

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

## Dataset:

Num of genes in input gene set: 10  
Total number of genes: 20834  
Prediction LLR threshold: 0

The CLIME PDF output two sections:

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

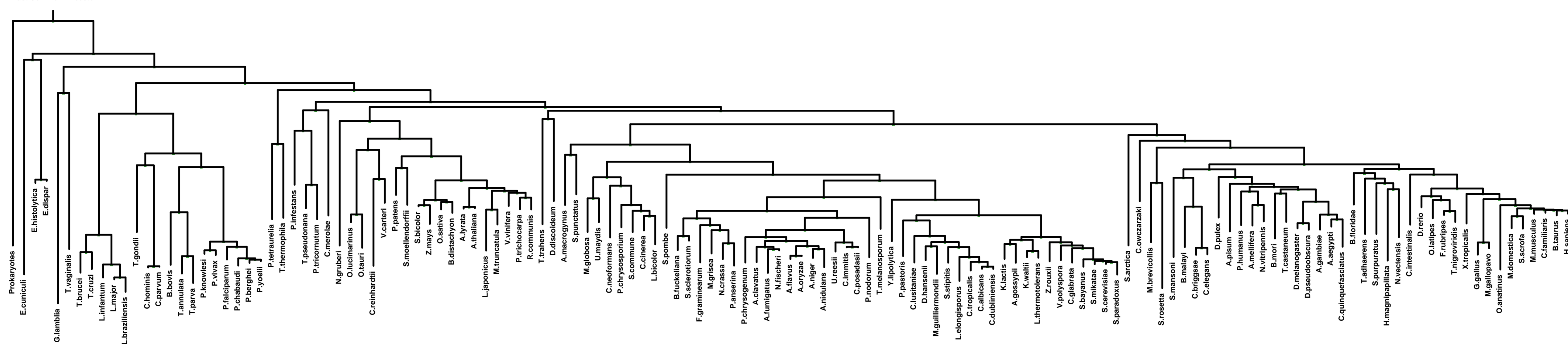
- Top panel shows the predefined species tree.
- Bottom panel shows the partition of input genes into Evolutionary Conserved Modules (ECMs), ordered by ECM strength (shown at right), and separated by horizontal lines.
- Each row show one gene, where the phylogenetic profile indicates presence (blue) 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)

Last Common Ancestor

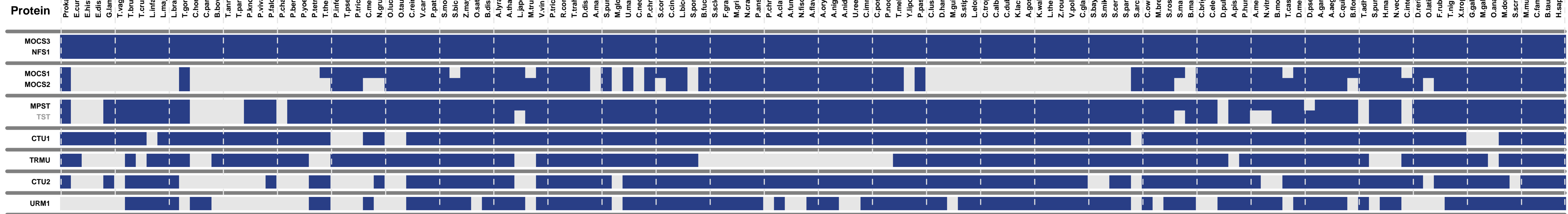


Protists

Plants

Fungi

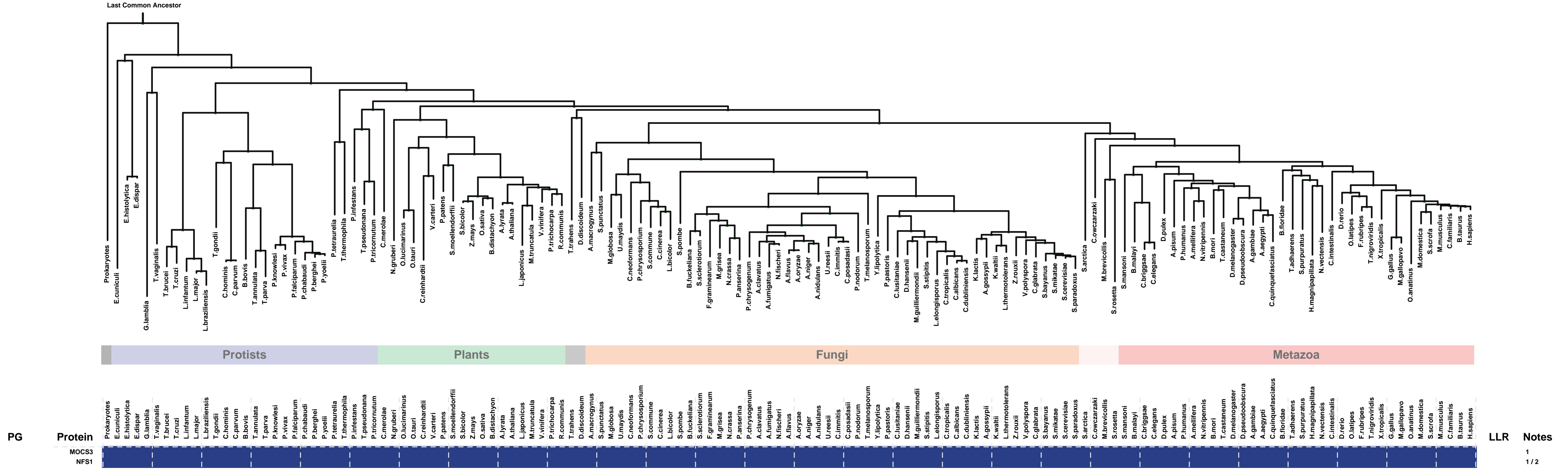
Metazoa



Strength

ECM 1, Gene set "Sulfur relay system", Page 1

Num of ECM Genes: 2. Num of Predicted Genes: 0. ECM Strength: 0.0

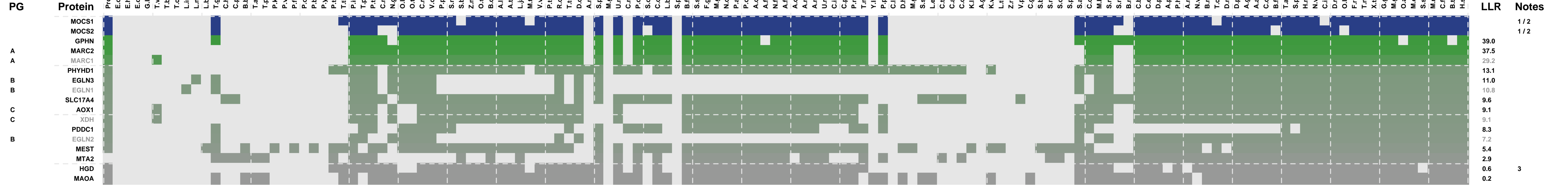
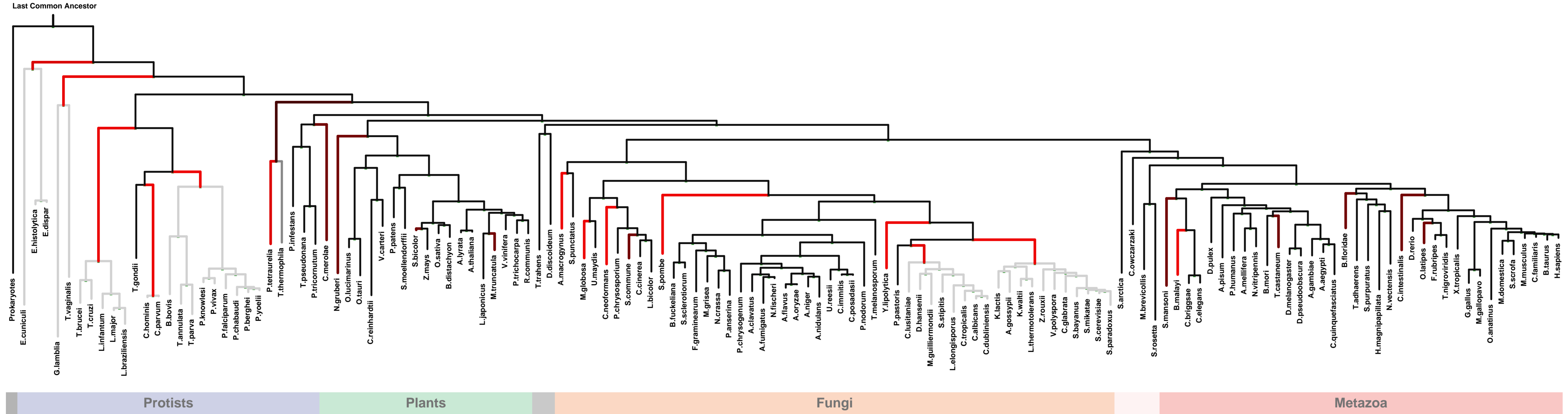
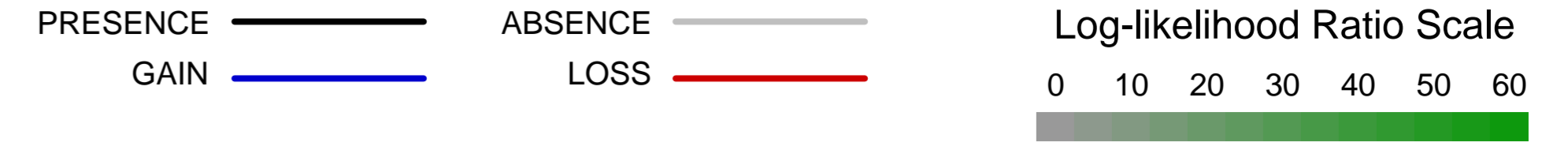


1: Sulfur relay system || 2: Thiamine metabolism

LLR Notes  
1  
1/2

ECM 2, Gene set "Sulfur relay system", Page 1

Num of ECM Genes: 2. Num of Predicted Genes: 15. ECM Strength: 0.0



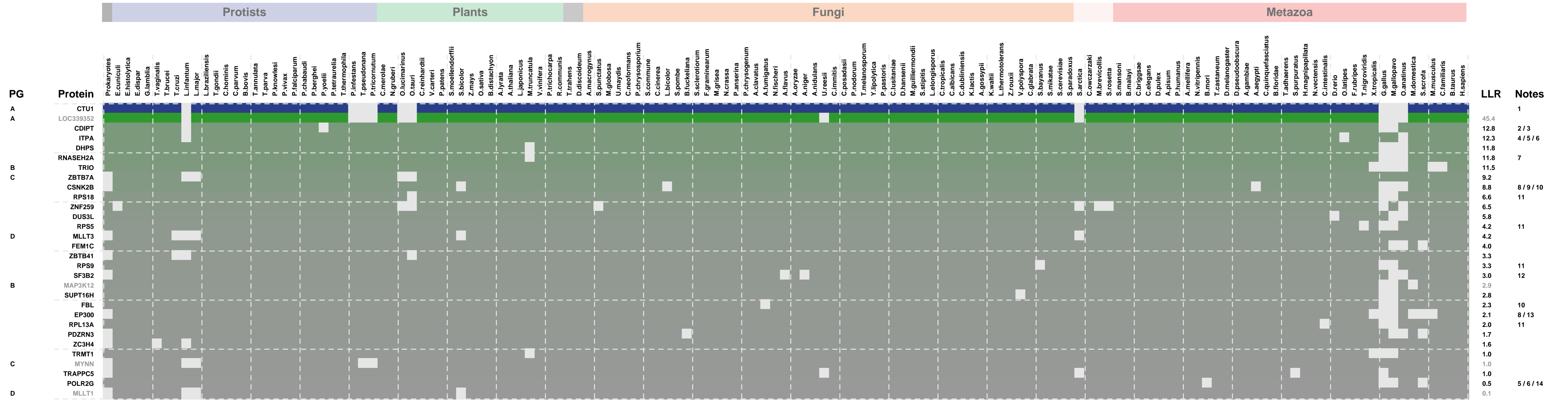
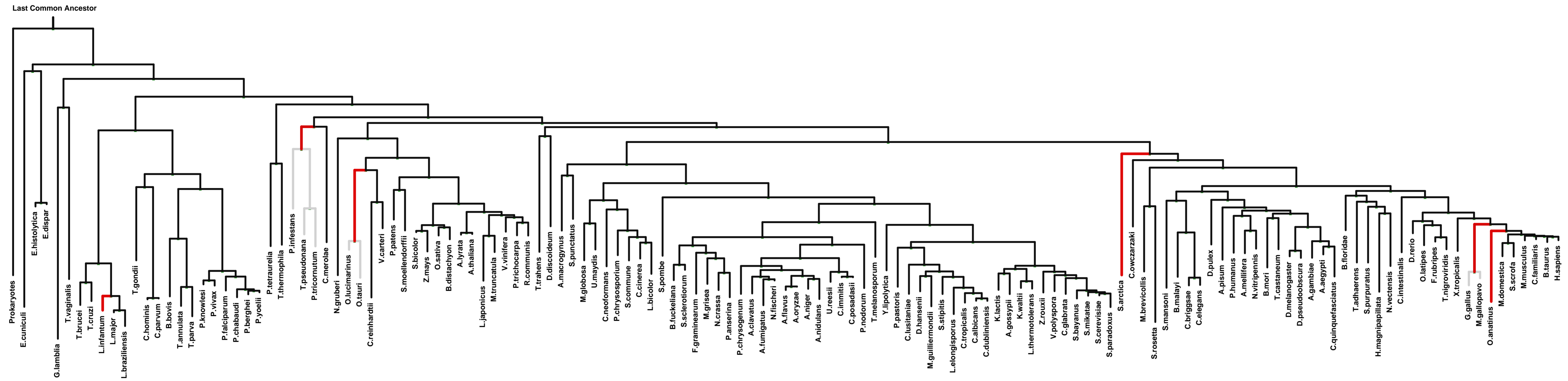
1: Folate biosynthesis || 2: Sulfur relay system || 3: Tyrosine metabolism





ECM 4, Gene set "Sulfur relay system", Page 1

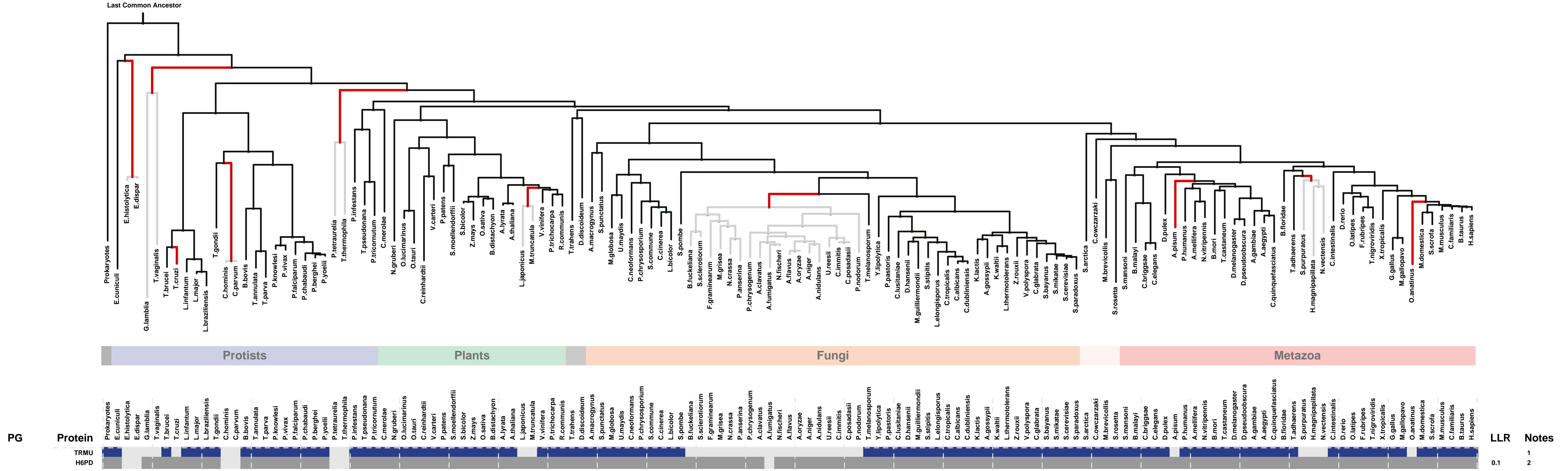
Num of ECM Genes: 1. Num of Predicted Genes: 29



1: Sulfur relay system || 2: Inositol phosphate metabolism || 3: Glycerophospholipid metabolism || 4: Drug metabolism - other enzymes || 5: Purine metabolism || 6: Pyrimidine metabolism || 7: DNA replication || 8: Adherens junction || 9: Tight junction || 10: Ribosome biogenesis in eukaryotes || 11: Ribosome || 12: Spliceosome || 13: Cell cycle || 14: RNA polymerase

ECM 5, Gene set "Sulfur relay system", Page 1

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

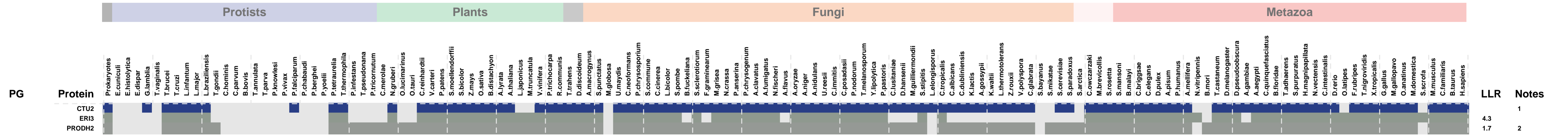
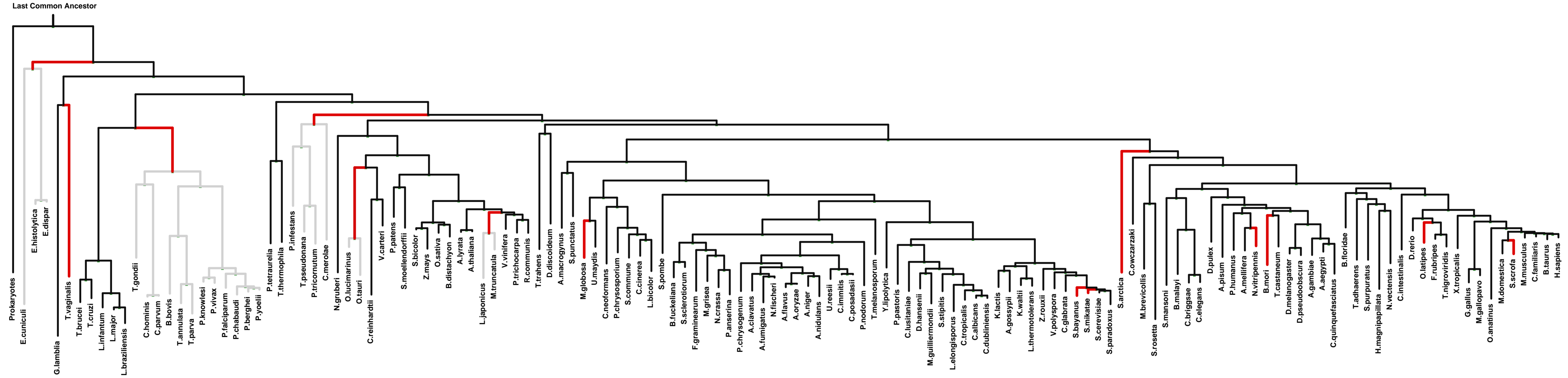


1: Sulfur relay system || 2: Pentose phosphate pathway



ECM 6, Gene set "Sulfur relay system", Page 1

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



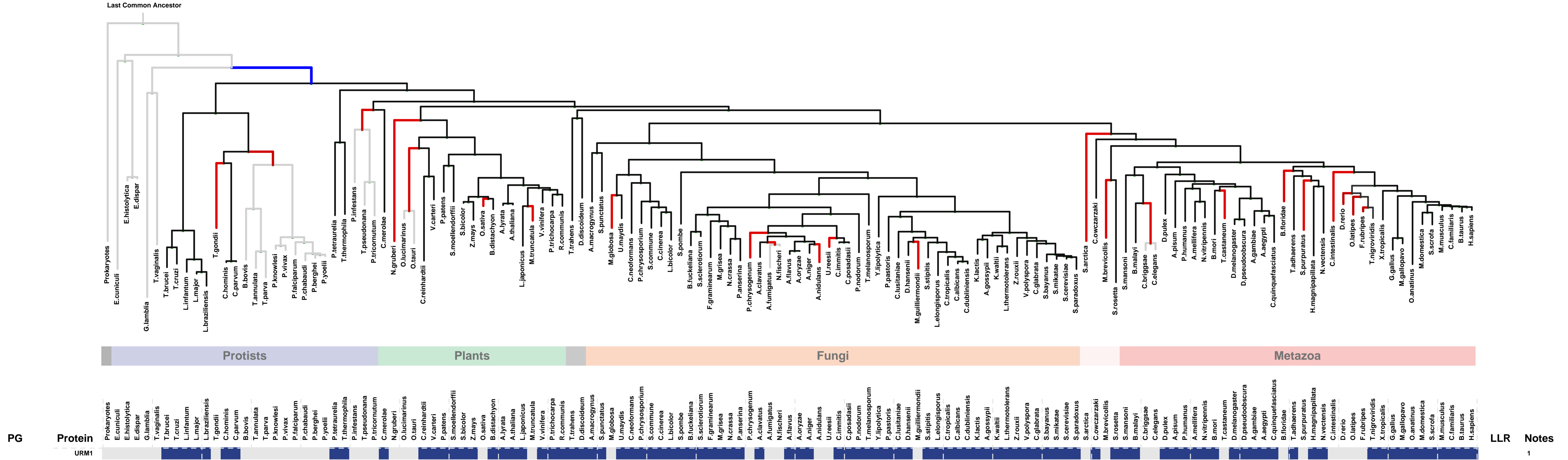
1: Sulfur relay system || 2: Arginine and proline metabolism

LLR	Notes
1	
4.3	
1.7	



ECM 7, Gene set "Sulfur relay system", Page 1

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



1: Sulfur relay system