

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

## Dataset:

Num of genes in input gene set: 2  
Total number of genes: 20834  
Prediction LLR threshold: 0

The CLIME PDF output two sections:

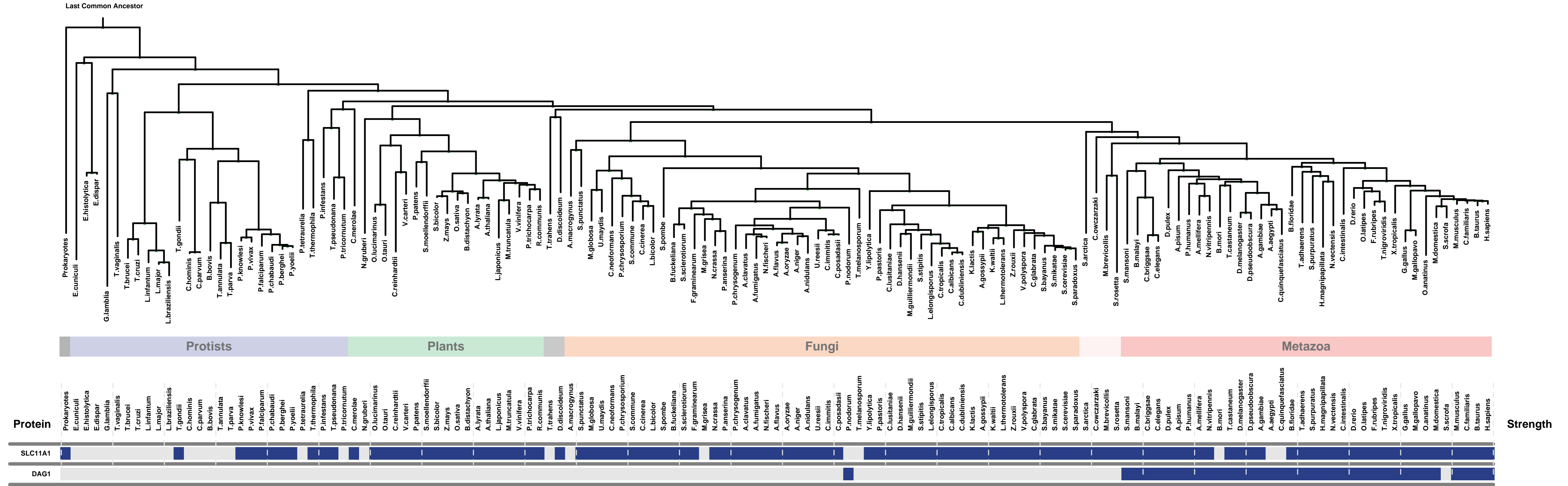
### 1) Overview of Evolutionarily Conserved Modules (ECMs)

- 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+

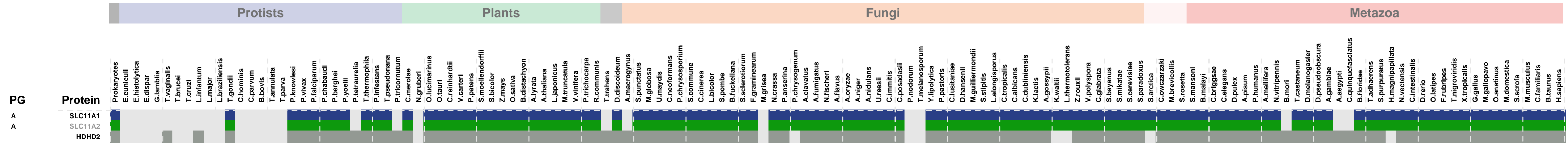
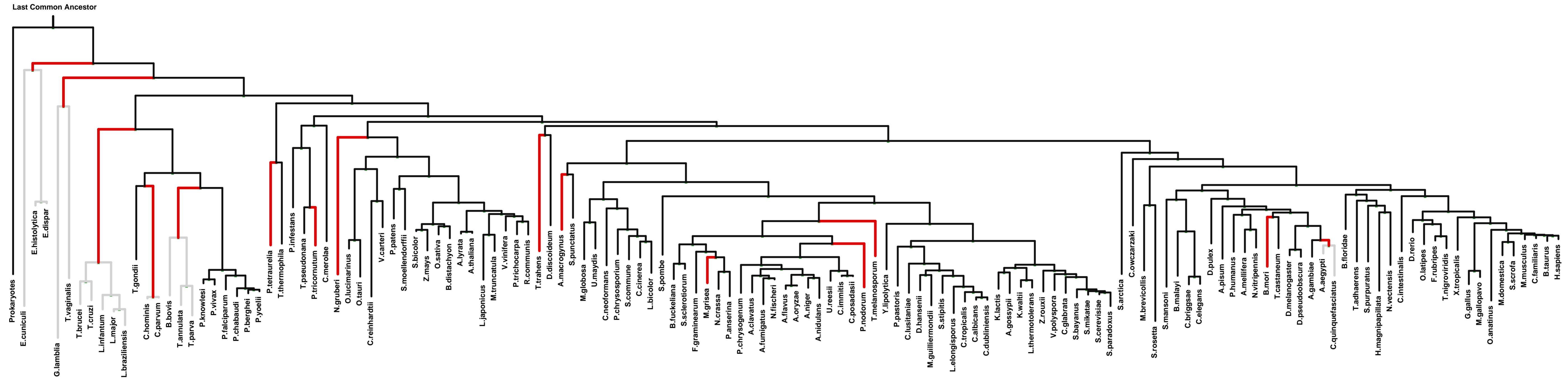
- Top panel shows the inferred evolutionary history on the predefined species tree. Branch color shows the gain event (blue) and loss events (red color, with brighter color indicating higher confidence in loss). Branches before the gain or after a loss are shown in gray.
- Bottom panel shows the input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

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

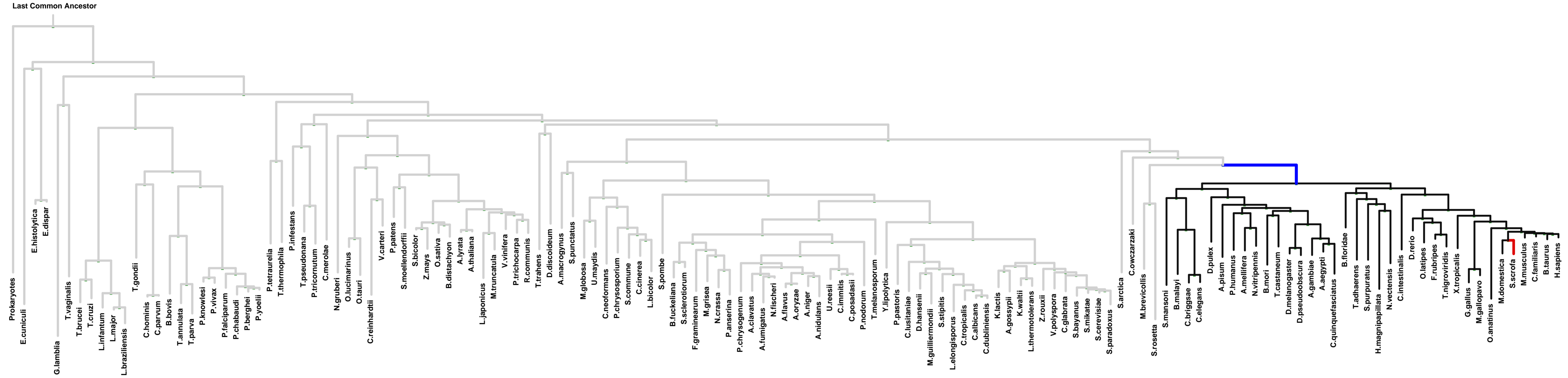


LLR 83.5  
Notes 1/2/3/4/5  
2/3/4/6/7/8/9/10/11/12/13/14/15

- 1: cell outer membrane || 2: late endosome || 3: late endosome membrane || 4: lysosome || 5: phagocytic vesicle membrane || 6: apical part of cell || 7: basal part of cell || 8: brush border || 9: cytoplasmic vesicle || 10: early endosome ||
- 11: endomembrane system || 12: lysosomal membrane || 13: recycling endosome || 14: trans-Golgi network || 15: vacuole

ECM 2, Gene set "cell outer membrane", Page 1

Num of ECM Genes: 1. Num of Predicted Genes: 3



PG	Protein	LLR	Notes
	DAG1		
	ATP5J	2.6	1/2/3/4/5/6/7/8/9/10/11/12/13/14/15
	CBFB	2.3	14/15
	LDLRAD1	1.1	

- 1: basement membrane || 2: cell outer membrane || 3: cell-cell adherens junction || 4: contractile ring || 5: costamere || 6: dystrophin-associated glycoprotein complex || 7: filopodium || 8: focal adhesion || 9: lamellipodium || 10: membrane raft || 11: node of Ranvier || 12: postsynaptic membrane || 13: sarcolemma || 14: mitochondrial proton-transporting ATP synthase complex || 15: mitochondrial proton-transporting ATP synthase complex, coupling factor F(o)