

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

Dataset:

Num of genes in input gene set: 12

Total number of genes: 20834

Prediction LLR threshold: 0

The CLIME PDF output two sections:

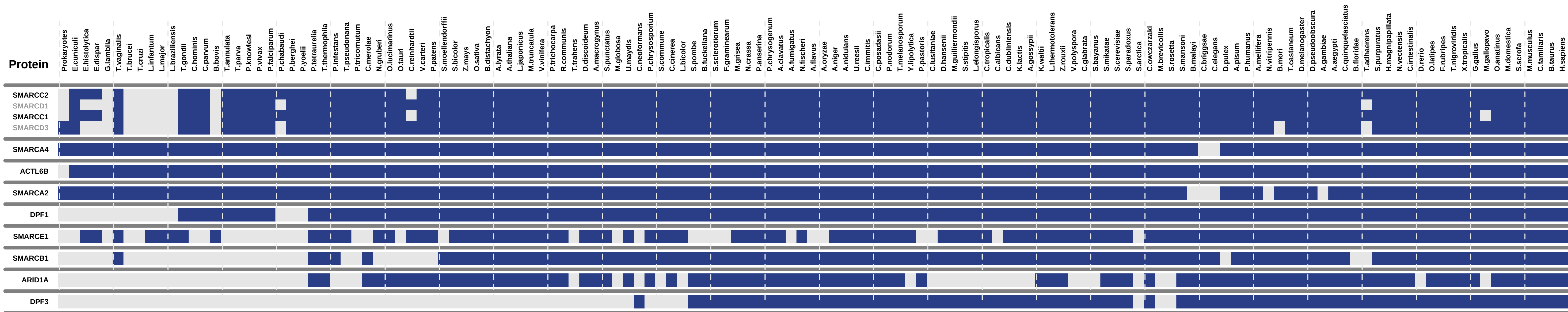
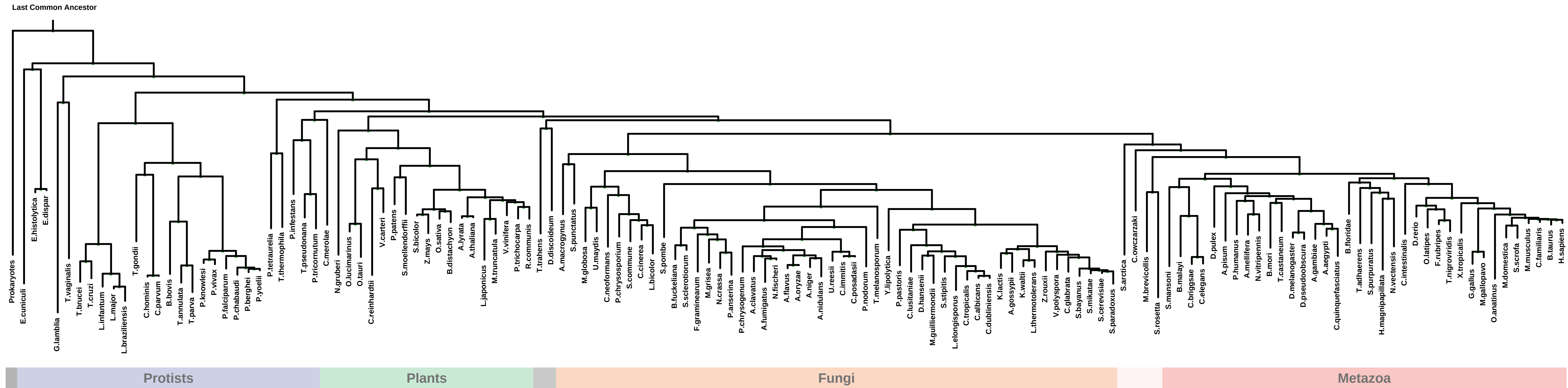
1) Overview of Evolutionarily Conserved Modules (ECMs)

- 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.

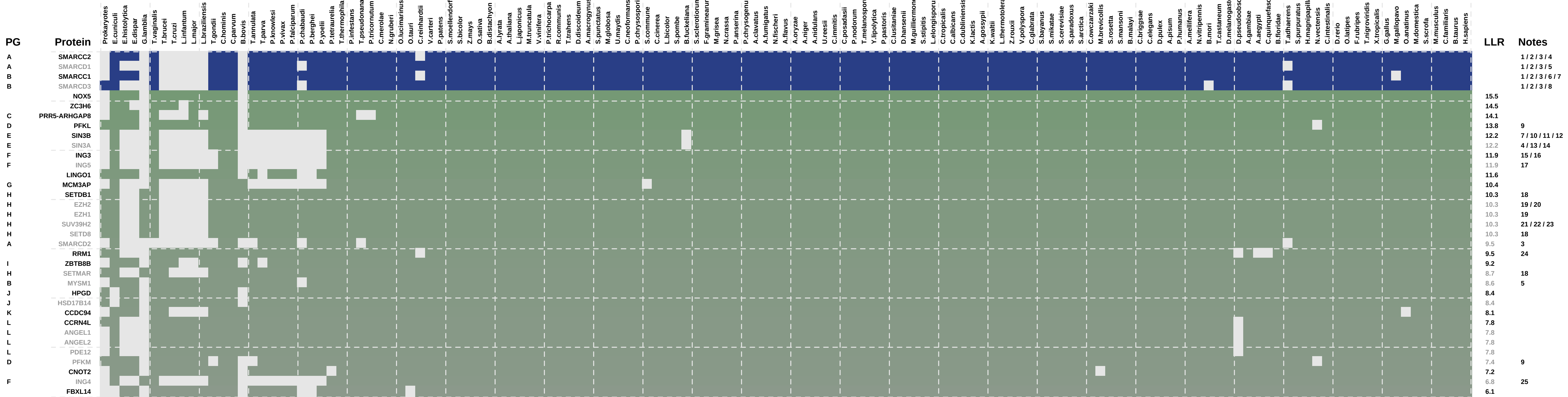
Overview of Evolutionarily Conserved Modules (ECMs)



Strength

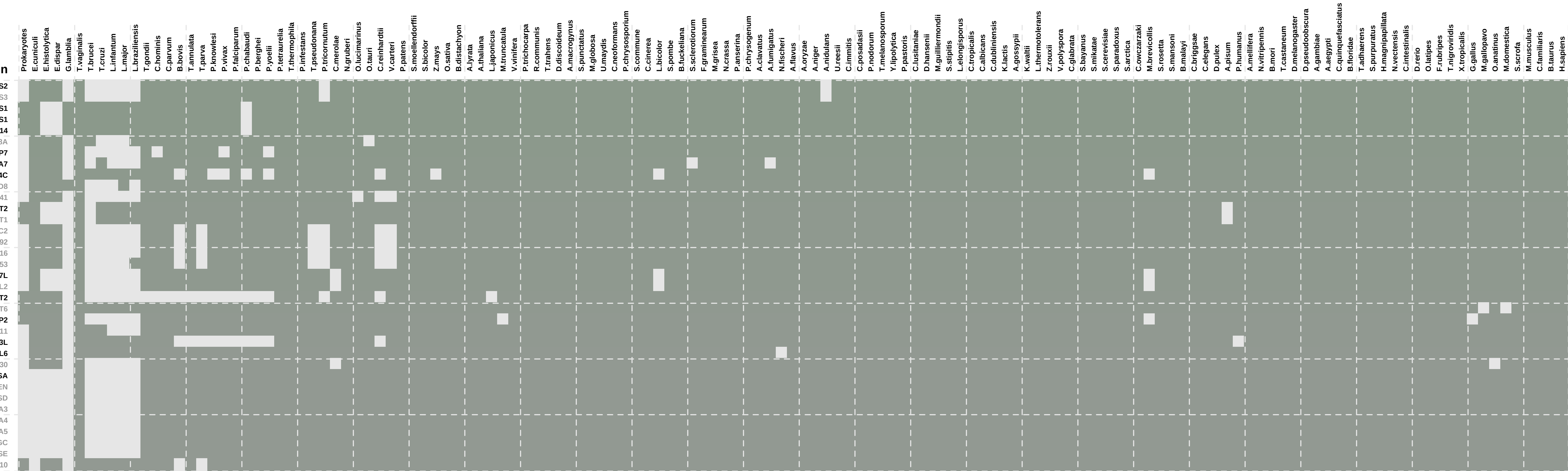
7.4

Num of ECM Genes: 4. Num of Predicted Genes: 130. ECM Strength: 7.4



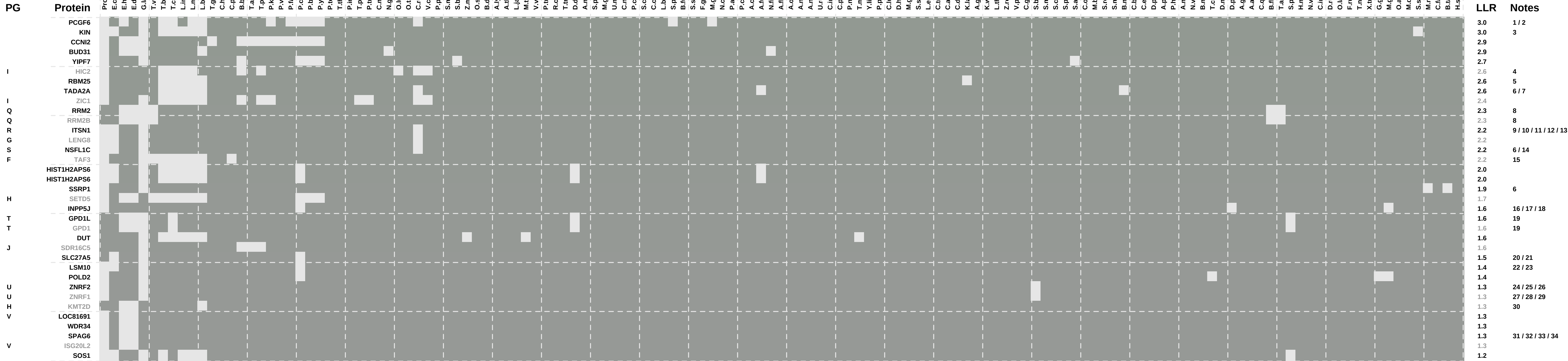
1: nBAF complex	2: npBAF complex	3: SWI/SNF complex	4: transcriptional repressor complex	5: chromatin remodeling complex	6: WINAC complex	7: XY body	8: nuclear chromatin	9: 6-phosphofructokinase complex	10: autosome	11: X chromosome	12: Y chromosome	13: kinetochore	14: Sin3 complex	15: NuA4 histone acetyltransferase complex	16: Piccolo NuA4 histone acetyltransferase complex	17: MOZ/MORF histone acetyltransferase complex	18: chromosome	19: ESC/E(Z) complex	20: pronucleus	21: chromatin	22: chromosome, centromeric region	23: nuclear heterochromatin	24: ribonucleoside-diphosphate reductase complex	25: histone acetyltransferase complex
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Num of ECM Genes: 4. Num of Predicted Genes: 130. ECM Strength: 7.4



LLR	Notes
6.0	
6.0	
5.8	1 / 2 / 3 / 4
5.8	
5.8	
5.4	
5.4	
5.2	
5.1	5
4.9	
4.8	
4.4	6 / 7 / 8
4.4	
4.4	
4.4	
4.4	
4.2	
4.1	
4.1	9
4.0	
3.8	
3.6	10 / 11
3.6	
3.3	9
3.1	
3.1	
3.1	12 / 13
3.1	14
3.1	13 / 15 / 16 / 17
3.1	
3.1	
3.1	
3.1	
3.1	18
3.0	

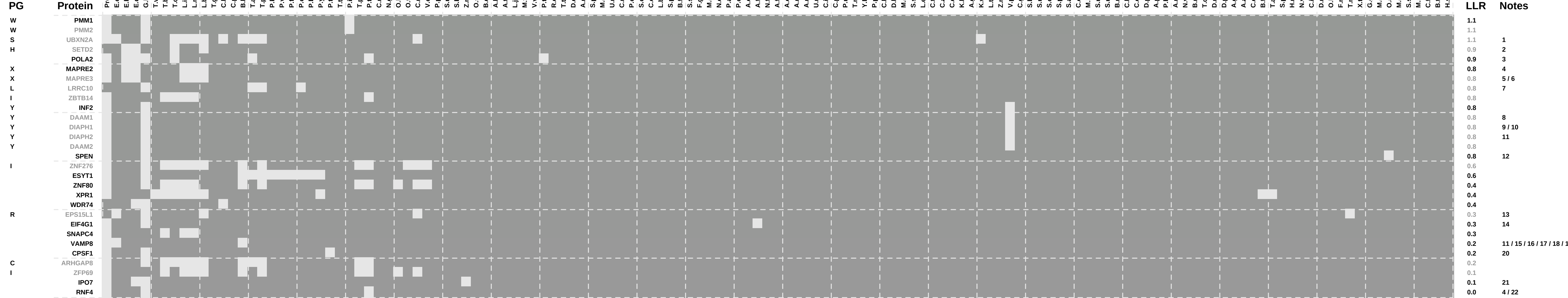
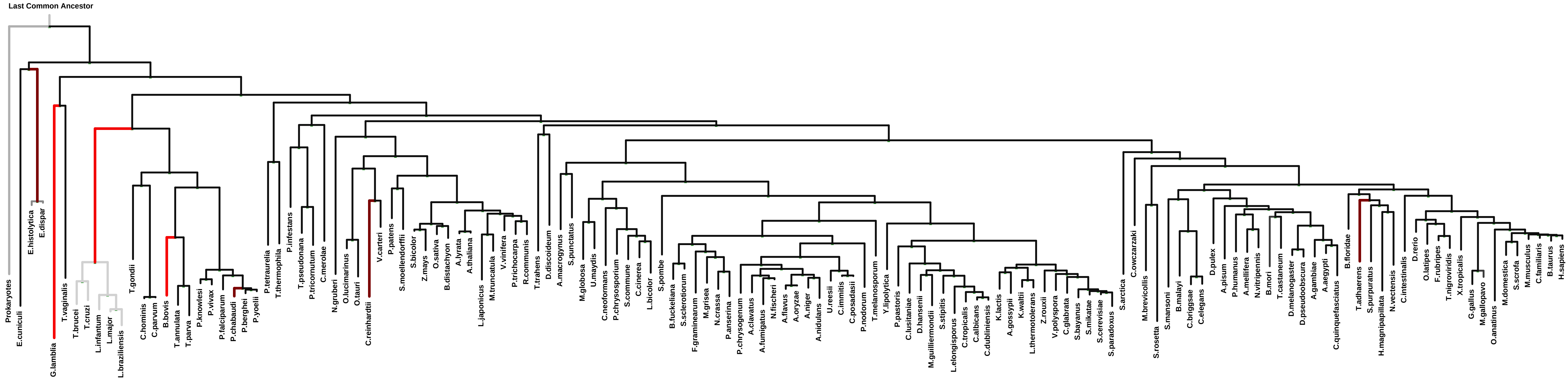
Num of ECM Genes: 4. Num of Predicted Genes: 130. ECM Strength: 7.4



1: PcG protein complex || 2: PRC1 complex || 3: nuclear matrix || 4: focal adhesion || 5: nuclear speck || 6: chromosome || 7: PCAF complex || 8: ribonucleoside-diphosphate reductase complex || 9: coated pit || 10: endocytic vesicle || 11: lamellipodium || 12: neuron projection || 13: synapse || 14: Golgi stack || 15: transcription factor TFIID complex || 16: dendritic shaft || 17: growth cone || 18: ruffle || 19: glycerol-3-phosphate dehydrogenase complex || 20: basal plasma membrane || 21: integral to endoplasmic reticulum membrane || 22: Cajal body || 23: U7 snRNP || 24: endosome membrane || 25: lysosomal membrane || 26: presynaptic membrane || 27: endosome || 28: lysosome ||

ECM 1, Gene set "nBAF complex", Page 4

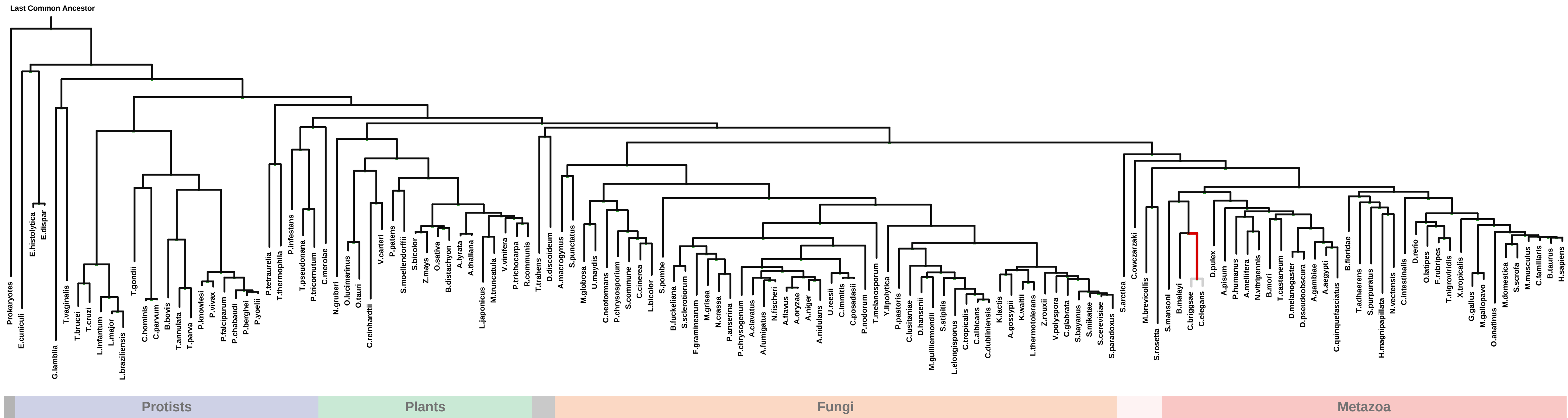
Num of ECM Genes: 4. Num of Predicted Genes: 130. ECM Strength: 7.4



1: cis-Golgi network || 2: chromosome || 3: alpha DNA polymerase:primase complex || 4: microtubule cytoskeleton || 5: cytoplasmic microtubule || 6: midbody || 7: myofibril || 8: stress fiber || 9: mitotic spindle || 10: ruffle membrane || 11: early endosome || 12: transcriptional repressor complex || 13: coated pit || 14: eukaryotic translation initiation factor 4F complex || 15: late endosome membrane || 16: lysosomal membrane || 17: recycling endosome || 18: secretory granule membrane || 19: SNARE complex || 20: mRNA cleavage and polyadenylation specificity factor complex || 21: nuclear pore || 22: PML body

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

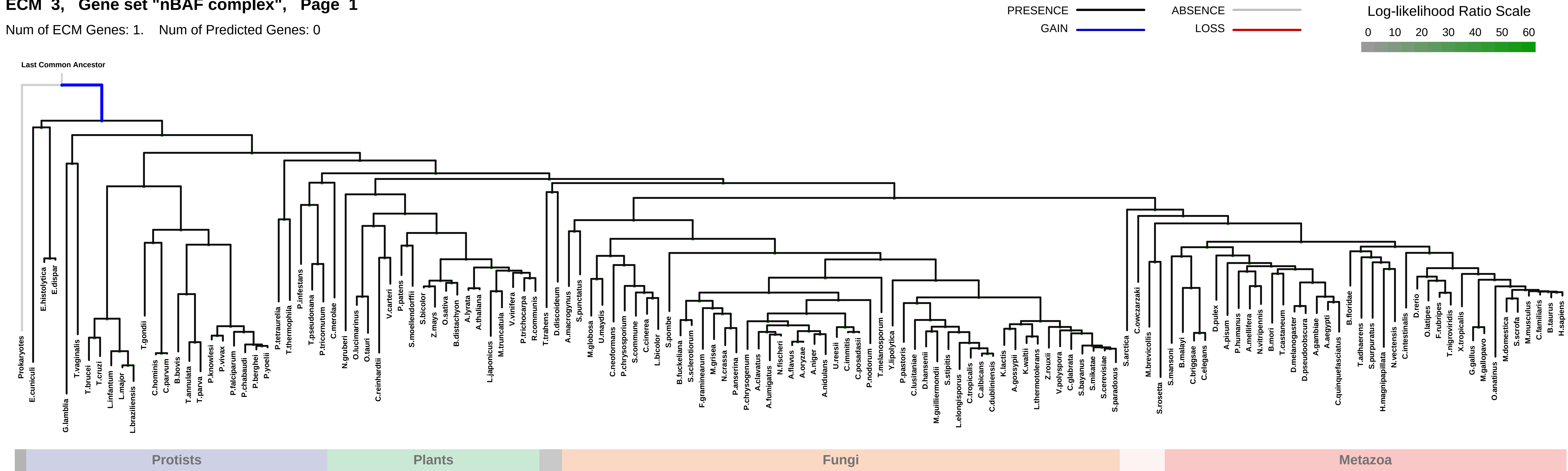
Num of ECM Genes: 1. Num of Predicted Genes: 0

[illegible]

1: nBAF complex || 2: npBAF complex || 3: nuclear chromatin || 4: SWI/SNF complex || 5: WINAC complex

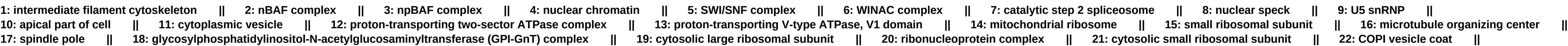
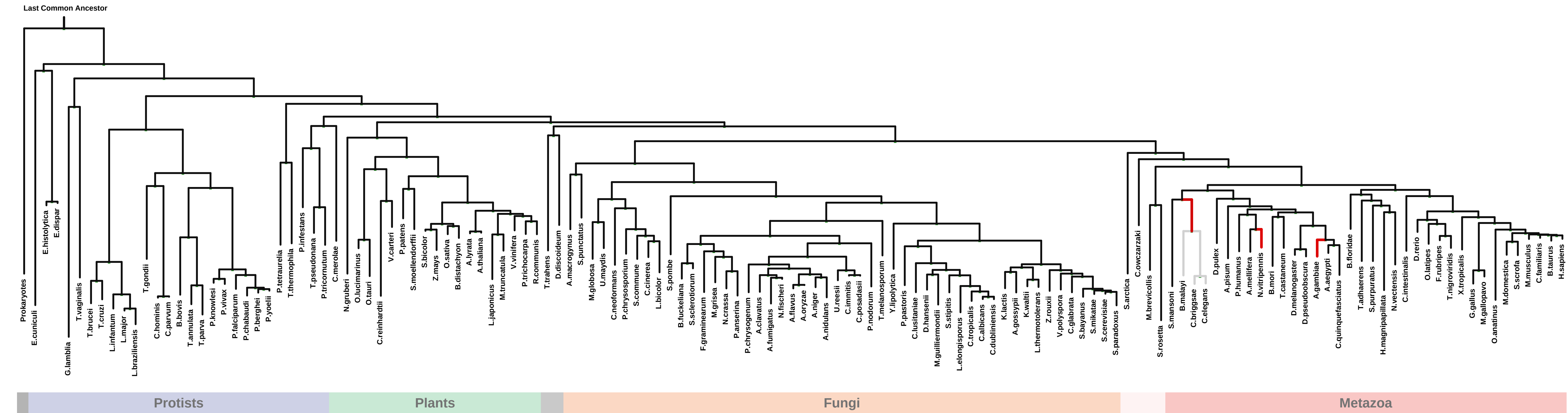
ECM 3, Gene set "nBAF complex", Page 1

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

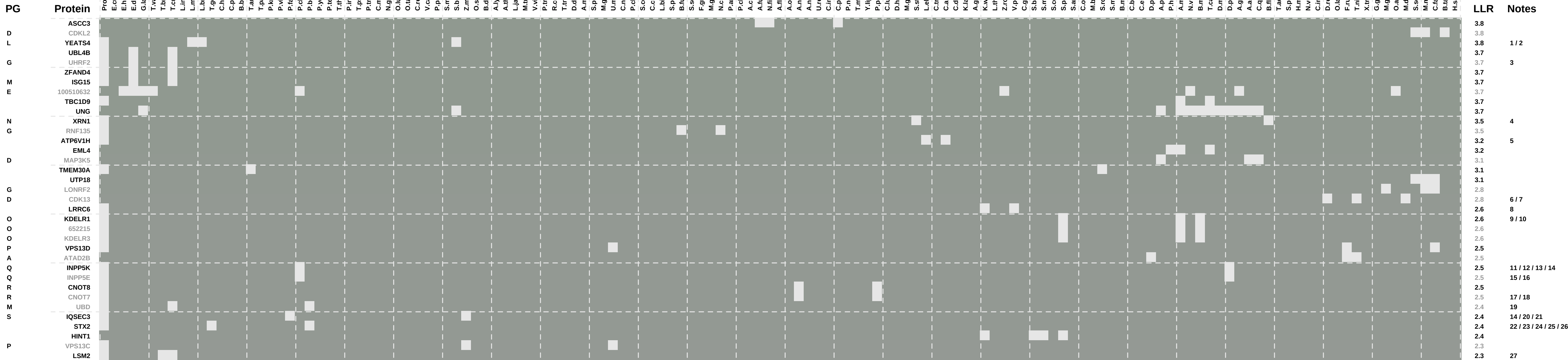
[illegible]

1: nBAF complex || 2: SWI/SNF complex

Num of ECM Genes: 1. Num of Predicted Genes: 139

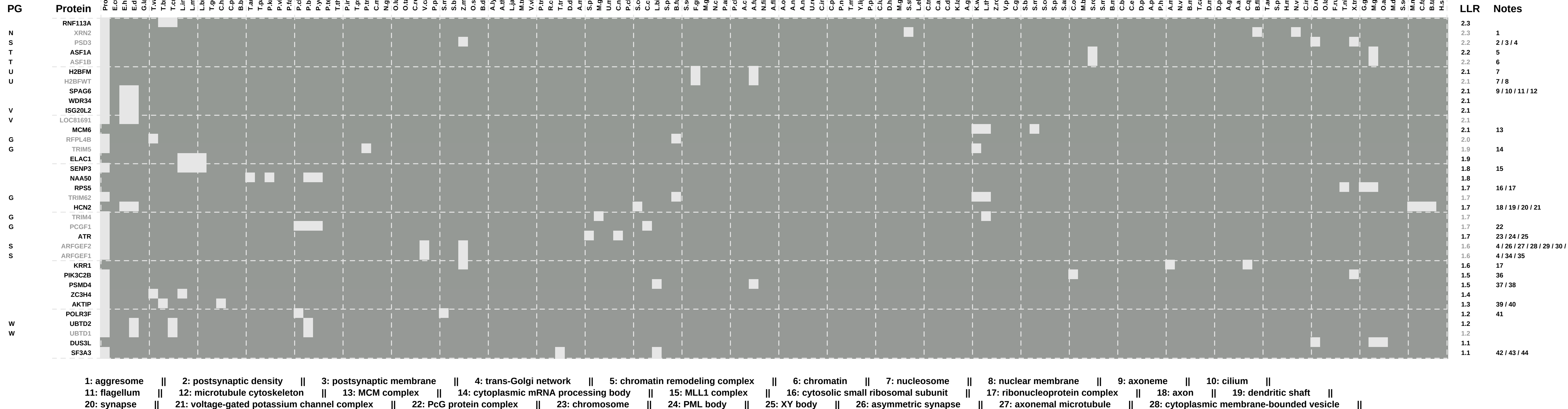


Num of ECM Genes: 1. Num of Predicted Genes: 139

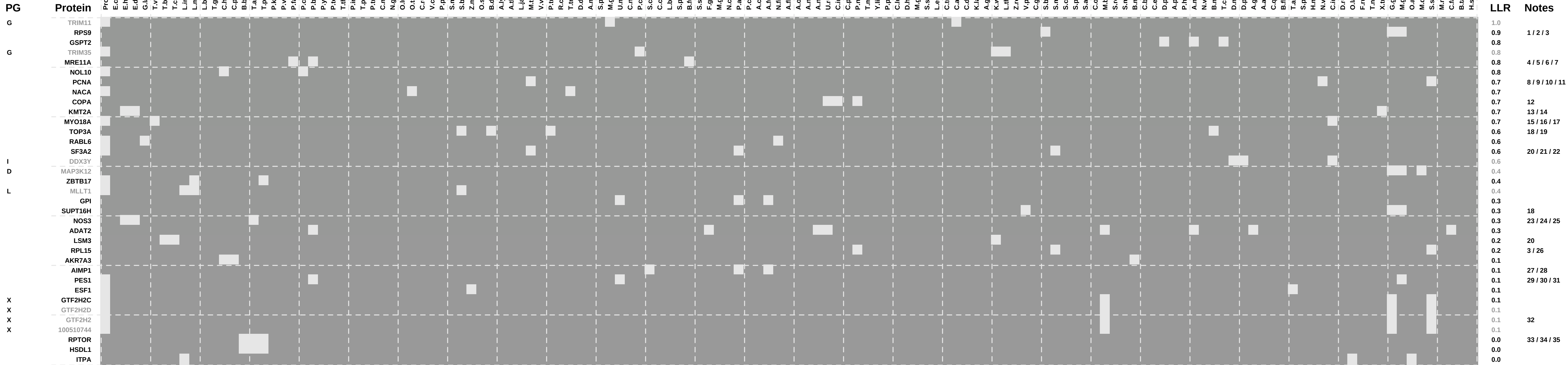


1: NuA4 histone acetyltransferase complex || 2: nuclear matrix || 3: nuclear heterochromatin || 4: intermediate filament cytoskeleton || 5: vacuolar proton-transporting V-type ATPase, V1 domain || 6: nuclear cyclin-dependent protein kinase holoenzyme complex ||
7: nuclear speck || 8: cilium || 9: cis-Golgi network || 10: endoplasmic reticulum-Golgi intermediate compartment || 11: neuron projection || 12: ruffle || 13: ruffle membrane || 14: trans-Golgi network || 15: cilium axoneme ||
16: Golgi cisterna membrane || 17: CCR4-NOT complex || 18: cytoplasmic mRNA processing body || 19: aggresome || 20: inhibitory synapse || 21: postsynaptic membrane || 22: basolateral plasma membrane || 23: cell-cell junction ||

Num of ECM Genes: 1. Num of Predicted Genes: 139

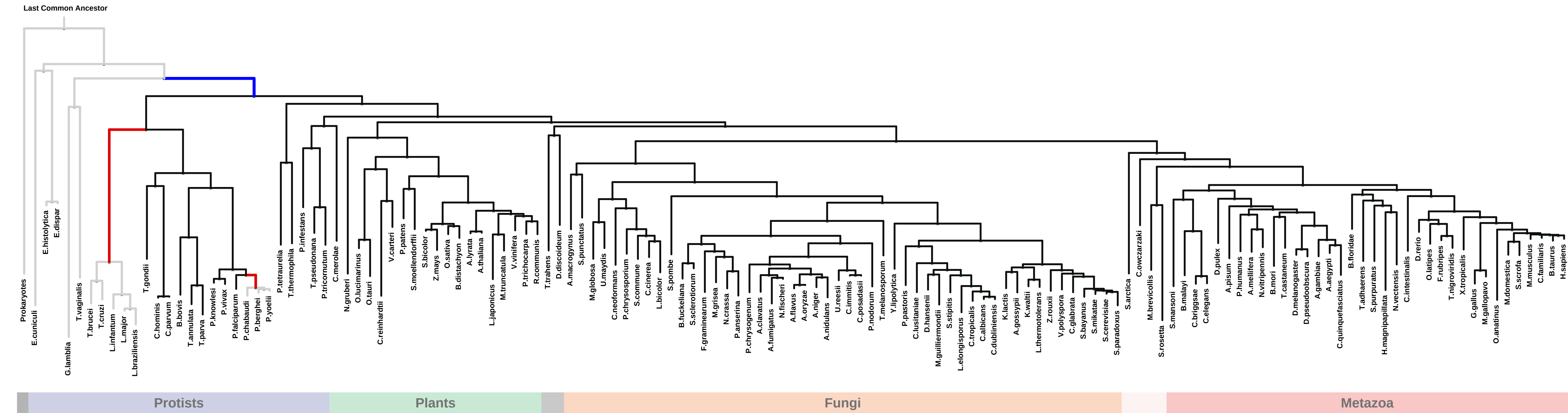


Num of ECM Genes: 1. Num of Predicted Genes: 139

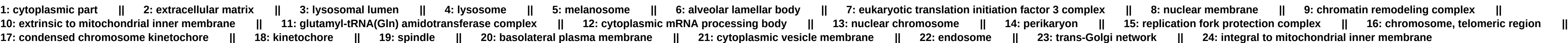
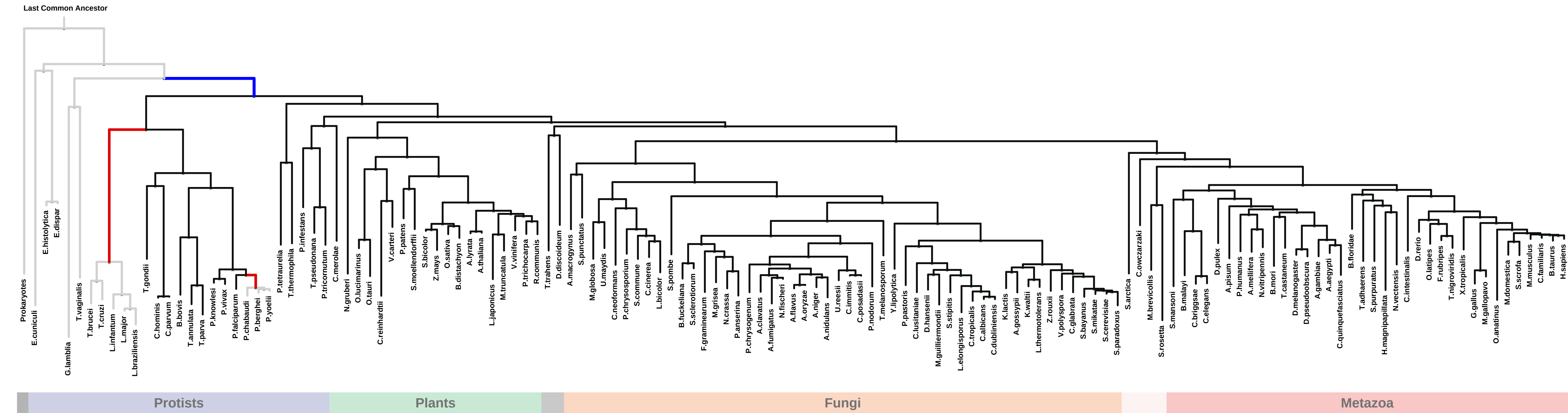


1: cytosolic small ribosomal subunit || 2: ribonucleoprotein complex || 3: ribosome || 4: chromosome, telomeric region || 5: condensed nuclear chromosome || 6: Mre11 complex || 7: nuclear chromatin || 8: DNA replication factor C complex || 9: microtubule cytoskeleton || 10: nuclear replication fork || 11: PCNA-p21 complex || 12: COPI vesicle coat || 13: histone methyltransferase complex || 14: MLL1 complex || 15: actomyosin || 16: endoplasmic reticulum-Golgi intermediate compartment || 17: myosin complex || 18: chromosome || 19: PML body || 20: catalytic step 2 spliceosome || 21: small nuclear ribonucleoprotein complex || 22: spliceosomal complex || 23: apical part of cell || 24: caveola || 25: endocytic vesicle membrane ||

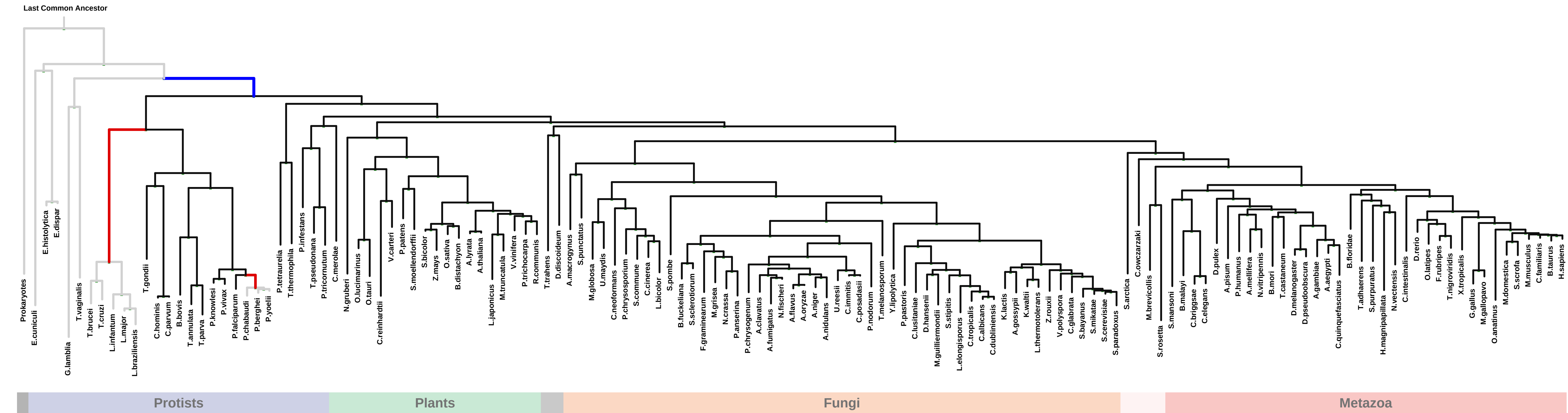
Num of ECM Genes: 1. Num of Predicted Genes: 93



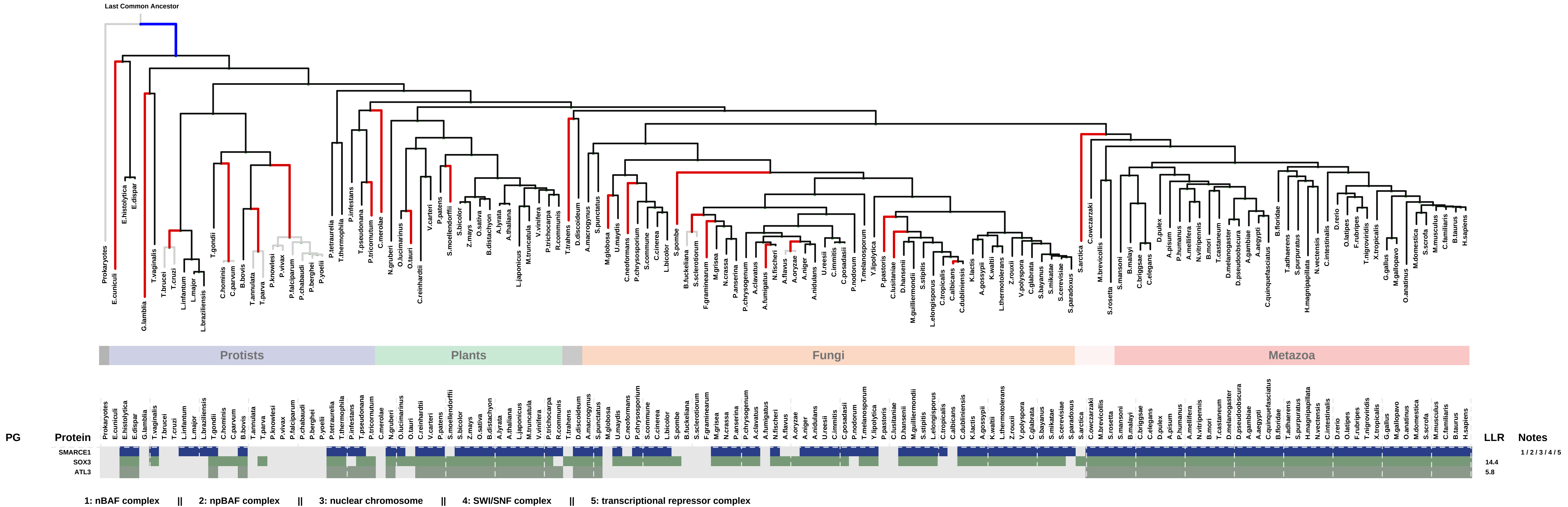
Num of ECM Genes: 1. Num of Predicted Genes: 93



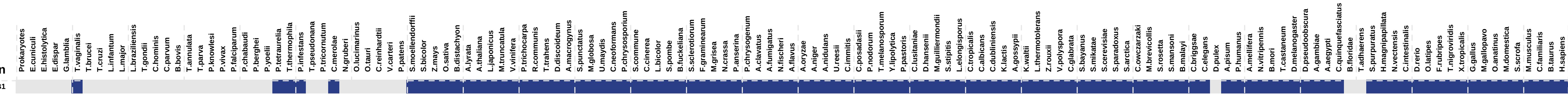
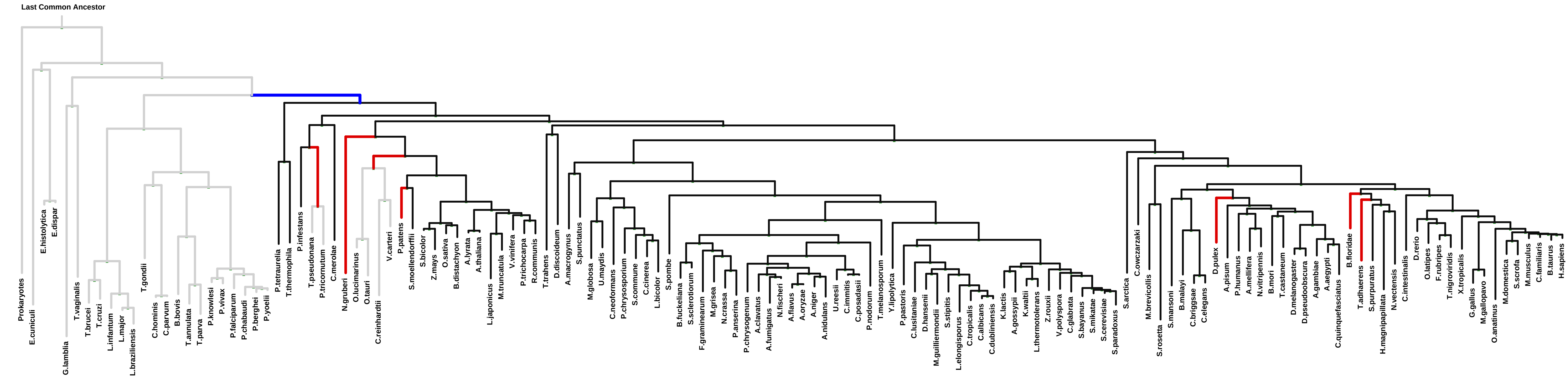
Num of ECM Genes: 1. Num of Predicted Genes: 93



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



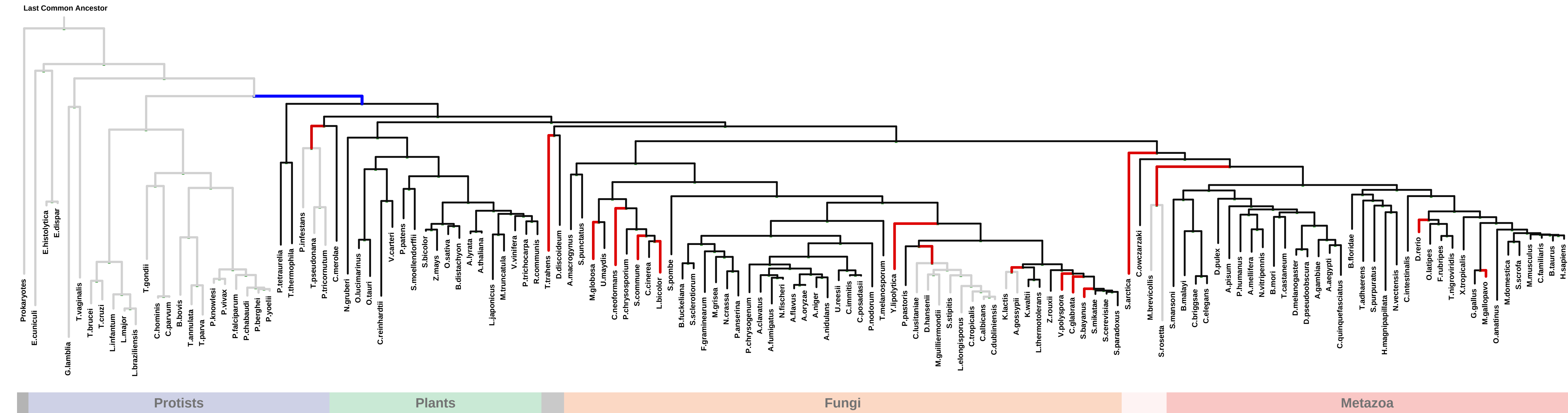
Num of ECM Genes: 1. Num of Predicted Genes: 0



1 / 2 / 3 / 4 / 5

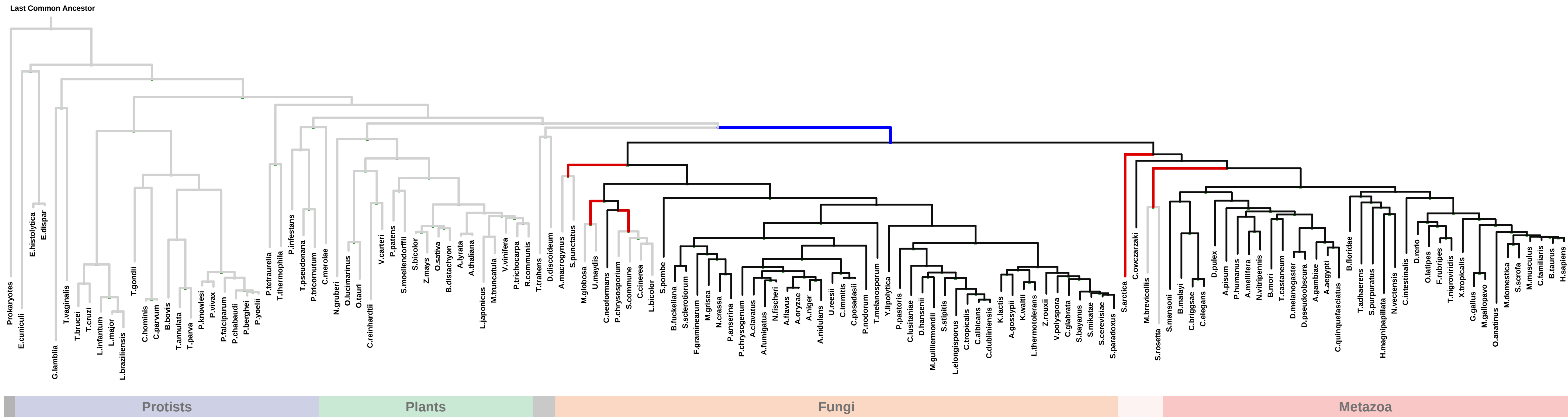
1: nBAF complex || 2: npBAF complex || 3: nuclear chromosome || 4: SWI/SNF complex || 5: XY body

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



ECM 9, Gene set "nBAF complex", Page 1

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

[illegible]

1: nBAF complex || 2: actin cytoskeleton || 3: Z disc