

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:

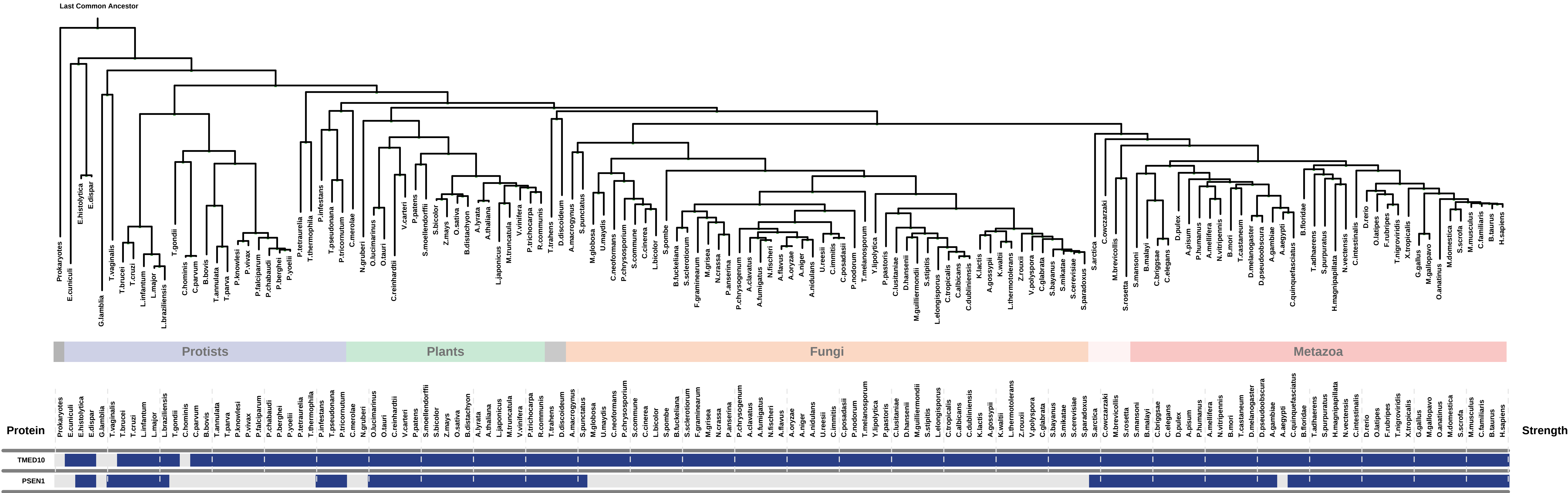
1) Overview of Evolutionarily Conserved Modules (ECMs)

- 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 $E < 1e-3$).

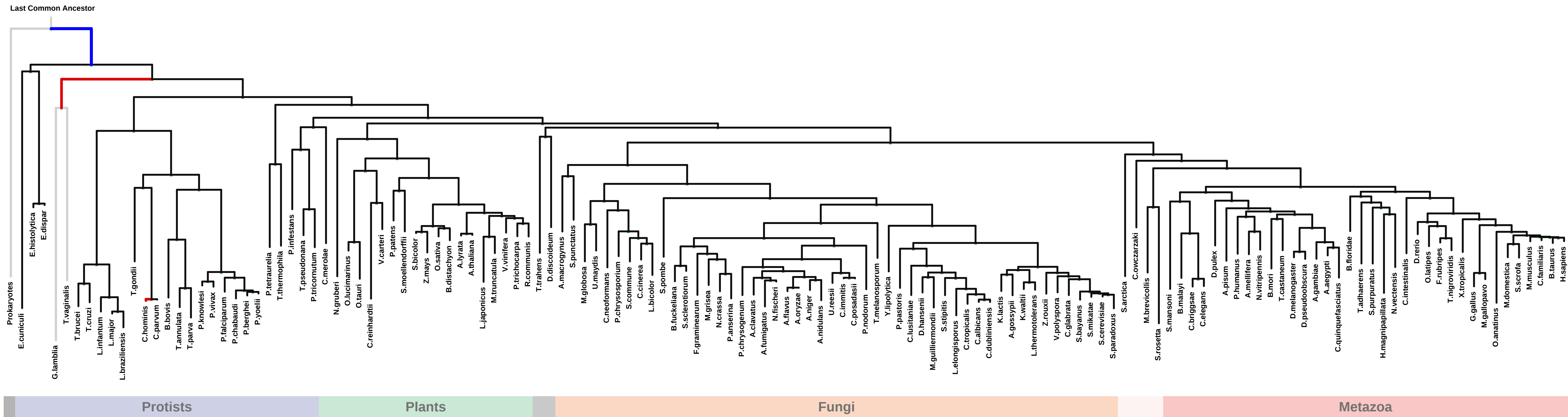
2) Details of each ECM and its expansion ECM+

- 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.

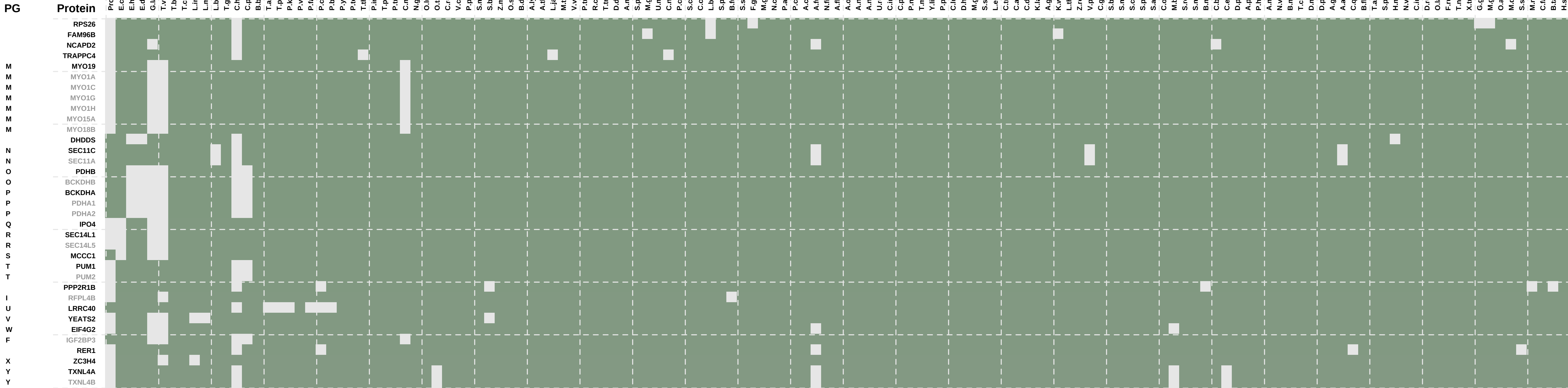
Overview of Evolutionarily Conserved Modules (ECMs)



Num of ECM Genes: 1. Num of Predicted Genes: 500

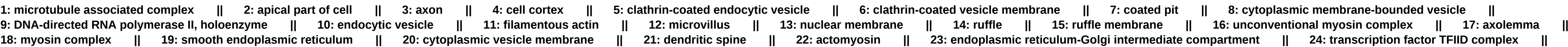
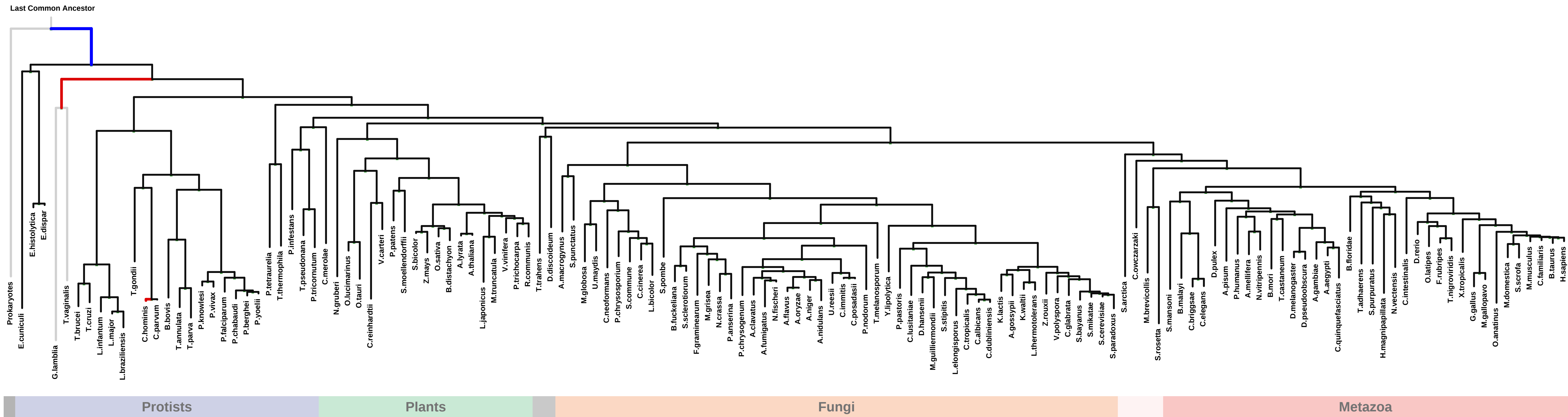


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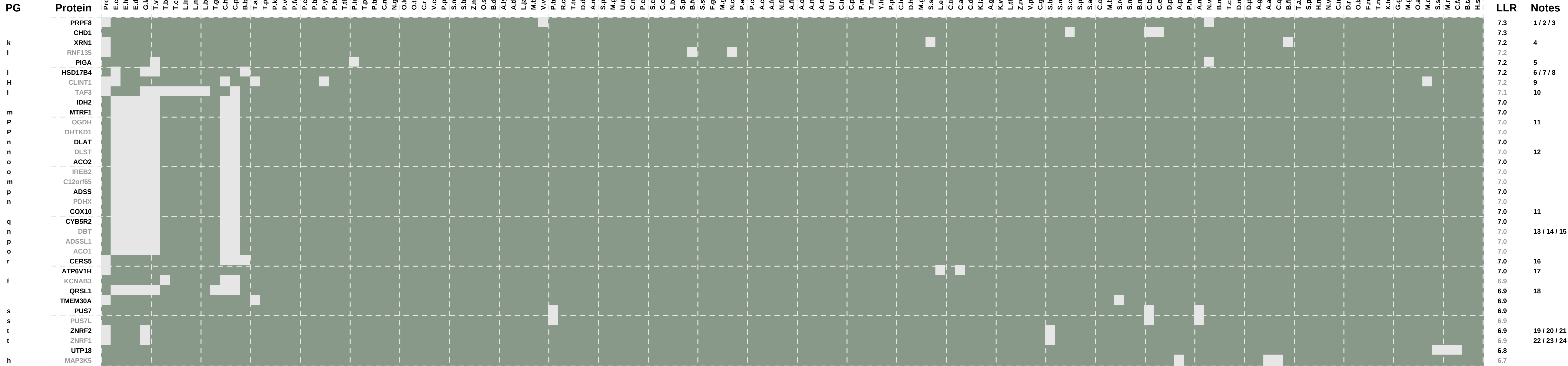


LLR	Notes
11.1	1 / 2
11.0	3 / 4 / 5
10.9	6 / 7 / 8 / 9
10.9	10 / 11 / 12 / 13 / 14
10.9	15 / 16
10.9	16 / 17 / 18 / 19 / 20 / 21
10.9	17 / 19 / 21 / 22 / 23 / 24
10.9	16
10.9	16
10.9	16 / 28
10.9	27 / 29
10.8	
10.7	
10.7	
10.5	30
10.5	31
10.5	31
10.5	
10.5	
10.4	24
10.4	
10.4	
10.4	
10.2	
10.2	32
10.1	
10.0	
10.0	
9.9	33
9.9	34
9.8	
9.7	35
9.5	
9.5	36
9.5	36

Num of ECM Genes: 1. Num of Predicted Genes: 500

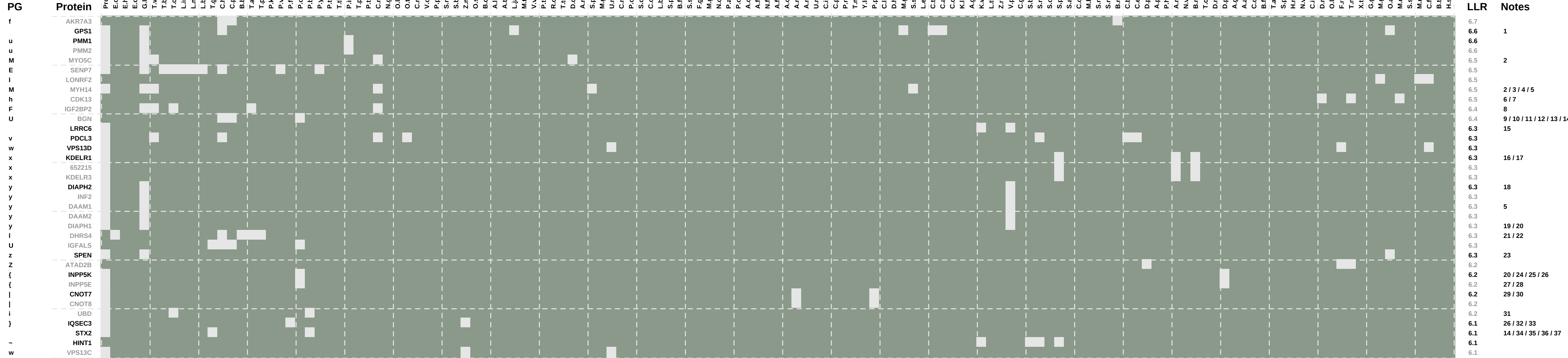


Num of ECM Genes: 1. Num of Predicted Genes: 500



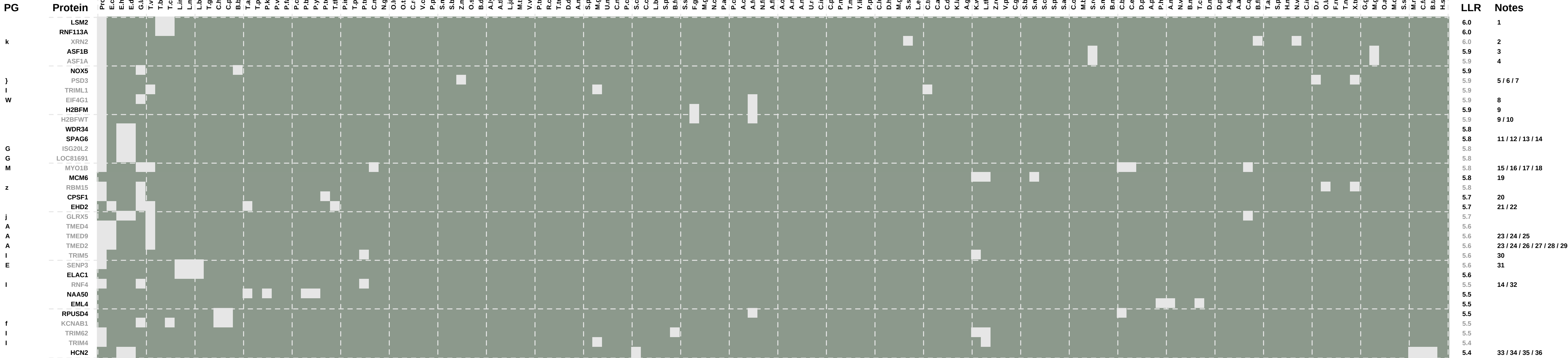
1: catalytic step 2 spliceosome || 2: nuclear speck || 3: U5 snRNP || 4: intermediate filament cytoskeleton || 5: glycosylphosphatidylinositol-N-acetylglucosaminyltransferase (GPI-GnT) complex || 6: peroxisomal matrix || 7: peroxisomal membrane || 8: peroxisome || 9: clathrin-coated vesicle || 10: transcription factor TFIID complex || 11: mitochondrial membrane || 12: oxoglutarate dehydrogenase complex || 13: microtubule cytoskeleton || 14: mitochondrial alpha-ketoglutarate dehydrogenase complex || 15: mitochondrial nucleoid || 16: nuclear membrane || 17: vacuolar proton-transporting V-type ATPase, V1 domain || 18: glutamyl-tRNA(Gln) amidotransferase complex || 19: endosome membrane || 20: lysosomal membrane || 21: presynaptic membrane ||

Num of ECM Genes: 1. Num of Predicted Genes: 500



1: signalosome || 2: myosin complex || 3: axon || 4: growth cone || 5: stress fiber || 6: nuclear cyclin-dependent protein kinase holoenzyme complex || 7: nuclear speck || 8: cytoskeletal part || 9: extracellular matrix ||
10: Golgi lumen || 11: lysosomal lumen || 12: proteinaceous extracellular matrix || 13: sarcolemma || 14: transport vesicle || 15: cilium || 16: cis-Golgi network || 17: endoplasmic reticulum-Golgi intermediate compartment ||
18: early endosome || 19: mitotic spindle || 20: ruffle membrane || 21: peroxisomal membrane || 22: peroxisome || 23: transcriptional repressor complex || 24: neuron projection || 25: ruffle || 26: trans-Golgi network

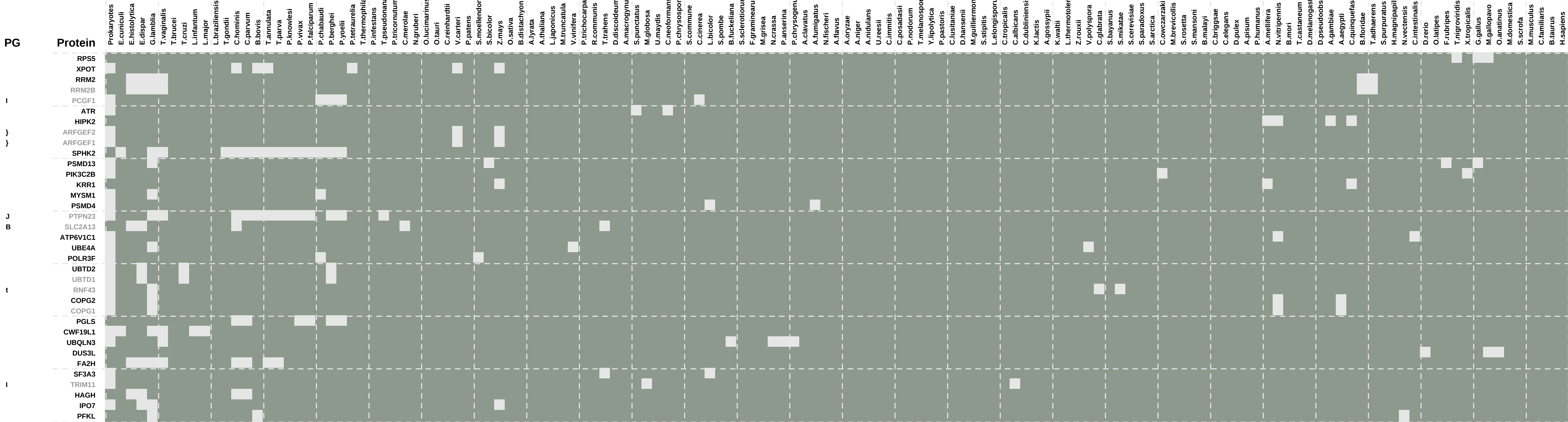
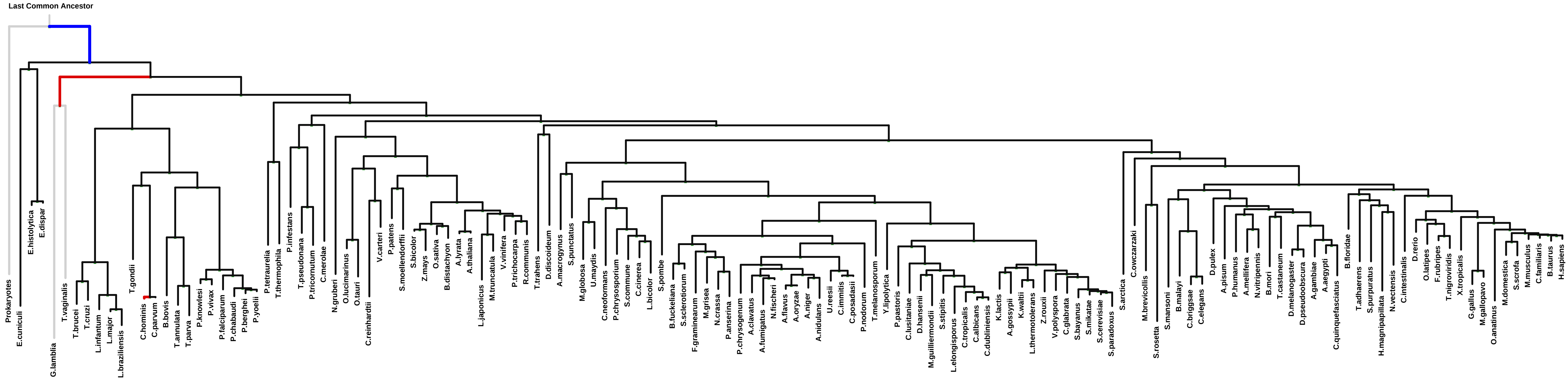
Num of ECM Genes: 1. Num of Predicted Genes: 500



1: catalytic step 2 spliceosome || 2: aggresome || 3: chromatin || 4: chromatin remodeling complex || 5: postsynaptic density || 6: postsynaptic membrane || 7: trans-Golgi network || 8: eukaryotic translation initiation factor 4F complex ||
9: nucleosome || 10: nuclear membrane || 11: axoneme || 12: cilium || 13: flagellum || 14: microtubule cytoskeleton || 15: brush border || 16: cell periphery || 17: filopodium || 18: myosin complex || 19: MCM complex ||
20: mRNA cleavage and polyadenylation specificity factor complex || 21: endosome membrane || 22: recycling endosome membrane || 23: endoplasmic reticulum-Golgi intermediate compartment || 24: endoplasmic reticulum-Golgi intermediate compartment membrane ||

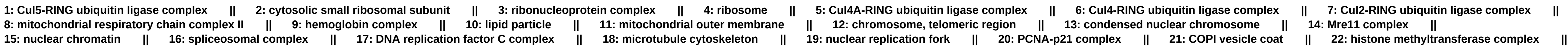
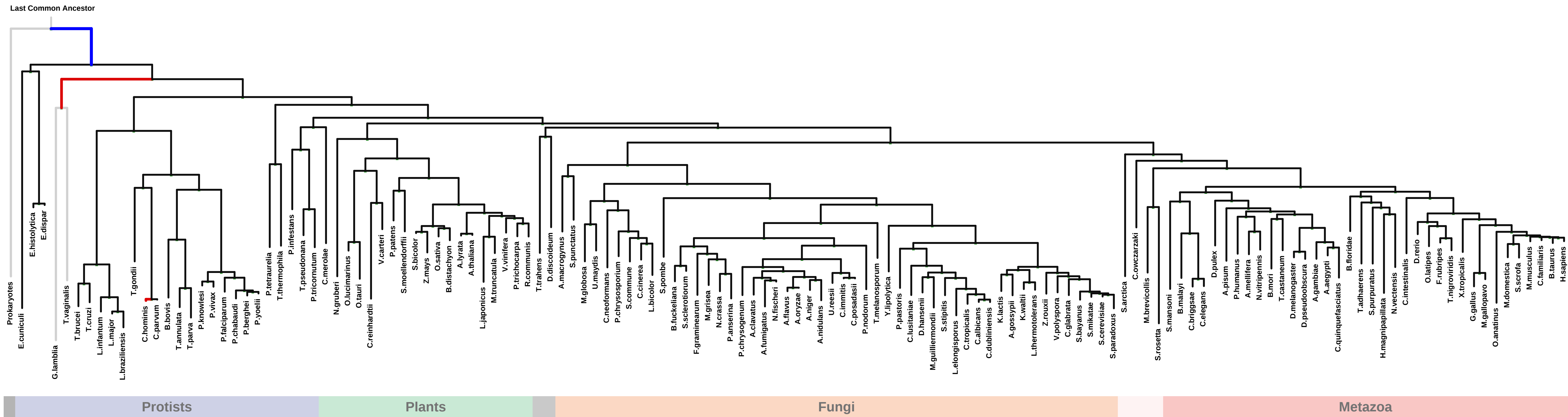
ECM 1, Gene set "gamma-secretase complex", Page 7

Num of ECM Genes: 1. Num of Predicted Genes: 500

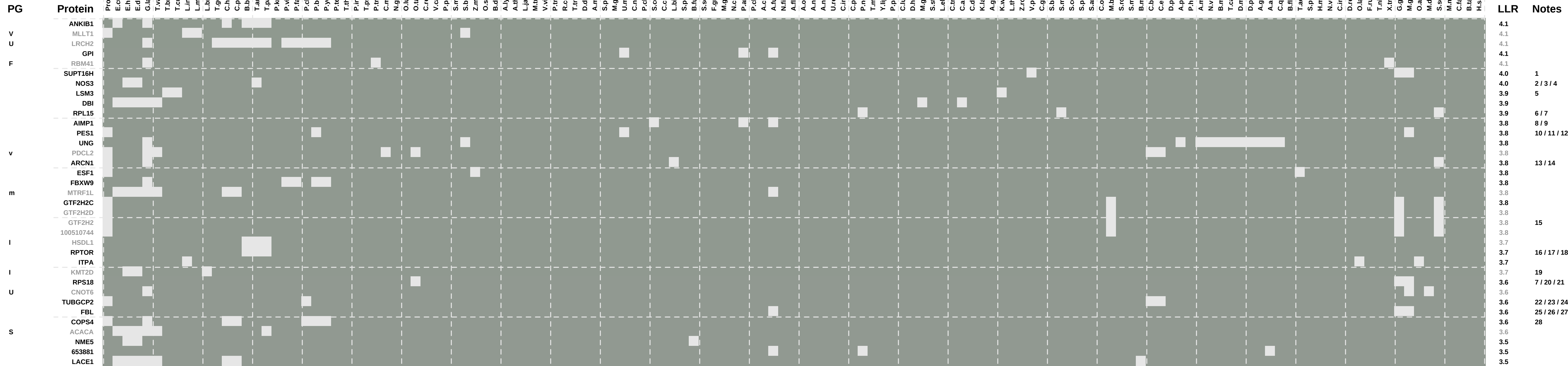


1: cytosolic small ribosomal subunit || 2: ribonucleoprotein complex || 3: nuclear pore || 4: ribonucleoside-diphosphate reductase complex || 5: PcG protein complex || 6: chromosome || 7: PML body || 8: XY body || 9: asymmetric synapse || 10: axonemal microtubule || 11: cytoplasmic membrane-bounded vesicle || 12: cytoplasmic vesicle || 13: dendritic spine || 14: microtubule organizing center || 15: recycling endosome || 16: symmetric synapse || 17: trans-Golgi network || 18: nuclear matrix || 19: small nuclear ribonucleoprotein complex || 20: lysosomal membrane || 21: proteasome accessory complex || 22: proteasome complex || 23: proteasome regulatory particle || 24: endocytic vesicle || 25: chromatin remodeling complex ||

Num of ECM Genes: 1. Num of Predicted Genes: 500

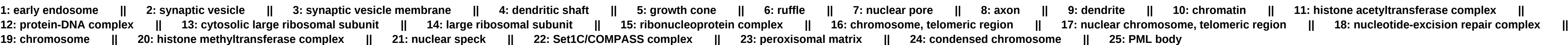
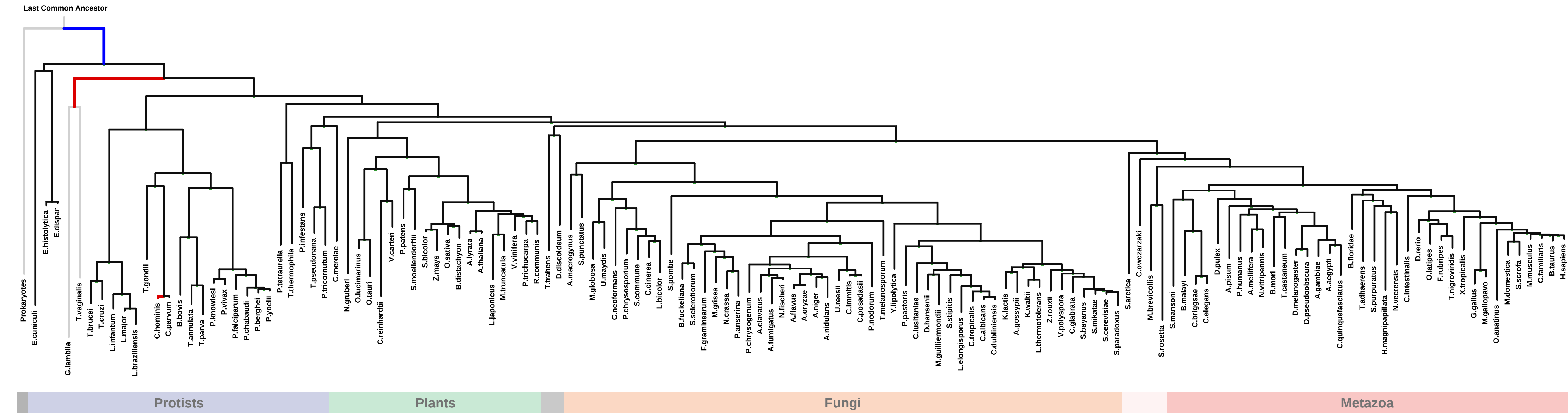


Num of ECM Genes: 1. Num of Predicted Genes: 500

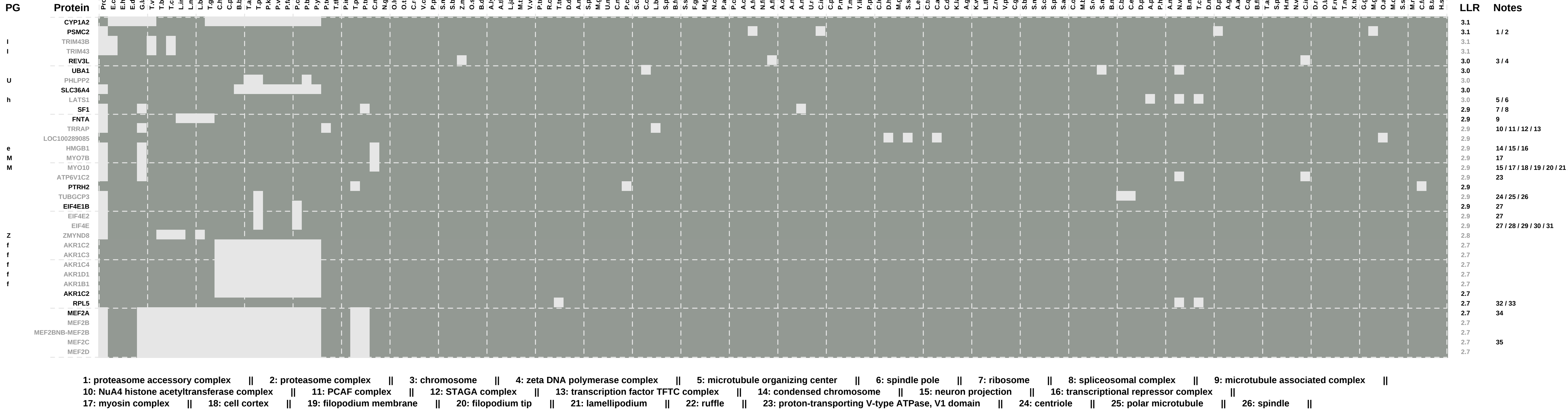


1: chromosome || 2: apical part of cell || 3: caveola || 4: endocytic vesicle membrane || 5: catalytic step 2 spliceosome || 6: cytosolic large ribosomal subunit || 7: ribosome || 8: aminoacyl-tRNA synthetase multienzyme complex || 9: transport vesicle || 10: condensed chromosome || 11: PeBoW complex || 12: preribosome, large subunit precursor || 13: clathrin adaptor complex || 14: COPI vesicle coat || 15: holo TFIIF complex || 16: dendrite || 17: lysosome || 18: TORC1 complex || 19: histone methyltransferase complex || 20: cytosolic small ribosomal subunit || 21: small ribosomal subunit || 22: cytoplasmic microtubule || 23: microtubule organizing center || 24: spindle pole || 25: box C/D snoRNP complex ||

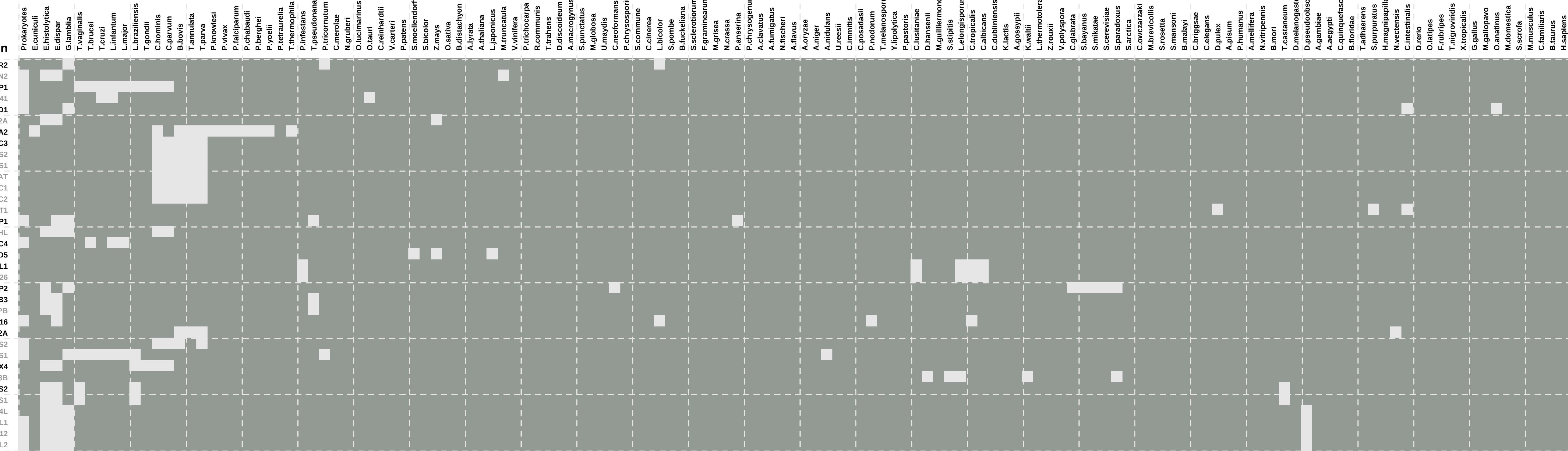
Num of ECM Genes: 1. Num of Predicted Genes: 500



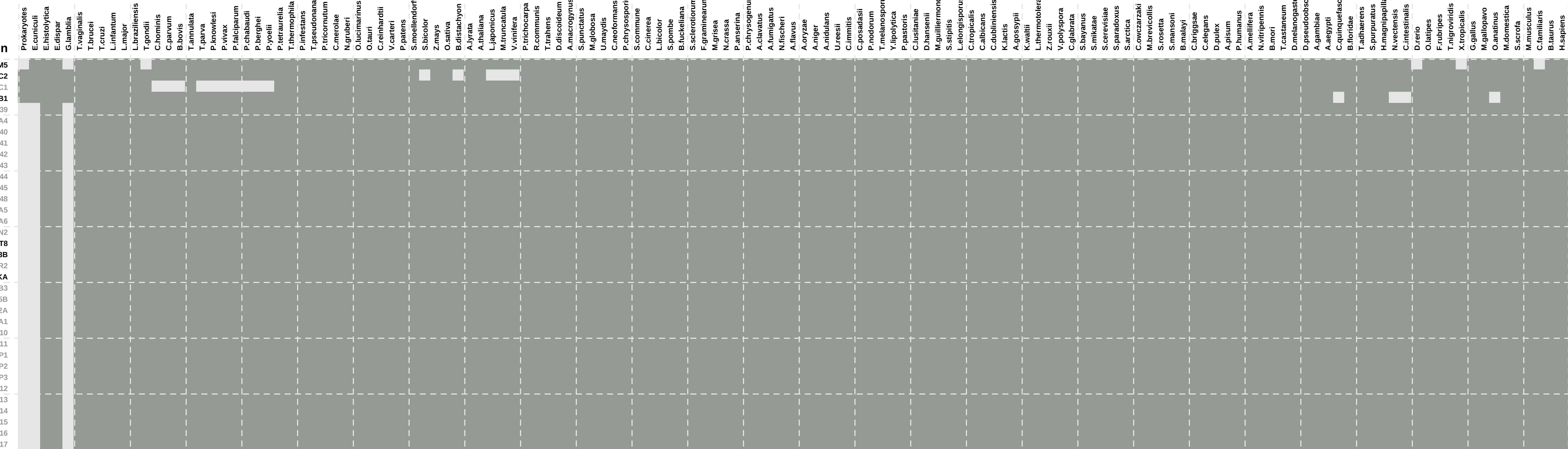
Num of ECM Genes: 1. Num of Predicted Genes: 500



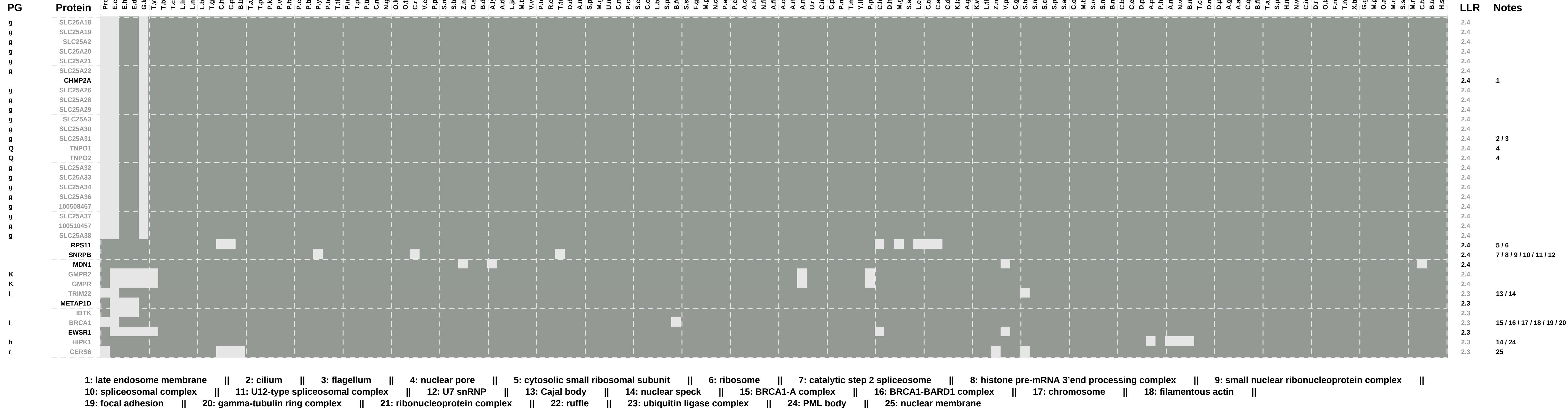
Num of ECM Genes: 1. Num of Predicted Genes: 500



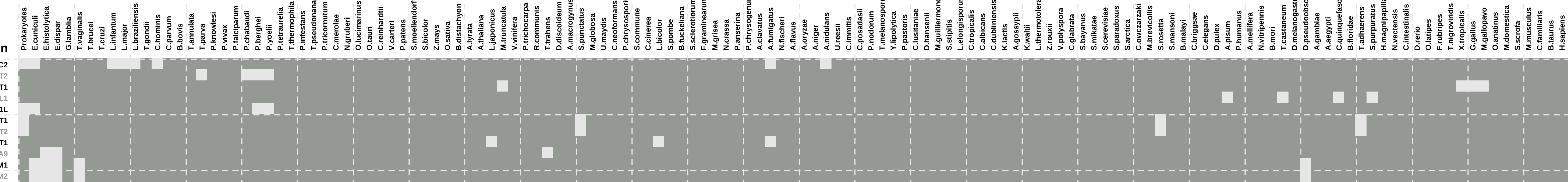
Num of ECM Genes: 1. Num of Predicted Genes: 500

[illegible]

Num of ECM Genes: 1. Num of Predicted Genes: 500

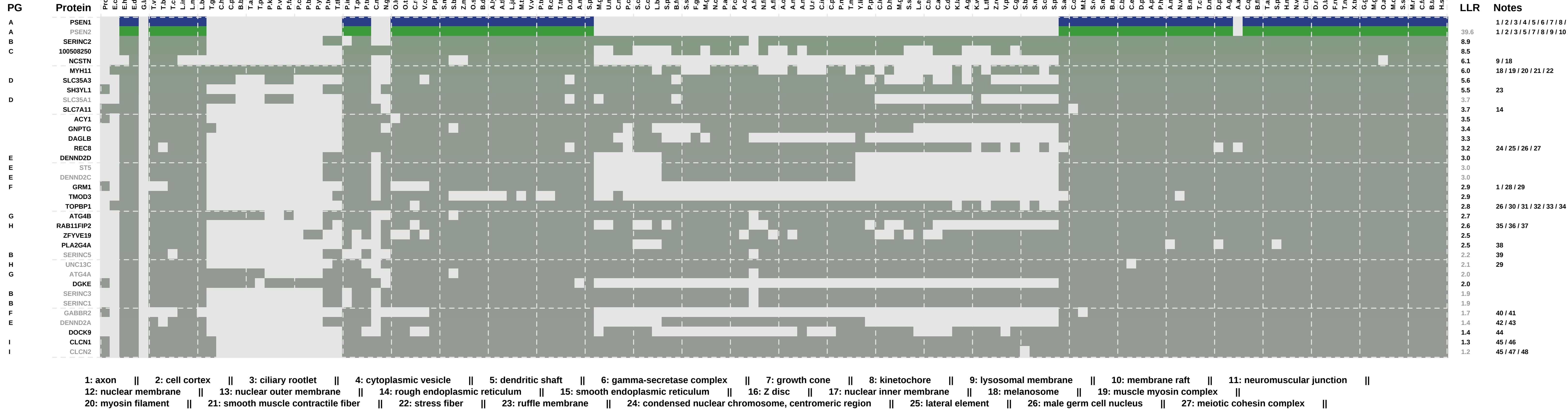


Num of ECM Genes: 1. Num of Predicted Genes: 500

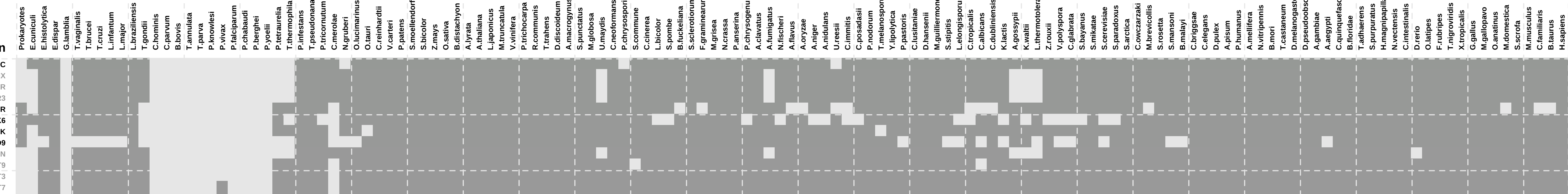


LLR	Notes
2.3	
2.3	
2.2	
2.2	1 / 2
2.2	1
2.2	
2.2	
2.1	3
2.1	
2.1	4

Num of ECM Genes: 1. Num of Predicted Genes: 46



Num of ECM Genes: 1. Num of Predicted Genes: 46



1: axon || 2: dendrite cytoplasm || 3: dendritic spine || 4: endoplasmic reticulum lumen || 5: integral to luminal side of endoplasmic reticulum membrane || 6: melanosome || 7: ribosome || 8: rough endoplasmic reticulum || 9: acrosomal vesicle || 10: external side of plasma membrane || 11: MHC class I peptide loading complex || 12: polysome || 13: proteinaceous extracellular matrix || 14: sarcoplasmic reticulum lumen || 15: supraspliceosomal complex || 16: mitochondrial membrane || 17: nuclear envelope || 18: dense core granule || 19: secretory granule membrane || 20: synaptic vesicle membrane || 21: endosome || 22: lysosome