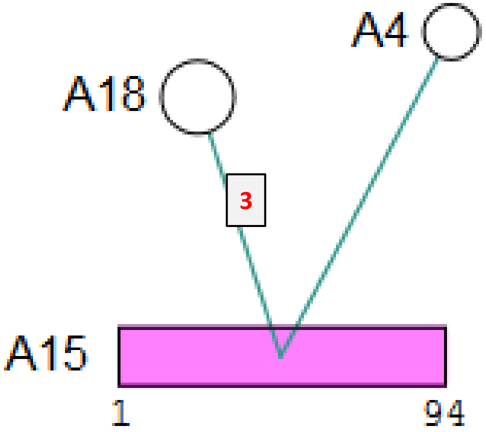
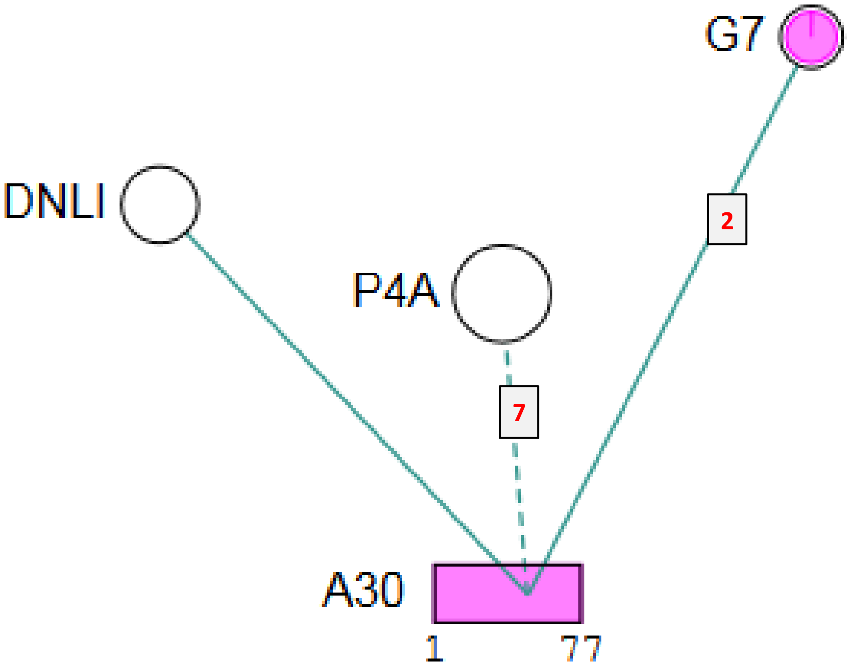
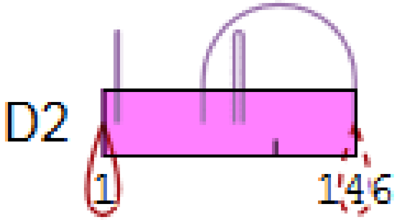
7PC

A15, A30 , D2, D3, G7, J1, VPK2


A4
A18
3
A15
1
94

A30-49/P4A-876: 0.080

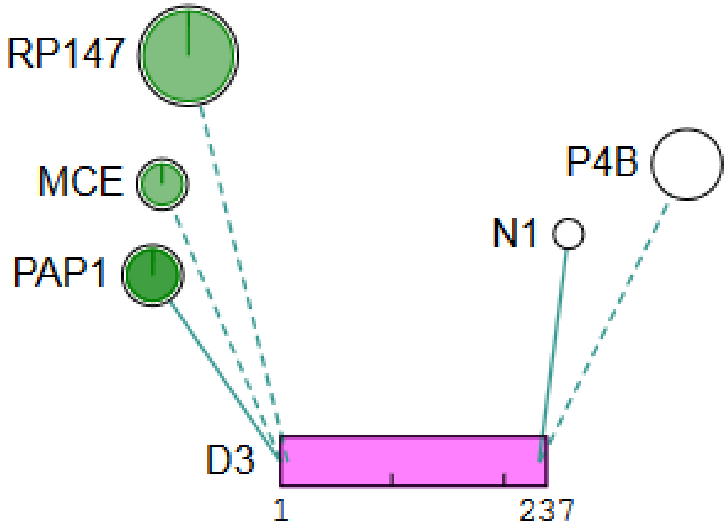



D2
1
146

D3-1/MCE-8: 0

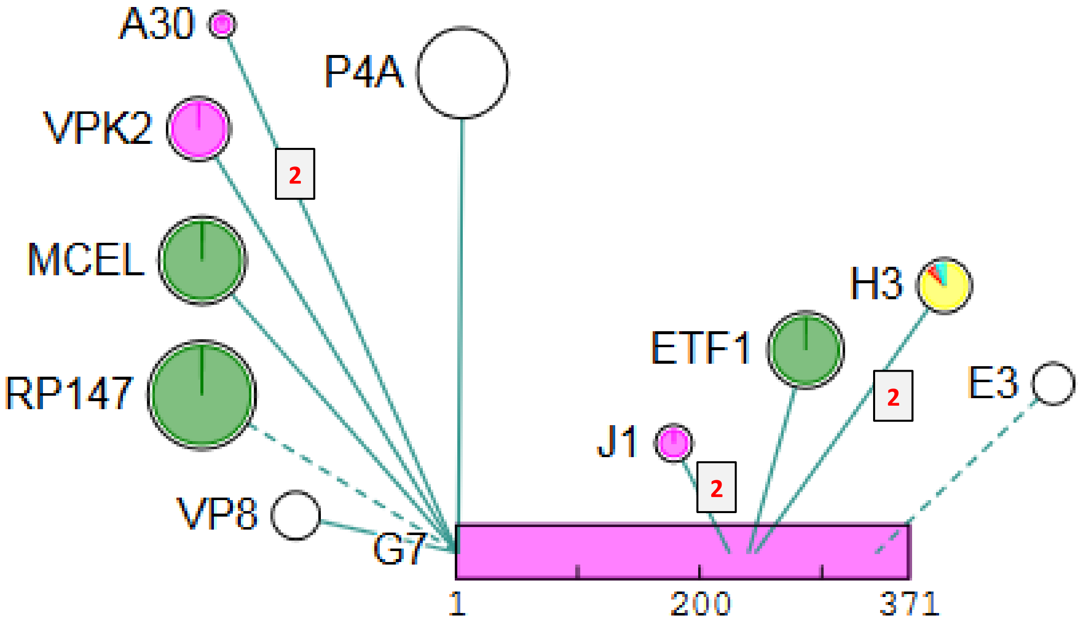
D3-7/RP147-54: 0

D3-232/P4B-189: 0



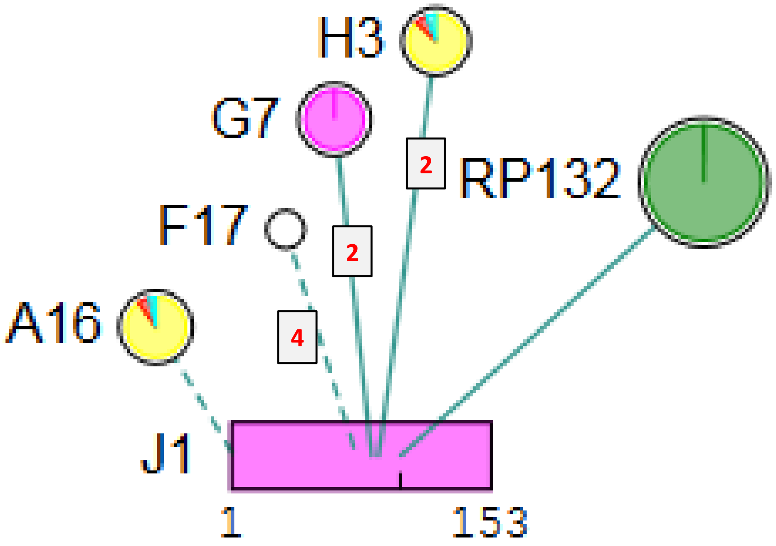
G7-1/RP147-75: 0

G7-345/E3-165: 0



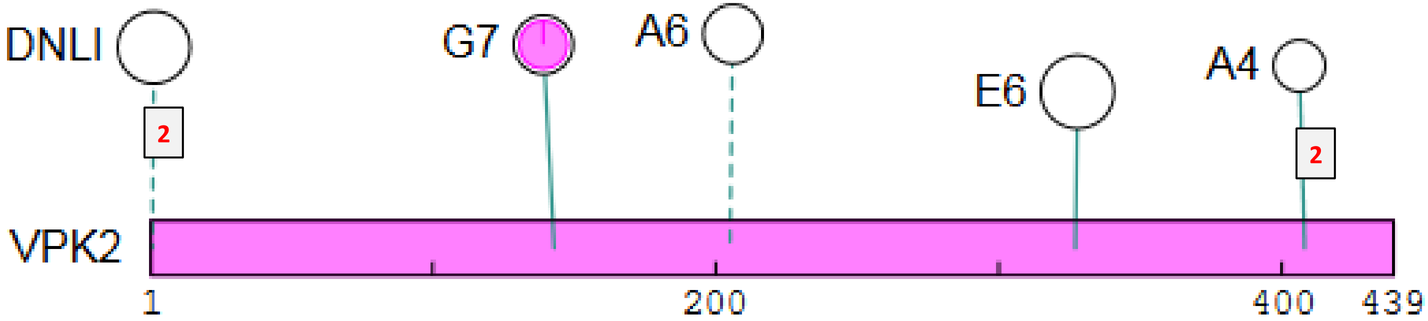
J1-2/A16-206: 0

J1-74/F17-74: 0



VPK2-1/DNLI-303: 0.667

VPK2-205/A6-352: 0.500



EFC/EFC-associated

A16, A21, A28, F9, G3, G9, H2, J5, L1, L5, O3

A16-22/RAP94-516: 0

A16-116/A27-37: 0

A16-133/P4A-754: 0

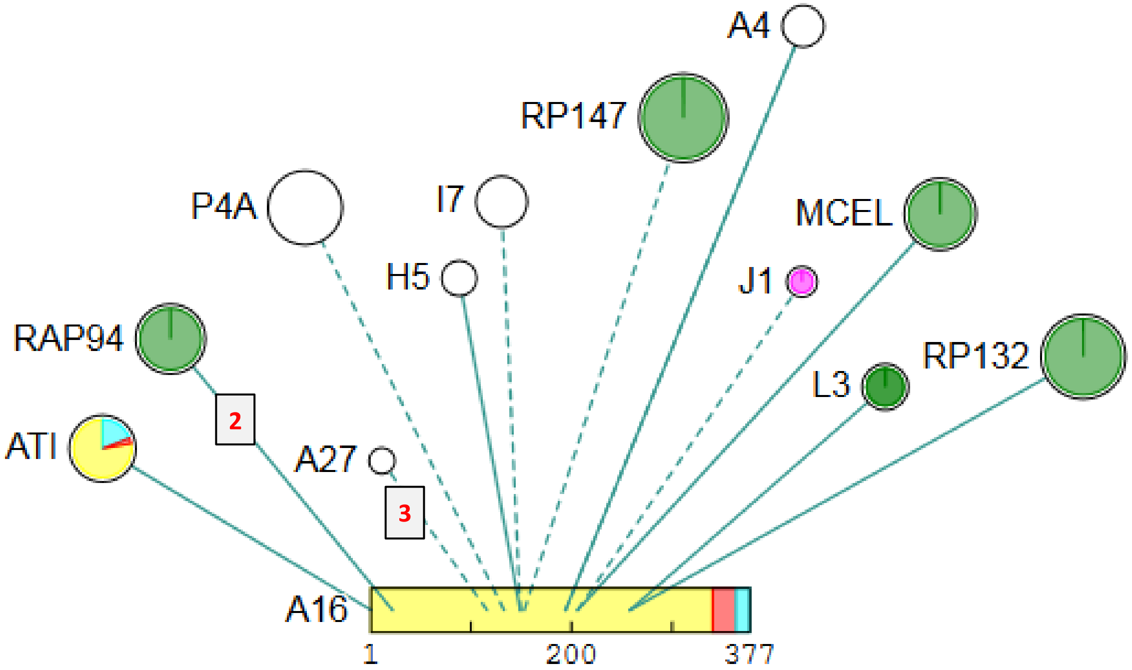
A16-149/I7-126: 0

A16-153/RP147-493: 0

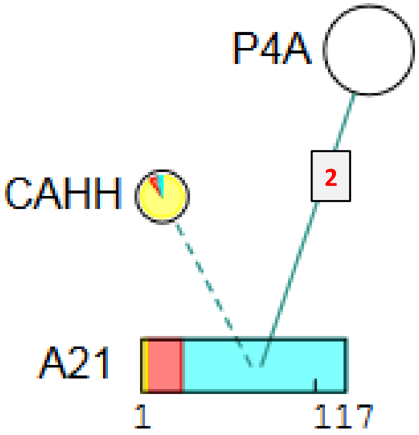
A16-194/A4-33: 1.000

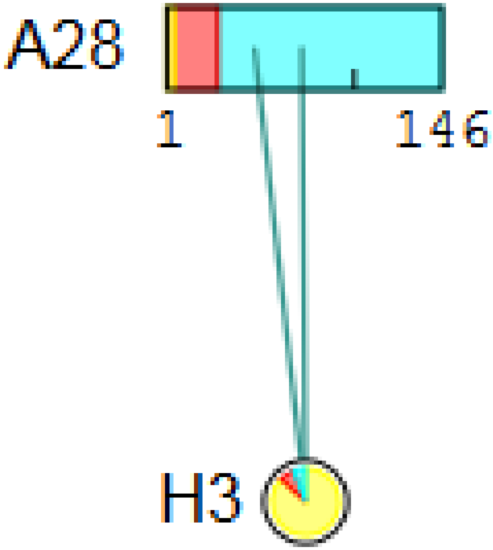
A16-194/A4-42: 1.000

A16-206/J1-2: 0



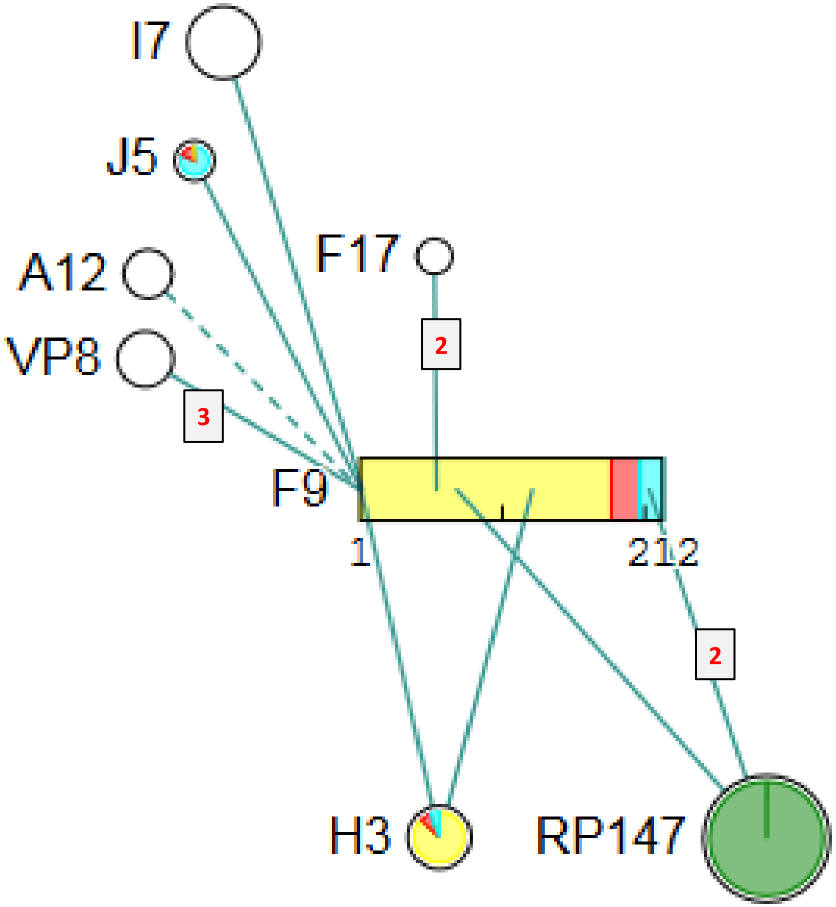
CAHH-100/A21-63: 0




A28
1
146
H3

F9-0/A12-75: 0

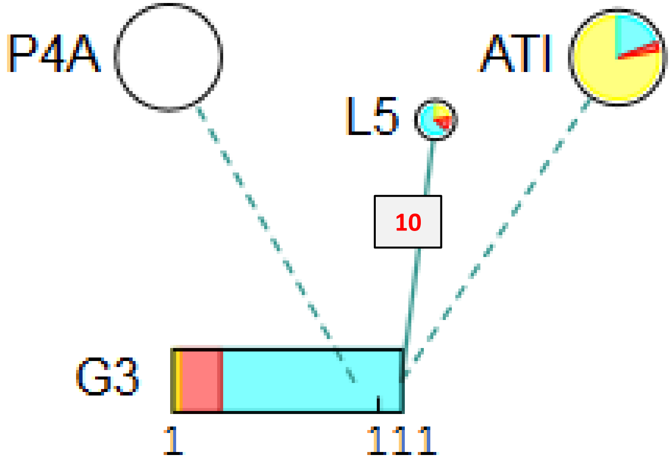
F9-203/RP147-148: 0.111



G3-88/P4A-876: 0.167

G3-111/ATI-38: 0.250

G3-111/L5-109: 0.750



G9-52/ATI-512: 0

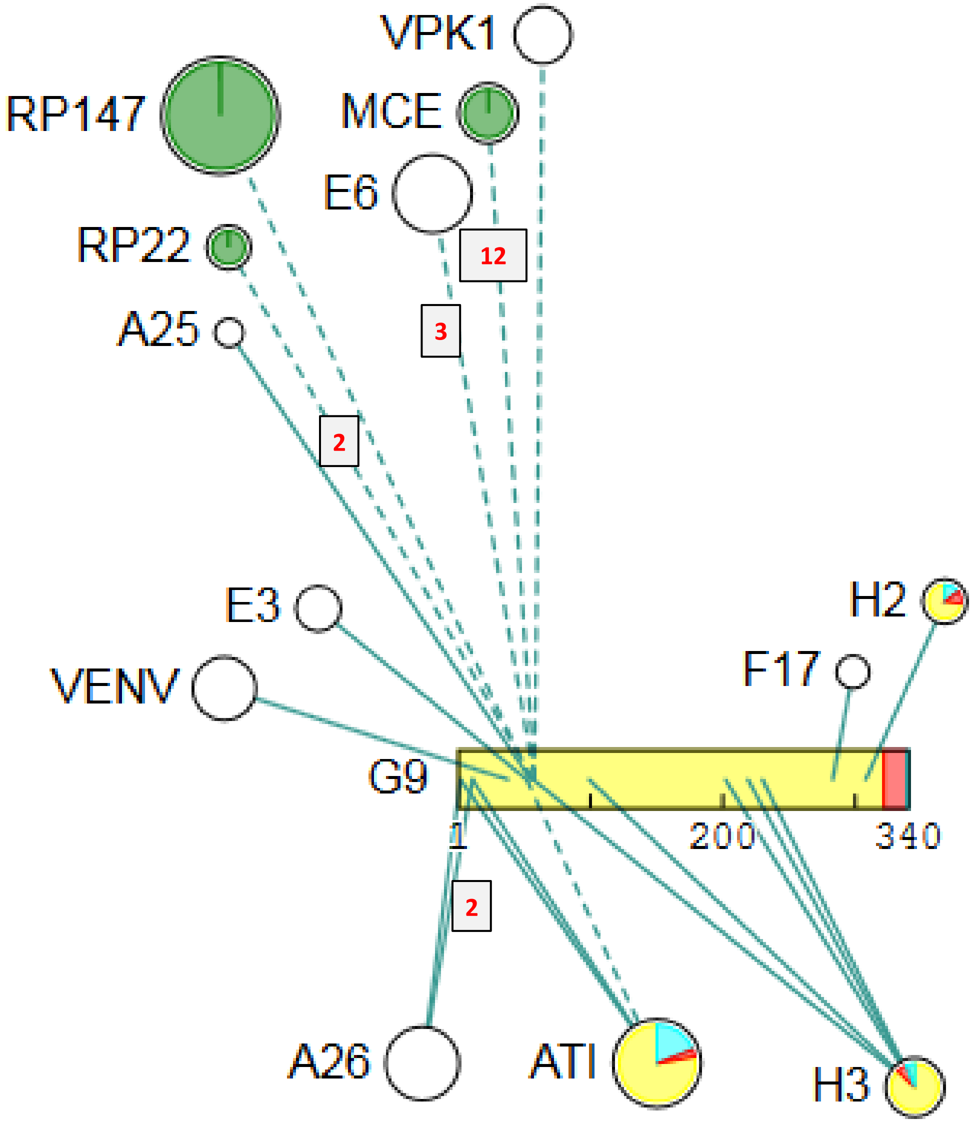
G9-55/RP147-956: 0.500

G9-57/RP22-1: 0

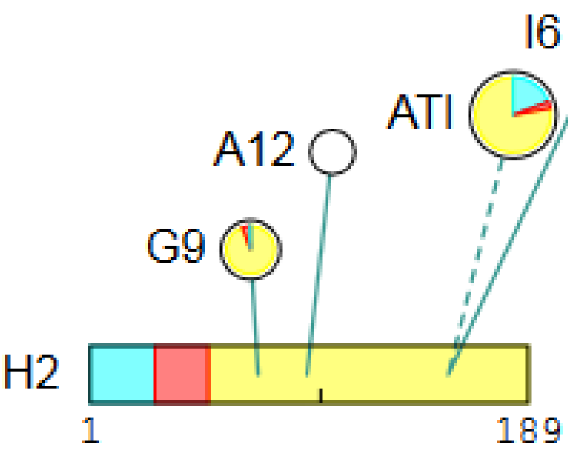
G9-58/E6-278: 0.143

G9-58/MCE-226: 0.857

G9-58/VPK1-121: 0

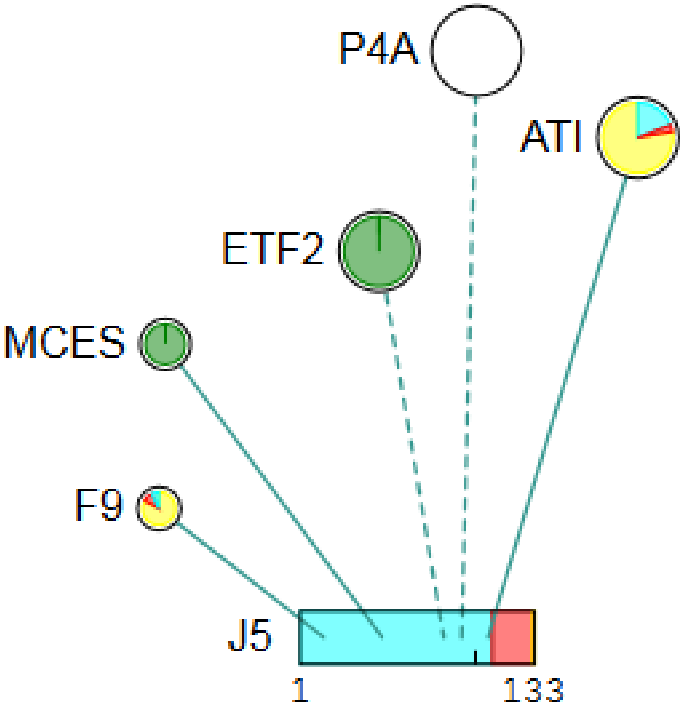


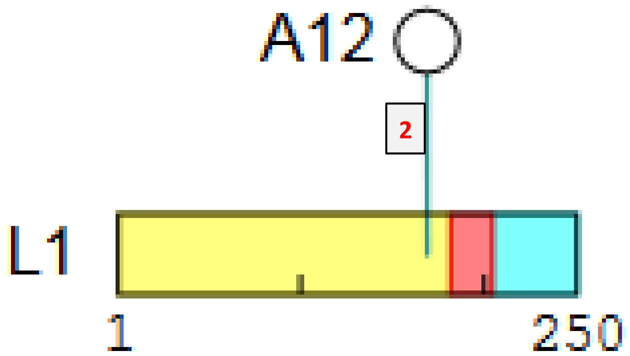
H2-155/ATI-175: 0.500



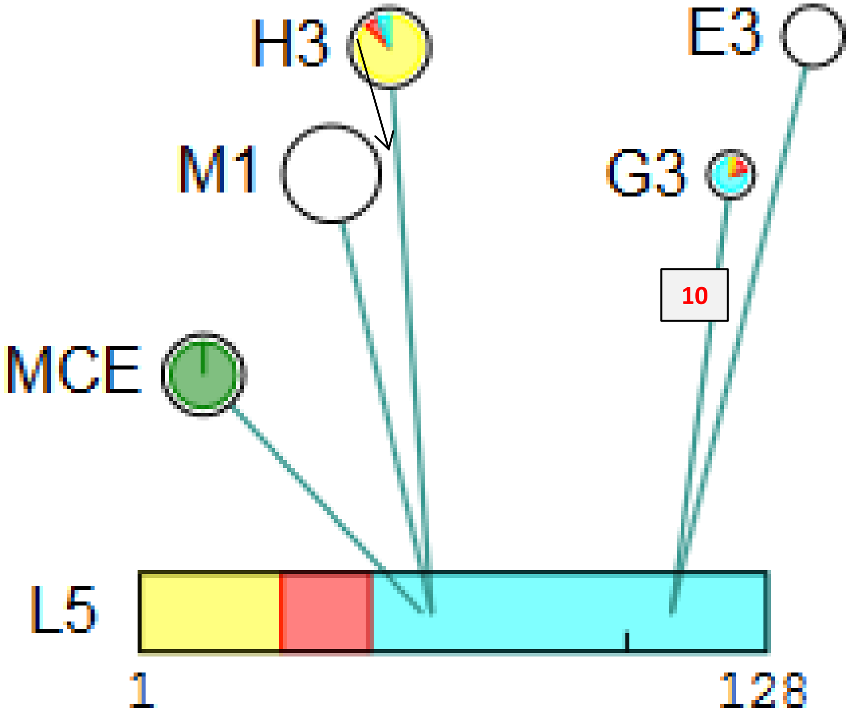
J5-82/ETF2-279: 0.500

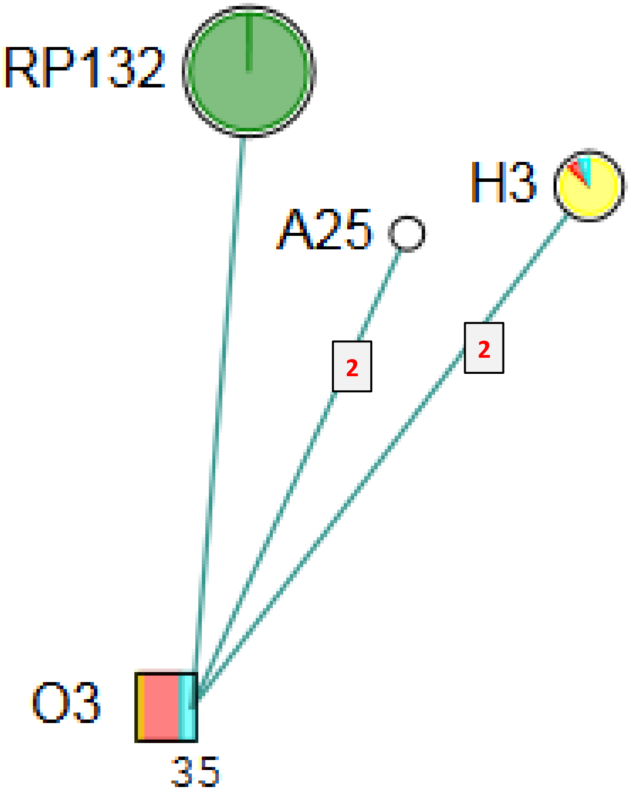
J5-92/P4A-736: 0




A12
2
L1
1
250

G3-111/L5-109: 0.750



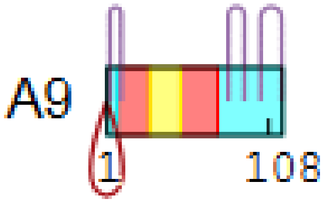

RP132
H3
A25
2
2
O3
35

Other transmembrane proteins

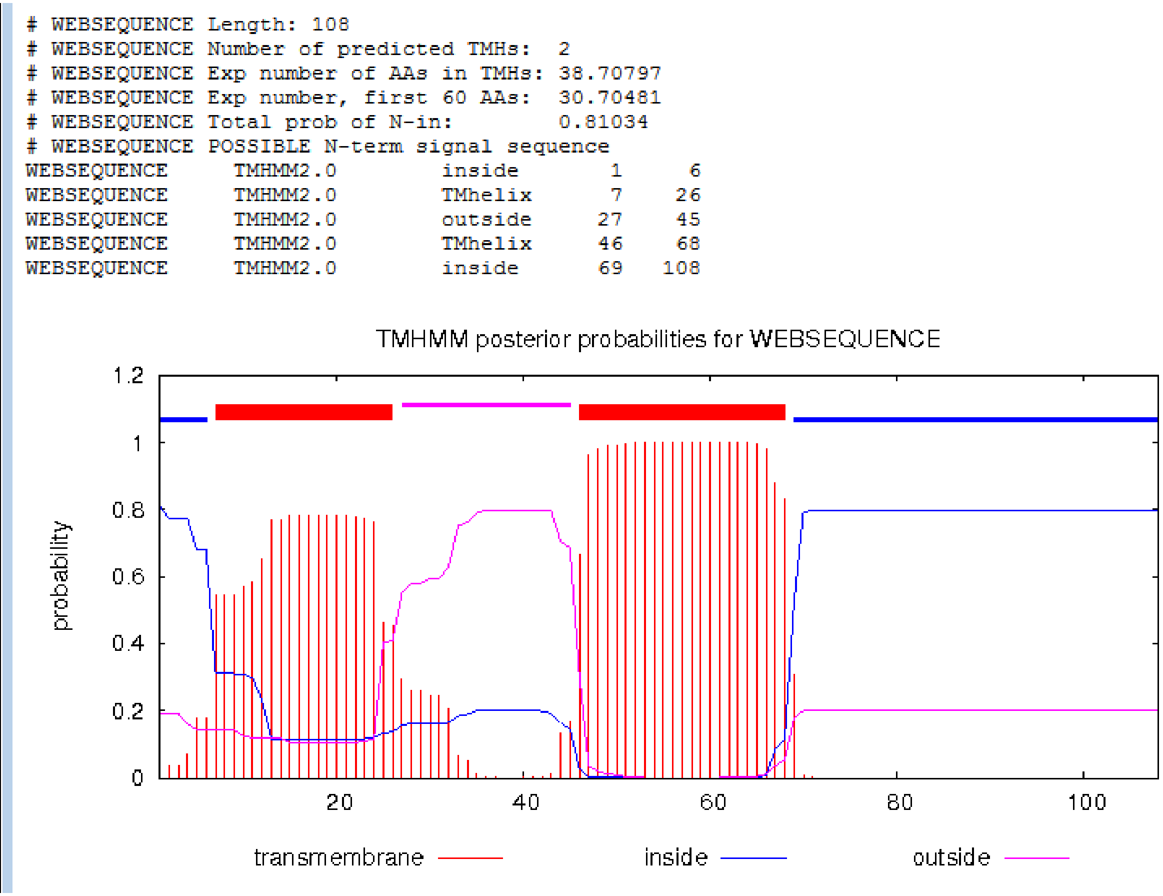
A9, A13, A17, ATI, CAHH, E8, F14.5, H3, I5

(Undetected: A14, I2)

No external XL.



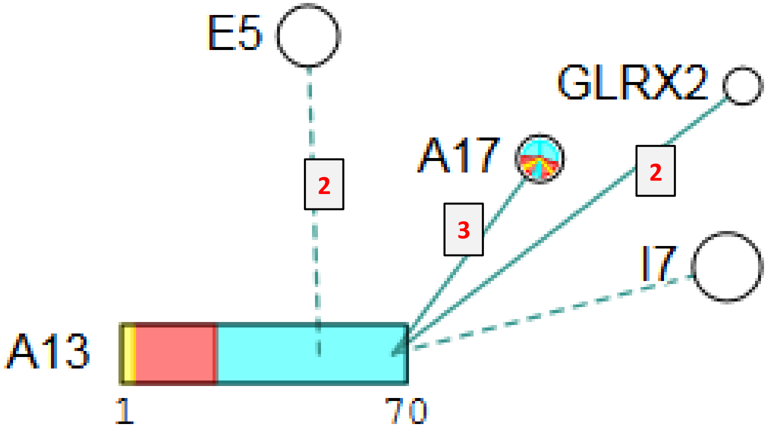
A9



```
# WEBSEQUENCE Length: 108
# WEBSEQUENCE Number of predicted TMHs:  2
# WEBSEQUENCE Exp number of AAs in TMHs: 38.70797
# WEBSEQUENCE Exp number, first 60 AAs:  30.70481
# WEBSEQUENCE Total prob of N-in:        0.81034
# WEBSEQUENCE POSSIBLE N-term signal sequence
WEBSEQUENCE     TMHMM2.0        inside       1     6
WEBSEQUENCE     TMHMM2.0        TMhelix      7    26
WEBSEQUENCE     TMHMM2.0        outside     27    45
WEBSEQUENCE     TMHMM2.0        TMhelix     46    68
WEBSEQUENCE     TMHMM2.0        inside      69   108
```

A13-49/E5-67: 0

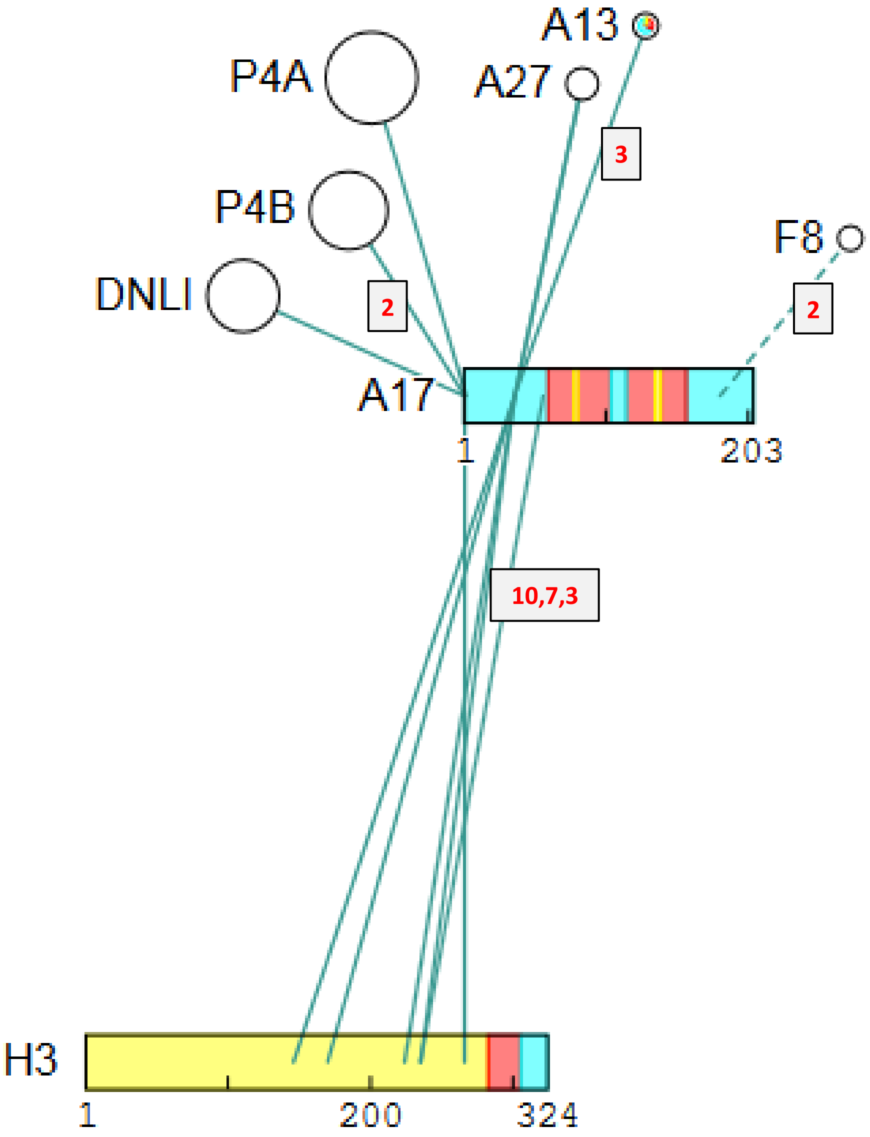
A13-67/I7-90: 0



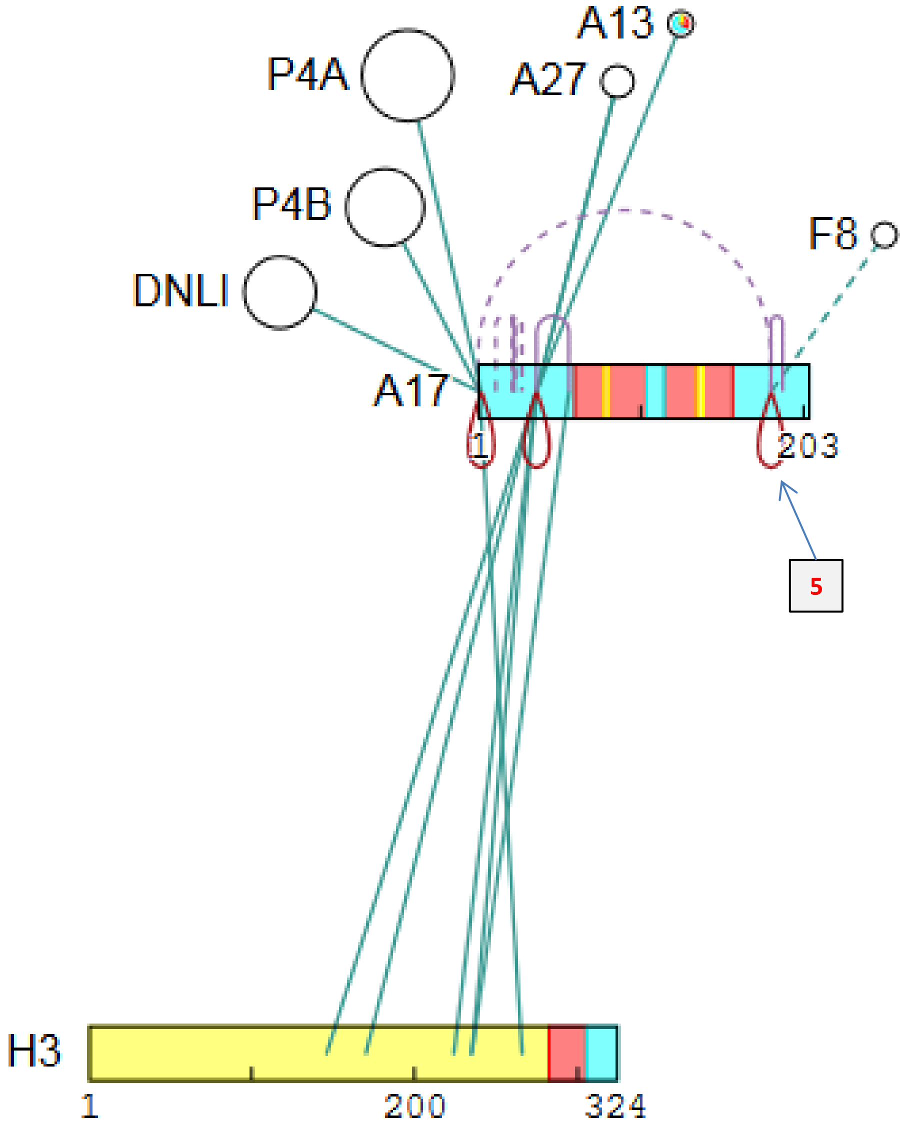
A17-36/H3-224: 0

A17-36/A27-98: 0

A17-180/F8-1: 0



As prior slide, showing intra-protein also



ATI-38/G3-111: 0.250

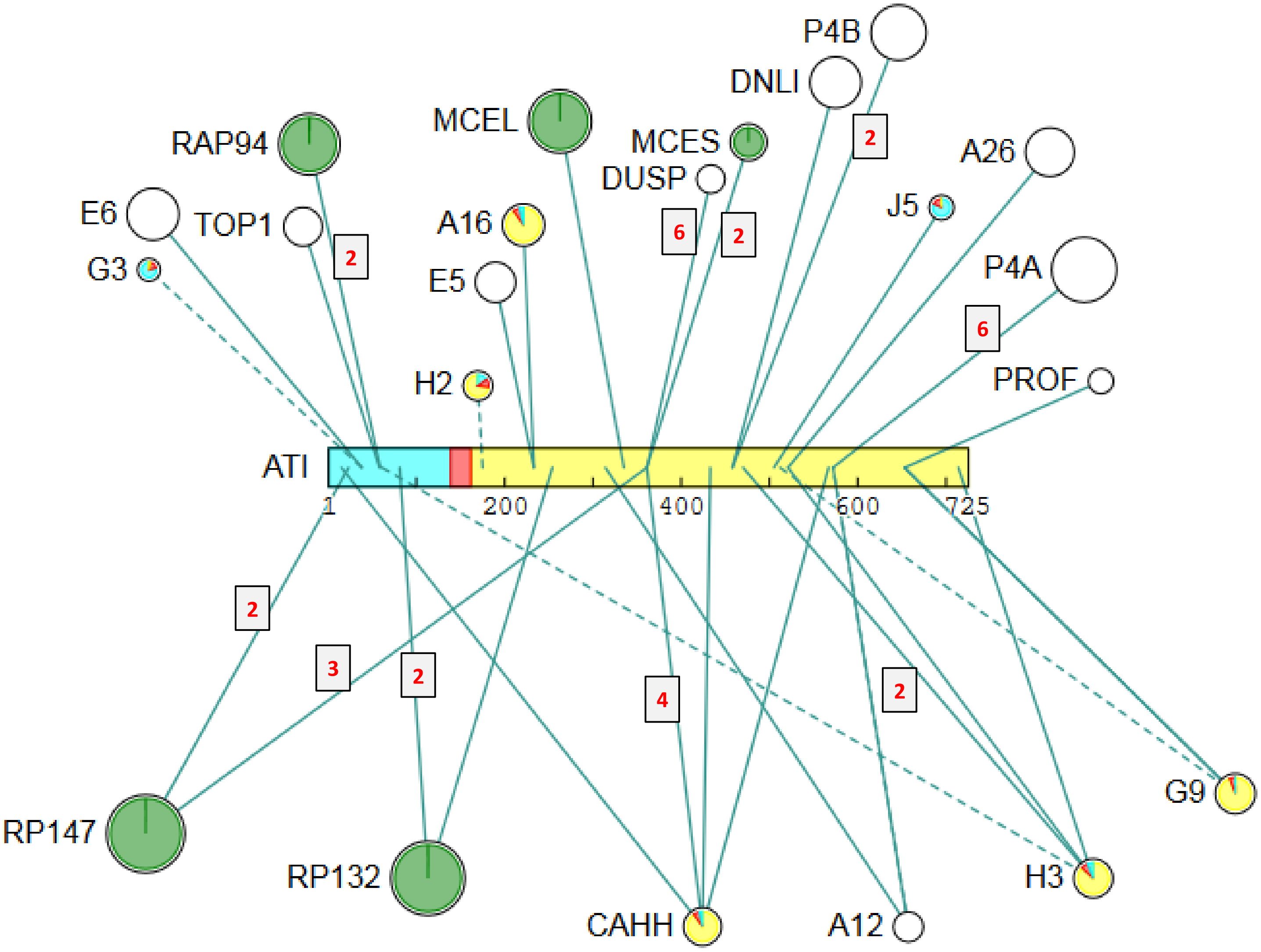
ATI-61/H3-147: 0.500

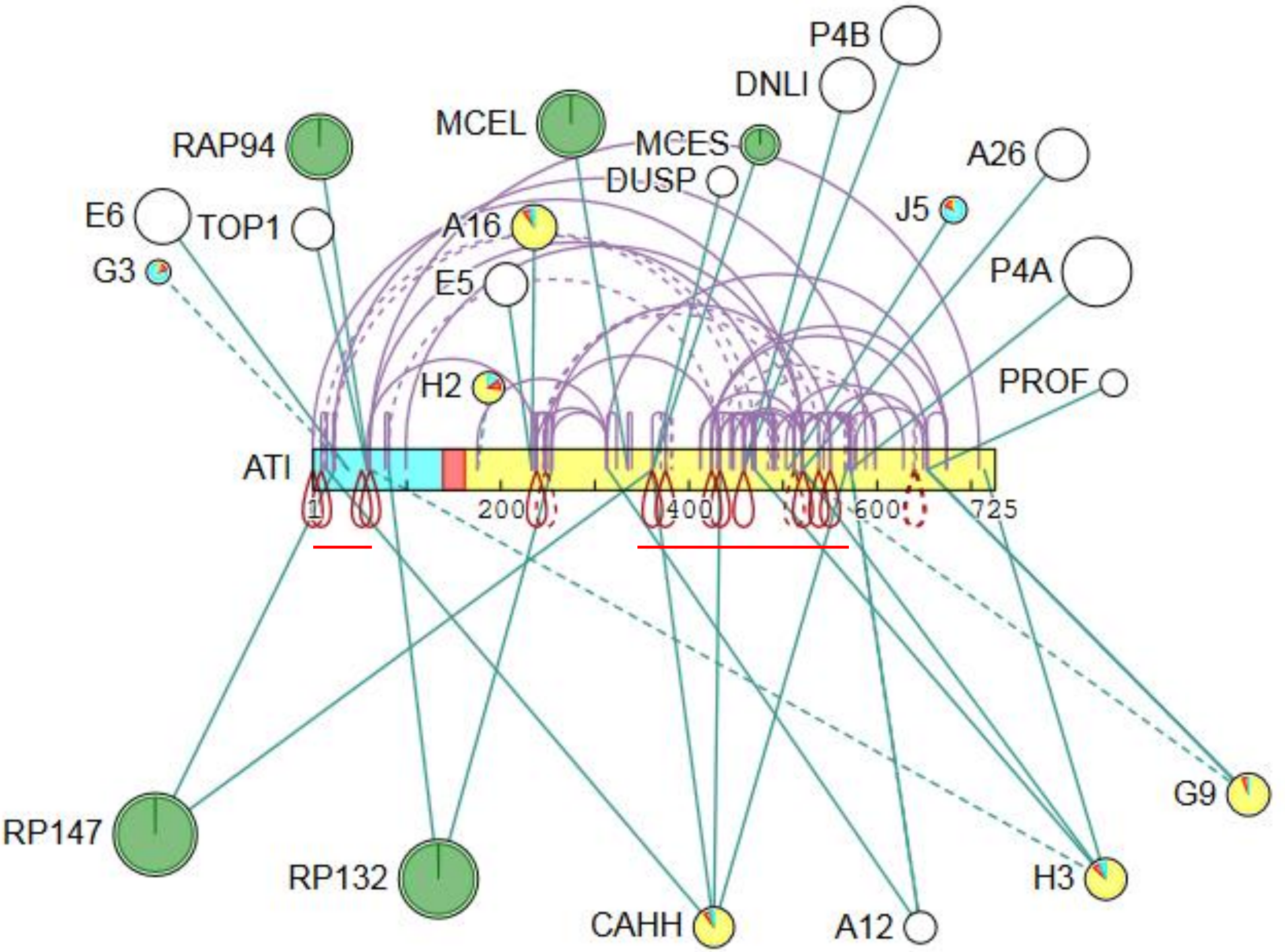
ATI-175/H2-155: 0.500

ATI-512/G9-52: 0

ATI-572/A12-88: 0

ATI-572/P4A-876: 0

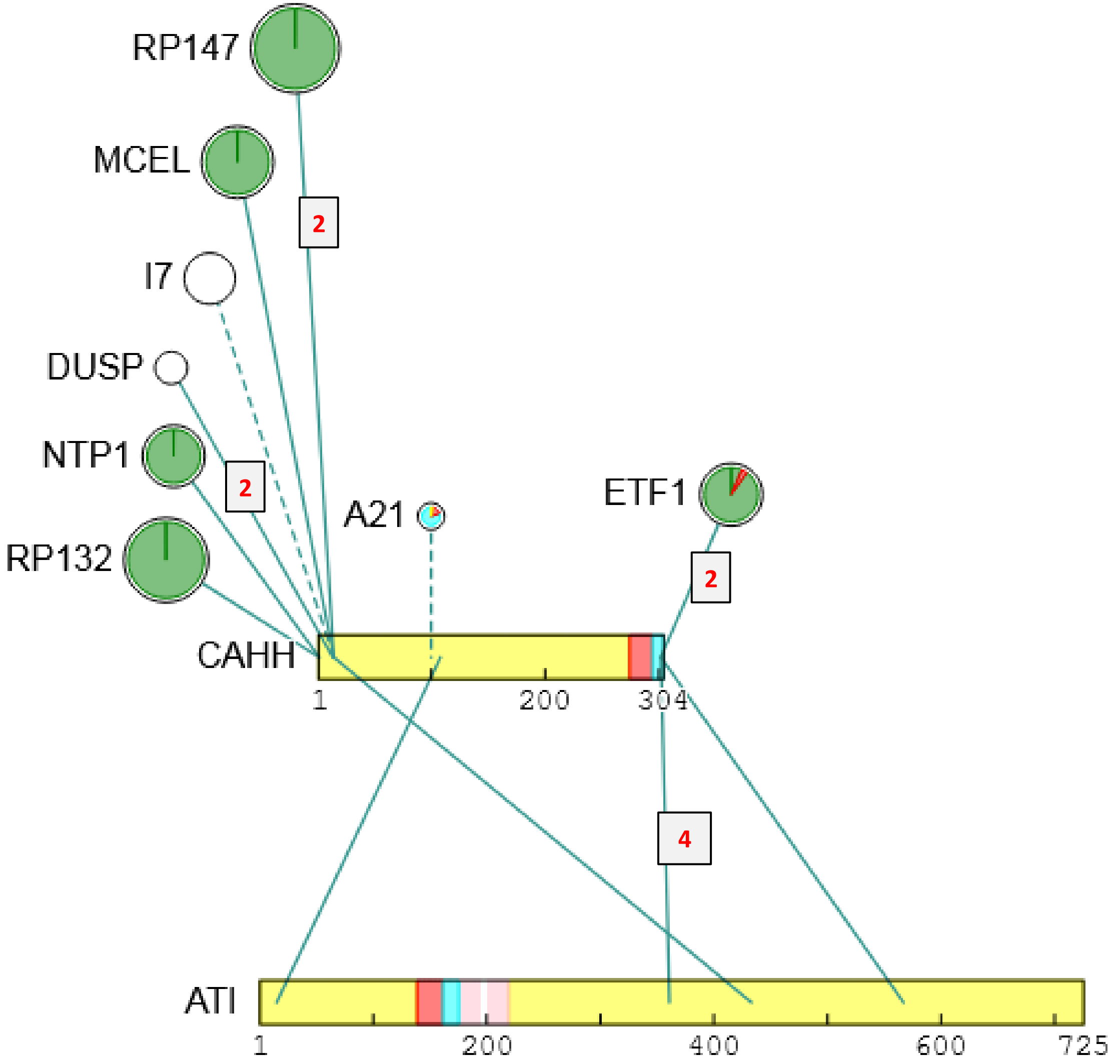




Horizontal red lines: Two dense regions of high-scoring intra-links = self-association?

CAHH-14/I7-146: 0

CAHH-100/A21-63: 0



E8 Griffiths topology (Residues 1 – 124 argued to be 'inside'):
Doglio et al. (2002) suggests N-term 120 aa is on the cytoplasmic side due to antibody reactivity.
aa144-237 would then be on non-cytoplasmic side.

E8 may loop around so that both inside (cyan) domains => transcriptosome

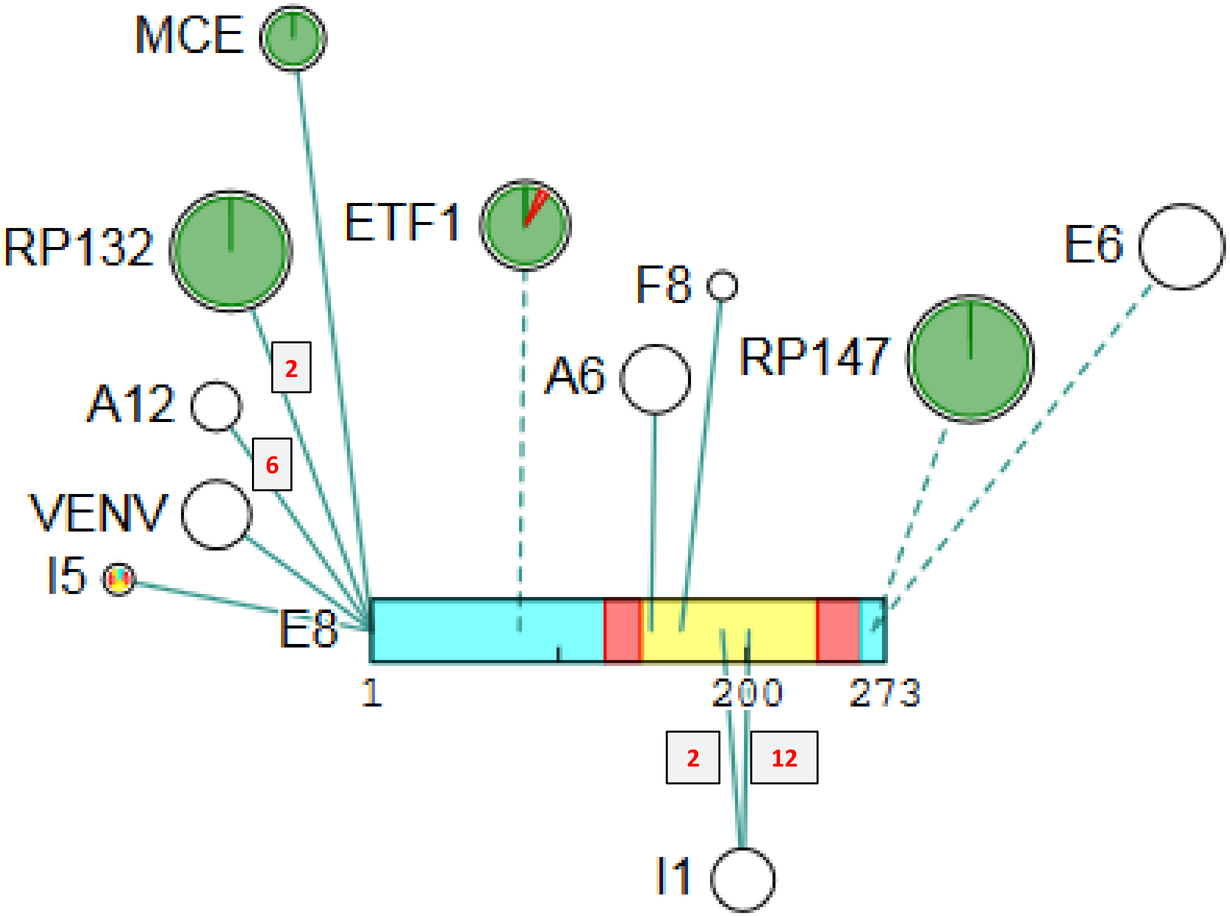
E8-1/A12-167: 0

E8-79/ETF1-229: 0

E8-201/I1-178: 1.000

E8-267/E6-552: 0

E8-267/RP147-603: 0



E8 TMHMM topology (Residues 1 – 124 argued to be 'outside'):
TMHMM suggests with 55% probability 'N-outside'
aa144-237 would then be on cytoplasmic (cyan) side.

Here, E8 may loop around so that both outside (yellow) domains => transcriptosome.

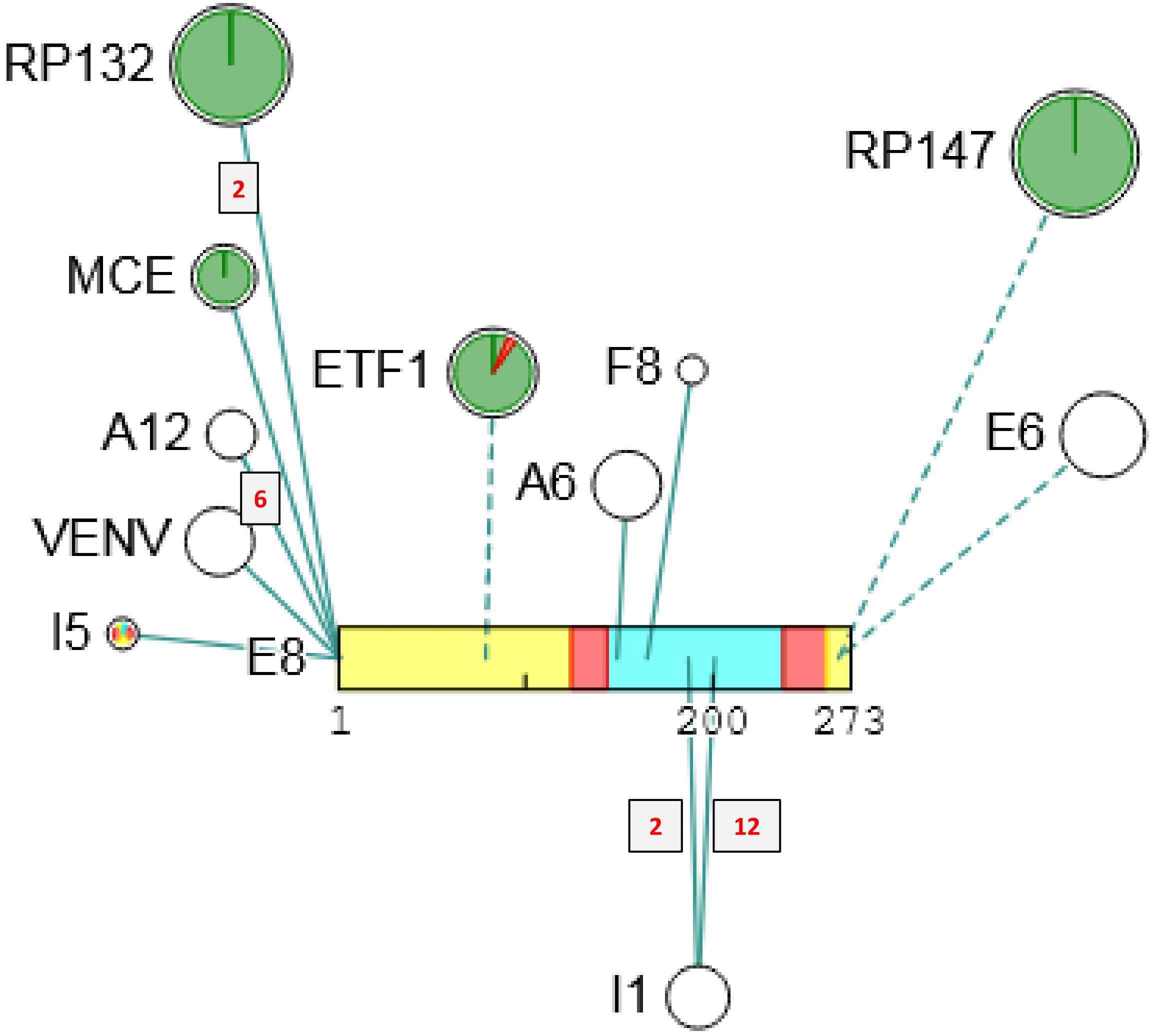
E8-1/A12-167: 0

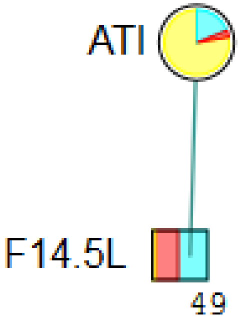
E8-79/ETF1-229: 0

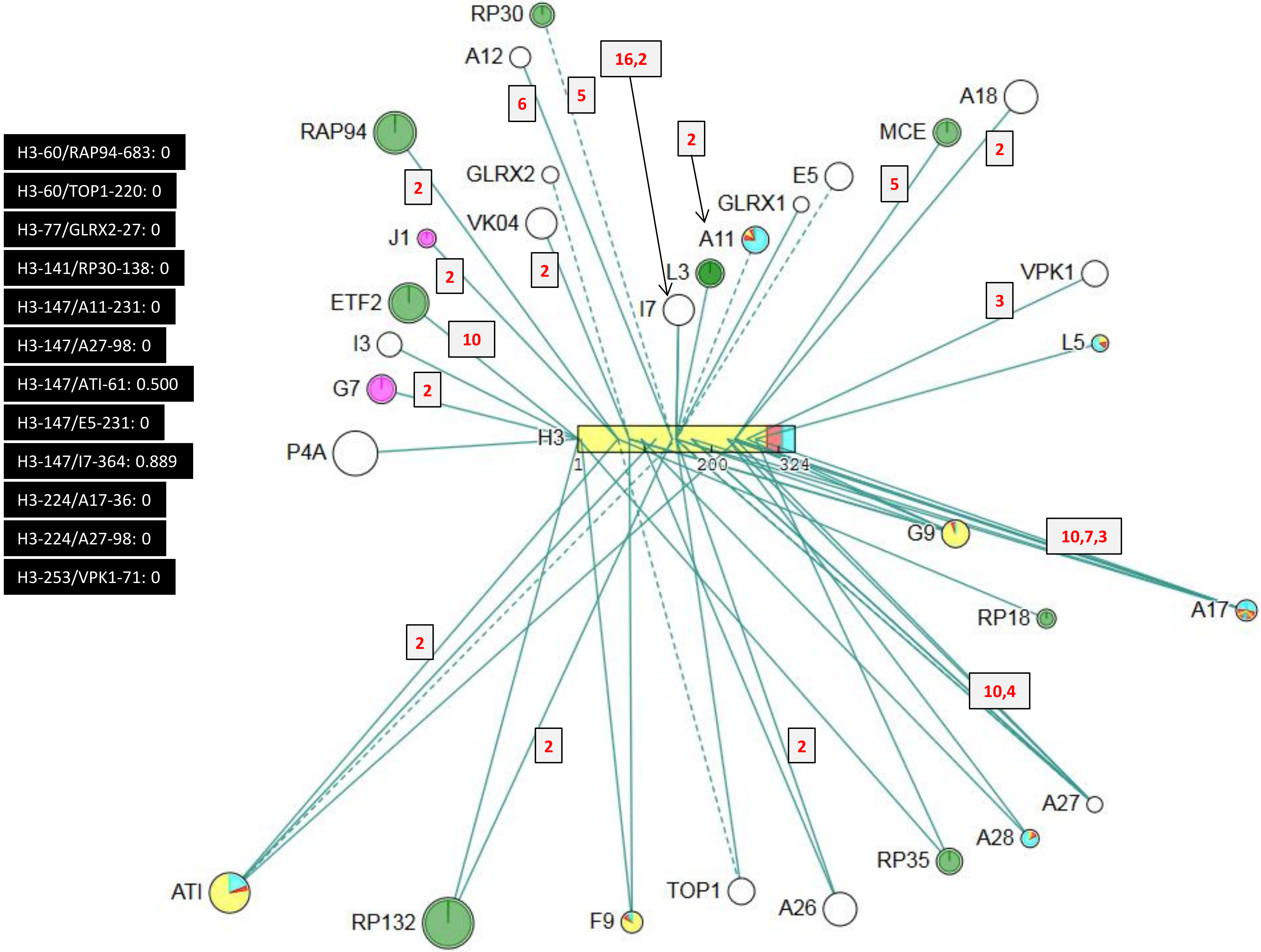
E8-201/I1-178: 1.000

E8-267/E6-552: 0

E8-267/RP147-603: 0




ATI
F14.5L
49



H3-60/RAP94-683: 0

H3-60/TOP1-220: 0

H3-77/GLRX2-27: 0

H3-141/RP30-138: 0

H3-147/A11-231: 0

H3-147/A27-98: 0

H3-147/ATI-61: 0.500

H3-147/E5-231: 0

H3-147/I7-364: 0.889

H3-224/A17-36: 0

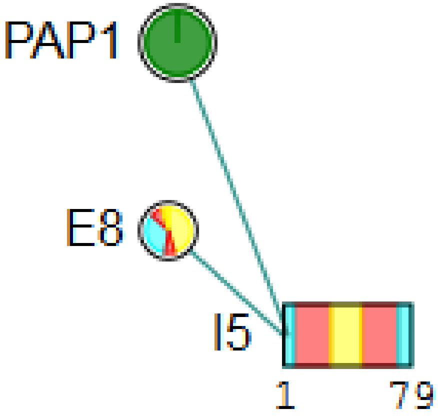
H3-224/A27-98: 0

H3-253/VPK1-71: 0

I5 is shown with N-inside topology (next page: TMHMM gives probability for N-inside = 55%).

Below: I5 N-terminal ‘inside’ (cyan) domain crosslinks to inside domain of E8, only if E8 is in ‘Griffiths’ topology (four pages back) as opposed to ‘TMHMM’ topology (three pages back).

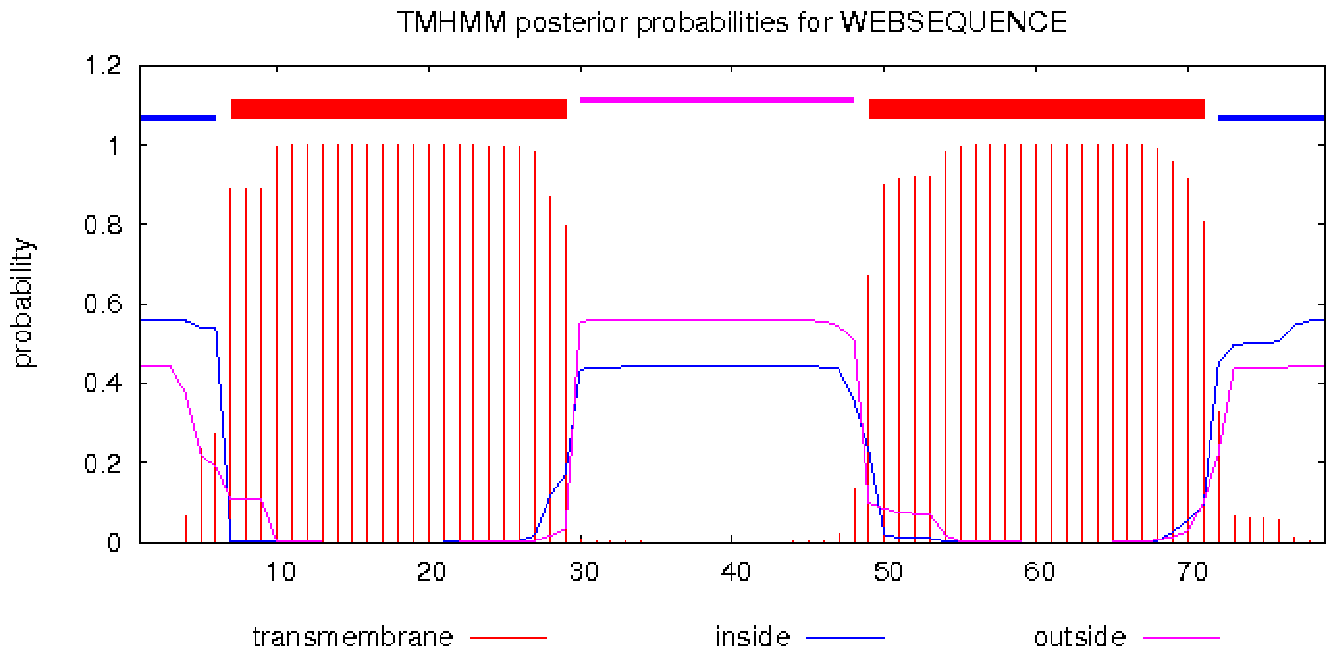
PARADOX: TMHMM topology is incorrect for either E8 or I5 according to the E8-I5 crosslink.



TMHMM result

HELP with output formats

```
# WEBSEQUENCE Length: 79
# WEBSEQUENCE Number of predicted TMHs:  2
# WEBSEQUENCE Exp number of AAs in TMHs: 45.57927
# WEBSEQUENCE Exp number, first 60 AAs:  34.33226
# WEBSEQUENCE Total prob of N-in:        0.55770
# WEBSEQUENCE POSSIBLE N-term signal sequence
WEBSEQUENCE     TMHMM2.0        inside       1     6
WEBSEQUENCE     TMHMM2.0        TMhelix      7    29
WEBSEQUENCE     TMHMM2.0        outside     30    48
WEBSEQUENCE     TMHMM2.0        TMhelix     49    71
WEBSEQUENCE     TMHMM2.0        inside      72    79
```



VMAPs

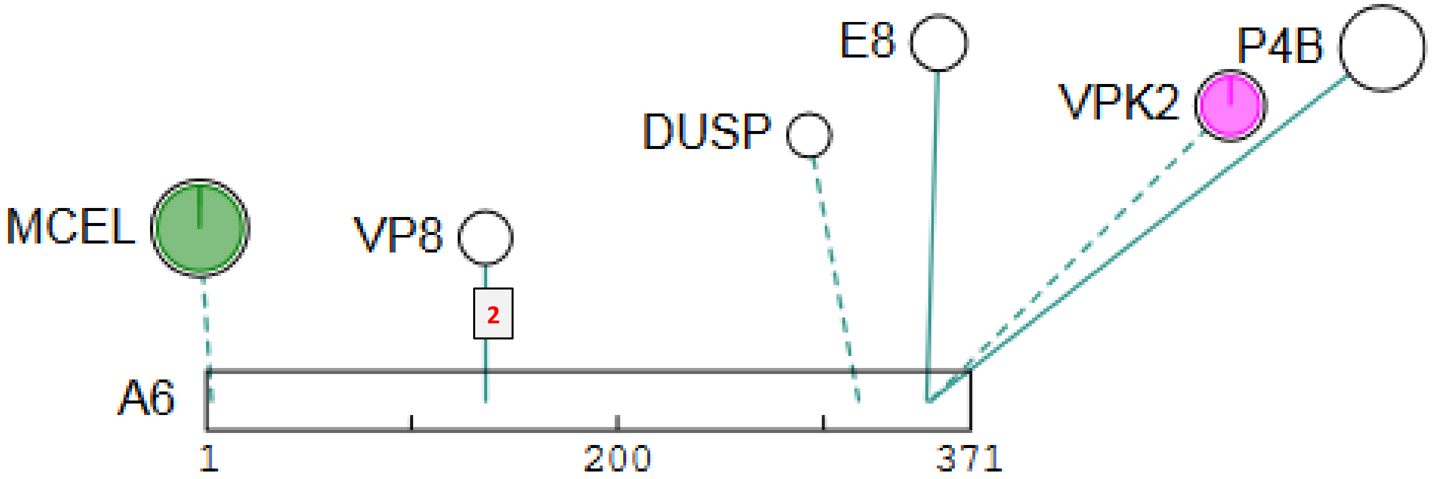
A6, A11

A6-3/MCEL-843: 0.500

A6-136/VP8-175: 0

A6-317/DUSP-8: 0

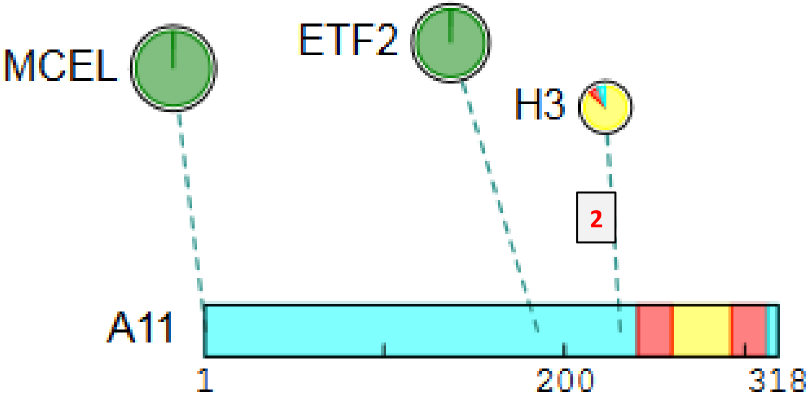
A6-352/VPK2-205: 0.500



A11-1/MCEL-797: 0.143

A11-185/ETF2-584: 0.500

A11-231/H3-147: 0



Membrane-associated non-TM proteins

A26, A27, VENV(F13)

A26-37/RP147-147: 0

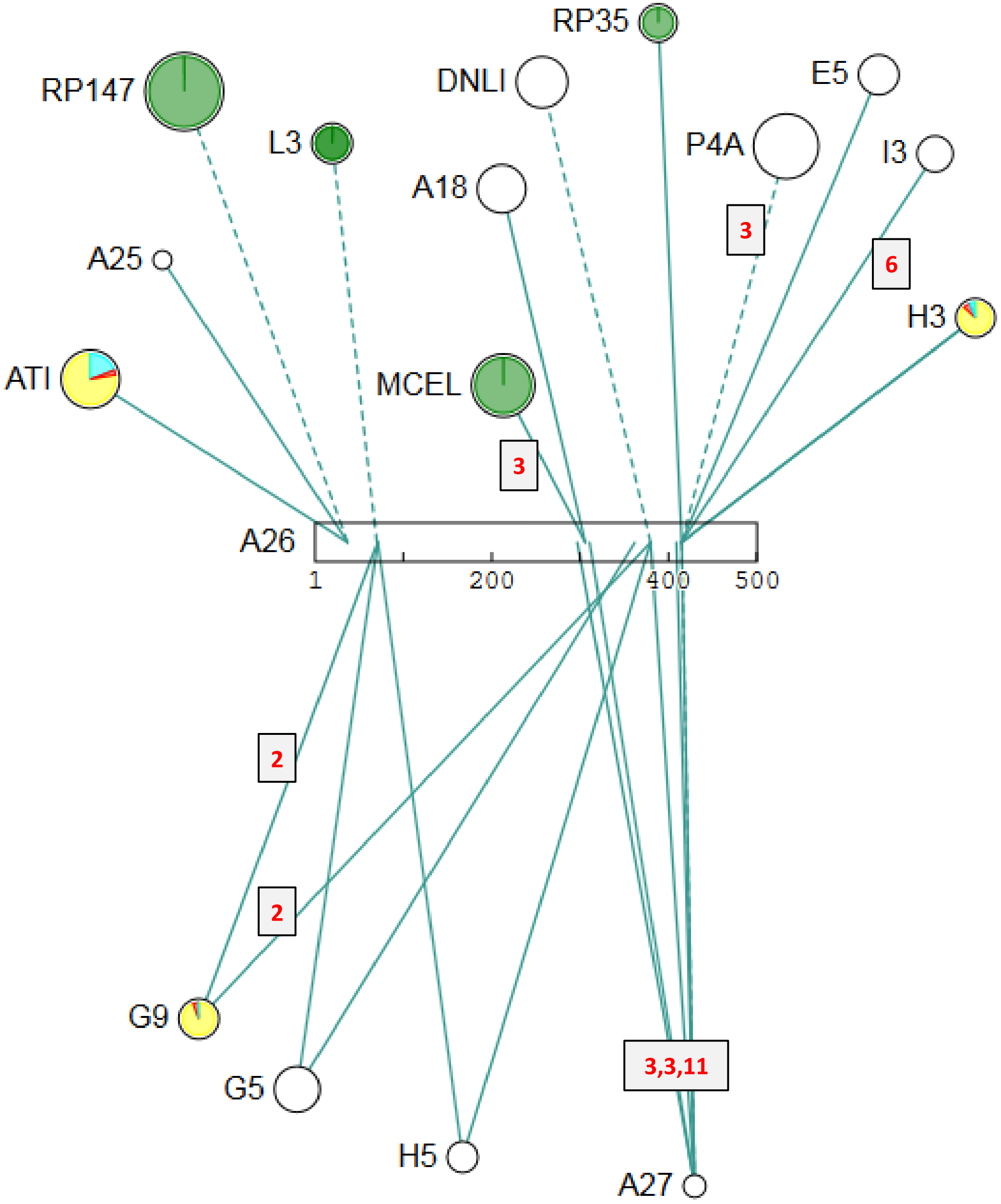
A26-70/L3-18: 0

A26-306/MCEL-588: 0

A26-380/DNLI-399: 0.500

A26-415/A27-48: 0

A26-415/P4A-660: 0



A27-37/A16-116: 0

A27-48/A26-415: 0

A27-57/E5-0: 0

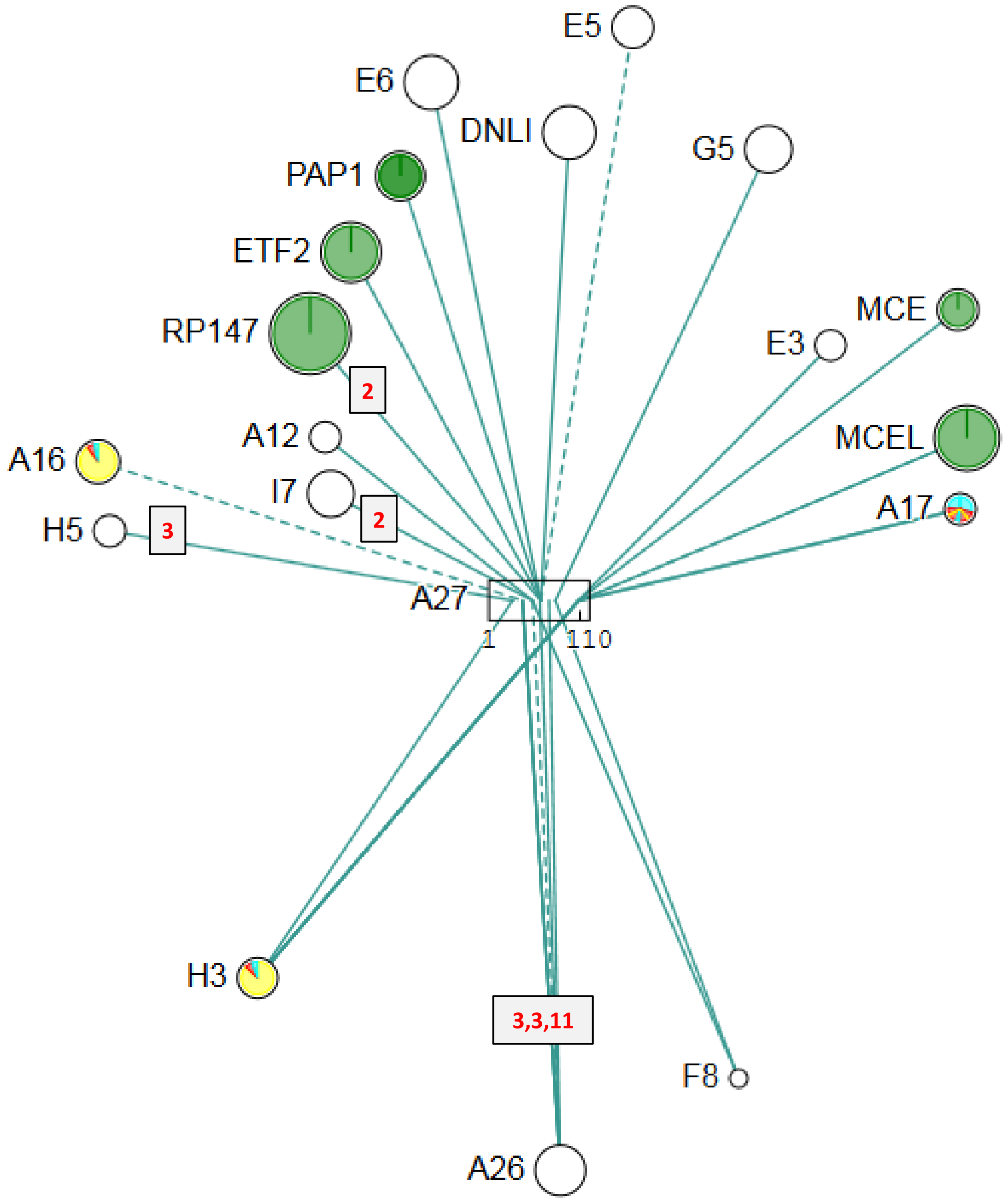
A27-57/RP147-956: 0

A27-98/A17-36: 0

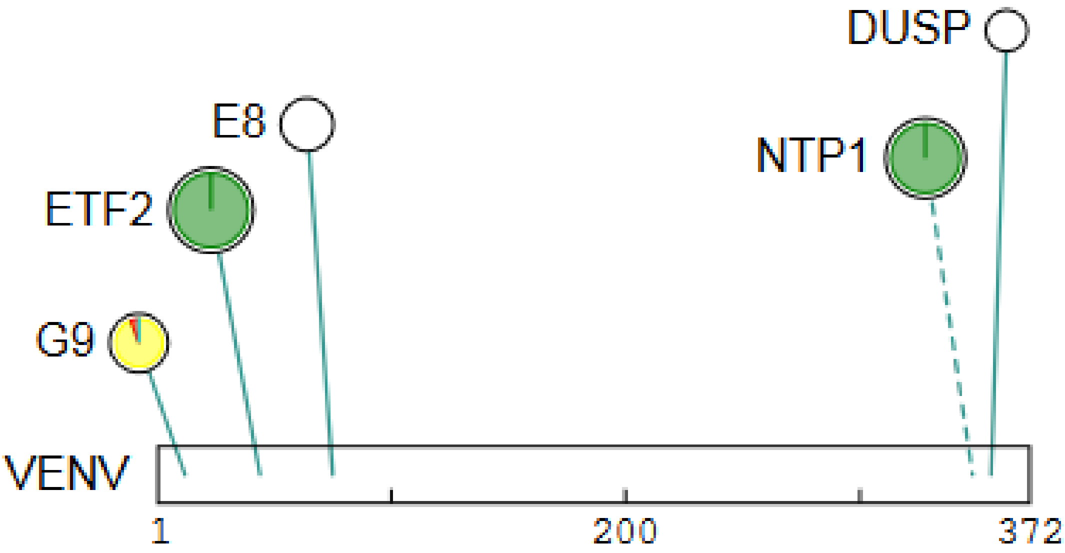
A27-98/H3-224: 0

A27-98/H3-147: 0

A27-99/MCEL-136: 0.500



VENV-348/NTP1-324: 0



Transcriptosome (mRNA biogenesis) proteins

ETF1, ETF2, L3, MCE, MCEL, MCES, NTP1, PAP1, NPH2, RP147, RP132, RAP94 , RP35 , RP30 , RP22 , RP19 , RP18, RP07

ETF1-229/E8-79: 0

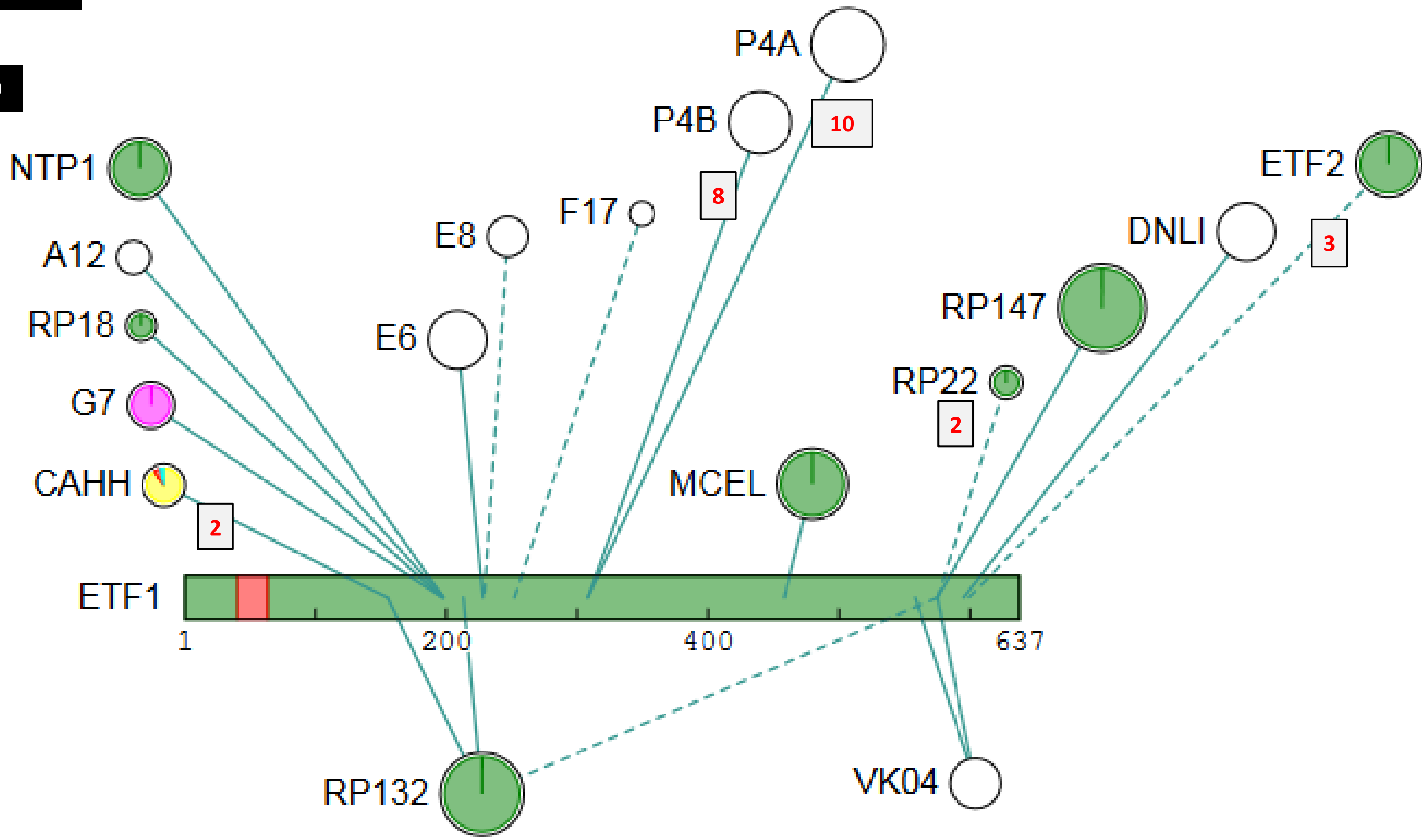
ETF1-252/F17-50: 0

ETF1-308/P4A-736: 0.333

ETF1-575/RP132-421: 0.500

ETF1-575/RP22-1: 0

ETF1-599/ETF2-647: 0



ETF2-67/P4B-185: 0

ETF2-112/I1-193: 0

ETF2-279/J5-82: 0.500

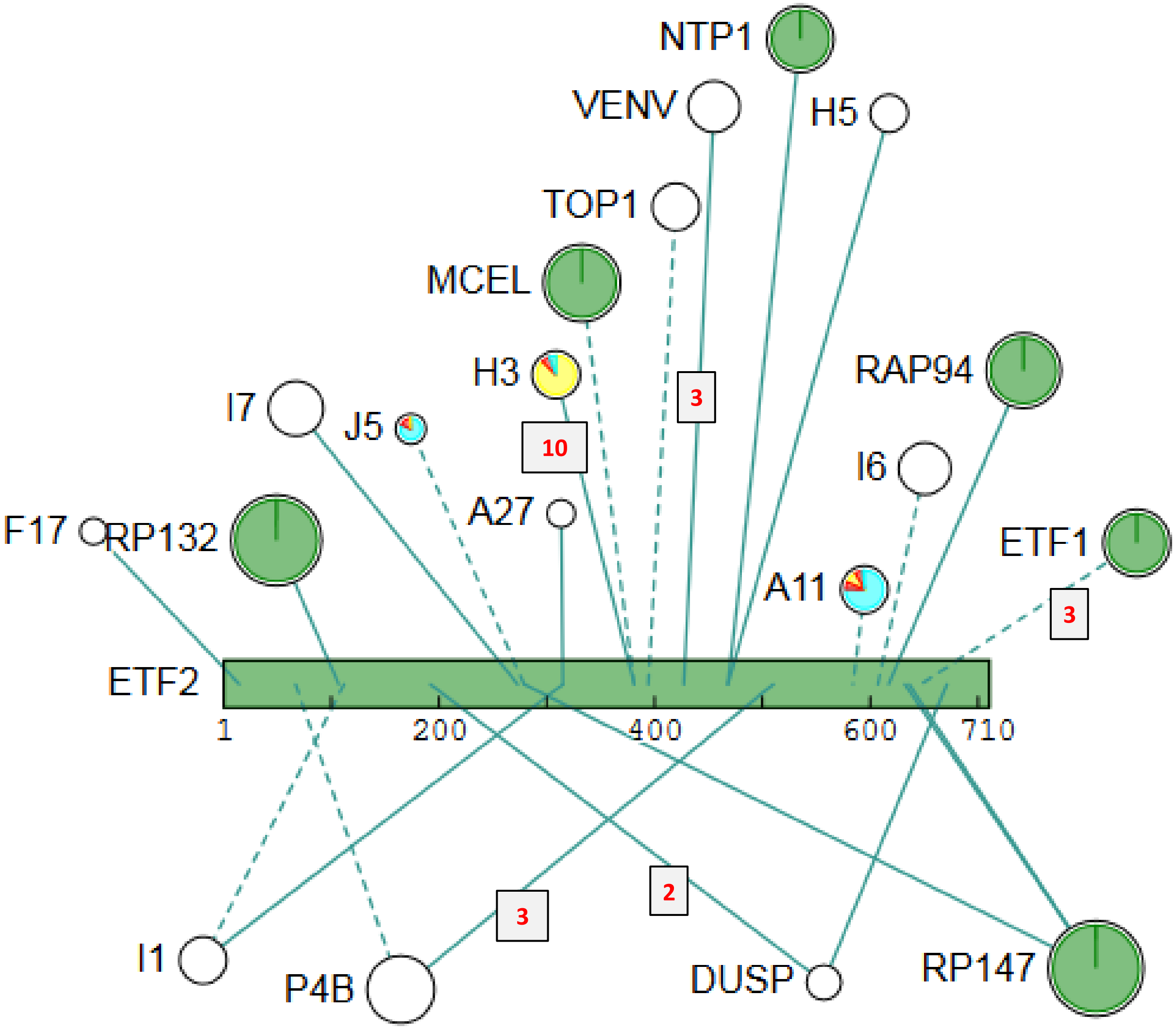
ETF2-381/MCEL-719: 0

ETF2-394/TOP1-207: 0

ETF2-584/A11-185: 0.500

ETF2-607/I6-305: 0.333

ETF2-647/ETF1-599: 0

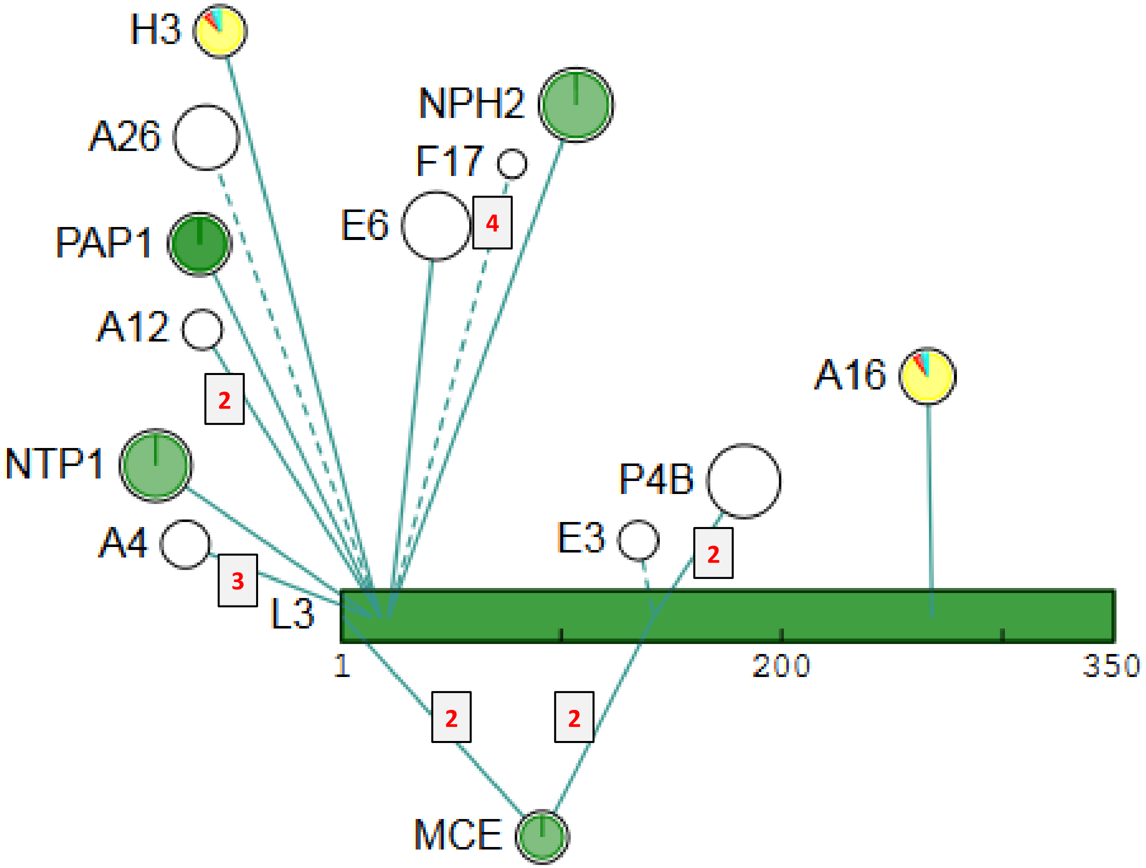


L3-18/A12-167: 0

L3-18/A26-70: 0

L3-22/F17-74: 0

L3-142/E3-165: 0.500

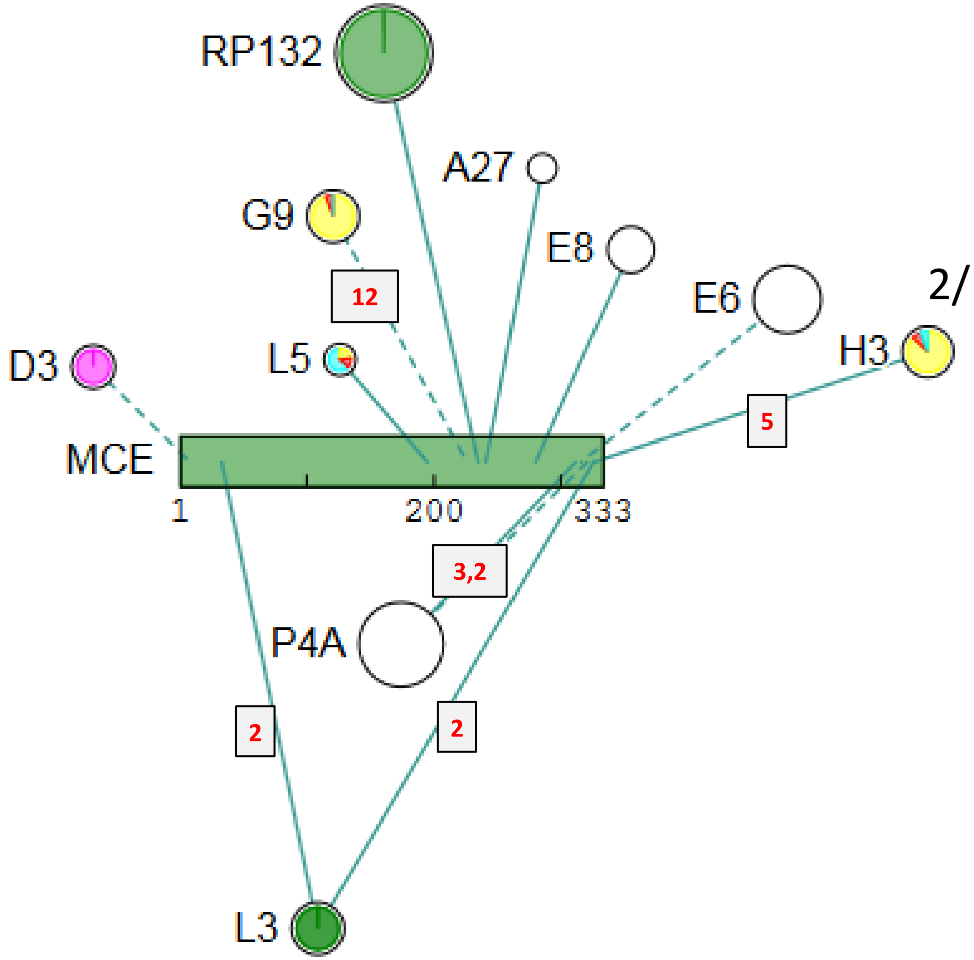


MCE-8/D3-1: 0

MCE-226/G9-58: 0.857

MCE-316/E6-440: 0.500

MCE-321/P4A-876: 0.018



2/10 = txn

MCEL-136/A27-99: 0.500

MCEL-136/G5-87: 0.500

MCEL-136/RP18-47: 1.000

MCEL-308/NTP1-280: 0

MCEL-386/RP19-156: 0

MCEL-433/P4B-83: 0.500

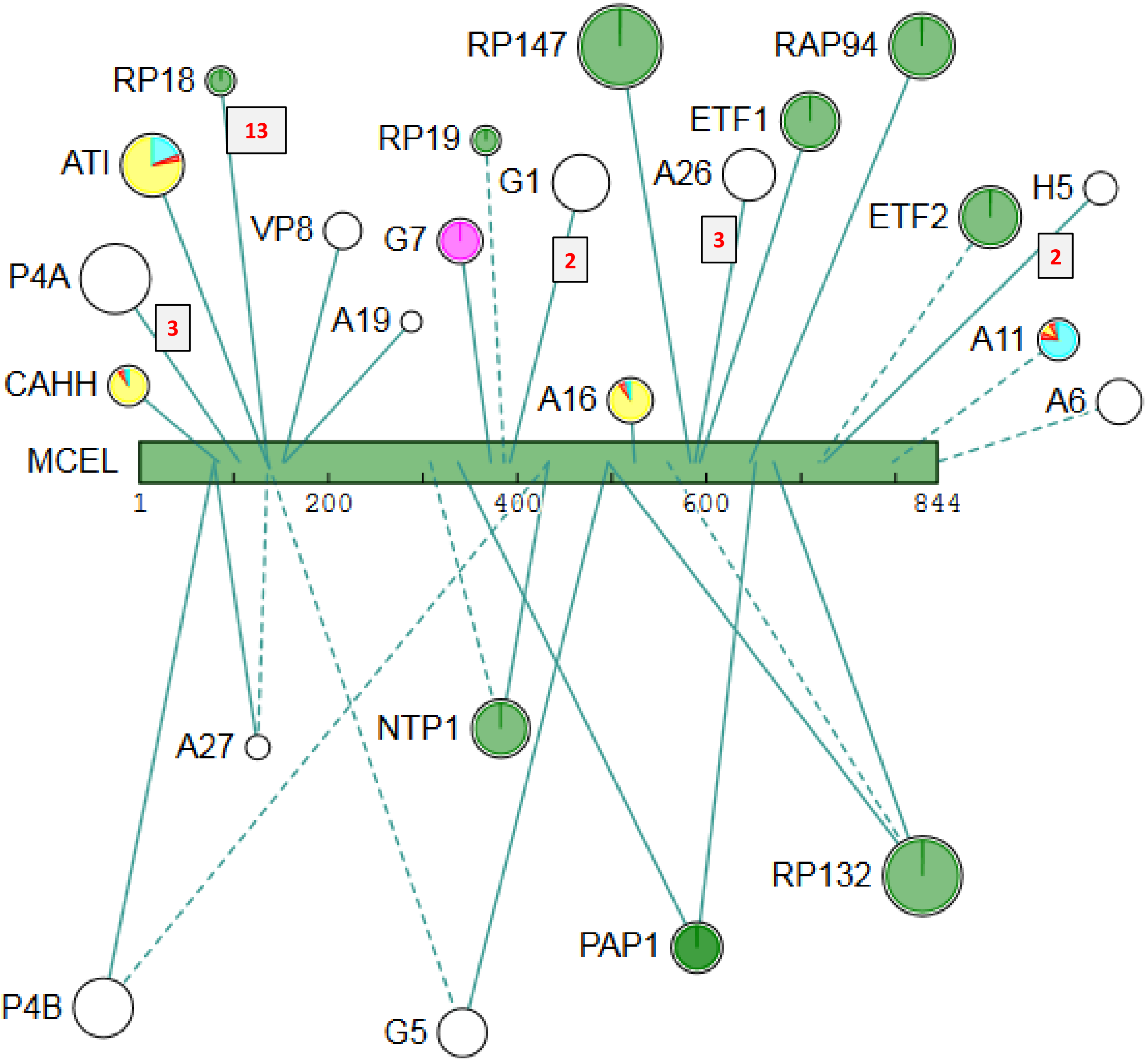
MCEL-559/RP132-1046: 0

MCEL-588/A26-306: 0

MCEL-719/ETF2-381: 0

MCEL-797/A11-1: 0.143

MCEL-843/A6-3: 0.500

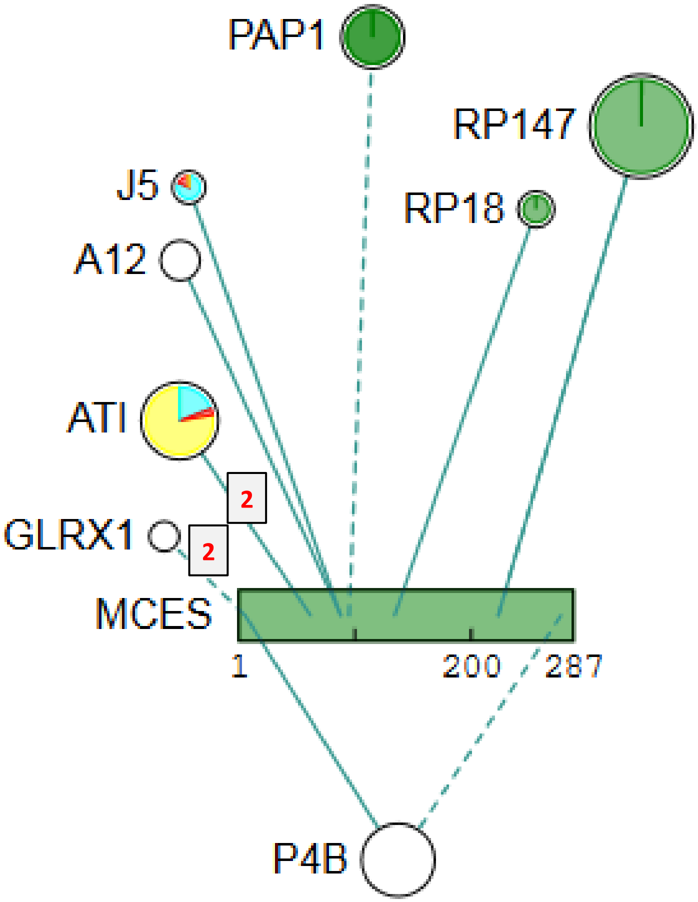


MCES-6/GLRX1-35: 0

MCES-95/PAP1-170: 0.500

MCES-223/RP147-242: 0

MCES-277/P4B-83: 0.500



NTP1-32/E11-62: 0

NTP1-56/G5-337: 1.000

NTP1-56/G5-350: 1.000

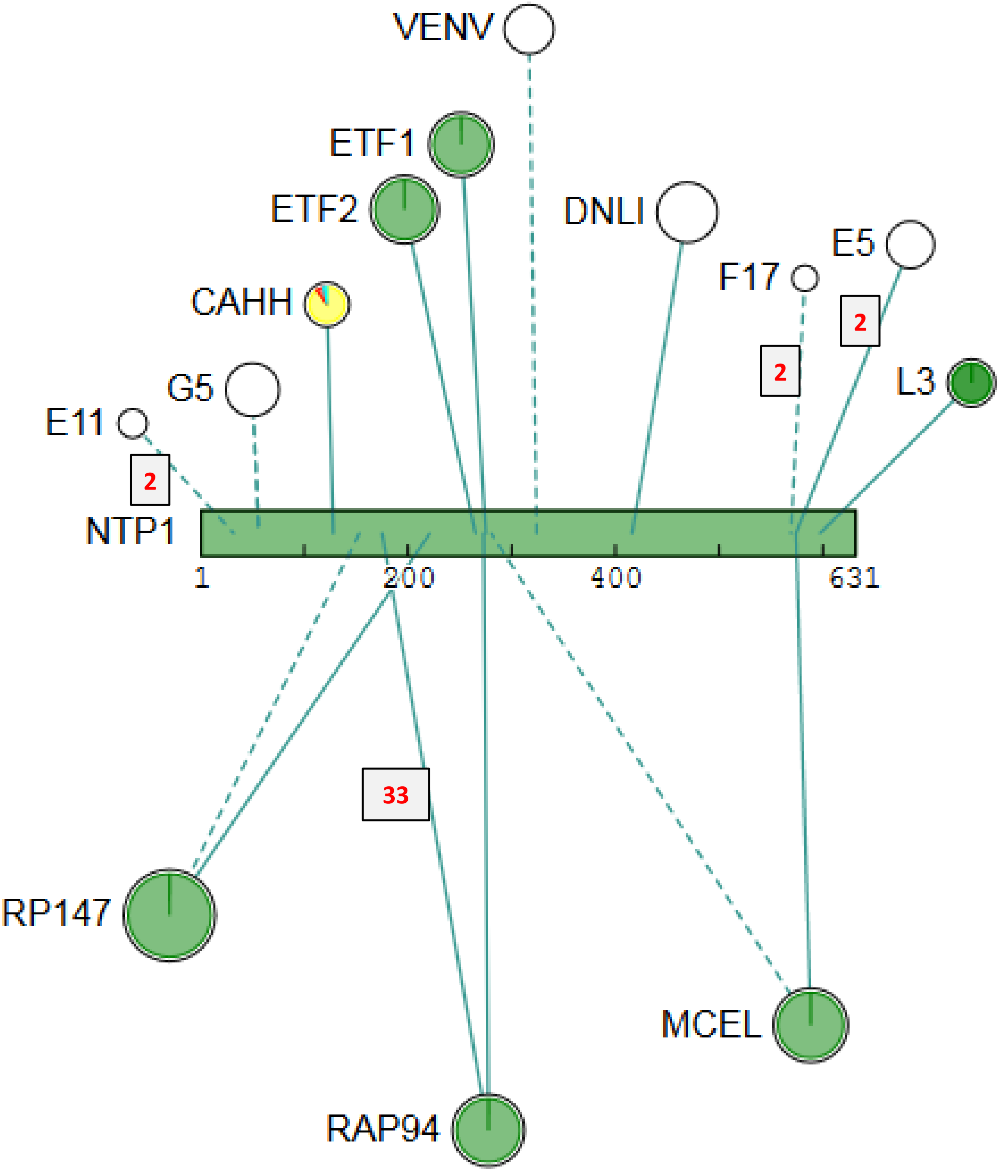
NTP1-153/RP147-724: 0.500

NTP1-175/RAP94-177: 1.000

NTP1-280/MCEL-308: 0

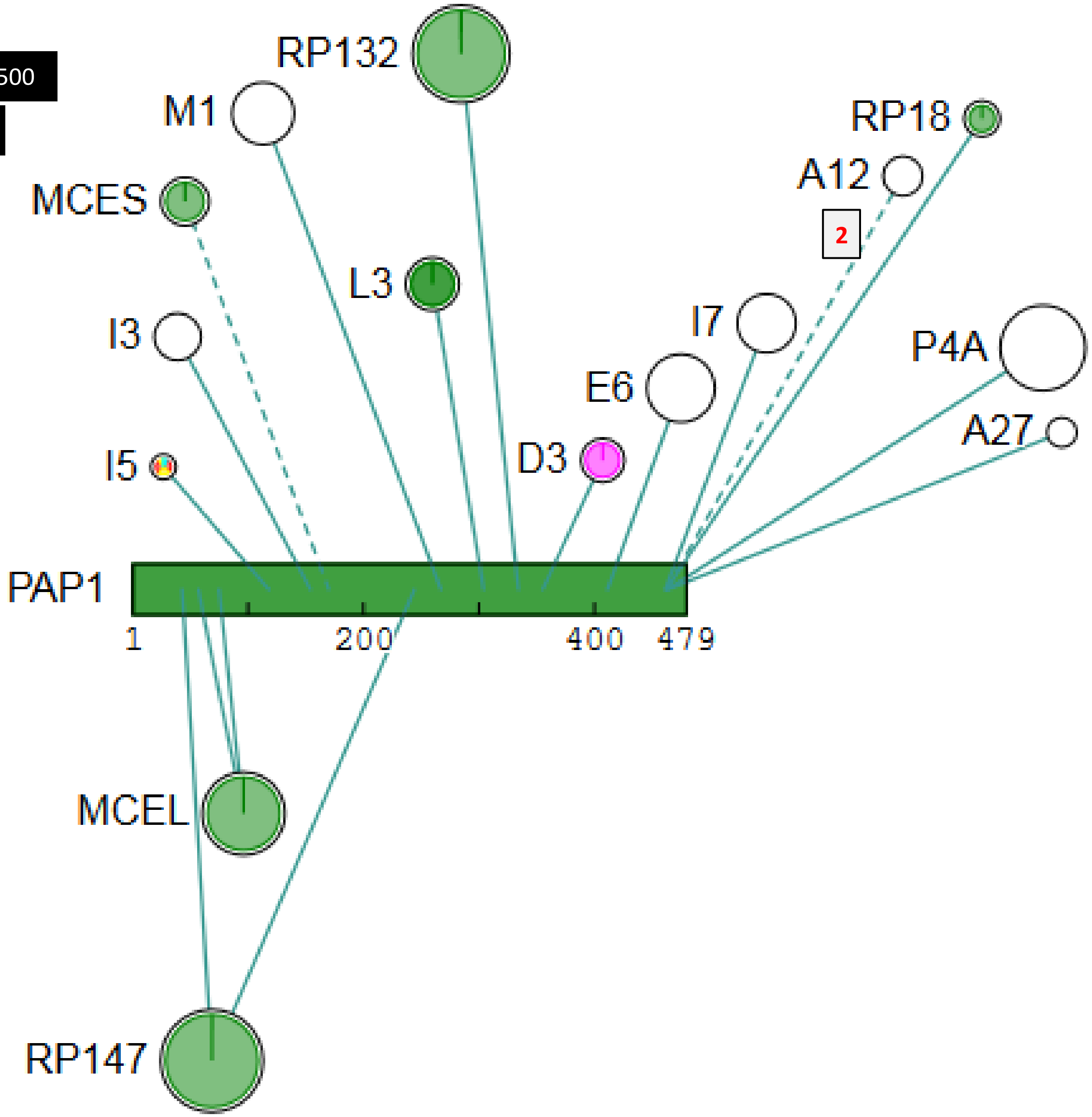
NTP1-324/VENV-348: 0

NTP1-569/F17-74: 0



PAP1-170/MCES-95: 0.500

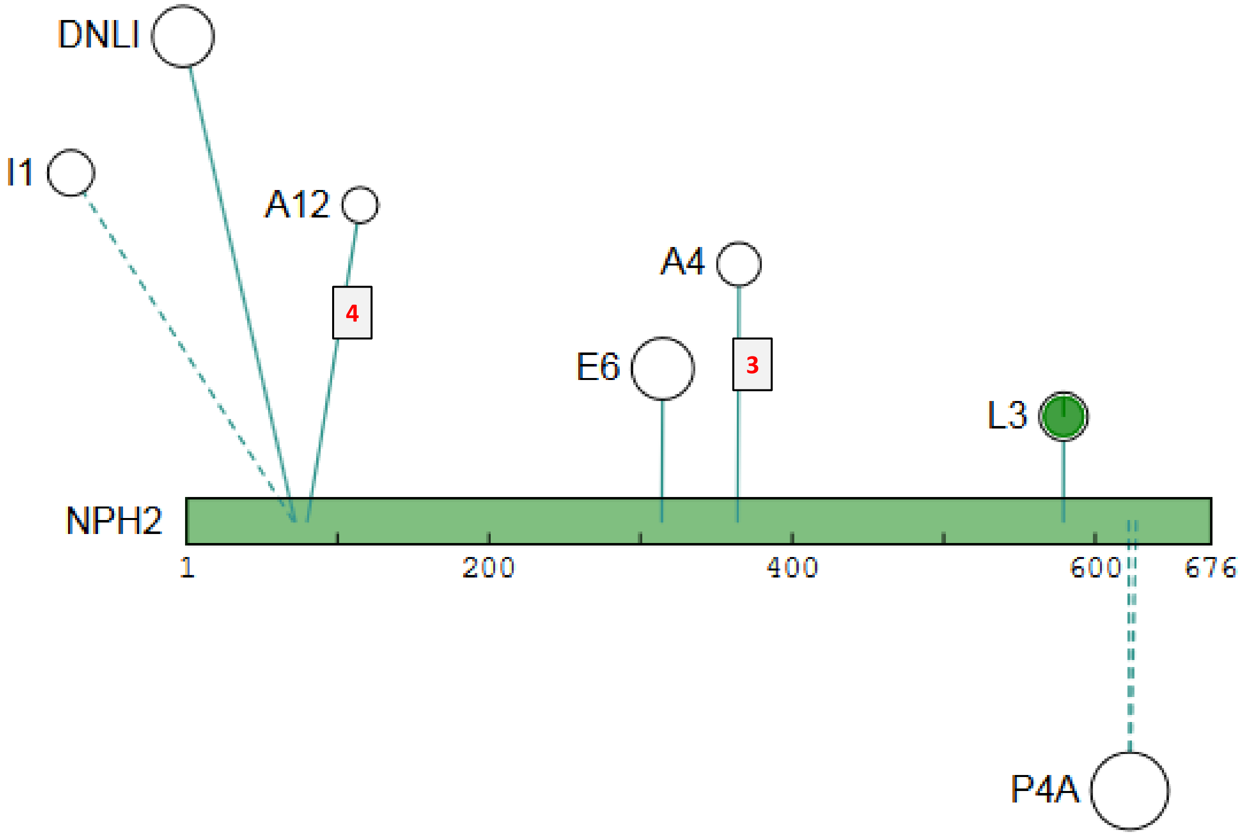
PAP1-462/A12-167: 0



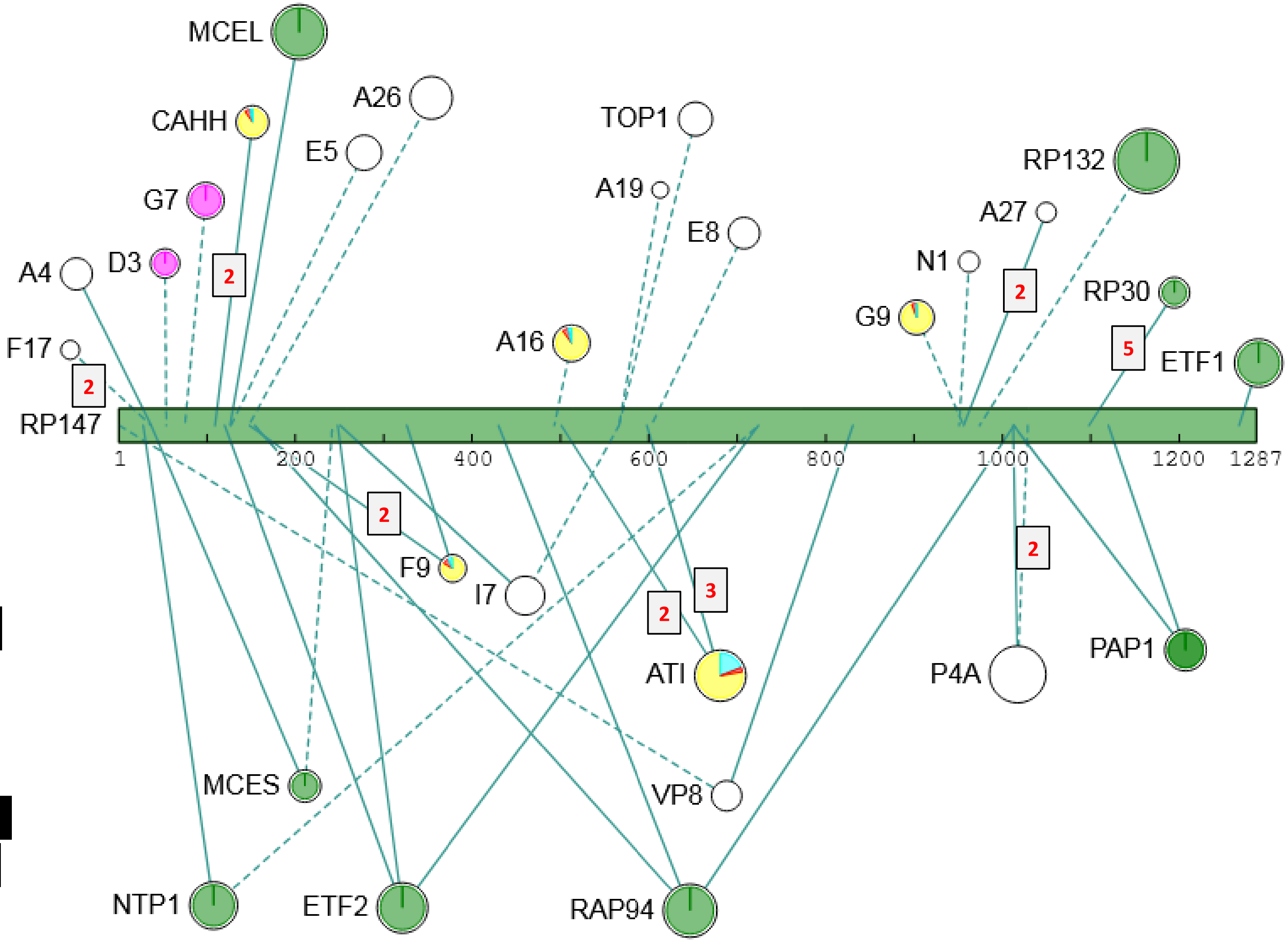
NPH2-71/I1-37: 0

NPH2-622/P4A-876: 0.167

NPH2-627/P4A-508: 0



RP147-1/VP8-153: 0
RP147-37/F17-17: 0
RP147-54/D3-7: 0
RP147-75/G7-1: 0
RP147-127/E5-314: 0
RP147-147/A26-37: 0
RP147-148/F9-203: 0.111
RP147-242/MCES-223: 0
RP147-493/A16-153: 0
RP147-566/A19-1: 0
RP147-566/I7-53: 0
RP147-566/TOP1-74: 0
RP147-603/E8-267: 0
RP147-724/NTP1-153: 0.500
RP147-951/N1-78: 0
RP147-956/A27-57: 0
RP147-956/G9-55: 0.500
RP147-974/RP132-452: 0.500
RP147-1029/P4A-876: 0.286



RP132-421/ETF1-575: 0.500

RP132-452/RP147-974: 0.500

RP132-511/A19-46: 0

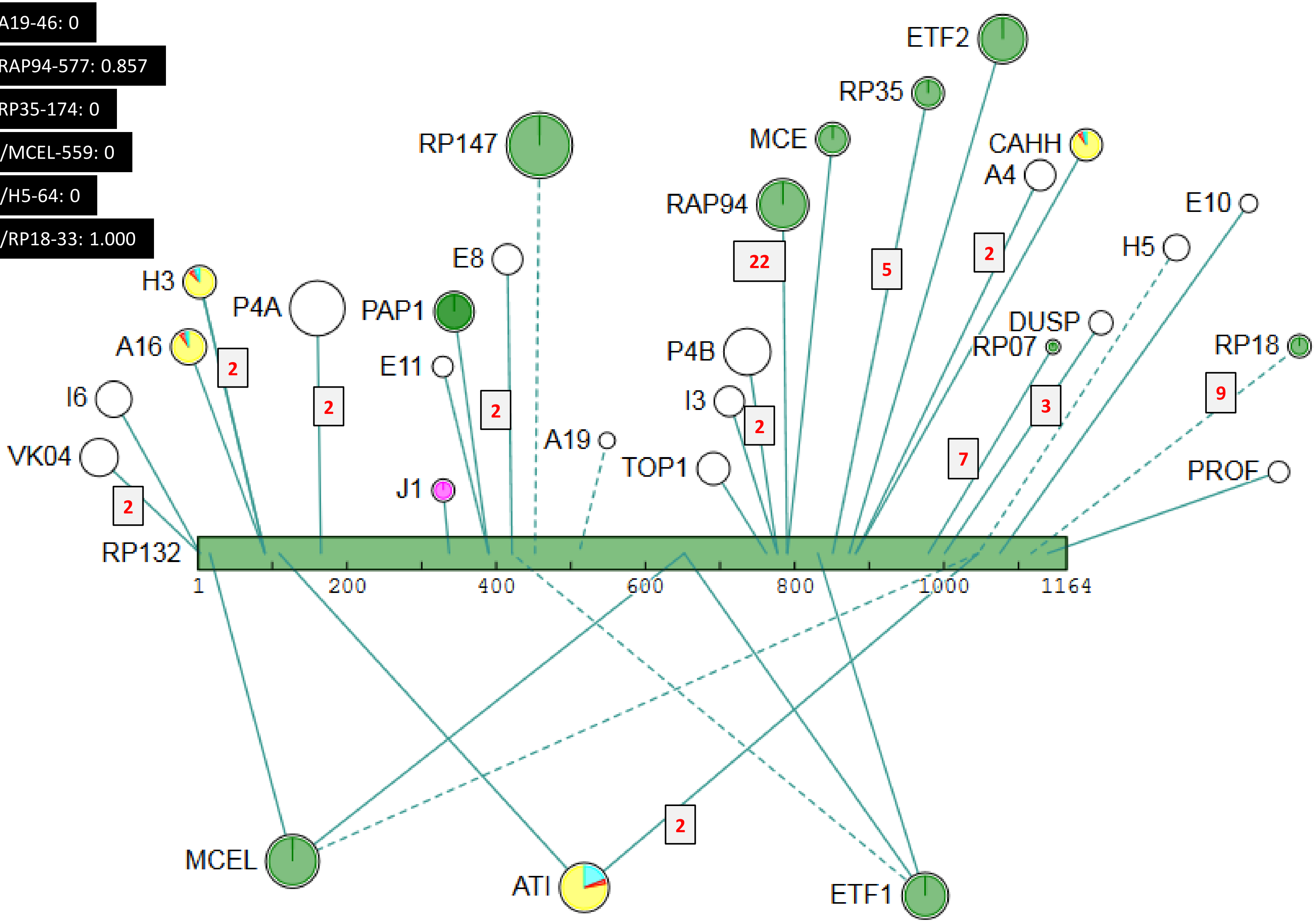
RP132-790/RAP94-577: 0.857

RP132-851/RP35-174: 0

RP132-1046/MCEL-559: 0

RP132-1046/H5-64: 0

RP132-1117/RP18-33: 1.000



RAP94-177/NTP1-175: 1.000

RAP94-206/E5-61: 0

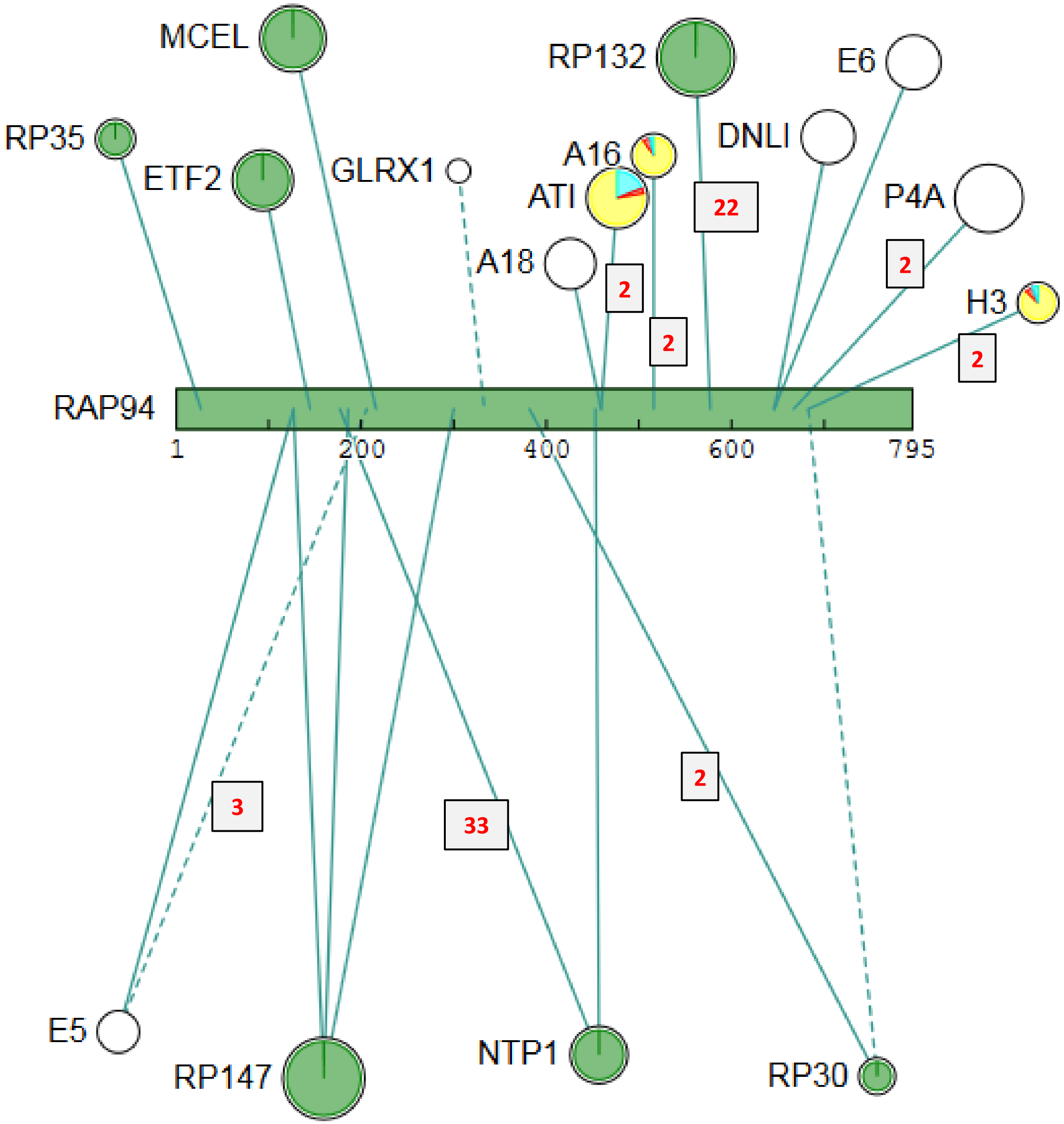
RAP94-333/GLRX1-1: 0.500

RAP94-516/A16-22: 0

RAP94-577/RP132-790: 0.857

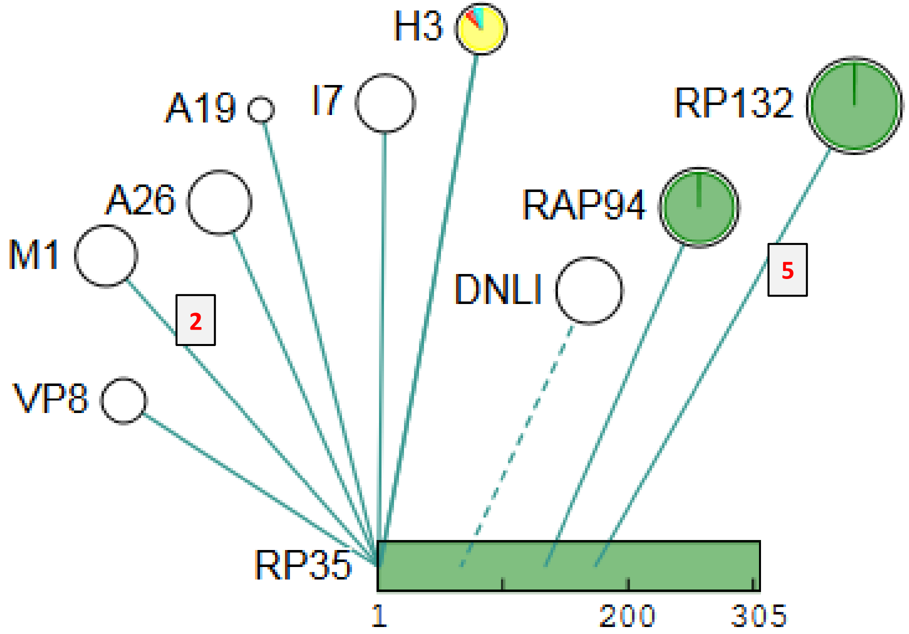
RAP94-683/H3-60: 0

RAP94-683/RP30-101: 0.500



RP35-67/DNLI-477: 0

RP35-174/RP132-851: 0



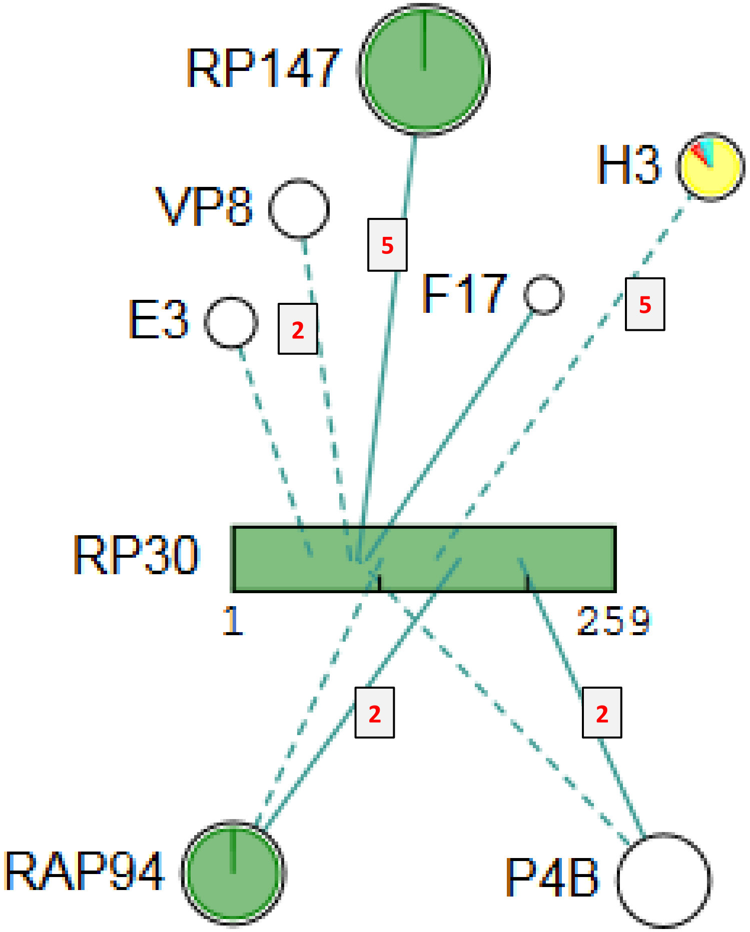
RP30-54/E3-3: 0.500

RP30-80/VP8-153: 0

RP30-85/P4B-83: 0

RP30-101/RAP94-683: 0.500

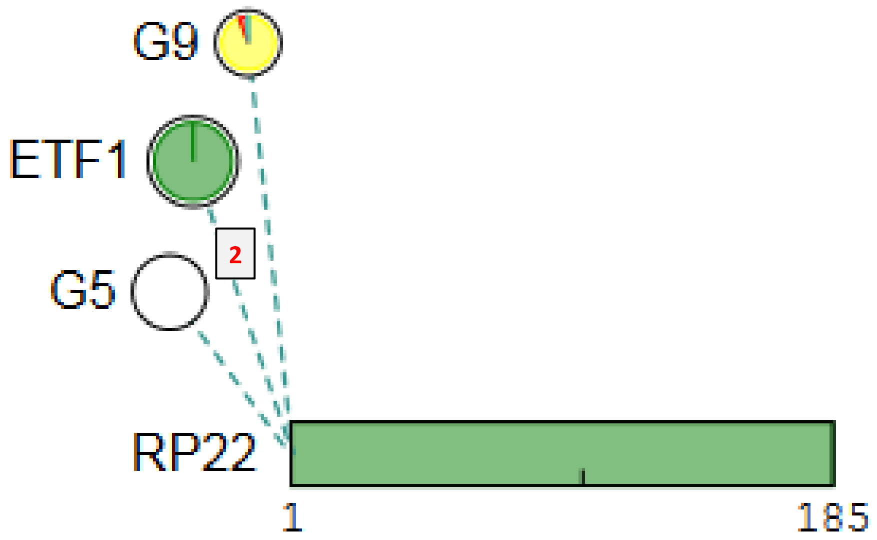
RP30-138/H3-141: 0



RP22-0/G5-90: 0

RP22-1/ETF1-575: 0

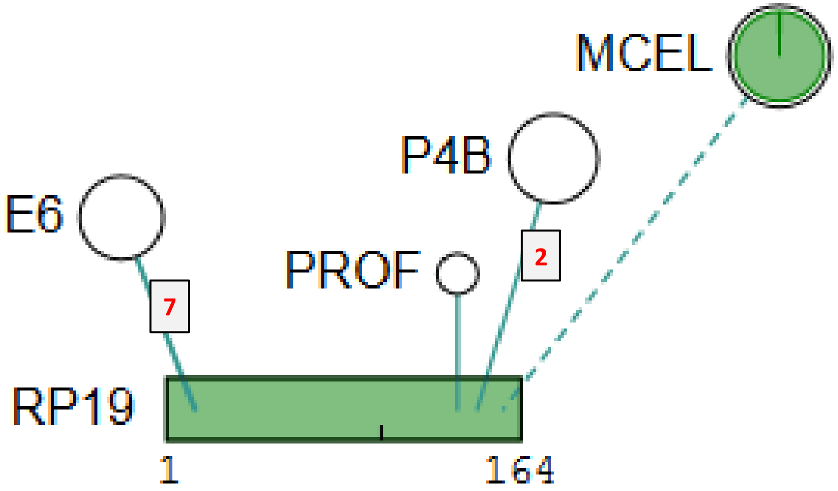
RP22-1/G9-57: 0



RP19-13/E6-404: 1.000

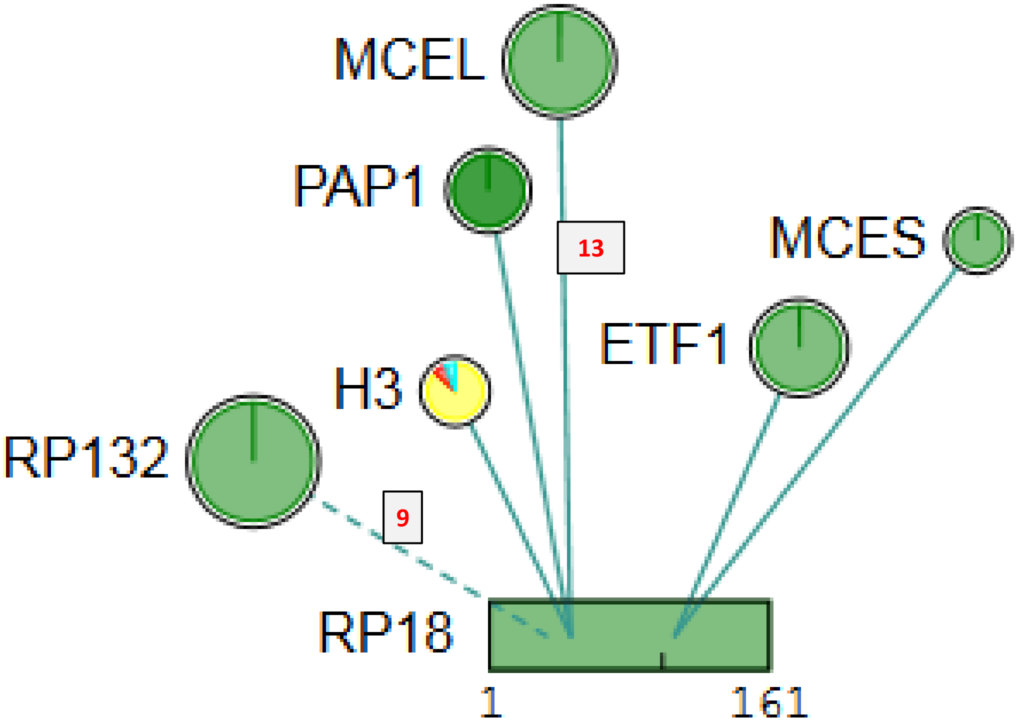
RP19-14/E6-404: 1.000

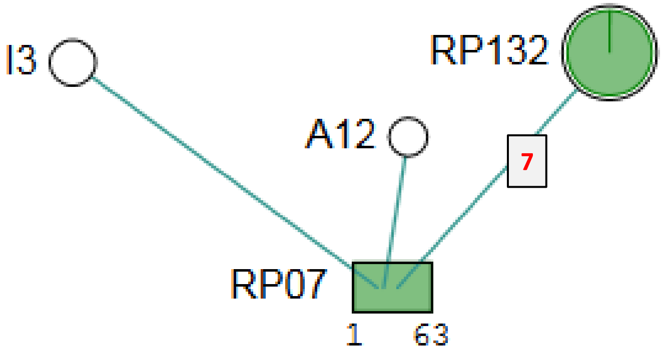
RP19-156/MCEL-386: 0



RP18-33/RP132-1117: 1.000

RP18-47/MCEL-136: 1.000




I3
RP132
A12
7
RP07
1
63

DNA-related proteins

DNLI, G5, H5, I1, I3, I6, K4, TOP1, VP8

DNLI-0/P4B-83: 0

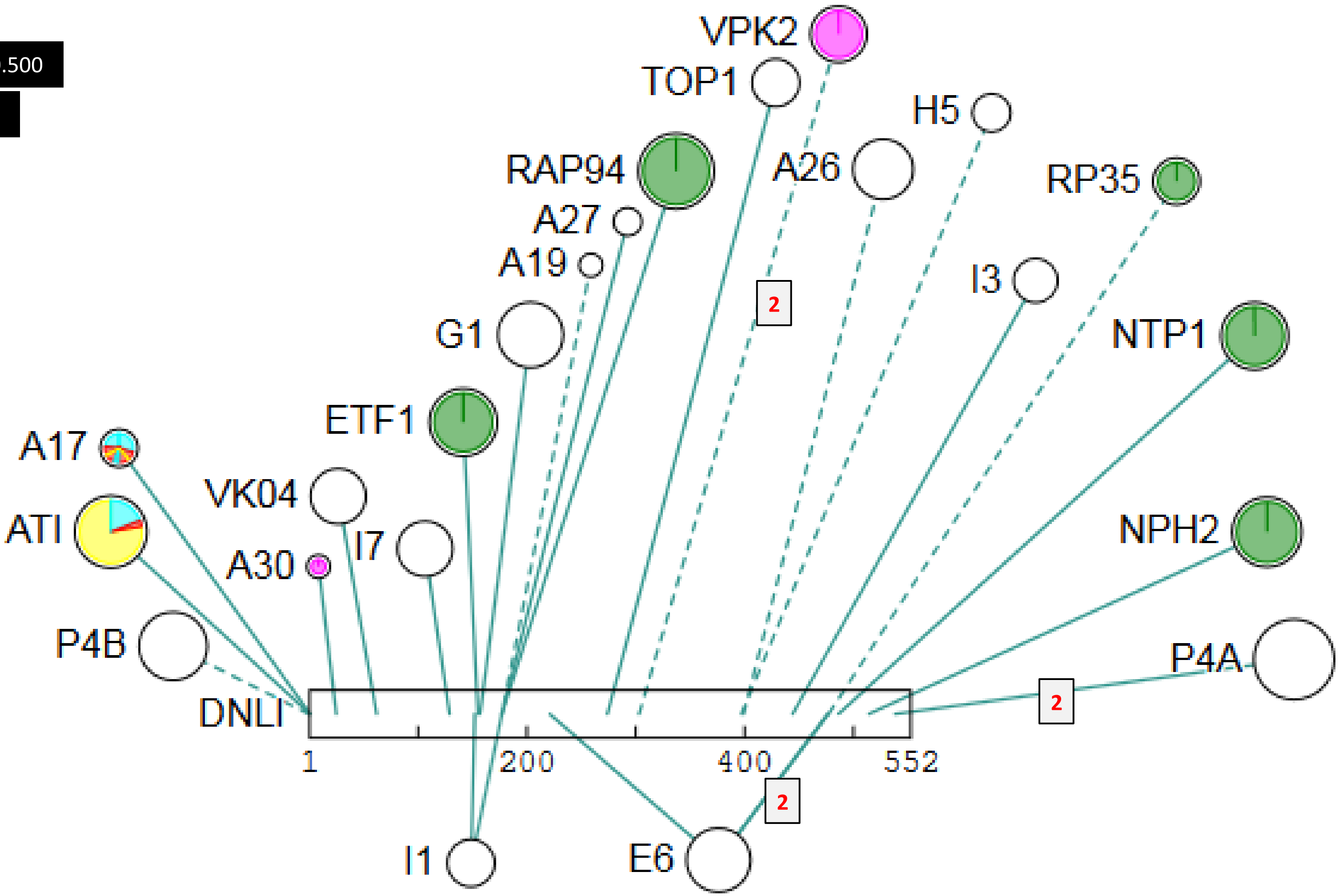
DNLI-177/A19-0: 0.500

DNLI-303/VPK2-1: 0.667

DNLI-397/H5-25: 0

DNLI-399/A26-380: 0.500

DNLI-477/RP35-67: 0

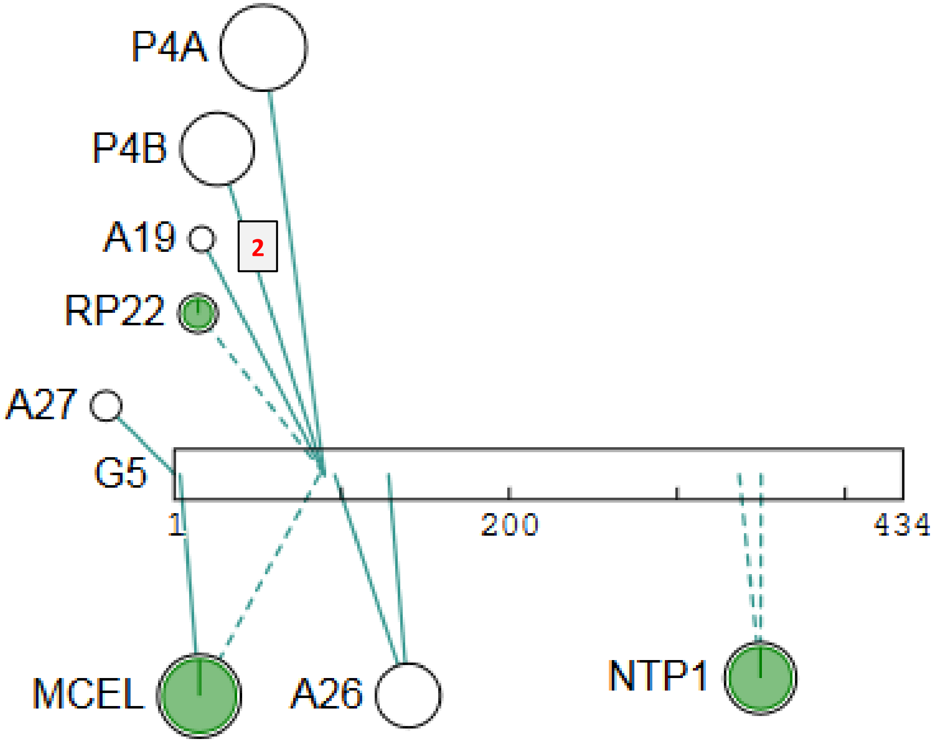


G5-87/MCEL-136: 0.500

G5-90/RP22-0: 0

G5-337/NTP1-56: 1.000

G5-350/NTP1-56: 1.000

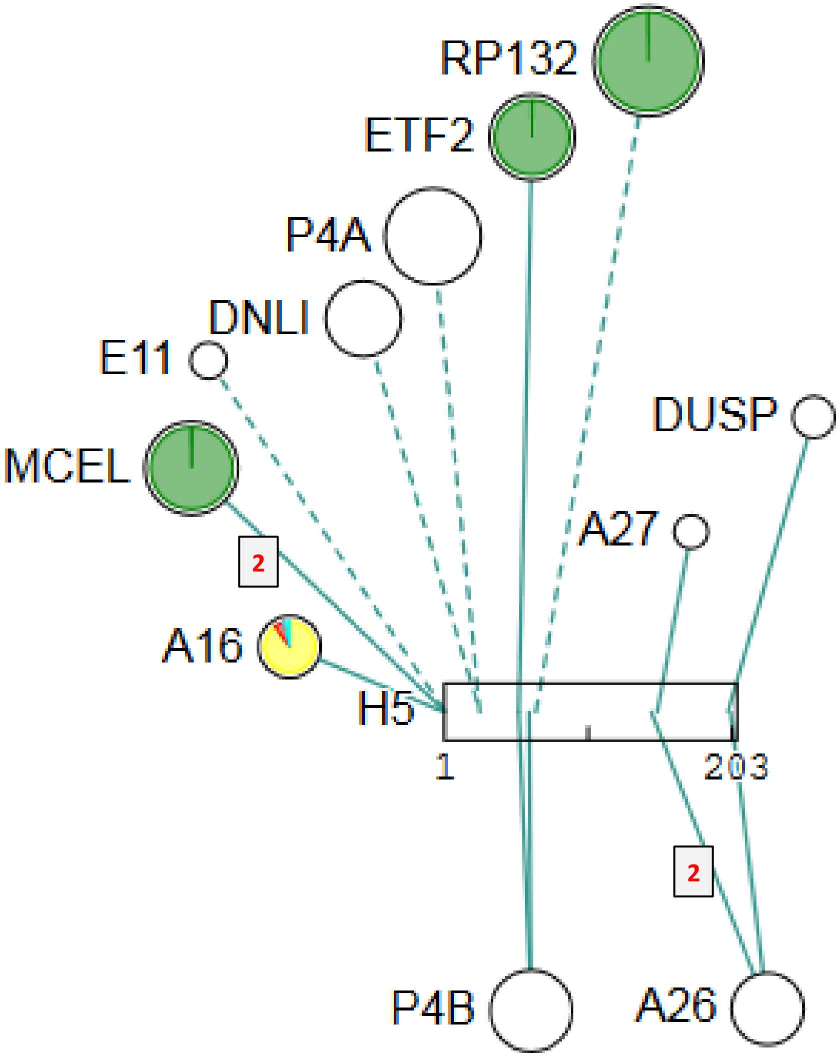


H5-1/E11-56: 0

H5-25/DNLI-397: 0

H5-25/P4A-487: 0.500

H5-64/RP132-1046: 0

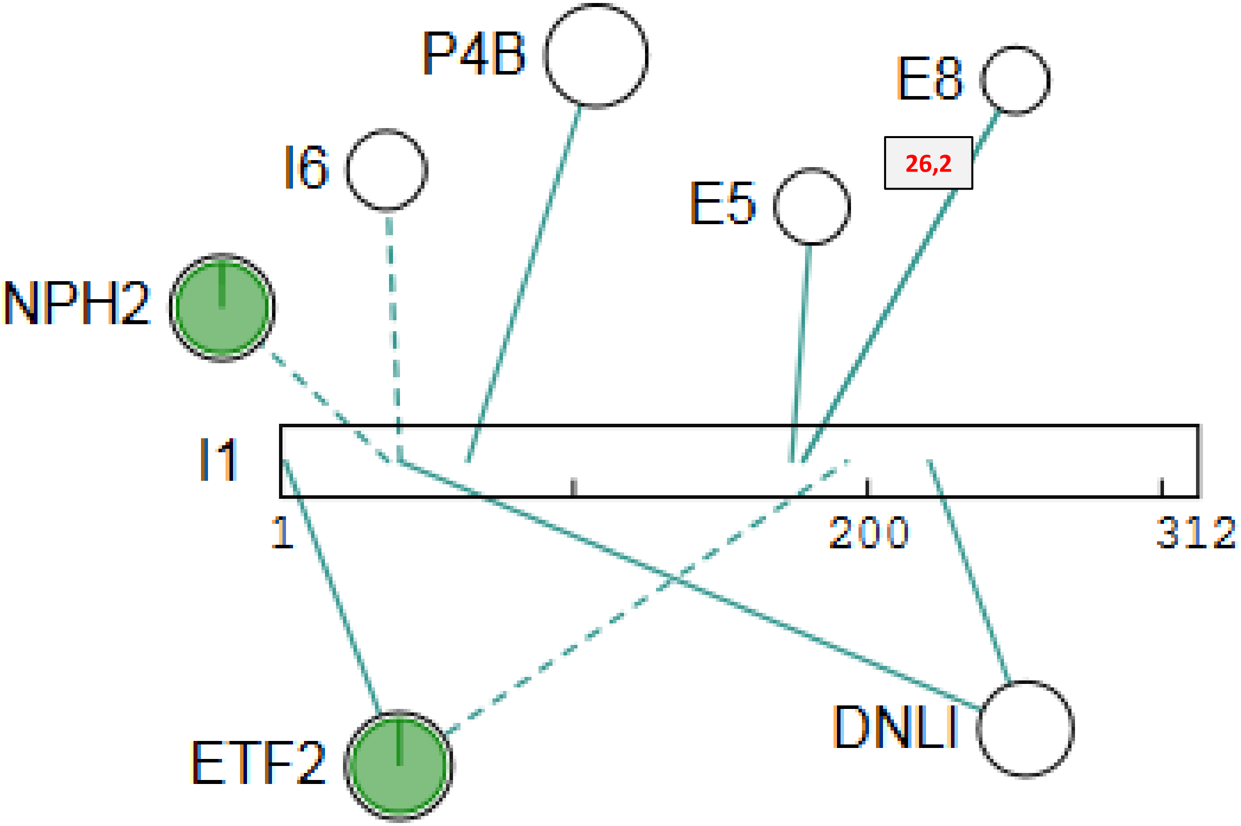


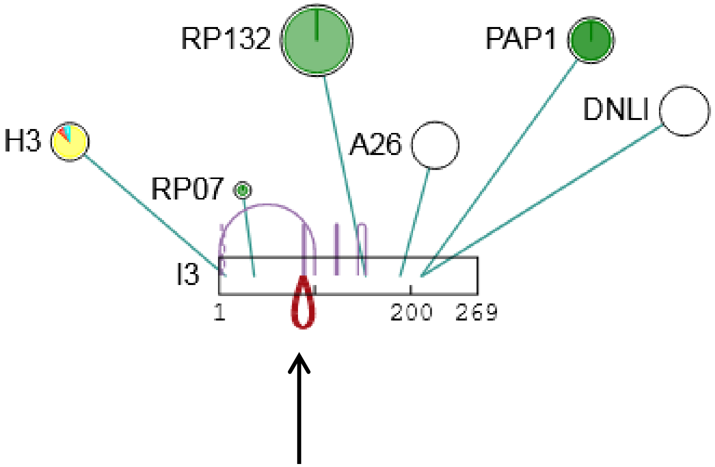
I1-37/NPH2-71: 0

I1-41/I6-359: 0

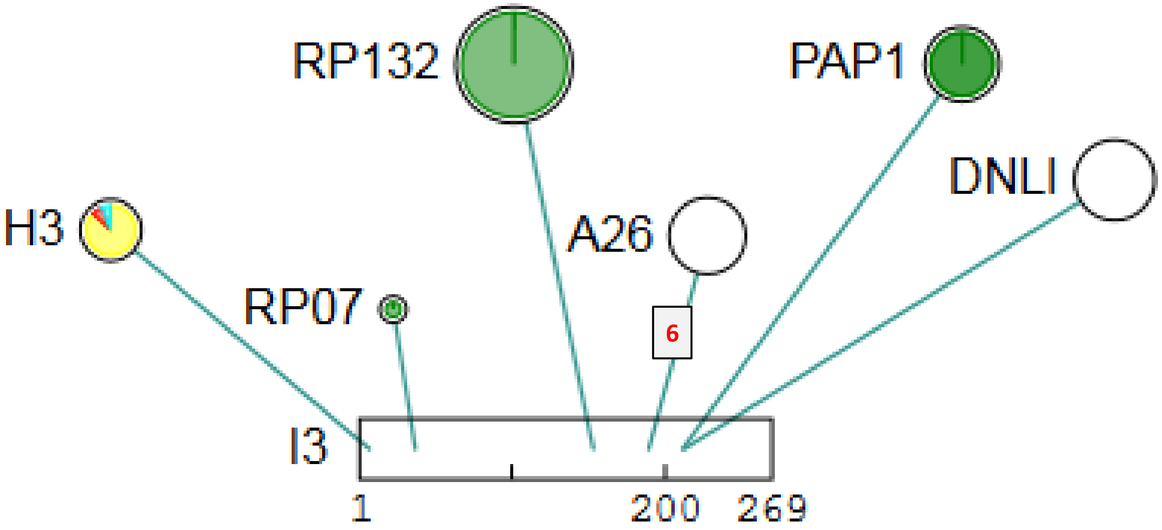
I1-178/E8-201: 1.000

I1-193/ETF2-112: 0





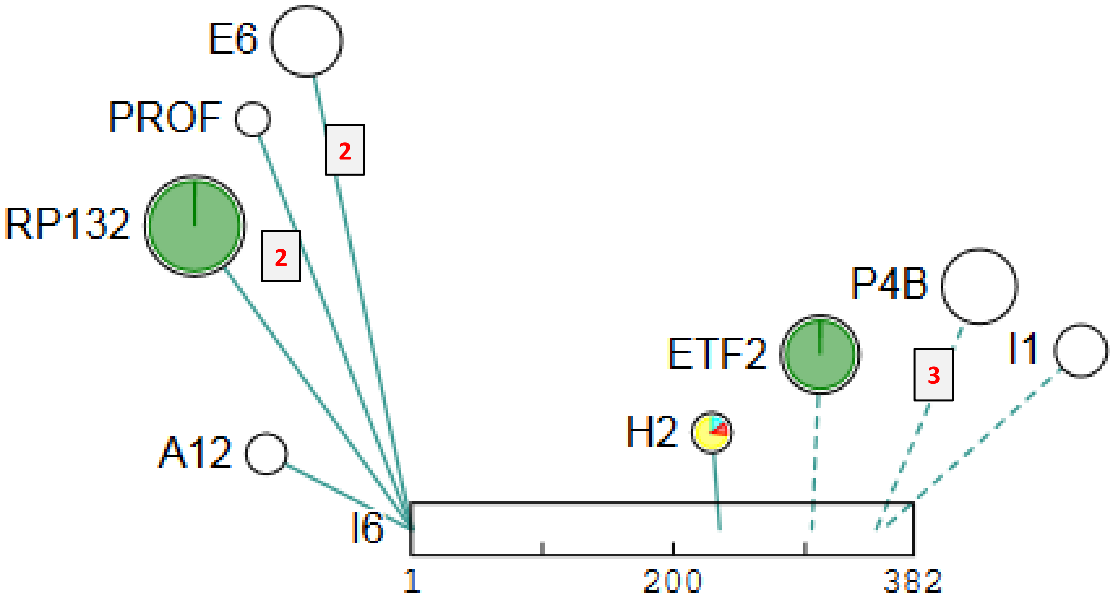
Self-interaction region of Greseth *et al*. [Traktman] 2012? At least three overlaid self-links (86-86, 88-88, 90-90)

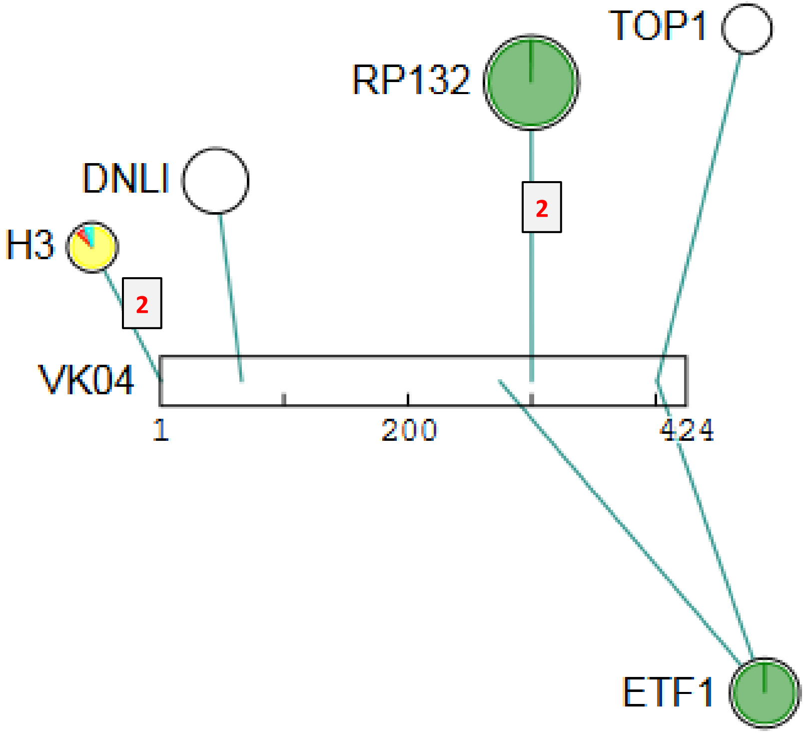


I6-305/ETF2-607: 0.333

I6-354/P4B-134: 0

I6-359/I1-41: 0




TOP1
RP132
DNLI
H3
2
2
VK04
1
200
424
ETF1

TOP1-74/RP147-566: 0

TOP1-167/P4A-876: 0.500

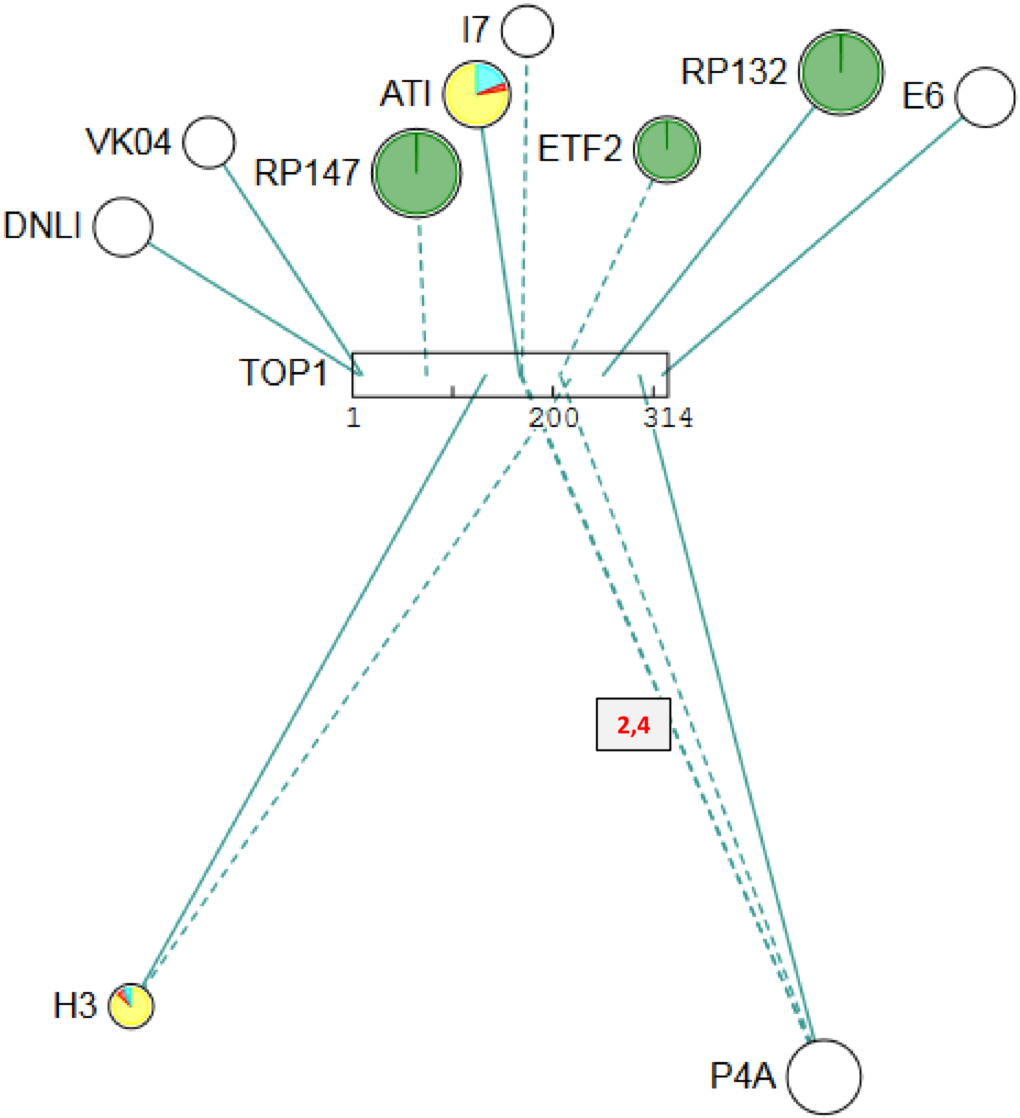
TOP1-169/I7-414: 0.500

TOP1-169/P4A-1: 0

TOP1-207/ETF2-394: 0

TOP1-207/P4A-876: 0

TOP1-220/H3-60: 0



VP8-125/P4B-83: 0

VP8-153/RP147-1: 0

VP8-153/RP30-80: 0

VP8-175/A6-136: 0

VP8-204/A12-75: 0

VP8-212/A12-63: 0

VP8-240/A12-63: 0

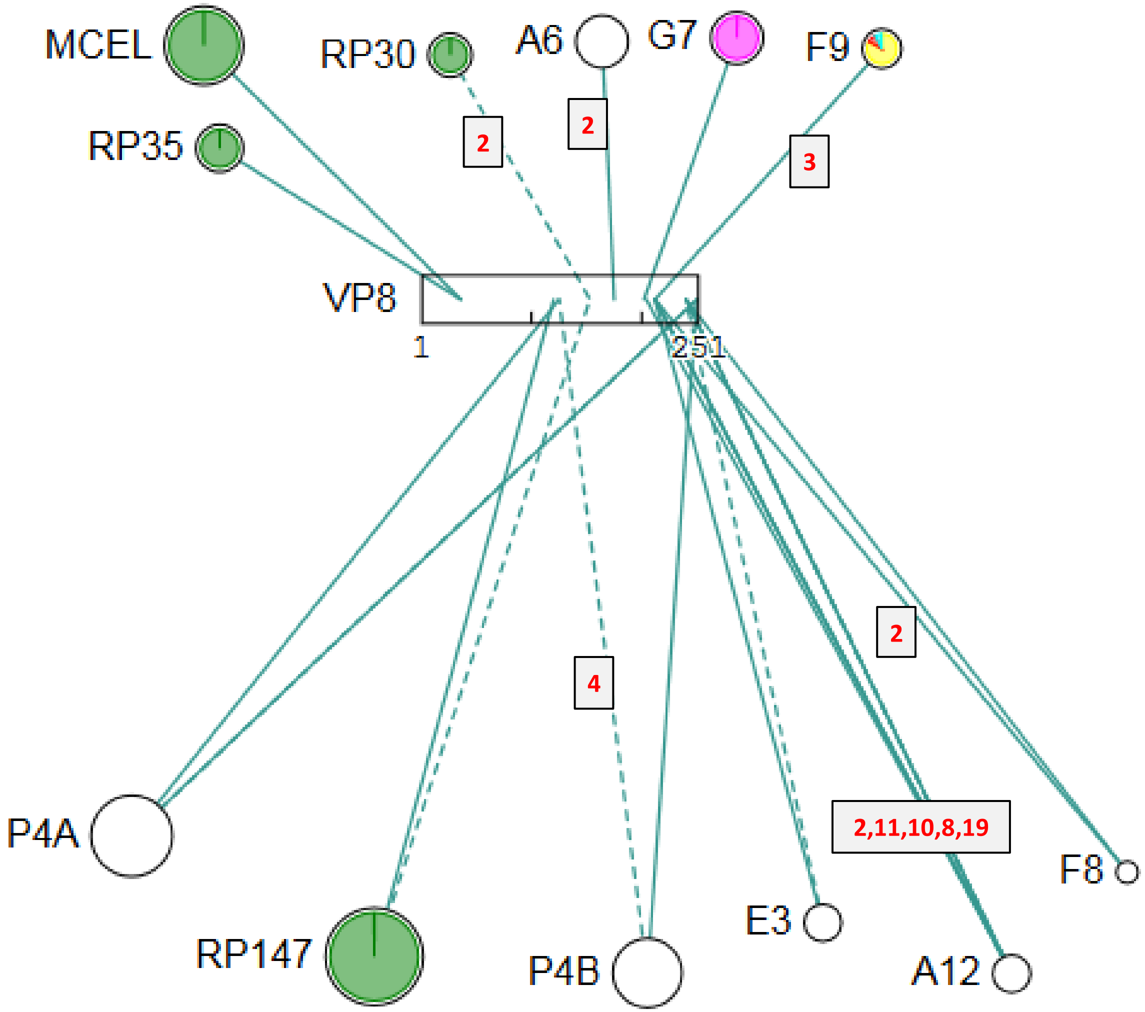
VP8-240/A12-75: 0

VP8-240/A12-88: 1.000

VP8-240/A12-166: 0

VP8-240/E3-40: 0

VP8-250/P4A-487: 0.500



‘Structural’ proteins

A4, p4a, p4b

A4-32/A12-88: 0

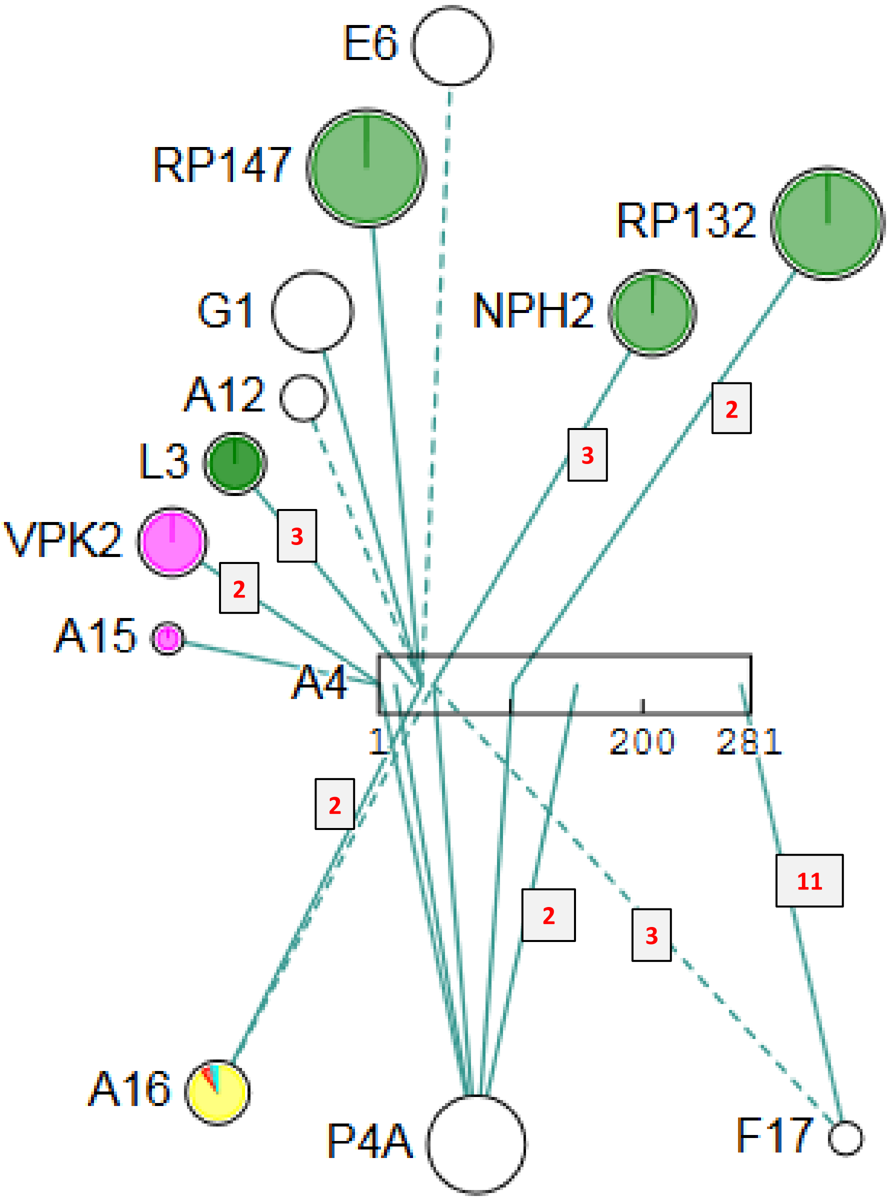
A4-33/A16-194: 1.000

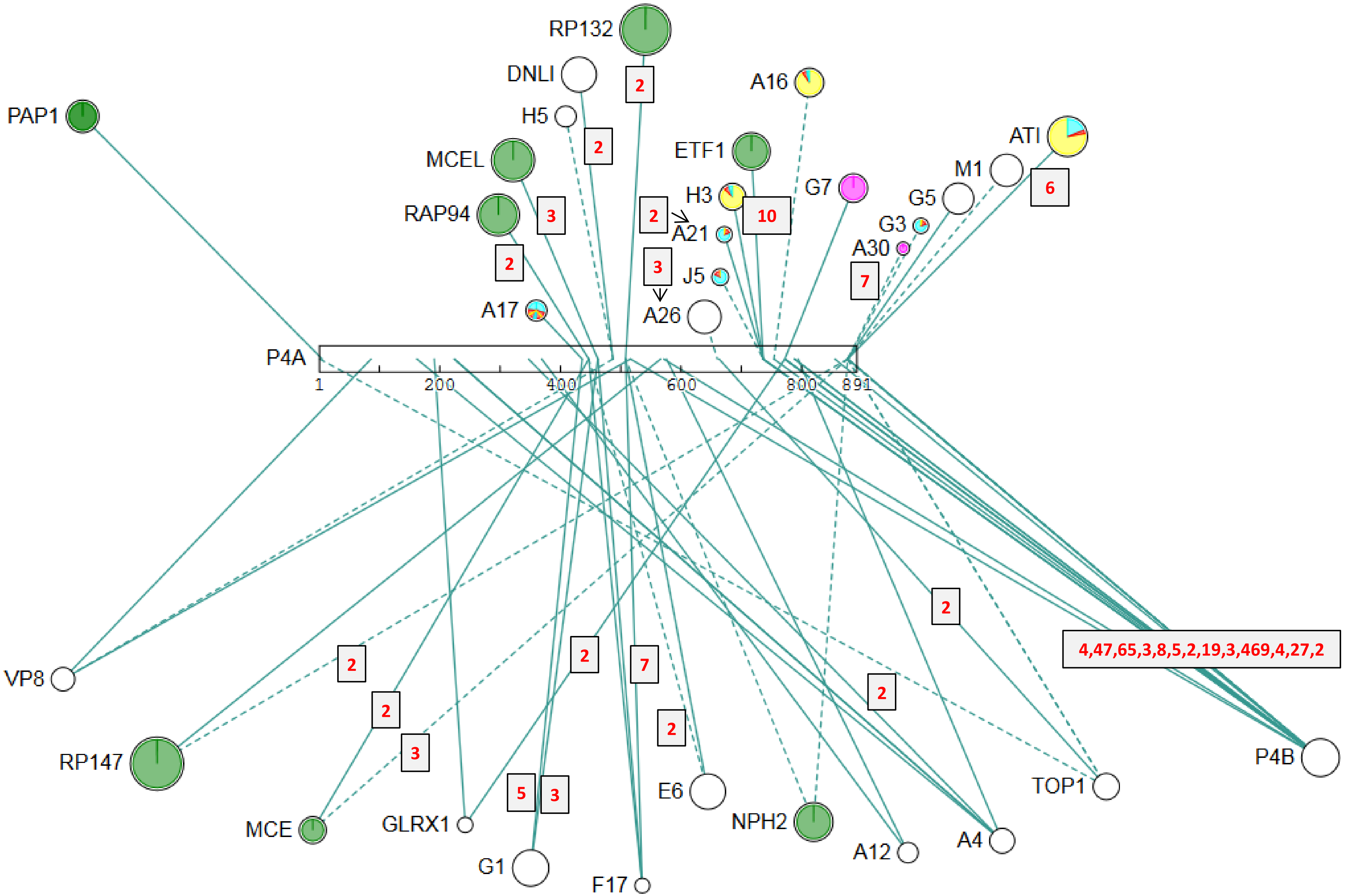
A4-33/E6-90: 0

A4-42/A16-194: 1.000

A4-42/F17-74: 0

A4-274/F17-74: 1.000




RP132
2
DNLI
A16
PAP1
H5
2
ATI
MCEL
ETF1
M1
6
G7
H3
G5
RAP94
3
2
10
A21
G3
A30
2
7
3
J5
A17
A26
P4A
1
200
400
600
800
891
2
4,47,65,3,8,5,2,19,3,469,4,27,2
VP8
2
2
7
2
2
2
RP147
3
P4B
E6
TOP1
MCE
GLRX1
5
3
NPH2
A4
A12
G1
F17

P4A-1/TOP1-169: 0

P4A-436/G1-96: 0

P4A-447/E6-484: 0

P4A-487/H5-25: 0.500

P4A-487/VP8-250: 0.500

P4A-508/NPH2-627: 0

P4A-508/F17-74: 0

P4A-660/A26-415: 0

P4A-736/J5-92: 0

P4A-736/ETF1-308: 0.333

P4A-736/P4B-393: 1.000

P4A-736/P4B-407: 1.000

P4A-754/A16-133: 0

P4A-788/P4B-567: 0.500

P4A-788/P4B-568: 0

P4A-875/P4B-563: 1.000

P4A-876/A30-49: 0.080

P4A-876/ATI-572: 0

P4A-876/G3-88: 0.167

P4A-876/NPH2-622: 0.167

P4A-876/MCE-321: 0.018

P4A-876/P4B-563: 0.500

P4A-876/P4B-564: 0.982

P4A-876/P4B-567: 1.000

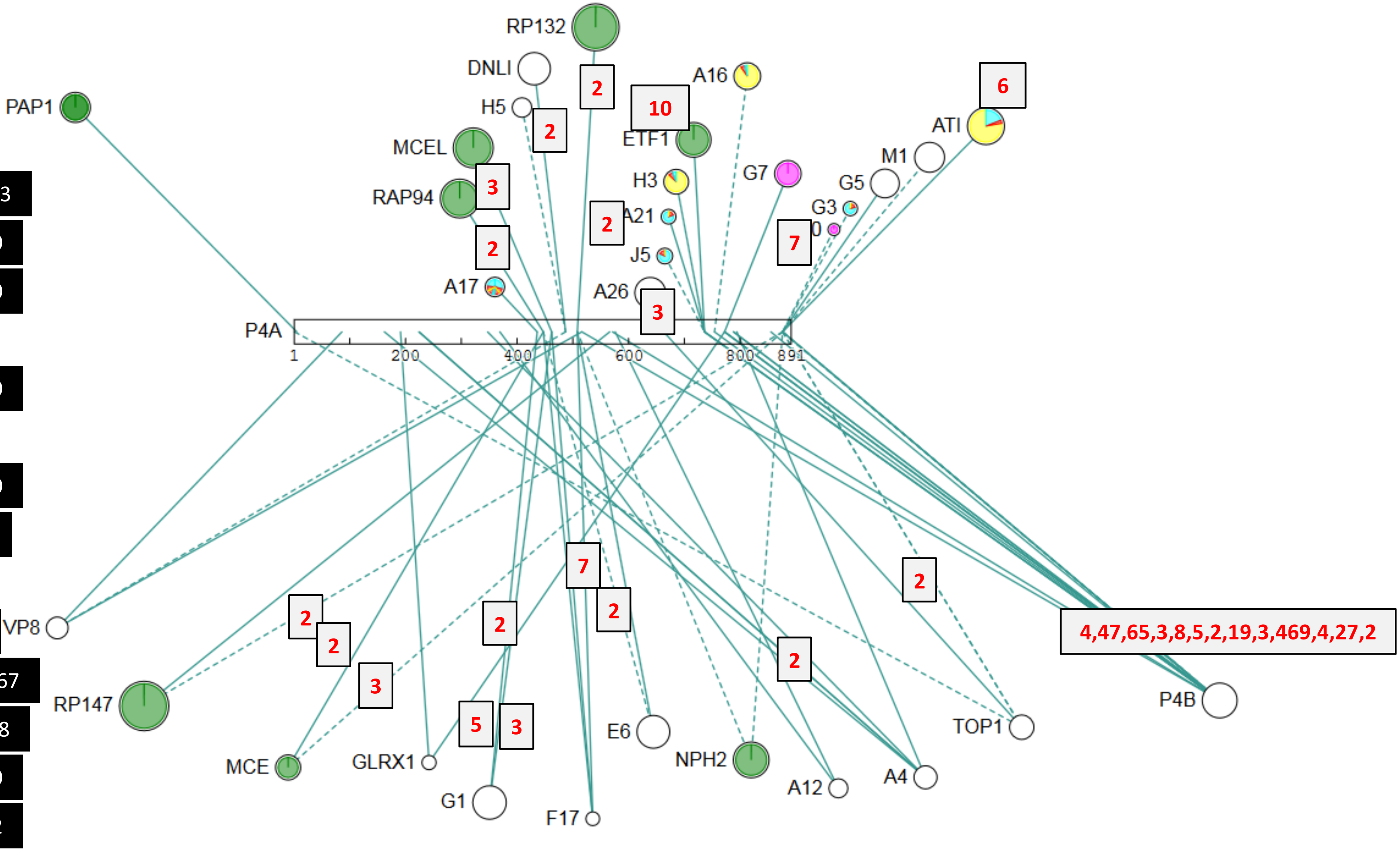
P4A-876/P4B-568: 0

P4A-876/RP147-1029: 0.286

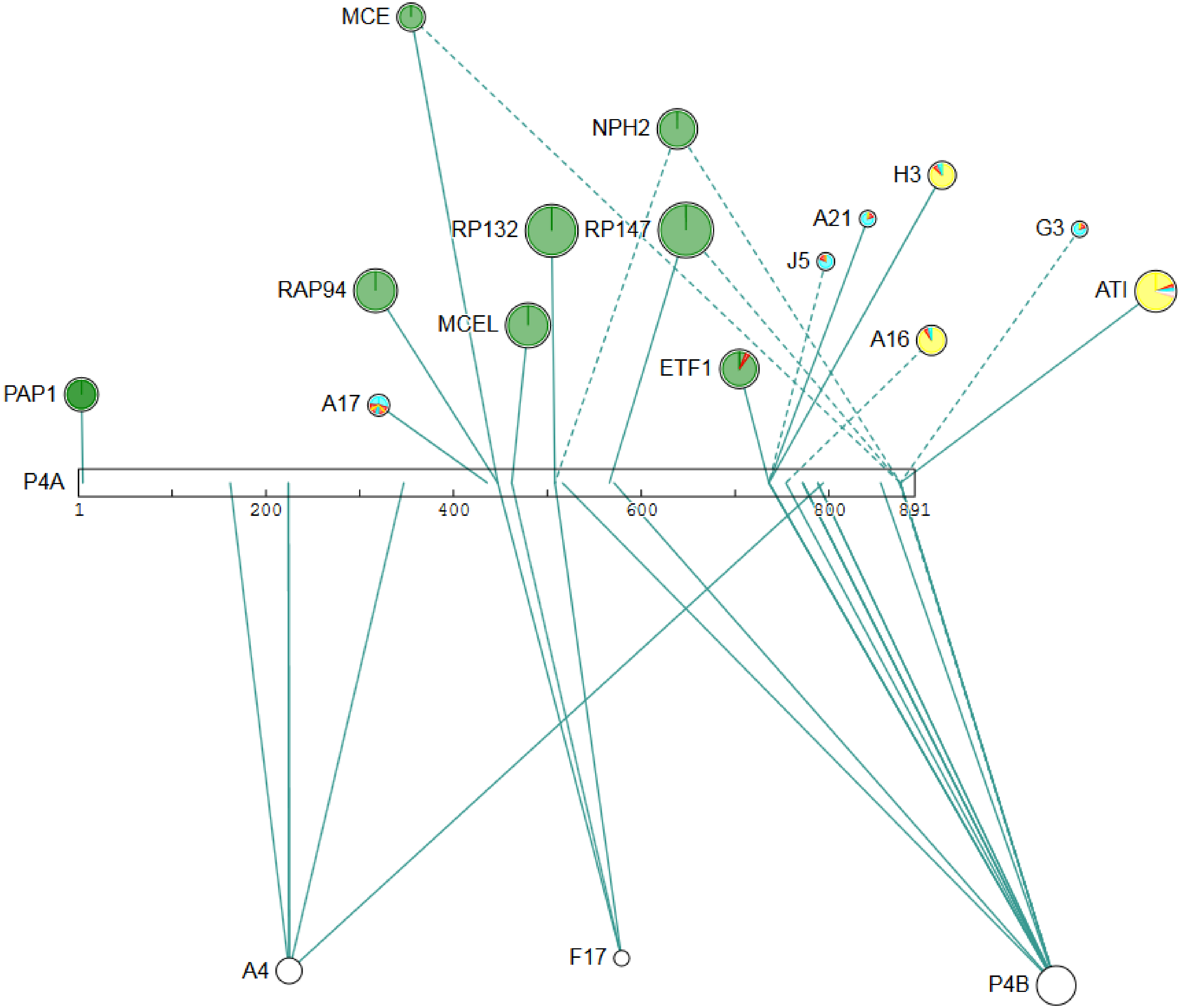
P4A-876/TOP1-167: 0.500

P4A-876/TOP1-207: 0

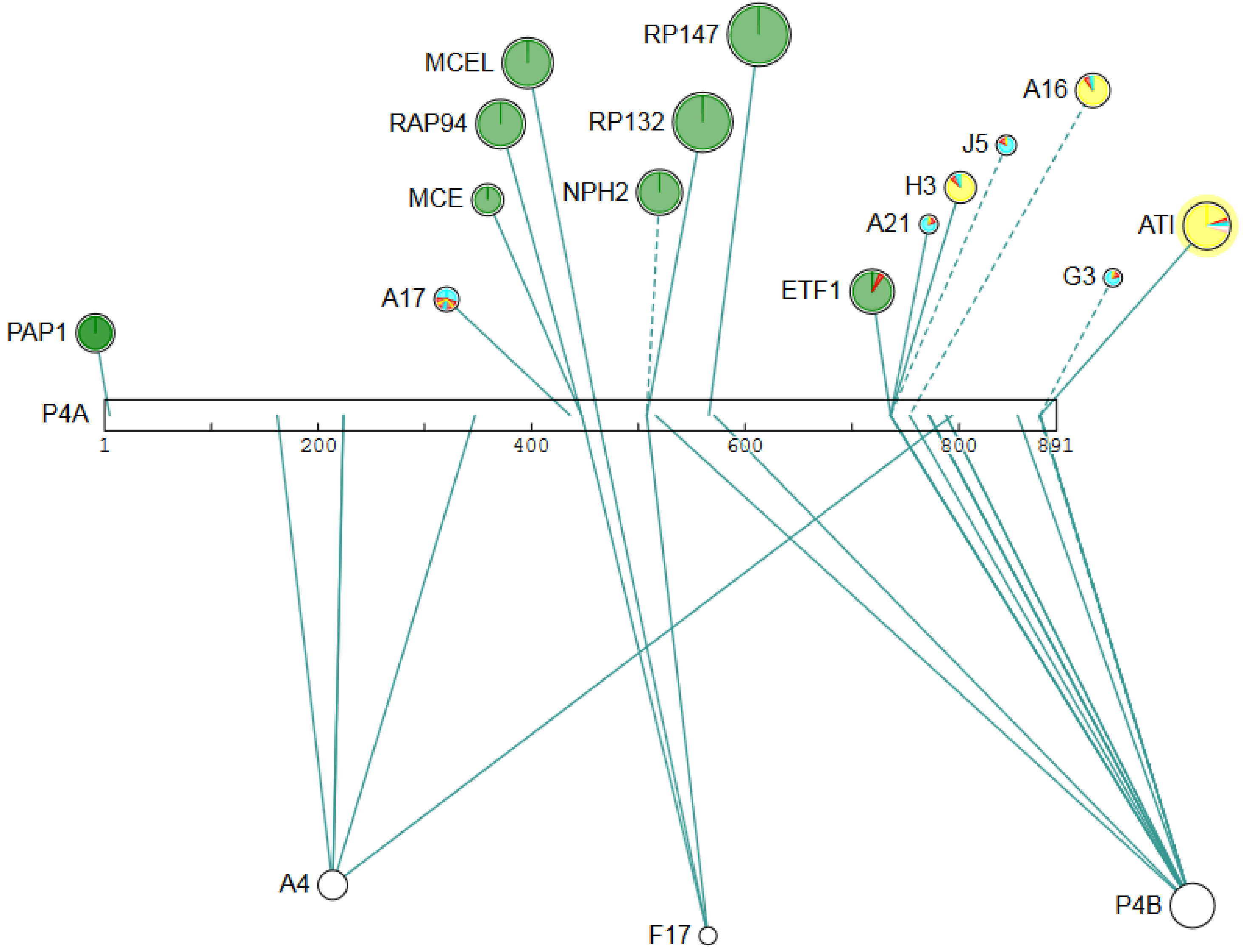
P4A-876/M1-149: 0



P4a, showing XL with transcriptosome, membrane, structural proteins only



P4a, showing XL with transcriptosome, membrane, structural proteins only:
After removal of three ‘ambig’. XL between transcriptosome proteins and p4a C-terminal residue.



P4B-83/DNLI-0: 0

P4B-83/GLRX1-0: 0

P4B-83/MCEL-433: 0.500

P4B-83/MCES-277: 0.500

P4B-83/M1-133: 0

P4B-83/VP8-125: 0

P4B-83/RP30-85: 0

P4B-134/I6-354: 0

P4B-185/ETF2-67: 0

P4B-189/D3-232: 0

P4B-189/A12-167: 1.000

P4B-189/F8-7: 0

P4B-393/P4A-736: 1.000

P4B-407/P4A-736: 1.000

P4B-563/P4A-875: 1.000

P4B-563/P4A-876: 0.500

P4B-564/P4A-876: 0.982

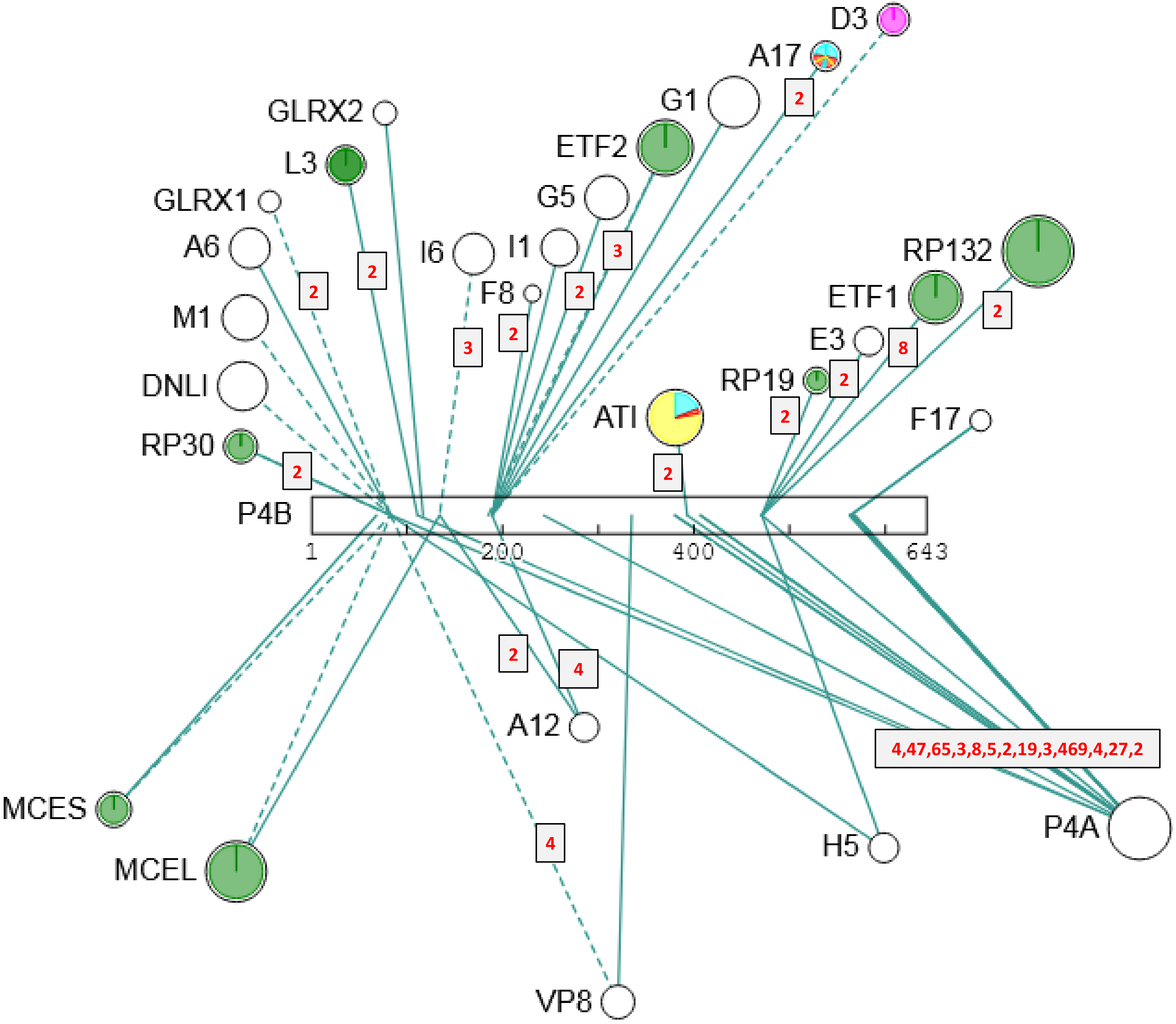
P4B-564/F17-74: 0

P4B-567/P4A-788: 0.500

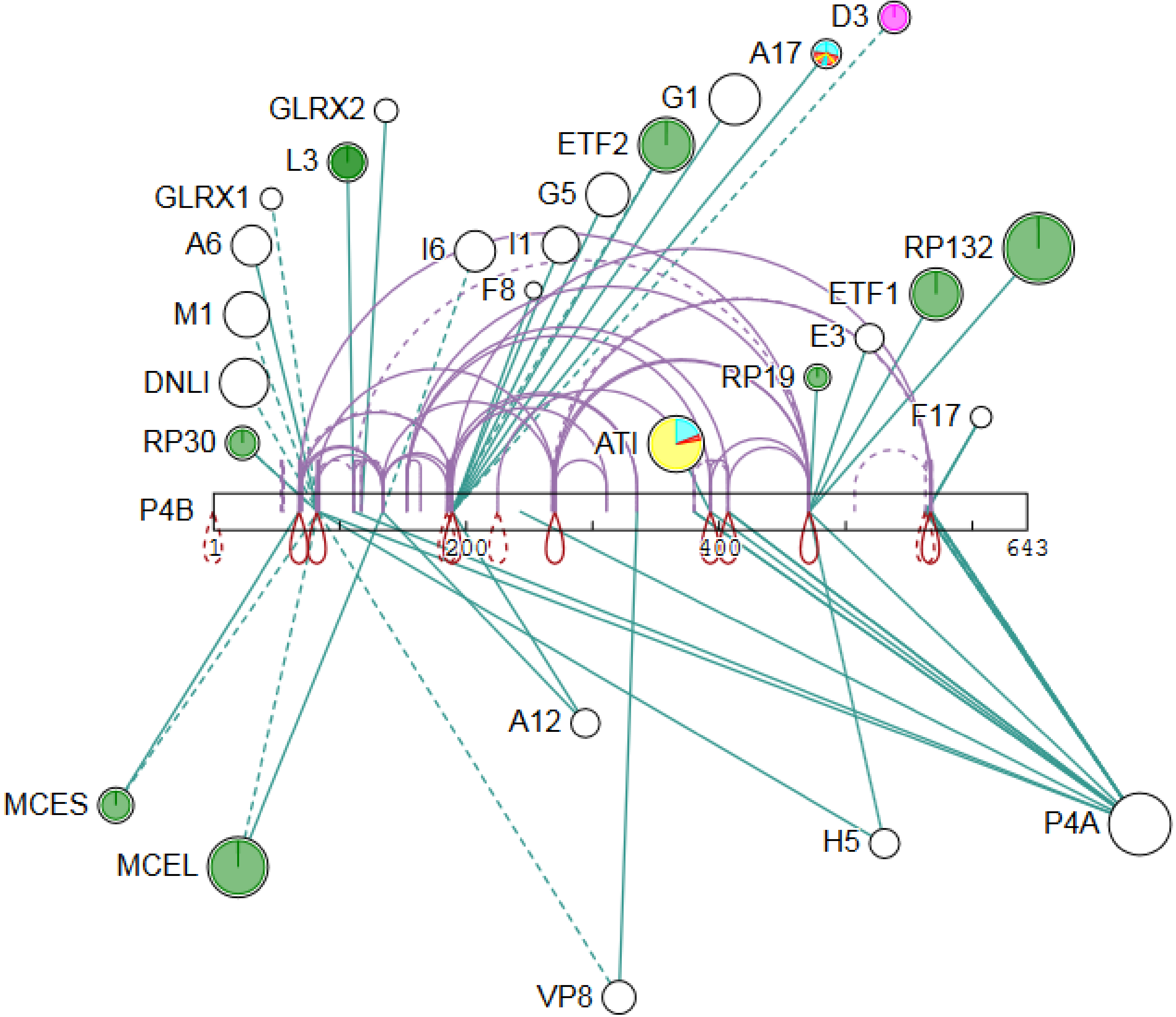
P4B-567/P4A-876: 1.000

P4B-568/P4A-788: 0

P4B-568/P4A-876: 0



P4b with intramolecular XL.



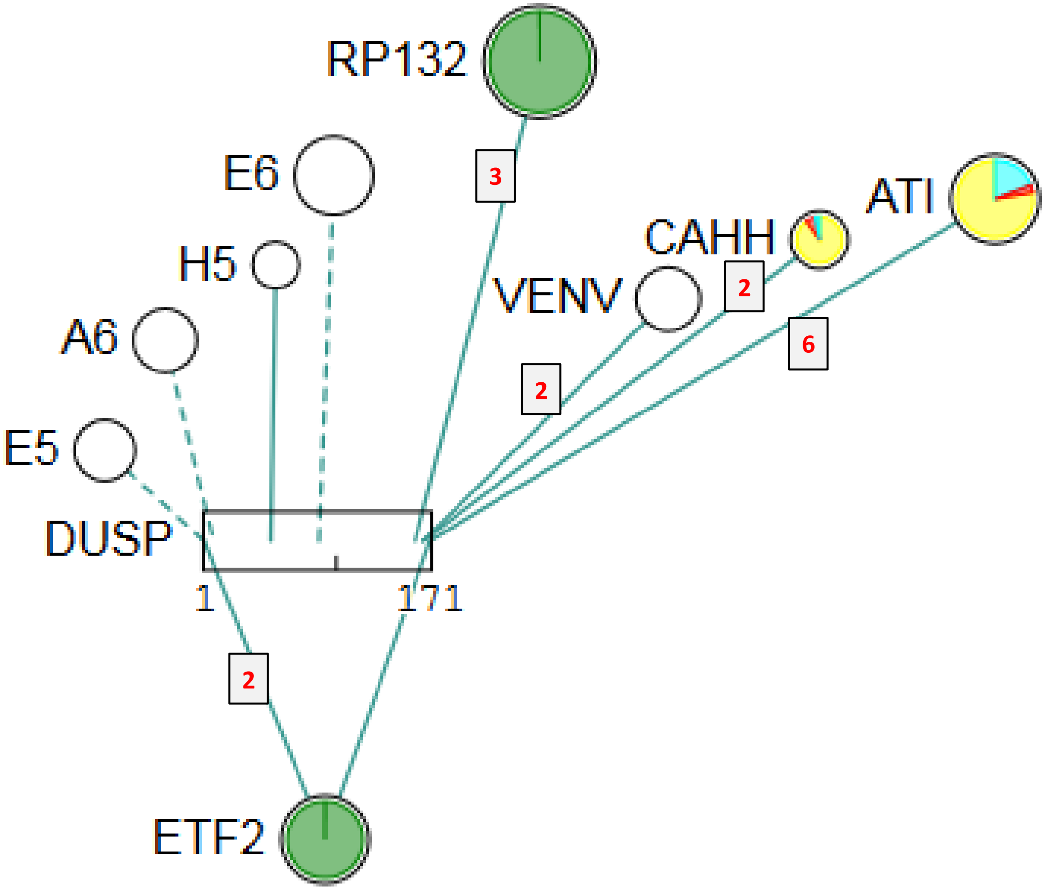
Other enzymes

DUSP, G1, GLRX1, GLRX2, I7, VPK1

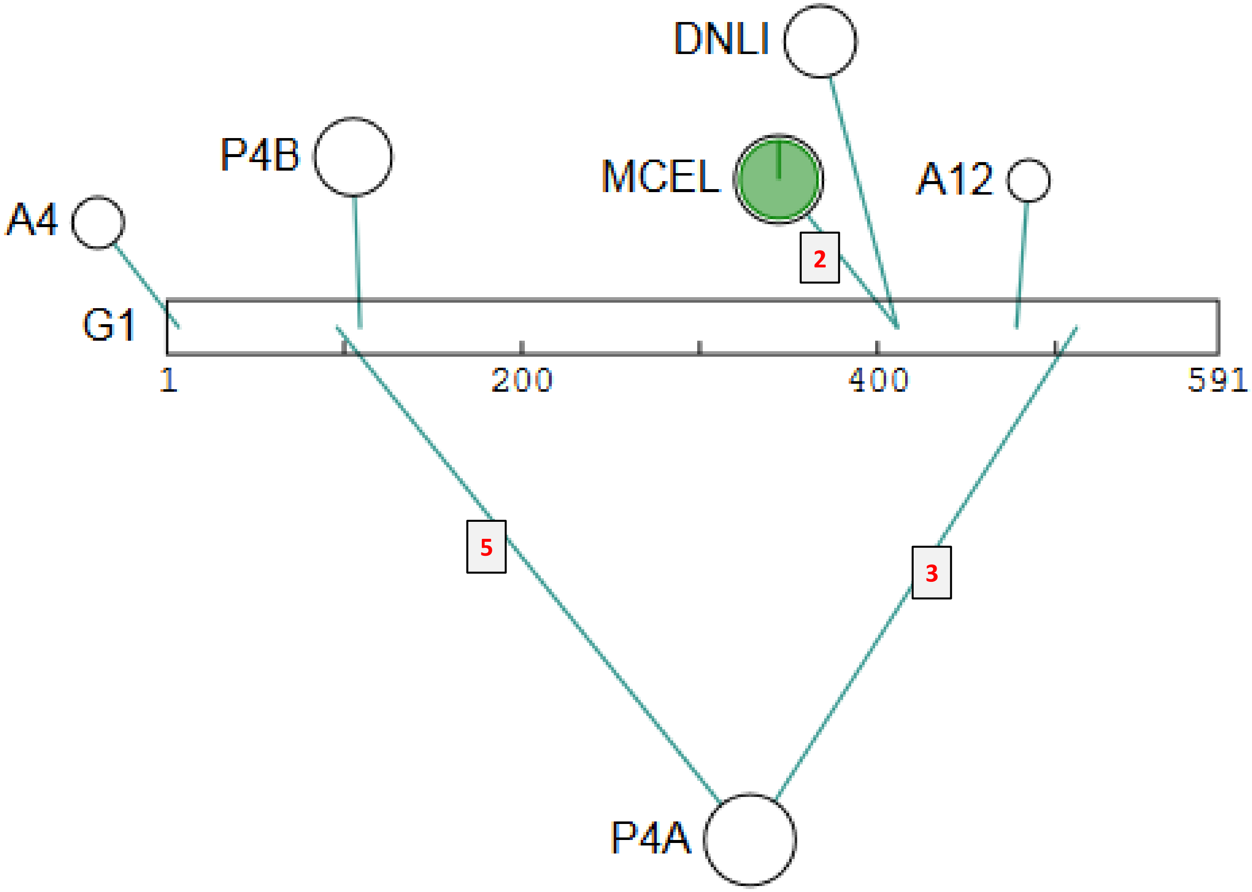
DUSP-1/E5-127: 0

DUSP-8/A6-317: 0

DUSP-87/E6-439: 0.500



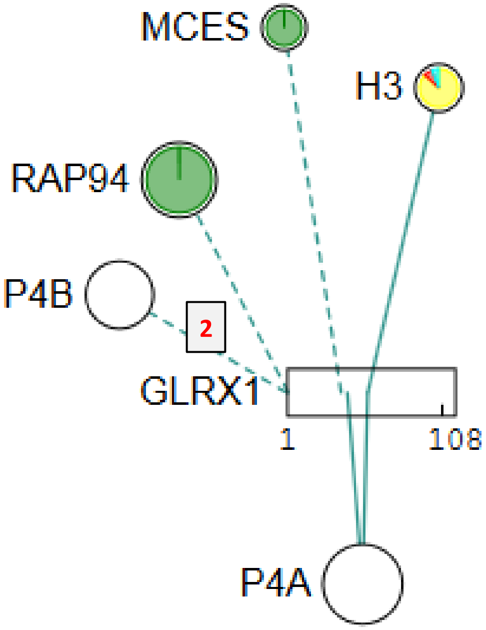
P4A-436/G1-96: 0



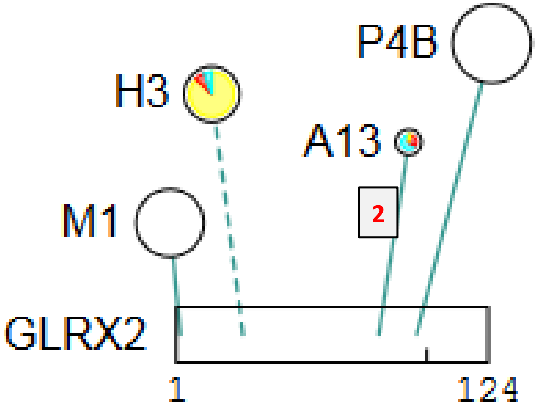
GLRX1-0/P4B-83: 0

GLRX1-1/RAP94-333: 0.500

GLRX1-35/MCES-6: 0



H3-77/GLRX2-27: 0



I7-53/RP147-566: 0

I7-90/A13-67: 0

I7-126/A16-149: 0

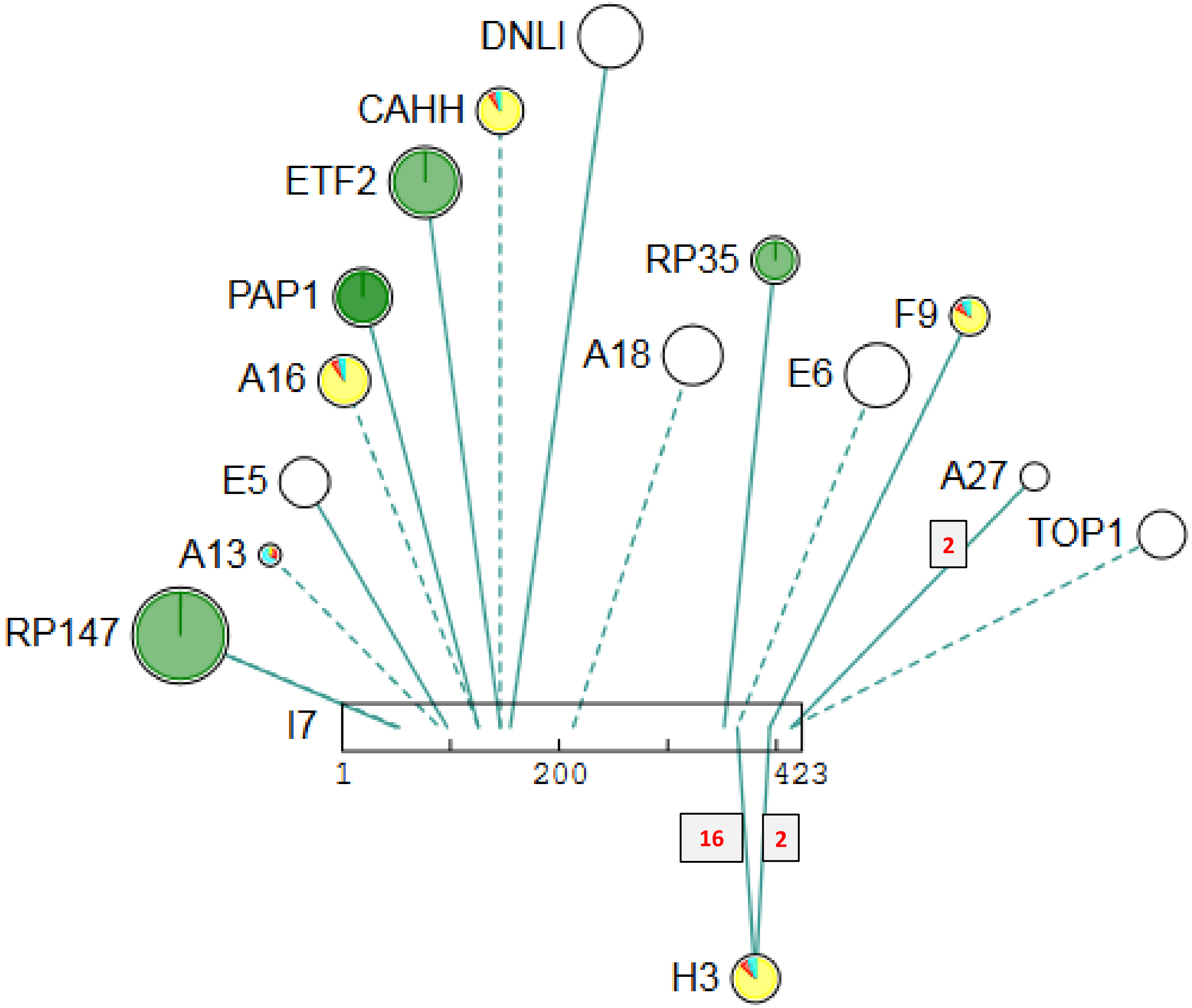
I7-146/CAHH-14: 0

I7-213/A18-458: 0

I7-364/E6-1: 0

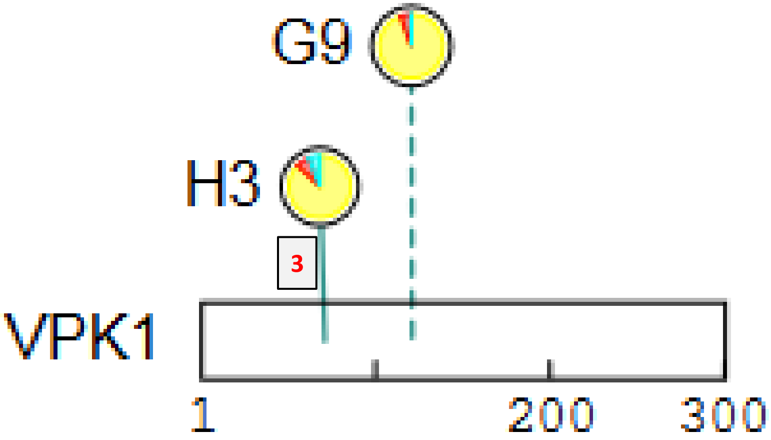
I7-364/H3-147: 0.889

I7-414/TOP1-169: 0.500



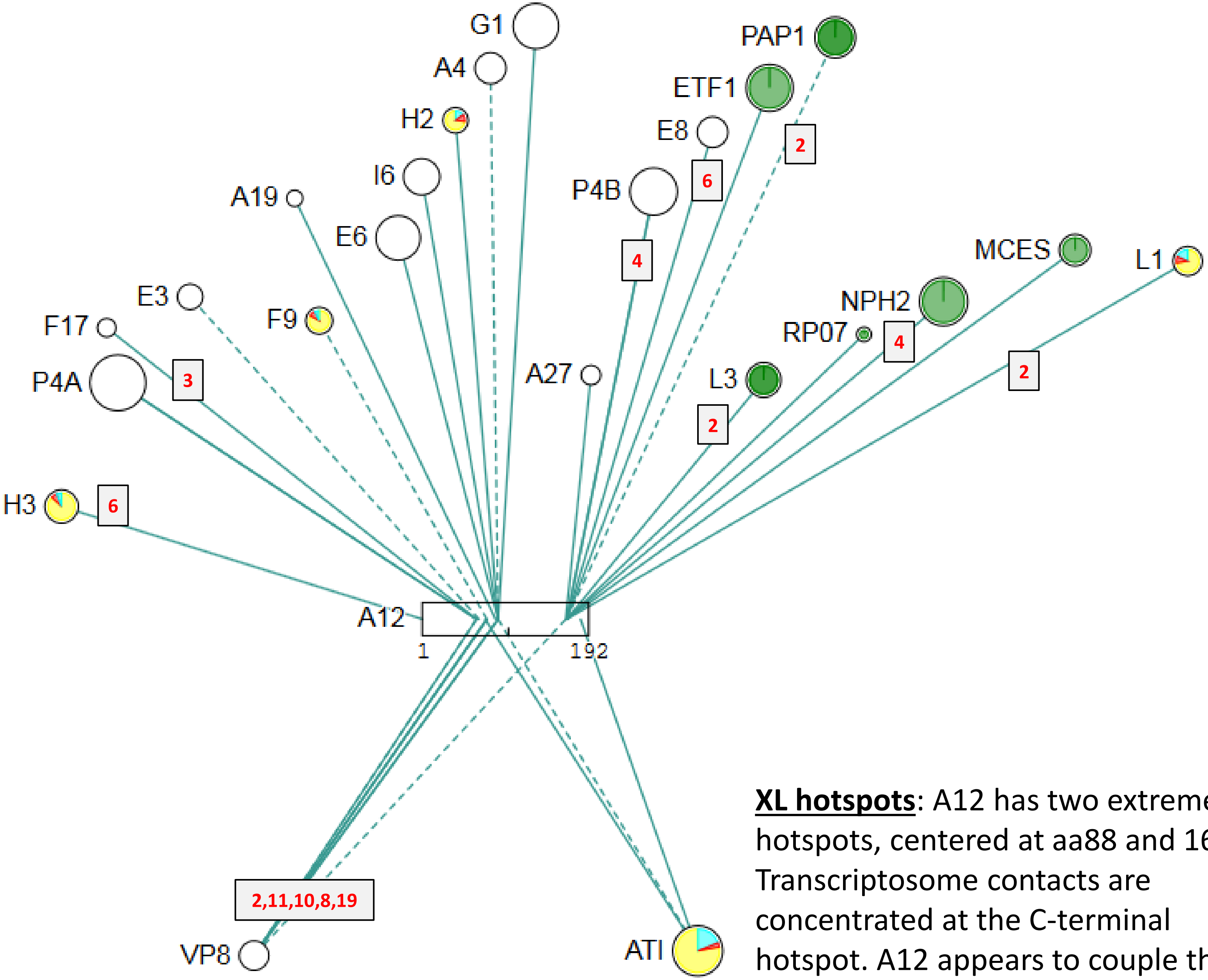
VPK1-71/H3-253: 0

VPK1-121/G9-58: 0

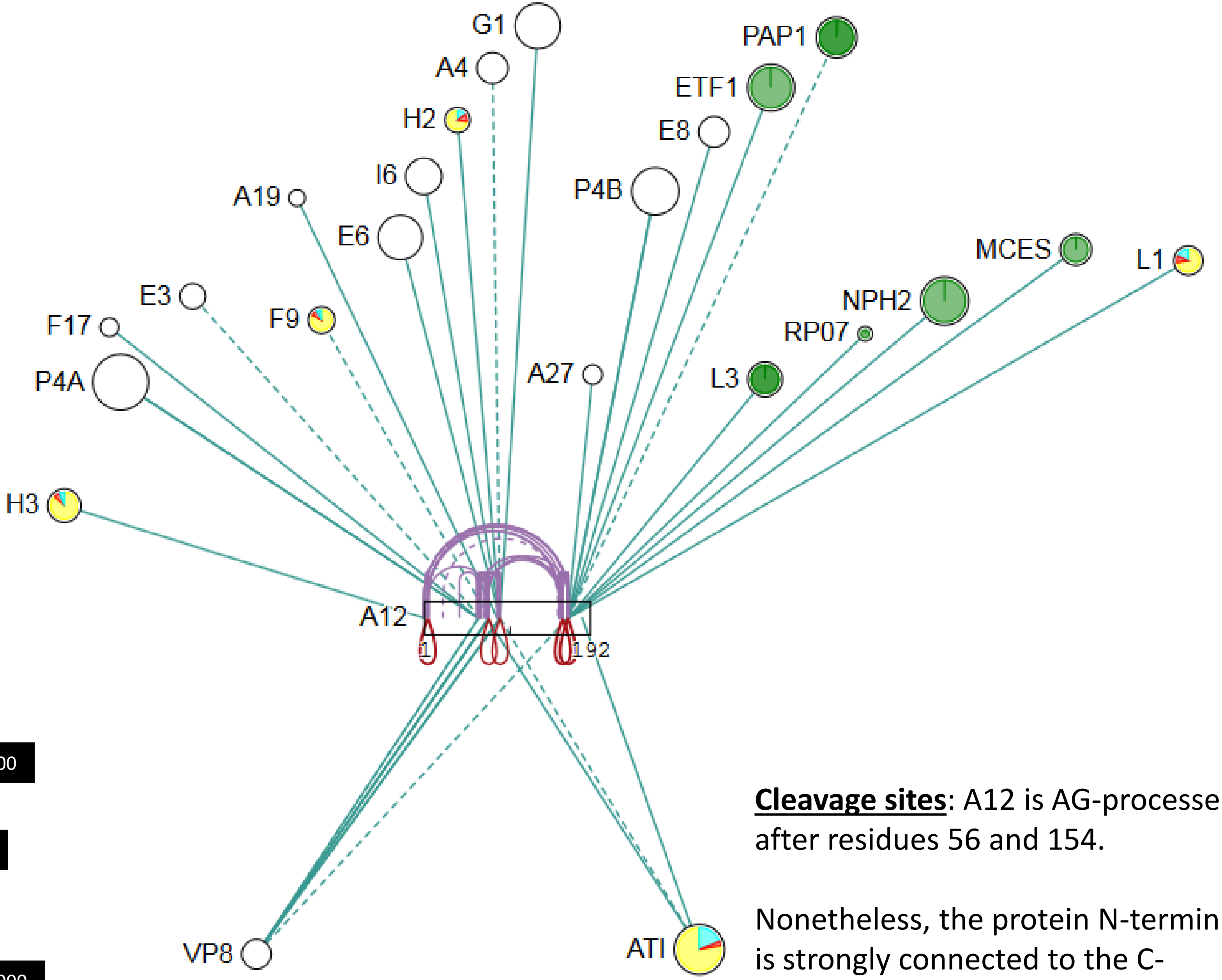


Other proteins

A12, A18, A19, A25(A2.5), A46, E3, E5, E6, E10, E11, F8, F17, M1, N1, PROF, SODL, A46



XL hotspots: A12 has two extreme XL hotspots, centered at aa88 and 167. Transcriptosome contacts are concentrated at the C-terminal hotspot. A12 appears to couple the transcription apparatus (C-terminus) with the VP8 interactome (N-terminal region).

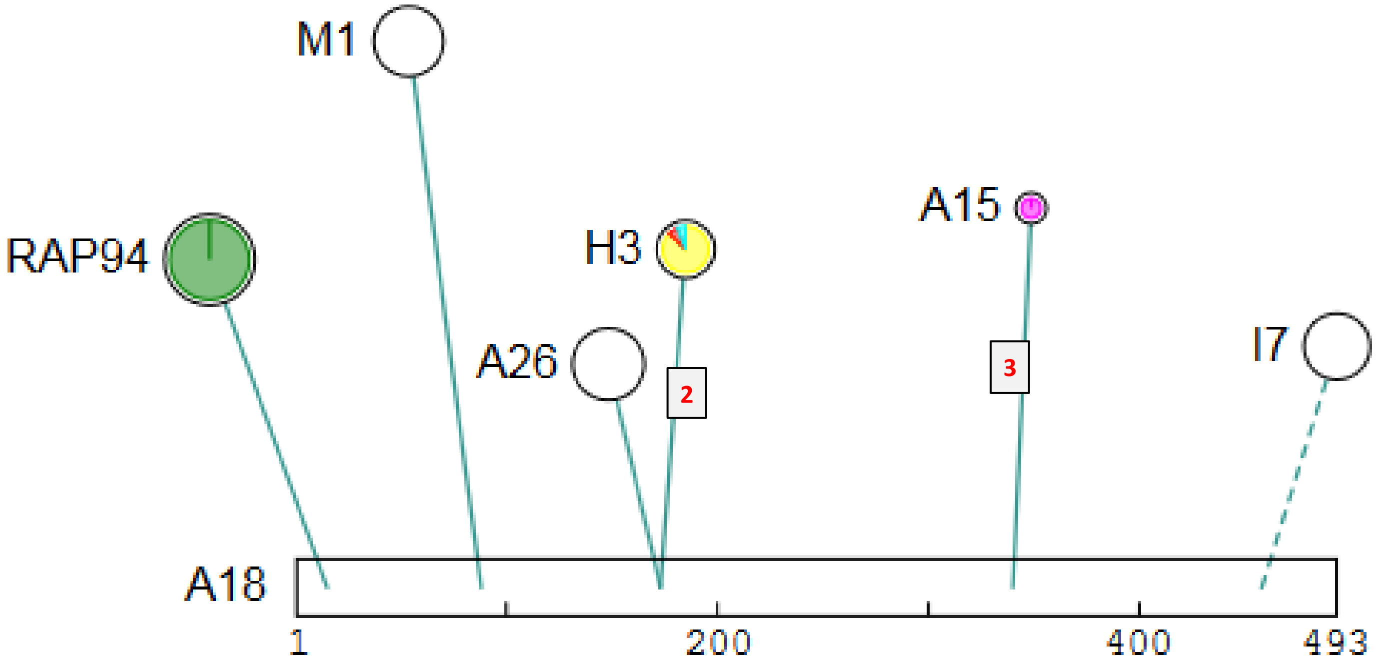


A12-63/VP8-240: 0
A12-63/VP8-212: 0
A12-66/E3-109: 0
A12-75/VP8-204: 0
A12-75/VP8-240: 0
A12-75/F9-0: 0
A12-88/A4-32: 0
A12-88/VP8-240: 1.000
A12-88/ATI-572: 0
A12-166/VP8-240: 0
A12-167/L3-18: 0
A12-167/E8-1: 0
A12-167/P4B-189: 1.000
A12-167/PAP1-462: 0

<u>Cleavage sites</u>: A12 is AG-processed after residues 56 and 154.

Nonetheless, the protein N-terminus is strongly connected to the C-terminal hotspot via intra-protein XL.

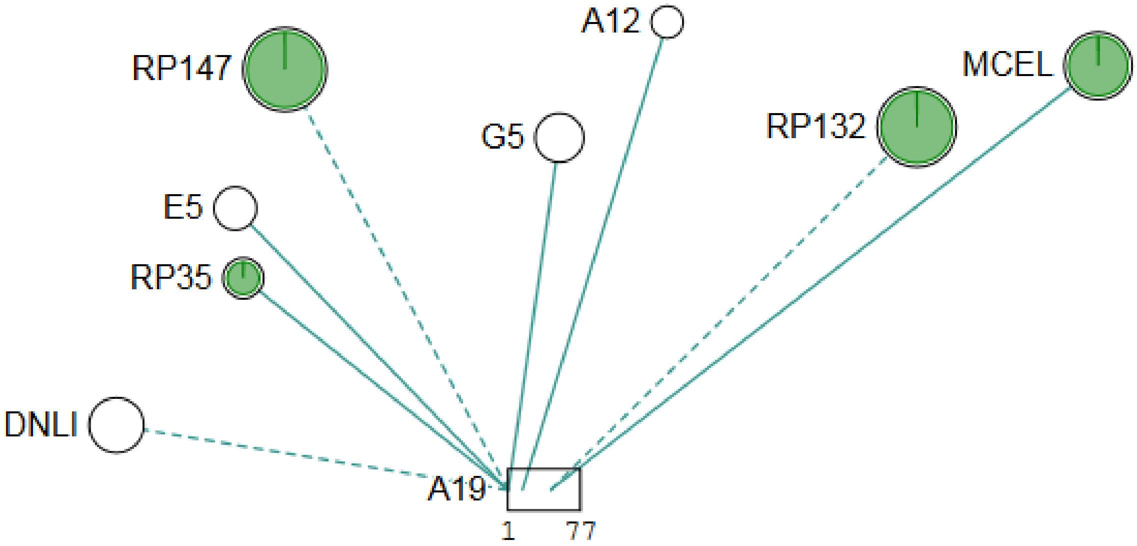
A18-458/I7-213: 0



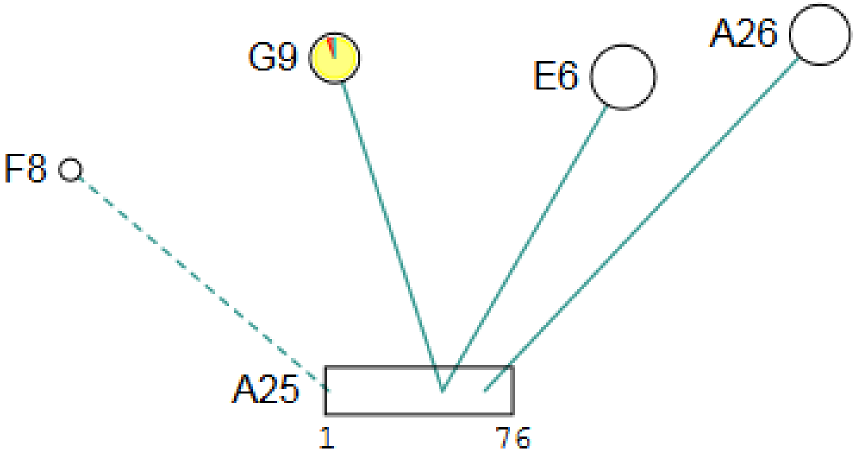
A19-0/DNLI-177: 0.500

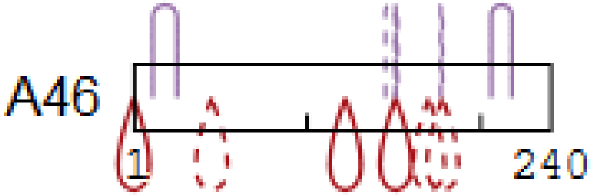
A19-1/RP147-566: 0

A19-46/RP132-511: 0



A25-2/F8-7: 0




A46
1
240

E3-3/RP30-54: 0.500

E3-40/VP8-240: 0

E3-45/F17-74: 0

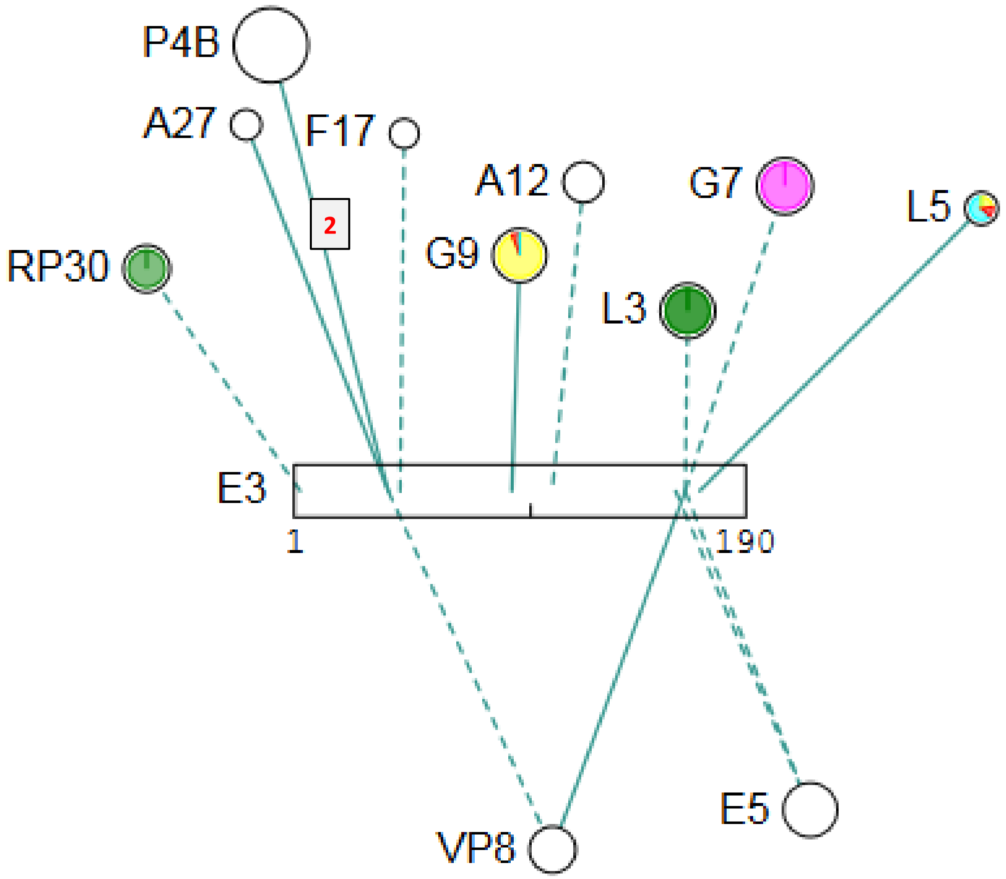
E3-109/A12-66: 0

E3-161/E5-223: 1.000

E3-165/E5-223: 1.000

E3-165/G7-345: 0

E3-165/L3-142: 0.500



E5-0/A27-57: 0

E5-61/RAP94-206: 0

E5-67/A13-49: 0

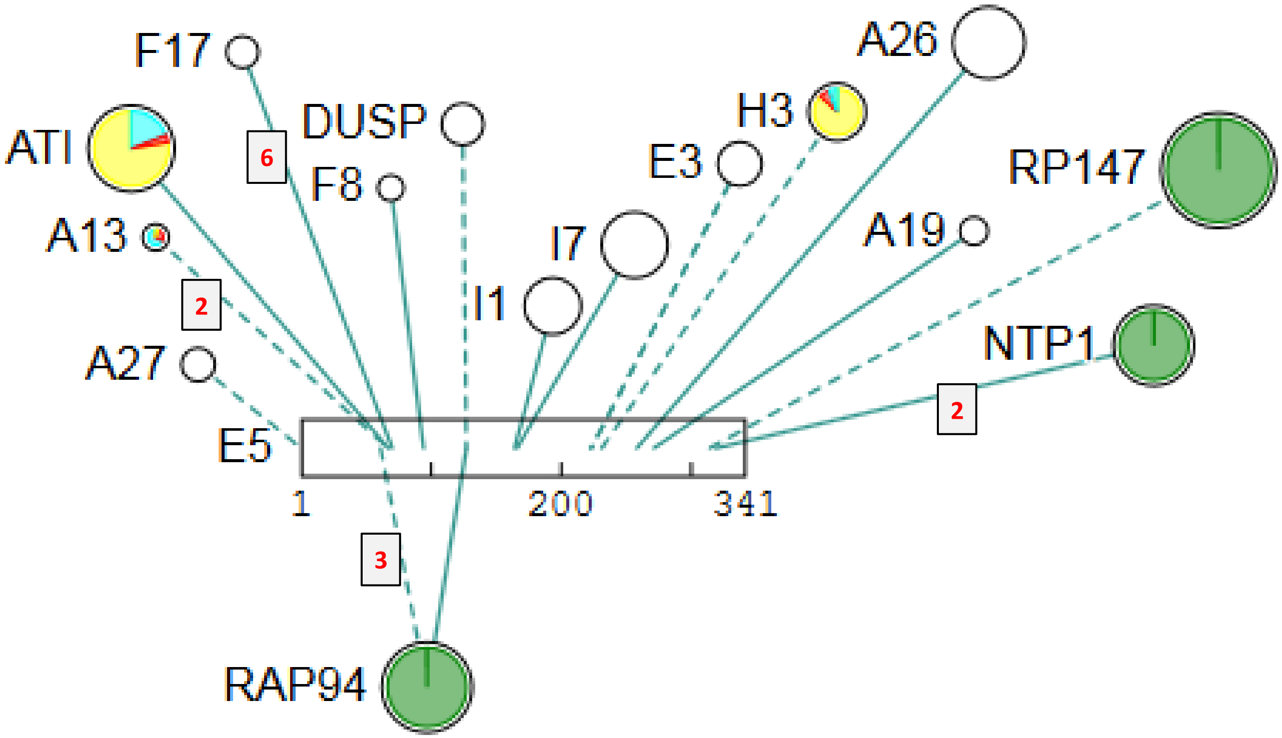
E5-127/DUSP-1: 0

E5-223/E3-161: 1.000

E5-223/E3-165: 1.000

E5-231/H3-147: 0

E5-314/RP147-127: 0



E6-1/I7-364: 0

E6-90/A4-33: 0

E6-118/F17-74: 0

E6-278/G9-58: 0.143

E6-404/RP19-13: 1.000

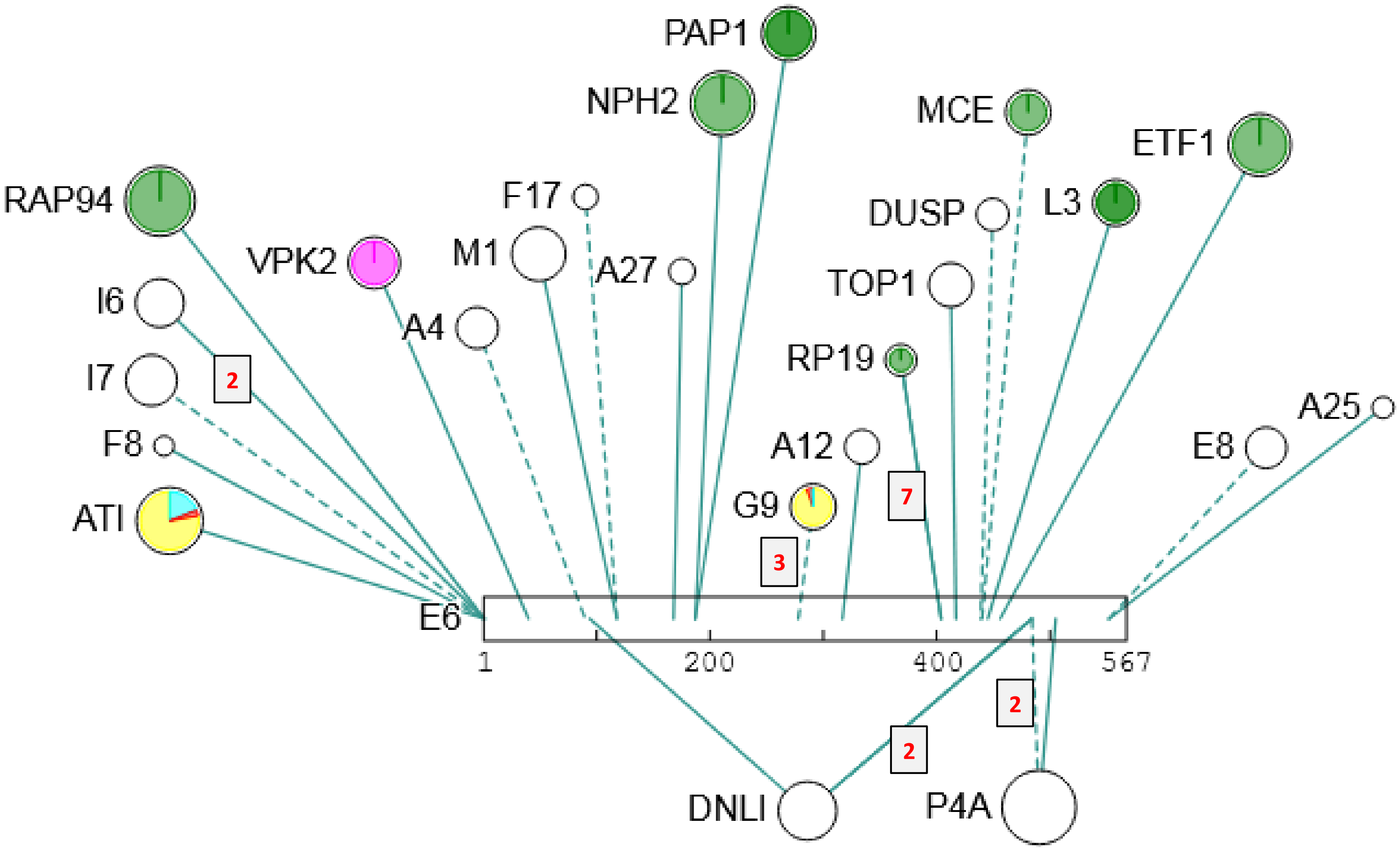
E6-404/RP19-14: 1.000

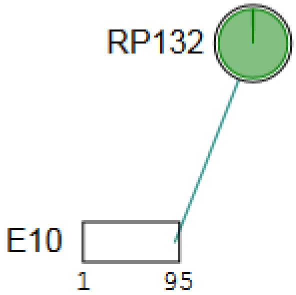
E6-439/DUSP-87: 0.500

E6-440/MCE-316: 0.500

E6-484/P4A-447: 0

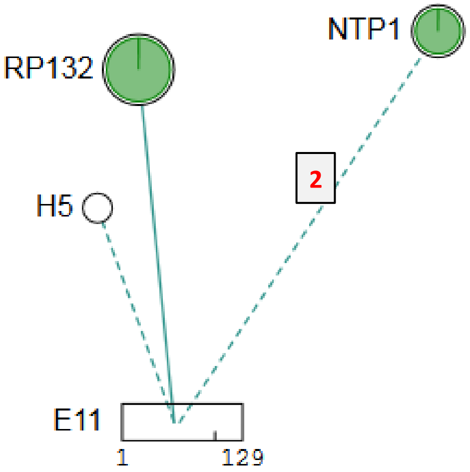
E6-552/E8-267: 0




RP132
E10
1
95

E11-56/H5-1: 0

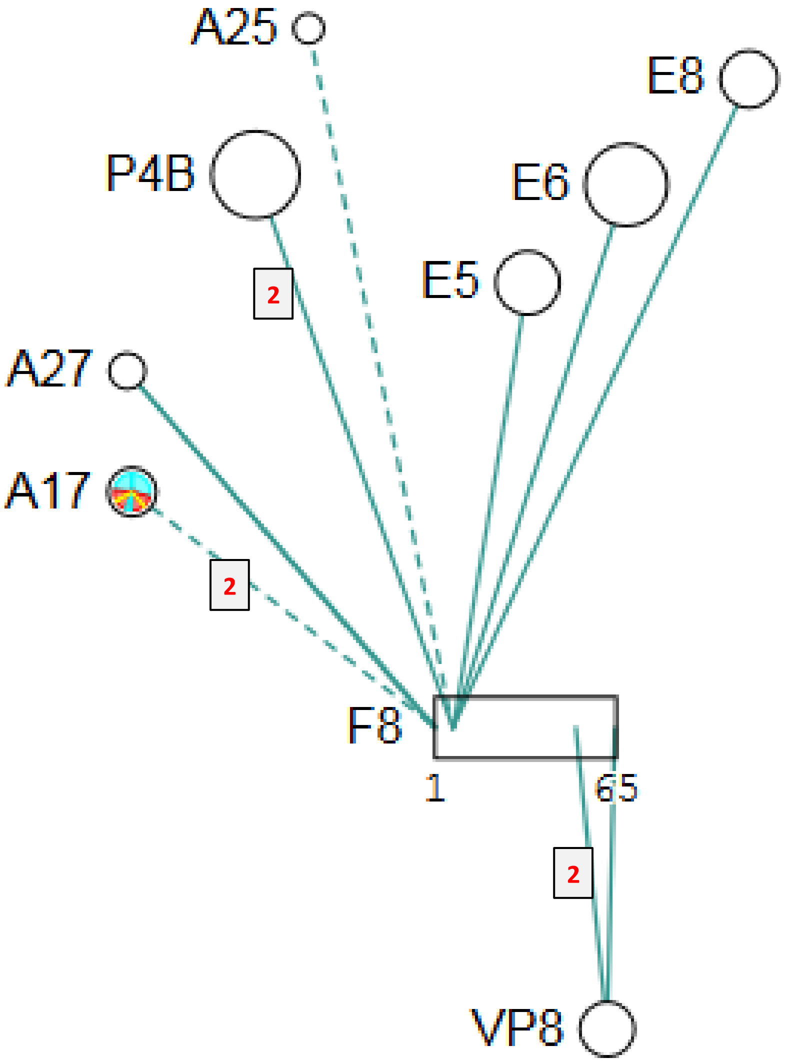
E11-62/NTP1-32: 0



F8-1/A17-180: 0

F8-7/A25-2: 0

F8-7/P4B-189: 0



F17-17/RP147-37: 0

F17-50/ETF1-252: 0

F17-74/A4-42: 0

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F17-74/P4A-508: 0

F17-74/E6-118: 0

F17-74/J1-74: 0

F17-74/L3-22: 0

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F17-74/P4B-564: 0

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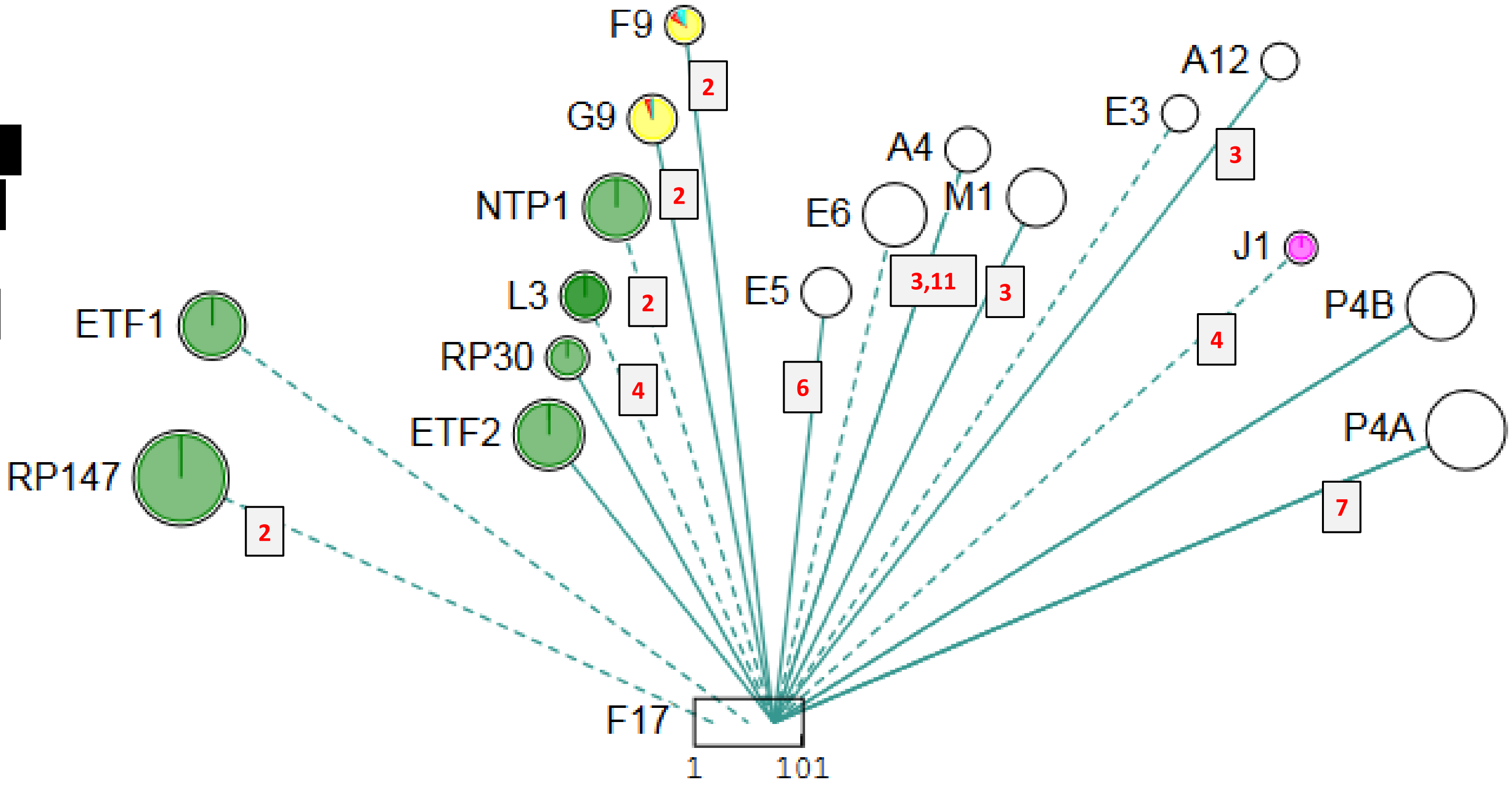
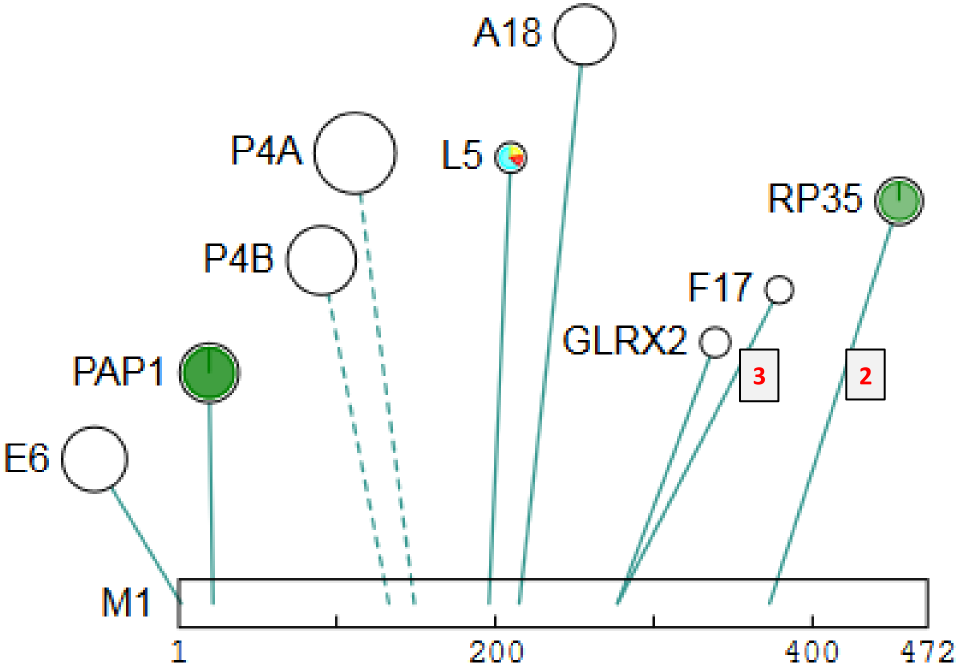


M1-133/P4B-83: 0

M1-149/P4A-876: 0

M1-277/F17-74: 0



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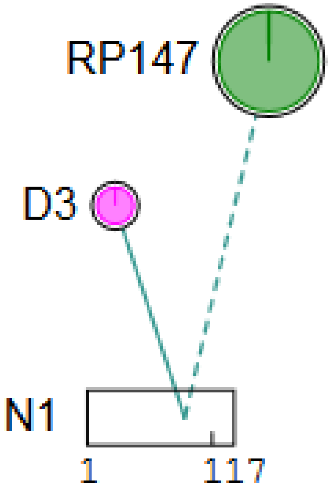
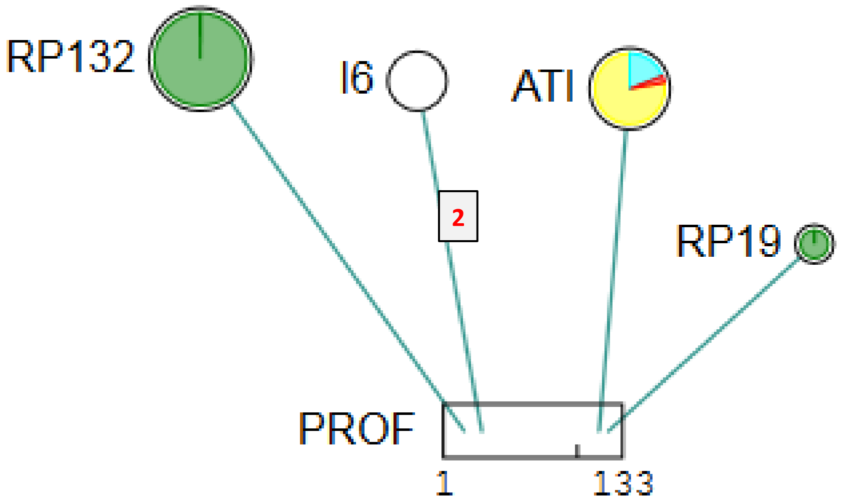
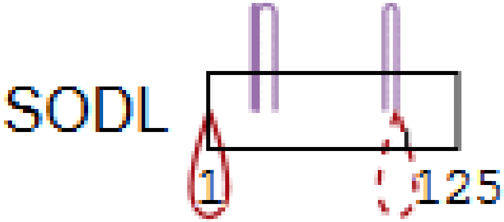



RP132
I6
ATI
2
RP19
PROF
1
133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125