

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

Dataset:

Num of genes in input gene set: 7
Total number of genes: 20834
Prediction LLR threshold: 0

The CLIME PDF output two sections:

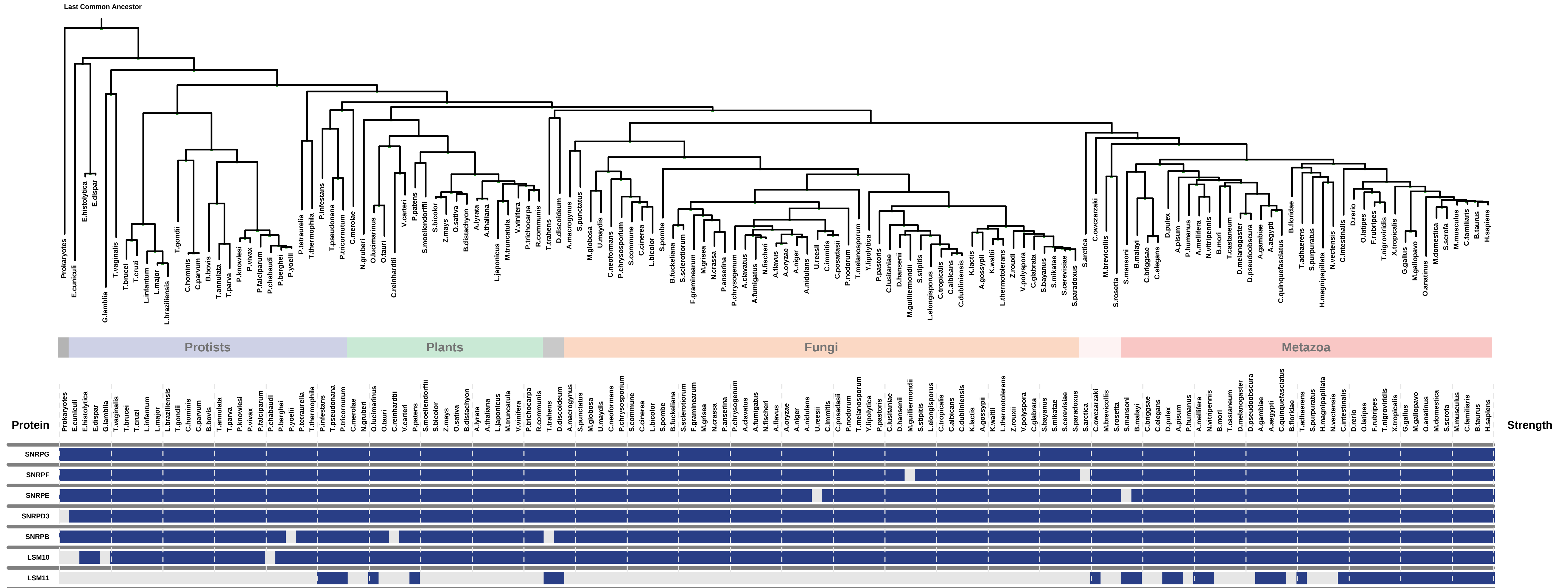
1) Overview of Evolutionarily Conserved Modules (ECMs)

- 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+

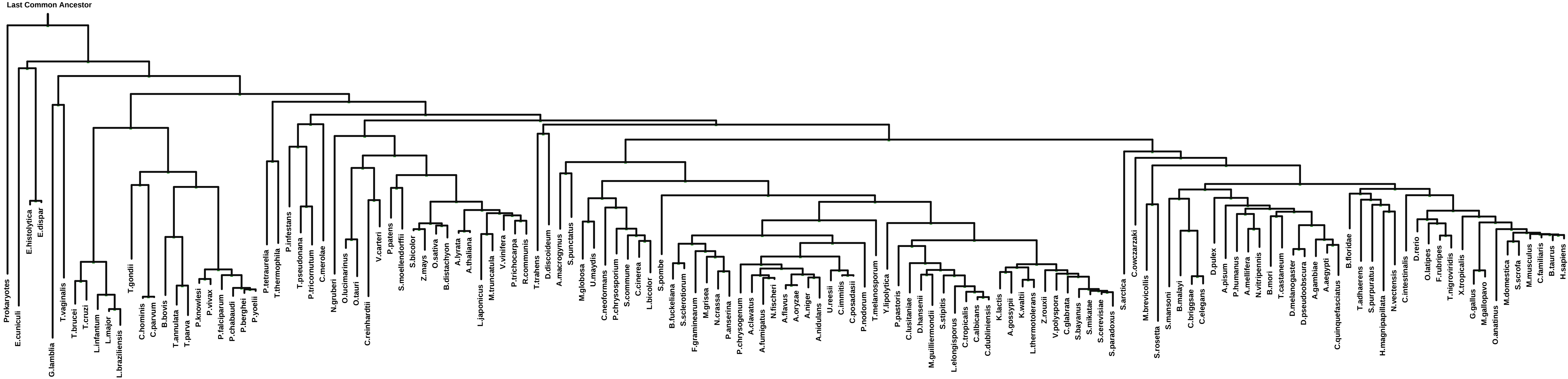
- Top panel shows the inferred evolutionary history on the predefined species tree. Branch color shows the gain event (blue) and loss events (red color, with brighter color indicating higher confidence in loss). Branches before the gain or after a loss are shown in gray.
- Bottom panel shows the input 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 "U7 snRNP", Page 1

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



PG

Protein	SNRPG
Prokaryotes	
E. cuniculi	
E. histolytica	
E. dispar	
G. lamblia	
T. vaginalis	
T. brucei	
T. cruzi	
L. infantum	
L. major	
L. braziliensis	
T. gondii	
C. hominis	
C. parvum	
B. bovis	
T. annulata	
T. parva	
P. knowlesi	
P. vivax	
P. falciparum	
P. chabaudi	
P. berghei	
P. yoelii	
P. tetraurelia	
T. thermophila	
P. infestans	
T. pseudonana	
P. tricornutum	
C. merolae	
N. gruberi	
O. lucimarinus	
O. tauri	
C. reinhardtii	
V. carteri	
P. patens	
S. moellendorffii	
S. bicolor	
Z. mays	
O. sativa	
B. distachyon	
A. lyrata	
A. thaliana	
L. japonicus	
M. truncatula	
V. vinifera	
P. trichocarpa	
R. communis	
T. trahens	
D. discoideum	
A. macrogynus	
S. punctatus	
M. globosa	
U. maydis	
C. neoformans	
P. chrysosporium	
S. commune	
C. cinerea	
L. bicolor	
S. pombe	
B. tuckeliana	
S. sclerotiorum	
F. graminearum	
M. grisea	
N. crassa	
P. anserina	
P. chrysogenum	
A. clavatus	
A. fumigatus	
N. fischeri	
A. flavus	
A. oryzae	
A. niger	
A. nidulans	
U. reesii	
C. immitis	
C. posadasii	
P. nodorum	
T. melanosporum	
Y. lipolytica	
P. pastoris	
C. lusitanae	
D. hansenii	
M. guilliermondii	
S. stipitidis	
L. elongisporus	
C. tropicalis	
C. albicans	
C. dubliniensis	
K. lactis	
A. gossypii	
K. waltii	
L. thermotolerans	
Z. rouxii	
V. polyspora	
C. glabrata	
S. bayanus	
S. mikatae	
S. cerevisiae	
S. paradoxus	
S. sacchari	
C. owczarzaki	
M. brevicollis	
S. rosetta	
S. mansoni	
B. malayi	
C. briggsae	
C. elegans	
D. pulex	
A. pisum	
P. humanus	
A. mellifera	
N. vitripennis	
B. mori	
T. castaneum	
D. melanogaster	
D. pseudoobscura	
A. gambiae	
A. aegypti	
C. quinquefasciatus	
B. floridae	
T. adhaerens	
S. purpuratus	
H. magnipapillata	
N. vectensis	
C. intestinalis	
D. rerio	
O. latipes	
F. rubripes	
T. nigroviridis	
X. tropicalis	
G. gallus	
M. gallopavo	
O. anatinus	
M. domestica	
S. scrofa	
M. musculus	
C. familiaris	
B. taurus	
H. sapiens	

LLR

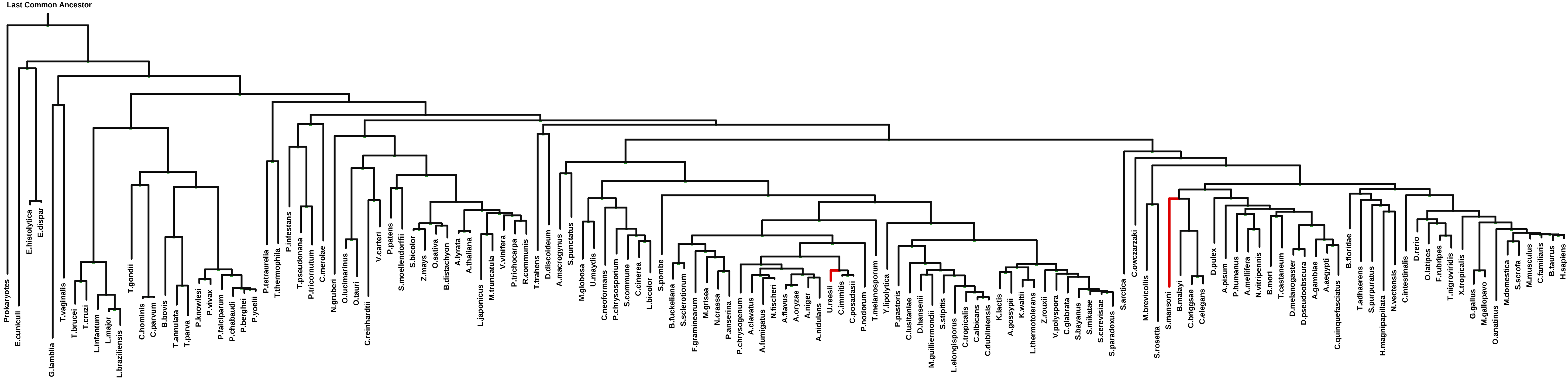
Notes

1 / 2 / 3 / 4 / 5

1: catalytic step 2 spliceosome || 2: small nuclear ribonucleoprotein complex || 3: spliceosomal complex || 4: U12-type spliceosomal complex || 5: U7 snRNP

ECM 3, Gene set "U7 snRNP", Page 1

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



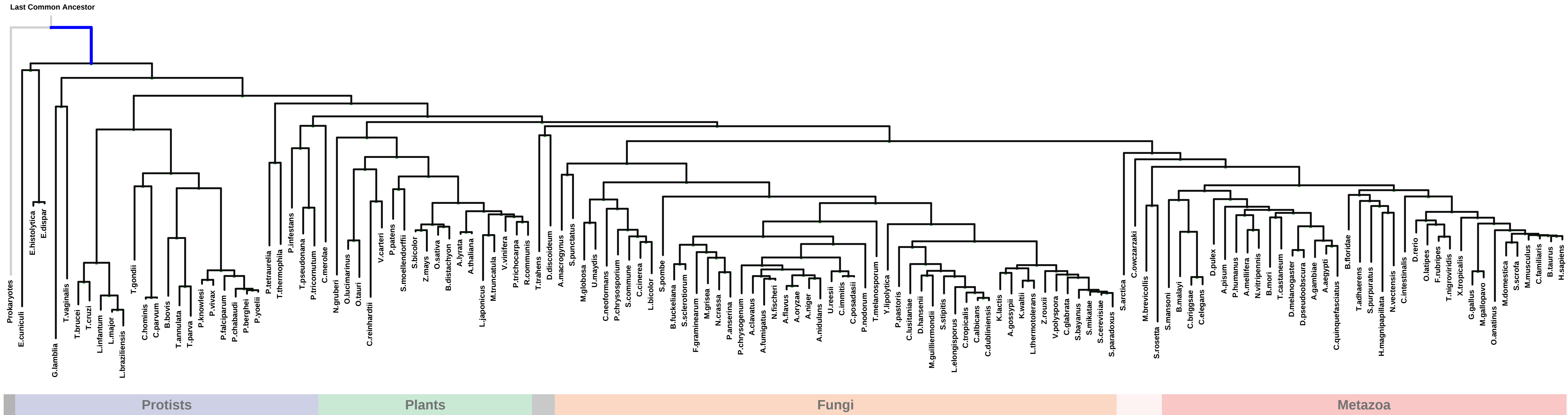
PG

Protein	SNRPE	LLR	Notes

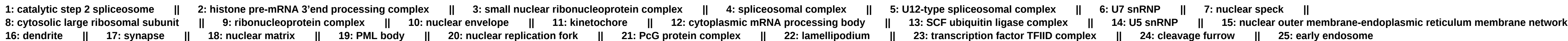
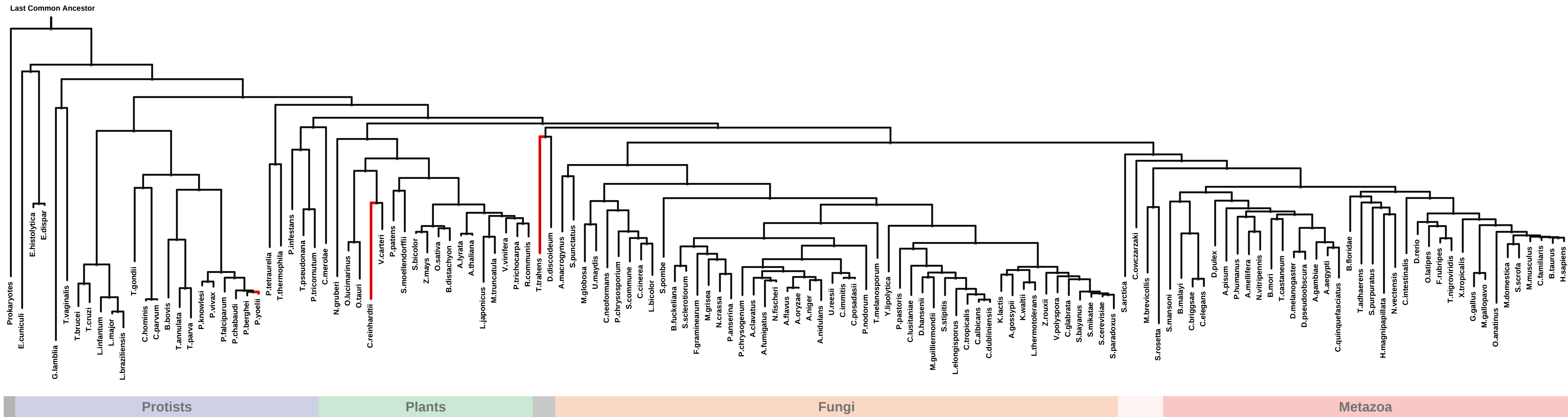
1: catalytic step 2 spliceosome || 2: small nuclear ribonucleoprotein complex || 3: spliceosomal complex || 4: U12-type spliceosomal complex || 5: U7 snRNP

ECM 4, Gene set "U7 snRNP", Page 1

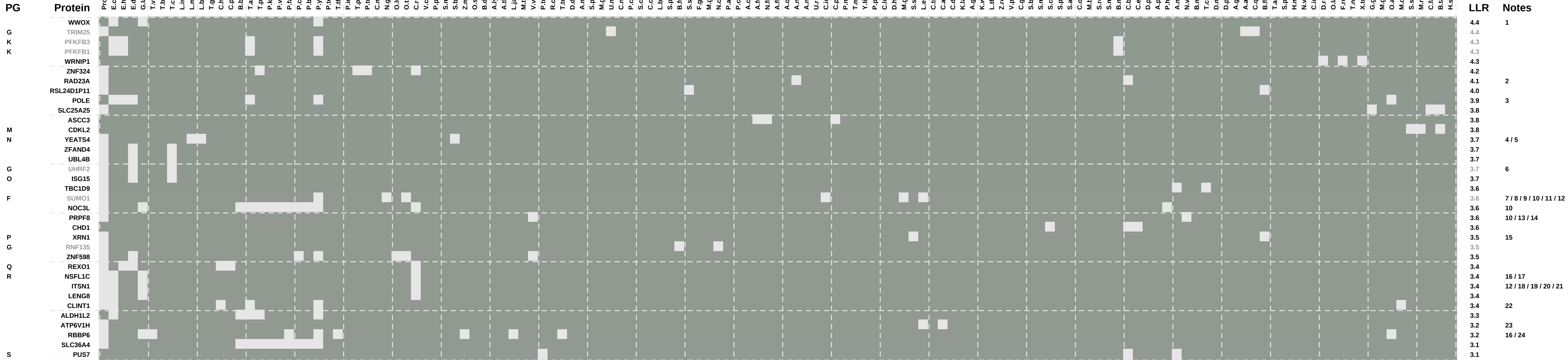
Num of ECM Genes: 1. Num of Predicted Genes: 0

[illegible]

Num of ECM Genes: 1. Num of Predicted Genes: 190

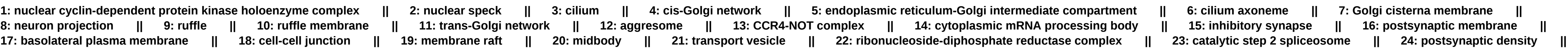
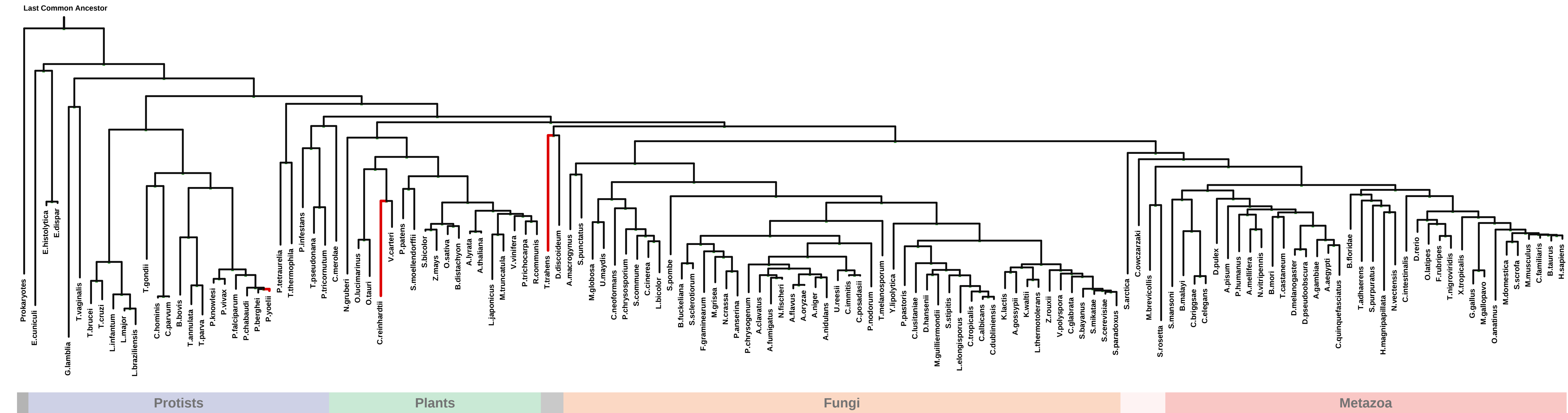


Num of ECM Genes: 1. Num of Predicted Genes: 190

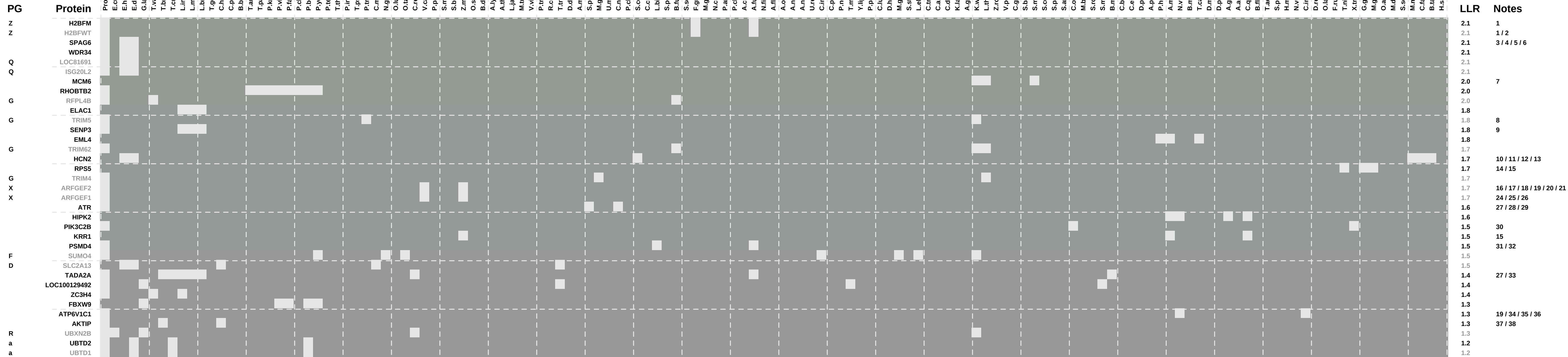


1: microvillus || 2: proteasome complex || 3: epsilon DNA polymerase complex || 4: NuA4 histone acetyltransferase complex || 5: nuclear matrix || 6: nuclear heterochromatin || 7: dendrite || 8: nuclear membrane || 9: nuclear pore ||
10: nuclear speck || 11: PML body || 12: synapse || 13: catalytic step 2 spliceosome || 14: U5 snRNP || 15: intermediate filament cytoskeleton || 16: chromosome || 17: Golgi stack || 18: coated pit || 19: endocytic vesicle ||
20: lamellipodium || 21: neuron projection || 22: clathrin-coated vesicle || 23: vacuolar proton-transporting V-type ATPase, V1 domain || 24: microtubule organizing center

Num of ECM Genes: 1. Num of Predicted Genes: 190



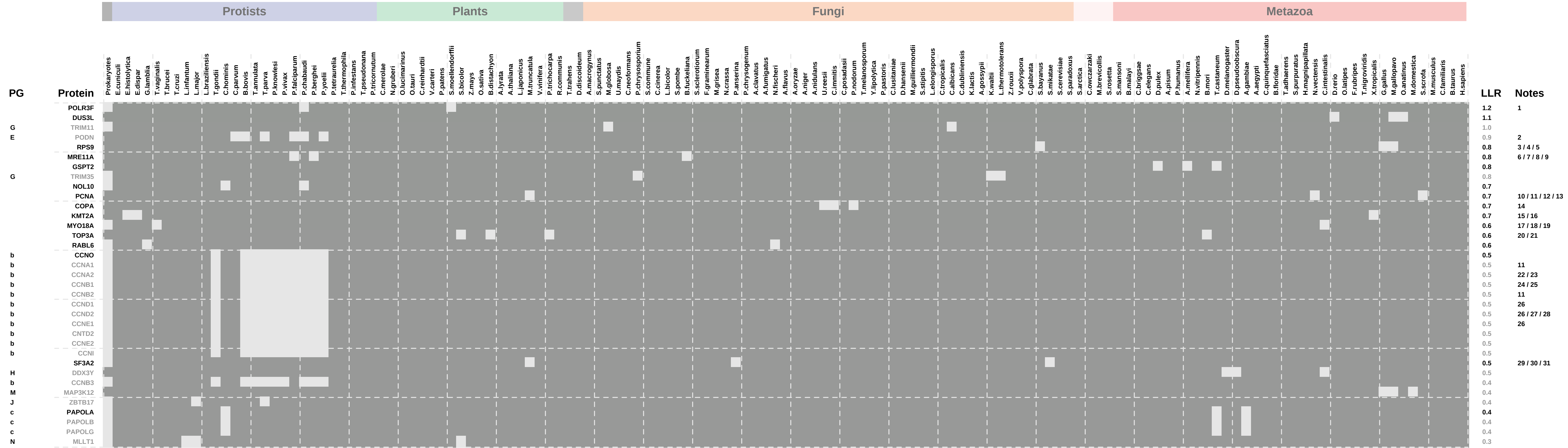
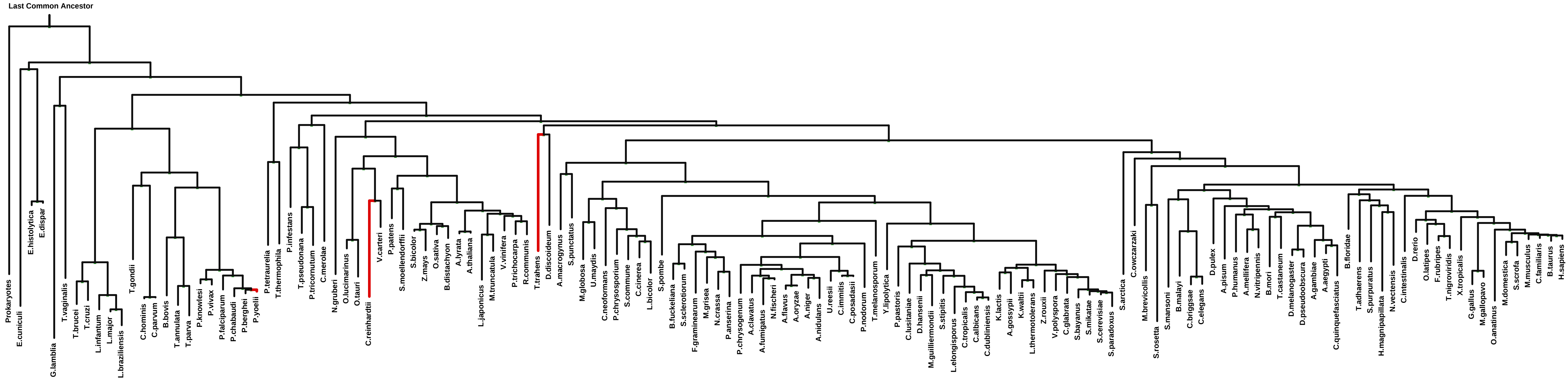
Num of ECM Genes: 1. Num of Predicted Genes: 190



1: nucleosome || 2: nuclear membrane || 3: axoneme || 4: cilium || 5: flagellum || 6: microtubule cytoskeleton || 7: MCM complex || 8: cytoplasmic mRNA processing body || 9: MLL1 complex || 10: axon || 11: dendritic shaft ||
12: synapse || 13: voltage-gated potassium channel complex || 14: cytosolic small ribosomal subunit || 15: ribonucleoprotein complex || 16: asymmetric synapse || 17: axonemal microtubule || 18: cytoplasmic membrane-bounded vesicle ||
19: cytoplasmic vesicle || 20: dendritic spine || 21: microtubule organizing center || 22: recycling endosome || 23: symmetric synapse || 24: trans-Golgi network || 25: nuclear matrix || 26: small nuclear ribonucleoprotein complex ||

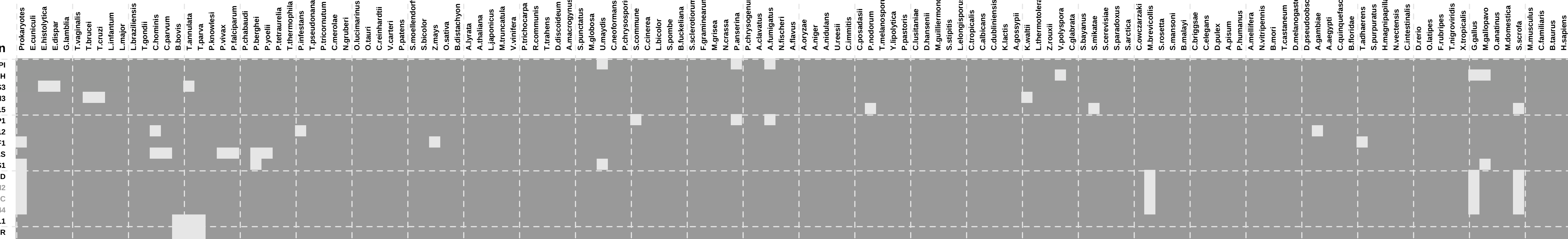
ECM 5, Gene set "U7 snRNP", Page 5

Num of ECM Genes: 1. Num of Predicted Genes: 190



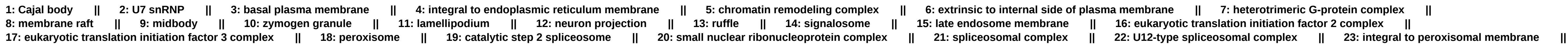
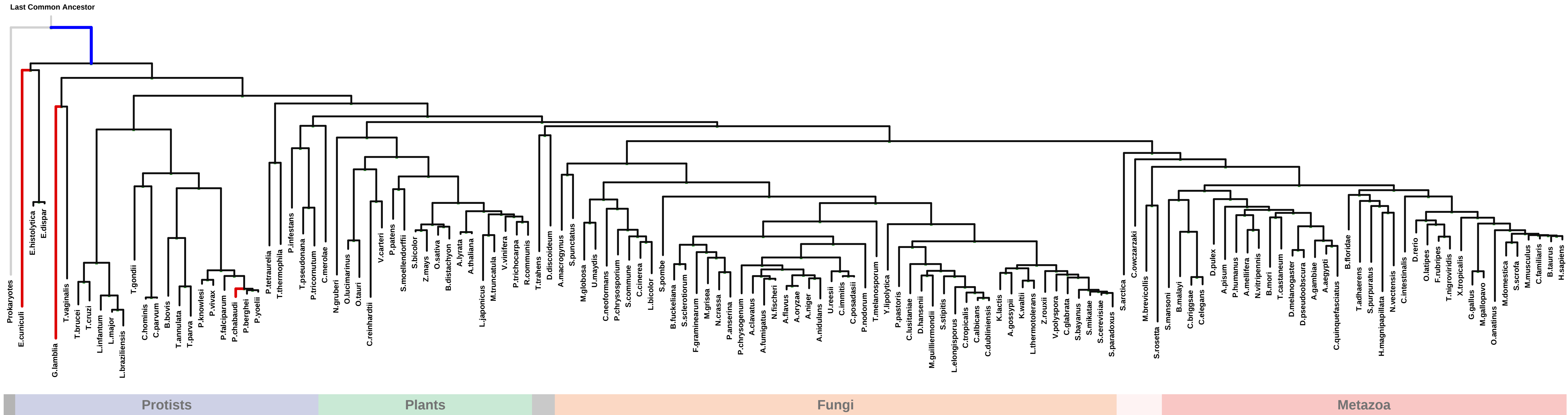
1: DNA-directed RNA polymerase III complex 2: proteinaceous extracellular matrix 3: cytosolic small ribosomal subunit 4: ribonucleoprotein complex 5: ribosome 6: chromosome, telomeric region 7: condensed nuclear chromosome 8: Mre11 complex 9: nuclear chromatin 10: DNA replication factor C complex 11: microtubule cytoskeleton 12: nuclear replication fork 13: PCNA-p21 complex 14: COPI vesicle coat 15: histone methyltransferase complex 16: MLL1 complex 17: actomyosin 18: endoplasmic reticulum-Golgi intermediate compartment 19: myosin complex 20: chromosome 21: PML body 22: female pronucleus 23: male pronucleus 24: condensed nuclear chromosome outer kinetochore

Num of ECM Genes: 1. Num of Predicted Genes: 190



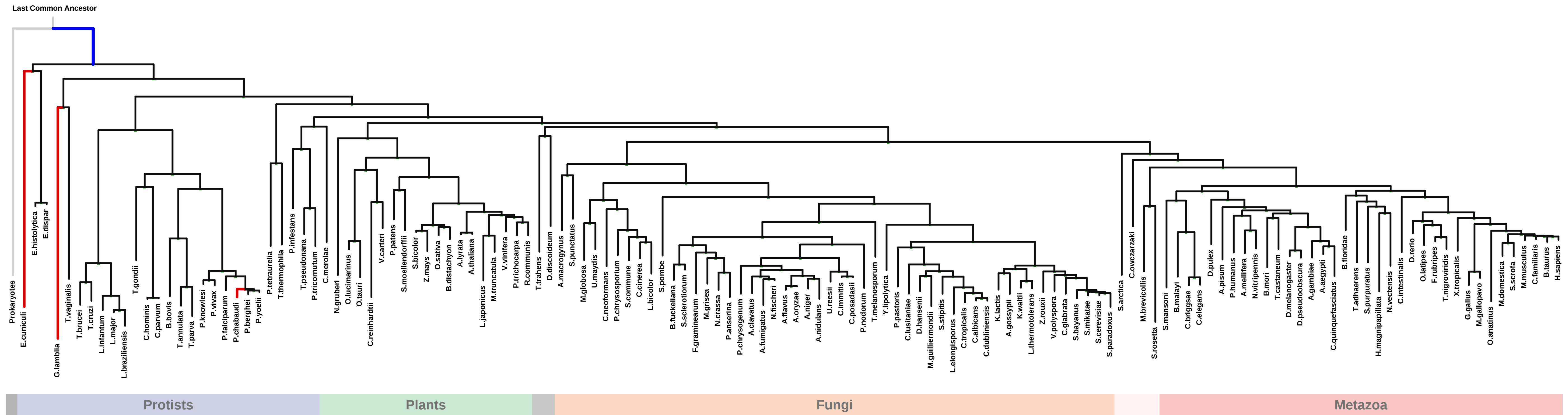
LLR	Notes
0.3	
0.3	1
0.2	2 / 3 / 4
0.2	5
0.2	6 / 7
0.1	8 / 9
0.1	10 / 11
0.1	
0.1	
0.1	12 / 13 / 14
0.0	
0.0	15
0.0	
0.0	
0.0	
0.0	16 / 17 / 18

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



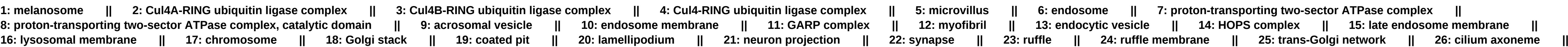
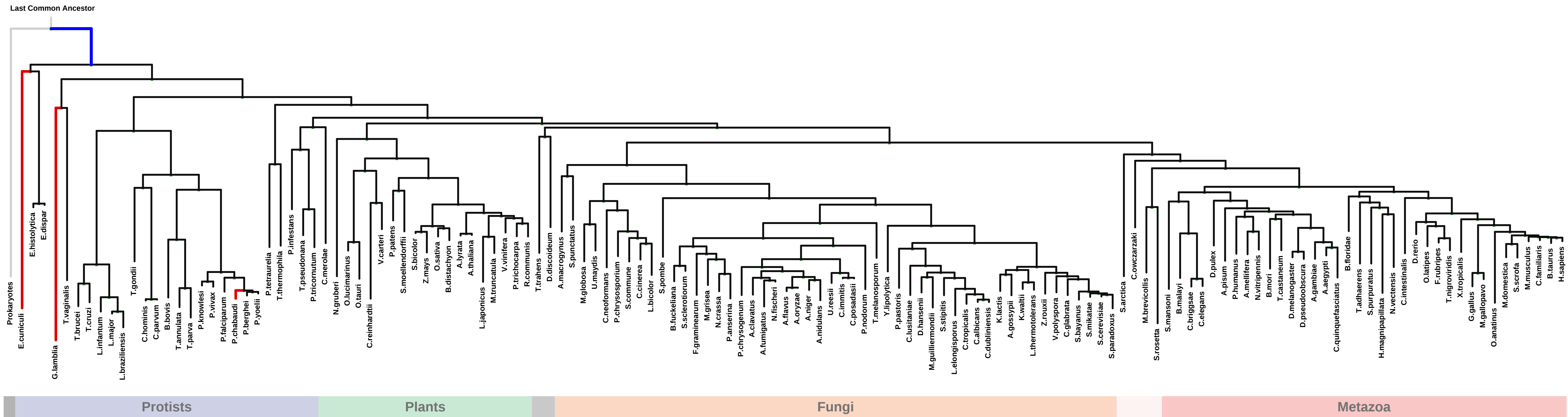
ECM 6, Gene set "U7 snRNP", Page 2

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

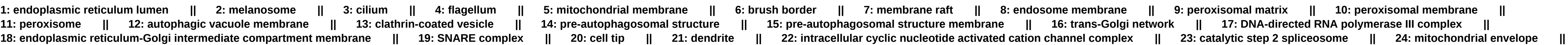
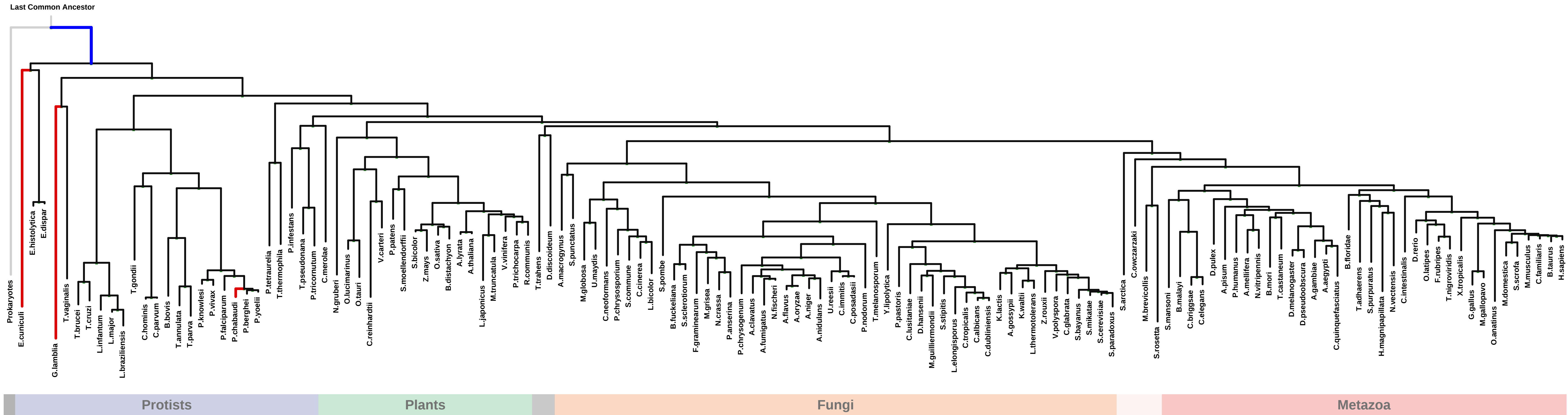
[illegible]

1: cilium || 2: flagellum || 3: mitochondrial outer membrane || 4: mitochondrial nucleoid || 5: MMXD complex || 6: mitochondrial inner membrane presequence translocase complex || 7: nuclear pore || 8: extrinsic to internal side of plasma membrane || 9: heterotrimeric G-protein complex || 10: nuclear membrane

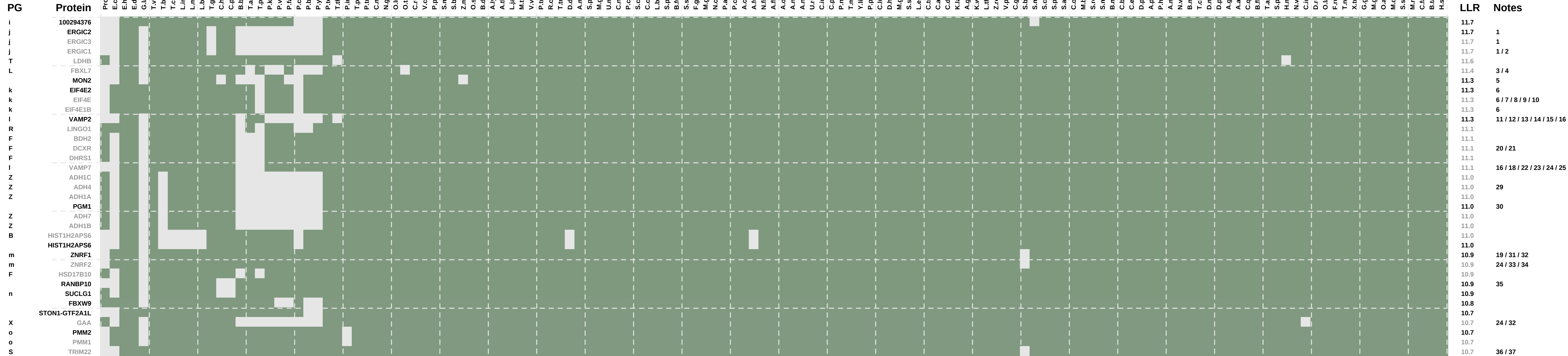
Num of ECM Genes: 1. Num of Predicted Genes: 500



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

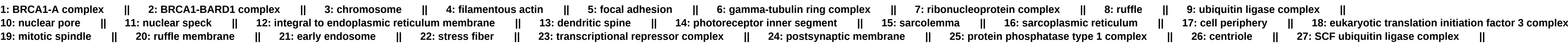
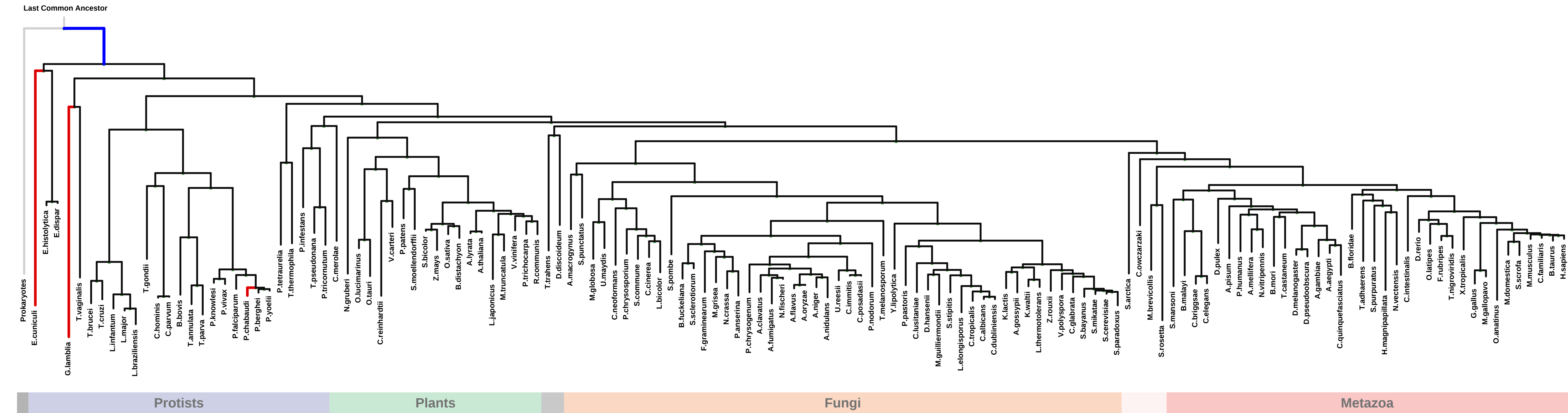


Num of ECM Genes: 1. Num of Predicted Genes: 500

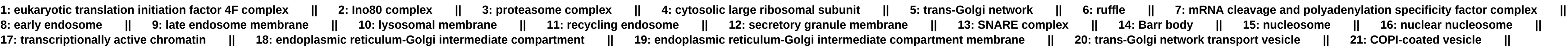
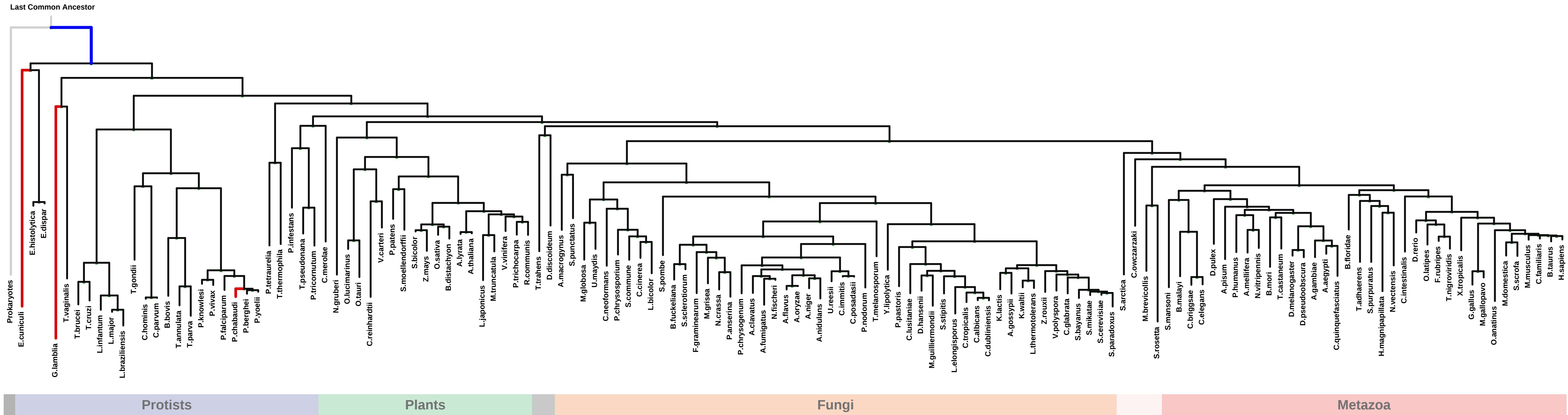


1: endoplasmic reticulum-Golgi intermediate compartment membrane || 2: endoplasmic reticulum-Golgi intermediate compartment || 3: SCF ubiquitin ligase complex || 4: ubiquitin ligase complex || 5: trans-Golgi network || 6: mRNA cap binding complex || 7: cytoplasmic mRNA processing body || 8: cytoplasmic stress granule || 9: eukaryotic translation initiation factor 4F complex || 10: RNA-induced silencing complex || 11: clathrin-coated vesicle || 12: clathrin-sculpted gamma-aminobutyric acid transport vesicle membrane || 13: clathrin-sculpted glutamate transport vesicle membrane || 14: clathrin-sculpted monoamine transport vesicle membrane || 15: endocytic vesicle membrane || 16: neuron projection || 17: secretory granule membrane || 18: SNARE complex ||

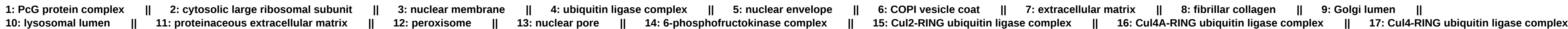
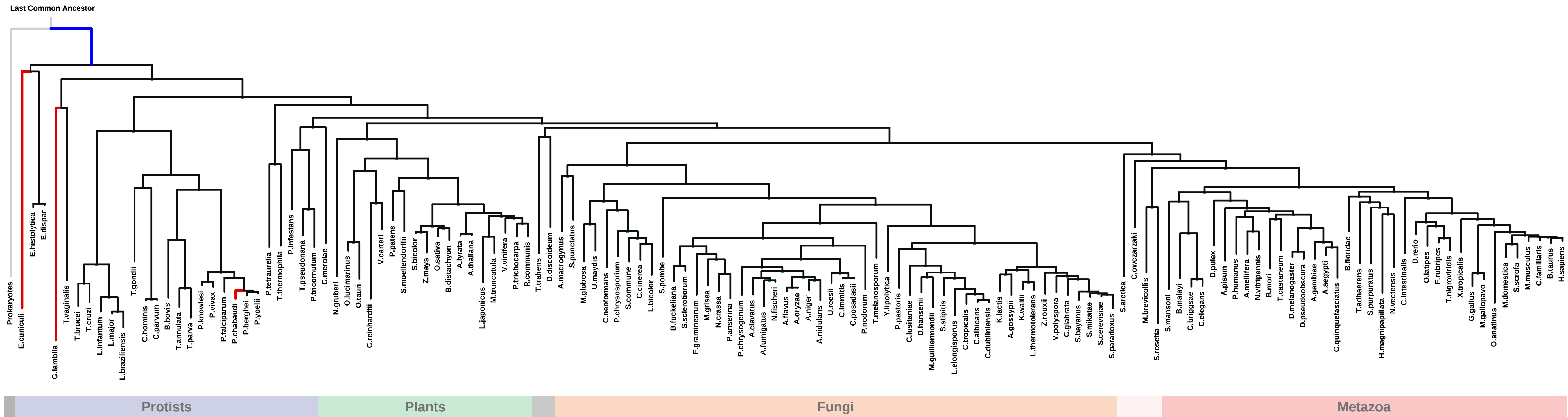
Num of ECM Genes: 1. Num of Predicted Genes: 500



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

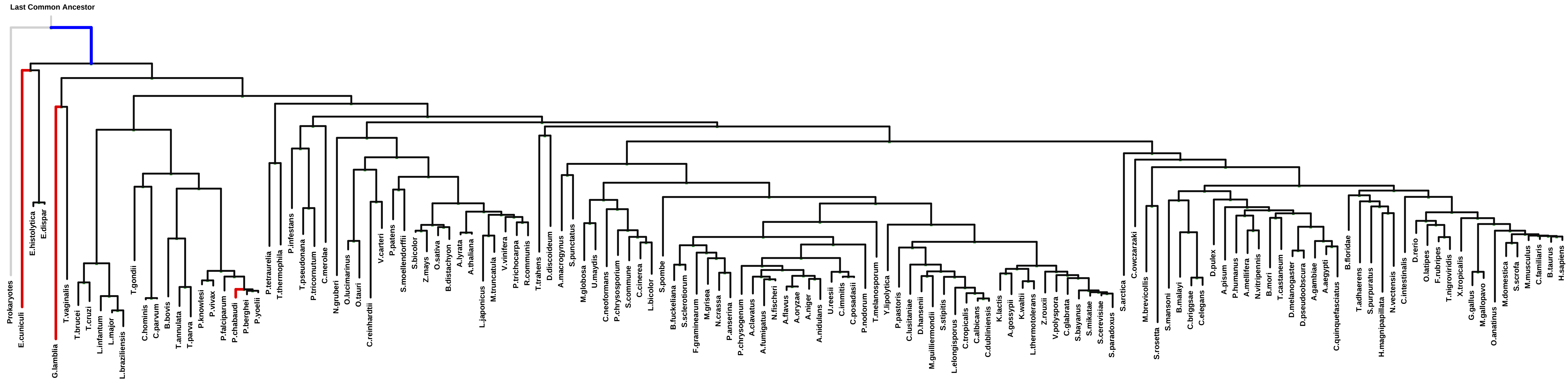


Num of ECM Genes: 1. Num of Predicted Genes: 500



ECM 6, Gene set "U7 snRNP", Page 9

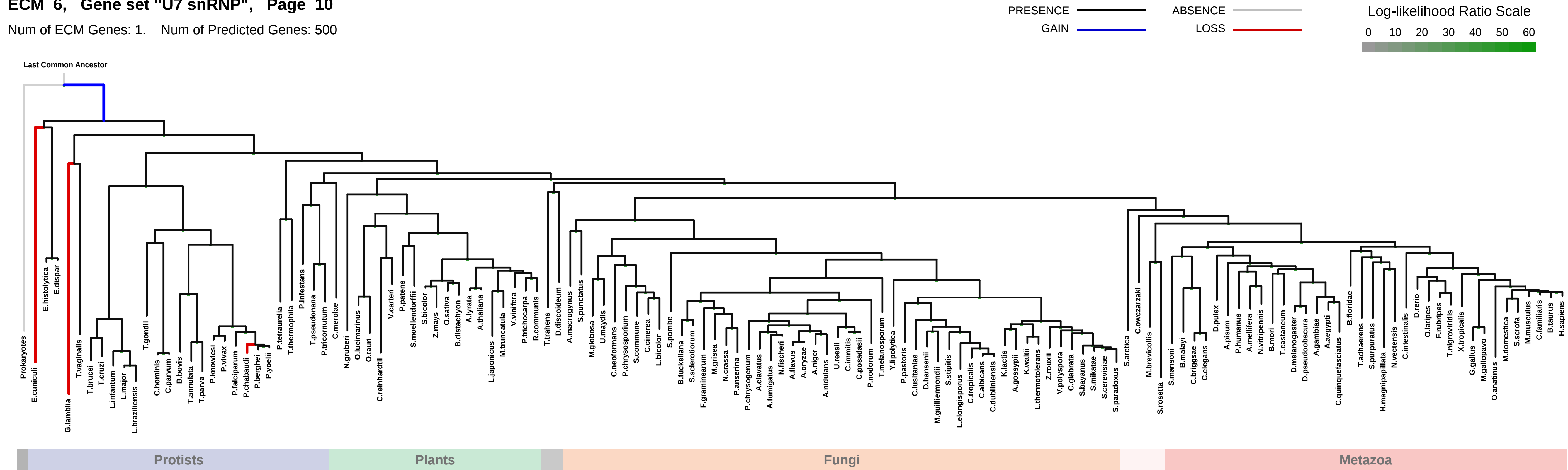
Num of ECM Genes: 1. Num of Predicted Genes: 500

[illegible]

1: spliceosomal complex || 2: mitochondrial outer membrane || 3: axon || 4: cell projection || 5: internal side of plasma membrane || 6: myelin sheath adaxonal region || 7: neuron projection || 8: PML body || 9: Schmidt-Lanterman incisure || 10: prefoldin complex || 11: endosome || 12: endosome membrane || 13: retromer complex || 14: vesicle || 15: acrosomal vesicle || 16: synaptic vesicle membrane || 17: early endosome || 18: HOPS complex || 19: late endosome || 20: late endosome membrane || 21: lysosomal membrane || 22: cleavage furrow || 23: microtubule cytoskeleton || 24: nuclear pore || 25: extracellular matrix || 26: Golgi lumen || 27: lysosomal lumen || 28: proteinaceous extracellular matrix

ECM 6, Gene set "U7 snRNP", Page 10

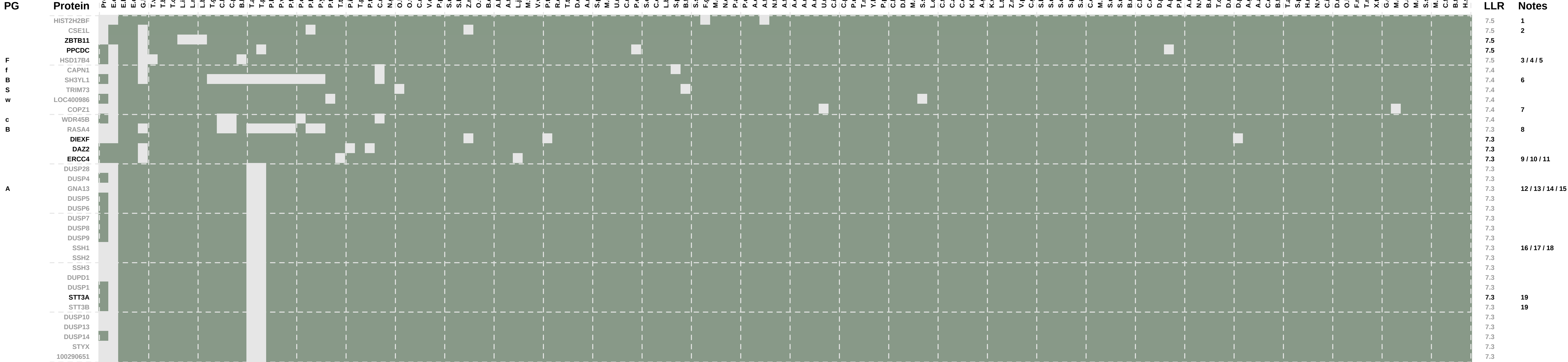
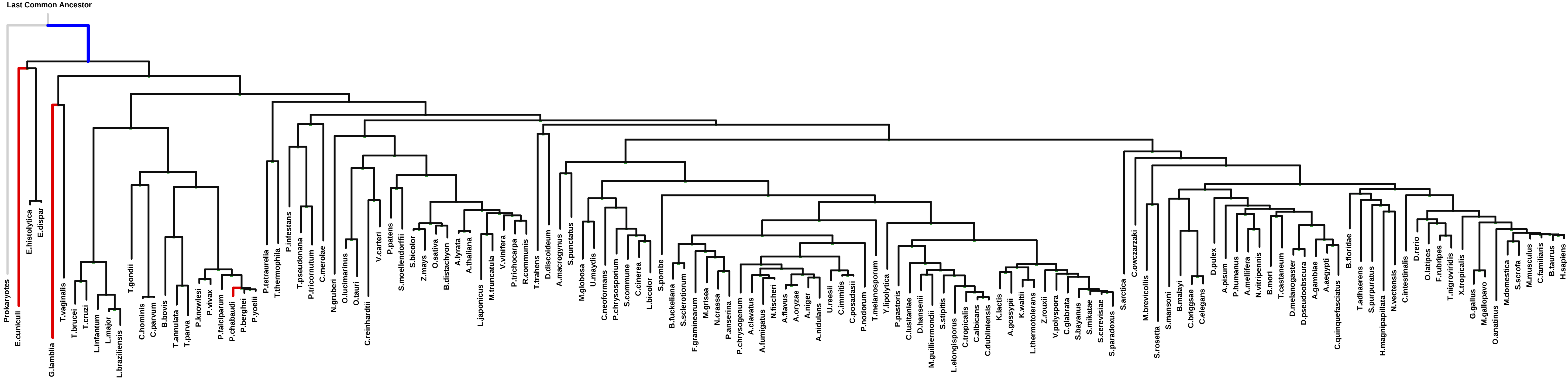
Num of ECM Genes: 1. Num of Predicted Genes: 500

[illegible]

1: extrinsic to internal side of plasma membrane || 2: heterotrimeric G-protein complex || 3: photoreceptor connecting cilium || 4: photoreceptor inner segment || 5: photoreceptor outer segment || 6: photoreceptor outer segment membrane || 7: guanyl-nucleotide exchange factor complex || 8: nuclear matrix || 9: synaptic vesicle membrane || 10: intermediate filament cytoskeleton || 11: catalytic step 2 spliceosome || 12: U5 snRNP || 13: cis-Golgi network || 14: COPI vesicle coat || 15: synaptic vesicle || 16: nucleosome || 17: extrinsic to plasma membrane

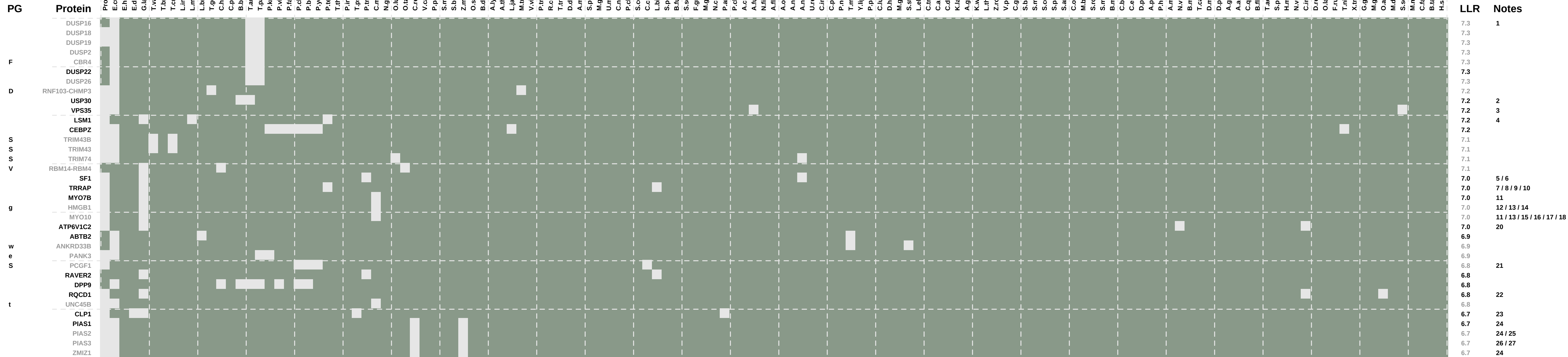
ECM 6, Gene set "U7 snRNP", Page 11

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



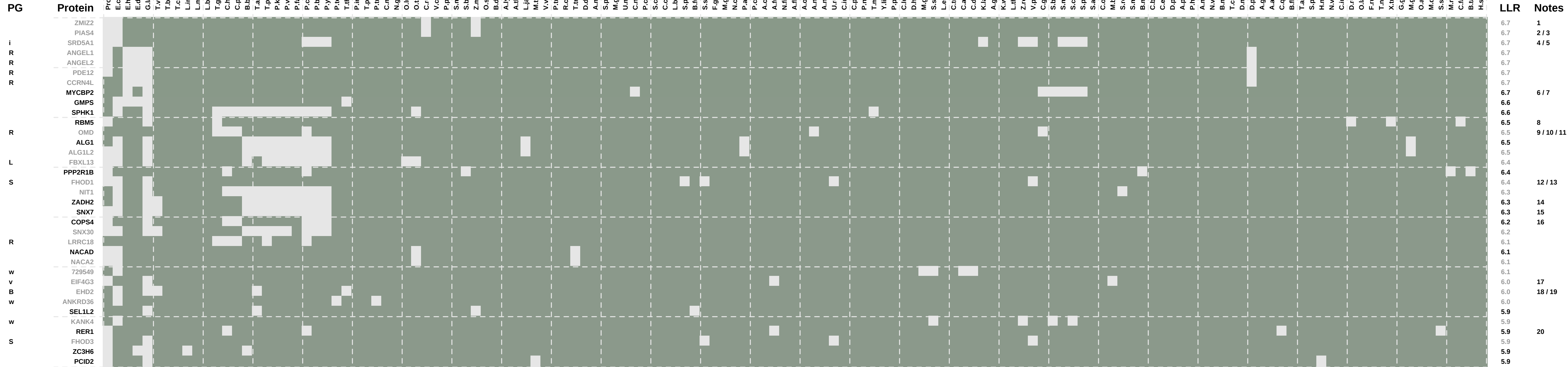
1: nucleosome || 2: nuclear pore || 3: peroxisomal matrix || 4: peroxisomal membrane || 5: peroxisome || 6: ruffle membrane || 7: COPI vesicle coat || 8: intrinsic to internal side of plasma membrane || 9: chromosome, telomeric region ||
10: nuclear chromosome, telomeric region || 11: nucleotide-excision repair complex || 12: brush border membrane || 13: extrinsic to internal side of plasma membrane || 14: heterotrimeric G-protein complex || 15: melanosome || 16: cleavage furrow ||
17: lamellipodium || 18: midbody || 19: oligosaccharyltransferase complex

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



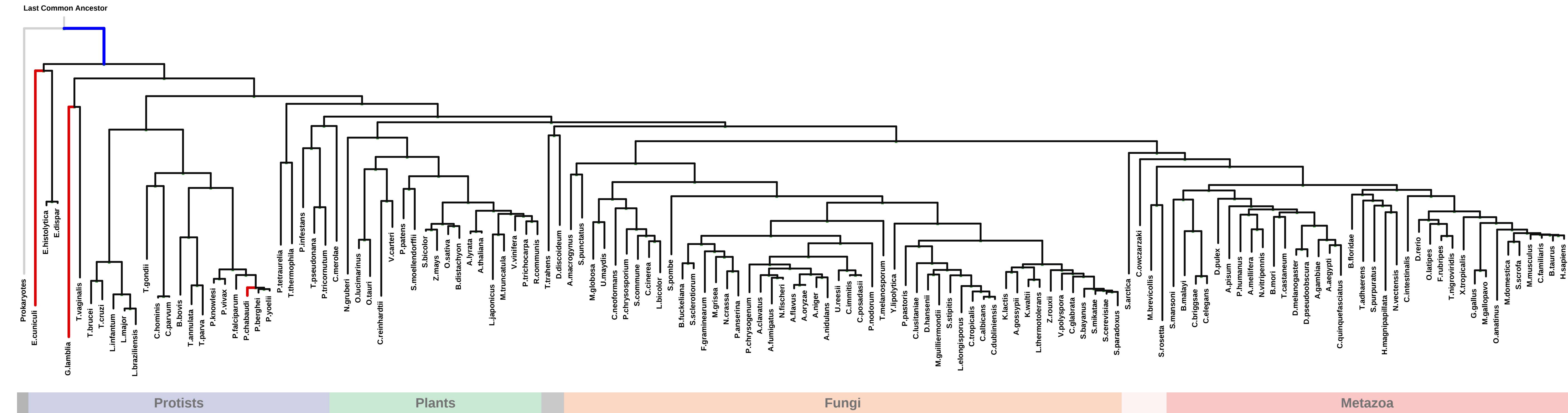
1: cytoplasmic membrane-bounded vesicle || 2: mitochondrial outer membrane || 3: endosome || 4: ribonucleoprotein complex || 5: ribosome || 6: spliceosomal complex || 7: NuA4 histone acetyltransferase complex || 8: PCAF complex || 9: STAGA complex || 10: transcription factor TFII complex || 11: myosin complex || 12: condensed chromosome || 13: neuron projection || 14: transcriptional repressor complex || 15: cell cortex || 16: filopodium membrane || 17: filopodium tip || 18: lamellipodium || 19: ruffle || 20: proton-transporting V-type ATPase, V1 domain || 21: PcG protein complex || 22: cytoplasmic mRNA processing body || 23: tRNA-intron endonuclease complex || 24: nuclear speck ||

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



1: nuclear replication fork || 2: nuclear matrix || 3: PML body || 4: cell body fiber || 5: myelin sheath || 6: axon || 7: microtubule cytoskeleton || 8: spliceosomal complex || 9: Golgi lumen || 10: lysosomal lumen || 11: proteinaceous extracellular matrix || 12: bleb || 13: stress fiber || 14: peroxisome || 15: cytoplasmic vesicle membrane || 16: signalosome || 17: eukaryotic translation initiation factor 4F complex || 18: endosome membrane || 19: recycling endosome membrane || 20: integral to Golgi membrane

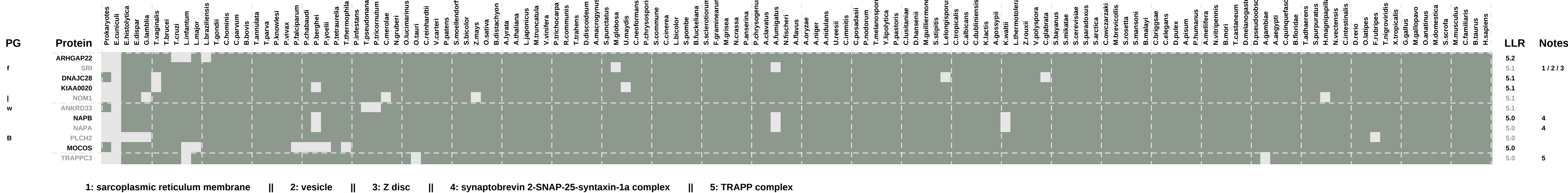
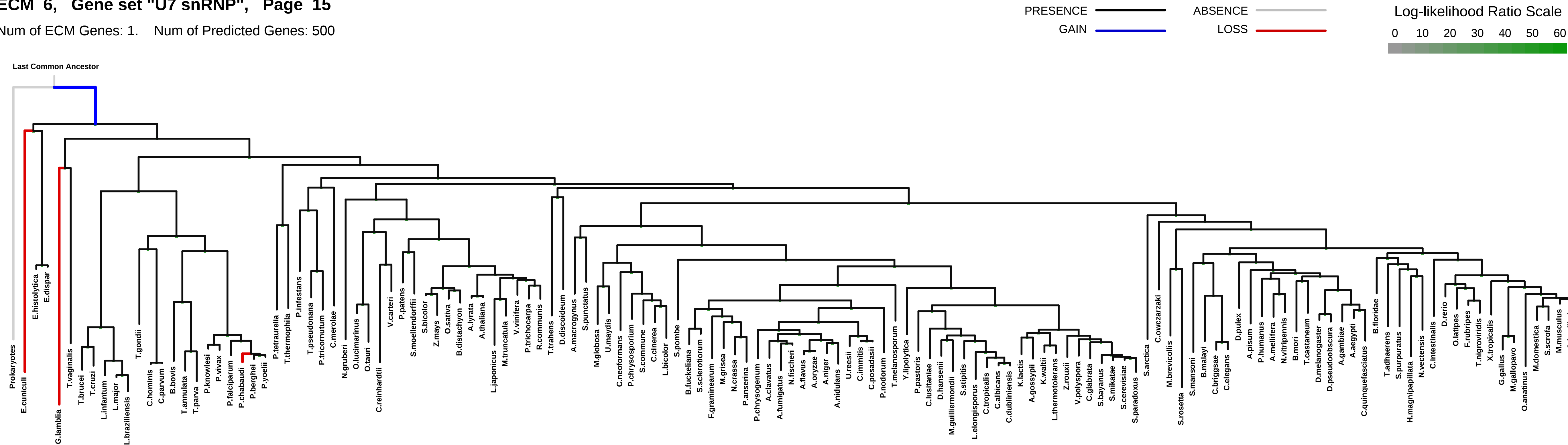
Num of ECM Genes: 1. Num of Predicted Genes: 500



9: eukaryotic translation initiation factor 2 complex || 10: chromosome, centromeric region || 11: microtubule cytoskeleton || 12: protein phosphatase type 2A complex || 13: lipid particle

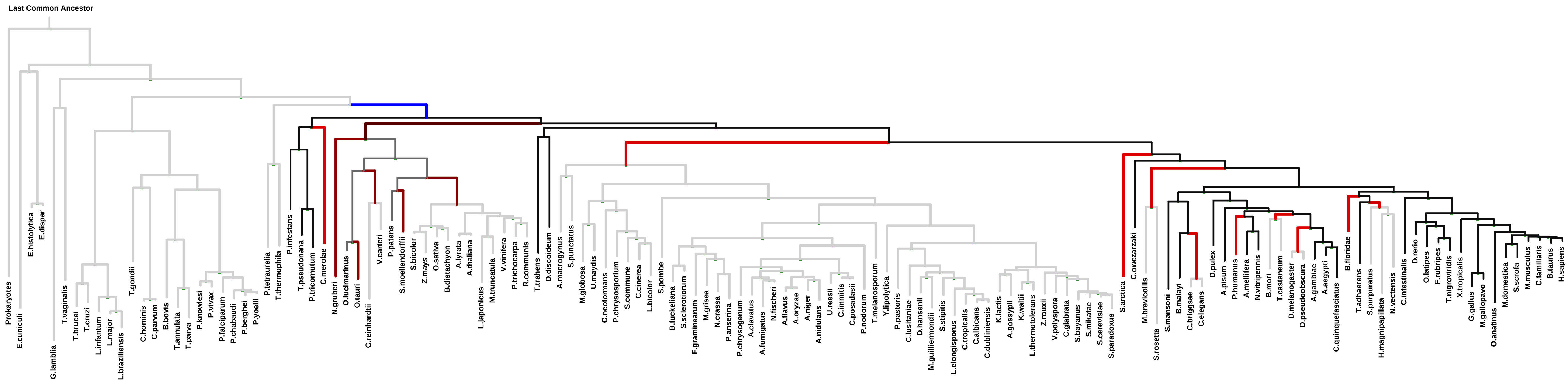
ECM 6, Gene set "U7 snRNP", Page 15

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



ECM 7, Gene set "U7 snRNP", Page 1

Num of ECM Genes: 1. Num of Predicted Genes: 2

[illegible]

1: histone pre-mRNA 3'end processing complex || 2: U7 snRNP || 3: lysosome || 4: Ragulator complex