

Output results of CLIME (CLustering by Inferred Models of Evolution)

Dataset:

Num of genes in input gene set: 6
Total number of genes: 20834
Prediction LLR threshold: 0

The CLIME PDF output two sections:

1) Overview of Evolutionarily Conserved Modules (ECMs)

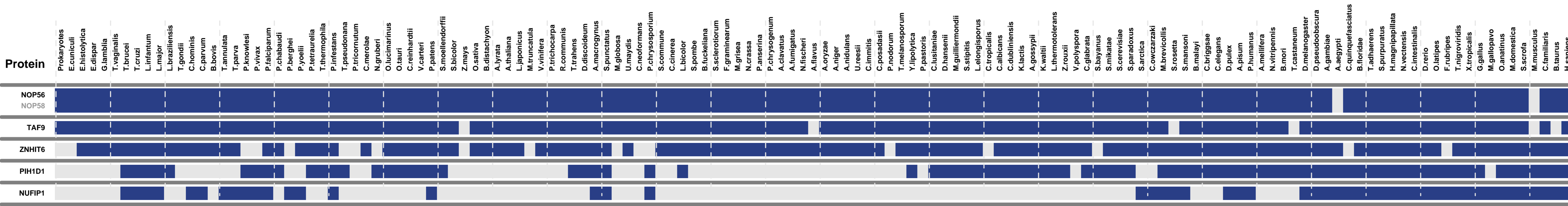
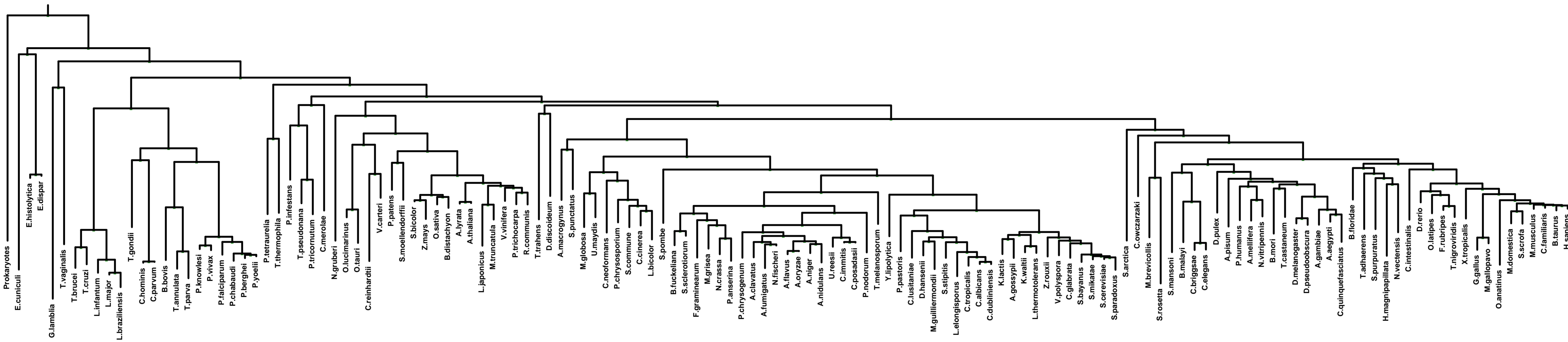
- Top panel shows the predefined species tree.
- Bottom panel shows the partition of input genes into Evolutionary Conserved Modules (ECMs), ordered by ECM strength (shown at right), and separated by horizontal lines.
- Each row show one gene, where the phylogenetic profile indicates presence (blue) or absence (gray) of homologs in each species (column).
- Gene symbols are shown at left. Gray color indicates that the gene is a paralog to a higher scoring gene within the same ECM (based on BLASTP $E < 1e-3$).

2) Details of each ECM and its expansion ECM+

- Top panel shows the inferred evolutionary history on the predefined species tree. Branch color shows the gain event (blue) and loss events (red color, with brighter color indicating higher confidence in loss). Branches before the gain or after a loss are shown in gray.
- Bottom panel shows the input genes that are within the ECM (blue/white rows) as well as all genes in the expanded ECM+ (green/gray rows). The ECM+ includes genes likely to have arisen under the inferred model of evolution relative to a background model, and scored using a log likelihood ratio (LLR).
- PG indicates "paralog group" and are labeled alphabetically (i.e., A, B). The first gene within each paralog group is shown in black color. All other genes sharing sequence similarity (BLAST $E < 1e-3$) are assigned to the same PG label and displayed in gray.

Overview of Evolutionarily Conserved Modules (ECMs)

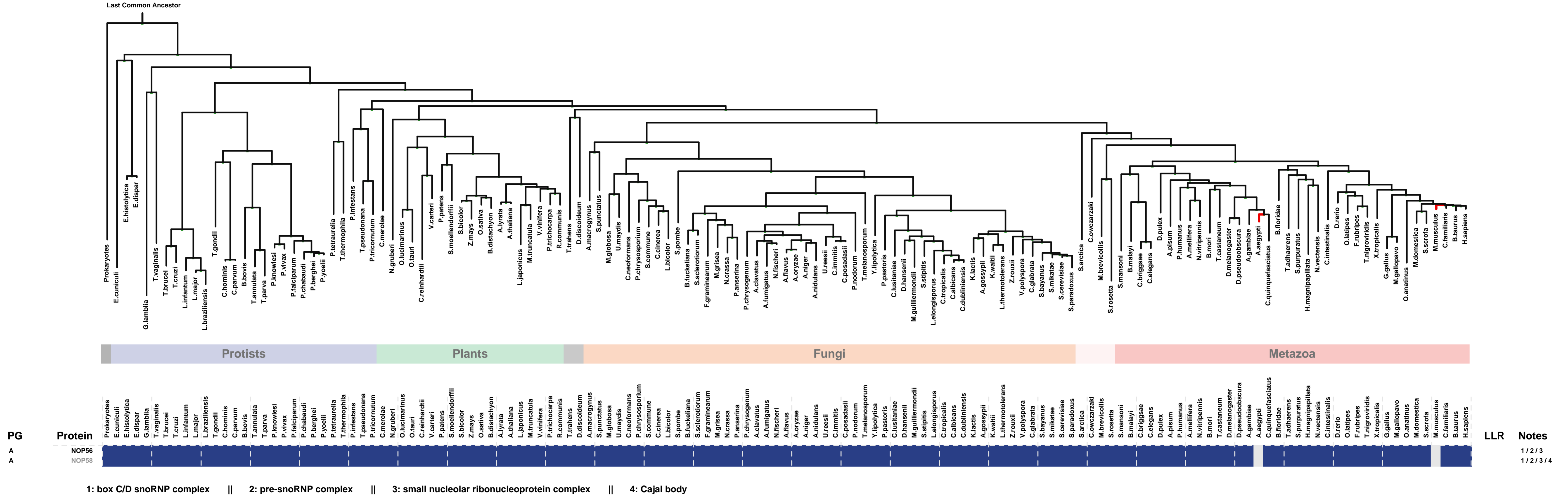
Last Common Ancestor



Strength

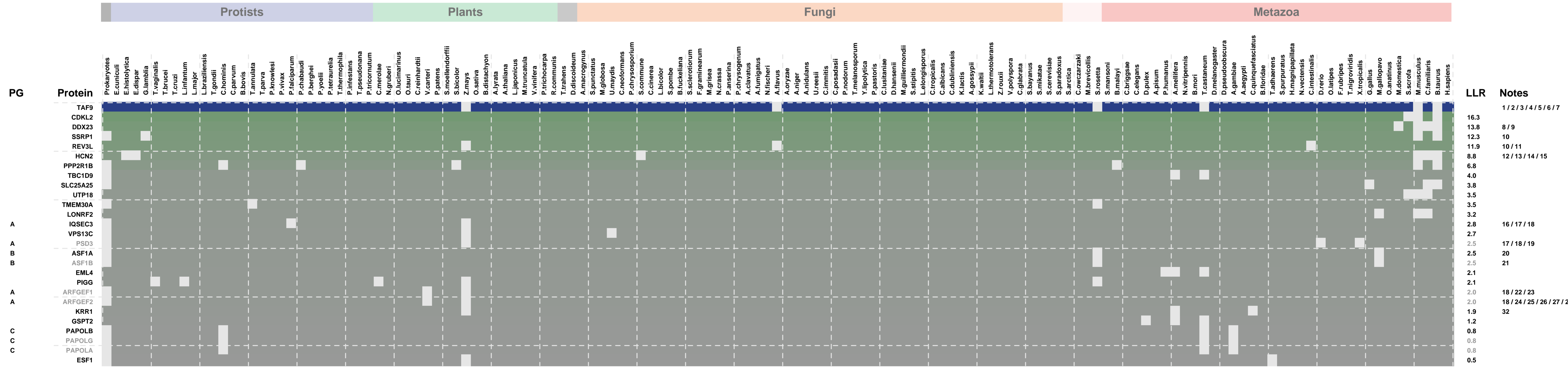
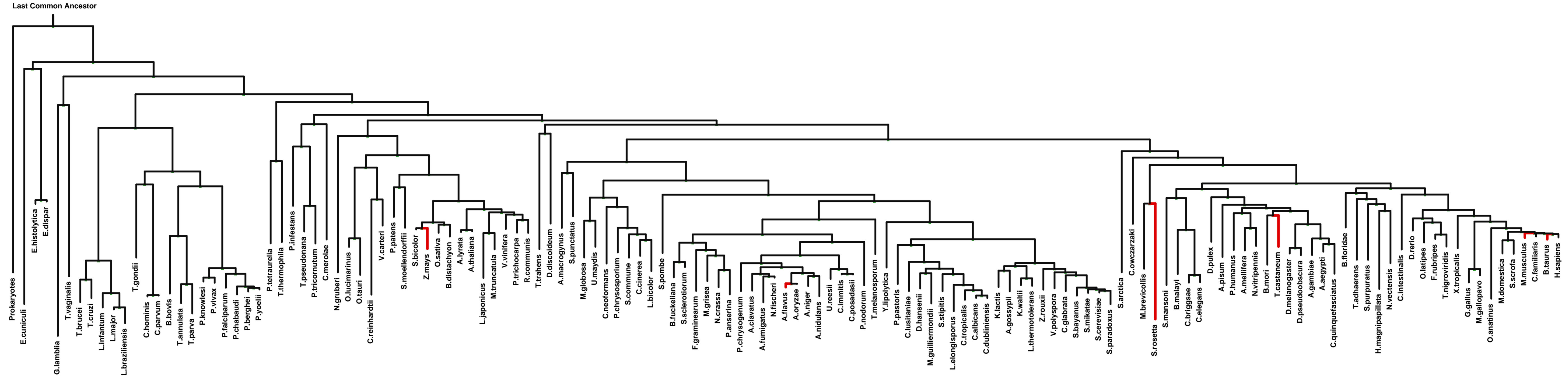
ECM 1, Gene set "pre-snoRNP complex", Page 1

Num of ECM Genes: 2. Num of Predicted Genes: 0. ECM Strength: 0.0



ECM 2, Gene set "pre-snoRNP complex", Page 1

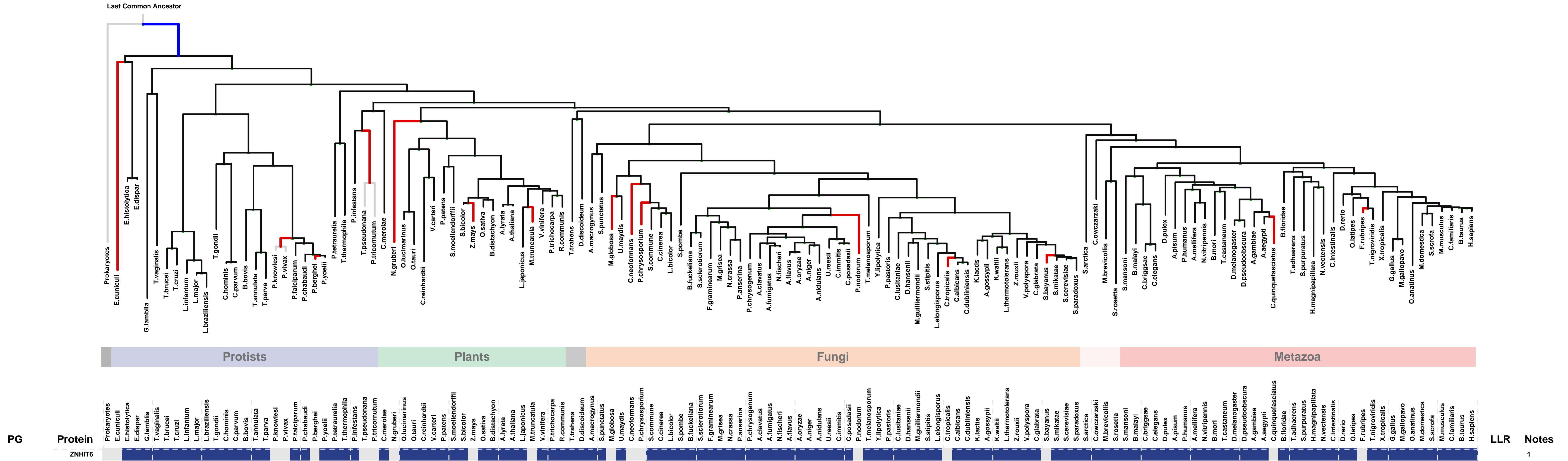
Num of ECM Genes: 1. Num of Predicted Genes: 26



1: Cajal body || 2: MLL1 complex || 3: PCAF complex || 4: pre-snoRNP complex || 5: STAGA complex || 6: transcription factor TFIID complex || 7: transcription factor TFIIIC complex || 8: catalytic step 2 spliceosome || 9: U5 snRNP || 10: chromosome || 11: zeta DNA polymerase complex || 12: axon || 13: dendritic shaft || 14: synapse || 15: voltage-gated potassium channel complex || 16: inhibitory synapse || 17: postsynaptic membrane || 18: trans-Golgi network || 19: postsynaptic density || 20: chromatin remodeling complex || 21: chromatin || 22: nuclear matrix || 23: small nuclear ribonucleoprotein complex || 24: asymmetric synapse || 25: axonemal microtubule || 26: cytoplasmic membrane-bounded vesicle || 27: cytoplasmic vesicle || 28: dendritic spine || 29: microtubule organizing center || 30: recycling endosome || 31: symmetric synapse || 32: ribonucleoprotein complex

ECM 3, Gene set "pre-snoRNP complex", Page 1

Num of ECM Genes: 1. Num of Predicted Genes: 0

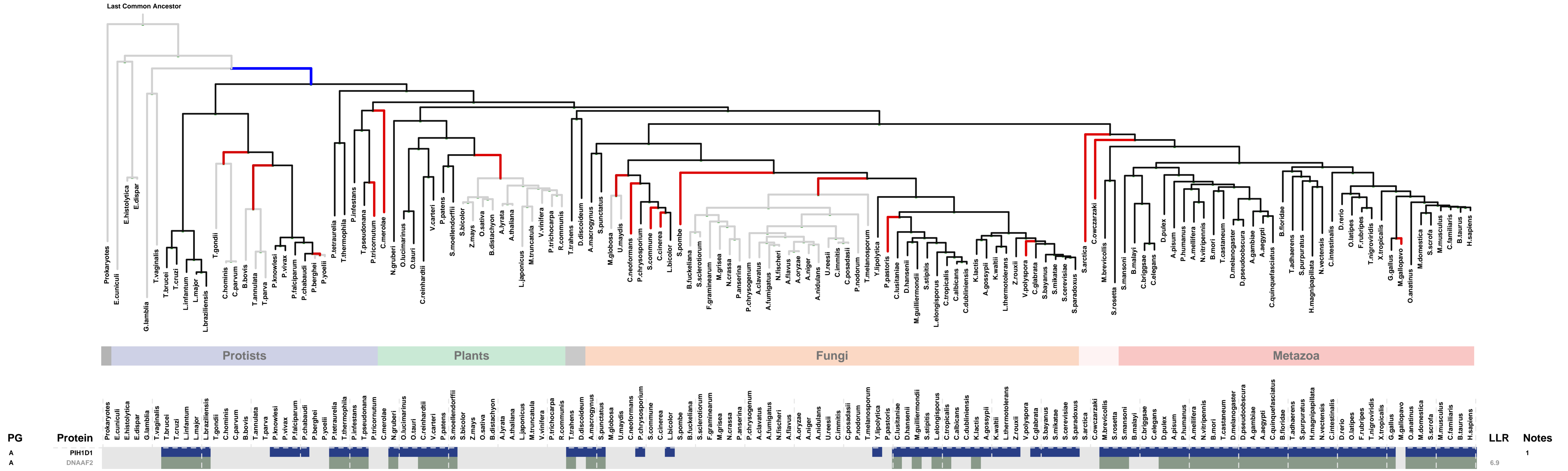
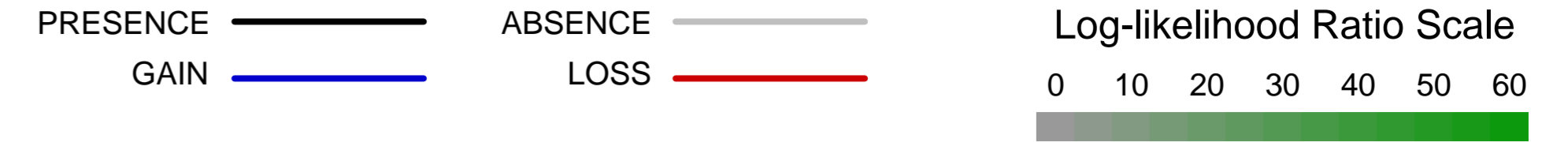


PG	Protein	LLR	Notes
ZNHIT6			

1: pre-snoRNP complex

ECM 4, Gene set "pre-snoRNP complex", Page 1

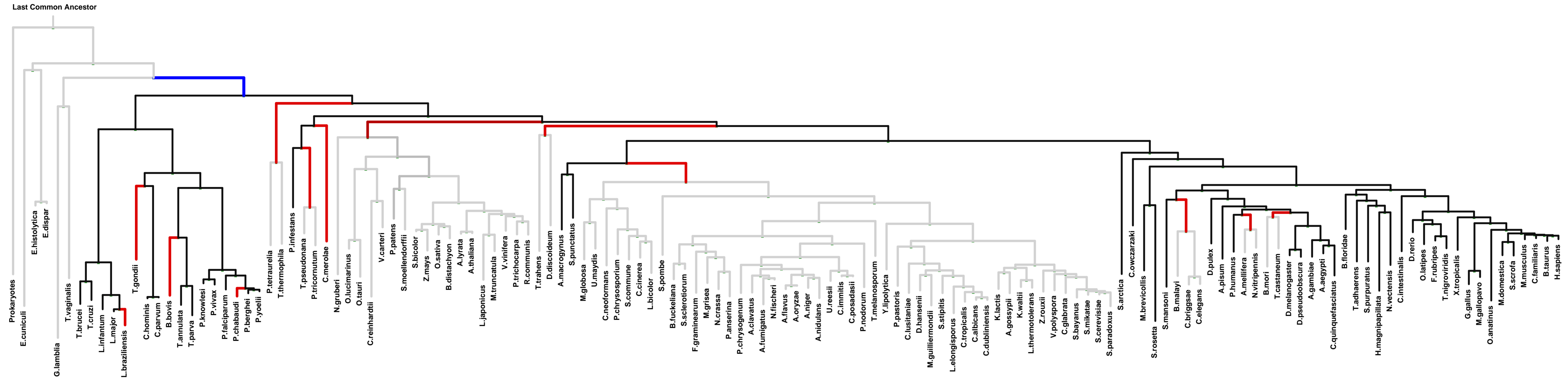
Num of ECM Genes: 1. Num of Predicted Genes: 1



1: pre-snoRNP complex

ECM 5, Gene set "pre-snoRNP complex", Page 1

Num of ECM Genes: 1. Num of Predicted Genes: 3



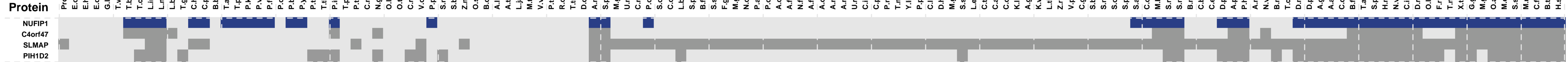
Protists

Plants

Fungi

Metazoa

PG



LLR Notes
1 2 3 4 5 6
0.5
0.4 7 8 9 10
0.2

1: cytosolic ribosome || 2: nuclear matrix || 3: perichromatin fibrils || 4: pre-snoRNP complex || 5: presynaptic active zone || 6: transcription elongation factor complex || 7: microtubule organizing center || 8: prefoldin complex || 9: sarcolemma || 10: smooth endoplasmic reticulum