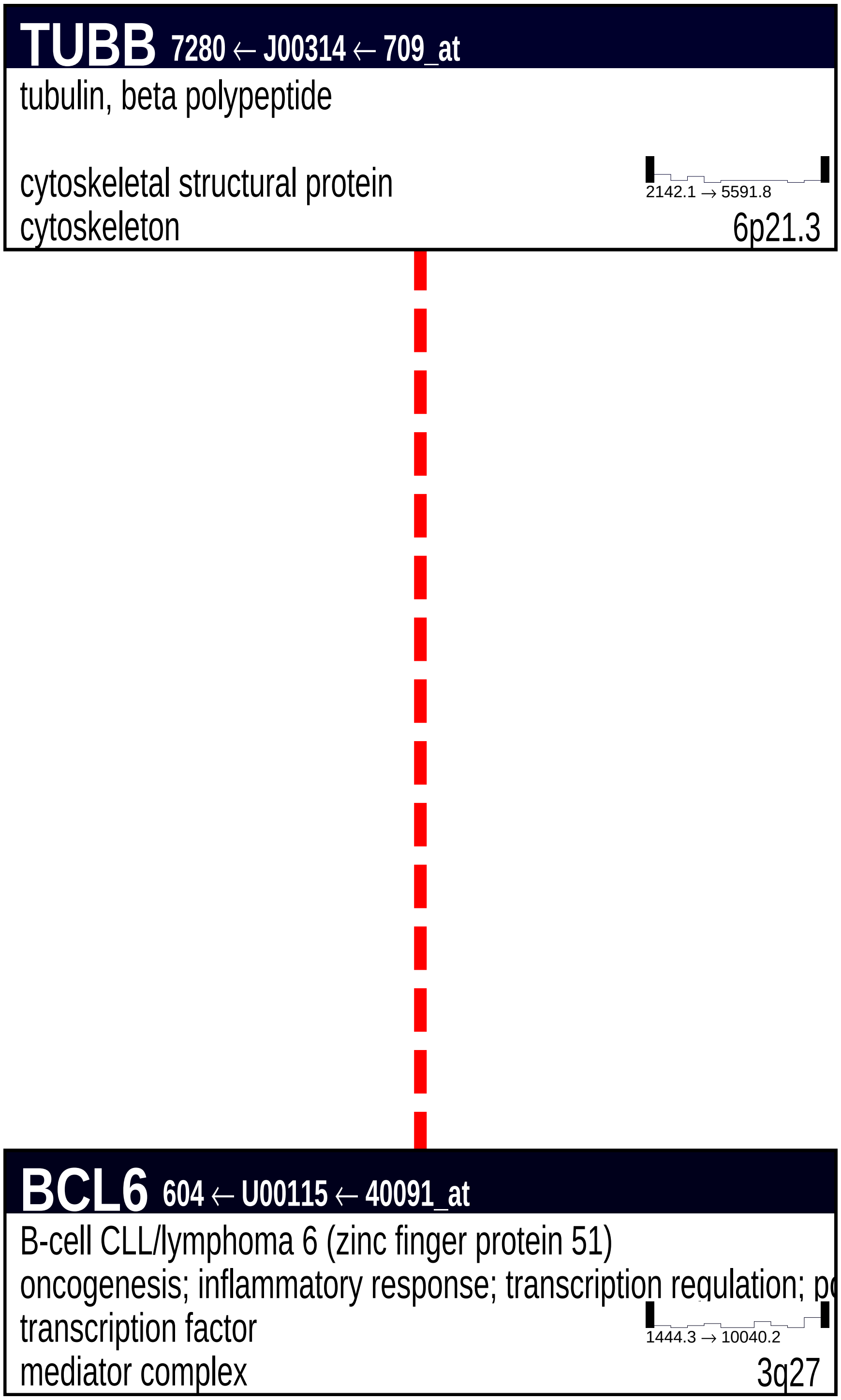
16q13-q24

NFATC3 4775 ← L41067 ← 40822_at

nuclear factor of activated T-cells, cytoplasmic, calcineurin-depe
inflammatory response; transcription from Pol II promoter; transc
transcription co-activator; transcription activating



16q13-q24



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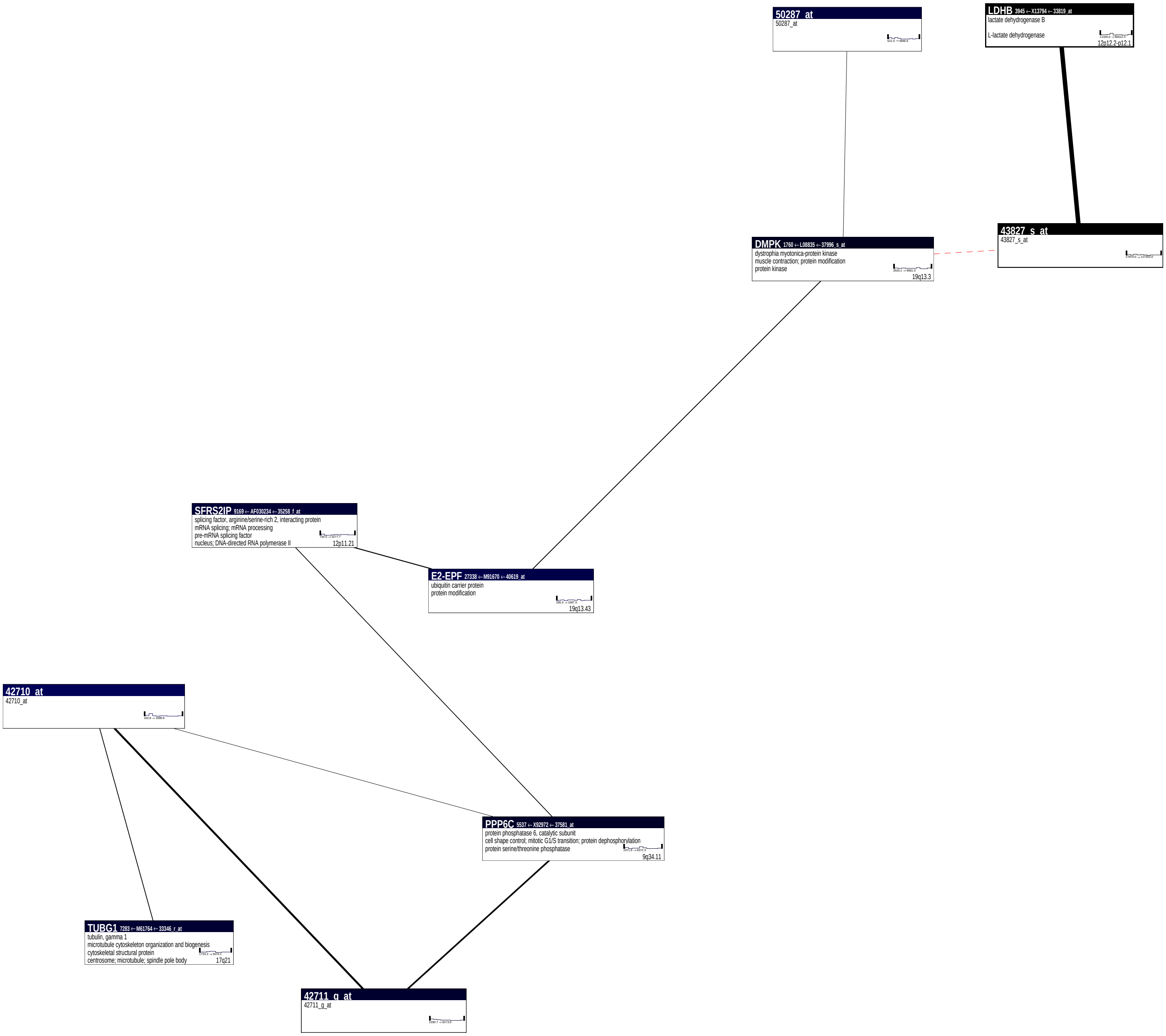

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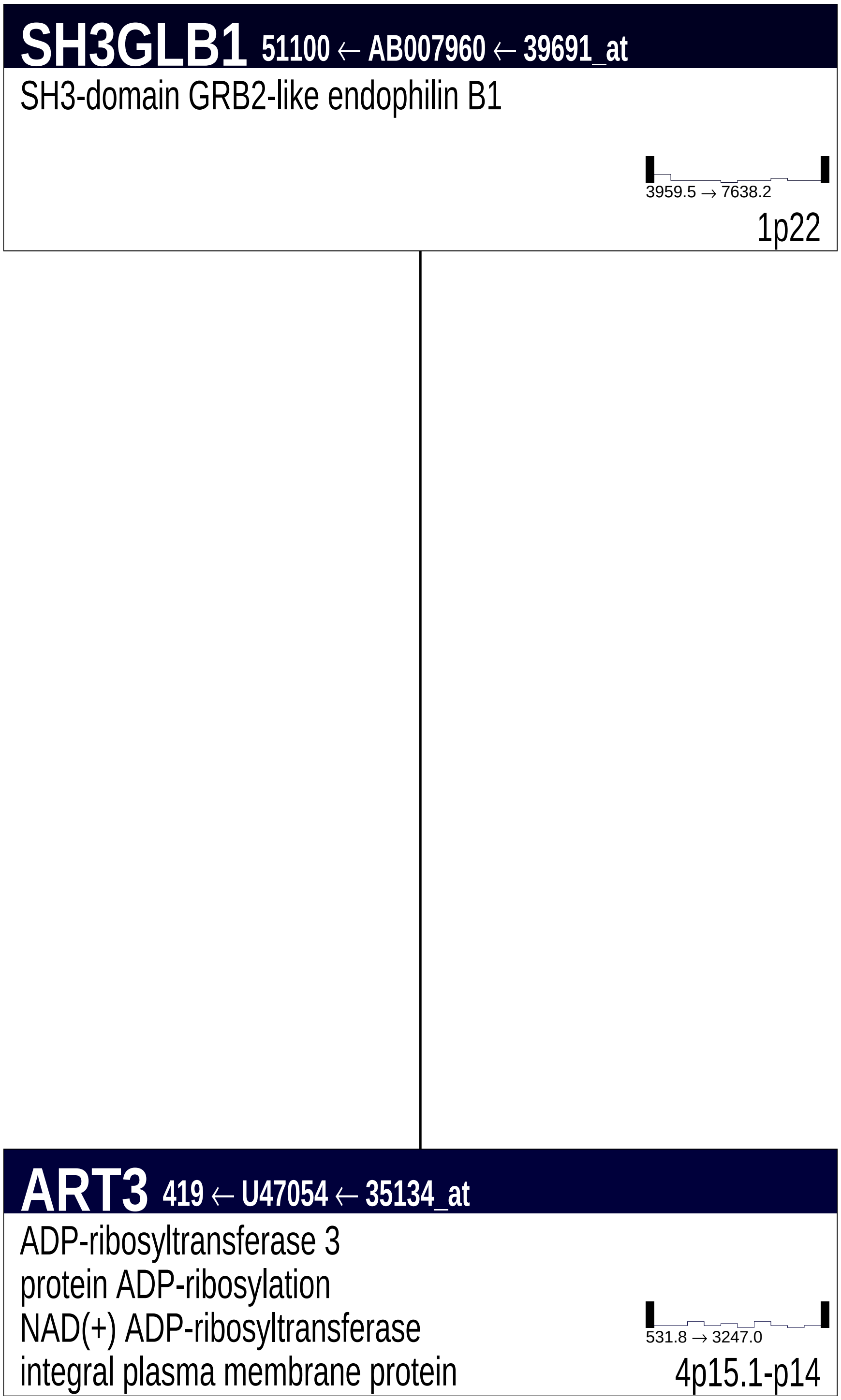
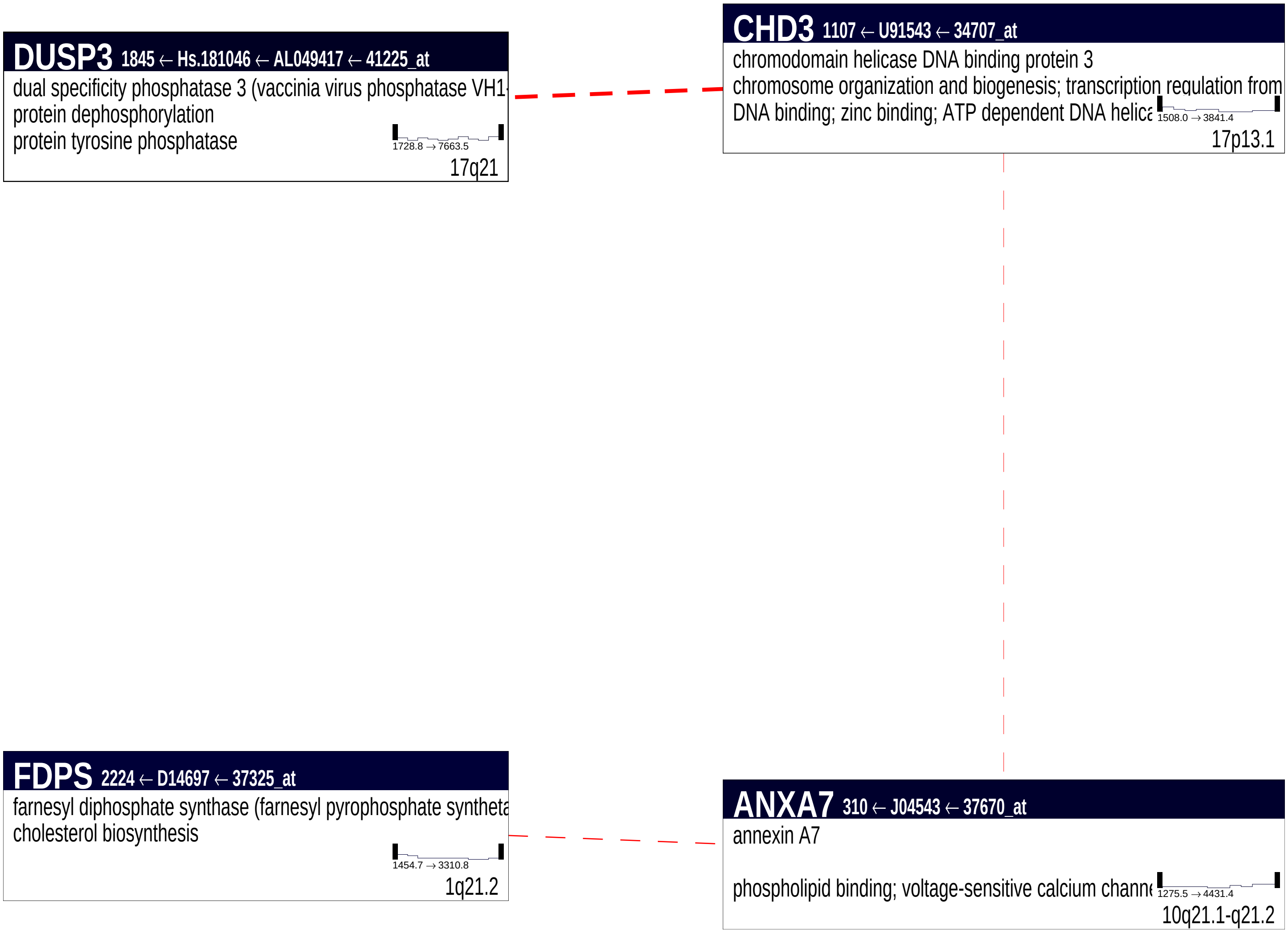
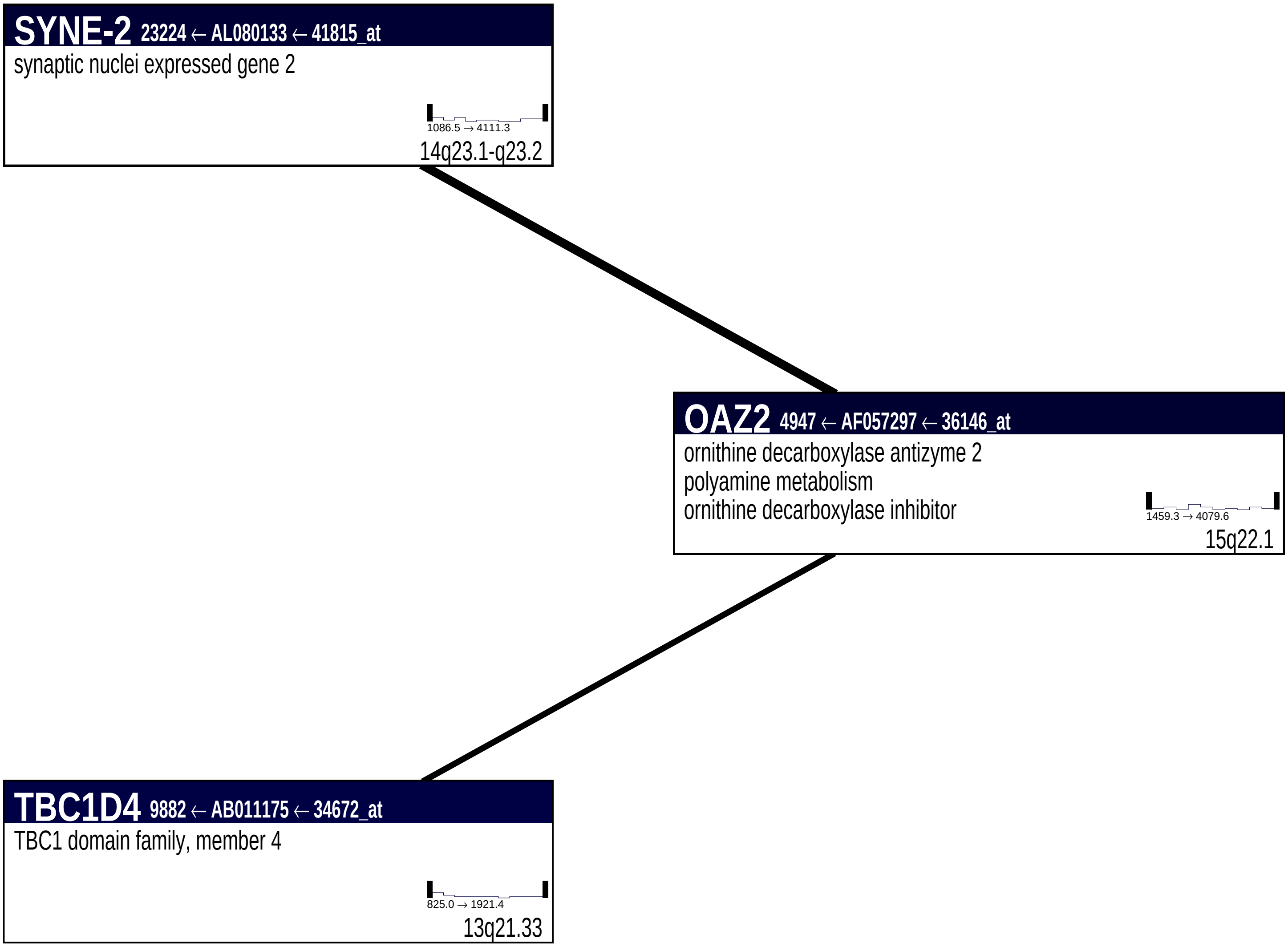


Network: 10 **Networks constructed: 13:41 09/30/2002**



Network: 11 Networks constructed: 13:41 09/30/2002



Network: 12 Networks constructed: 13:41 09/30/2002

DKFZP564B1162 83478 ← Hs.93589 ← AA166703 ←

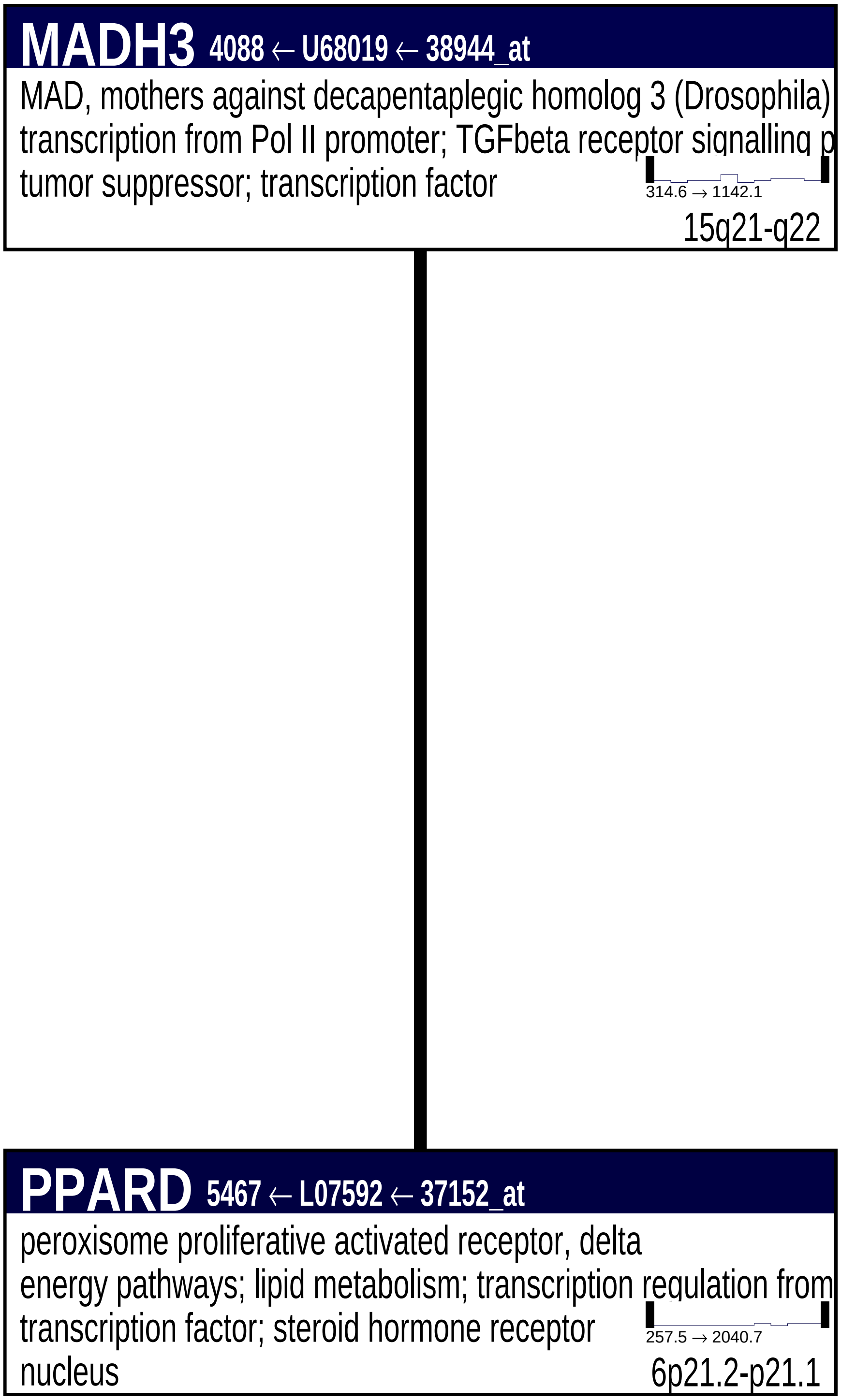
hypothetical protein DKFZp564B1162

4q21.23-q21.3

NEDD4 4734 ← D42055 ← 32078_at

neural precursor cell expressed, developmentally down-regulate
developmental processes; sodium ion homeostasis; small molec
ubiquitin--protein ligase
cytoplasm

15q



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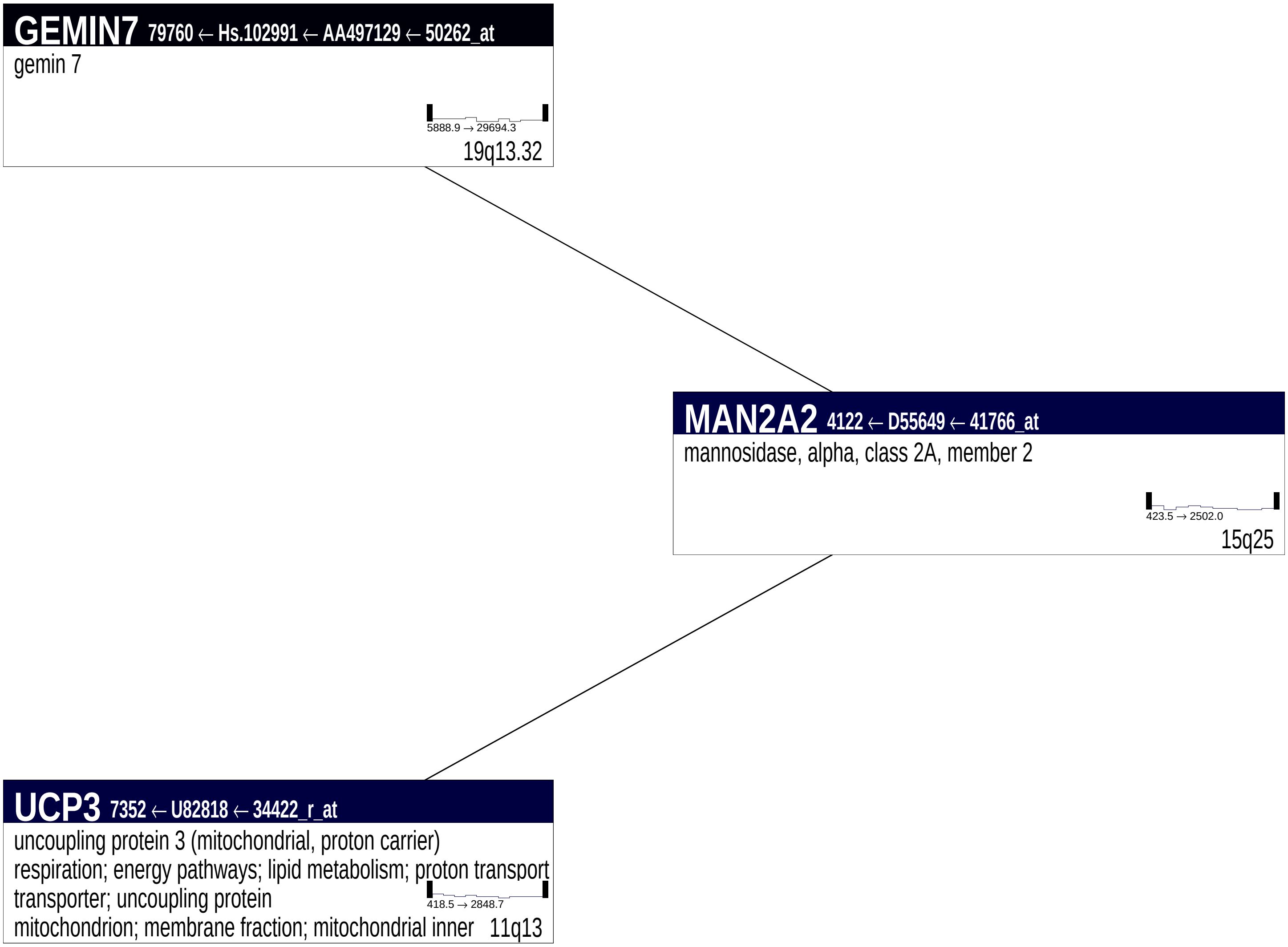
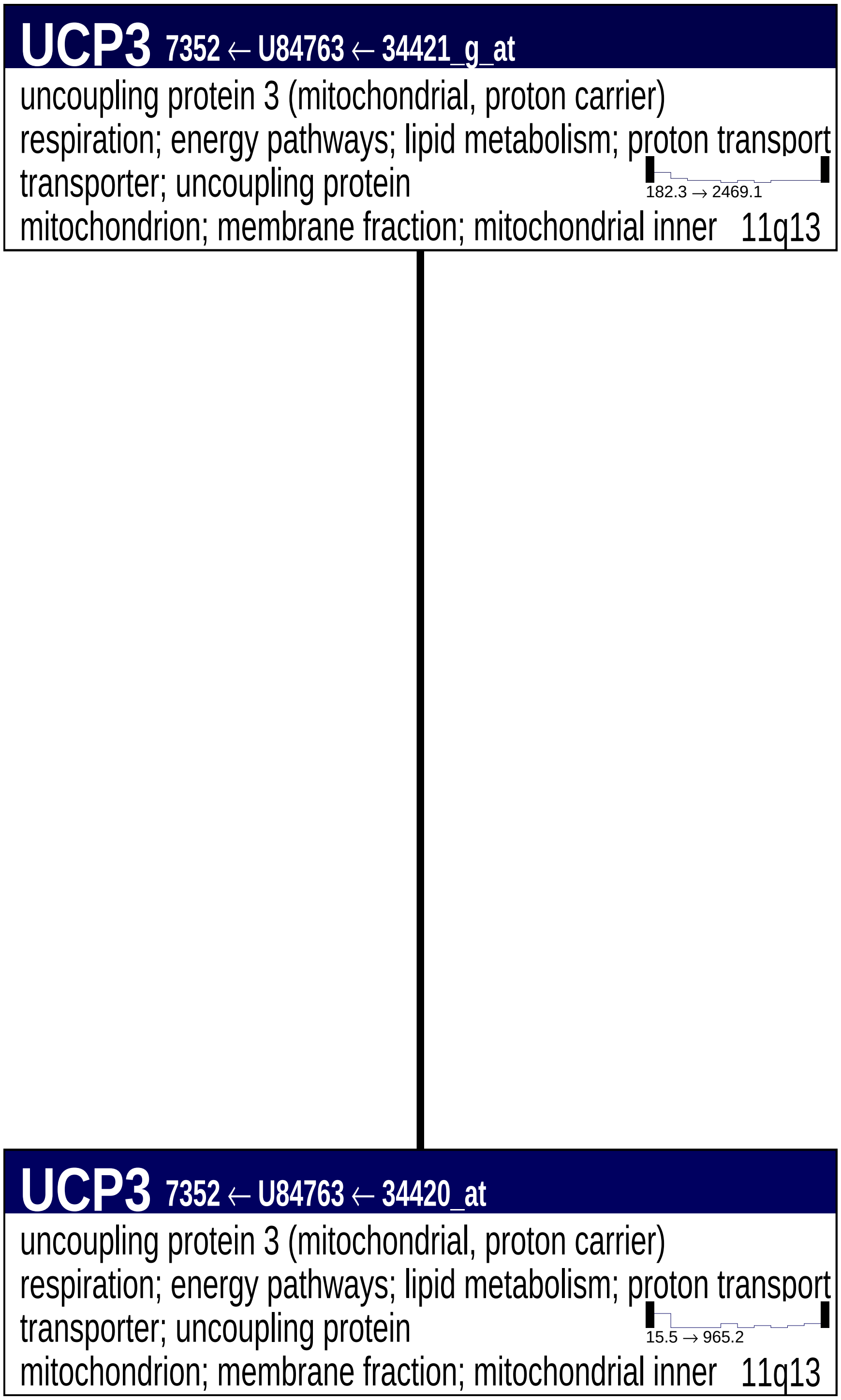


Network: 15 Networks constructed: 13:41 09/30/2002



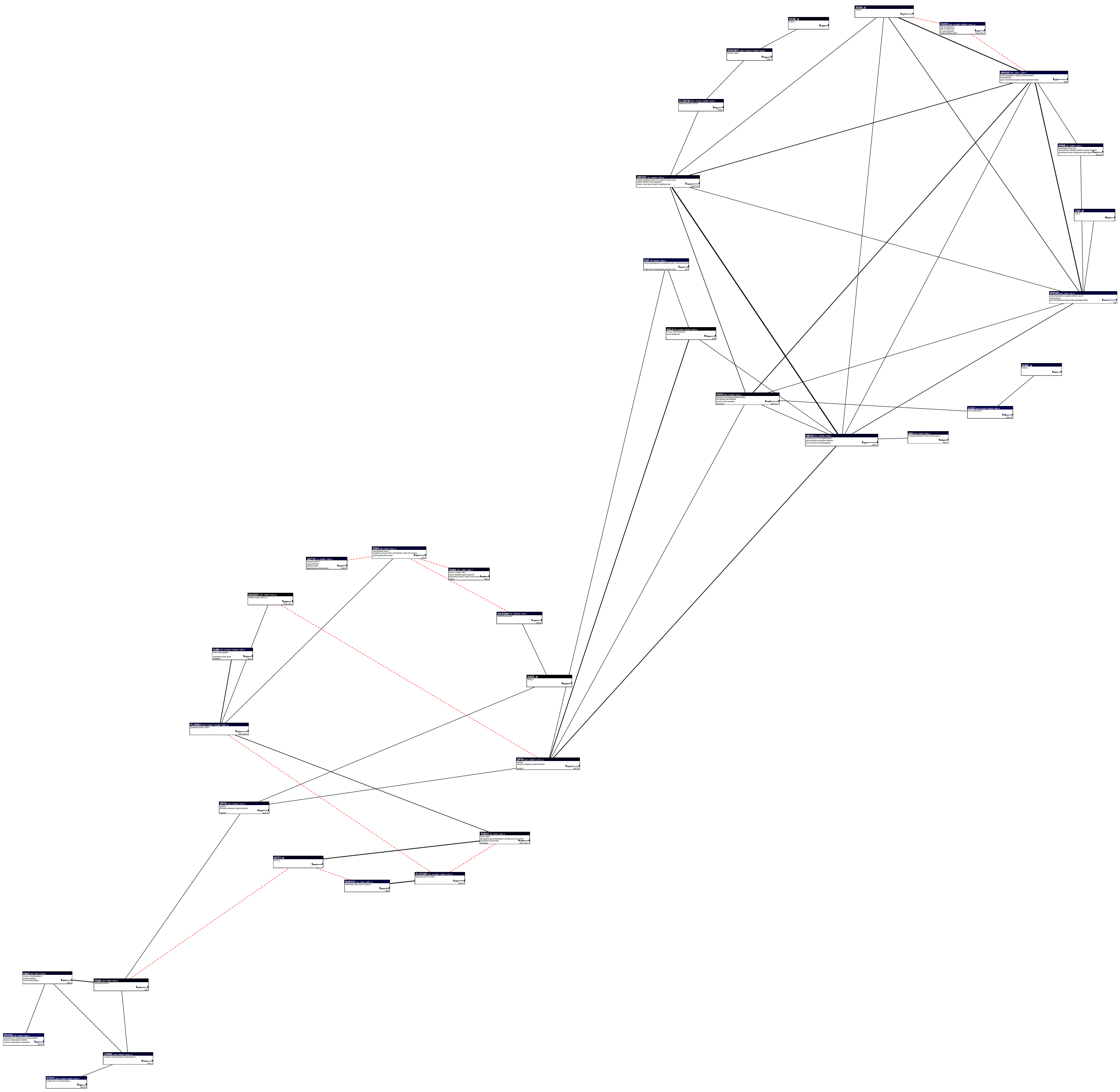
UCP3 7352 ← U84763 ← 34421_g_at

uncoupling protein 3 (mitochondrial, proton carrier)
respiration; energy pathways; lipid metabolism; proton transport
transporter; uncoupling protein
mitochondrion; membrane fraction; mitochondrial inner 11q13

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 11q13

Network: 16 Networks constructed: 13:41 09/30/2002



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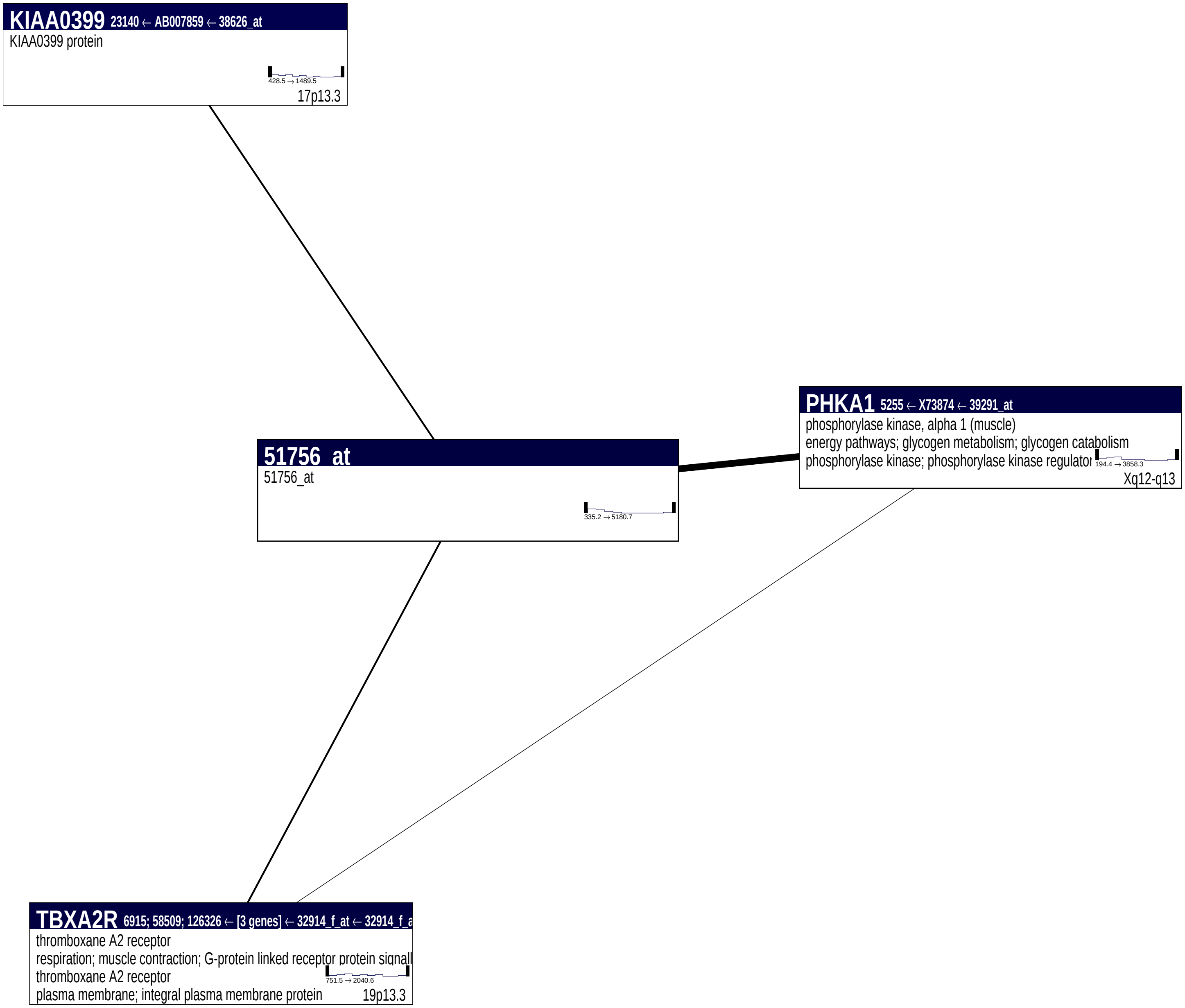

Network: 18 Networks constructed: 13:41 09/30/2002