

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

Dataset:

Num of genes in input gene set: 4
Total number of genes: 20834
Prediction LLR threshold: 0

The CLIME PDF output two sections:

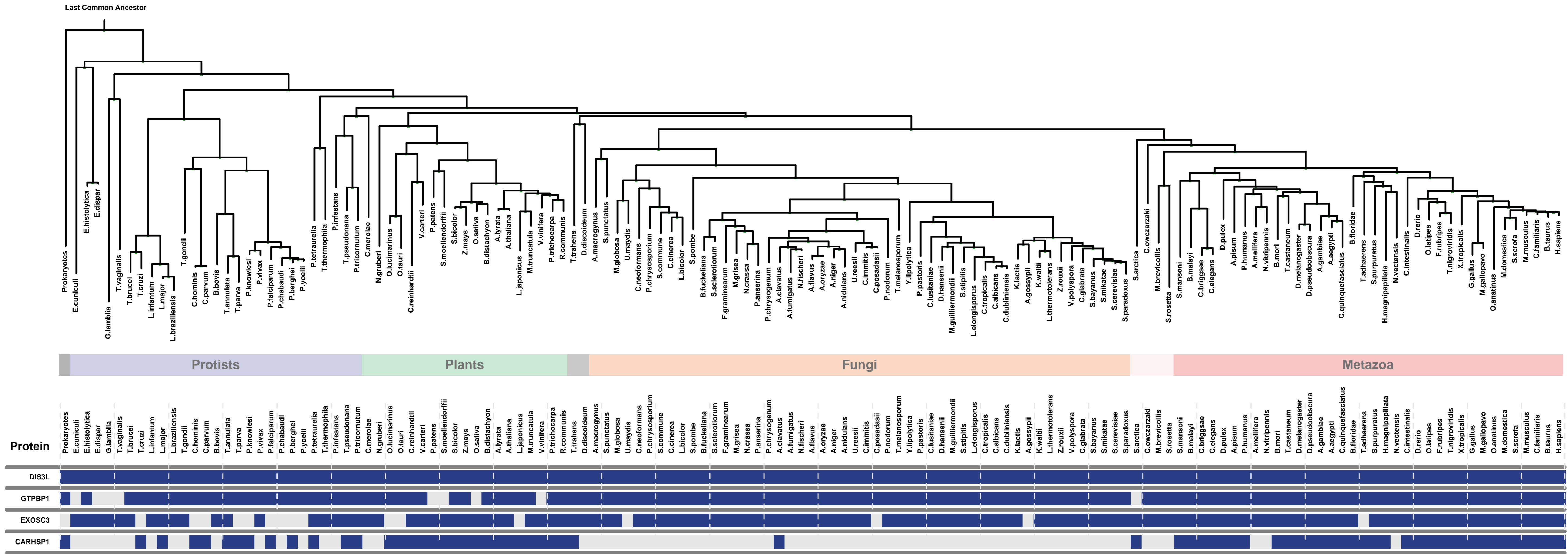
1) Overview of Evolutionarily Conserved Modules (ECMs)

- 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+

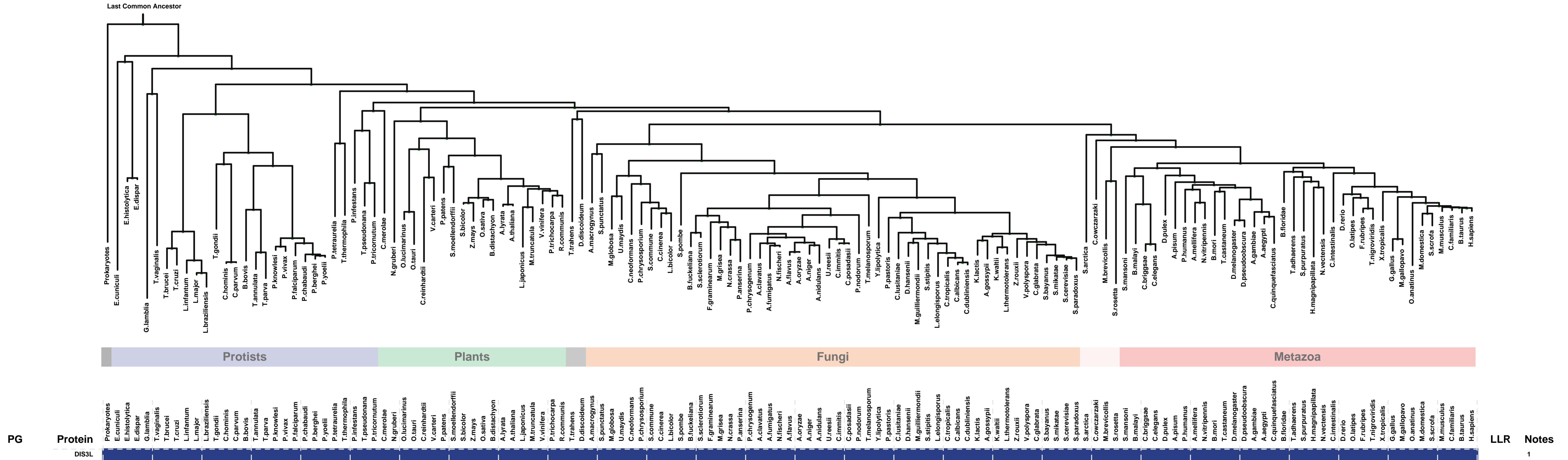
- Top panel shows the inferred evolutionary history on the predefined species tree. Branch color shows the gain event (blue) and loss events (red color, with brighter color indicating higher confidence in loss). Branches before the gain or after a loss are shown in gray.
- Bottom panel shows the input 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 "cytoplasmic exosome (RNase complex)", Page 1

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

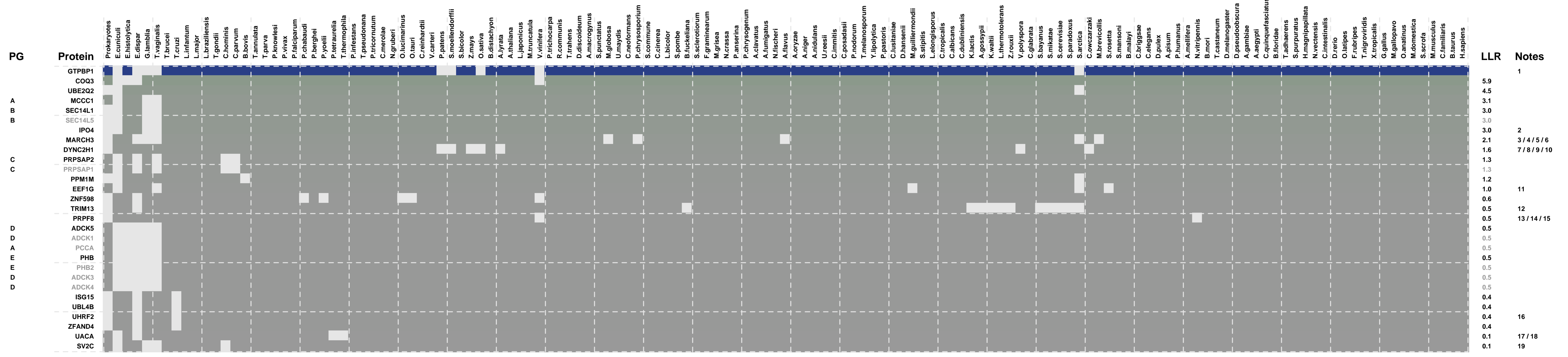
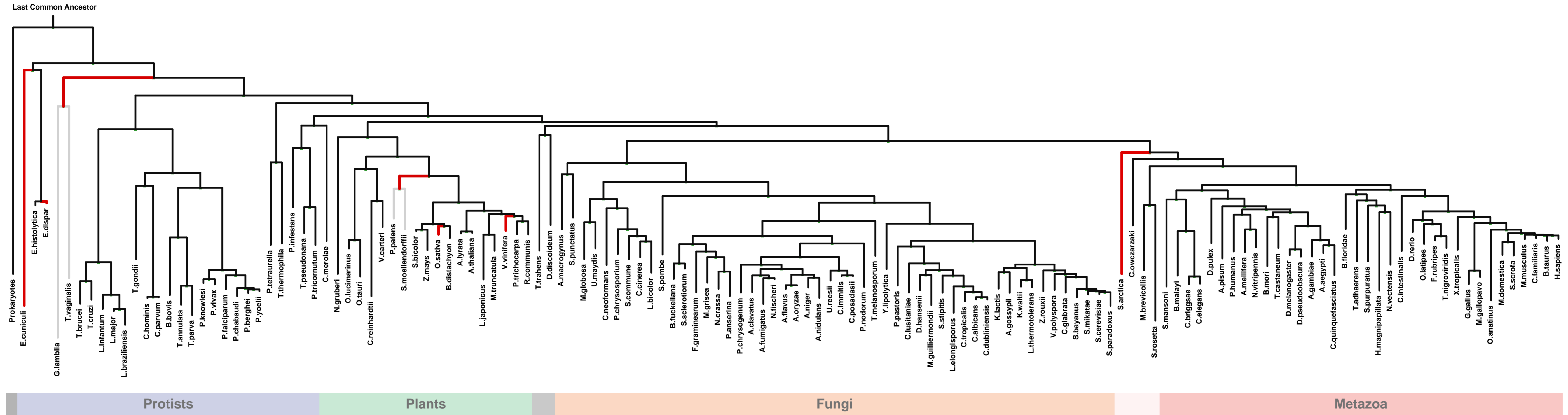


1: cytoplasmic exosome (RNase complex)

LLR Notes

ECM 2, Gene set "cytoplasmic exosome (RNase complex)", Page 1

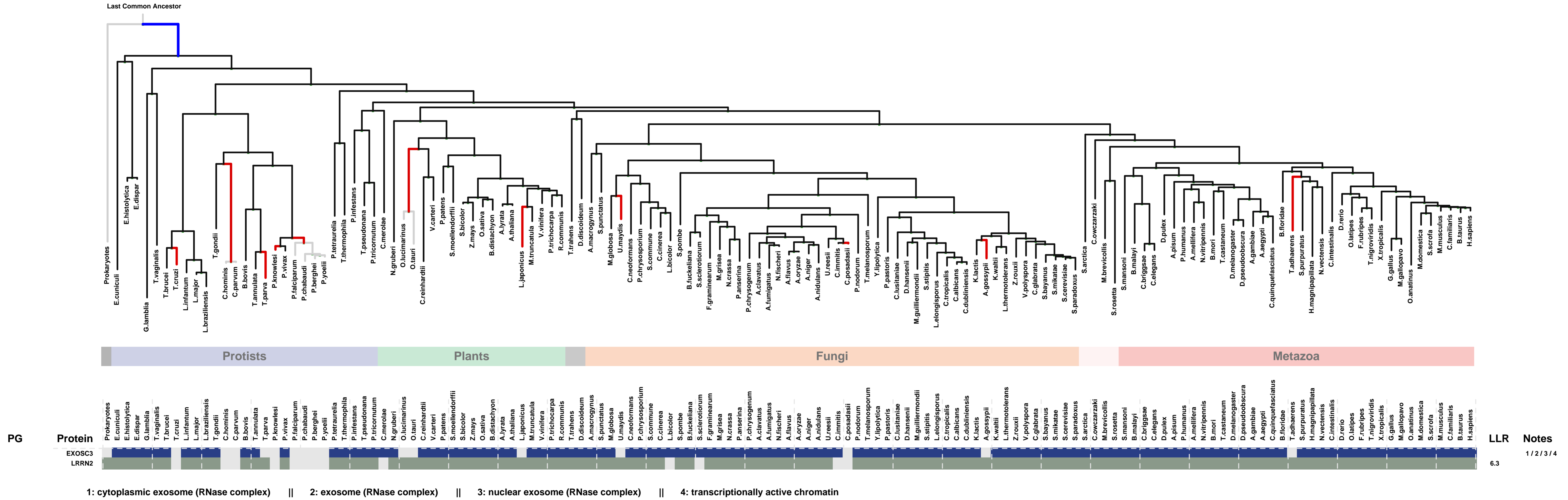
Num of ECM Genes: 1. Num of Predicted Genes: 28



1: cytoplasmic exosome (RNase complex) || 2: nuclear pore || 3: cytoplasmic vesicle membrane || 4: early endosome membrane || 5: endosome || 6: lysosome || 7: apical part of cell || 8: cilium axoneme || 9: dynein complex || 10: motile primary cilium || 11: eukaryotic translation elongation factor 1 complex || 12: perinuclear endoplasmic reticulum || 13: catalytic step 2 spliceosome || 14: nuclear speck || 15: U5 snRNP || 16: nuclear heterochromatin || 17: apoptosome || 18: nuclear envelope || 19: synaptic vesicle membrane

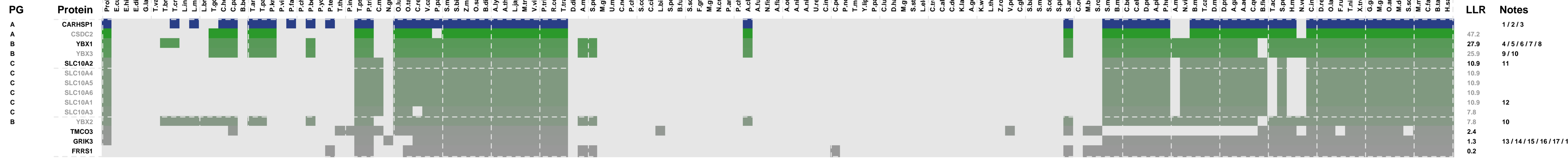
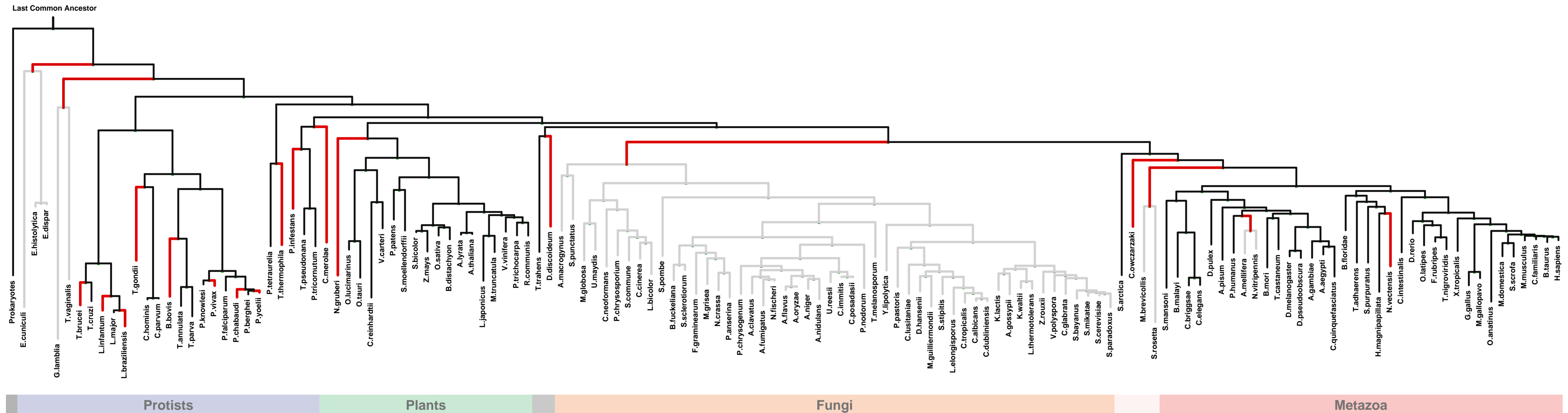
ECM 3, Gene set "cytoplasmic exosome (RNase complex)", Page 1

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



ECM 4, Gene set "cytoplasmic exosome (RNase complex)", Page 1

Num of ECM Genes: 1. Num of Predicted Genes: 13



1: cytoplasmic exosome (RNase complex) || 2: cytoplasmic mRNA processing body || 3: P granule || 4: CRD-mediated mRNA stability complex || 5: cytoplasmic stress granule || 6: histone pre-mRNA 3'end processing complex || 7: ribonucleoprotein complex || 8: U12-type spliceosomal complex || 9: gap junction || 10: polysome || 11: proteasome complex || 12: basolateral plasma membrane || 13: axon || 14: dendrite || 15: dendrite cytoplasm || 16: perikaryon || 17: postsynaptic membrane || 18: terminal button