

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

Dataset:

Num of genes in input gene set: 5
Total number of genes: 20834
Prediction LLR threshold: 0

The CLIME PDF output two sections:

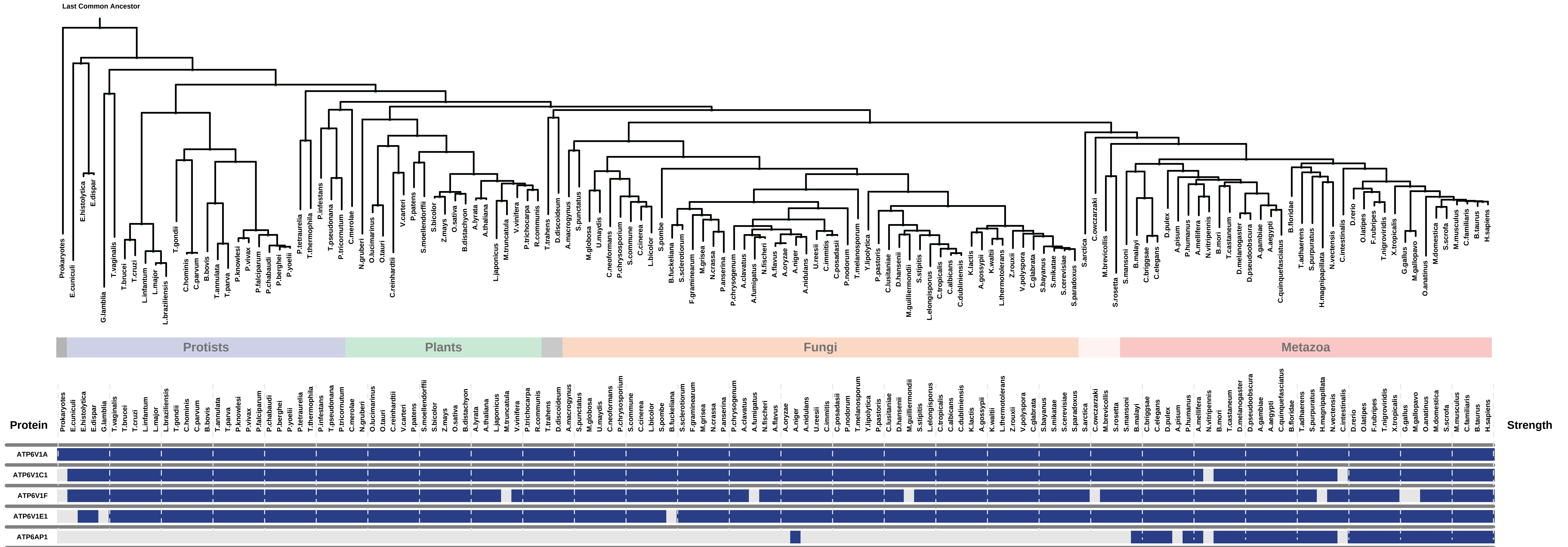
1) Overview of Evolutionarily Conserved Modules (ECMs)

- 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+

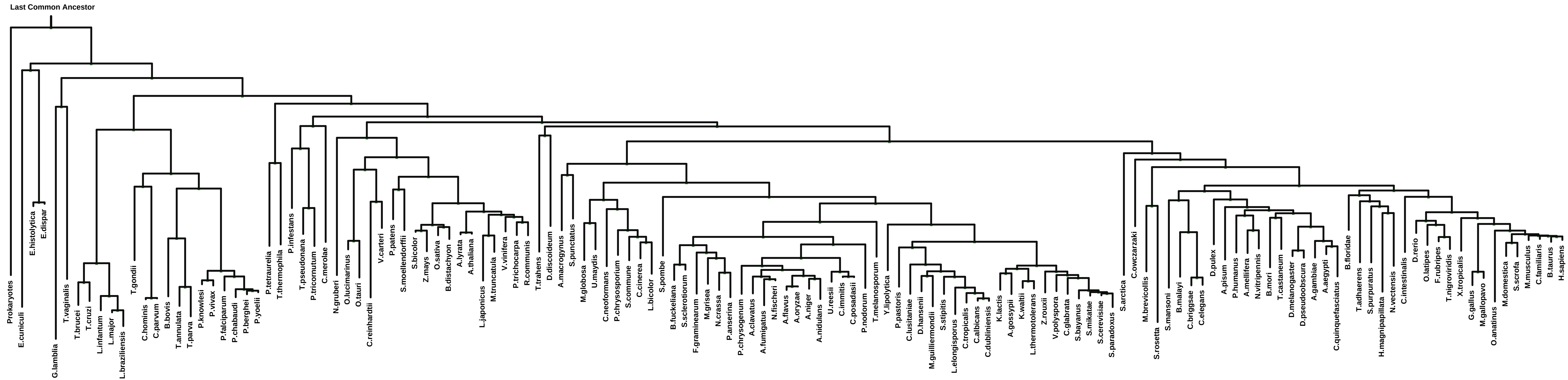
- Top panel shows the inferred evolutionary history on the predefined species tree. Branch color shows the gain event (blue) and loss events (red color, with brighter color indicating higher confidence in loss). Branches before the gain or after a loss are shown in gray.
- Bottom panel shows the input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



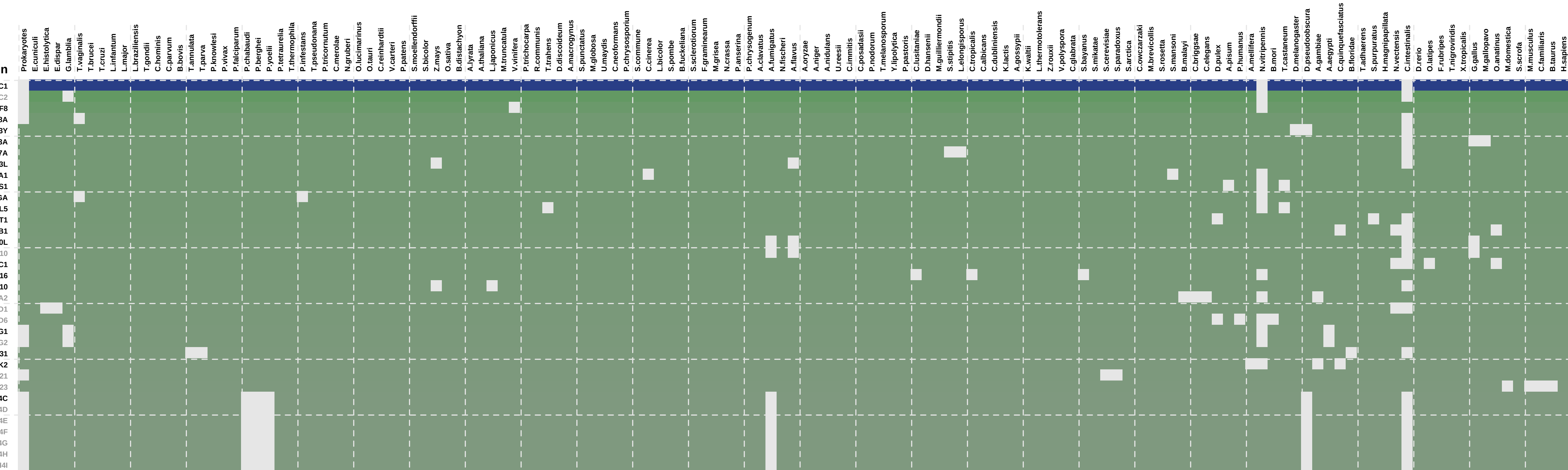
ECM 1, Gene set "proton-transporting two-sector ATPase complex", Page 1

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

[illegible]

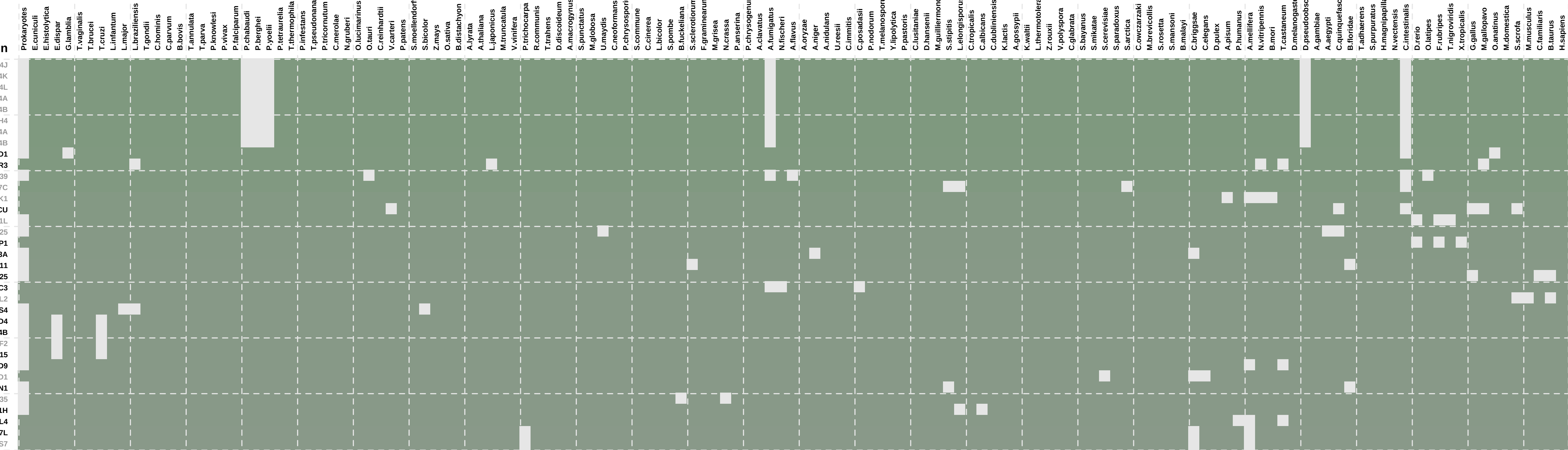
1: microvillus || 2: proton-transporting two-sector ATPase complex || 3: proton-transporting V-type ATPase, V1 domain

Num of ECM Genes: 1. Num of Predicted Genes: 392



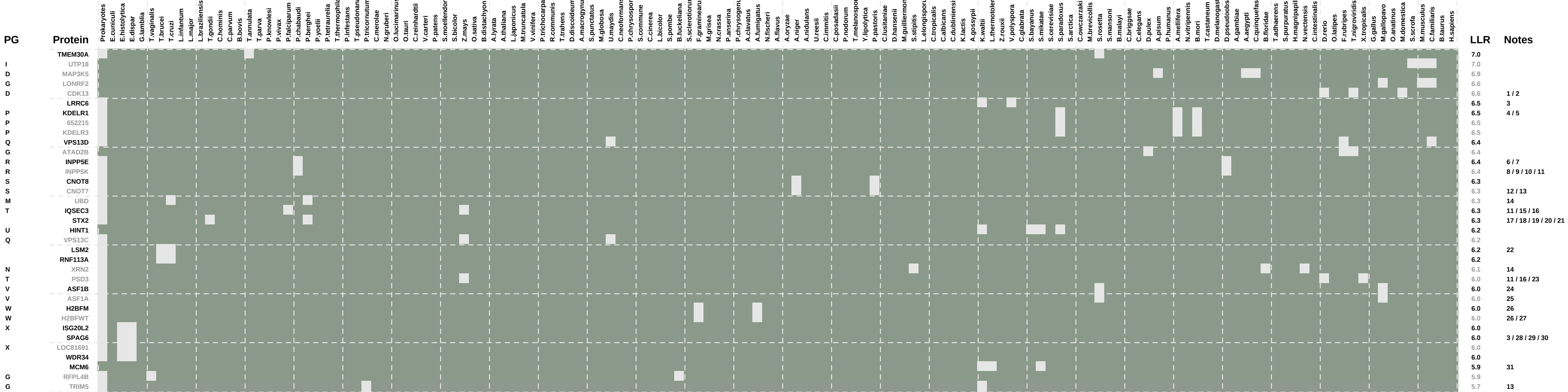
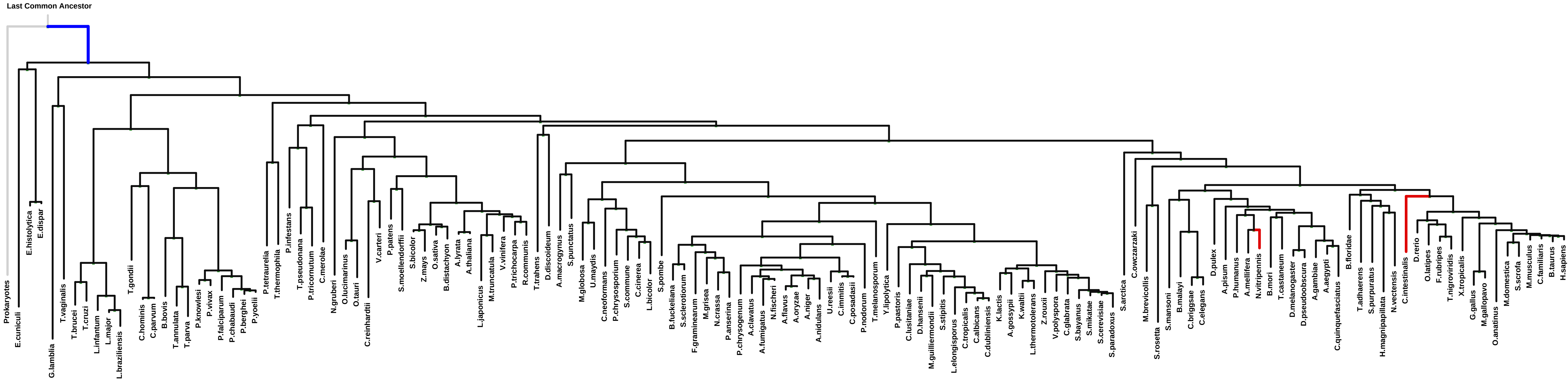
1: apical part of cell || 2: cytoplasmic vesicle || 3: proton-transporting two-sector ATPase complex || 4: proton-transporting V-type ATPase, V1 domain || 5: catalytic step 2 spliceosome || 6: nuclear speck || 7: U5 snRNP || 8: actomyosin ||
9: endoplasmic reticulum-Golgi intermediate compartment || 10: myosin complex || 11: cytosolic large ribosomal subunit || 12: large ribosomal subunit || 13: ribonucleoprotein complex || 14: chromosome || 15: zeta DNA polymerase complex ||
16: microtubule organizing center || 17: spindle pole || 18: glycosylphosphatidylinositol-N-acetylglucosaminyltransferase (GPI-GnT) complex || 19: condensed chromosome kinetochore || 20: condensed nuclear chromosome, centromeric region ||

Num of ECM Genes: 1. Num of Predicted Genes: 392



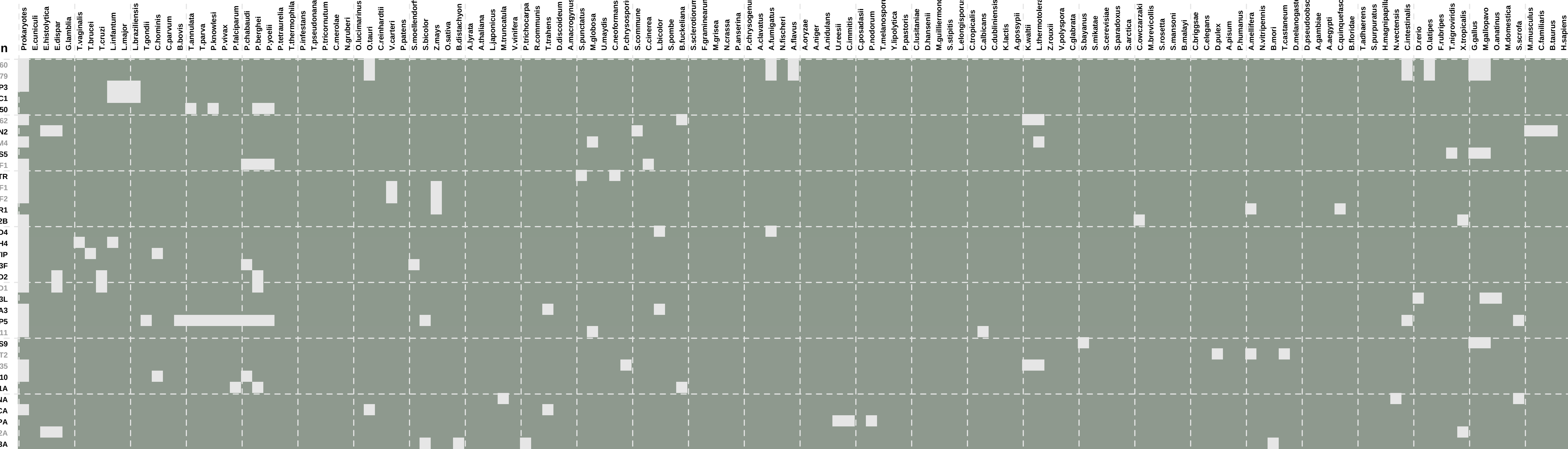
ECM 2, Gene set "proton-transporting two-sector ATPase complex", Page 3

Num of ECM Genes: 1. Num of Predicted Genes: 392



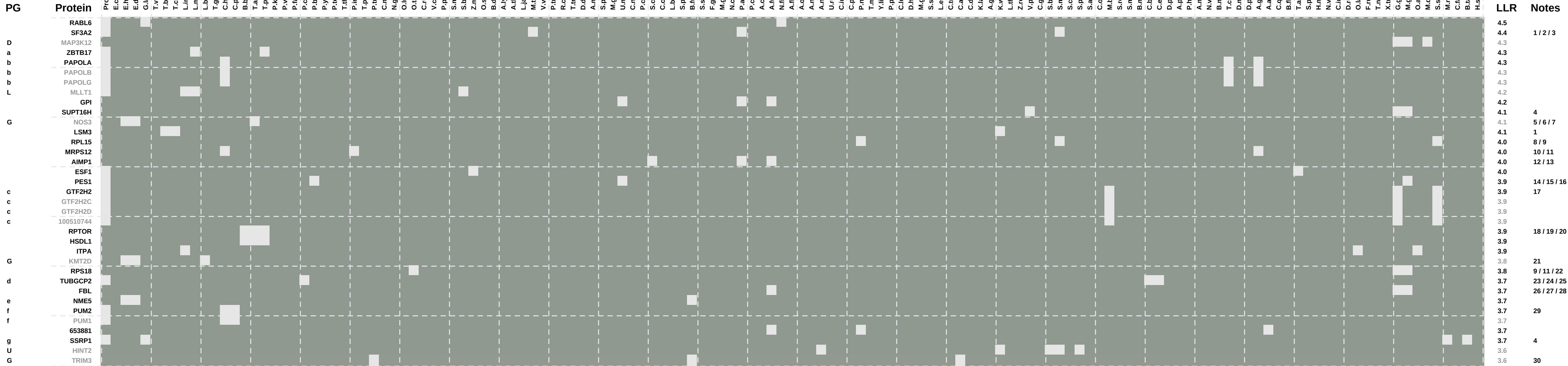
1: nuclear cyclin-dependent protein kinase holoenzyme complex || 2: nuclear speck || 3: cilium || 4: cis-Golgi network || 5: endoplasmic reticulum-Golgi intermediate compartment || 6: cilium axoneme || 7: Golgi cisterna membrane ||
8: neuron projection || 9: ruffle || 10: ruffle membrane || 11: trans-Golgi network || 12: CCR4-NOT complex || 13: cytoplasmic mRNA processing body || 14: aggresome || 15: inhibitory synapse || 16: postsynaptic membrane ||
17: basolateral plasma membrane || 18: cell-cell junction || 19: membrane raft || 20: midbody || 21: transport vesicle || 22: catalytic step 2 spliceosome || 23: postsynaptic density || 24: chromatin || 25: chromatin remodeling complex ||

Num of ECM Genes: 1. Num of Predicted Genes: 392



1: MLL1 complex || 2: axon || 3: dendritic shaft || 4: synapse || 5: voltage-gated potassium channel complex || 6: cytosolic small ribosomal subunit || 7: ribonucleoprotein complex || 8: PcG protein complex || 9: chromosome || 10: PML body || 11: XY body || 12: nuclear matrix || 13: small nuclear ribonucleoprotein complex || 14: trans-Golgi network || 15: asymmetric synapse || 16: axonemal microtubule || 17: cytoplasmic membrane-bounded vesicle || 18: cytoplasmic vesicle || 19: dendritic spine || 20: microtubule organizing center || 21: recycling endosome || 22: symmetric synapse || 23: endocytic vesicle || 24: proteasome accessory complex || 25: proteasome complex ||

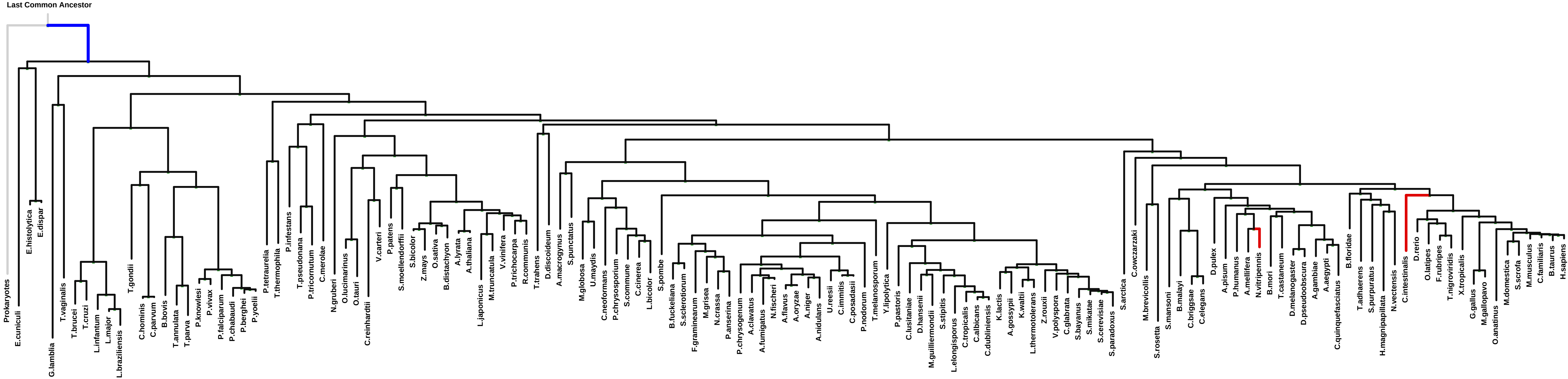
Num of ECM Genes: 1. Num of Predicted Genes: 392



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

ECM 2, Gene set "proton-transporting two-sector ATPase complex", Page 6

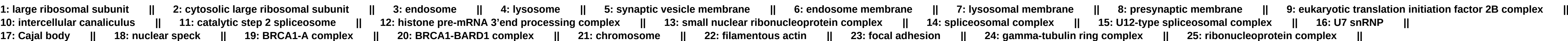
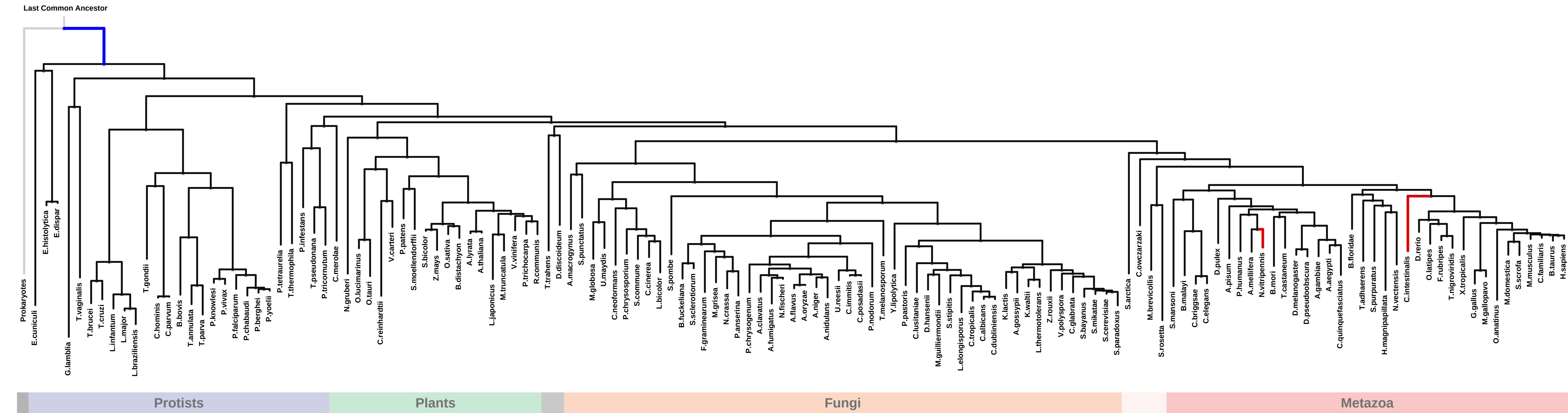
Num of ECM Genes: 1. Num of Predicted Genes: 392



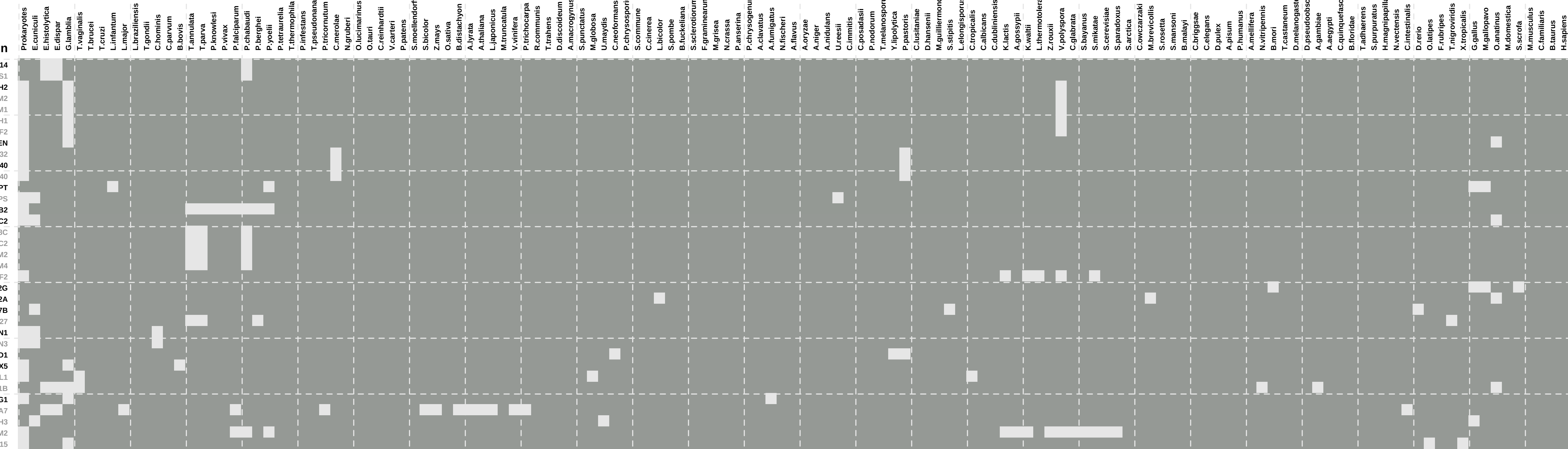
PG	Protein	Protists	Plants	Fungi	Metazoa	LLR	Notes
	UNG					3.6	
R	INPP5J					3.5	1 / 2 / 3
	IARS					3.5	
Y	HCN1					3.5	4 / 5
Q	EP300					3.5	6 / 7 / 8
Q	VPS13A					3.3	
g	SETD1A					3.3	9 / 10 / 11 / 12
g	HMGB3P27					3.3	9
g	100508670					3.3	
g	HMGB2					3.3	13
	PPAN-P2RY11					3.3	
h	LRG1					3.3	
	RFWD3					3.3	
h	FEM1C					3.3	14
	PSMC2					3.2	
h	PHLPP2					3.2	15 / 16
	SLC36A4					3.2	
i	FNTA					3.1	
h	LOC100289085					3.1	17
	PTRH2					3.0	
d	TUBGCP3					3.0	18 / 19 / 20
j	EIF4F2					3.0	21
j	EIF4E					3.0	21 / 22 / 23 / 24 / 25
j	EIF4E1B					3.0	21
k	SLC2A6					3.0	
k	SLC2A8					3.0	26 / 27
X	LOC100288562					3.0	
X	REXO1L11P					3.0	
X	REXO1L1					3.0	
X	REXO1L10P					3.0	
G	ZMYND8					3.0	
	CHRA1C1					2.9	28 / 29
X	PAN2					2.9	
a	ZBTB41					2.8	
Y	PRKAR2A					2.8	30 / 31

1: dendritic shaft 2: growth cone 3: ruffle 4: axon 5: dendrite 6: chromatin 7: histone acetyltransferase complex 8: protein-DNA complex 9: chromosome 10: histone methyltransferase complex 11: nuclear speck 12: Set1C/COMPASS complex 13: condensed chromosome 14: PML body 15: proteasome accessory complex 16: proteasome complex 17: microtubule associated complex 18: centriole 19: polar microtubule 20: spindle 21: mRNA cap binding complex 22: cytoplasmic mRNA processing body 23: cytoplasmic stress granule 24: eukaryotic translation initiation factor 4F complex 25: RNA-induced silencing complex 26: cytoplasmic vesicle membrane

Num of ECM Genes: 1. Num of Predicted Genes: 392



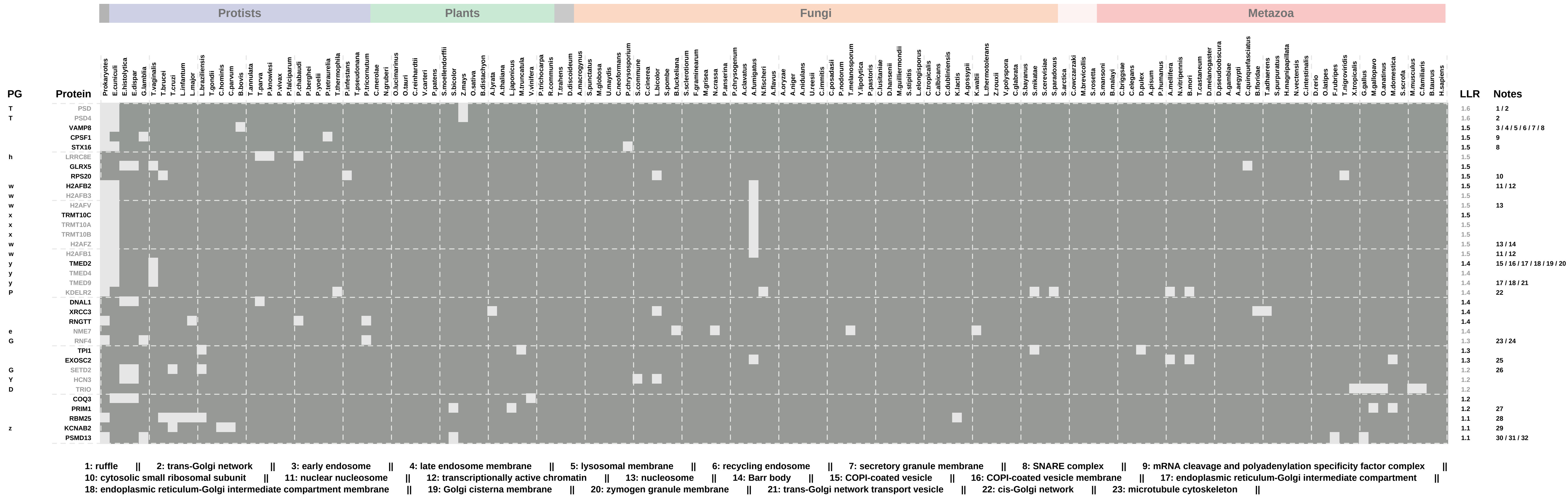
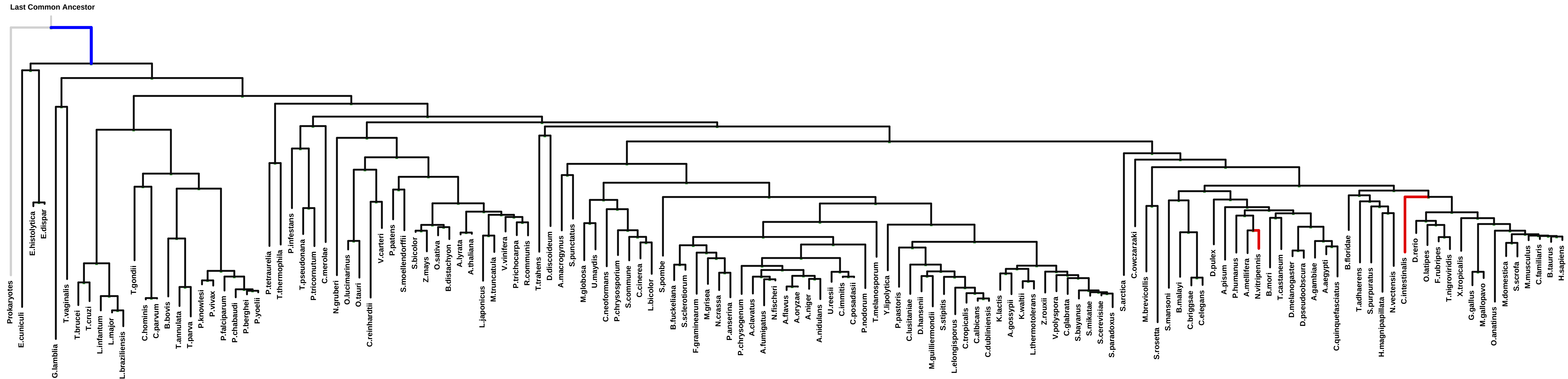
Num of ECM Genes: 1. Num of Predicted Genes: 392



1: dendritic spine || 2: photoreceptor inner segment || 3: sarcolemma || 4: sarcoplasmic reticulum || 5: early endosome || 6: stress fiber || 7: mitotic spindle || 8: ruffle membrane || 9: transcriptional repressor complex ||
10: protein phosphatase type 1 complex || 11: postsynaptic membrane || 12: MLL1 complex || 13: nuclear body || 14: PcG protein complex || 15: PRC1 complex || 16: sex chromatin || 17: ubiquitin ligase complex || 18: DNA-directed RNA polymerase II, core complex ||
19: centriole || 20: nuclear chromosome || 21: nucleoid || 22: synaptonemal complex || 23: anaphase-promoting complex || 24: spindle || 25: spindle microtubule || 26: coated pit || 27: clathrin-coated vesicle || 28: eukaryotic translation initiation factor 4F complex

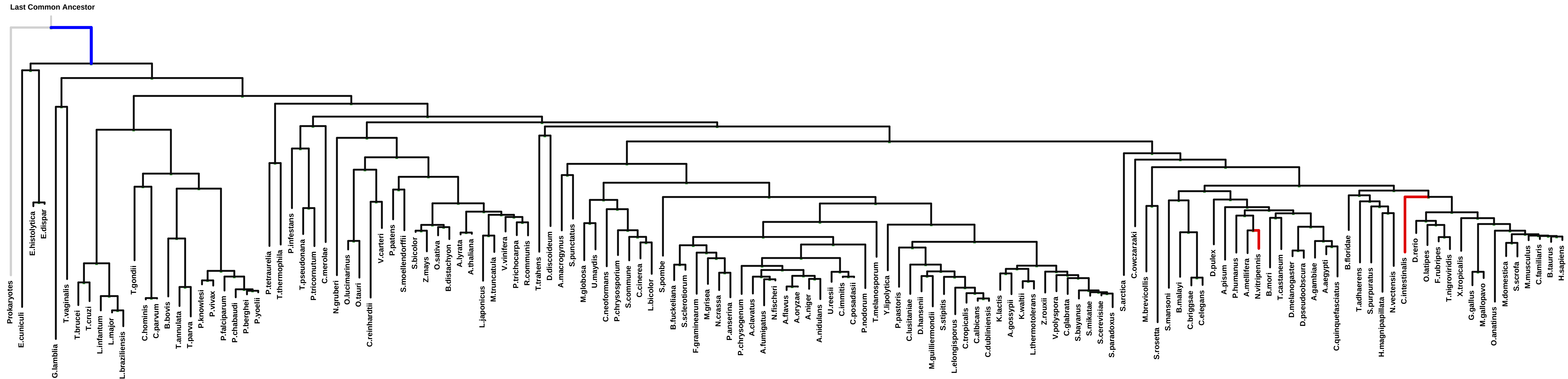
ECM 2, Gene set "proton-transporting two-sector ATPase complex", Page 9

Num of ECM Genes: 1. Num of Predicted Genes: 392



ECM 2, Gene set "proton-transporting two-sector ATPase complex", Page 10

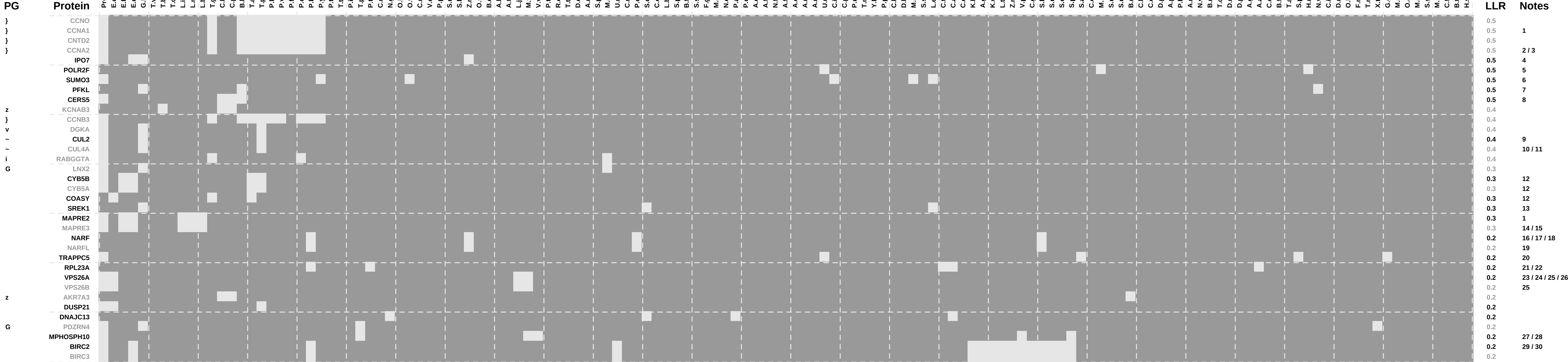
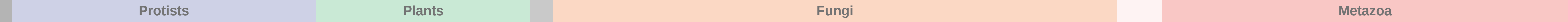
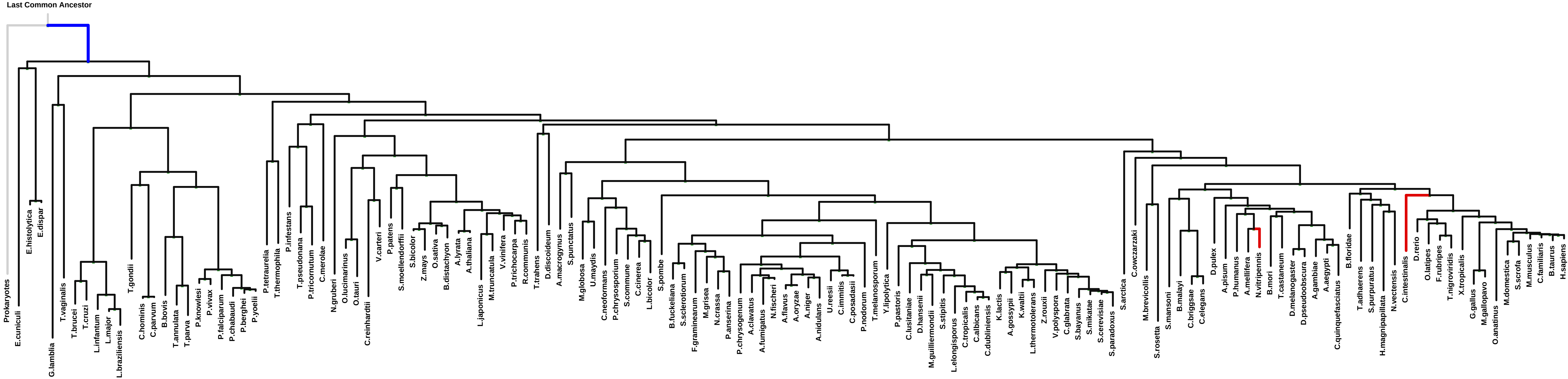
Num of ECM Genes: 1. Num of Predicted Genes: 392

[illegible]

1: chromatin remodeling complex || 2: ribonuclease H2 complex || 3: neuromuscular junction || 4: extrinsic to internal side of plasma membrane || 5: heterotrimeric G-protein complex || 6: membrane raft || 7: midbody || 8: zymogen granule ||
9: cytosolic large ribosomal subunit || 10: cytosolic small ribosomal subunit || 11: ribosome || 12: ubiquitin ligase complex || 13: nuclear envelope || 14: Cajal body || 15: MLL1 complex || 16: PCAF complex || 17: pre-snoRNP complex ||
18: STAGA complex || 19: transcription factor TFIID complex || 20: transcription factor TFIIIC complex || 21: extracellular matrix || 22: fibrillar collagen || 23: Golgi lumen || 24: lysosomal lumen || 25: proteinaceous extracellular matrix ||

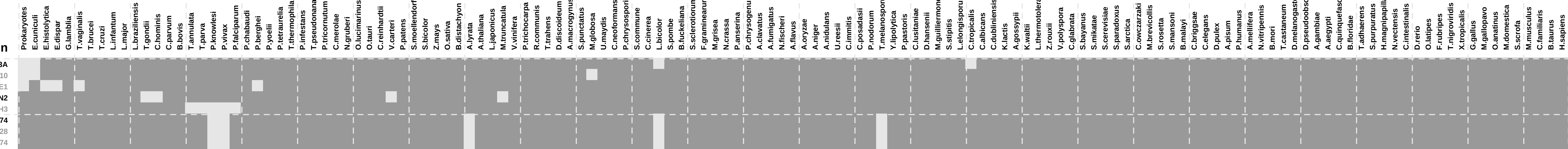
ECM 2, Gene set "proton-transporting two-sector ATPase complex", Page 11

Num of ECM Genes: 1. Num of Predicted Genes: 392



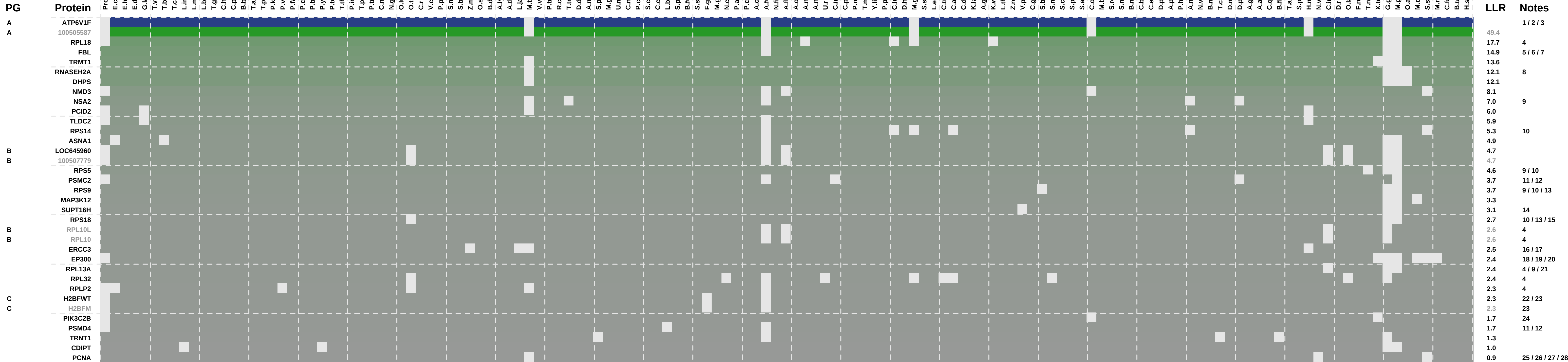
1: microtubule cytoskeleton || 2: female pronucleus || 3: male pronucleus || 4: nuclear pore || 5: DNA-directed RNA polymerase II, core complex || 6: kinetochore || 7: 6-phosphofructokinase complex || 8: nuclear membrane ||
9: Cul2-RING ubiquitin ligase complex || 10: Cul4A-RING ubiquitin ligase complex || 11: Cul4-RING ubiquitin ligase complex || 12: mitochondrial outer membrane || 13: spliceosomal complex || 14: cytoplasmic microtubule || 15: midbody ||
16: lamin filament || 17: nuclear lamina || 18: nuclear lumen || 19: CIA complex || 20: TRAPP complex || 21: cytosolic large ribosomal subunit || 22: TORC2 complex || 23: endosome || 24: endosome membrane || 25: retromer complex ||

Num of ECM Genes: 1. Num of Predicted Genes: 392



LLR	Notes
0.1	1 / 2 / 3 / 4 / 5
0.1	
0.1	6
0.1	
0.1	
0.1	
0.1	
0.1	

Num of ECM Genes: 1. Num of Predicted Genes: 39



1: proton-transporting two-sector ATPase complex || 2: proton-transporting V-type ATPase, V1 domain || 3: vacuolar proton-transporting V-type ATPase complex || 4: cytosolic large ribosomal subunit || 5: box C/D snoRNP complex || 6: Cajal body || 7: granular component || 8: ribonuclease H2 complex || 9: ribonucleoprotein complex || 10: cytosolic small ribosomal subunit || 11: proteasome accessory complex || 12: proteasome complex || 13: ribosome || 14: chromosome || 15: small ribosomal subunit || 16: holo TFIIH complex || 17: SSL2-core TFIIH complex || 18: chromatin || 19: histone acetyltransferase complex || 20: protein-DNA complex || 21: large ribosomal subunit || 22: nuclear membrane ||

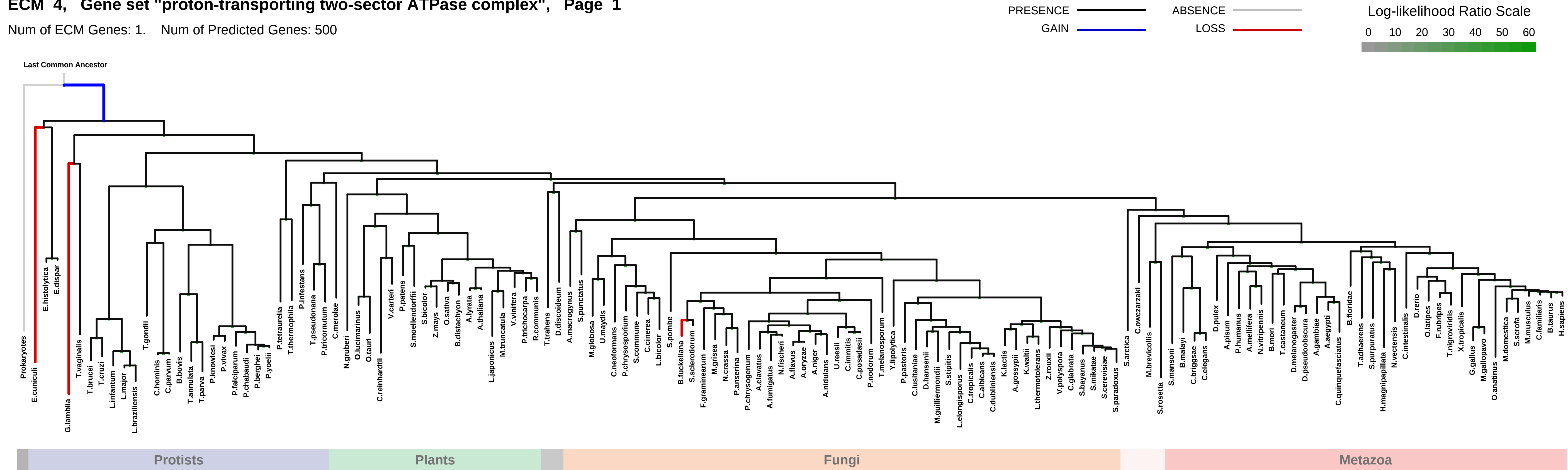
Num of ECM Genes: 1. Num of Predicted Genes: 39



1: DNA-directed RNA polymerase II, core complex || 2: catalytic step 2 spliceosome || 3: small nuclear ribonucleoprotein complex || 4: spliceosomal complex || 5: aminoacyl-tRNA synthetase multienzyme complex || 6: transport vesicle

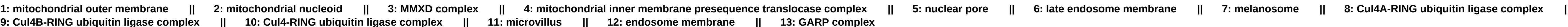
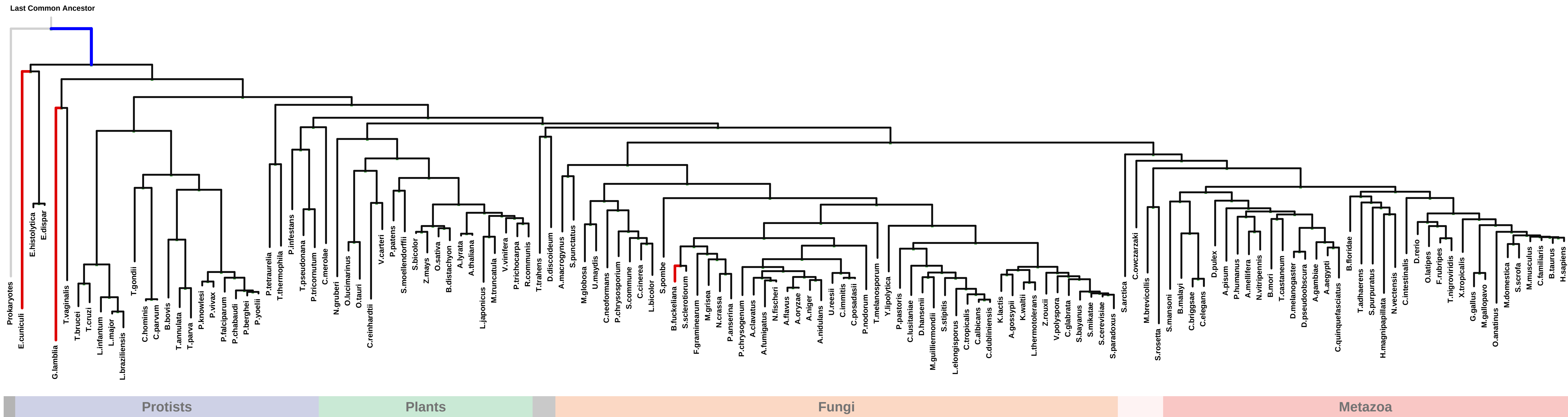
ECM 4, Gene set "proton-transporting two-sector ATPase complex", Page 1

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

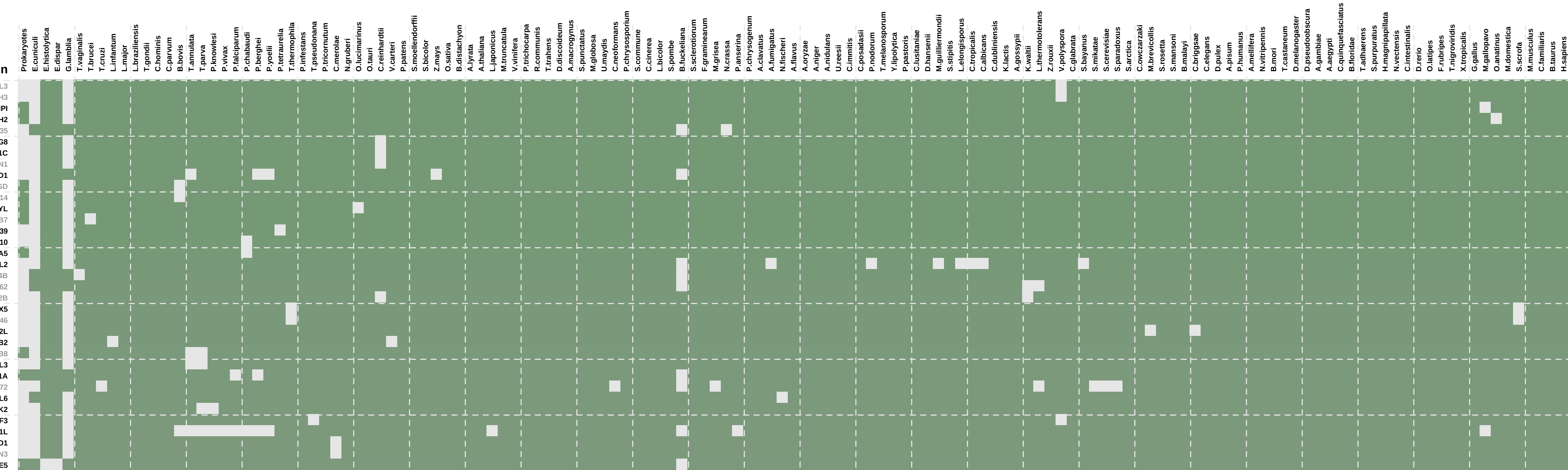
[illegible]

1: endosome || 2: microvillus || 3: proton-transporting two-sector ATPase complex || 4: proton-transporting two-sector ATPase complex, catalytic domain || 5: acrosomal vesicle || 6: BRCA1-A complex || 7: BRCA1-BARD1 complex || 8: chromosome || 9: filamentous actin || 10: focal adhesion || 11: gamma-tubulin ring complex || 12: ribonucleoprotein complex || 13: ruffle || 14: ubiquitin ligase complex || 15: peroxisome || 16: eukaryotic translation initiation factor 2 complex || 17: eukaryotic translation initiation factor 3 complex || 18: catalytic step 2 spliceosome || 19: small nuclear ribonucleoprotein complex || 20: spliceosomal complex || 21: U12-type spliceosomal complex || 22: integral to peroxisomal membrane ||

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

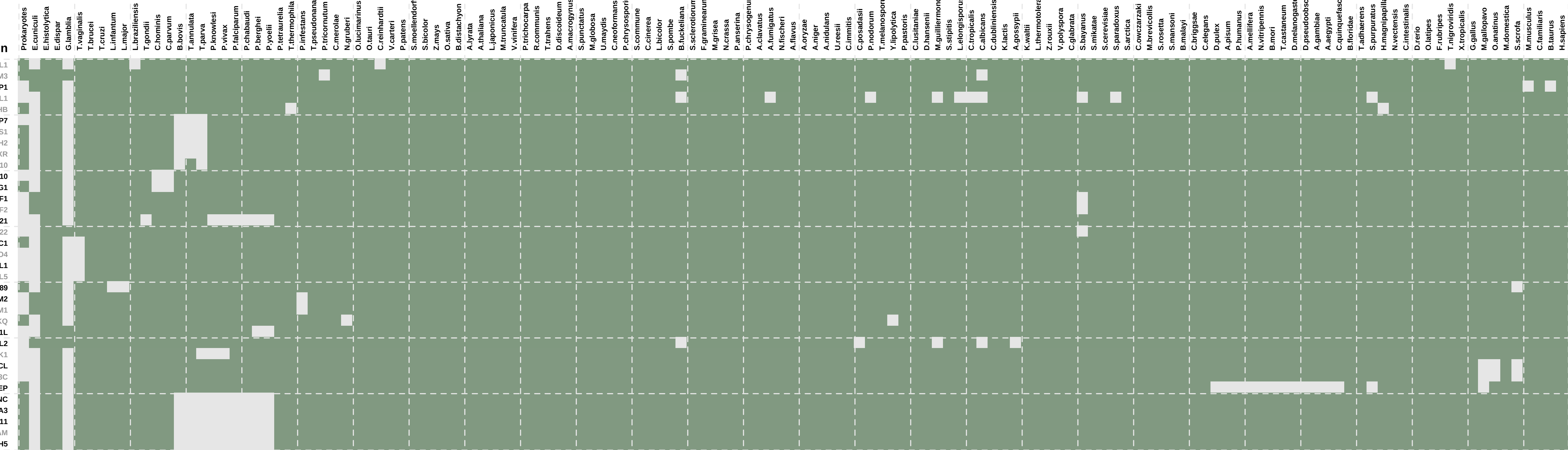


Num of ECM Genes: 1. Num of Predicted Genes: 500



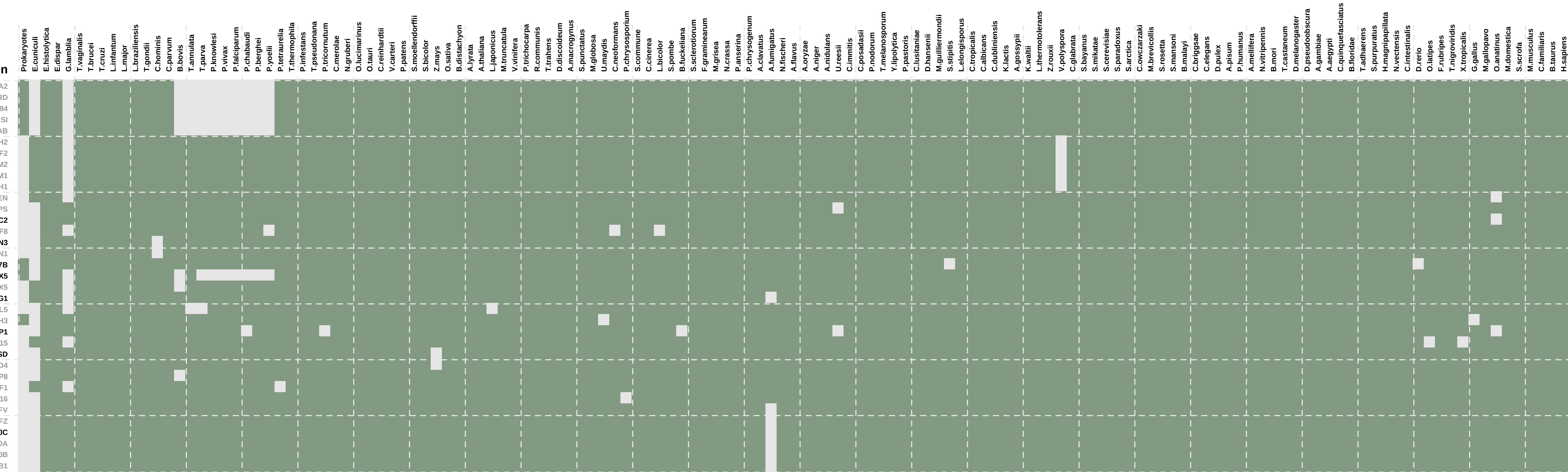
1: chromosome || 2: Golgi stack || 3: coated pit || 4: endocytic vesicle || 5: lamellipodium || 6: neuron projection || 7: synapse || 8: Cajal body || 9: U7 snRNP || 10: basal plasma membrane || 11: integral to endoplasmic reticulum membrane || 12: nuclear matrix || 13: endoplasmic reticulum-Golgi intermediate compartment membrane || 14: SNARE complex || 15: catalytic step 2 spliceosome || 16: mitochondrial envelope || 17: chromosome, telomeric region || 18: condensed nuclear chromosome || 19: Mre11 complex || 20: nuclear chromatin || 21: cytoplasmic vesicle membrane || 22: sarcolemma || 23: mitochondrial intermembrane space || 24: endosome || 25: myofibril || 26: T-tubule || 27: Z disc

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



1: coated pit || 2: early endosome || 3: chromosome || 4: cortical actin cytoskeleton || 5: lamellipodium membrane || 6: nuclear matrix || 7: ruffle membrane || 8: apical part of cell || 9: late endosome membrane || 10: lysosomal membrane ||
11: neuron projection || 12: phagocytic vesicle || 13: phagocytic vesicle membrane || 14: SNARE complex || 15: synapse || 16: transport vesicle membrane || 17: brush border || 18: microvillus || 19: cytoplasmic microtubule ||
20: endosome || 21: lysosome || 22: synaptic vesicle membrane || 23: endosome membrane || 24: presynaptic membrane || 25: Cajal body || 26: nuclear speck || 27: nuclear pore || 28: integral to endoplasmic reticulum membrane ||

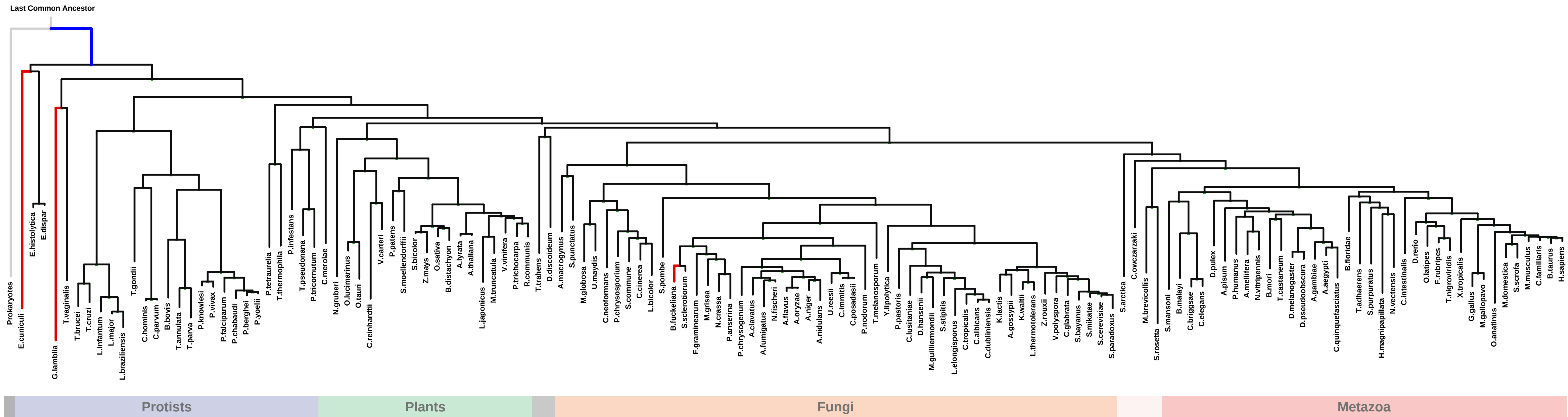
Num of ECM Genes: 1. Num of Predicted Genes: 500



1: cilium || 2: flagellum || 3: mitochondrial membrane || 4: brush border || 5: membrane raft || 6: endoplasmic reticulum lumen || 7: melanosome || 8: early endosome || 9: stress fiber || 10: mitotic spindle || 11: ruffle membrane || 12: transcriptional repressor complex || 13: clathrin-coated vesicle || 14: coated pit || 15: peroxisomal matrix || 16: peroxisomal membrane || 17: peroxisome || 18: eukaryotic translation initiation factor 4F complex || 19: Ino80 complex || 20: proteasome complex || 21: cytosolic large ribosomal subunit || 22: ruffle || 23: trans-Golgi network || 24: late endosome membrane || 25: lysosomal membrane || 26: recycling endosome || 27: secretory granule membrane ||

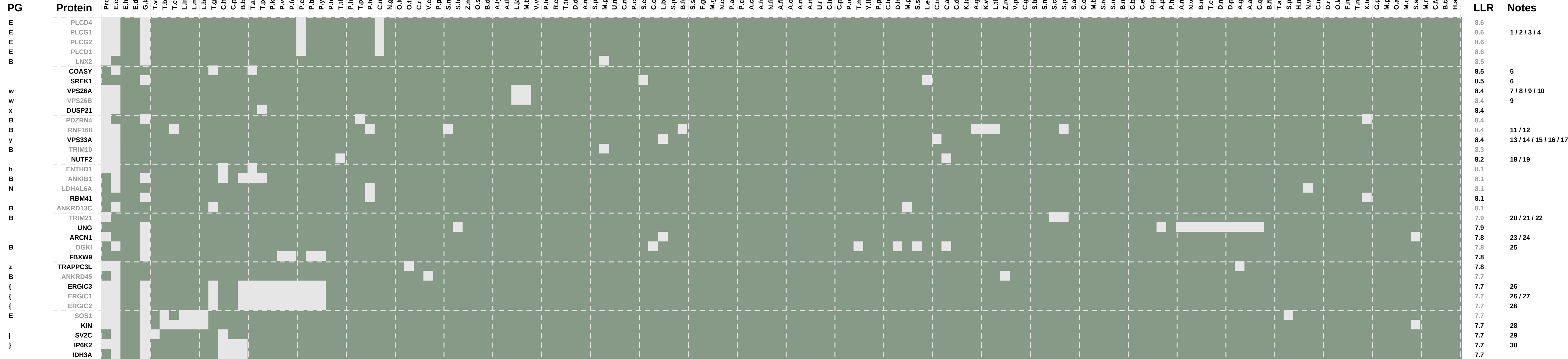
ECM 4, Gene set "proton-transporting two-sector ATPase complex", Page 6

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

[illegible]

1: nuclear nucleosome || 2: transcriptionally active chromatin || 3: endoplasmic reticulum-Golgi intermediate compartment || 4: endoplasmic reticulum-Golgi intermediate compartment membrane || 5: trans-Golgi network transport vesicle ||
6: COPI-coated vesicle || 7: COPI-coated vesicle membrane || 8: Golgi cisterna membrane || 9: zymogen granule membrane || 10: microtubule cytoskeleton || 11: PML body || 12: bleb || 13: cell cortex || 14: phagocytic vesicle ||
15: actin cytoskeleton || 16: cortical actin cytoskeleton || 17: mitochondrial respiratory chain complex III || 18: proteasome accessory complex || 19: proteasome complex || 20: proteasome regulatory particle || 21: chromatin remodeling complex ||

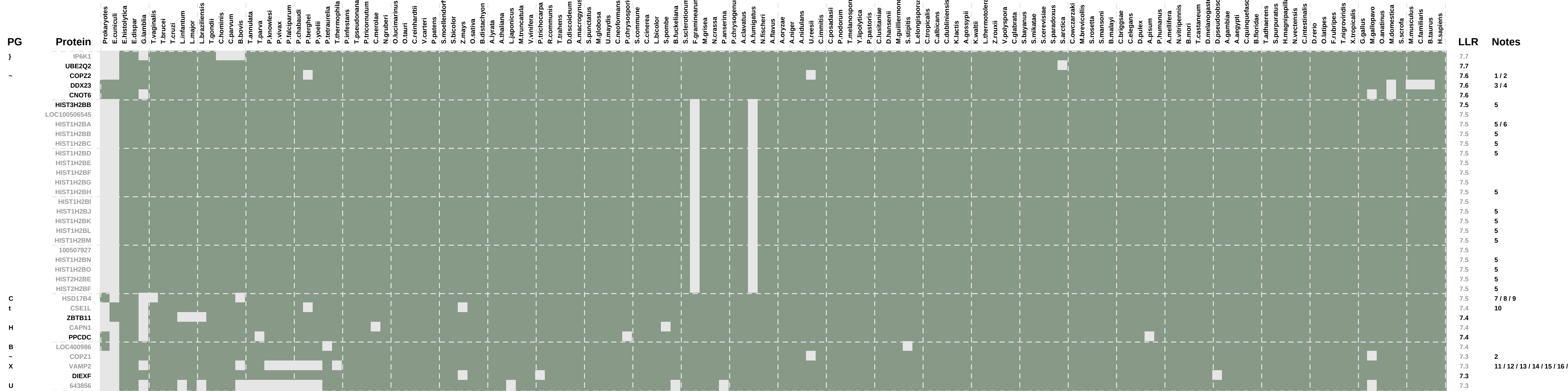
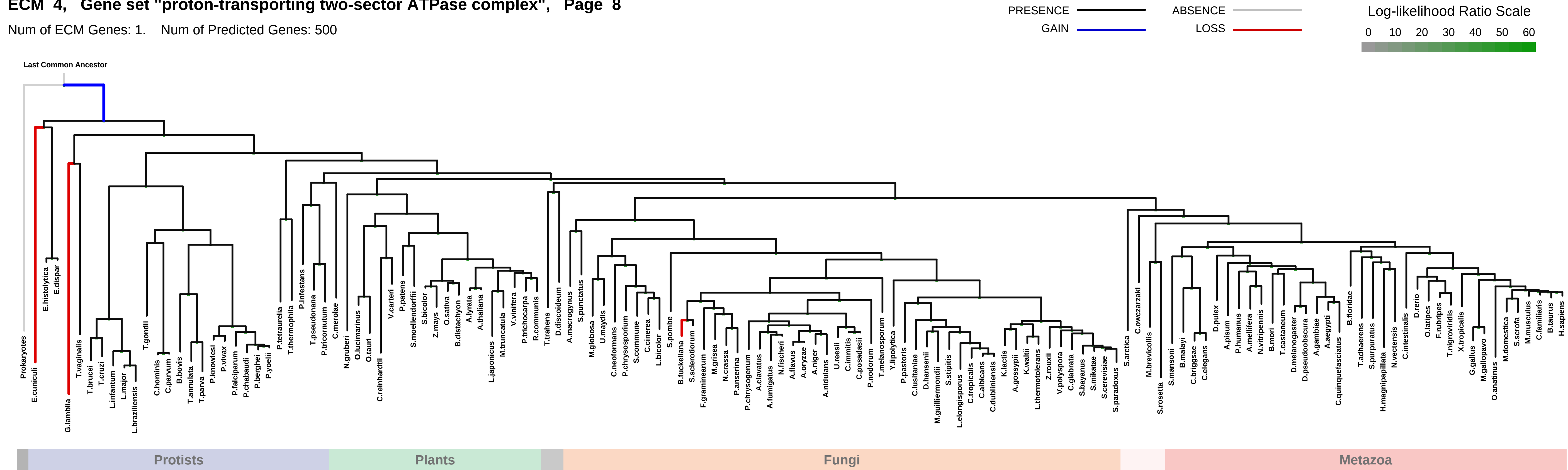
Num of ECM Genes: 1. Num of Predicted Genes: 500



1: lamellipodium || 2: neuron projection || 3: ruffle || 4: signalosome || 5: mitochondrial outer membrane || 6: spliceosomal complex || 7: endosome || 8: endosome membrane || 9: retromer complex || 10: vesicle || 11: site of double-strand break || 12: ubiquitin ligase complex || 13: early endosome || 14: HOPS complex || 15: late endosome || 16: late endosome membrane || 17: lysosomal membrane || 18: microtubule cytoskeleton || 19: nuclear pore || 20: cytoplasmic mRNA processing body || 21: ribonucleoprotein complex || 22: SCF ubiquitin ligase complex || 23: clathrin adaptor complex || 24: COPI vesicle coat || 25: guanyl-nucleotide exchange factor complex ||

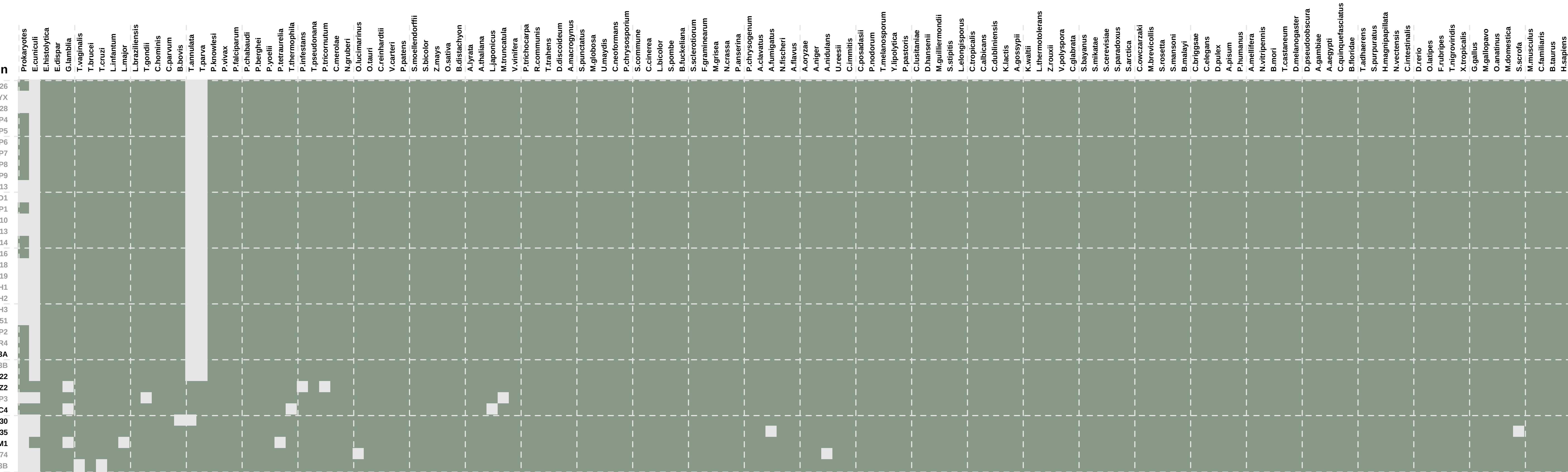
ECM 4, Gene set "proton-transporting two-sector ATPase complex", Page 8

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



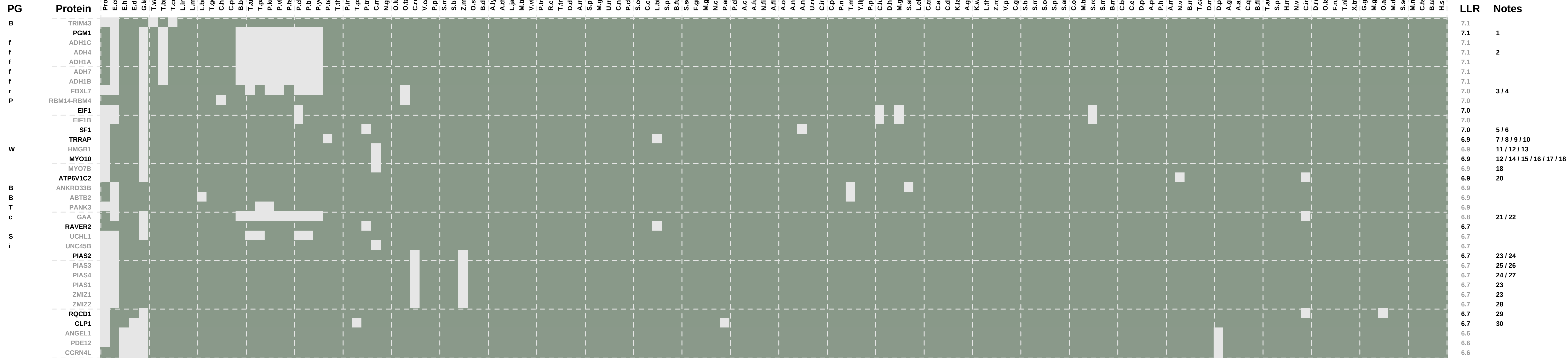
1: cis-Golgi network || 2: COPI vesicle coat || 3: catalytic step 2 spliceosome || 4: U5 snRNP || 5: nucleosome || 6: extrinsic to plasma membrane || 7: peroxisomal matrix || 8: peroxisomal membrane || 9: peroxisome || 10: nuclear pore || 11: clathrin-coated vesicle || 12: clathrin-sculpted gamma-aminobutyric 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 || 19: synaptic vesicle membrane

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



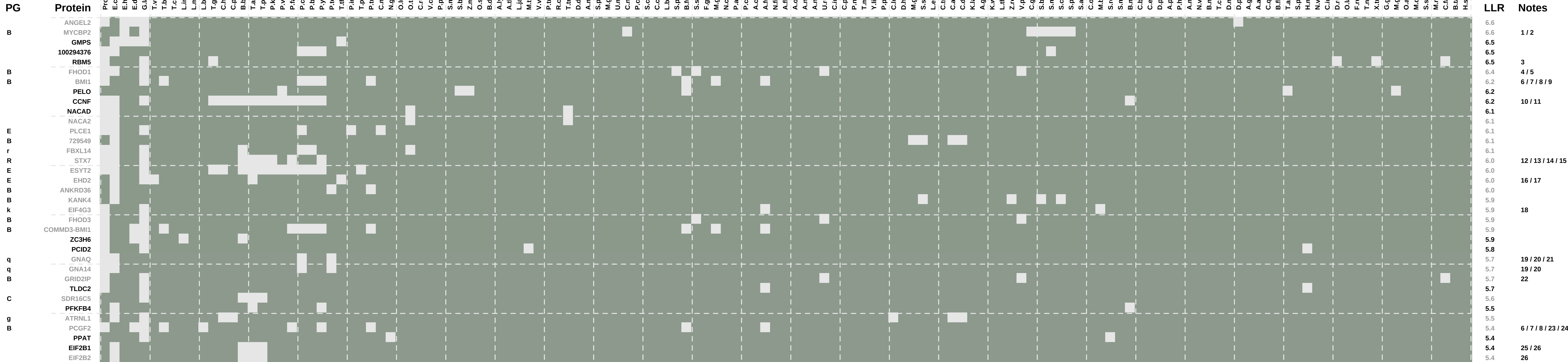
LLR	Notes
7.2	
7.2	
7.2	
7.2	
7.2	
7.2	
7.2	
7.2	
7.2	1 / 2 / 3 / 4
7.2	
7.2	
7.2	
7.2	
7.2	5
7.2	
7.2	6 / 7 / 8
7.2	
7.2	
7.2	
7.2	
7.2	9
7.2	9
7.2	
7.2	
7.2	
7.2	10 / 11 / 12
7.2	13
7.2	14
7.1	15
7.1	
7.1	

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



1: actin cytoskeleton || 2: microtubule cytoskeleton || 3: SCF ubiquitin ligase complex || 4: ubiquitin ligase complex || 5: ribosome || 6: spliceosomal complex || 7: NuA4 histone acetyltransferase complex || 8: PCAF complex || 9: STAGA complex || 10: transcription factor TFII complex || 11: condensed chromosome || 12: neuron projection || 13: transcriptional repressor complex || 14: cell cortex || 15: filopodium membrane || 16: filopodium tip || 17: lamellipodium || 18: myosin complex || 19: ruffle || 20: proton-transporting V-type ATPase, V1 domain || 21: lysosomal membrane || 22: lysosome || 23: nuclear speck || 24: PML body || 25: dendrite || 26: synapse ||

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



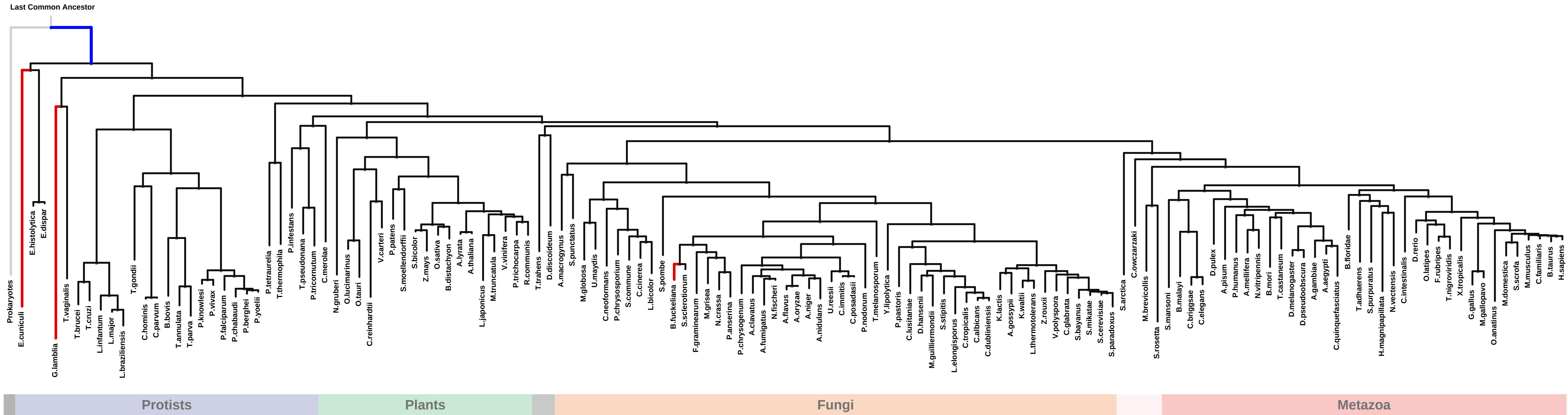
1: axon || 2: microtubule cytoskeleton || 3: spliceosomal complex || 4: bleb || 5: stress fiber || 6: nuclear body || 7: PcG protein complex || 8: PRC1 complex || 9: ubiquitin ligase complex || 10: centriole || 11: SCF ubiquitin ligase complex || 12: early endosome membrane || 13: late endosome membrane || 14: lysosomal membrane || 15: SNARE complex || 16: endosome membrane || 17: recycling endosome membrane || 18: eukaryotic translation initiation factor 4F complex || 19: extrinsic to internal side of plasma membrane || 20: heterotrimeric G-protein complex || 21: nuclear membrane || 22: postsynaptic membrane || 23: nuclear chromatin || 24: sex chromatin || 25: eukaryotic translation initiation factor 2 complex ||

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



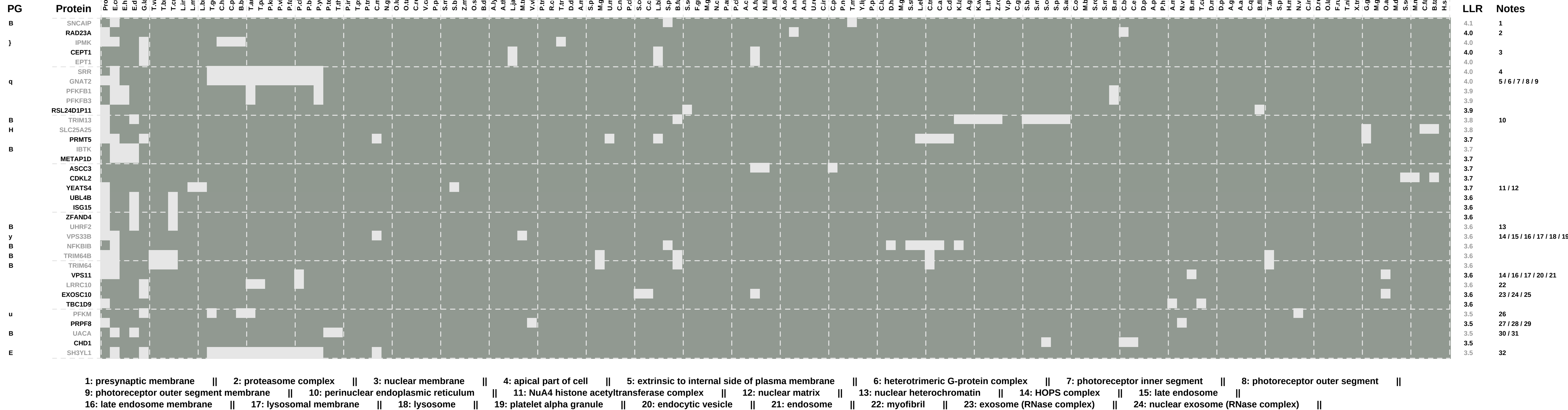
ECM 4, Gene set "proton-transporting two-sector ATPase complex", Page 13

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

[illegible]

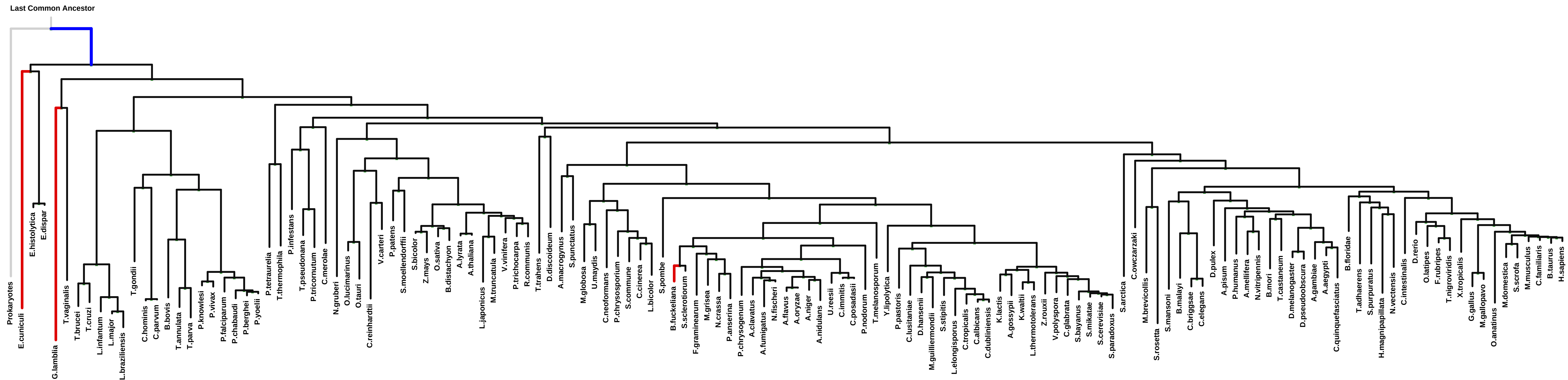
1: Cul5-RING ubiquitin ligase complex || 2: transcription factor TFIID complex || 3: proteasome regulatory particle || 4: proteasome regulatory particle, base subcomplex || 5: axon || 6: cell projection || 7: internal side of plasma membrane || 8: myelin sheath adaxonal region || 9: neuron projection || 10: PML body || 11: Schmidt-Lanterman incisure || 12: focal adhesion || 13: chromatin assembly complex || 14: extrinsic to internal side of plasma membrane || 15: heterotrimeric G-protein complex || 16: chromatin || 17: transcription factor TFIIA complex || 18: proteasome accessory complex || 19: proteasome complex

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



ECM 4, Gene set "proton-transporting two-sector ATPase complex", Page 15

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

[illegible]

1: endosome || 2: endosome membrane || 3: intermediate filament cytoskeleton || 4: intrinsic to internal side of plasma membrane || 5: clathrin-coated vesicle || 6: ubiquitin ligase complex || 7: acrosomal vesicle || 8: synaptic vesicle membrane

Num of ECM Genes: 1. Num of Predicted Genes: 33

