

A Phylogenetic Analysis of GPT and GPT2 Evolution

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What is GPT/GPT2?

- Glutamic pyruvate transaminase (2)
 - Also called Alanine Aminotransferase (ALT1/ALT2)
- GPT is expressed in the cytosol of humans and mouse
- GPT2 is in the mitochondria
 - Chromosomal gene



Why Study GPT2?

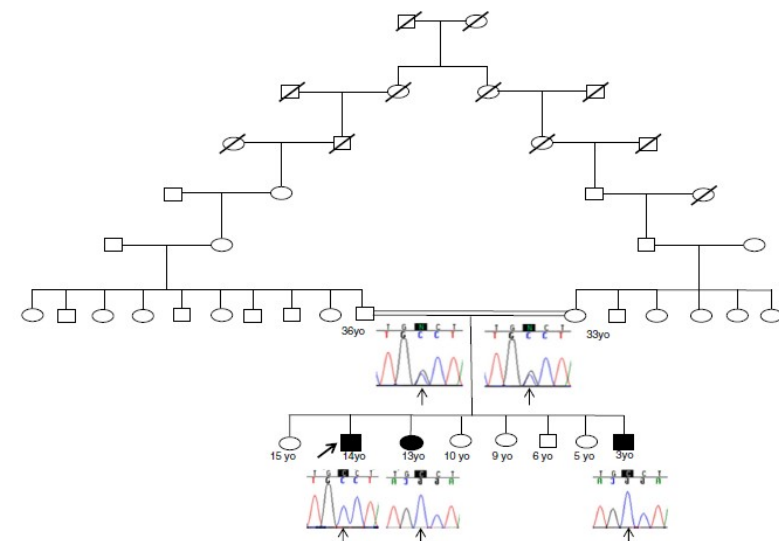
- Loss of GPT2 has been shown to cause developmental encephalopathy

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ORIGINAL ARTICLE

Loss of function mutation in glutamic pyruvate transaminase 2 (*GPT2*) causes developmental encephalopathy

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My Question

GPT and GPT2 are conserved in a number of species. Did they evolve separately from a common ancestor or have they evolved uniquely in each species?

Methods

- Identify gene and protein sequences using data from Homologene
 - I chose to only use species with both GPT and GPT2
- Using a process similar to that from hydroildolina assignment
 - Alignment with mafft → RAxML
 - GTRGAMMA for mRNA data
 - PROTGAMMAWAG



HomoloGene

An automated system for constructing putative homology groups from the complete gene sets of a wide range of eukaryotic species.

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HomoloGene:68832. Gene conserved in Eukaryota

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Genes

Genes identified as putative homologs of one another during the construction of HomoloGene.

- [GPT2, *H.sapiens*](#)
glutamic pyruvate transaminase (alanine aminotransferase) 2
- [GPT2, *P.troglodytes*](#)
glutamic pyruvate transaminase (alanine aminotransferase) 2
- [LOC716305, *M.mulatta*](#)
alanine aminotransferase 2-like
- [GPT2, *B.taurus*](#)
glutamic pyruvate transaminase (alanine aminotransferase) 2
- [Gpt2, *M.musculus*](#)
glutamic pyruvate transaminase (alanine aminotransferase) 2
- [Gpt2, *R.norvegicus*](#)
glutamic pyruvate transaminase (alanine aminotransferase) 2
- [GPT2, *G.gallus*](#)
glutamic pyruvate transaminase (alanine aminotransferase) 2
- [LOC100494152, *X.tropicalis*](#)
alanine aminotransferase 2-like
- [gpt2, *D.rerio*](#)
glutamic pyruvate transaminase (alanine aminotransferase) 2
- [CG1640, *D.melanogaster*](#)
CG1640
- [AgaP_AGAP000901, *A.gambiae*](#)
AgaP_AGAP000901
- [CELE_C32F10.8, *C.elegans*](#)
CELE_C32F10.8
- [ALT1, *S.cerevisiae*](#)

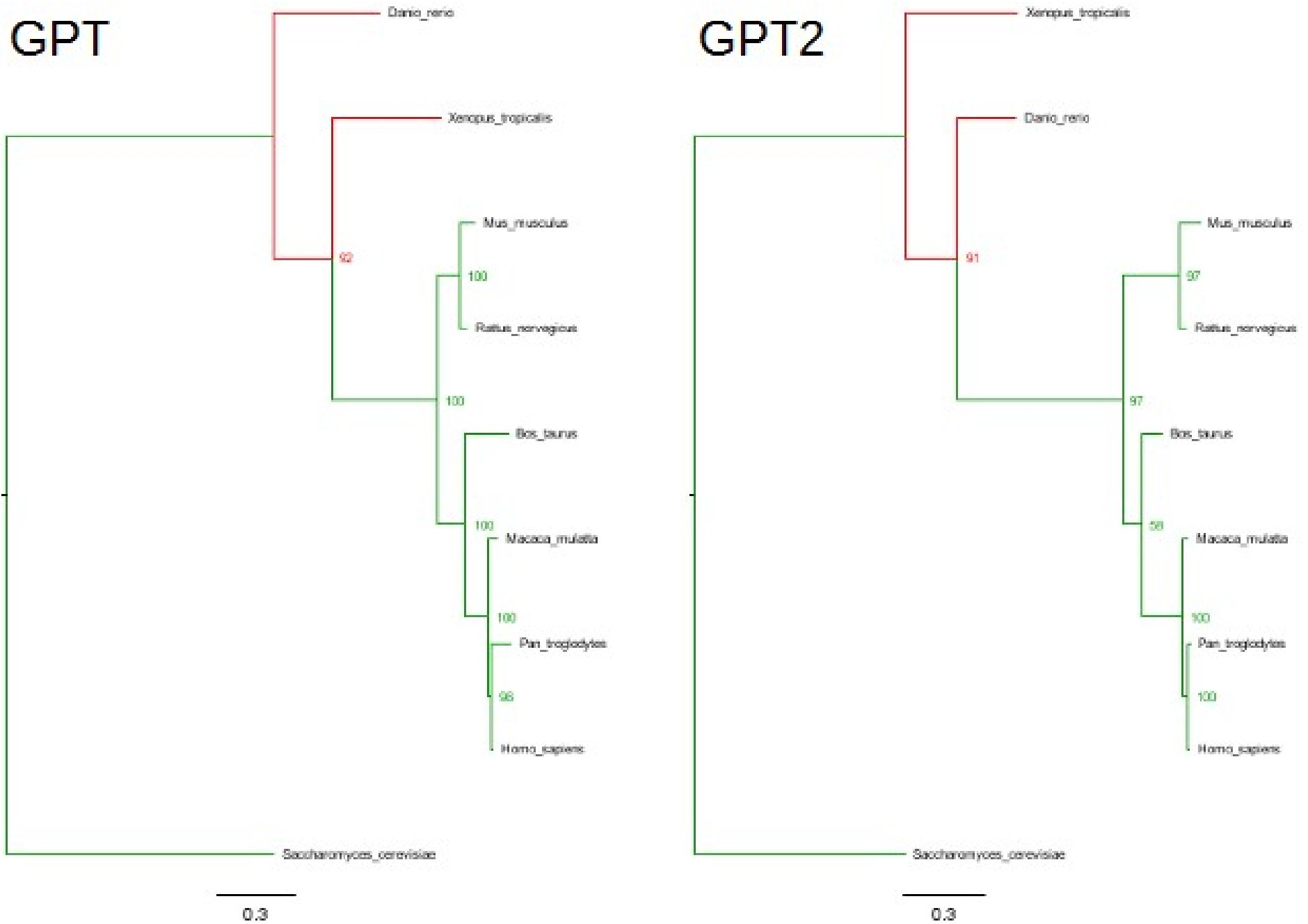
Proteins

Proteins used in sequence comparisons and their conserved domain architectures.

- [NP_597700.1](#) 523 aa
- [XP_003952890.1](#) 523 aa
- [XP_001113757.2](#) 599 aa
- [NP_001180116.1](#) 523 aa
- [NP_776291.1](#) 522 aa
- [NP_001012057.1](#) 522 aa
- [XP_414111.3](#) 544 aa
- [XP_002931716.1](#) 538 aa
- [NP_001092227.2](#) 484 aa
- [NP_572879.2](#) 568 aa
- [XP_316880.5](#) 552 aa
- [NP_001021021.1](#) 504 aa
- [NP_012180.1](#)

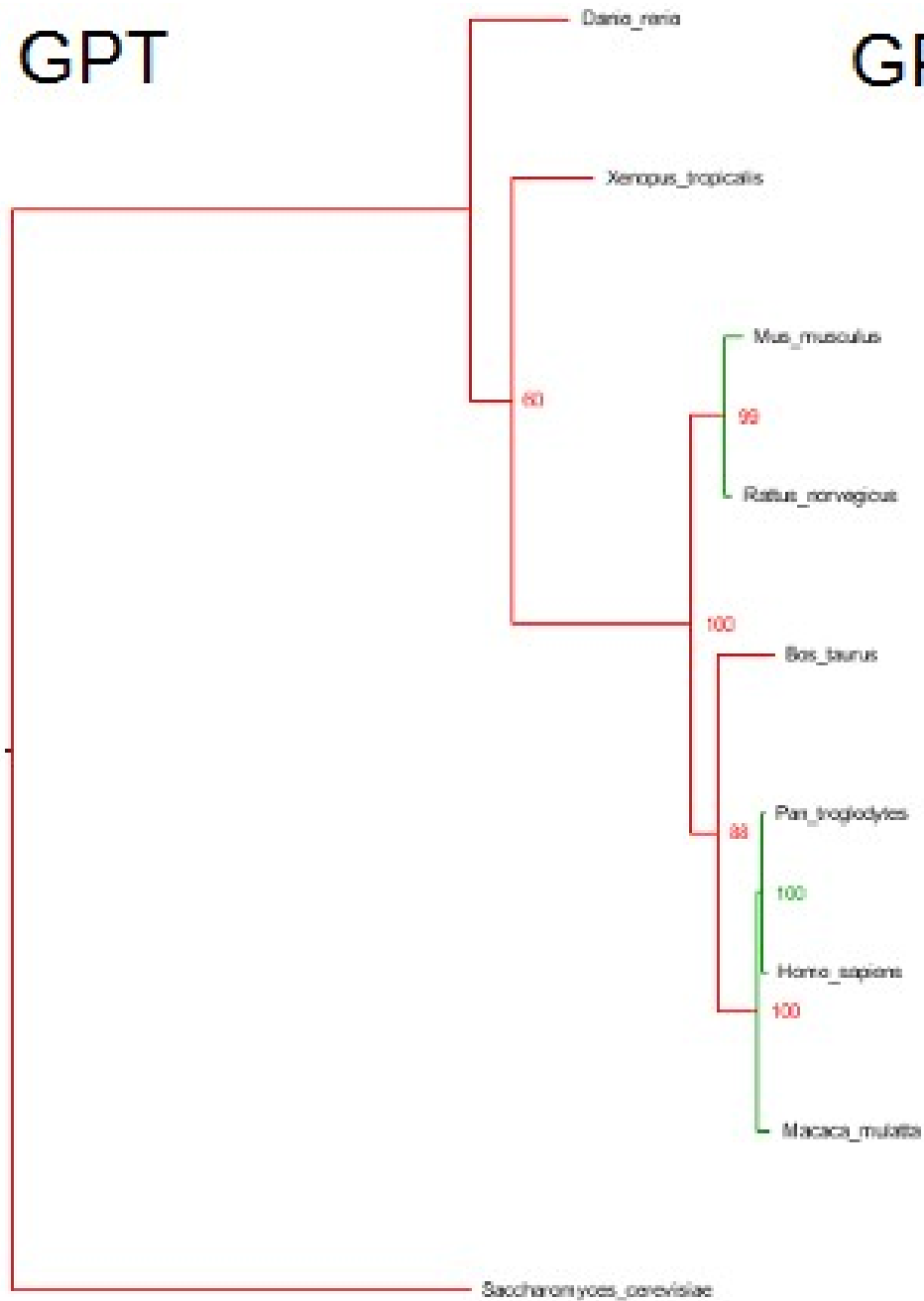
Species	Protein Family	Gene Name
Homo sapiens	GPT	GPT
Pan troglodytes	GPT	GPT
Macaca mulatta	GPT	GPT
Bos taurus	GPT	GPT
Mus musculus	GPT	Gpt
Rattus norvegicus	GPT	Gpt
Xenopus tropicalis	GPT	gpt2
Danio rerio	GPT	gpt2l
Saccharomyces cerevisiae	GPT	ALT2
Homo sapiens	GPT2	GPT2
Pan troglodytes	GPT2	GPT2
Macaca mulatta	GPT2	GPT2
Bos taurus	GPT2	GPT2
Mus musculus	GPT2	Gpt2
Rattus norvegicus	GPT2	Gpt2
Xenopus tropicalis	GPT2	gpt2
Danio rerio	GPT2	gpt2
Saccharomyces cerevisiae	GPT2	ALT1

Results: mRNA “control” trees

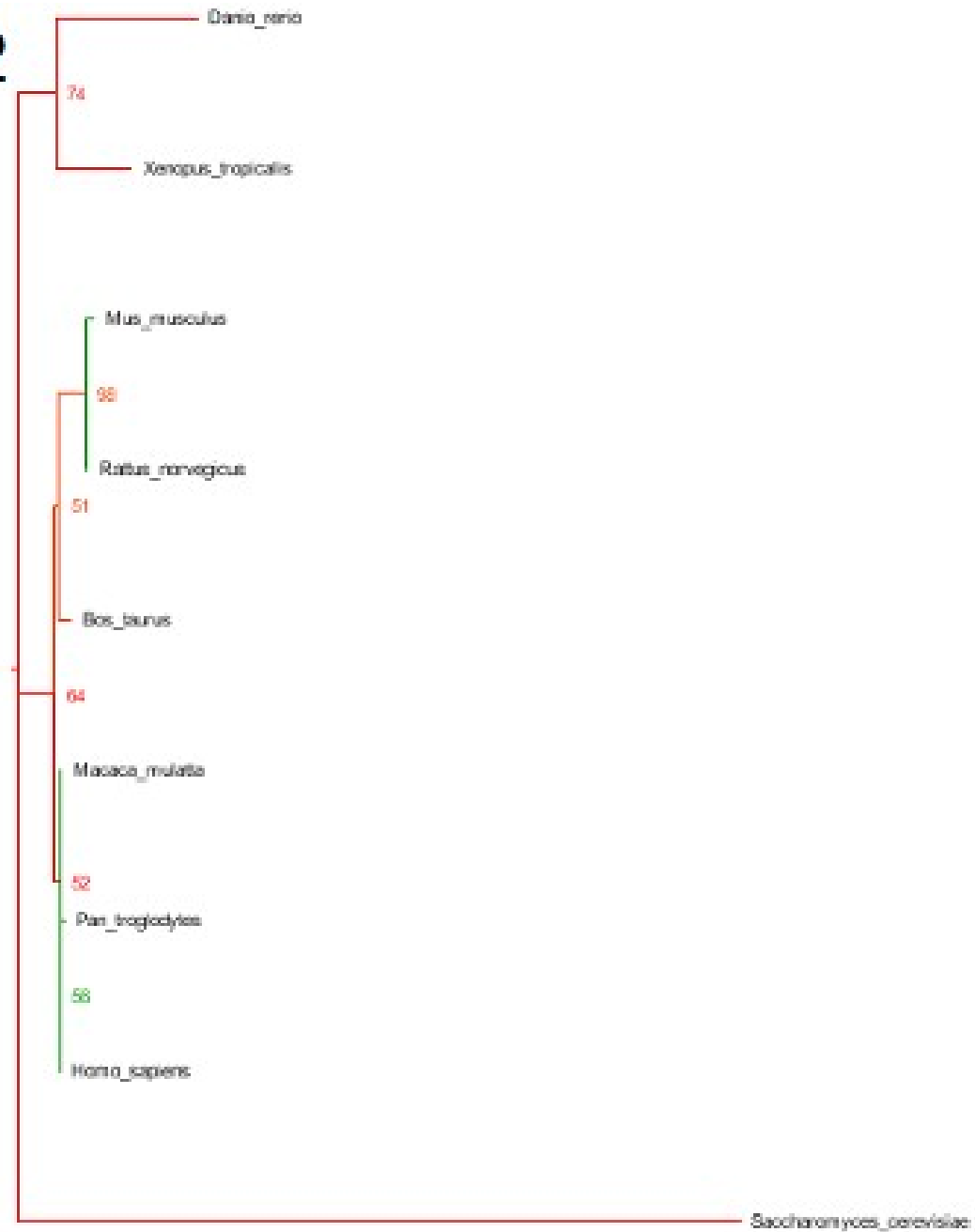


Results: protein “control” trees

GPT

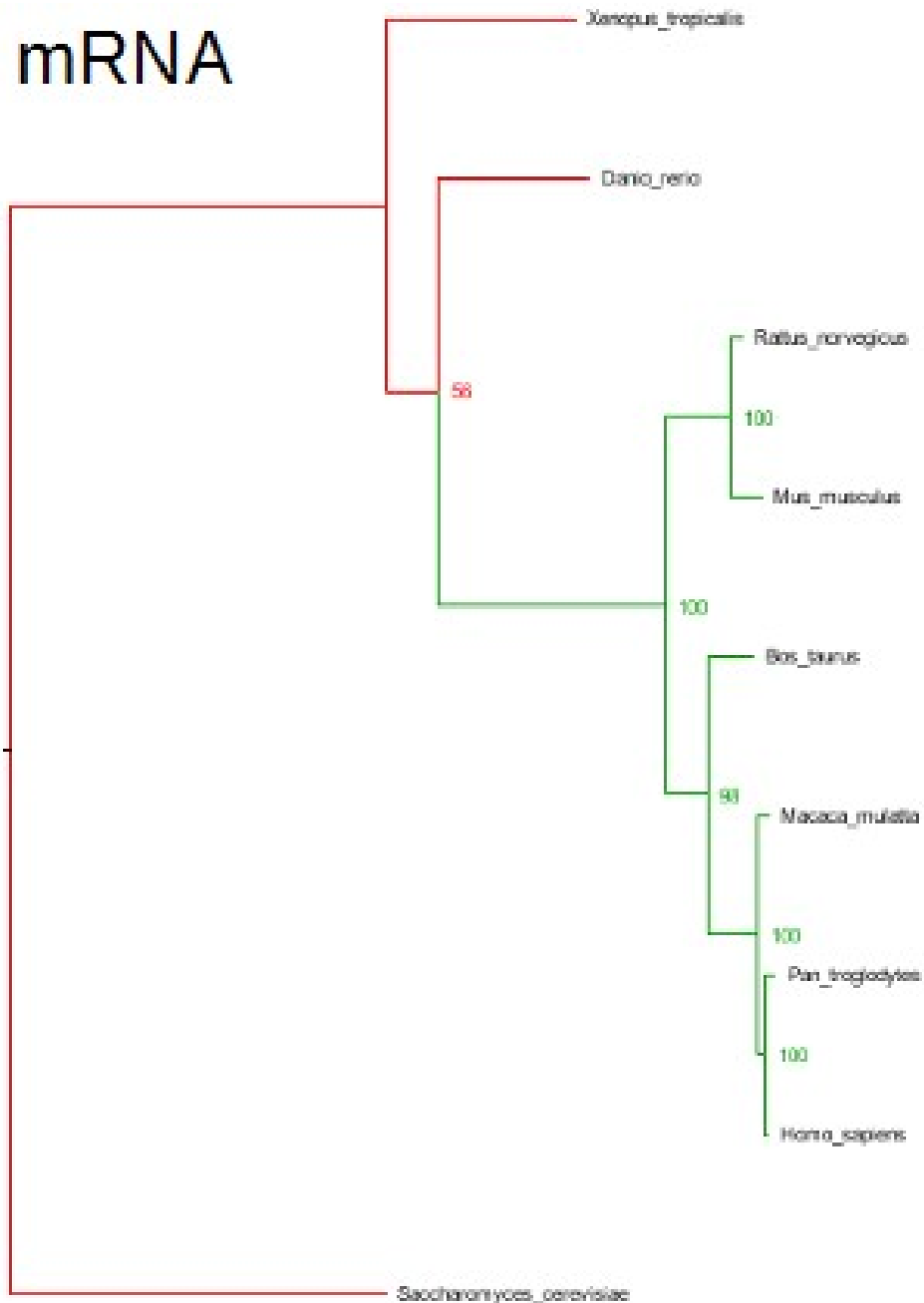


GPT2

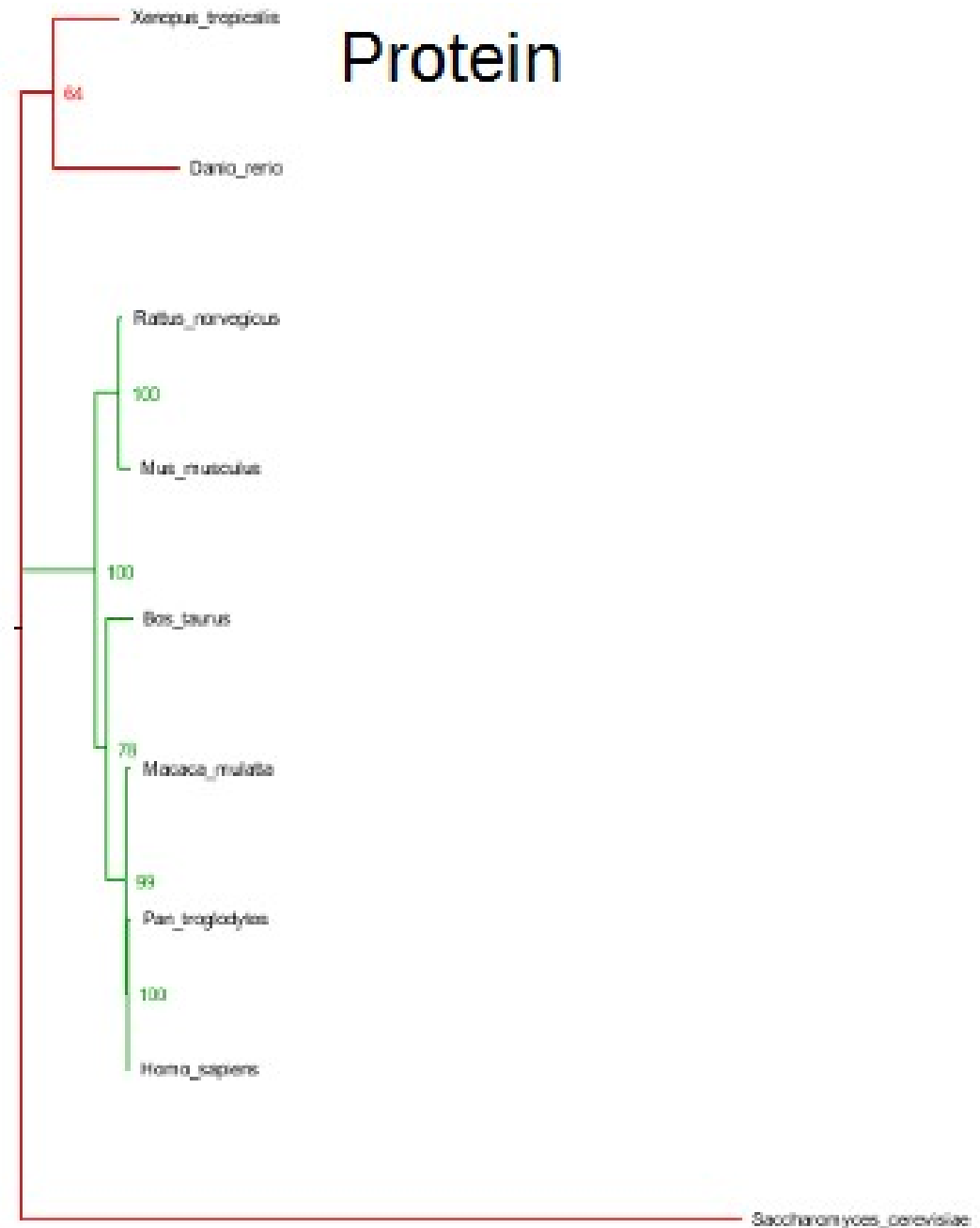


Results: concatenated “control” trees

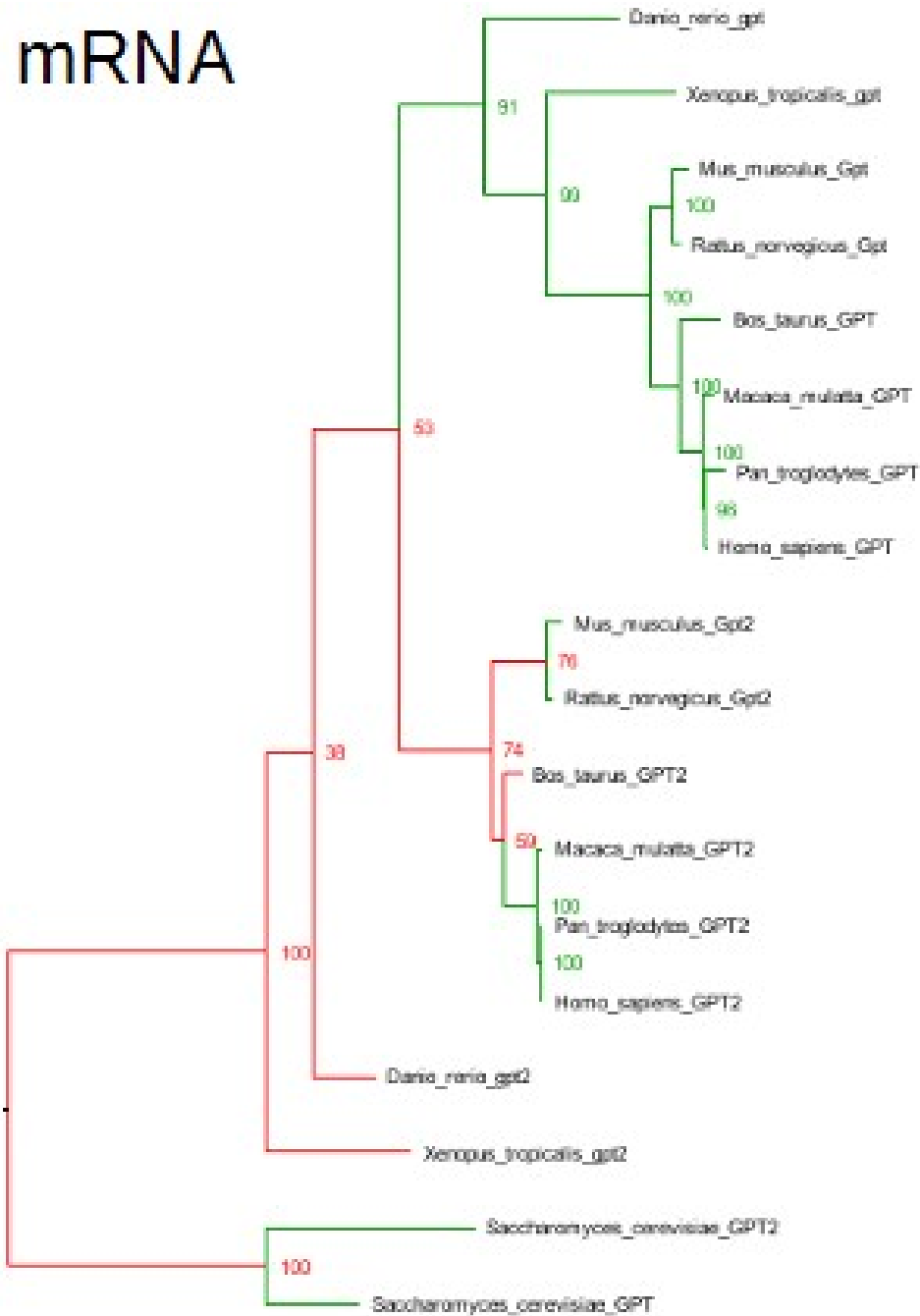
mRNA



Protein

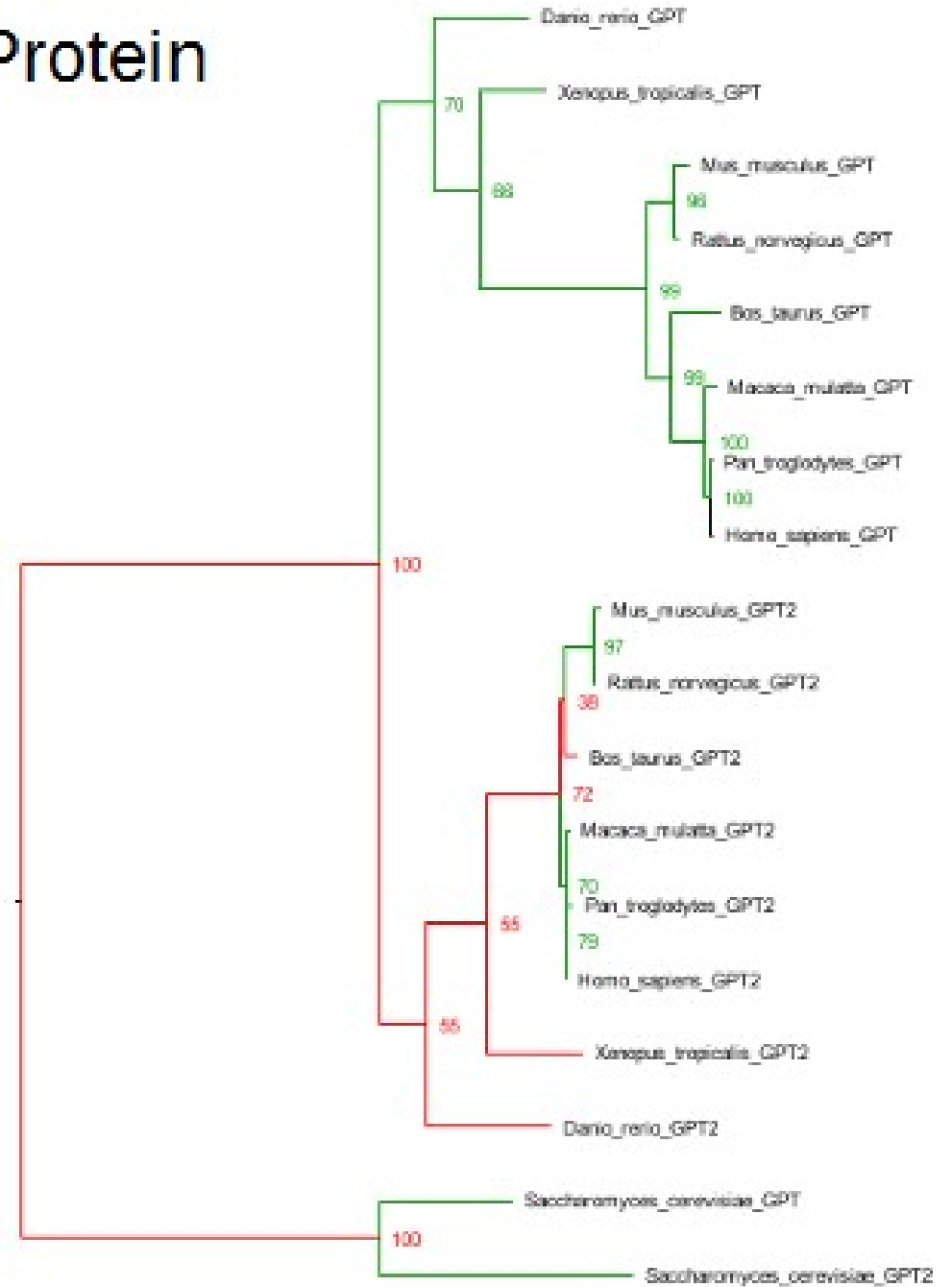


mRNA



0.4

Protein



0.2

Conclusions

- Difficult to draw conclusions about cellular localizations as I could only find data for human mouse and rat.
- Raises some questions for me about homologue:
 - They use protein sequence as opposed to mRNA?
 - Why does yeast group separately in both but are assigned to different homologue groups?