

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:

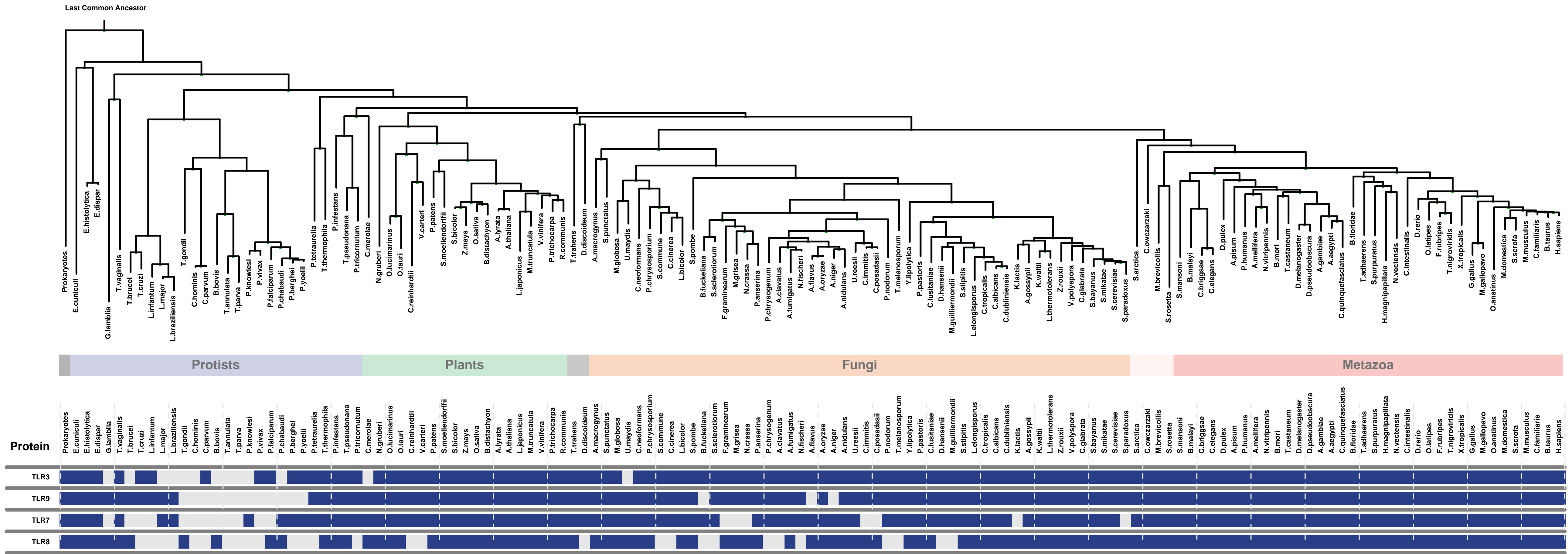
1) Overview of Evolutionarily Conserved Modules (ECMs)

- 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+

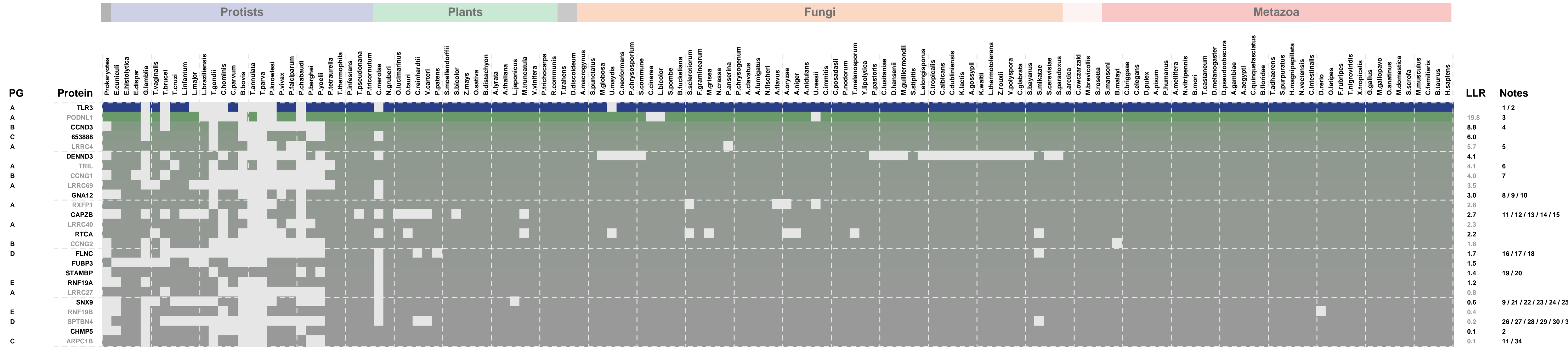
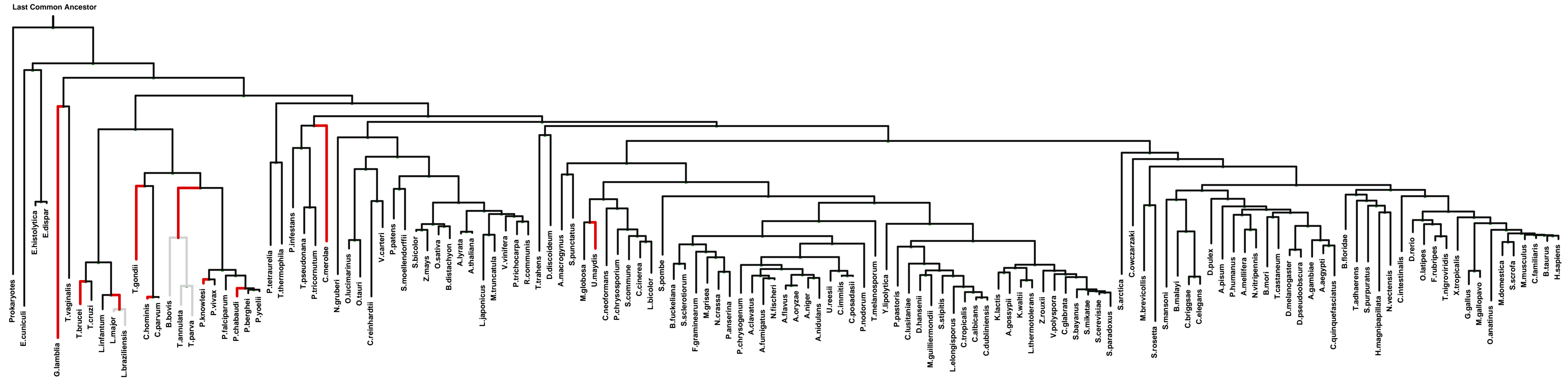
- Top panel shows the inferred evolutionary history on the predefined species tree. Branch color shows the gain event (blue) and loss events (red color, with brighter color indicating higher confidence in loss). Branches before the gain or after a loss are shown in gray.
- Bottom panel shows the input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

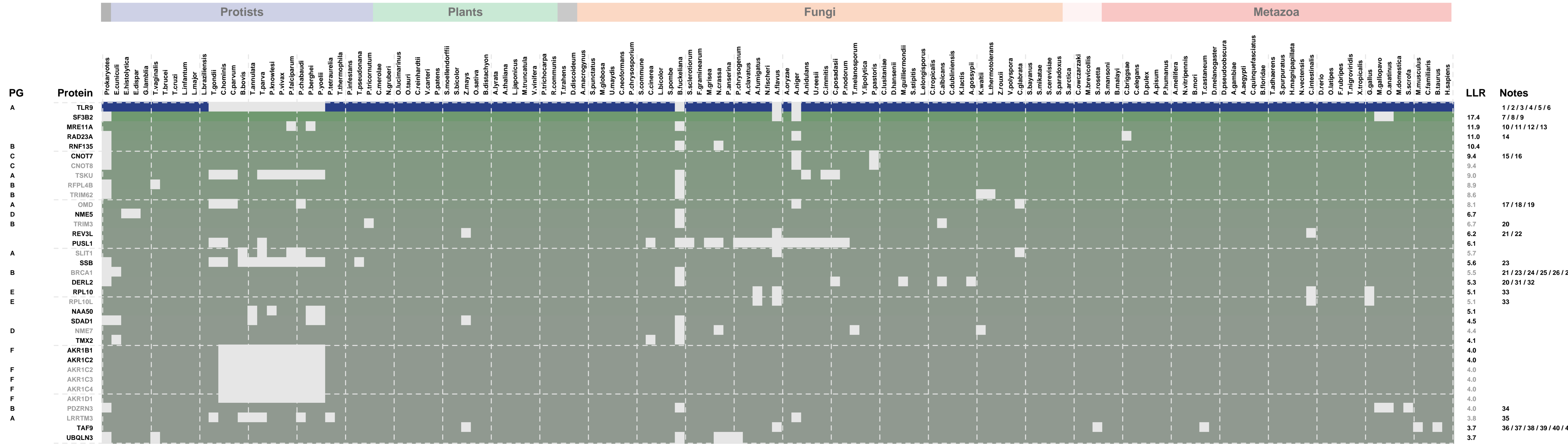
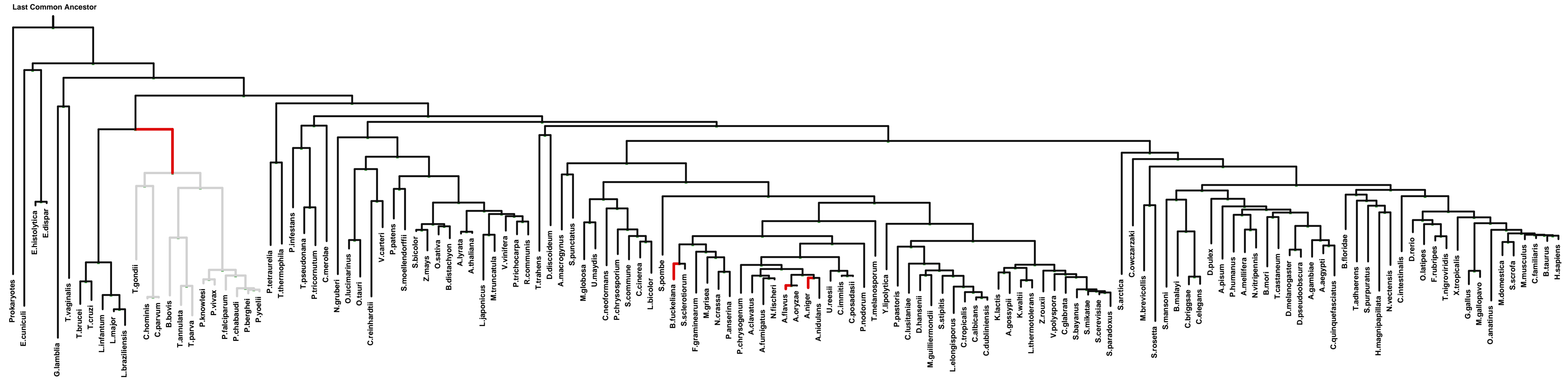
Num of ECM Genes: 1. Num of Predicted Genes: 24



1: endolysosome membrane || 2: endosome membrane || 3: proteinaceous extracellular matrix || 4: cyclin-dependent protein kinase holoenzyme complex || 5: postsynaptic membrane || 6: lipopolysaccharide receptor complex || 7: dendrite || 8: brush border membrane || 9: extrinsic to internal side of plasma membrane || 10: heterotrimeric G-protein complex || 11: actin cytoskeleton || 12: cortical cytoskeleton || 13: F-actin capping protein complex || 14: lamellipodium || 15: WASH complex || 16: costamere || 17: sarcolemma || 18: Z disc || 19: cleavage furrow || 20: early endosome || 21: clathrin-coated vesicle || 22: cytoplasmic membrane-bounded vesicle || 23: cytoplasmic vesicle membrane || 24: ruffle || 25: trans-Golgi network || 26: adherens junction || 27: axon hillock || 28: axon initial segment || 29: cell body fiber || 30: node of Ranvier || 31: nuclear matrix || 32: PML body || 33: spectrin || 34: Arp2/3 protein complex

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

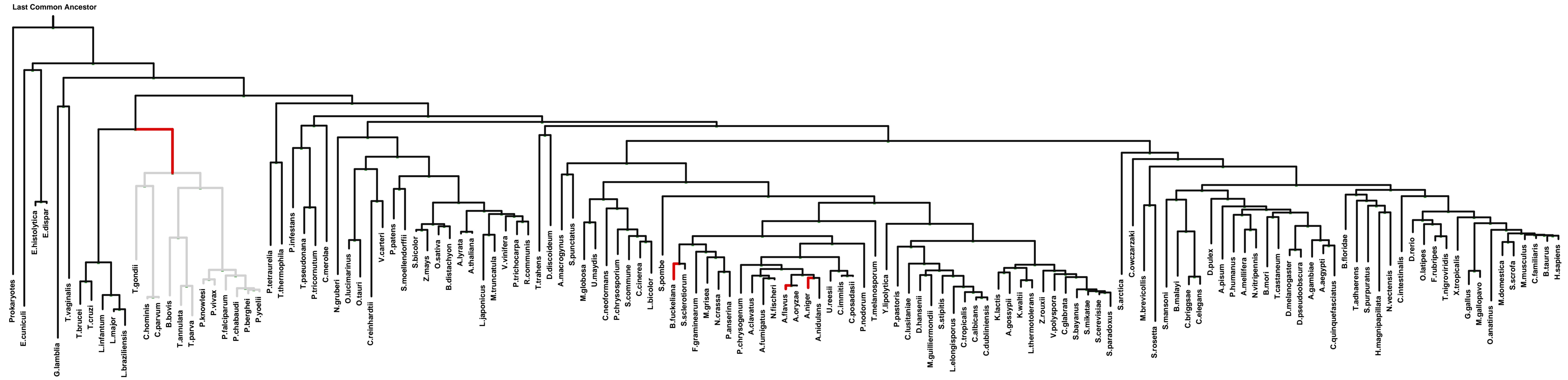
Num of ECM Genes: 1. Num of Predicted Genes: 64



1: basolateral plasma membrane || 2: early phagosome || 3: endolysosome membrane || 4: endosome || 5: endosome membrane || 6: lysosome || 7: catalytic step 2 spliceosome || 8: spliceosomal complex || 9: U12-type spliceosomal complex || 10: chromosome, telomeric region || 11: condensed nuclear chromosome || 12: Mre11 complex || 13: nuclear chromatin || 14: proteasome complex || 15: CCR4-NOT complex || 16: cytoplasmic mRNA processing body || 17: Golgi lumen || 18: lysosomal lumen || 19: proteinaceous extracellular matrix || 20: early endosome || 21: chromosome || 22: zeta DNA polymerase complex || 23: ribonucleoprotein complex || 24: BRCA1-A complex || 25: BRCA1-BARD1 complex ||

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

Num of ECM Genes: 1. Num of Predicted Genes: 64

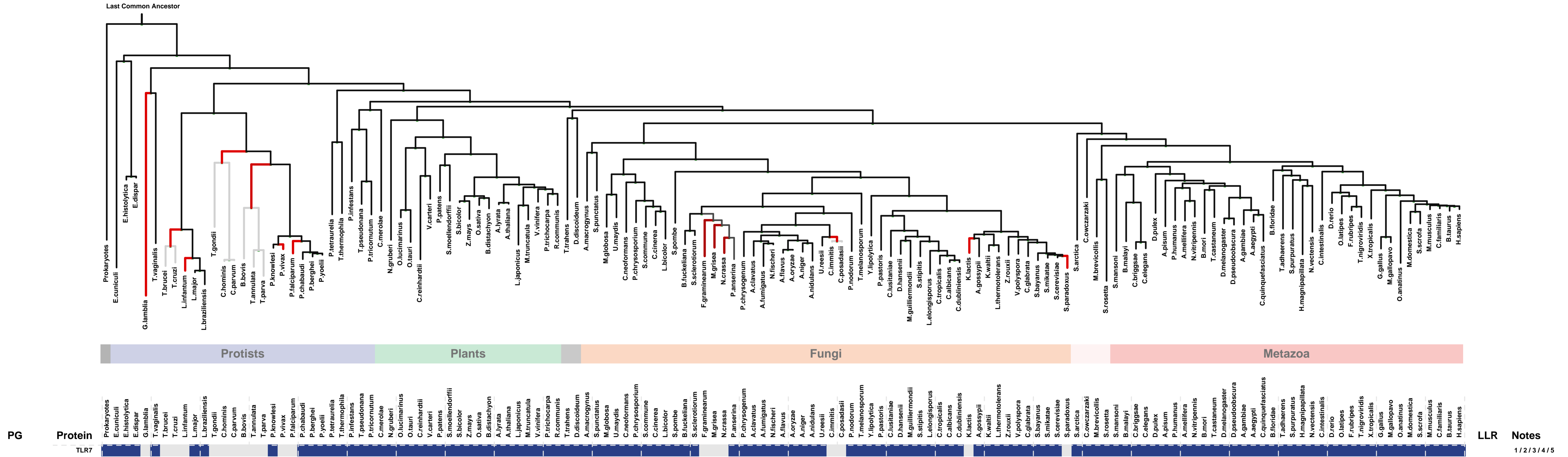


PG	Protein	Protists	Plants	Fungi	Metazoa	LLR	Notes
F	AKR1C1					3.6	
	ACPP					3.2	1 / 2 / 3 / 4 / 5 / 6
	PELO					3.2	
A	LRR59					3.2	7
A	LRCH2					2.9	
	SEL1L2					2.8	
B	TRIM21					2.7	8 / 9 / 10
	SRR					2.7	1
	GNAT2					2.6	11 / 12 / 13 / 14 / 15
	NMD3					2.6	
	DDX23					2.5	16 / 17
	FIP1L1					2.3	18
F	AKR1E2					2.3	
F	LRR28					2.3	
F	AKR1B15					2.3	
B	TRIM73					2.2	
	RBKS					2.0	
	NIP7					1.6	
A	LRCH3					1.6	
	STX2					1.4	19 / 20 / 21 / 22 / 23
A	LRCH1					1.1	
	PGLS					1.0	
E	100293539					1.0	
	PCGF1					0.8	24
	NLRP1					0.8	25
A	LRG1					0.6	
A	PHLPP2					0.4	
A	LRR40					0.3	
A	IGFALS					0.1	
	TMEM30A					0.0	

1: apical part of cell || 2: filopodium || 3: Golgi cisterna || 4: lysosomal membrane || 5: multivesicular body || 6: secretory granule || 7: mitochondrial nucleoid || 8: cytoplasmic mRNA processing body || 9: ribonucleoprotein complex || 10: SCF ubiquitin ligase complex || 11: extrinsic to internal side of plasma membrane || 12: heterotrimeric G-protein complex || 13: photoreceptor inner segment || 14: photoreceptor outer segment || 15: photoreceptor outer segment membrane || 16: catalytic step 2 spliceosome || 17: U5 snRNP || 18: mRNA cleavage and polyadenylation specificity factor complex || 19: basolateral plasma membrane || 20: cell-cell junction || 21: membrane raft || 22: midbody || 23: transport vesicle || 24: PcG protein complex || 25: NLRP1 inflammasome complex

ECM 3, Gene set "endolysosome membrane", Page 1

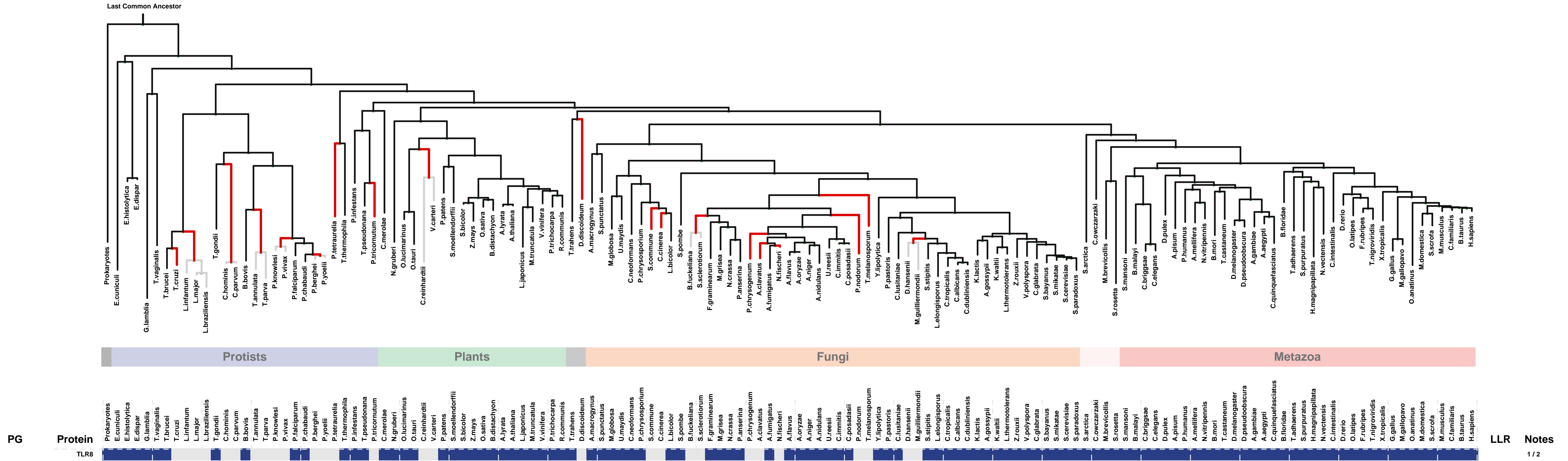
Num of ECM Genes: 1. Num of Predicted Genes: 0



1: early phagosome || 2: endolysosome membrane || 3: endosome || 4: endosome membrane || 5: lysosome

ECM 4, Gene set "endolysosome membrane", Page 1

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



1: endolysosome membrane || 2: endosome membrane