

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)

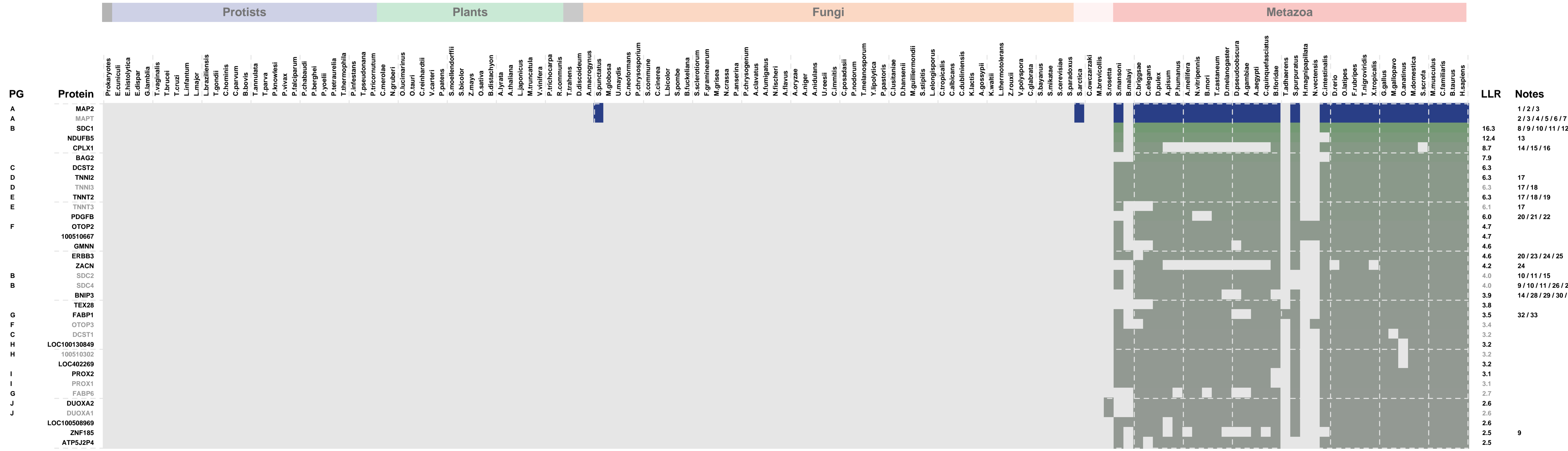
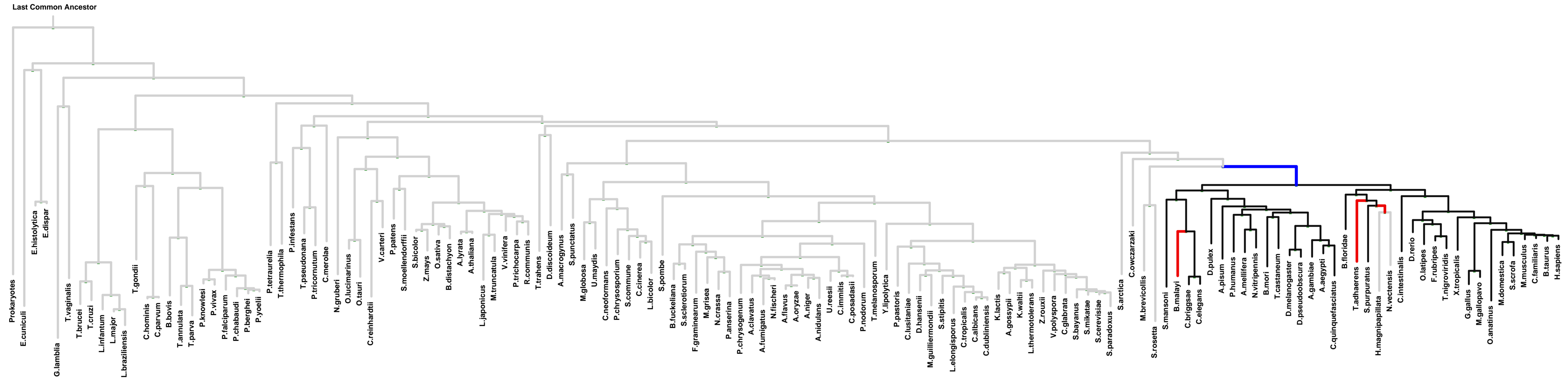
- Top panel shows the predefined species tree.
- Bottom panel shows the partition of input genes into Evolutionary Conserved Modules (ECMs), ordered by ECM strength (shown at right), and separated by horizontal lines.
- Each row show one gene, where the phylogenetic profile indicates presence (blue)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

ECM 1, Gene set "nuclear periphery", Page 1

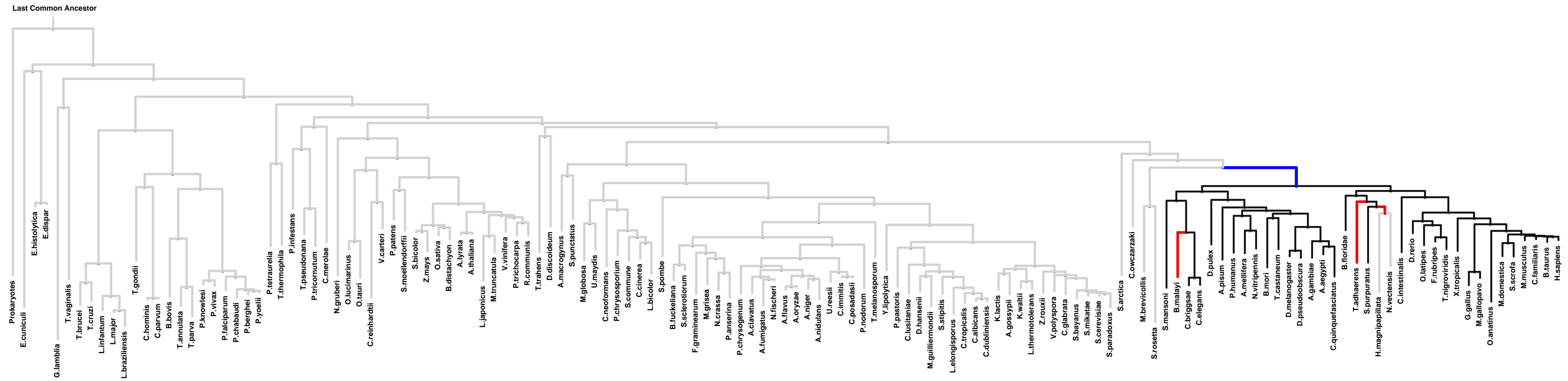
Num of ECM Genes: 2. Num of Predicted Genes: 77. ECM Strength: 3.0



1: dendritic shaft || 2: microtubule associated complex || 3: nuclear periphery || 4: axon || 5: cilium axoneme || 6: growth cone || 7: tubulin complex || 8: external side of plasma membrane || 9: focal adhesion || 10: Golgi lumen || 11: lysosomal lumen || 12: uropod || 13: mitochondrial respiratory chain complex I || 14: dendrite || 15: synapse || 16: synaptobrevin 2-SNAP-25-syntaxin-1a-complexin I complex || 17: troponin complex || 18: sarcomere || 19: striated muscle thin filament || 20: basolateral plasma membrane || 21: endoplasmic reticulum lumen || 22: platelet alpha granule lumen || 23: lateral plasma membrane || 24: postsynaptic membrane || 25: receptor complex ||

ECM 1, Gene set "nuclear periphery", Page 2

Num of ECM Genes: 2. Num of Predicted Genes: 77. ECM Strength: 3.0

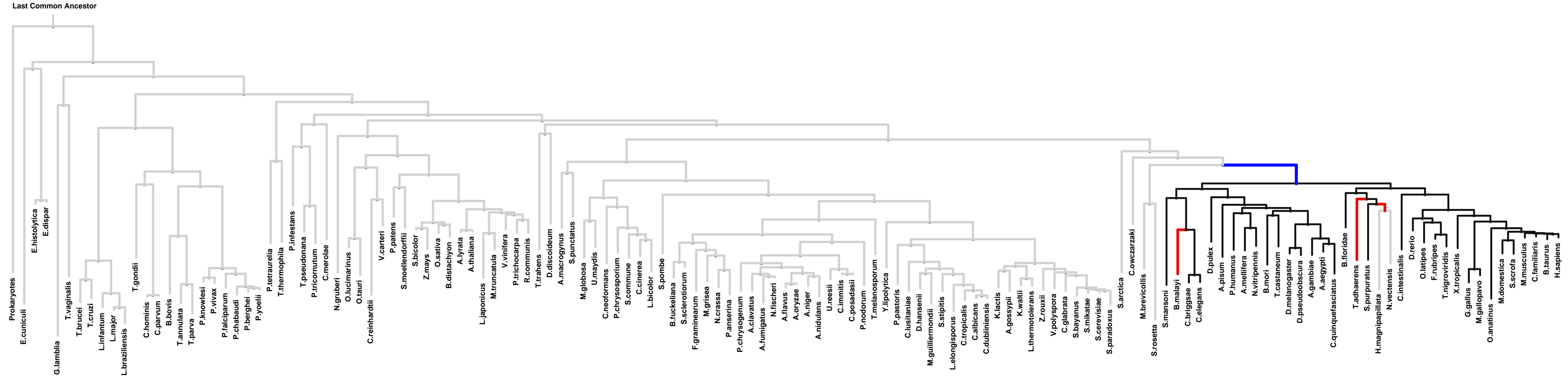


PG	Protein	Protists	Plants	Fungi	Metazoa	LLR	Notes
E	TNNT1					2.4	1
K	OLFML1					1.8	
K	OLFML2A					1.8	
K	OLFML2B					1.8	2
K	OLFML3					1.8	
L	TSC22D2					1.8	
L	TSC22D3					1.8	
M	EFNA1					1.8	3
M	EFNA5					1.8	4/5
D	100508475					1.8	
K	TNNI1					1.8	1
	OLFM2					1.8	
	BAG5					1.6	6
	GPM6B					1.5	7
	FBXO28					1.5	
N	C1QTNF5					1.4	8
N	C1QTNF6					1.4	8
N	C1QTNF7					1.4	8
N	C1QTNF8					1.4	8
	TEDDM1					1.4	
N	CBLN2					1.4	
N	CBLN3					1.4	9
N	CBLN4					1.4	9
N	COL10A1					1.4	8/10/11
N	COL8A1					1.4	2/11/12
N	COL8A2					1.4	2/8/11/12/13
N	C1QC					1.4	8
N	C1QL1					1.4	8
N	C1QL2					1.4	8
N	C1QL3					1.4	8
N	C1QL4					1.4	8
N	C1QTNF2					1.4	8
N	C1QTNF3					1.4	8
N	C1QTNF4					1.4	8
	CCR10					1.3	

1: troponin complex || 2: extracellular matrix || 3: anchored to plasma membrane || 4: anchored to external side of plasma membrane || 5: caveola || 6: inclusion body || 7: membrane raft || 8: collagen || 9: synapse ||
 10: cell cortex || 11: endoplasmic reticulum lumen || 12: basement membrane || 13: proteinaceous extracellular matrix

ECM 1, Gene set "nuclear periphery", Page 3

Num of ECM Genes: 2. Num of Predicted Genes: 77. ECM Strength: 3.0

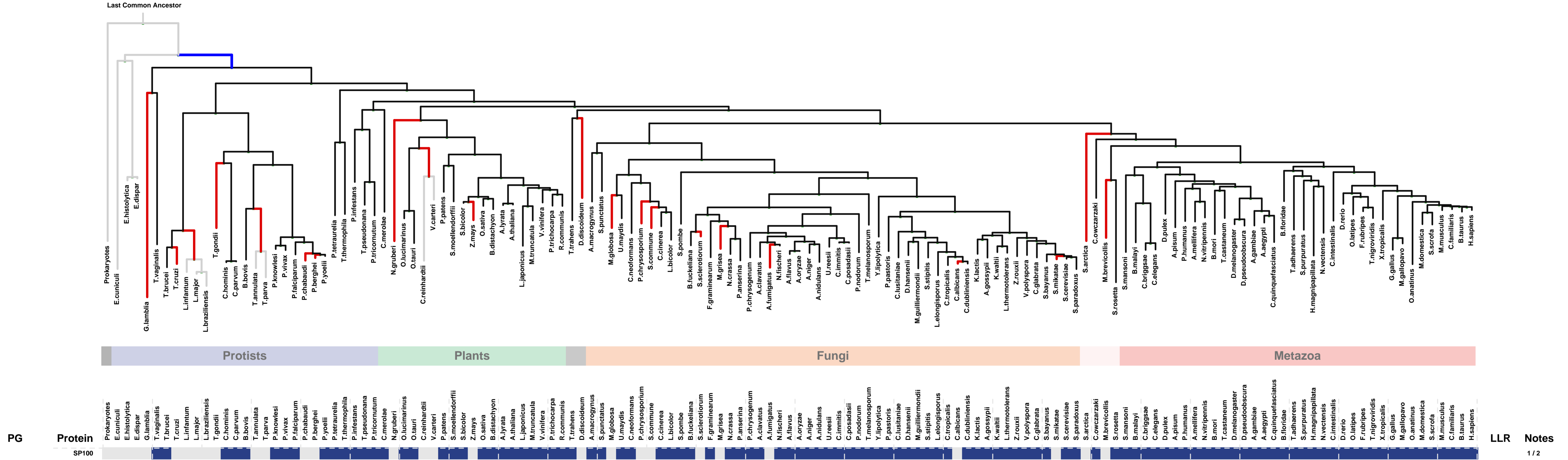


PG	Protein	Prokaryotes	Protists	Plants	Fungi	Metazoa	LLR	Notes
N	CBLN1						1.3	1
	KCNJ13						1.1	2
	TWSG1						1.1	
	TSHZ1						0.9	
	FAM195A						0.9	
O	IL1RAP						0.2	
	CCDC85B						0.2	
F	OTOP1						0.2	
O	IL18R1						0.2	

1: synapse || 2: voltage-gated potassium channel complex

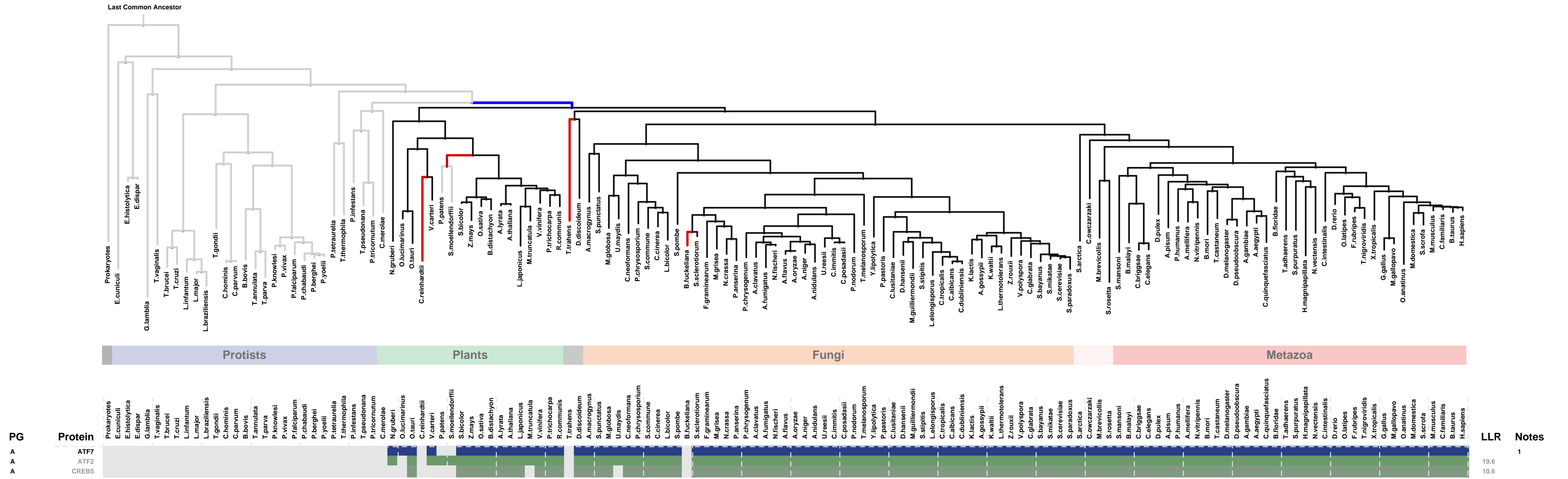
ECM 2, Gene set "nuclear periphery", Page 1

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



ECM 3, Gene set "nuclear periphery", Page 1

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



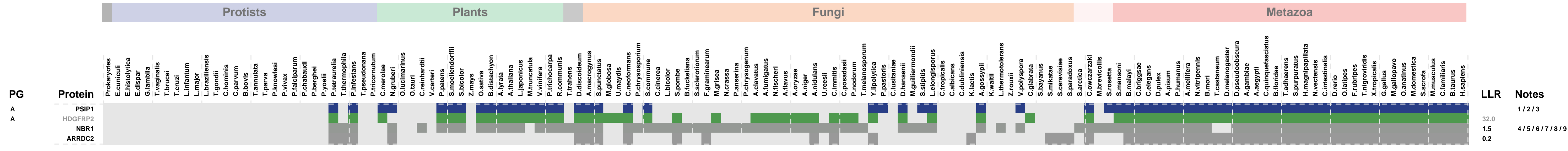
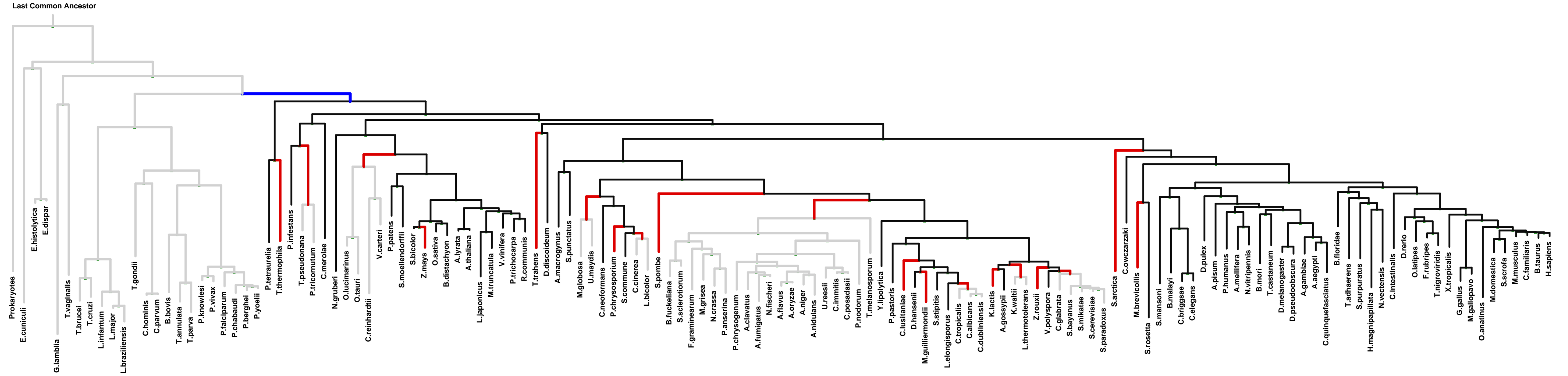
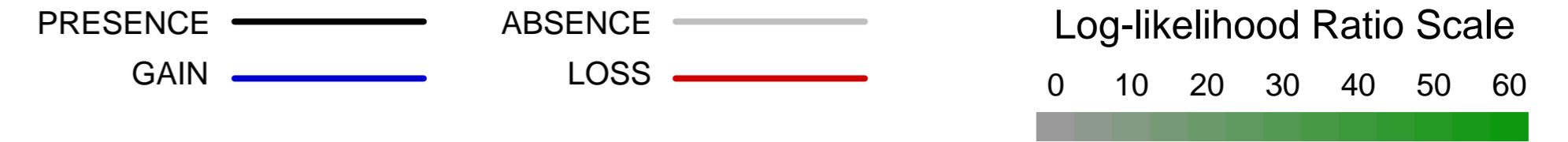
PG
A
A
A

Protein	Prokaryotes	Protists	Plants	Fungi	Metazoa	LLR	Notes
ATF7							
ATF2						19.6	1
CREB5						10.6	

1: nuclear periphery

ECM 4, Gene set "nuclear periphery", Page 1

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



1: nuclear heterochromatin || 2: nuclear periphery || 3: transcriptionally active chromatin || 4: autophagic vacuole || 5: cytoplasmic vesicle || 6: late endosome || 7: lysosome || 8: M band || 9: pre-autophagosomal structure