

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

Dataset:

Num of genes in input gene set: 2
Total number of genes: 20834
Prediction LLR threshold: 0

The CLIME PDF output two sections:

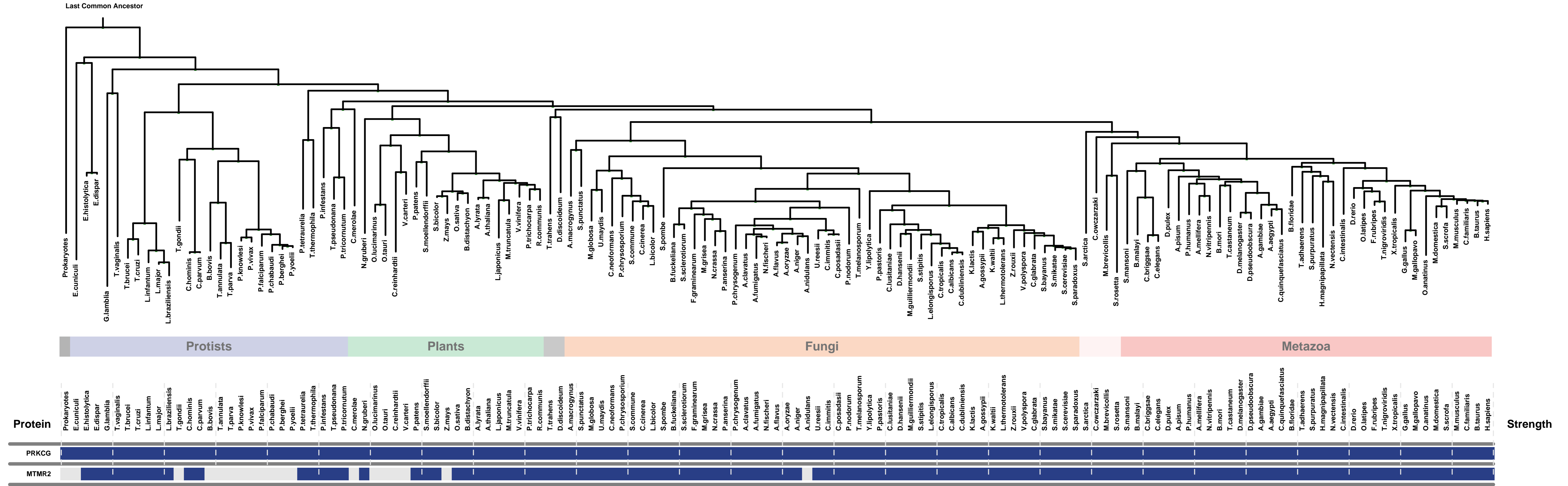
1) Overview of Evolutionarily Conserved Modules (ECMs)

- 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+

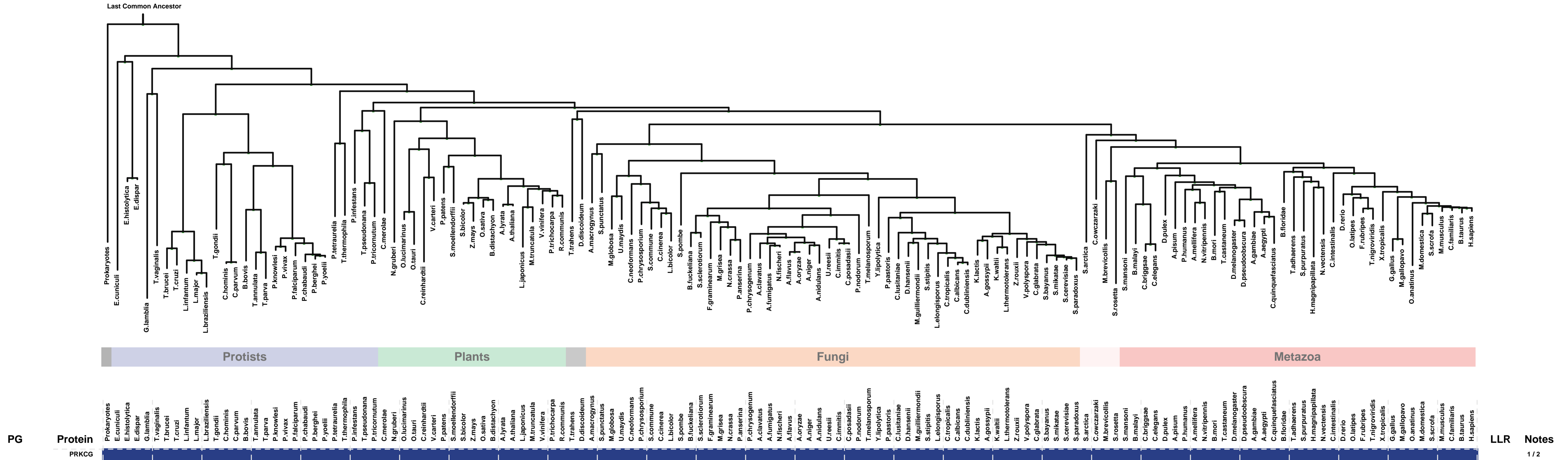
- Top panel shows the inferred evolutionary history on the predefined species tree. Branch color shows the gain event (blue) and loss events (red color, with brighter color indicating higher confidence in loss). Branches before the gain or after a loss are shown in gray.
- Bottom panel shows the input 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)



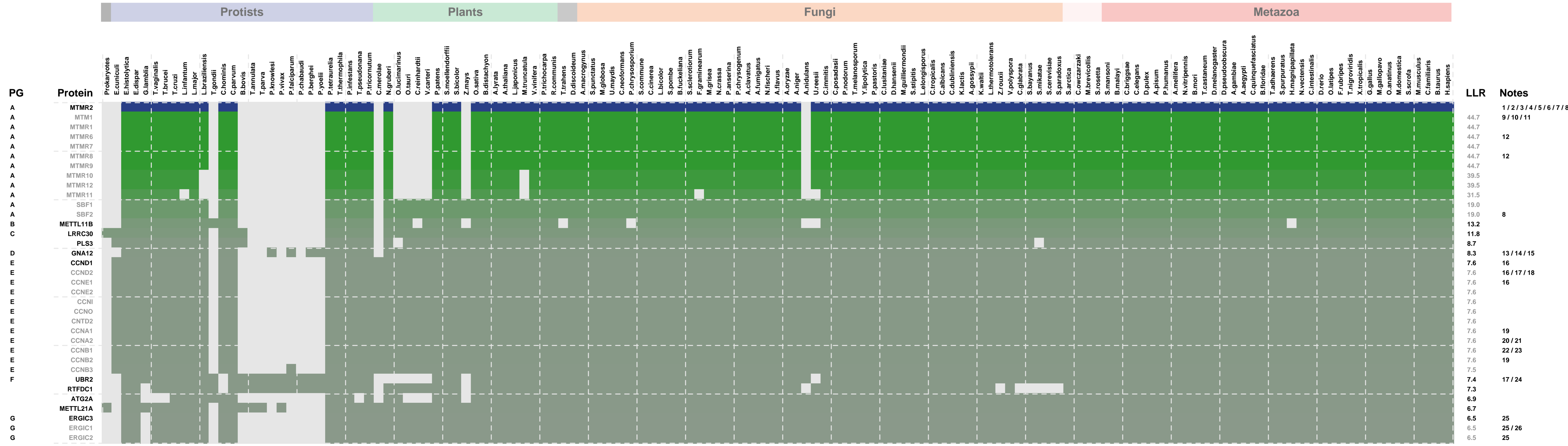
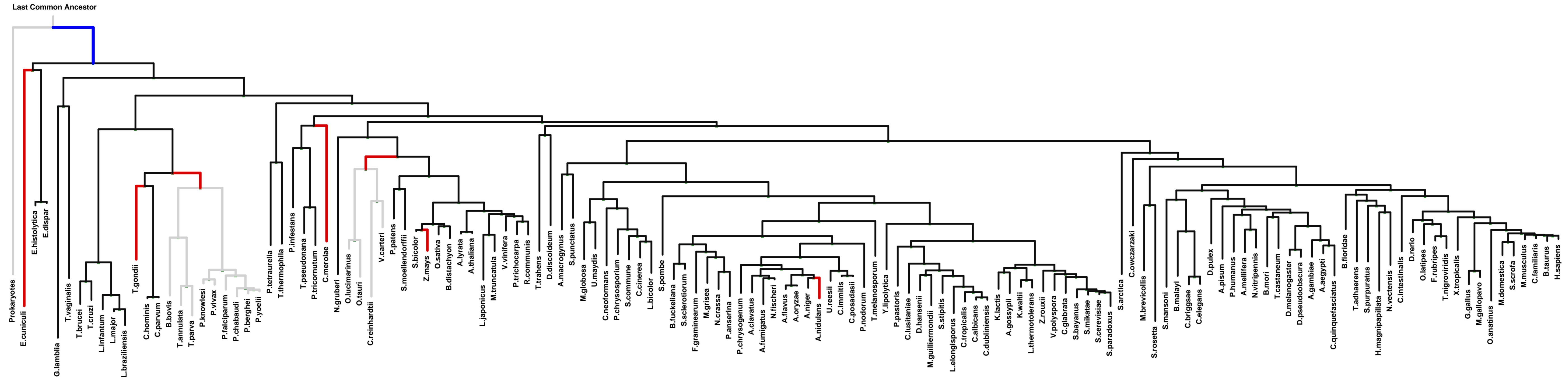
ECM 1, Gene set "synaptic membrane", Page 1

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



ECM 2, Gene set "synaptic membrane", Page 1

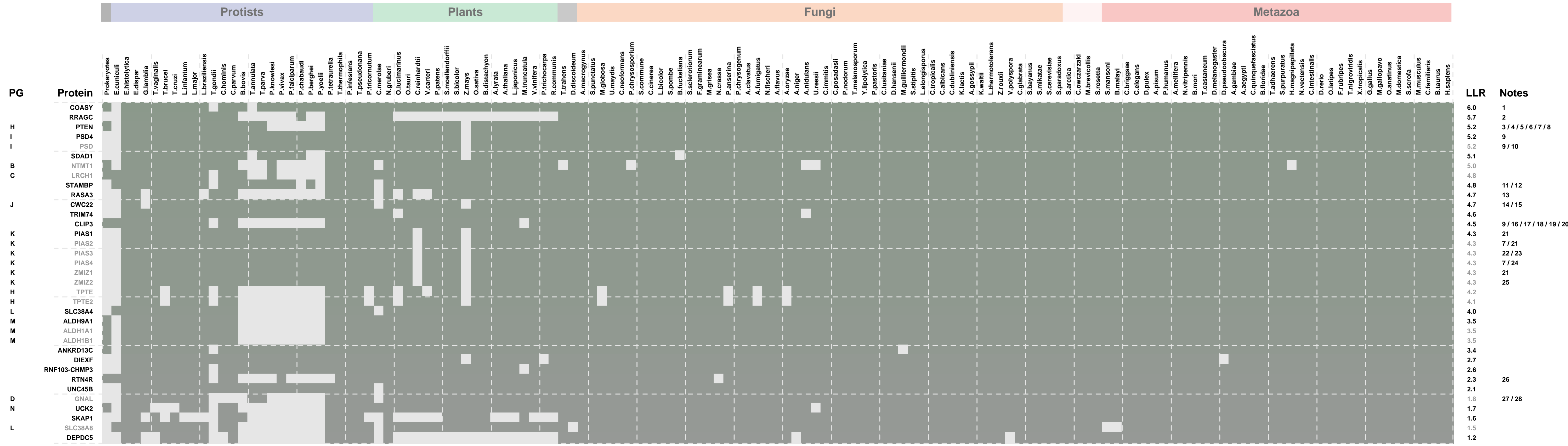
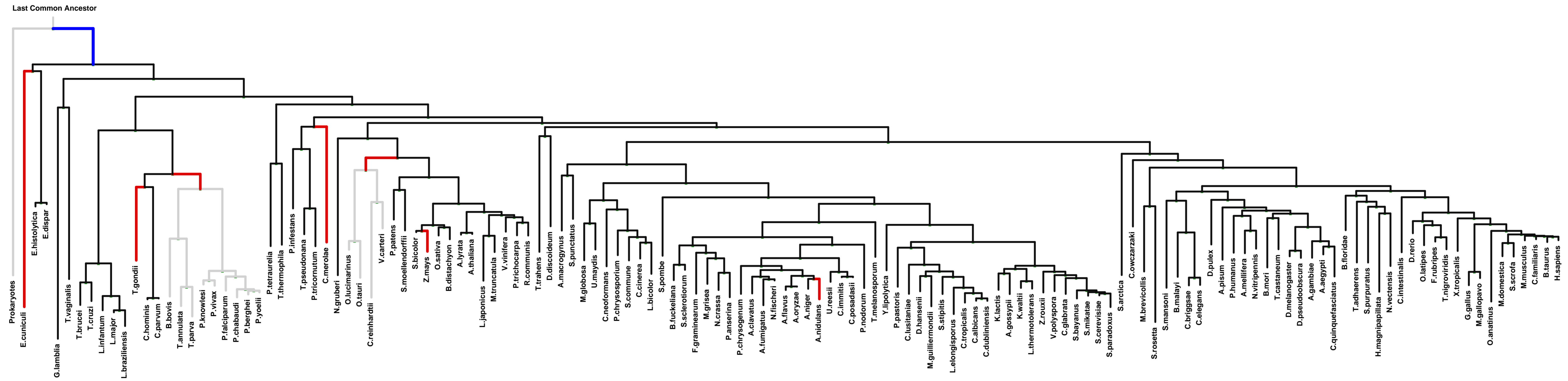
Num of ECM Genes: 1. Num of Predicted Genes: 81



1: axon || 2: dendrite || 3: dendritic spine || 4: early endosome membrane || 5: postsynaptic density || 6: synaptic membrane || 7: synaptic vesicle || 8: vacuolar membrane || 9: filopodium || 10: late endosome || 11: ruffle || 12: nuclear envelope || 13: brush border membrane || 14: extrinsic to internal side of plasma membrane || 15: heterotrimeric G-protein complex || 16: cyclin-dependent protein kinase holoenzyme complex || 17: chromatin || 18: nuclear membrane || 19: microtubule cytoskeleton || 20: female pronucleus || 21: male pronucleus || 22: condensed nuclear chromosome outer kinetochore || 23: spindle pole || 24: ubiquitin ligase complex || 25: endoplasmic reticulum-Golgi intermediate compartment membrane ||

ECM 2, Gene set "synaptic membrane", Page 2

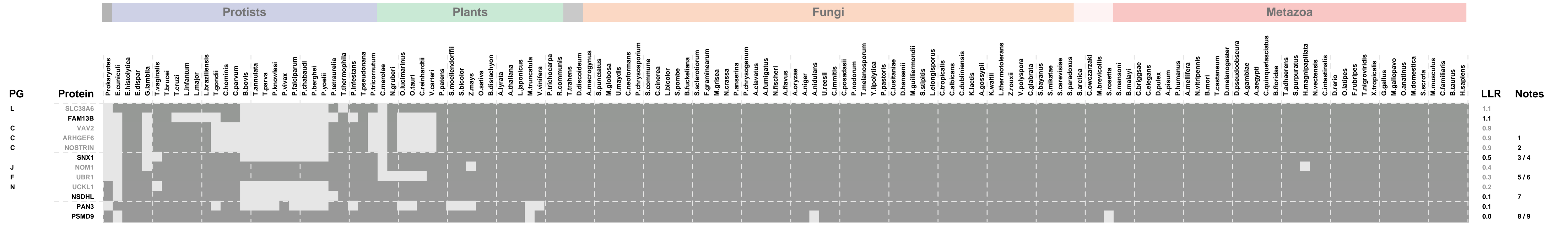
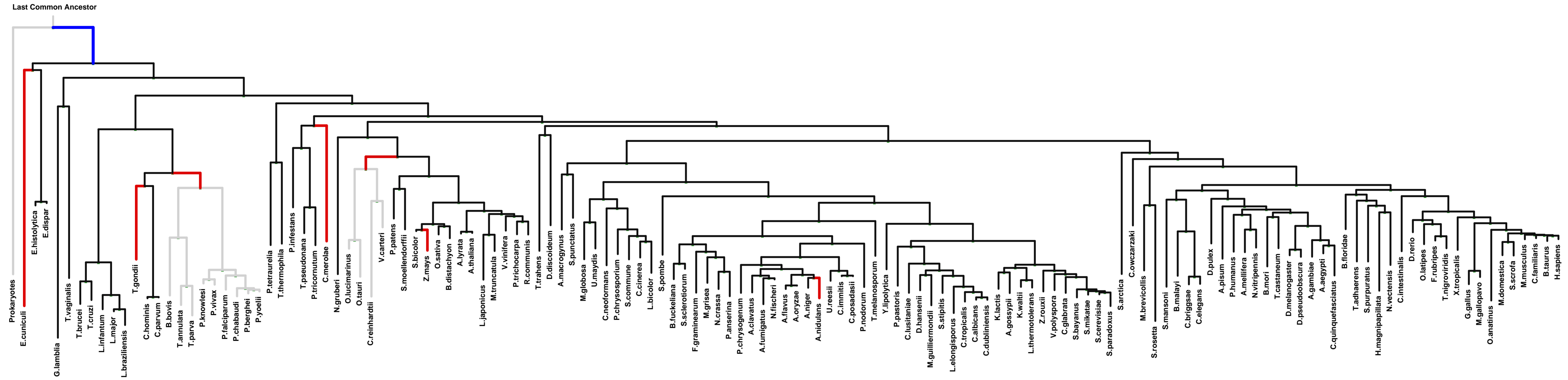
Num of ECM Genes: 1. Num of Predicted Genes: 81



1: mitochondrial outer membrane || 2: lysosome || 3: cell projection || 4: internal side of plasma membrane || 5: myelin sheath axonal region || 6: neuron projection || 7: PML body || 8: Schmidt-Lanterman incisure || 9: trans-Golgi network || 10: ruffle || 11: cleavage furrow || 12: early endosome || 13: intrinsic to internal side of plasma membrane || 14: catalytic step 2 spliceosome || 15: spliceosomal complex || 16: early endosome membrane || 17: Golgi stack || 18: membrane raft || 19: recycling endosome membrane || 20: trans-Golgi network membrane || 21: nuclear speck || 22: dendrite || 23: synapse || 24: nuclear matrix || 25: nuclear replication fork || 26: anchored to membrane ||

ECM 2, Gene set "synaptic membrane", Page 3

Num of ECM Genes: 1. Num of Predicted Genes: 81



1: lamellipodium || 2: endocytic vesicle membrane || 3: early endosome membrane || 4: endosome membrane || 5: proteasome complex || 6: ubiquitin ligase complex || 7: lipid particle || 8: proteasome regulatory particle || 9: proteasome regulatory particle, base subcomplex