

# 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:

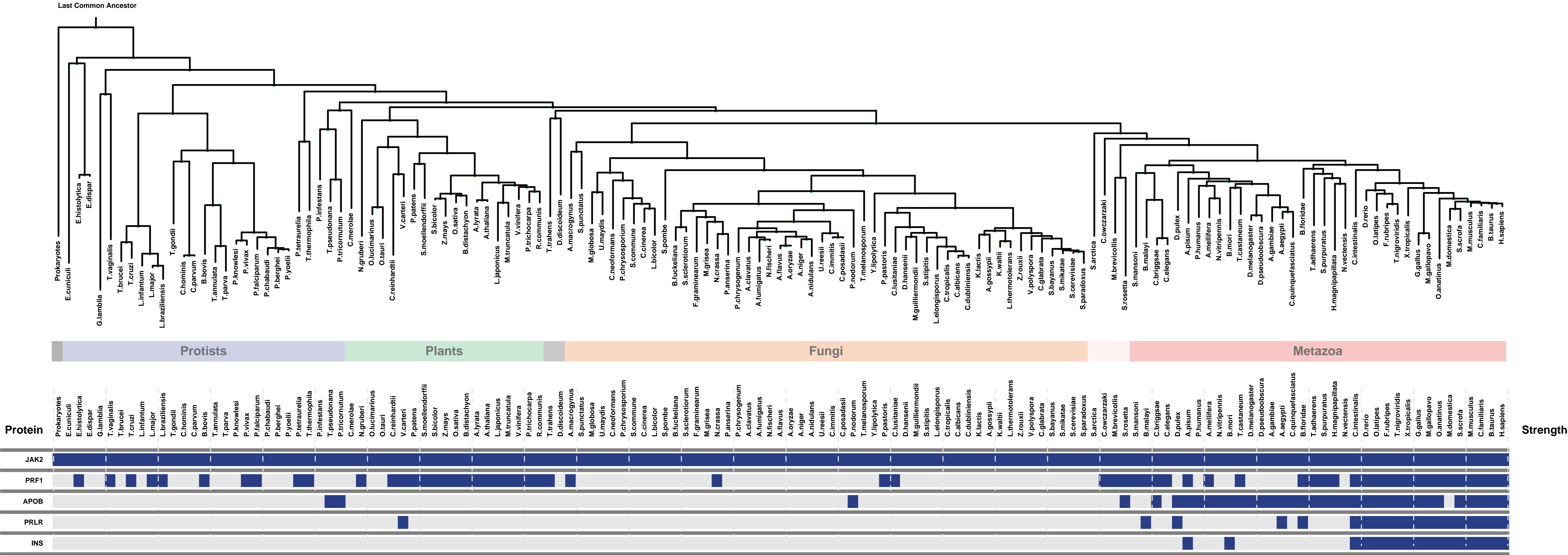
### 1) Overview of Evolutionarily Conserved Modules (ECMs)

- 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+

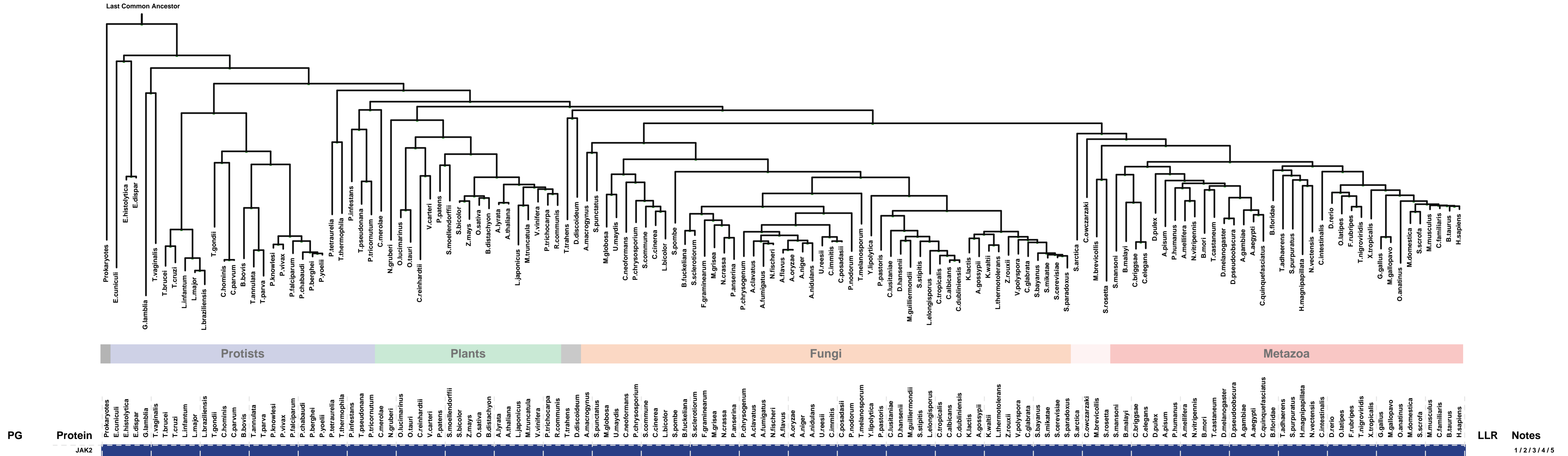
- Top panel shows the inferred evolutionary history on the predefined species tree. Branch color shows the gain event (blue) and loss events (red color, with brighter color indicating higher confidence in loss). Branches before the gain or after a loss are shown in gray.
- Bottom panel shows the input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

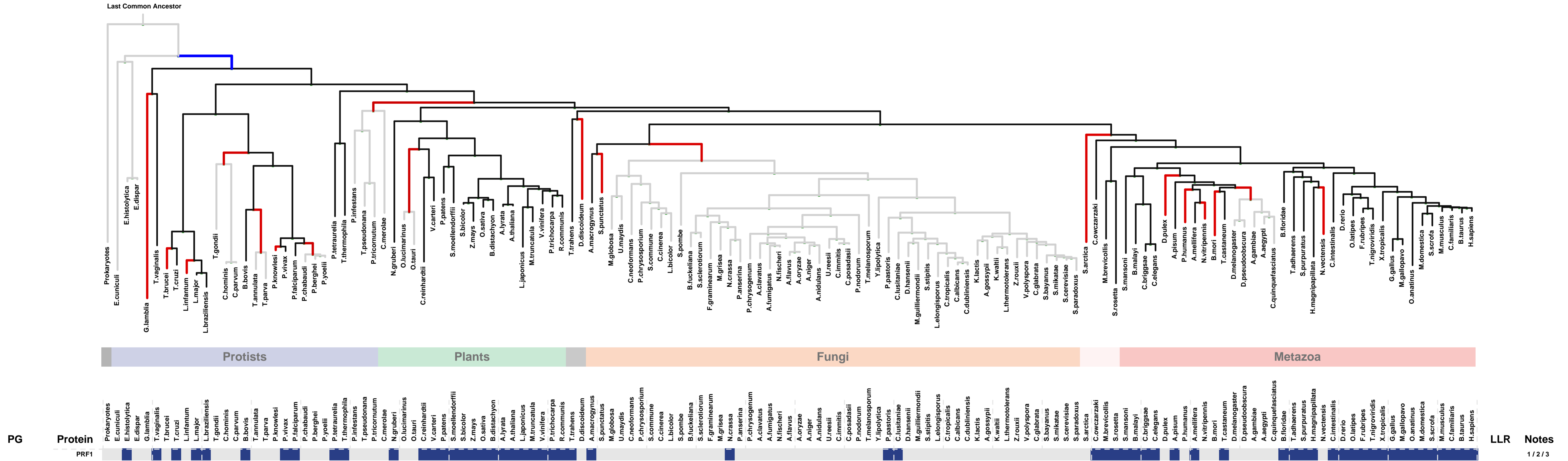
Num of ECM Genes: 1. Num of Predicted Genes: 0



1: caveola || 2: endomembrane system || 3: endosome lumen || 4: membrane raft || 5: nuclear matrix

ECM 2, Gene set "endosome lumen", Page 1

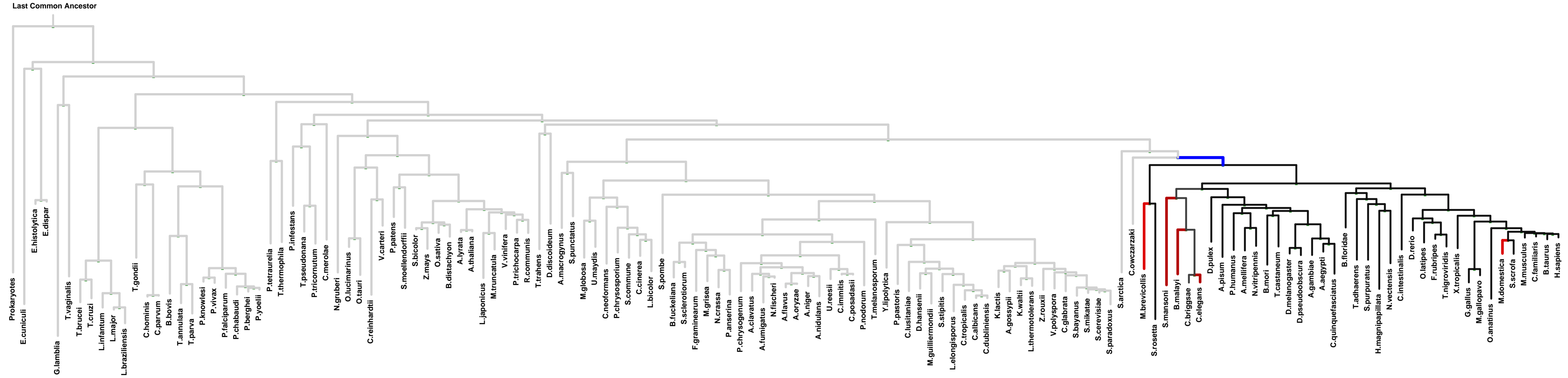
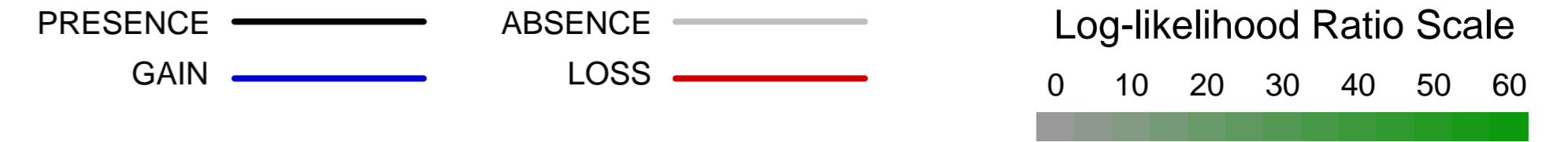
Num of ECM Genes: 1. Num of Predicted Genes: 0



1: cytotytic granule || 2: cytoplasmic membrane-bounded vesicle || 3: endosome lumen

ECM 3, Gene set "endosome lumen", Page 1

Num of ECM Genes: 1. Num of Predicted Genes: 9

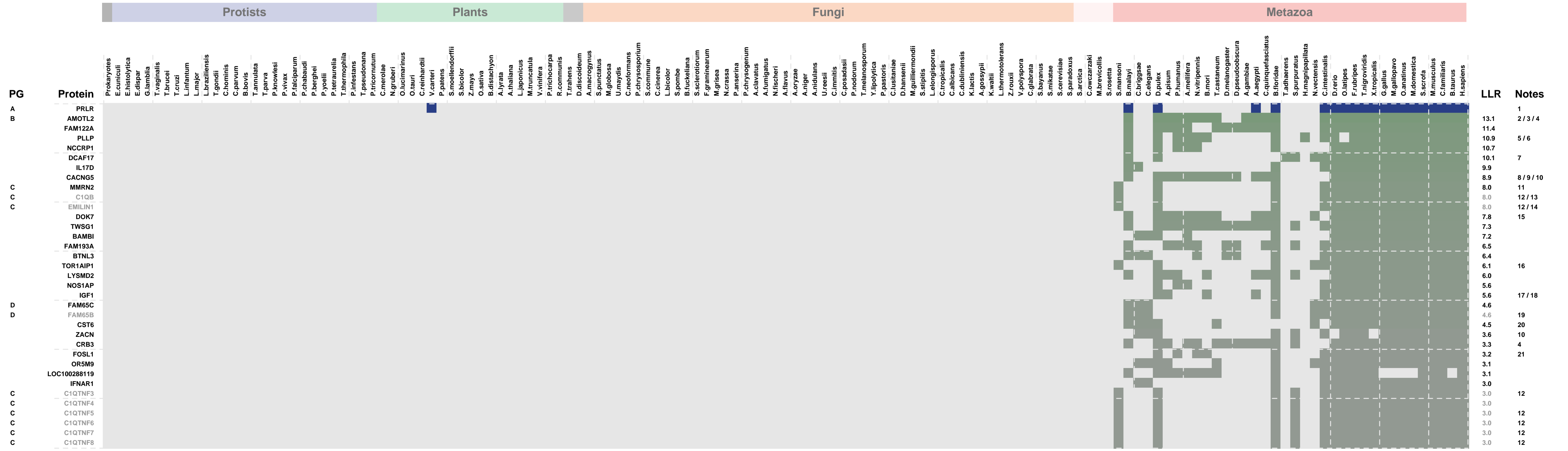
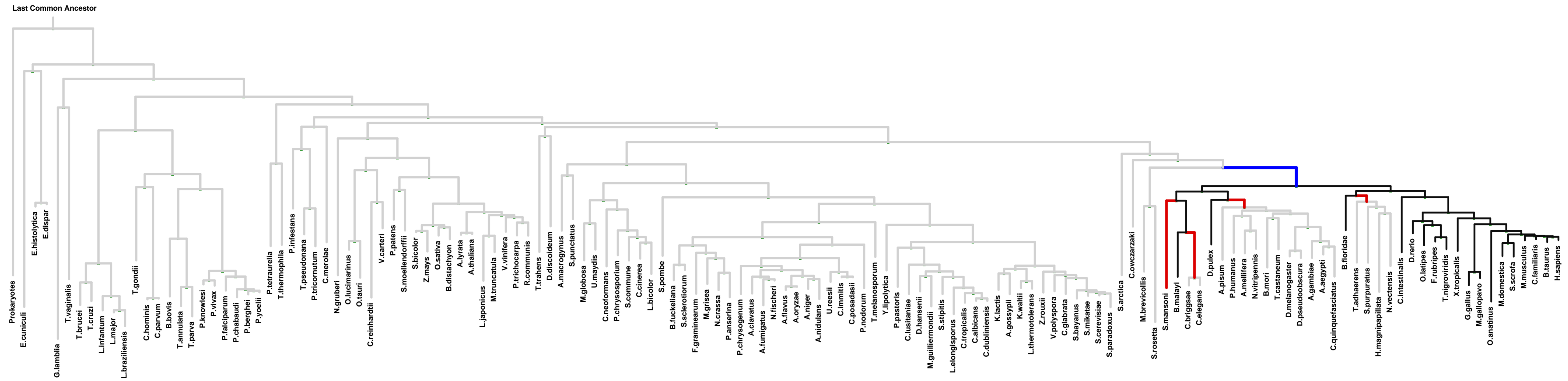


PG	Protein	LLR	Notes
	APOB	3.5	1/2/3/4/5/6/7/8/9/10/11/12/13/14/15/16
	PRG2	10	
	MMACHC	3.4	
A	ATP1B2	0.8	
A	ATP1B3	0.8	11/12/13
B	MUC5B	0.2	14
B	MUC6	0.2	14
B	OTOG	0.2	15
B	MUC5AC	0.2	14/16
B	100510563	0.2	

1: chylomicron || 2: clathrin-coated endocytic vesicle membrane || 3: endoplasmic reticulum lumen || 4: endosome lumen || 5: endosome membrane || 6: intermediate-density lipoprotein particle || 7: low-density lipoprotein particle || 8: very-low-density lipoprotein particle || 9: vesicle lumen || 10: transport vesicle || 11: caveola || 12: melanosome || 13: sodium:potassium-exchanging ATPase complex || 14: Golgi lumen || 15: proteinaceous extracellular matrix || 16: fibril

# ECM 4, Gene set "endosome lumen", Page 1

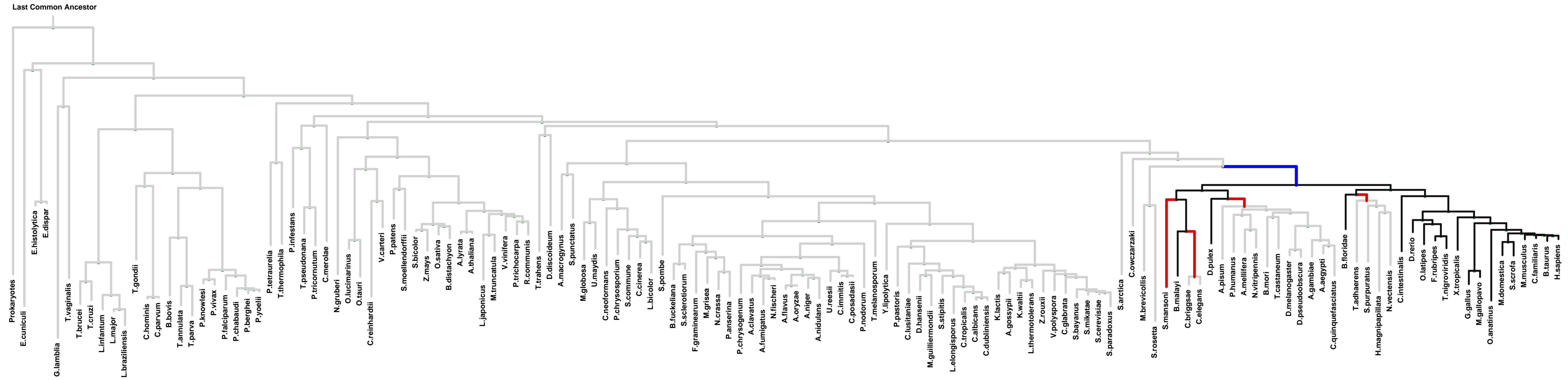
Num of ECM Genes: 1. Num of Predicted Genes: 80



1: endosome lumen || 2: cytoplasmic vesicle || 3: recycling endosome || 4: tight junction || 5: compact myelin || 6: membrane raft || 7: Cul4-RING ubiquitin ligase complex || 8: alpha-amino-3-hydroxy-5-methyl-4-isoxazolepropionic acid selective glutamate receptor complex || 9: postsynaptic density || 10: postsynaptic membrane || 11: basement membrane || 12: collagen || 13: complement component C1 complex || 14: extracellular matrix || 15: neuromuscular junction || 16: nuclear inner membrane || 17: insulin-like growth factor binding protein complex || 18: platelet alpha granule lumen || 19: filopodium || 20: cornified envelope || 21: presynaptic membrane

ECM 4, Gene set "endosome lumen", Page 2

Num of ECM Genes: 1. Num of Predicted Genes: 80

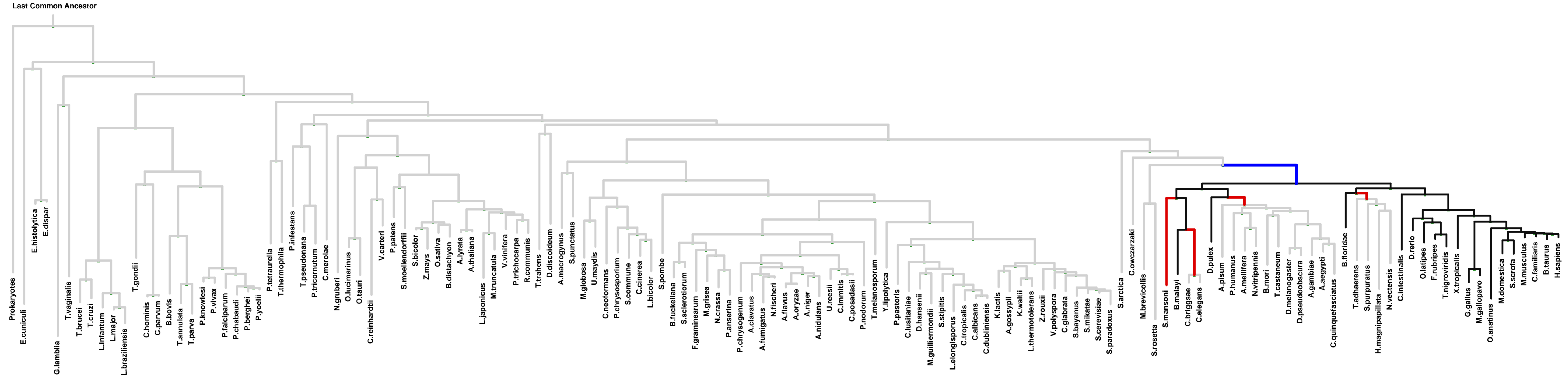


PG	Protein	LLR	Notes
C	C1QC	3.0	1
C	CBLN2	3.0	
C	CBLN3	3.0	
C	CBLN4	3.0	
C	COL10A1	3.0	
C	COL8A1	3.0	1/3/4
C	COL8A2	3.0	4/5/6
C	C1QL1	3.0	1/4/5/6/7
C	C1QL2	3.0	
C	TEDDM1	3.0	
C	C1QL3	3.0	
C	C1QL4	3.0	
C	C1QTNF2	3.0	
E	PHYHIPL	2.9	
E	PHYHIP	2.9	
C	CBLN1	2.8	2
B	AMOT	2.7	8/9/10/11/12/13/14
B	AMOTL1	2.7	11/13/15/16
F	TMIE	2.6	
F	CICP25	2.5	
A	TMEM211	2.0	
A	EBI3	1.9	
G	INTS10	1.8	17
G	NR0B2	1.8	
G	LYPD6B	1.6	18
G	LYPD6	1.6	
G	LILRA3	1.6	
G	TMEM200A	1.4	
G	ZNF488	1.3	
G	LOC728715	1.3	
F	LOC728715	1.3	
F	LOC100288119	1.2	
H	TNFSF12-TNFSF13	1.2	
H	TNFSF13	1.2	
F	CICP23	1.1	10

1: collagen || 2: synapse || 3: cell cortex || 4: endoplasmic reticulum lumen || 5: basement membrane || 6: extracellular matrix || 7: proteinaceous extracellular matrix || 8: actin filament || 9: endocytic vesicle || 10: external side of plasma membrane || 11: lamellipodium || 12: ruffle || 13: signalosome || 14: stress fiber || 15: tight junction || 16: cytoplasmic vesicle || 17: integrator complex || 18: anchored to membrane

ECM 4, Gene set "endosome lumen", Page 3

Num of ECM Genes: 1. Num of Predicted Genes: 80



PG	Protein	Prokaryotes	Protists	Plants	Fungi	Metazoa	LLR	Notes
F	LOC100505953						1.1	
	POLR3G						1.0	1
	PANX2						0.9	2
	IGSF5						0.9	3
	PID1						0.9	
	IL1RL2						0.8	
	HSPB9						0.7	
	ATP6V1G2						0.6	4/5
	TJAP1						0.5	3
	EPN2						0.5	
	CDC42EP4						0.2	6/7/8

1: DNA-directed RNA polymerase III complex || 2: gap junction || 3: tight junction || 4: melanosome || 5: vacuolar proton-transporting V-type ATPase complex || 6: actin cytoskeleton || 7: endomembrane system || 8: microtubule cytoskeleton



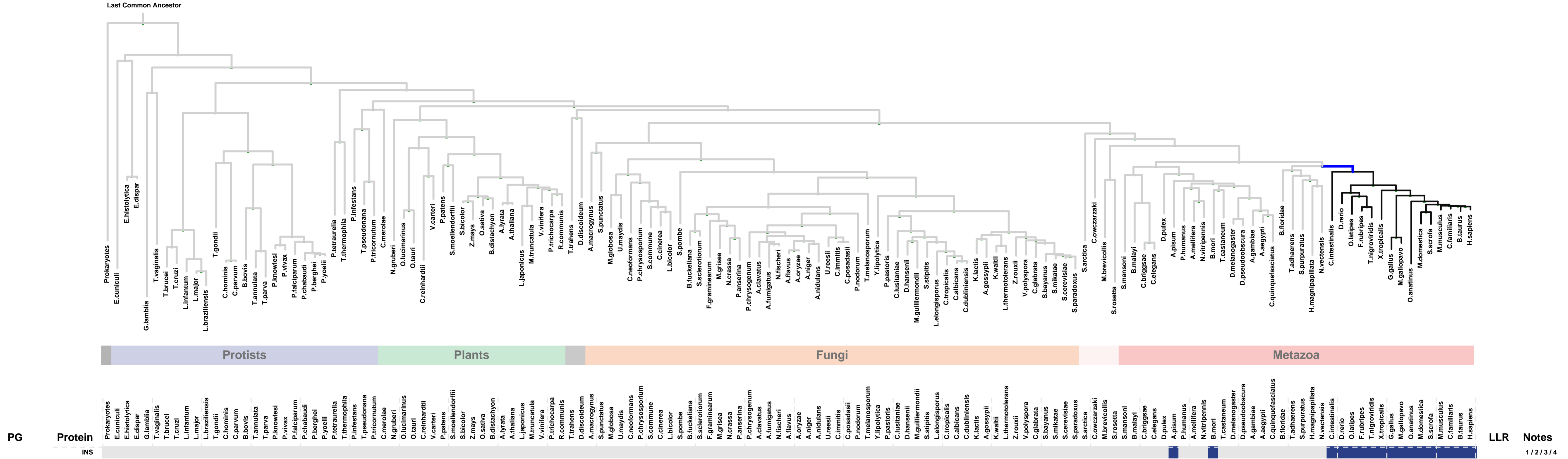
ECM 5, Gene set "endosome lumen", Page 1

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

PRESENCE ——— ABSENCE ———  
GAIN ——— LOSS ———

Log-likelihood Ratio Scale

0 10 20 30 40 50 60



1: endoplasmic reticulum lumen || 2: endosome lumen || 3: Golgi lumen || 4: secretory granule