

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

Dataset:

Num of genes in input gene set: 23

Total number of genes: 20834

Prediction LLR threshold: 0

The CLIME PDF output two sections:

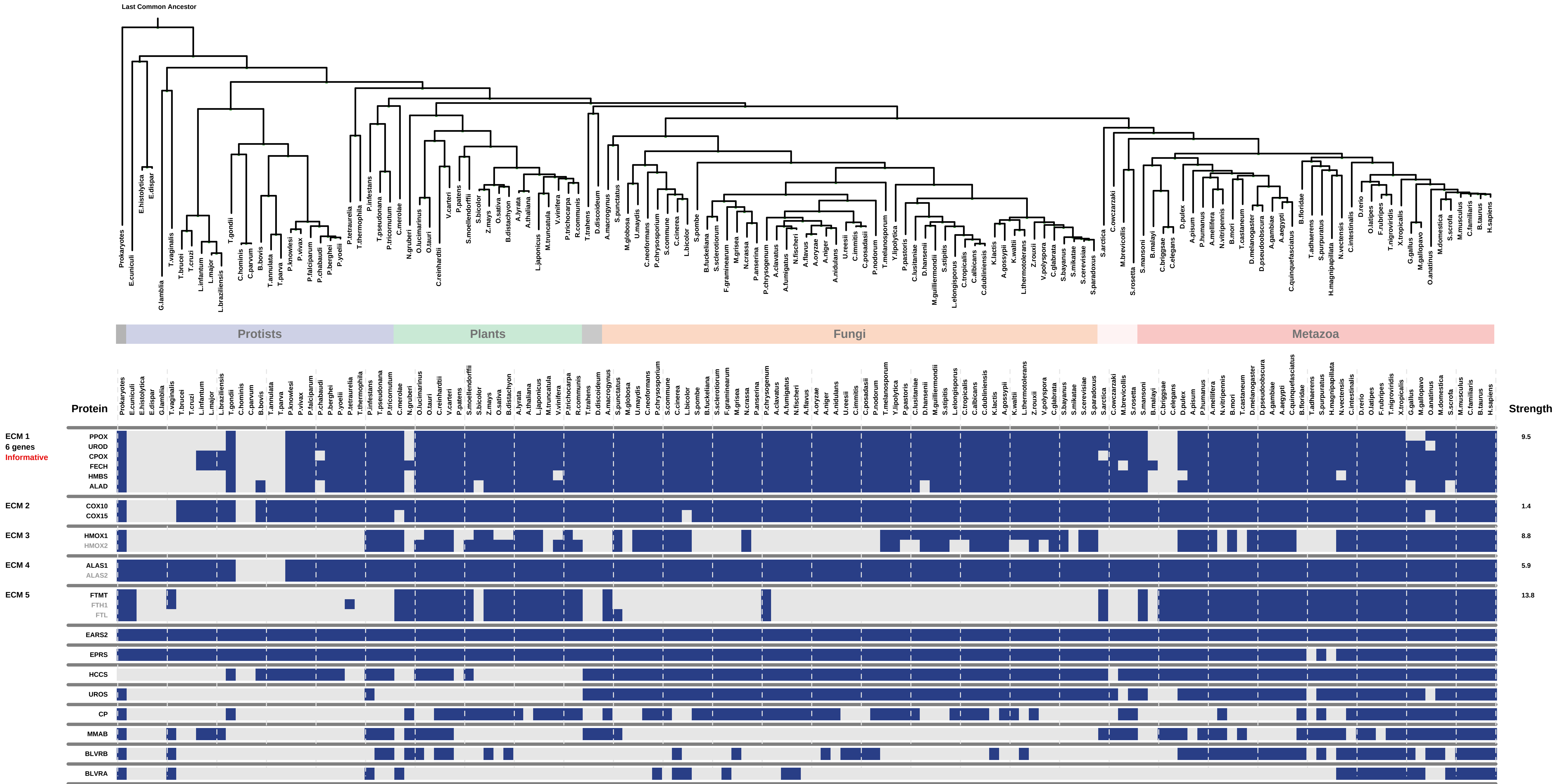
1) Overview of Evolutionarily Conserved Modules (ECMs)

- 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 $E < 1e-3$).

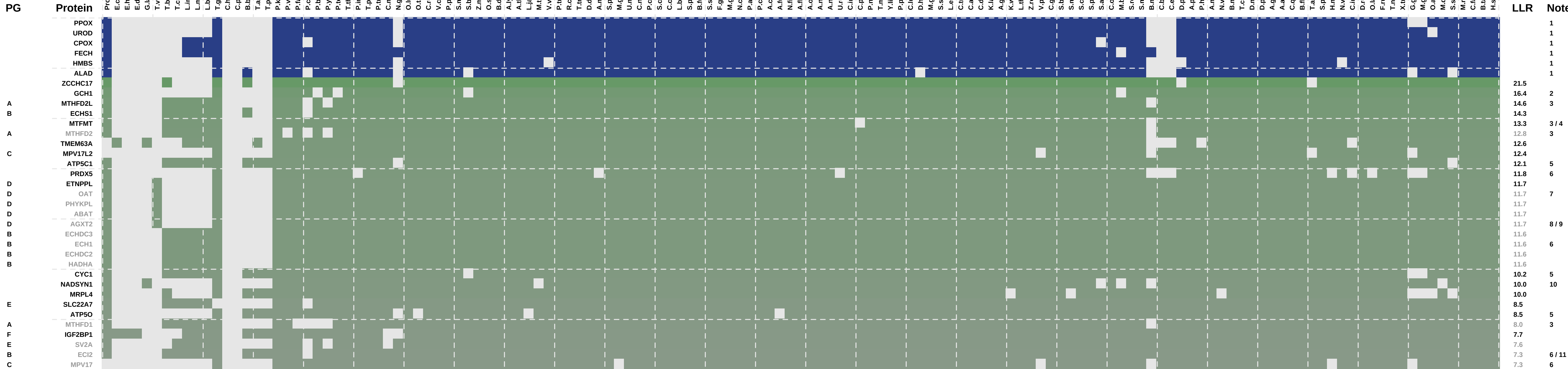
2) Details of each ECM and its expansion ECM+

- 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.

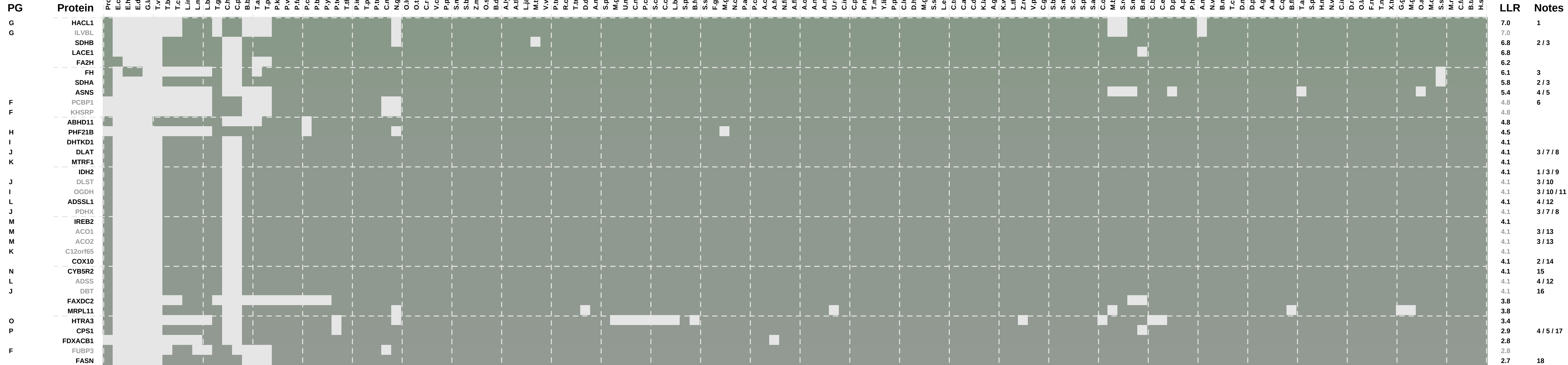
Overview of Evolutionarily Conserved Modules (ECMs)



Num of ECM Genes: 6. Num of Predicted Genes: 92. ECM Strength: 9.5

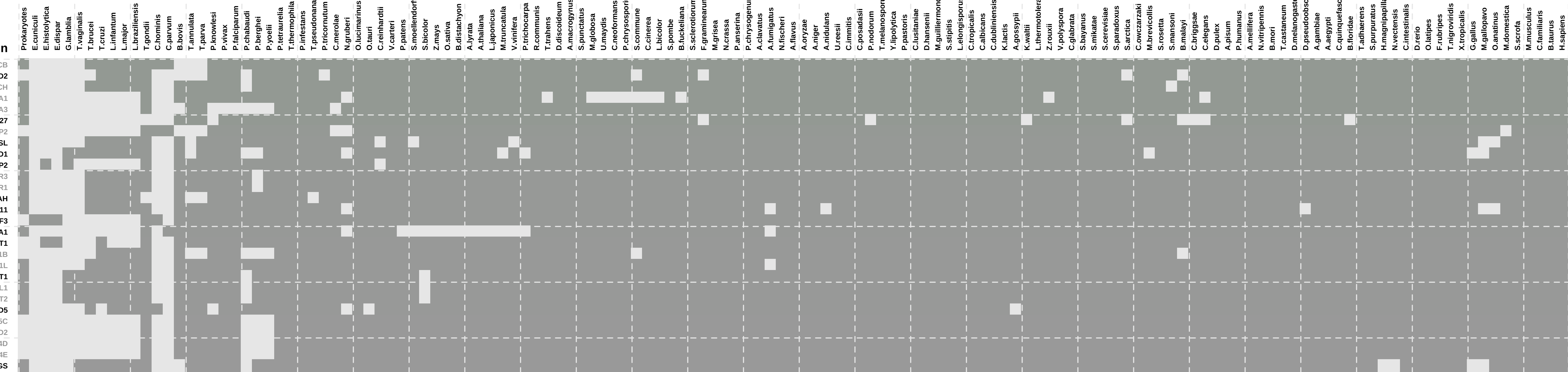


Num of ECM Genes: 6. Num of Predicted Genes: 92. ECM Strength: 9.5



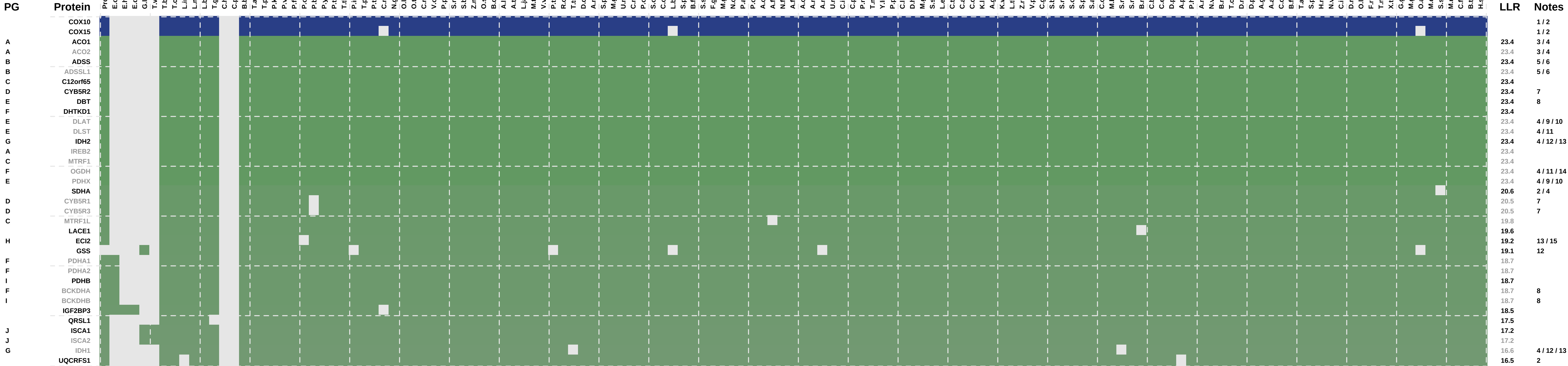
1: Peroxisome || 2: Oxidative phosphorylation || 3: Citrate cycle (TCA cycle) || 4: Alanine, aspartate and glutamate metabolism || 5: Nitrogen metabolism || 6: Spliceosome || 7: Pyruvate metabolism || 8: Glycolysis / Gluconeogenesis || 9: Glutathione metabolism || 10: Lysine degradation || 11: Tryptophan metabolism || 12: Purine metabolism || 13: Glyoxylate and dicarboxylate metabolism || 14: Porphyrin and chlorophyll metabolism || 15: Amino sugar and nucleotide sugar metabolism || 16: Valine, leucine and isoleucine degradation || 17: Arginine and proline metabolism || 18: Fatty acid biosynthesis

Num of ECM Genes: 6. Num of Predicted Genes: 92. ECM Strength: 9.5

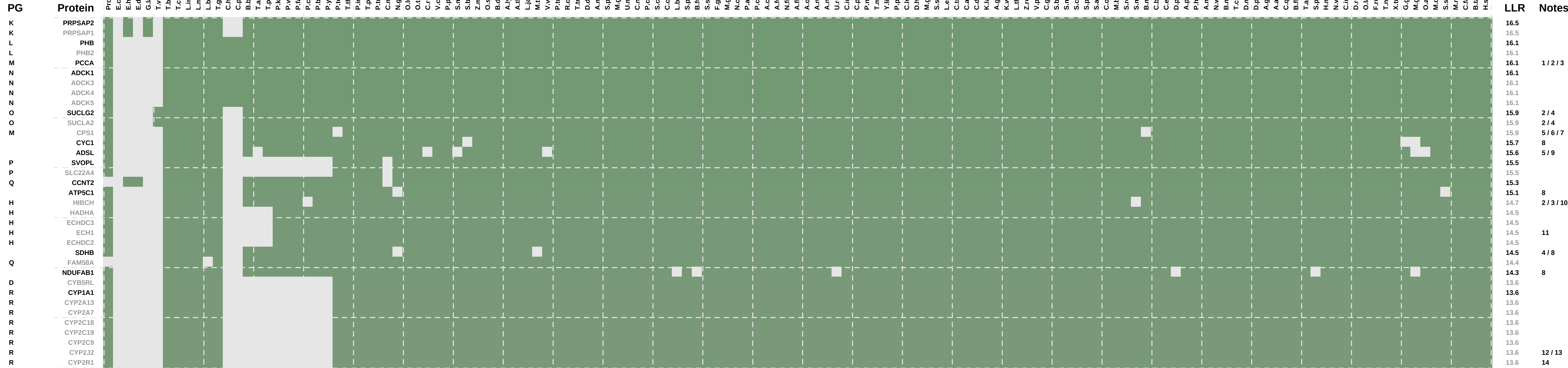


1: Propanoate metabolism || 2: Pyruvate metabolism || 3: Fatty acid biosynthesis || 4: Valine, leucine and isoleucine degradation || 5: beta-Alanine metabolism || 6: Alanine, aspartate and glutamate metabolism || 7: Purine metabolism || 8: Riboflavin metabolism || 9: Amino sugar and nucleotide sugar metabolism || 10: Oxidative phosphorylation || 11: Basal transcription factors || 12: Glycosphingolipid biosynthesis - ganglio series || 13: Folate biosynthesis

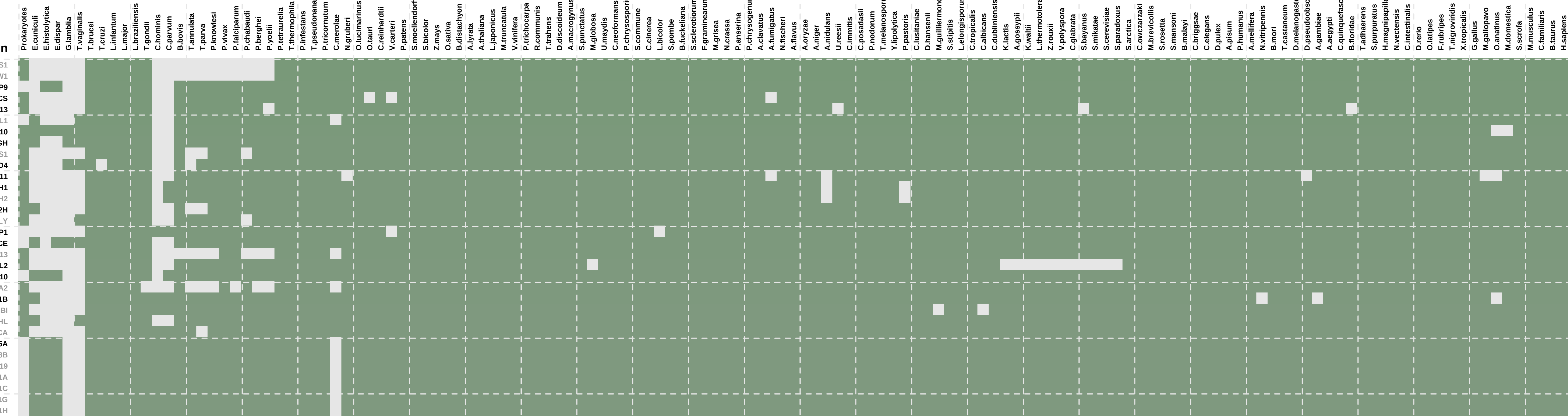
Num of ECM Genes: 2. Num of Predicted Genes: 100. ECM Strength: 1.4



Num of ECM Genes: 2. Num of Predicted Genes: 100. ECM Strength: 1.4

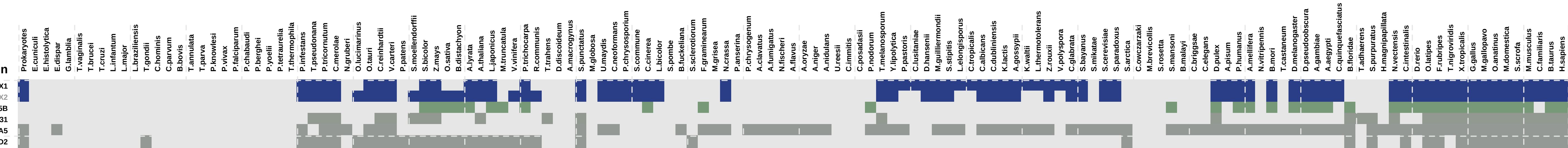


Num of ECM Genes: 2. Num of Predicted Genes: 100. ECM Strength: 1.4



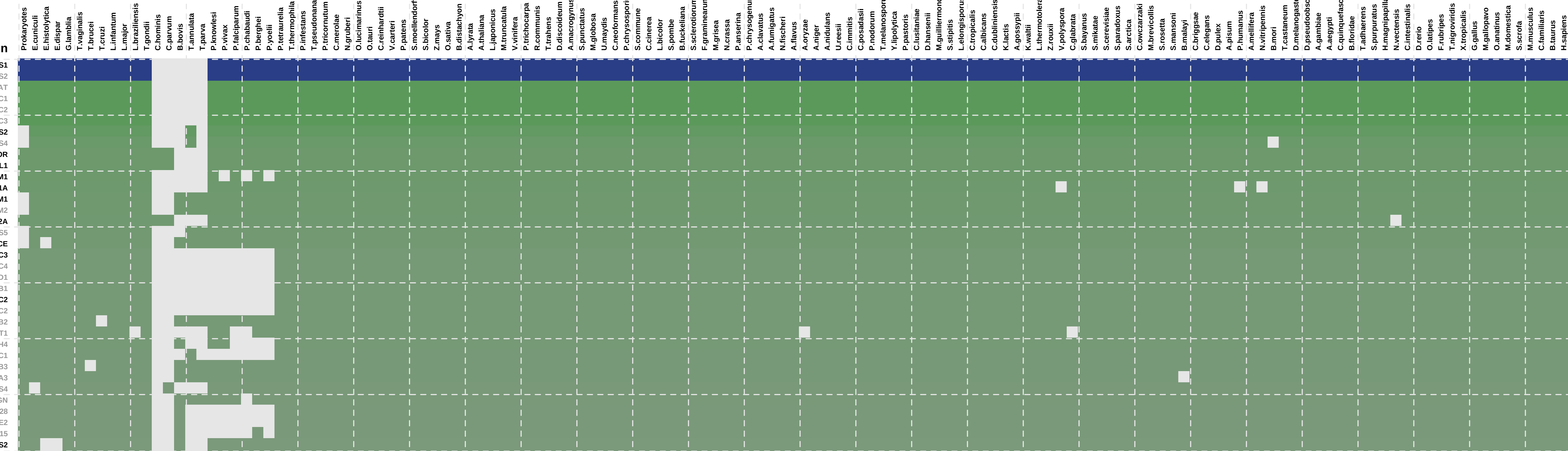
1: Arachidonic acid metabolism || 2: p53 signaling pathway || 3: Apoptosis || 4: Ribosome || 5: Pyruvate metabolism || 6: Oxidative phosphorylation || 7: Drug metabolism - other enzymes || 8: Purine metabolism || 9: Citrate cycle (TCA cycle) || 10: Propanoate metabolism || 11: Fatty acid biosynthesis

Num of ECM Genes: 2. Num of Predicted Genes: 4. ECM Strength: 8.8



LLR	Notes
1	
1	

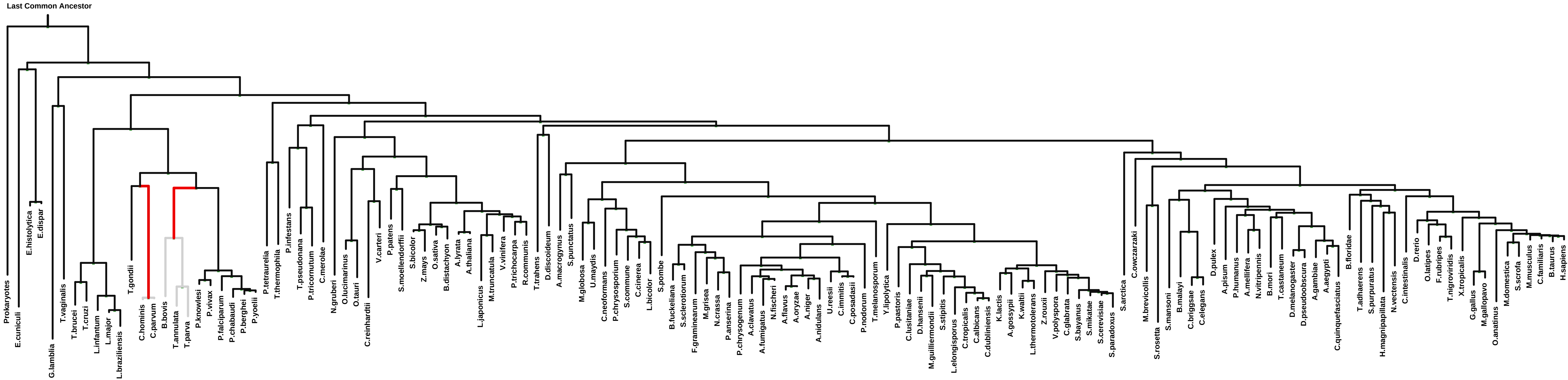
Num of ECM Genes: 2. Num of Predicted Genes: 100. ECM Strength: 5.9



LLR	Note
	1 / 2
	1 / 2
26.7	2
26.7	3
26.7	3
26.7	3
23.0	
20.1	
18.7	
18.7	
18.6	
18.4	
17.7	
17.7	
17.2	
16.7	
16.5	
14.9	4 / 5 / 6
14.9	4 / 5 / 7
14.9	4 / 7
14.9	
14.9	4 / 5
14.9	
14.8	
14.8	
14.6	4 / 5
14.2	
13.9	
13.8	8 / 9
13.6	
13.3	
13.3	
13.3	
13.0	10 / 11

ECM 4, Gene set "Porphyrin and chlorophyll metabolism", Page 2

Num of ECM Genes: 2. Num of Predicted Genes: 100. ECM Strength: 5.9



PG

H
H
C

D

I
I
I
B
C

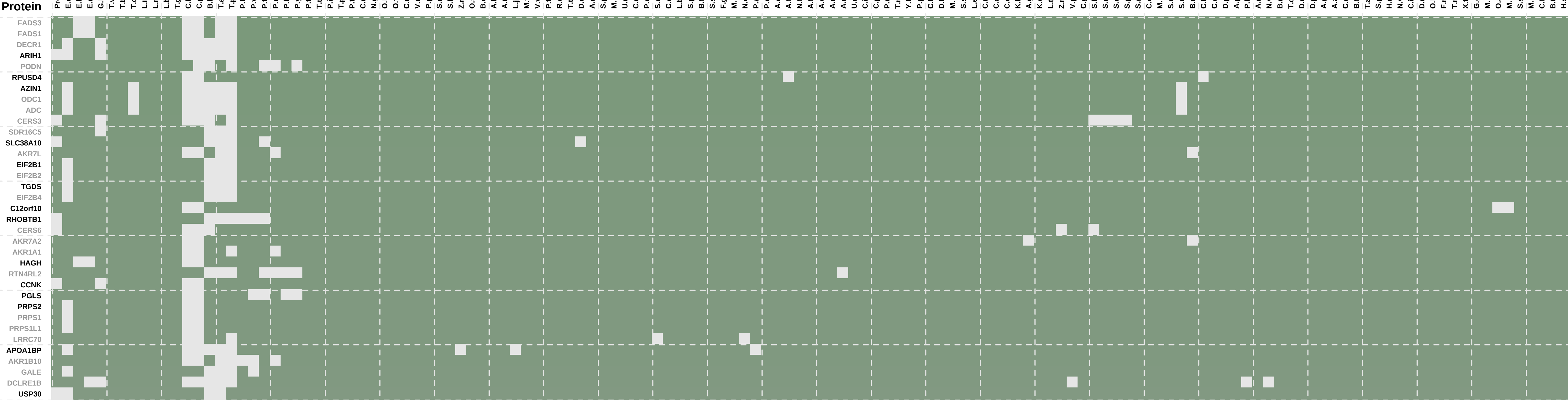
G
J
J
K
J

B
G
G

D

L
L
L
D

G
K
E



LLR

13.0
13.0
12.9
12.9
12.8
12.4
12.3
12.3
12.3
12.0
11.9
11.8
11.7
11.7
11.7
11.7
11.6
11.5
11.4
11.3
11.3
11.0
11.0
10.9
10.8
10.7
10.7
10.7
10.7
10.7
10.7
10.6
10.2
10.1
10.0

Notes

1

2 / 3
3

4
4

4

5

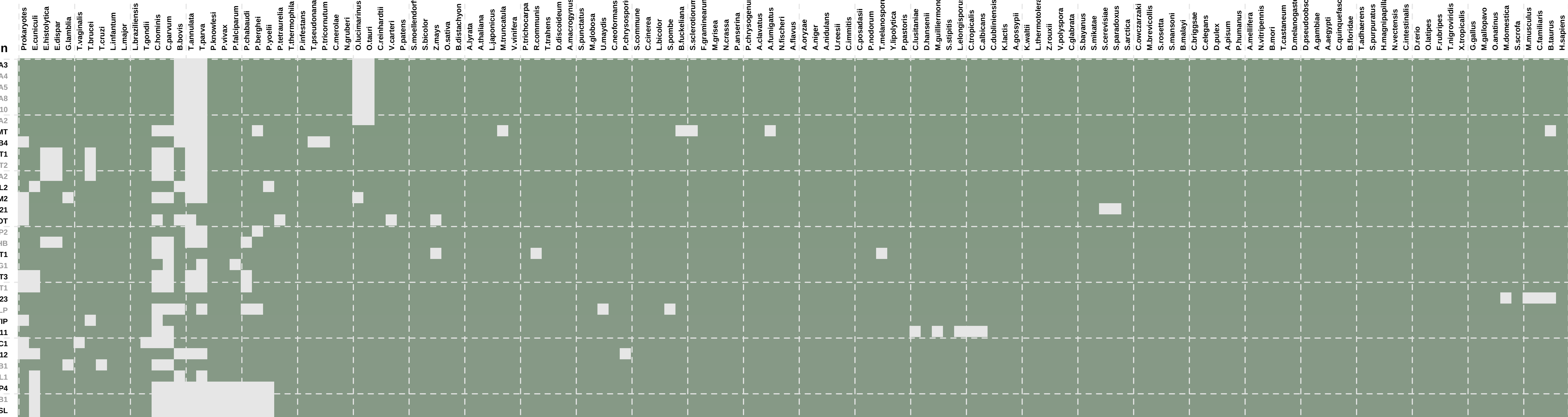
6 / 7
8

9
9 / 10
9 / 10
9 / 10

11 / 12 / 13
14 / 15

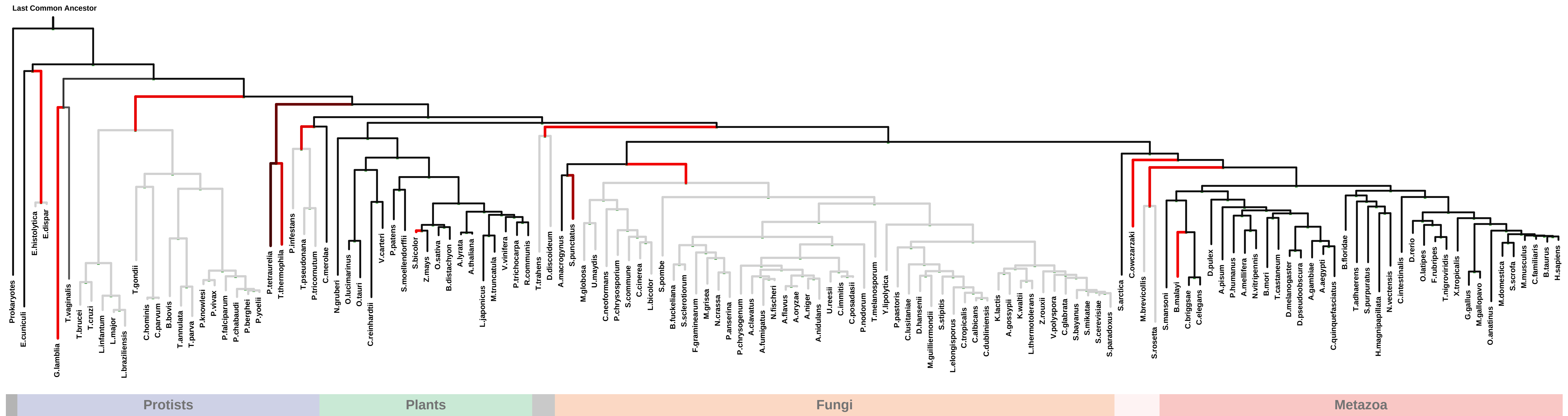
1: Biosynthesis of unsaturated fatty acids 2: Glutathione metabolism 3: Arginine and proline metabolism 4: RNA transport 5: Ubiquitin mediated proteolysis 6: Glycolysis / Gluconeogenesis 7: Glycerolipid metabolism 8: Pyruvate metabolism 9: Pentose phosphate pathway 10: Purine metabolism 11: Linoleic acid metabolism 12: Fructose and mannose metabolism 13: Butanoate metabolism 14: Amino sugar and nucleotide sugar metabolism 15: Galactose metabolism

Num of ECM Genes: 2. Num of Predicted Genes: 100. ECM Strength: 5.9



ECM 5, Gene set "Porphyrin and chlorophyll metabolism", Page 1

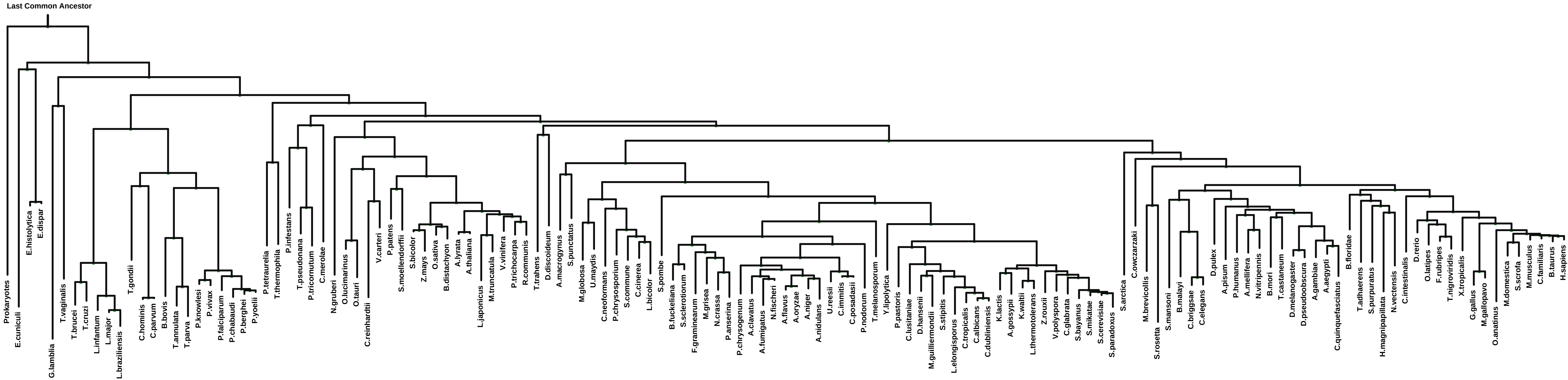
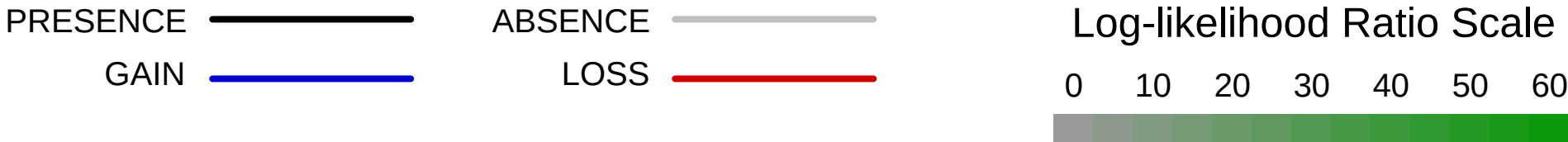
Num of ECM Genes: 3. Num of Predicted Genes: 1. ECM Strength: 13.8

[illegible]

1: Porphyrin and chlorophyll metabolism

ECM 6, Gene set "Porphyrin and chlorophyll metabolism", Page 1

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



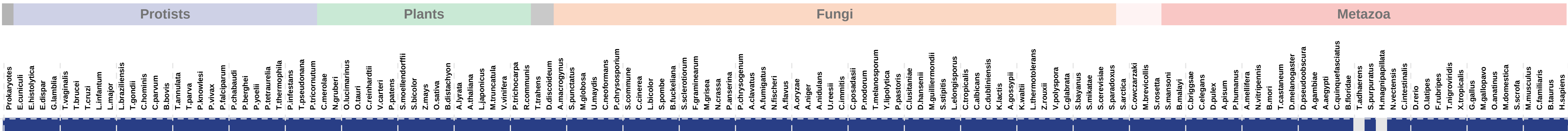
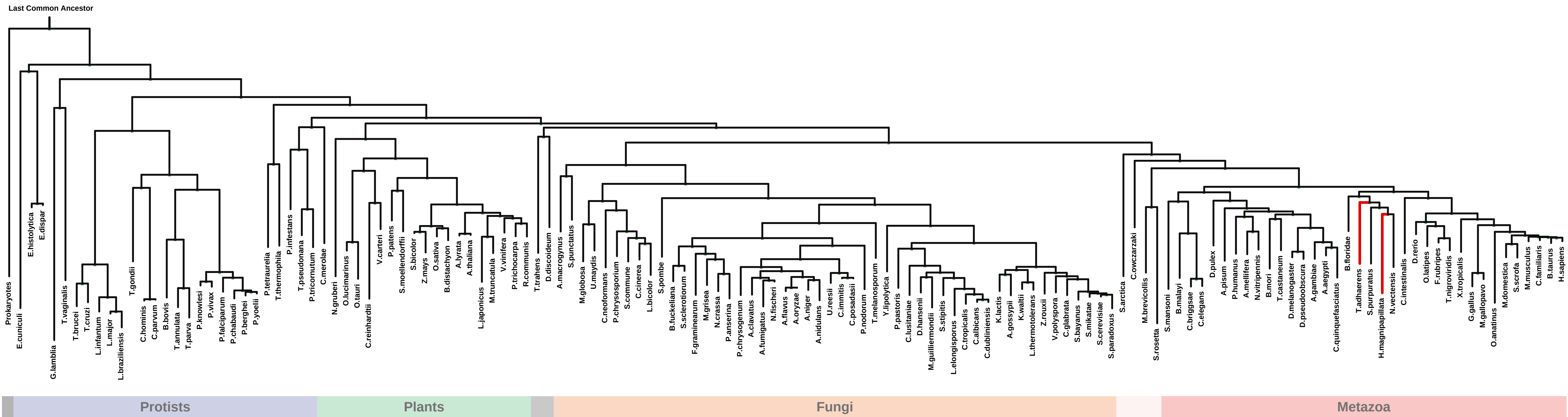
PG

Protein	LLR	Notes
EARS2		

1: Porphyrin and chlorophyll metabolism || 2: Aminoacyl-tRNA biosynthesis

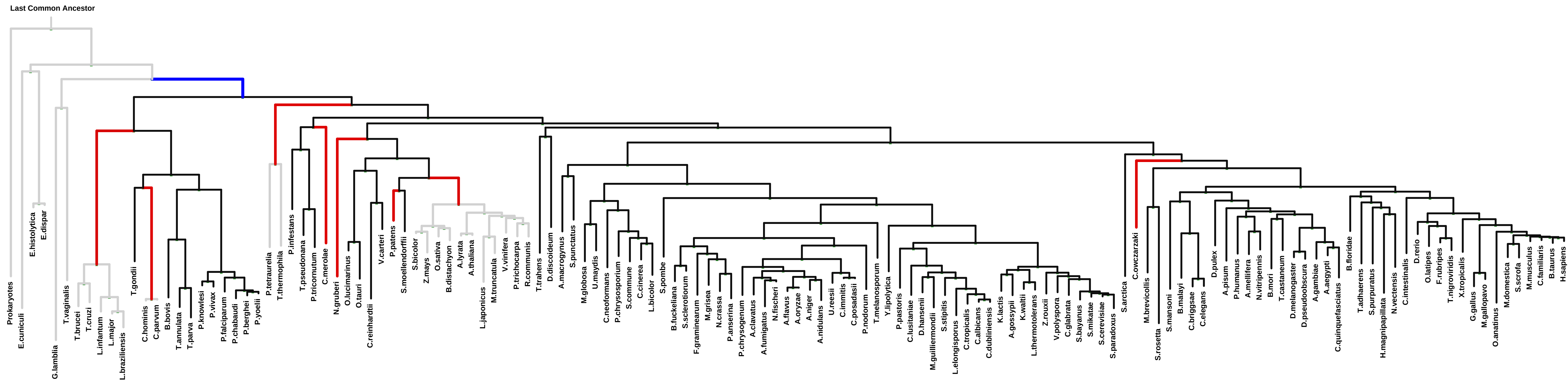
ECM 7, Gene set "Porphyrin and chlorophyll metabolism", Page 1

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



ECM 8, Gene set "Porphyrin and chlorophyll metabolism", Page 1

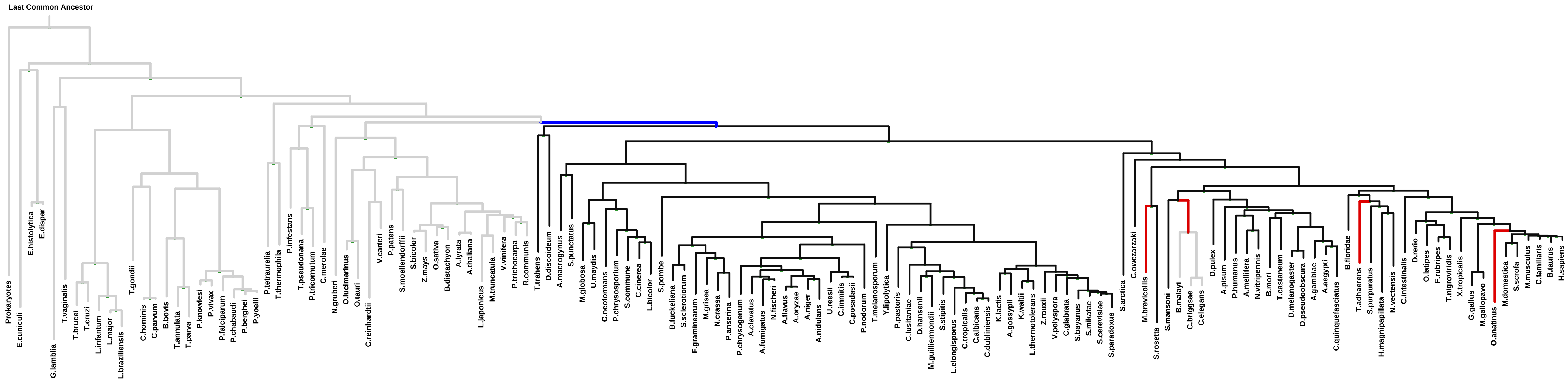
Num of ECM Genes: 1. Num of Predicted Genes: 8

[illegible]

1: Porphyrin and chlorophyll metabolism || 2: Glycosphingolipid biosynthesis - ganglio series

ECM 9, Gene set "Porphyrin and chlorophyll metabolism", Page 1

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

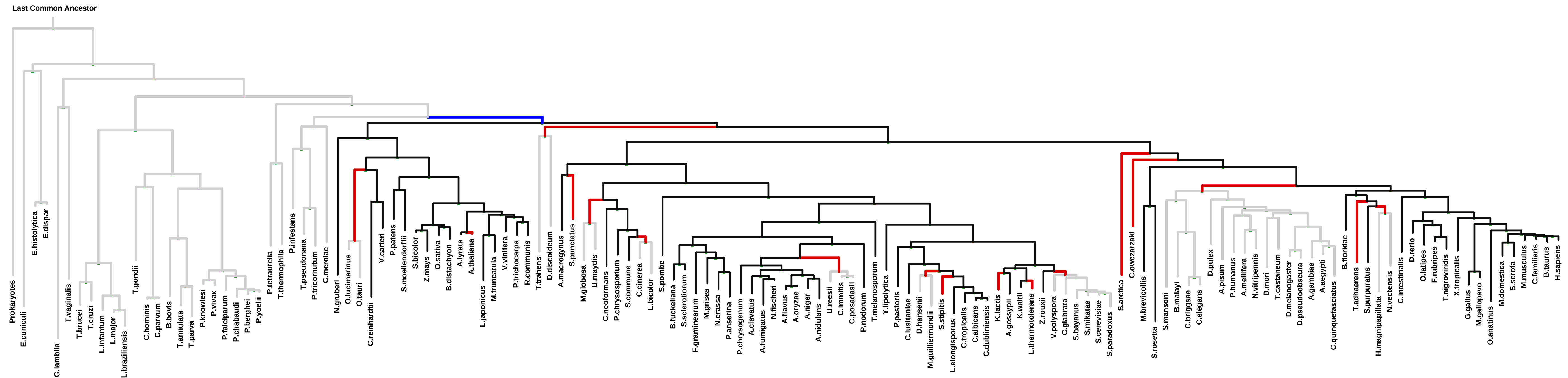
[illegible]

1

1

ECM 10, Gene set "Porphyrin and chlorophyll metabolism", Page 1

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

PG[illegible]

LLR Notes

1

27.7

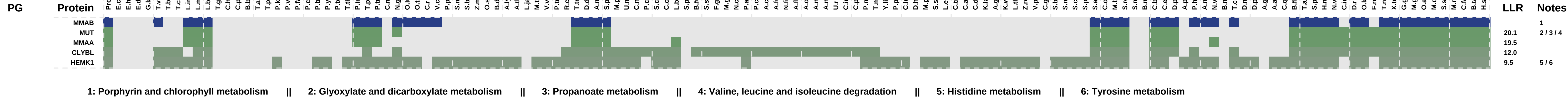
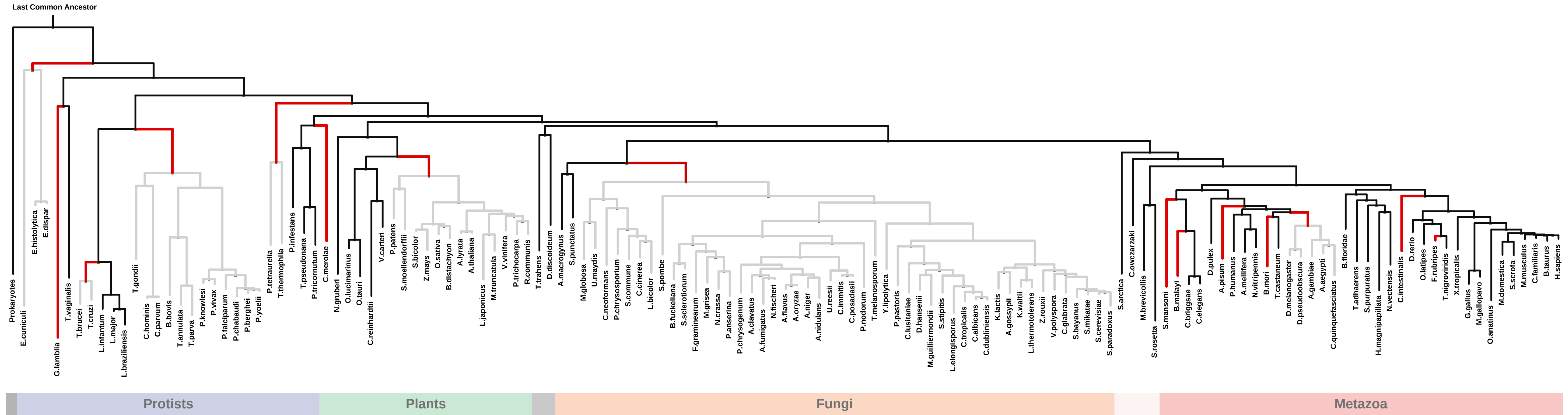
7.4

3.1

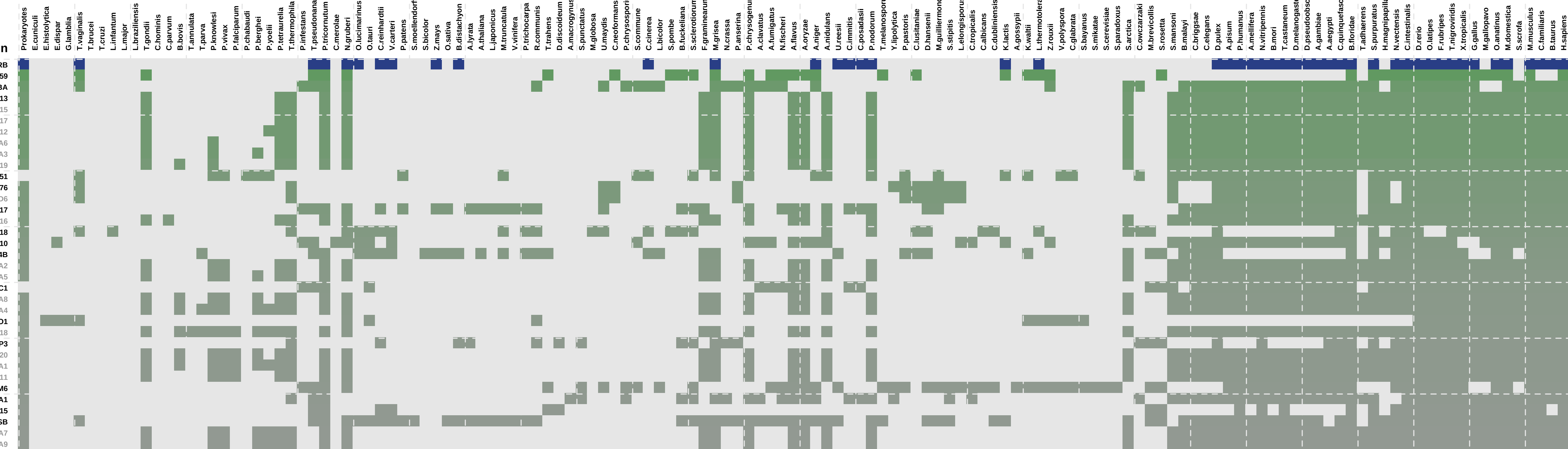
1: Porphyrin and chlorophyll metabolism

ECM 11, Gene set "Porphyrin and chlorophyll metabolism", Page 1

Num of ECM Genes: 1. Num of Predicted Genes: 4



Num of ECM Genes: 1. Num of Predicted Genes: 42

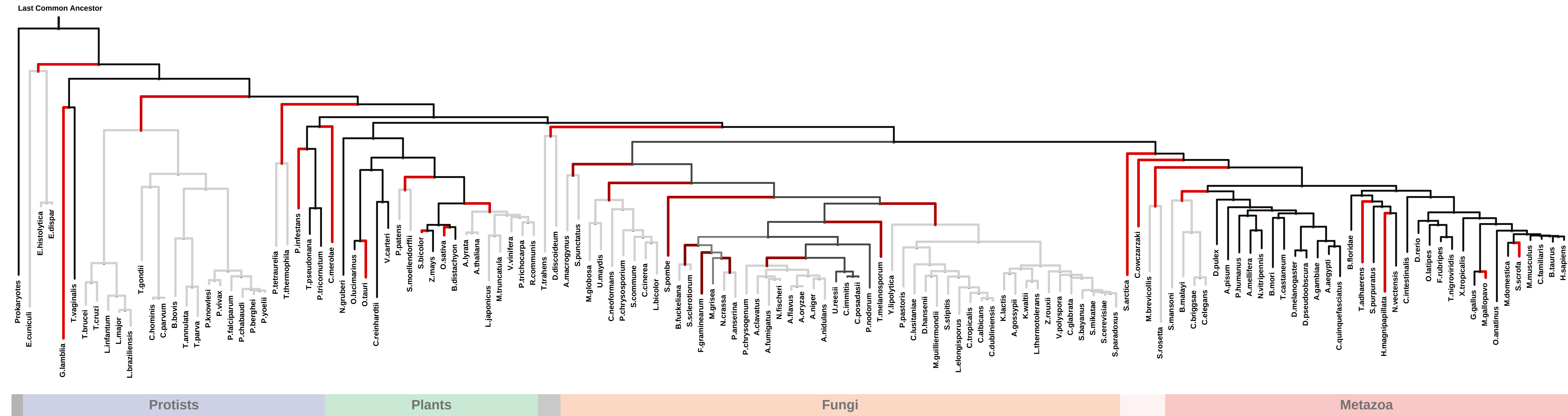
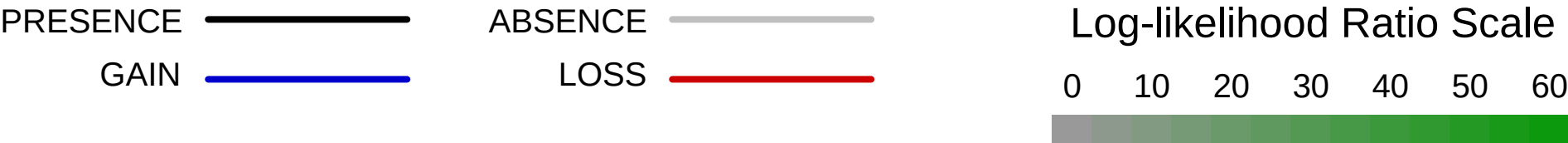


1: Porphyrin and chlorophyll metabolism || 2: Riboflavin metabolism || 3: Other glycan degradation || 4: Sphingolipid metabolism || 5: Lysosome || 6: Mucin type O-Glycan biosynthesis || 7: Glycosaminoglycan biosynthesis - chondroitin sulfate

LLR	Notes
	1 / 2
24.0	
18.7	3 / 4 / 5
16.6	
16.6	
16.6	
16.6	
16.5	
14.4	
12.8	
12.3	
12.3	
11.4	
11.0	
10.0	
8.9	
8.8	
8.0	
7.1	
7.0	6
6.6	
6.5	
6.2	
6.0	
4.8	
4.8	
4.5	
4.5	
4.2	
3.9	
3.3	7
3.3	
3.0	
3.0	

ECM 12, Gene set "Porphyrin and chlorophyll metabolism", Page 2

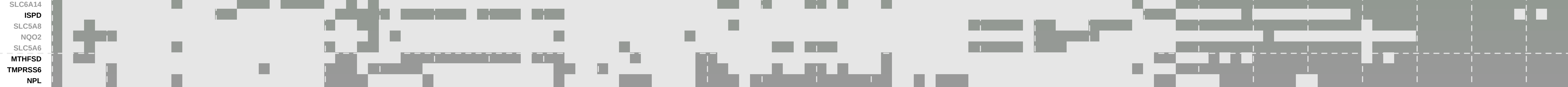
Num of ECM Genes: 1. Num of Predicted Genes: 42



PG

A
C
D
C

Protein



LLR

Notes

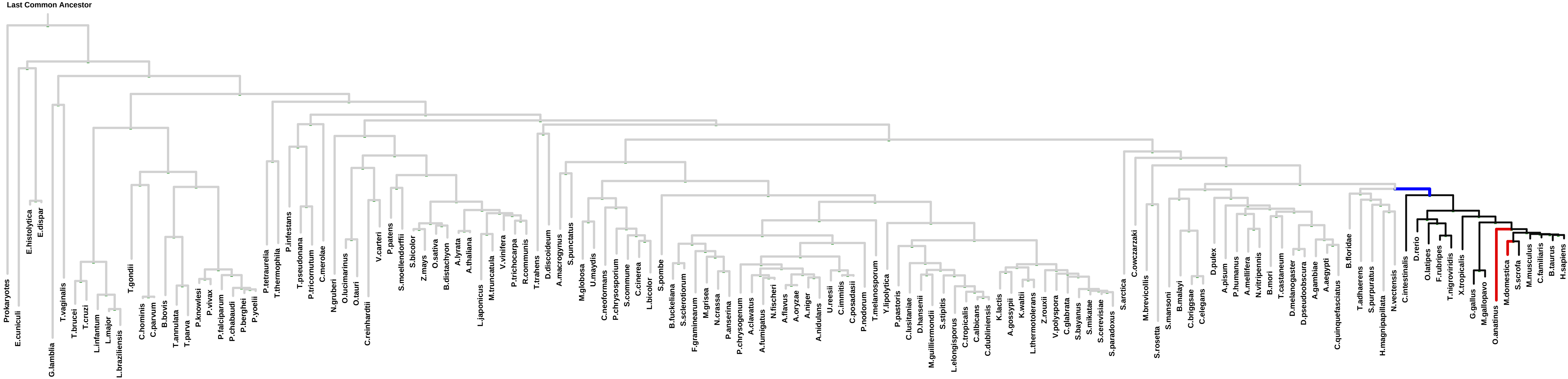
2.9
2.6
2.4
1.8
1.6
0.5
0.2
0.2

1

1: Amino sugar and nucleotide sugar metabolism

ECM 13, Gene set "Porphyrin and chlorophyll metabolism", Page 1

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



PG

Protein	Protists	Plants	Fungi	Metazoa
BLVRA	■			
FLJ38723	■			
LOC390638				
LOC441736				

1: Porphyrin and chlorophyll metabolism

LLR Notes

1
0.5
0.5
0.5