

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

Dataset:

Num of genes in input gene set: 4
Total number of genes: 20834
Prediction LLR threshold: 0

The CLIME PDF output two sections:

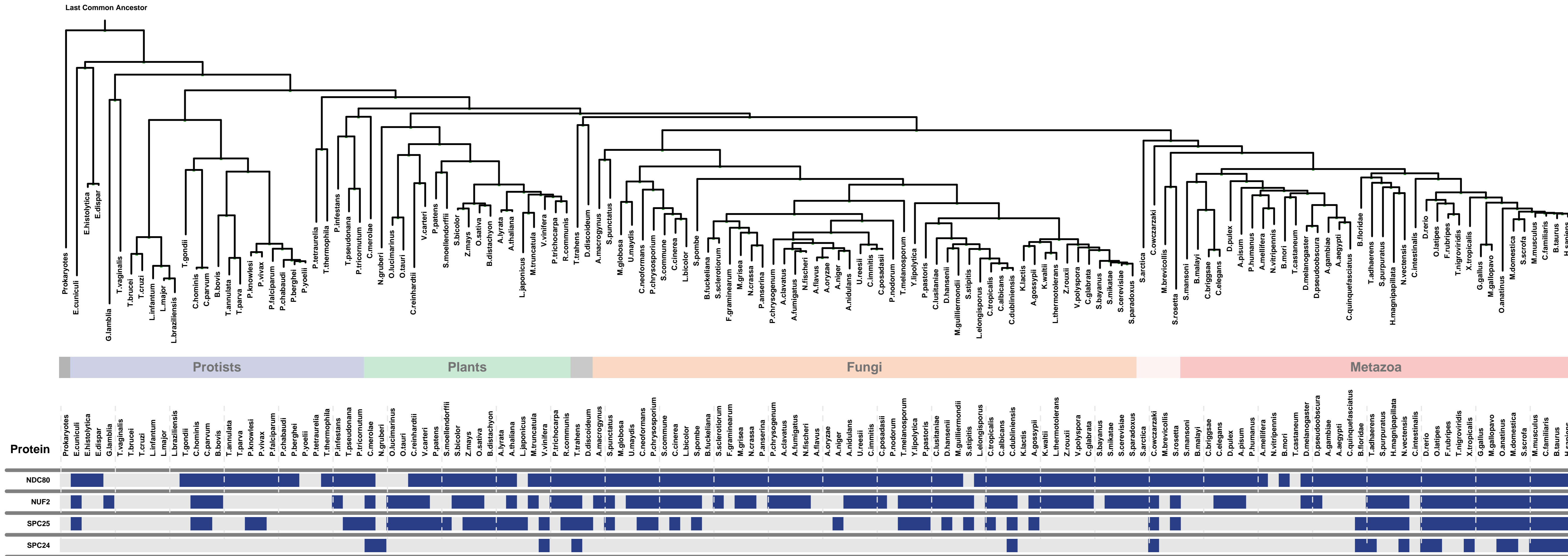
1) Overview of Evolutionarily Conserved Modules (ECMs)

- 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)



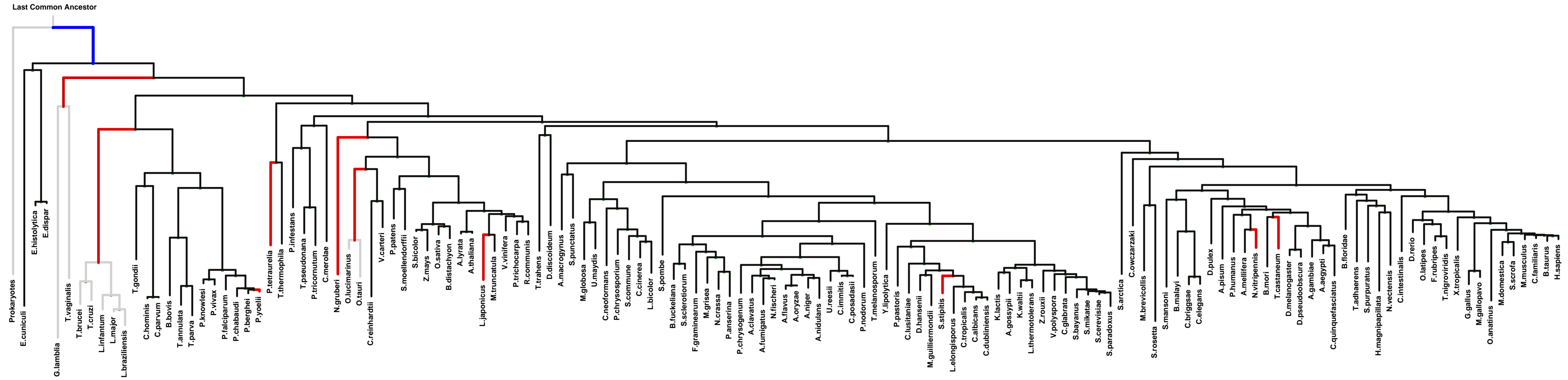
ECM 1, Gene set "Ndc80 complex", Page 1

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

PRESENCE ————
GAIN ————
ABSENCE ————
LOSS ————

Log-likelihood Ratio Scale

0 10 20 30 40 50 60

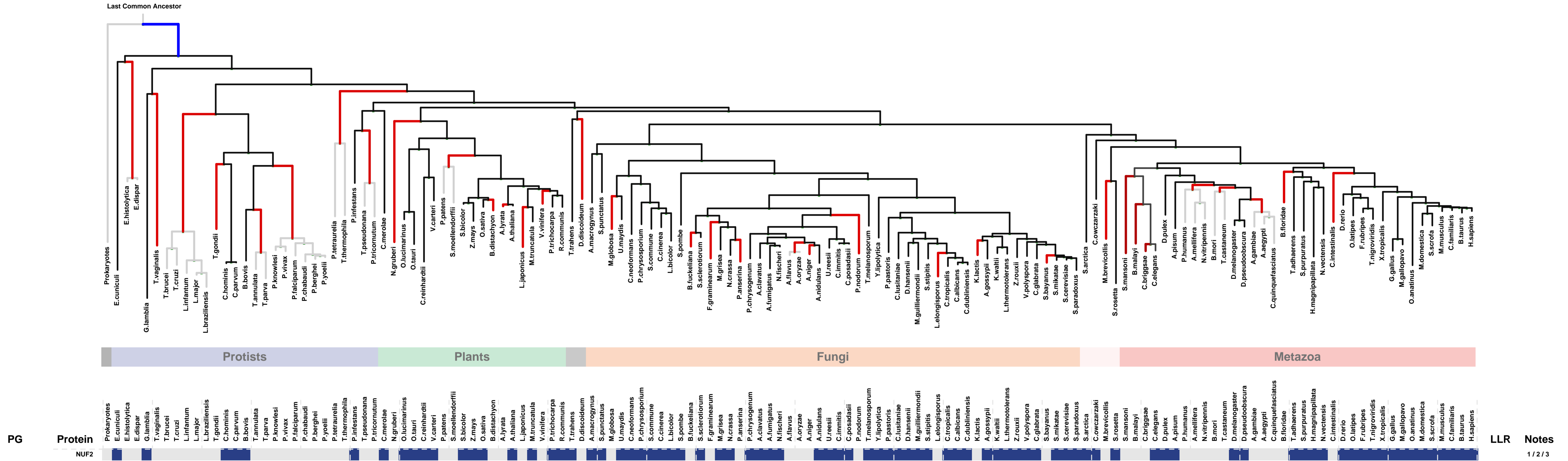


PG	Protein	Species	LLR	Notes
NDC80	NDC80	<i>E. cuniculi</i>	5.4	1 2 3 4 5
TSR3	TSR3	<i>E. histiolytica</i>	0.2	6
MNAT1	MNAT1	<i>E. dispar</i>	0.2	6

1: chromosome, centromeric region || 2: condensed chromosome kinetochore || 3: condensed nuclear chromosome outer kinetochore || 4: kinetochore || 5: Ndc80 complex || 6: holo TFIIF complex

ECM 2, Gene set "Ndc80 complex", Page 1

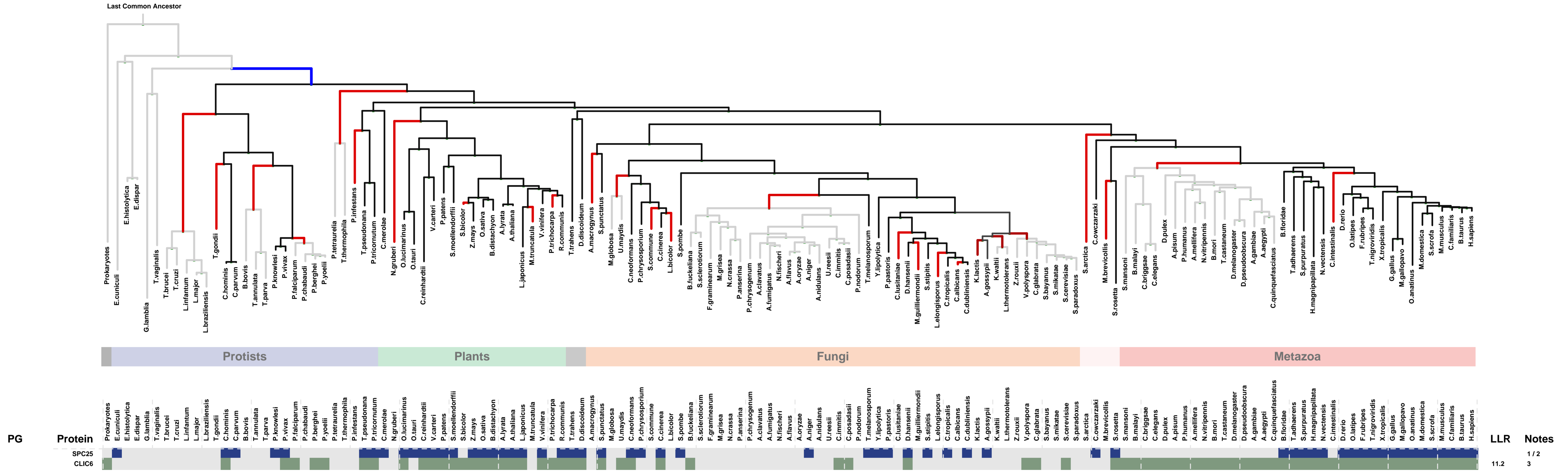
Num of ECM Genes: 1. Num of Predicted Genes: 0



1: chromosome, centromeric region || 2: condensed chromosome kinetochore || 3: Ndc80 complex

ECM 3, Gene set "Ndc80 complex", Page 1

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

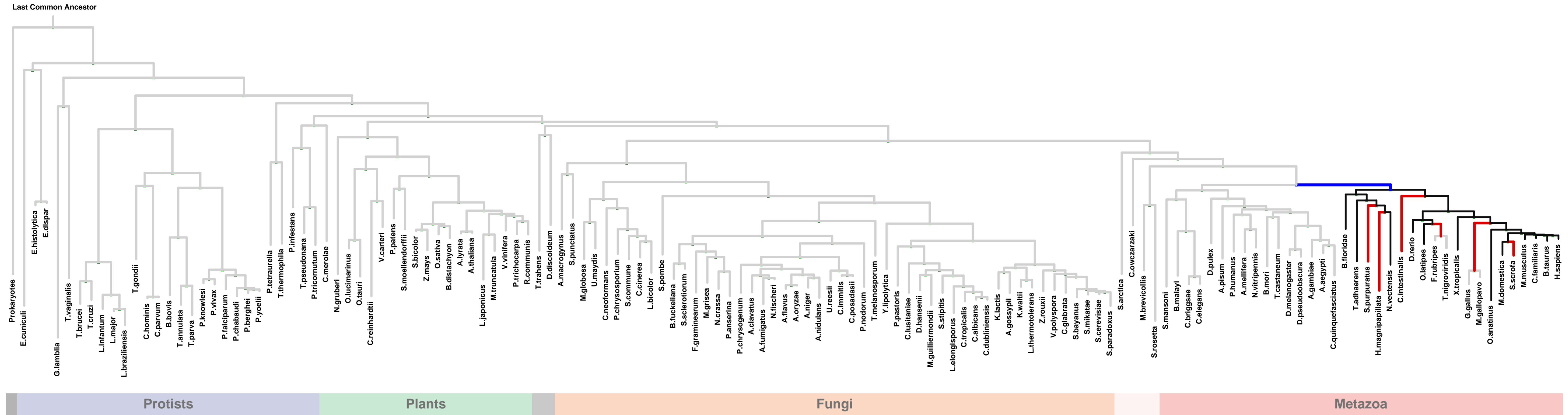


1: condensed chromosome kinetochore || 2: Ndc80 complex || 3: chloride channel complex

LLR Notes
1/2
3

ECM 4, Gene set "Ndc80 complex", Page 1

Num of ECM Genes: 1. Num of Predicted Genes: 19



PG	Protein	Protists	Plants	Fungi	Metazoa	LLR	Notes
SPC24							1 / 2
C7orf43						12.1	
C20orf201						10.2	
C19orf55						7.4	
CD3EAP						7.2	3 / 4 / 5
C10orf35						6.6	
FANCE						5.5	6
CCDC24						5.2	
HAUS7						4.8	7 / 8
FAM47A						4.6	
C12orf63						4.2	
C12orf63						4.2	
C10orf67						3.6	
CASC5						1.6	1 / 9
RD3L						1.4	
CCDC14						1.2	
MAP10						0.9	
C6orf118						0.8	
PNMA5						0.6	
KIAA0753						0.2	

1: condensed chromosome kinetochore || 2: Ndc80 complex || 3: chromosome || 4: DNA-directed RNA polymerase I complex || 5: RNA polymerase I transcription factor complex || 6: Fanconi anaemia nuclear complex || 7: HAUS complex || 8: spindle || 9: acrosomal vesicle