

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

Dataset:

Num of genes in input gene set: 3
Total number of genes: 20834
Prediction LLR threshold: 0

The CLIME PDF output two sections:

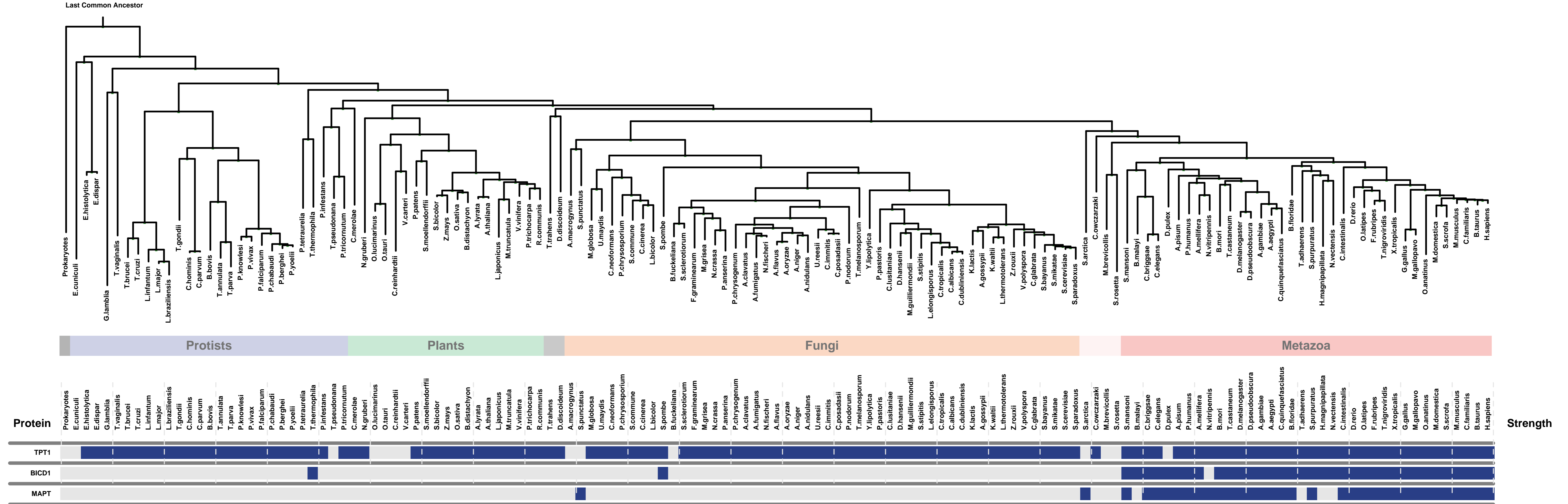
1) Overview of Evolutionarily Conserved Modules (ECMs)

- 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+

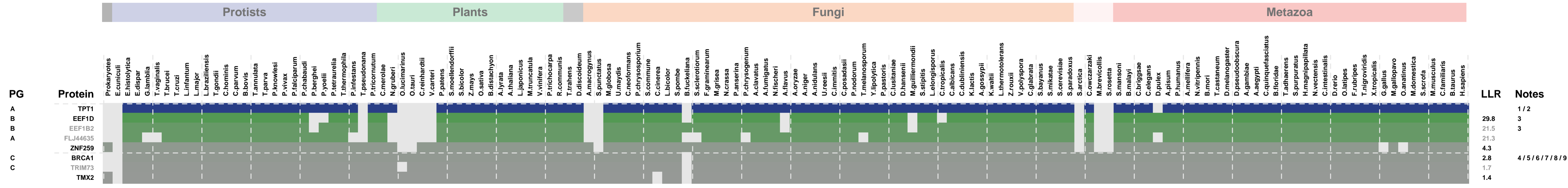
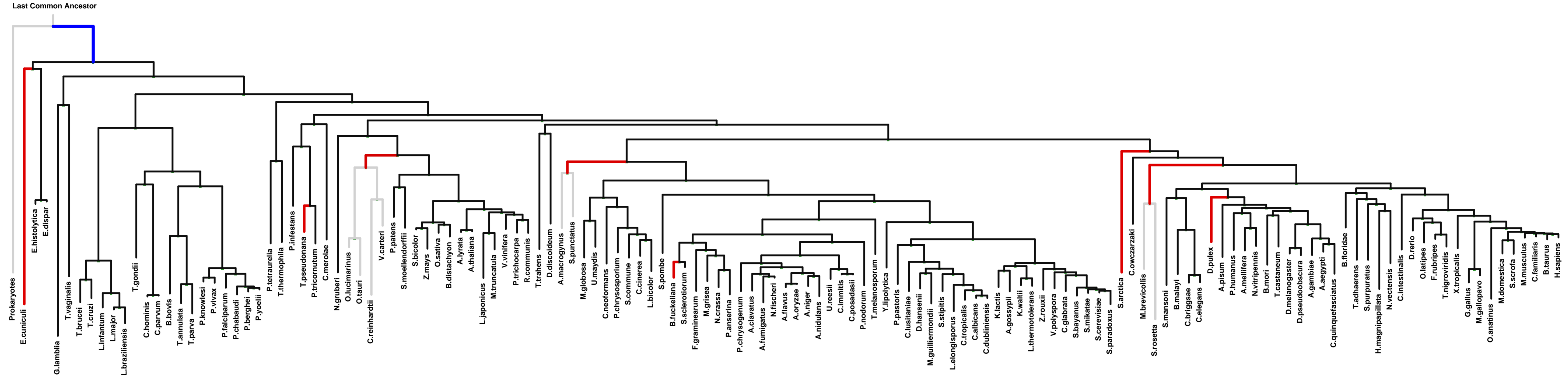
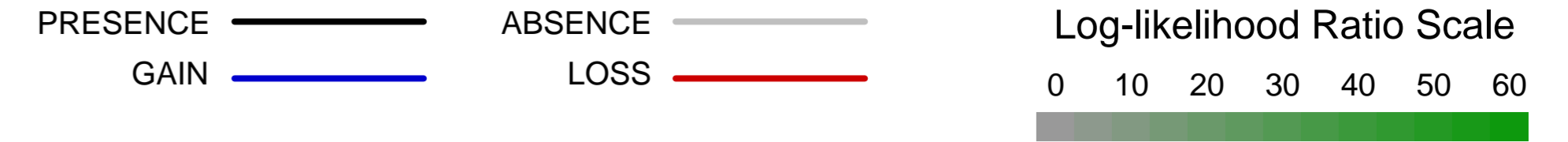
- Top panel shows the inferred evolutionary history on the predefined species tree. Branch color shows the gain event (blue) and loss events (red color, with brighter color indicating higher confidence in loss). Branches before the gain or after a loss are shown in gray.
- Bottom panel shows the input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

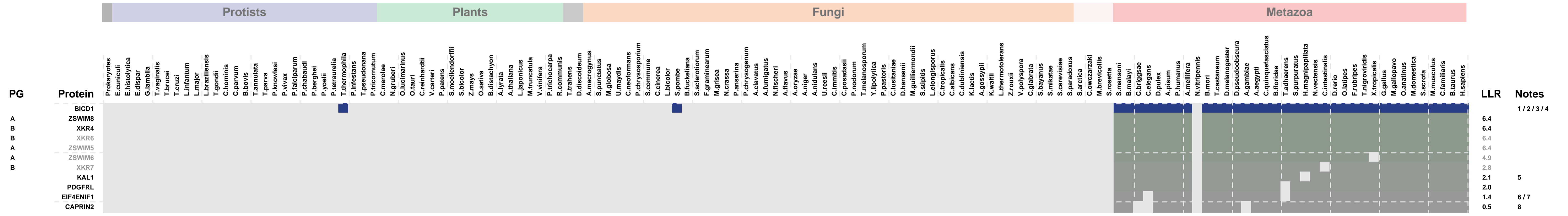
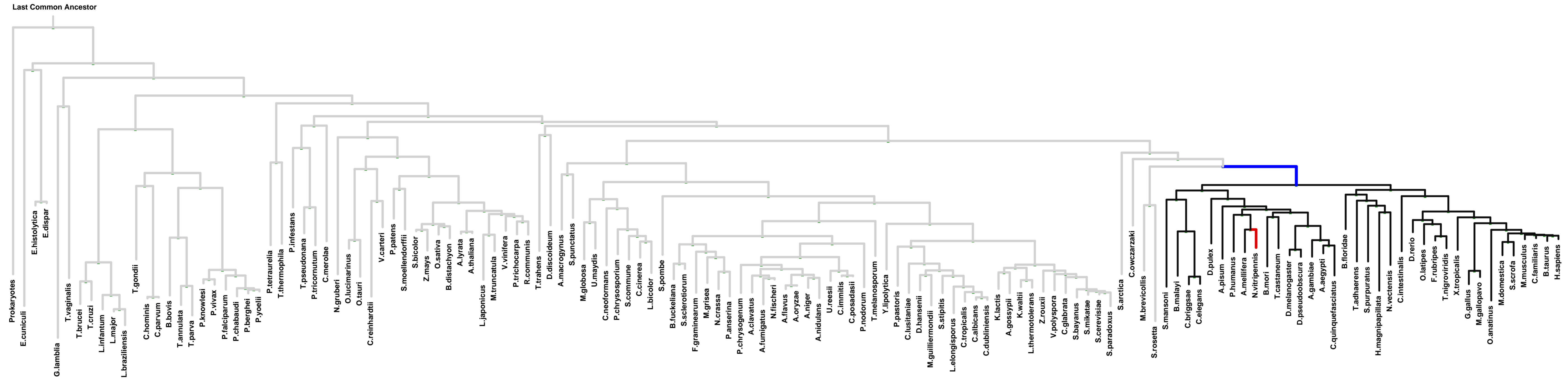
Num of ECM Genes: 1. Num of Predicted Genes: 7



1: multivesicular body || 2: tubulin complex || 3: eukaryotic translation elongation factor 1 complex || 4: BRCA1-A complex || 5: BRCA1-BARD1 complex || 6: chromosome || 7: filamentous actin || 8: focal adhesion || 9: gamma-tubulin ring complex || 10: ribonucleoprotein complex || 11: ruffle || 12: ubiquitin ligase complex

ECM 2, Gene set "tubulin complex", Page 1

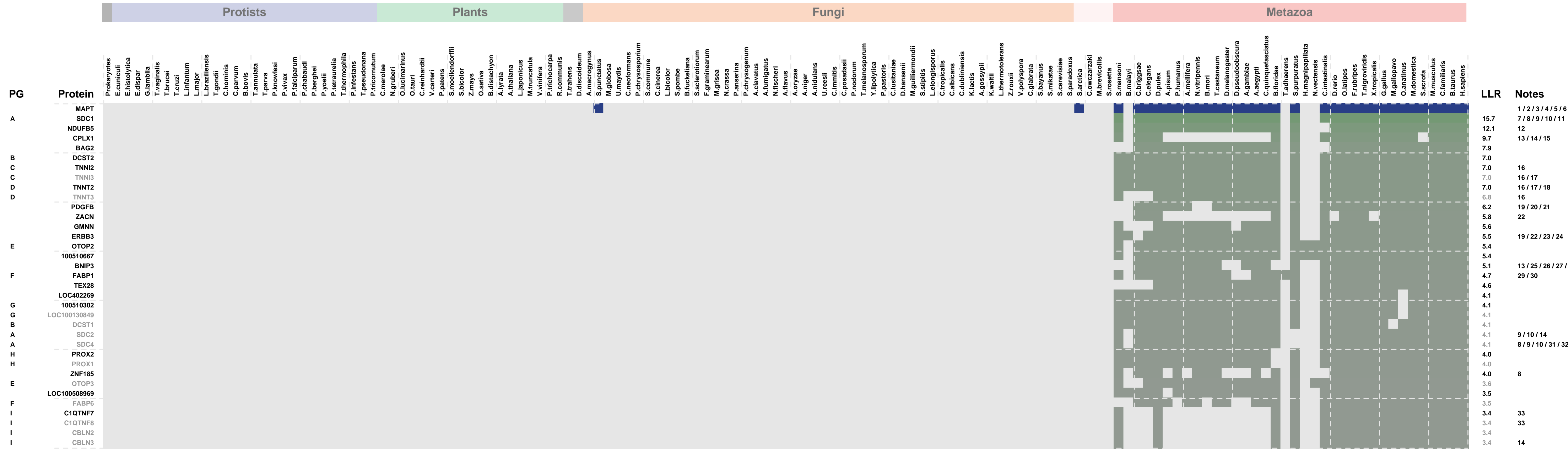
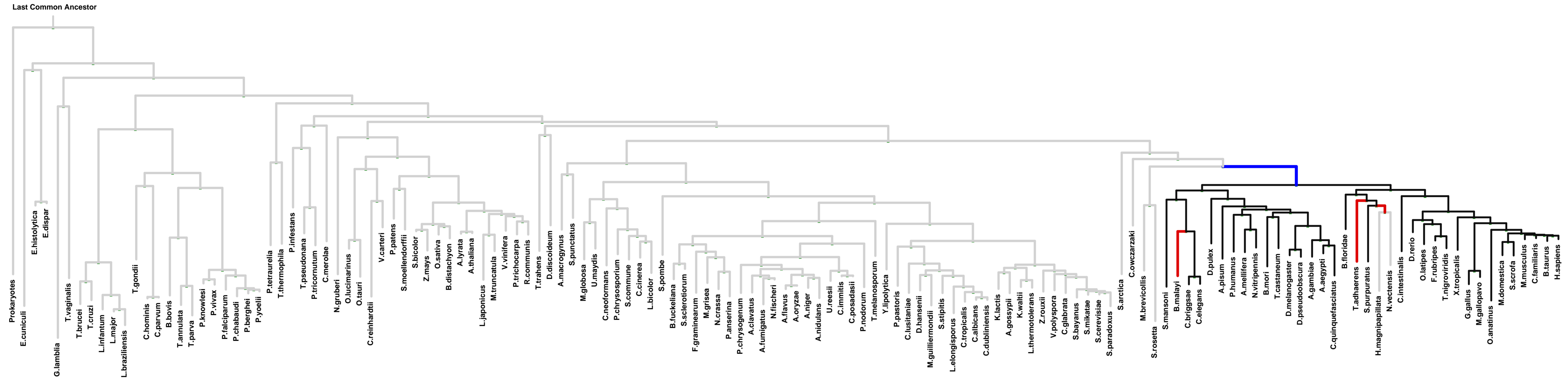
Num of ECM Genes: 1. Num of Predicted Genes: 10



1: cytoplasmic microtubule || 2: cytoplasmic vesicle || 3: trans-Golgi network || 4: tubulin complex || 5: proteinaceous extracellular matrix || 6: nuclear speck || 7: PML body || 8: receptor complex

ECM 3, Gene set "tubulin complex", Page 1

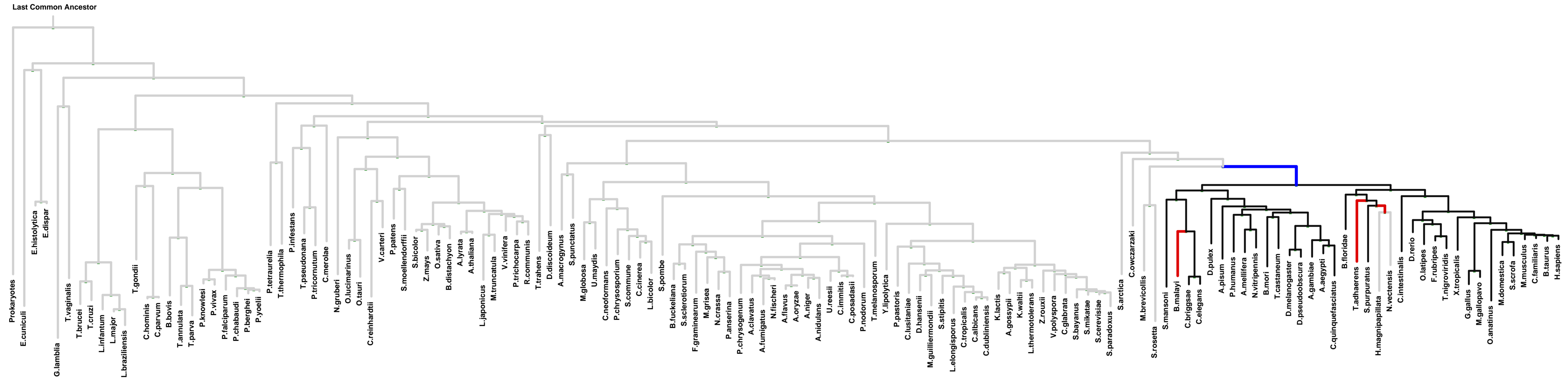
Num of ECM Genes: 1. Num of Predicted Genes: 88



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

ECM 3, Gene set "tubulin complex", Page 2

Num of ECM Genes: 1. Num of Predicted Genes: 88

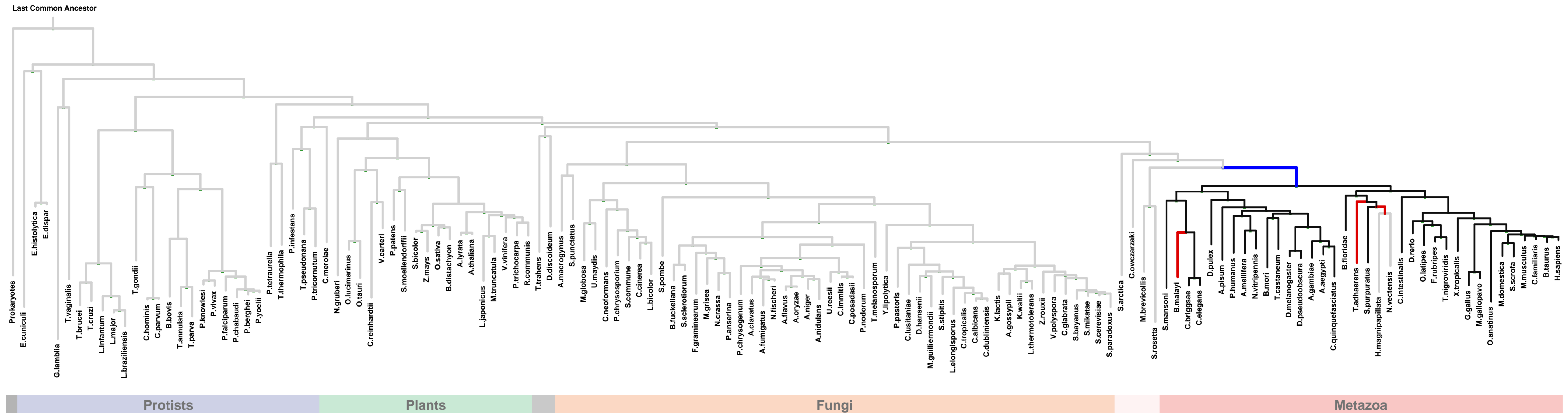


PG	Protein	Protists	Plants	Fungi	Metazoa	LLR	Notes
I	CBLN4					3.4	1
I	COL10A1					3.4	2/3/4
I	COL8A1					3.4	4/5/6
I	COL8A2					3.4	3/4/5/6/7
I	C1QC					3.4	3
I	TEDDM1					3.4	
I	C1QL1					3.4	3
I	C1QL2					3.4	3
I	C1QL3					3.4	3
I	C1QL4					3.4	3
I	C1QTNF2					3.4	3
I	C1QTNF3					3.4	3
I	C1QTNF4					3.4	3
I	C1QTNF5					3.4	3
I	C1QTNF6					3.4	3
D	TNNT1					3.4	8
I	CBLN1					3.3	1
J	GPM6B					3.2	9
J	FBXO28					3.2	
K	ATP5J2P4					2.8	
K	OLFML2A					2.8	6
K	OLFML2B					2.8	6
K	OLFML3					2.8	
L	EFNA1					2.8	10
M	TSC22D2					2.8	
M	TSC22D3					2.8	
L	EFNA5					2.8	11/12
K	OLFM2					2.8	
C	100508475					2.8	
C	TNNI1					2.8	8
K	OLFML1					2.8	
K	BAG5					2.6	13
K	CCR10					2.4	
N	DUOXA1					2.3	
N	DUOXA2					2.3	

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

ECM 3, Gene set "tubulin complex", Page 3

Num of ECM Genes: 1. Num of Predicted Genes: 88



PG	Protein	Prokaryotes	Protists	Plants	Fungi	Metazoa	LLR	Notes
	TSHZ1						2.2	
	TWSG1						2.0	
	FAM195A						2.0	
	EVPLL						1.8	
	KCNJ13						1.2	1
B	DCSTAMP						1.2	2/3/4
J	GPM6A						1.1	5/6/7/8
	CCDC85B						1.1	
	OTOP1						1.1	
E	IL18R1						1.1	
O	IL1RAP						1.1	
	SMDT1						1.0	
P	CDK5R1						0.9	6/9/10/11/12/13/14
	CDK5R2						0.9	11
	PCP2						0.3	
	RABEP2						0.2	16
	SH3BGR						0.1	
	TMEM47						0.1	17
	TAX1BP3						0.1	

1: voltage-gated potassium channel complex || 2: endoplasmic reticulum-Golgi intermediate compartment membrane || 3: endosome membrane || 4: integral to endoplasmic reticulum membrane || 5: axonal growth cone || 6: dendritic spine || 7: filopodium || 8: neuron projection || 9: axon || 10: contractile fiber || 11: cyclin-dependent protein kinase 5 holoenzyme complex || 12: dendrite || 13: growth cone || 14: neuromuscular junction || 15: postsynaptic density || 16: early endosome || 17: cell-cell junction