

# 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)

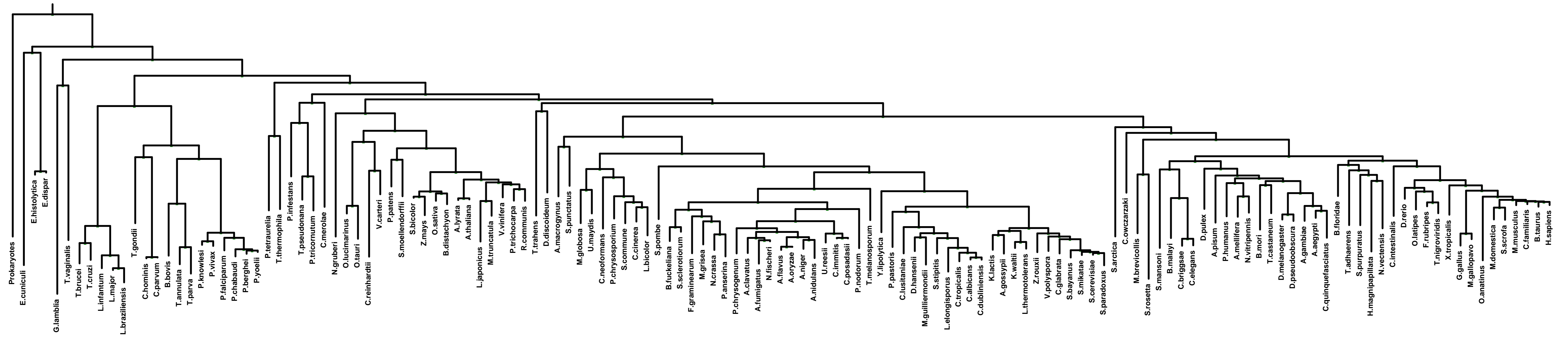
- Top panel shows the predefined species tree.
- Bottom panel shows the partition of input genes into Evolutionary Conserved Modules (ECMs), ordered by ECM strength (shown at right), and separated by horizontal lines.
- Each row show one gene, where the phylogenetic profile indicates presence (blue)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

Last Common Ancestor

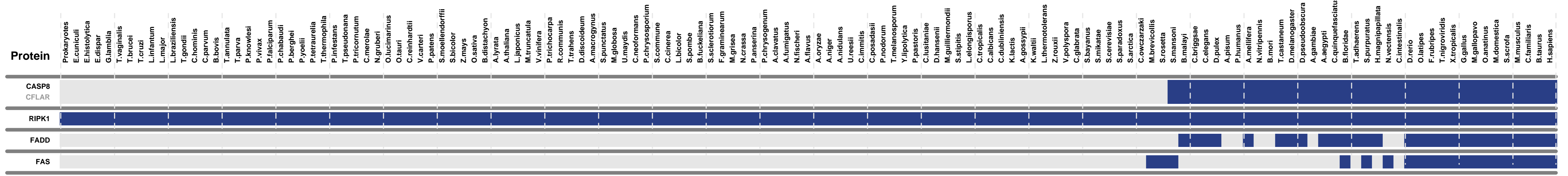


Protists

Plants

Fungi

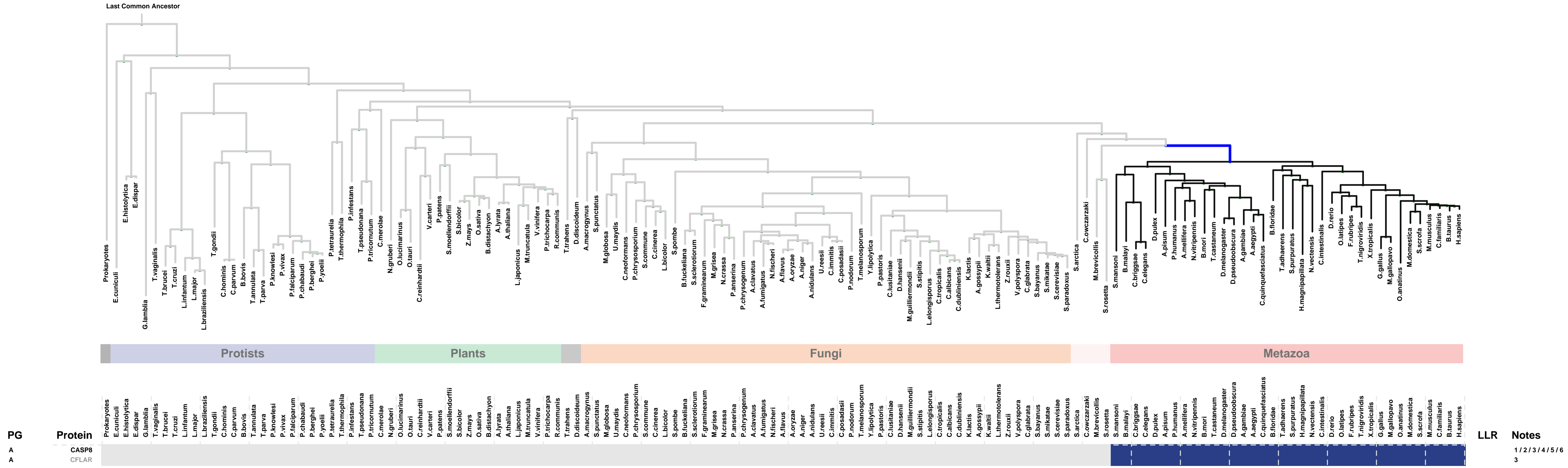
Metazoa



Strength

# ECM 1, Gene set "death-inducing signaling complex", Page 1

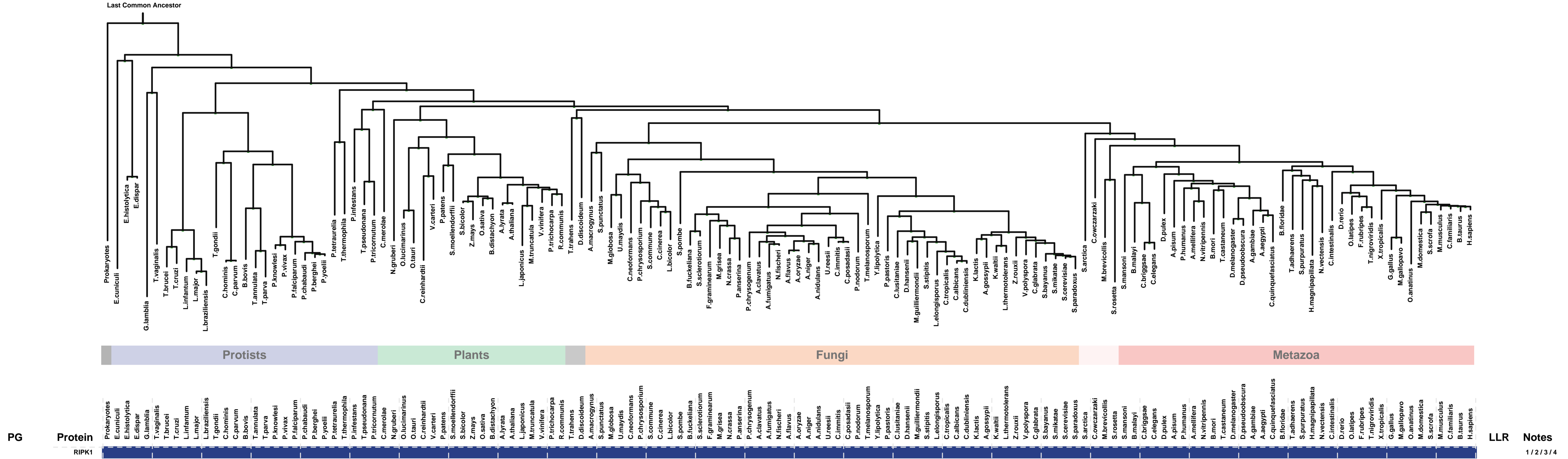
Num of ECM Genes: 2. Num of Predicted Genes: 0. ECM Strength: 0.0



1: CD95 death-inducing signaling complex || 2: cell body || 3: death-inducing signaling complex || 4: membrane raft || 5: mitochondrial outer membrane || 6: neuron projection

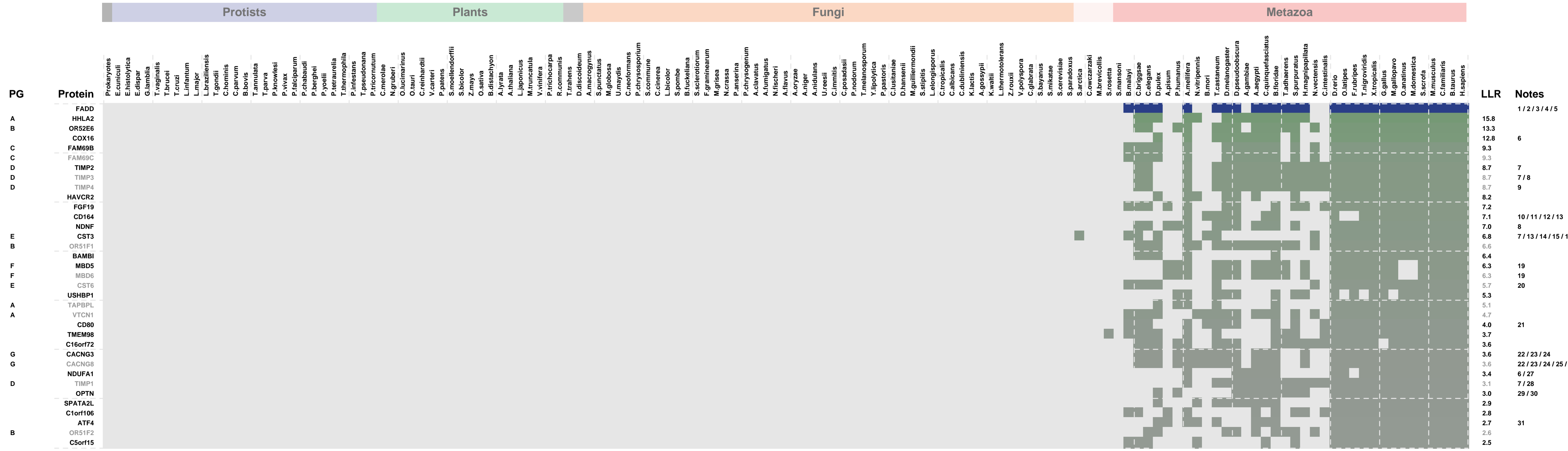
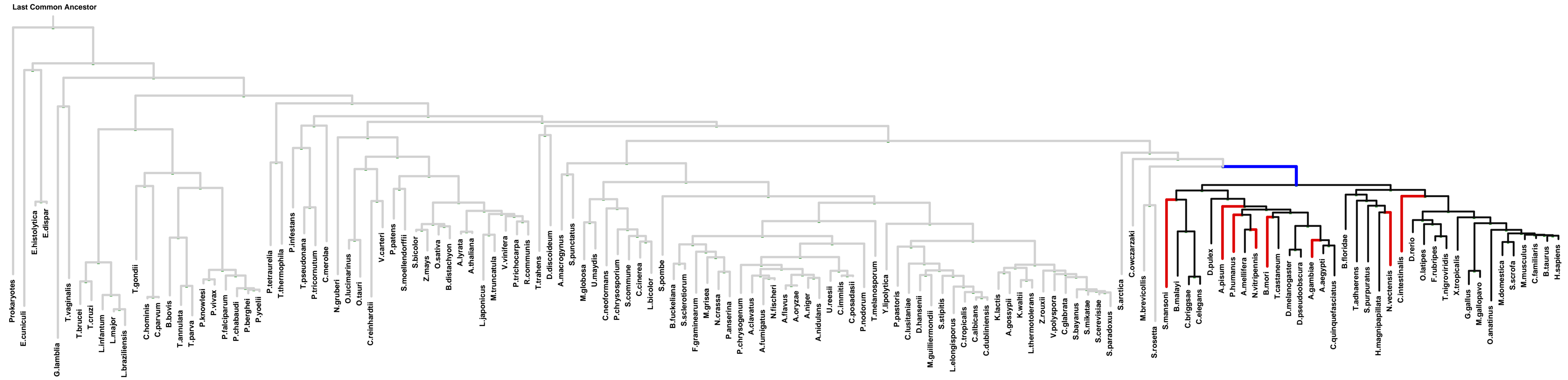
ECM 2, Gene set "death-inducing signaling complex", Page 1

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



# ECM 3, Gene set "death-inducing signaling complex", Page 1

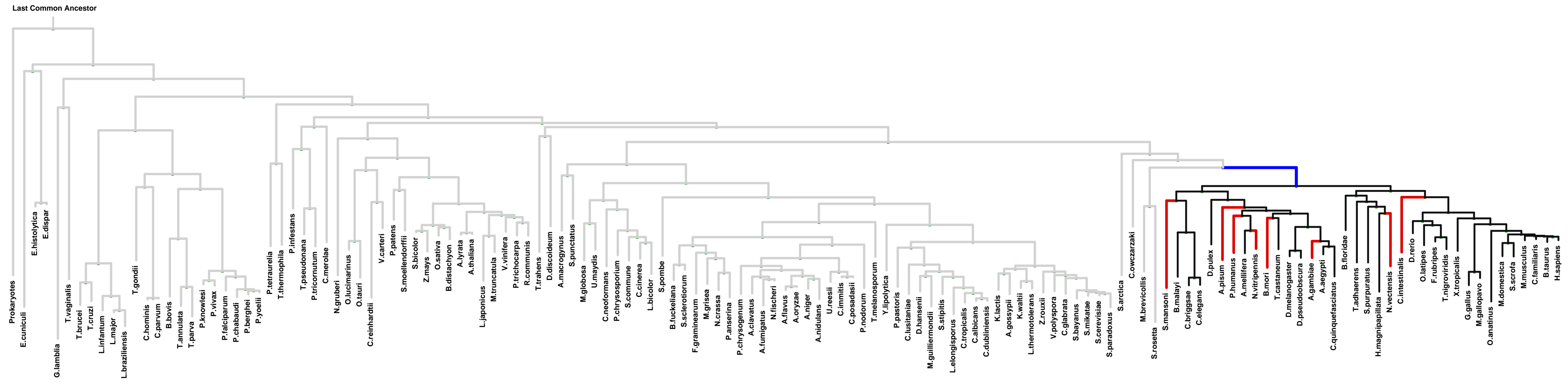
Num of ECM Genes: 1. Num of Predicted Genes: 49



1: CD95 death-inducing signaling complex || 2: cell body || 3: death-inducing signaling complex || 4: membrane raft || 5: neuron projection || 6: mitochondrial membrane || 7: basement membrane || 8: extracellular matrix || 9: sarcomere || 10: endosome || 11: endosome membrane || 12: lysosomal membrane || 13: lysosome || 14: axon part || 15: contractile fiber || 16: multivesicular body || 17: nuclear membrane || 18: vesicle || 19: chromosome || 20: cornified envelope || 21: external side of plasma membrane || 22: alpha-amino-3-hydroxy-5-methyl-4-isoxazolepropionic acid selective glutamate receptor complex || 23: endocytic vesicle membrane || 24: voltage-gated calcium channel complex ||

ECM 3, Gene set "death-inducing signaling complex", Page 2

Num of ECM Genes: 1. Num of Predicted Genes: 49



PG	Protein	Prokaryotes	Protists	Plants	Fungi	Metazoa	LLR	Notes
	CD200R1L						2.2	
	BORA						2.2	
	LECT2						2.1	
	PHYHIPL						1.8	
	PHYHIP						1.8	
	MMS22L						1.6	1 / 2 / 3
	GPRC5C						1.5	4
	APOOL						0.8	
	PTGFRN						0.7	
	FABP6						0.7	
	ARL6IP6						0.7	
	VEGFA						0.5	5 / 6 / 7 / 8
	KTN1						0.3	
	MFN						0.3	
	QSER1						0.1	9 / 10 / 11

1: FACT complex || 2: MCM complex || 3: nuclear replication fork || 4: cytoplasmic vesicle membrane || 5: basement membrane || 6: platelet alpha granule lumen || 7: proteinaceous extracellular matrix || 8: secretory granule || 9: integral to mitochondrial membrane || 10: mitochondrial outer membrane || 11: peroxisome

