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

Dataset:

Num of genes in input gene set: 21
Total number of genes: 20834
Prediction LLR threshold: 0

The CLIME PDF output two sections:

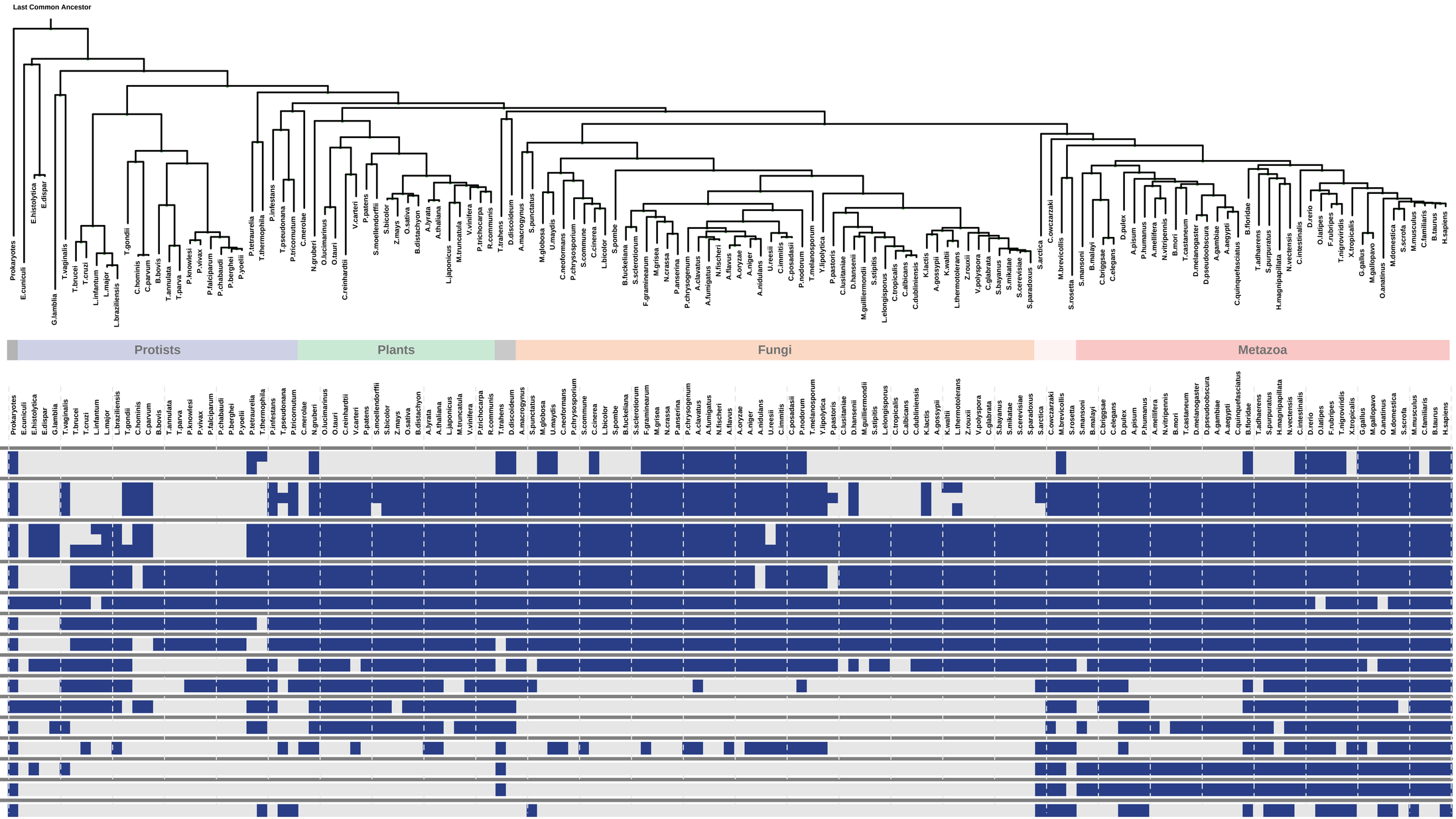
1) Overview of Evolutionarily Conserved Modules (ECMs)

- 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+

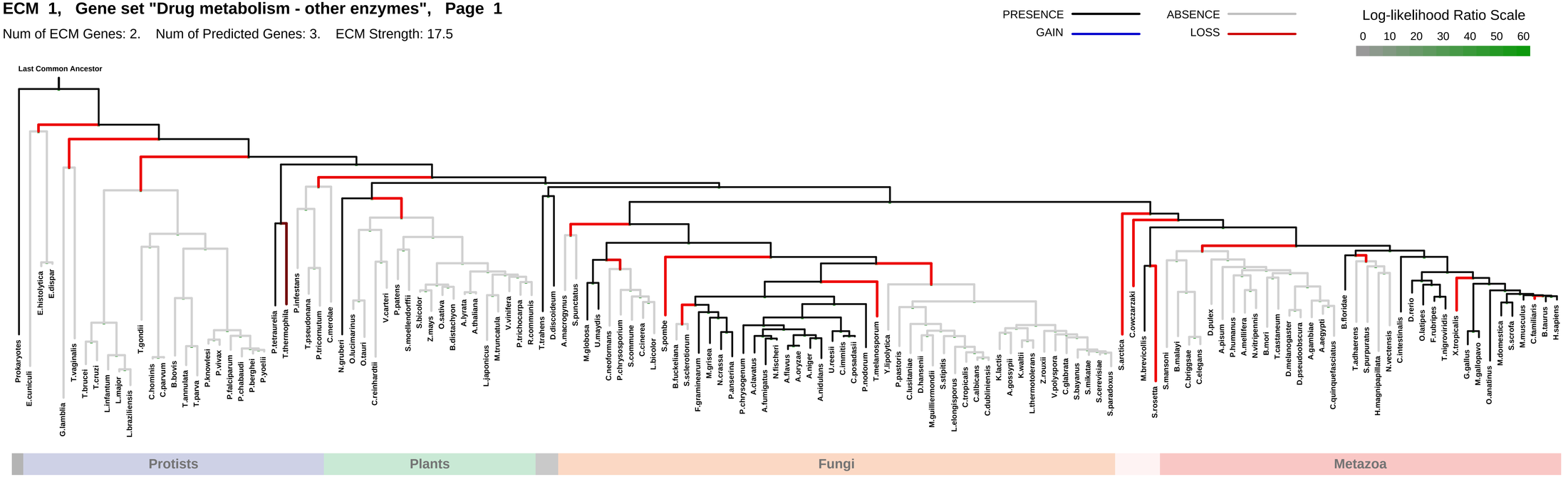
- Top panel shows the inferred evolutionary history on the predefined species tree. Branch color shows the gain event (blue) and loss events (red color, with brighter color indicating higher confidence in loss). Branches before the gain or after a loss are shown in gray.
- Bottom panel shows the input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

Num of ECM Genes: 2. Num of Predicted Genes: 3. ECM Strength: 17.5

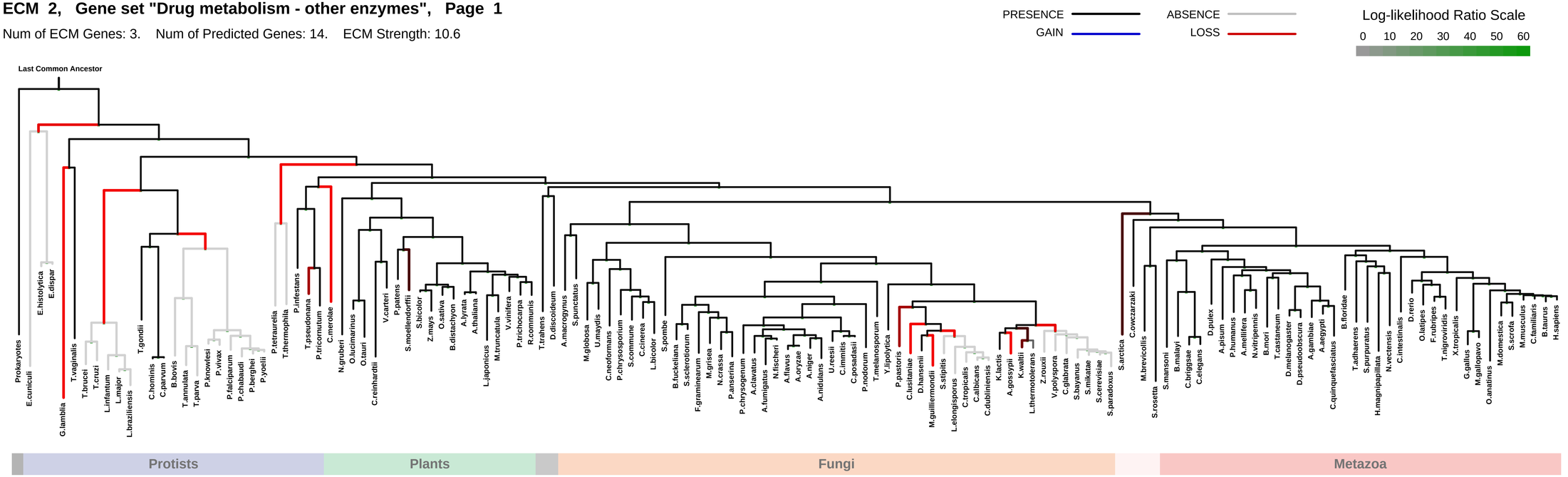


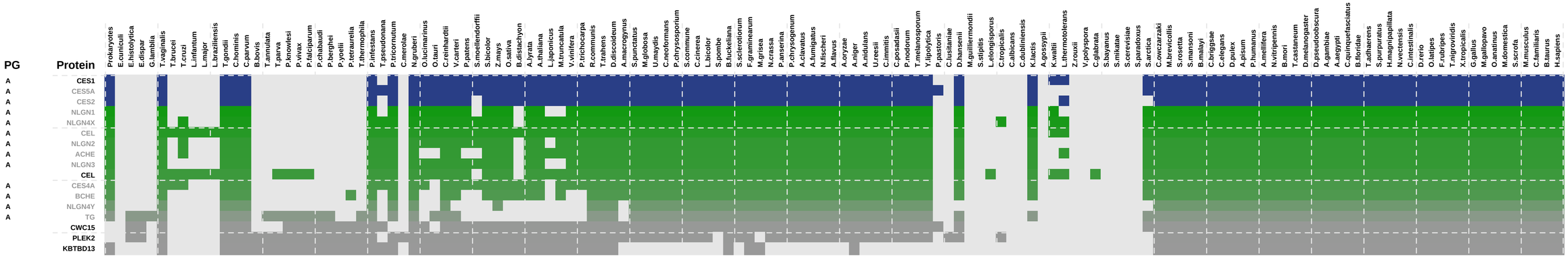
PG	Protein	LLR	Notes
A	NAT2		1 / 2
A	NAT1		1 / 2
	SLFNL1	10.9	
	OGFRL1	2.3	
	NUDT19	1.4	3

1: Caffeine metabolism || 2: Drug metabolism - other enzymes || 3: Peroxisome

ECM 2, Gene set "Drug metabolism - other enzymes", Page 1

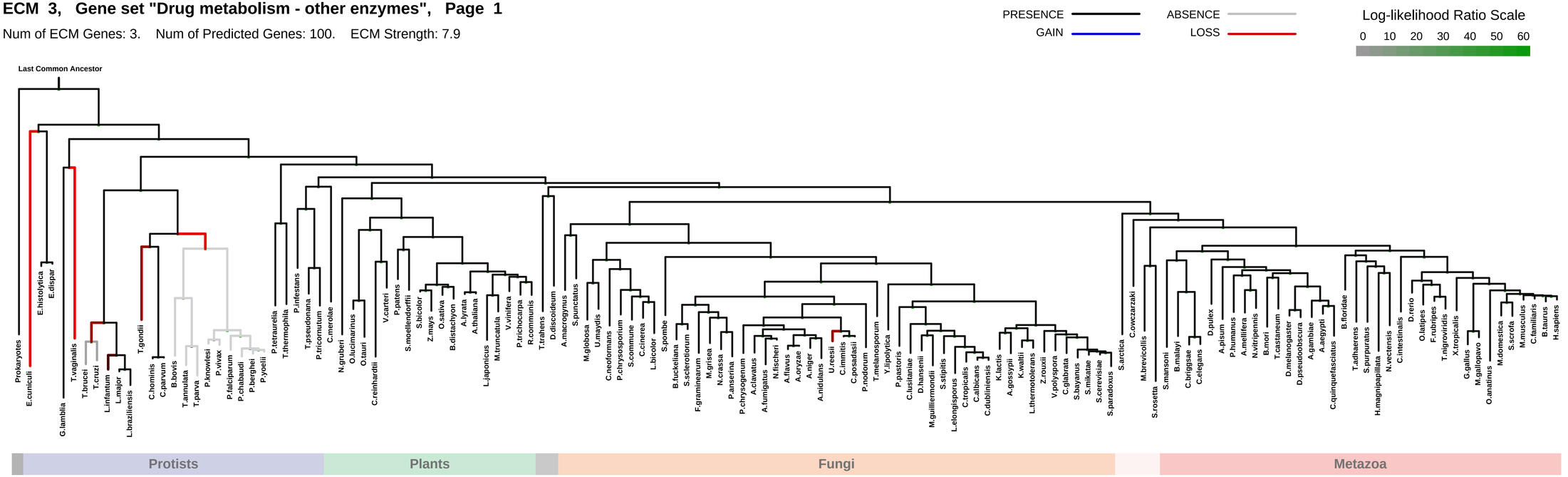
Num of ECM Genes: 3. Num of Predicted Genes: 14. ECM Strength: 10.6

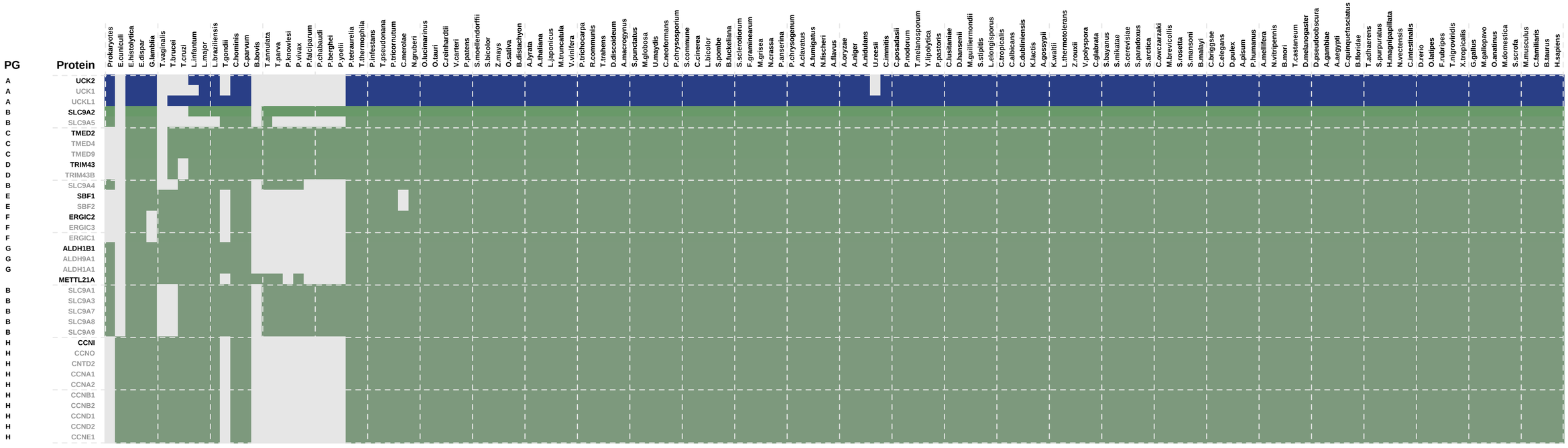




ECM 3, Gene set "Drug metabolism - other enzymes", Page 1

Num of ECM Genes: 3. Num of Predicted Genes: 100. ECM Strength: 7.9



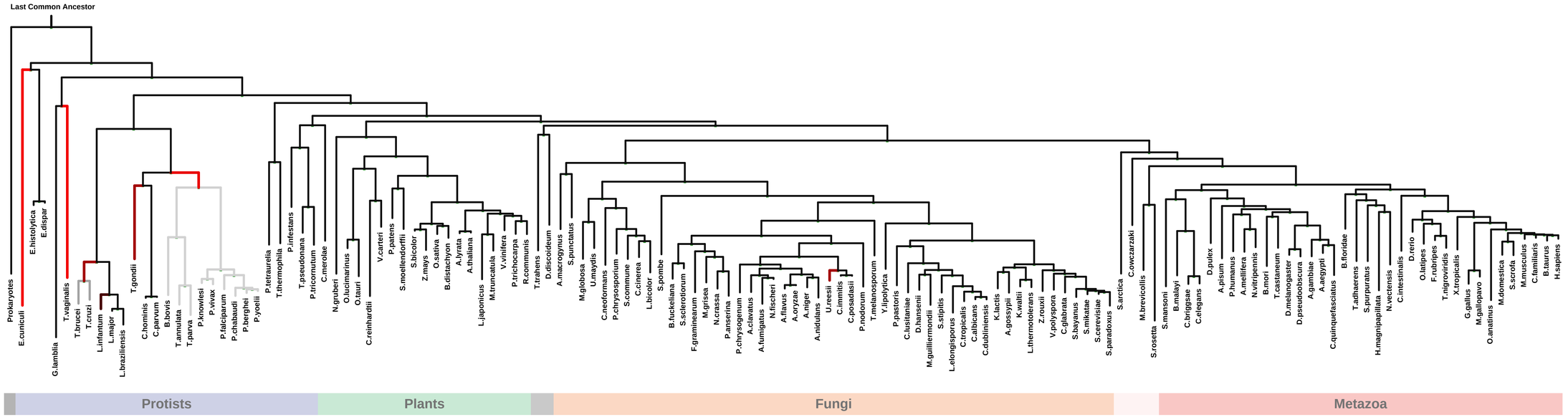


1: Drug metabolism - other enzymes || 2: Pyrimidine metabolism || 3: Retinol metabolism || 4: Regulation of actin cytoskeleton || 5: Cell cycle || 6: p53 signaling pathway || 7: Oocyte meiosis || 8: Focal adhesion

ECM 3, Gene set "Drug metabolism - other enzymes", Page 2

Num of ECM Genes: 3. Num of Predicted Genes: 100. ECM Strength: 7.9

PRESENCE ABSENCE
GAIN LOSS
Log-likelihood Ratio Scale
0 10 20 30 40 50 60

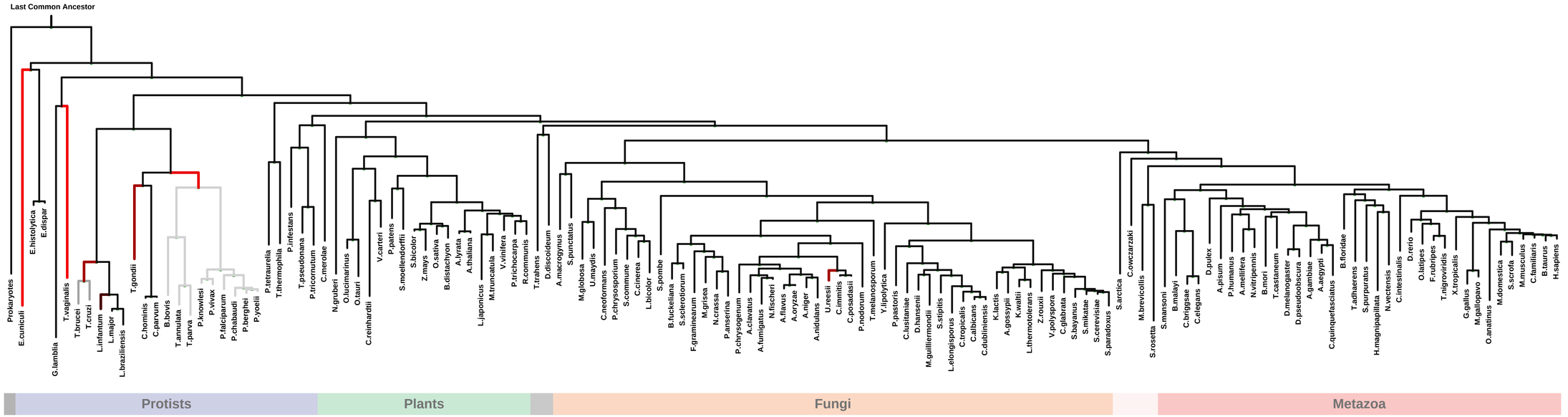


PG	Protein	LLR	Notes
H	CCNE2	12.0	1 / 2 / 3
	KIAA0020	12.0	
H	CCNB3	11.9	1 / 2
I	SMYD1	11.8	
B	SLC9A6	11.7	
	NFYC	11.6	
	ABCC3	11.5	
	ZADH2	11.5	
J	SNX7	11.5	
J	SNX30	11.4	
	COASY	11.3	4
	ZC3H4	11.1	
	YIPF6	11.0	
	CAPS	10.9	
	AADAT	10.8	5 / 6 / 7
K	COPZ2	10.4	
	PCCB	10.2	8 / 9 / 10
L	ADH6	9.9	
	DNAJC28	9.5	
M	LRCH1	9.3	
	TRIT1	9.0	
N	SLC36A1	8.8	
	NSDHL	8.7	11
	CLIP3	8.6	
	ANKRD13C	8.3	
	RPS25	8.3	12
	SVOP	8.3	
O	ARHGAP25	8.0	
C	TMED7	7.6	
K	COPZ1	7.6	
	RNF103-CHMP3	7.5	
	UTP11L	7.5	
P	POLH	7.4	
	SETD1A	7.1	6
D	TRIM64B	7.1	

1: Cell cycle || 2: p53 signaling pathway || 3: Oocyte meiosis || 4: Pantothenate and CoA biosynthesis || 5: Tryptophan metabolism || 6: Lysine degradation || 7: Lysine biosynthesis || 8: Glyoxylate and dicarboxylate metabolism ||
9: Propanoate metabolism || 10: Valine, leucine and isoleucine degradation || 11: Steroid biosynthesis || 12: Ribosome

ECM 3, Gene set "Drug metabolism - other enzymes", Page 3

Num of ECM Genes: 3. Num of Predicted Genes: 100. ECM Strength: 7.9

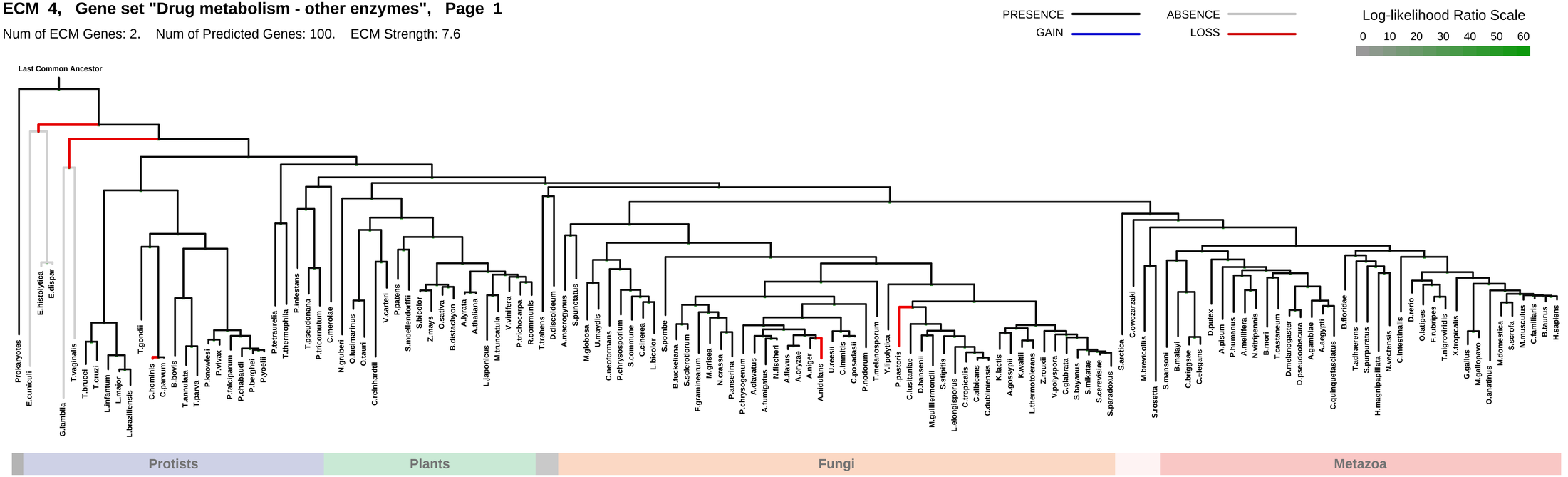


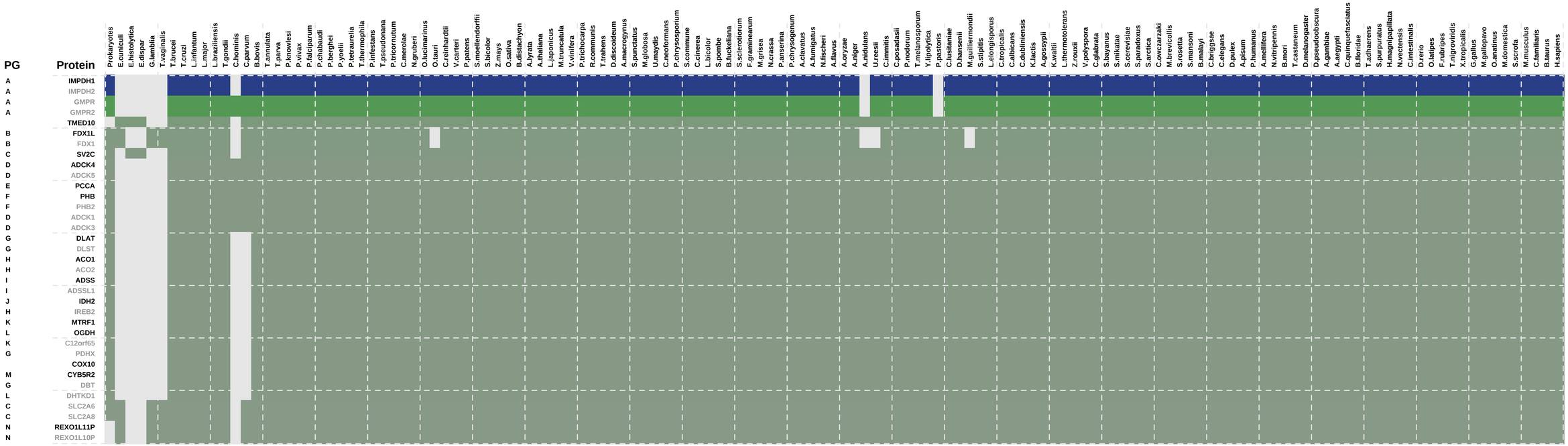
PG	Protein	LLR	Notes
D	TRIM64	7.1	
	LRRC29	6.9	
	PAXIP1	6.9	
M	GP5	6.8	
	TRMT61A	6.6	
A	UPRT	6.5	1
	PPP4R1	6.4	
O	ARHGAP24	6.0	
M	RTN4R	6.0	
	IMPA2	5.9	2
	STON1-GTF2A1L	5.8	
I	SMYD3	5.8	
L	SORD	5.7	3
Q	GANAB	5.7	4 / 5
Q	SI	5.7	6
Q	GANC	5.7	6 / 7
Q	MGAM	5.7	6 / 7
G	ALDH1A3	5.7	
L	ADH5	5.7	
G	ALDH1A2	5.7	8
R	ALG11	5.7	4
Q	100508894	5.7	
I	SMYD2	5.6	
N	SLC36A2	5.6	
	SETD3	5.4	
P	POLK	5.3	
	PEX5	5.3	9
	TBC1D21	5.2	
	MTPAP	5.2	
N	SLC36A4	5.0	
	NFYB	5.0	
J	SNX1	4.9	
R	ALG2	4.7	4

1: Pyrimidine metabolism || 2: Inositol phosphate metabolism || 3: Fructose and mannose metabolism || 4: N-Glycan biosynthesis || 5: Protein processing in endoplasmic reticulum || 6: Starch and sucrose metabolism || 7: Galactose metabolism || 8: Retinol metabolism || 9: Peroxisome

ECM 4, Gene set "Drug metabolism - other enzymes", Page 1

Num of ECM Genes: 2. Num of Predicted Genes: 100. ECM Strength: 7.6

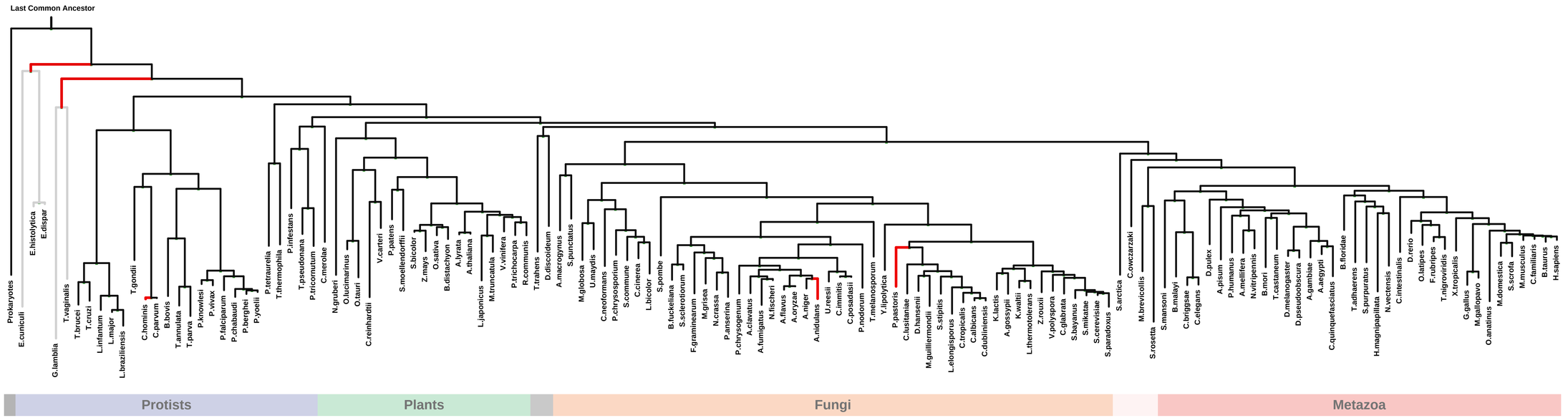


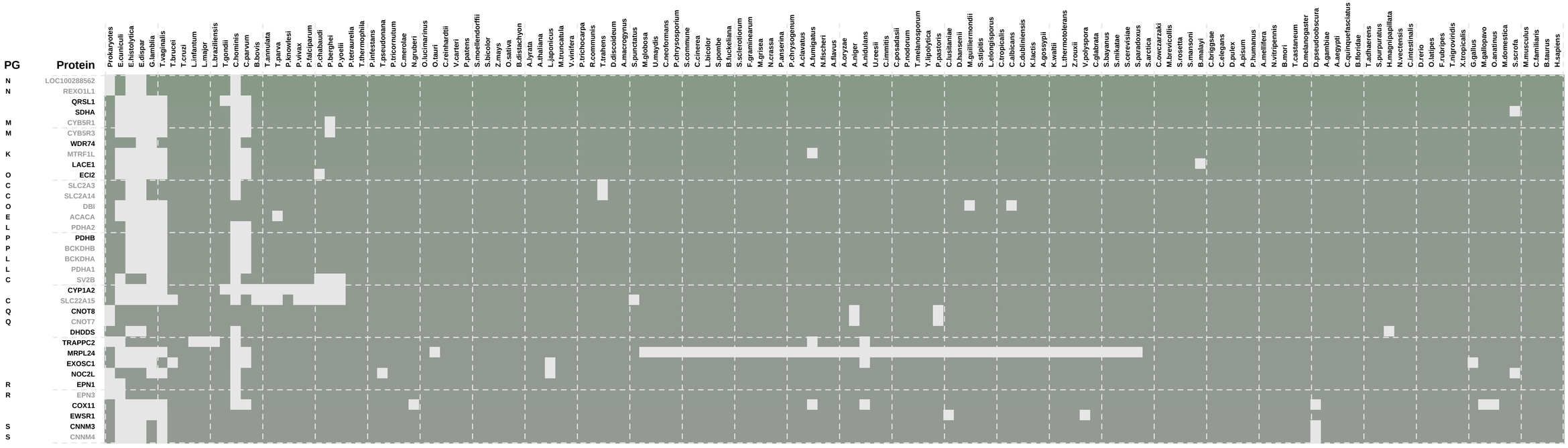


1: Drug metabolism - other enzymes || 2: Purine metabolism || 3: Glyoxylate and dicarboxylate metabolism || 4: Propanoate metabolism || 5: Valine, leucine and isoleucine degradation || 6: Pyruvate metabolism || 7: Glycolysis / Gluconeogenesis || 8: Citrate cycle (TCA cycle) || 9: Lysine degradation || 10: Alanine, aspartate and glutamate metabolism || 11: Glutathione metabolism || 12: Peroxisome || 13: Tryptophan metabolism || 14: Porphyrin and chlorophyll metabolism || 15: Oxidative phosphorylation || 16: Amino sugar and nucleotide sugar metabolism

ECM 4, Gene set "Drug metabolism - other enzymes", Page 2

Num of ECM Genes: 2. Num of Predicted Genes: 100. ECM Strength: 7.6

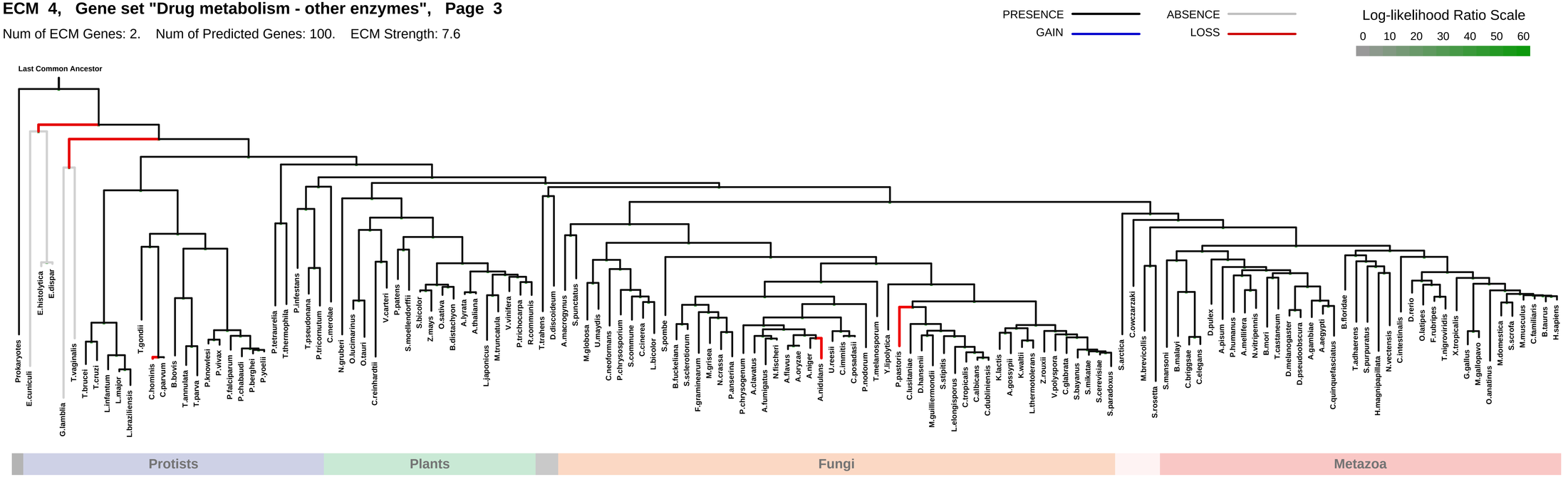


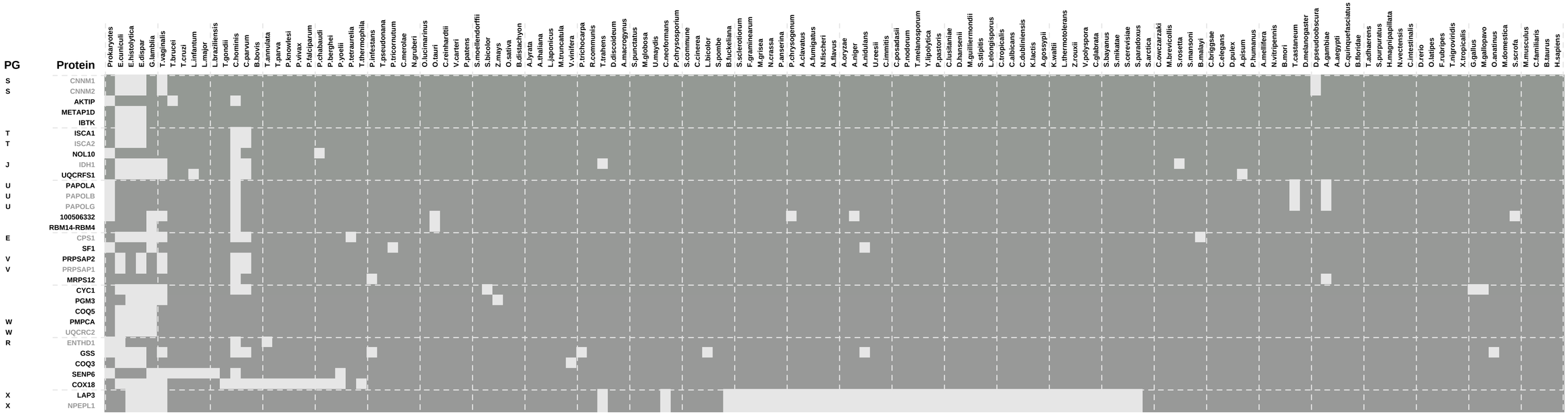


1: Ribosome biogenesis in eukaryotes || 2: Oxidative phosphorylation || 3: Citrate cycle (TCA cycle) || 4: Amino sugar and nucleotide sugar metabolism || 5: Peroxisome || 6: Fatty acid metabolism || 7: Propanoate metabolism ||
8: Pyruvate metabolism || 9: Fatty acid biosynthesis || 10: Valine, leucine and isoleucine degradation || 11: RNA degradation || 12: Terpenoid backbone biosynthesis || 13: Endocytosis

ECM 4, Gene set "Drug metabolism - other enzymes", Page 3

Num of ECM Genes: 2. Num of Predicted Genes: 100. ECM Strength: 7.6

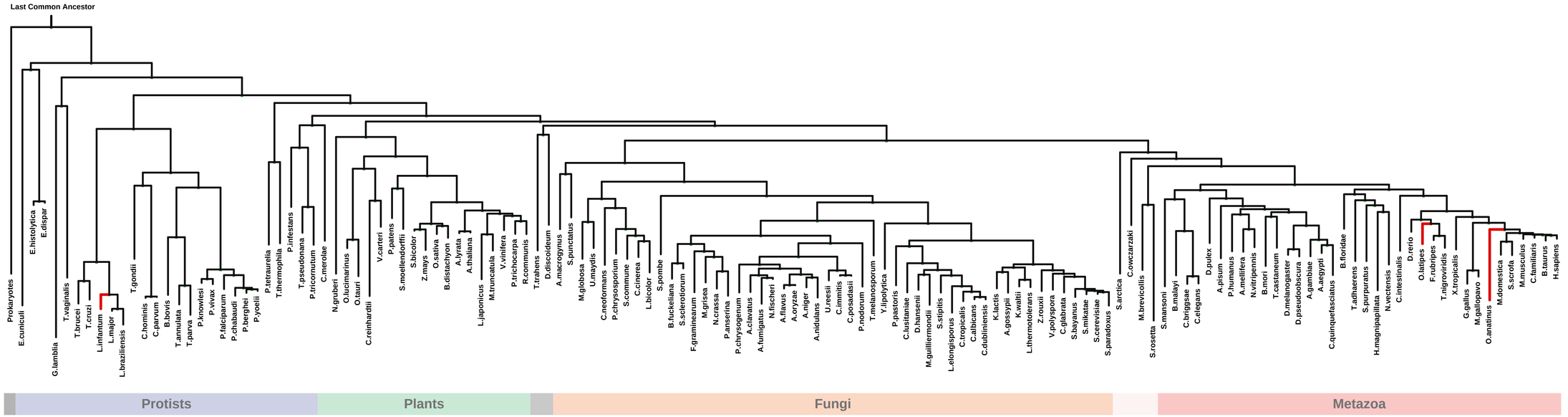


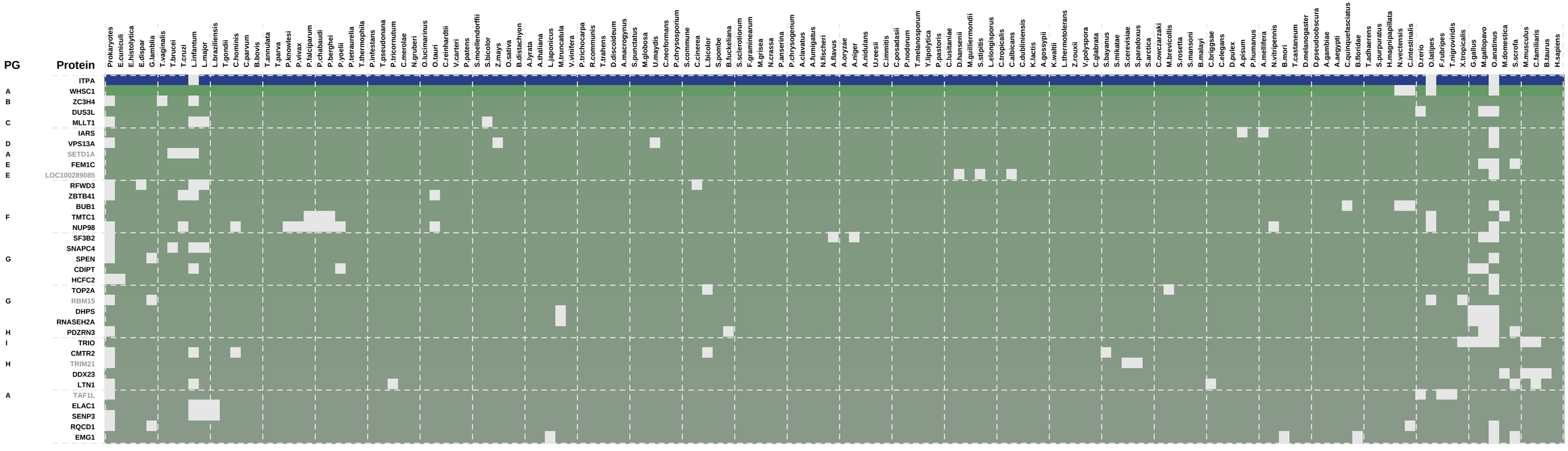


1: Glutathione metabolism || 2: Citrate cycle (TCA cycle) || 3: Peroxisome || 4: Oxidative phosphorylation || 5: mRNA surveillance pathway || 6: Alanine, aspartate and glutamate metabolism || 7: Arginine and proline metabolism ||
8: Nitrogen metabolism || 9: Amino sugar and nucleotide sugar metabolism || 10: Ubiquinone and other terpenoid-quinone biosynthesis

ECM 5, Gene set "Drug metabolism - other enzymes", Page 1

Num of ECM Genes: 1. Num of Predicted Genes: 100

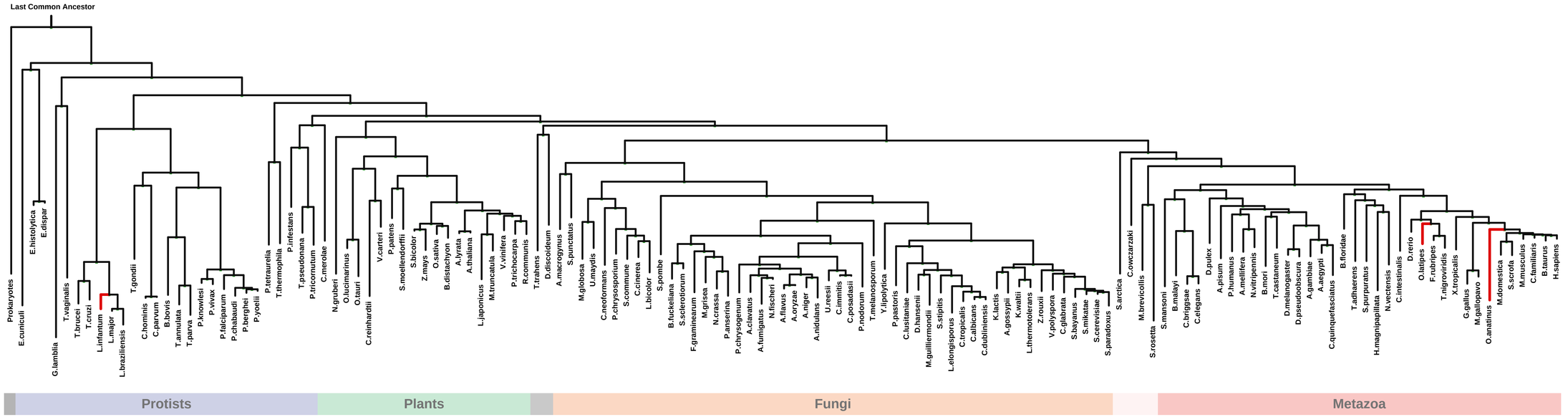


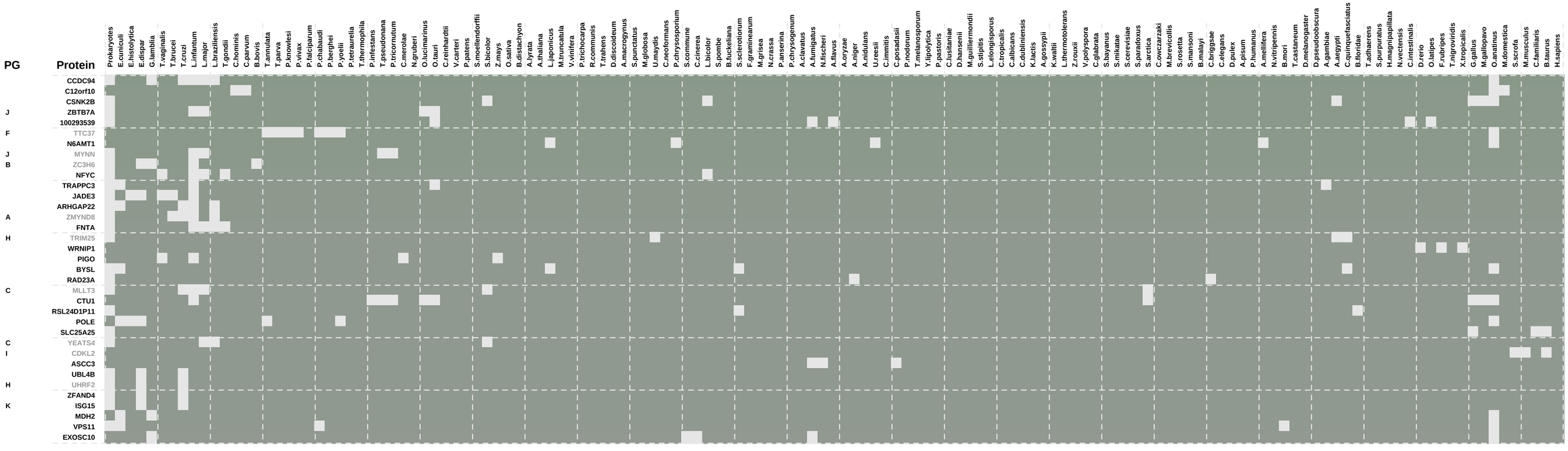


1: Drug metabolism - other enzymes || 2: Purine metabolism || 3: Pyrimidine metabolism || 4: Lysine degradation || 5: Aminoacyl-tRNA biosynthesis || 6: Valine, leucine and isoleucine biosynthesis || 7: Cell cycle || 8: Oocyte meiosis ||
9: RNA transport || 10: Spliceosome || 11: Inositol phosphate metabolism || 12: Glycerophospholipid metabolism || 13: DNA replication || 14: Basal transcription factors || 15: RNA degradation || 16: Ribosome biogenesis in eukaryotes

ECM 5, Gene set "Drug metabolism - other enzymes", Page 2

Num of ECM Genes: 1. Num of Predicted Genes: 100

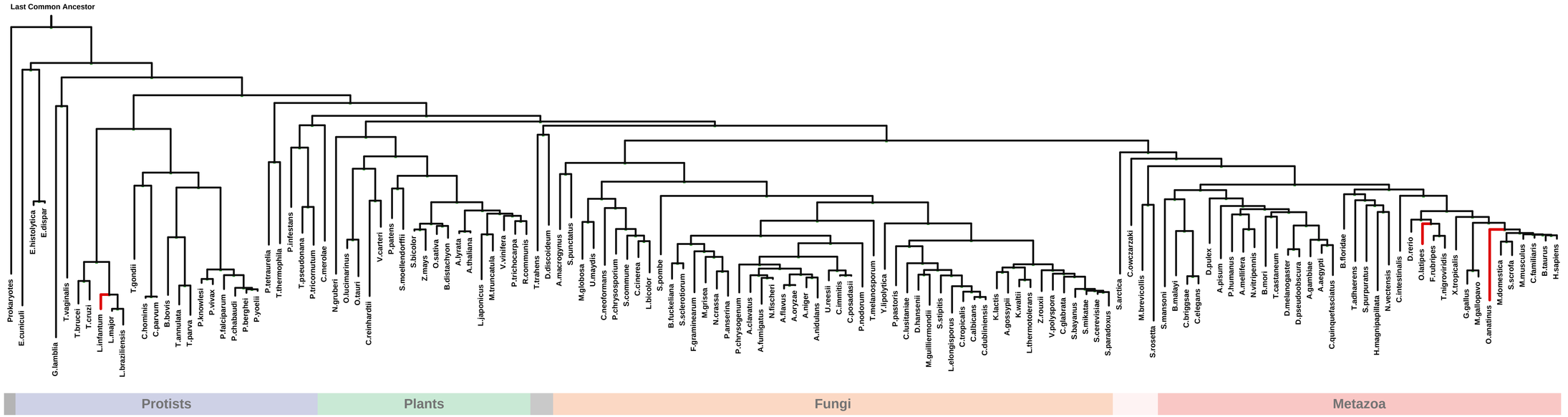


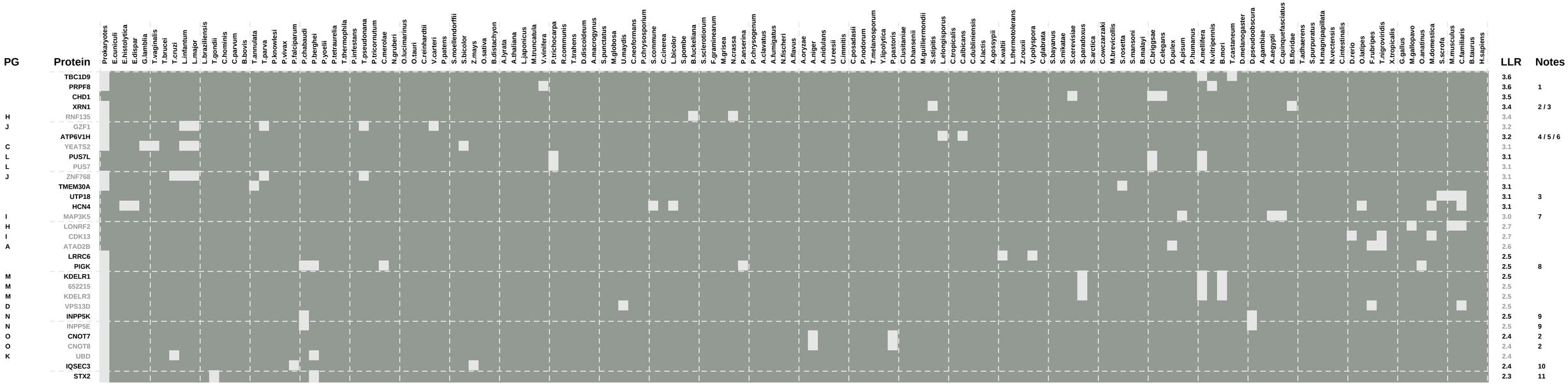


1: Adherens junction || 2: Tight junction || 3: Ribosome biogenesis in eukaryotes || 4: RNA degradation || 5: Glycosylphosphatidylinositol(GPI)-anchor biosynthesis || 6: Protein processing in endoplasmic reticulum || 7: Nucleotide excision repair ||
8: Sulfur relay system || 9: Ribosome || 10: Glyoxylate and dicarboxylate metabolism || 11: Pyruvate metabolism || 12: Citrate cycle (TCA cycle)

ECM 5, Gene set "Drug metabolism - other enzymes", Page 3

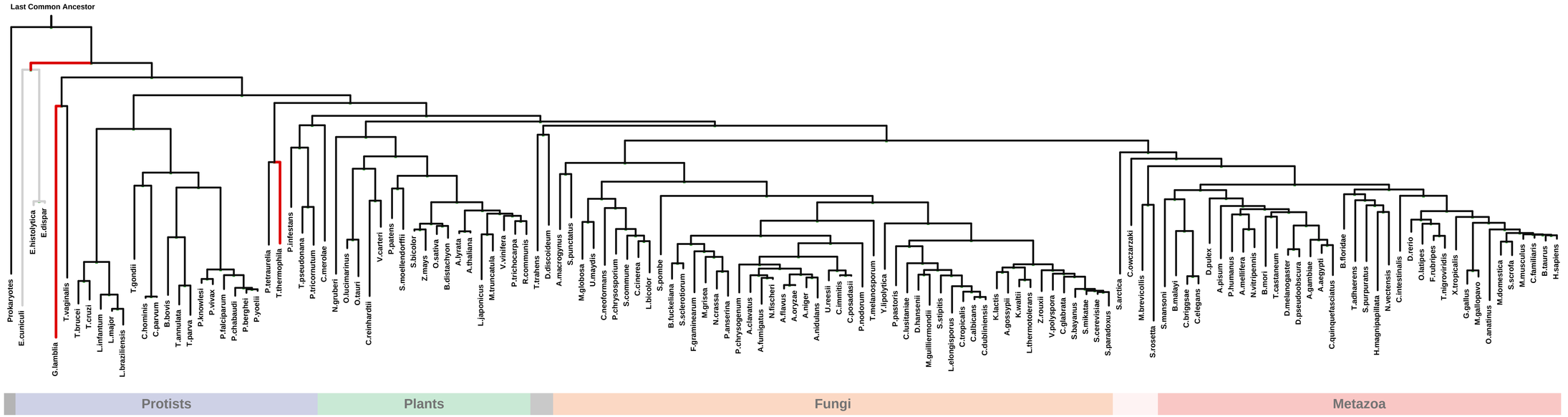
Num of ECM Genes: 1. Num of Predicted Genes: 100

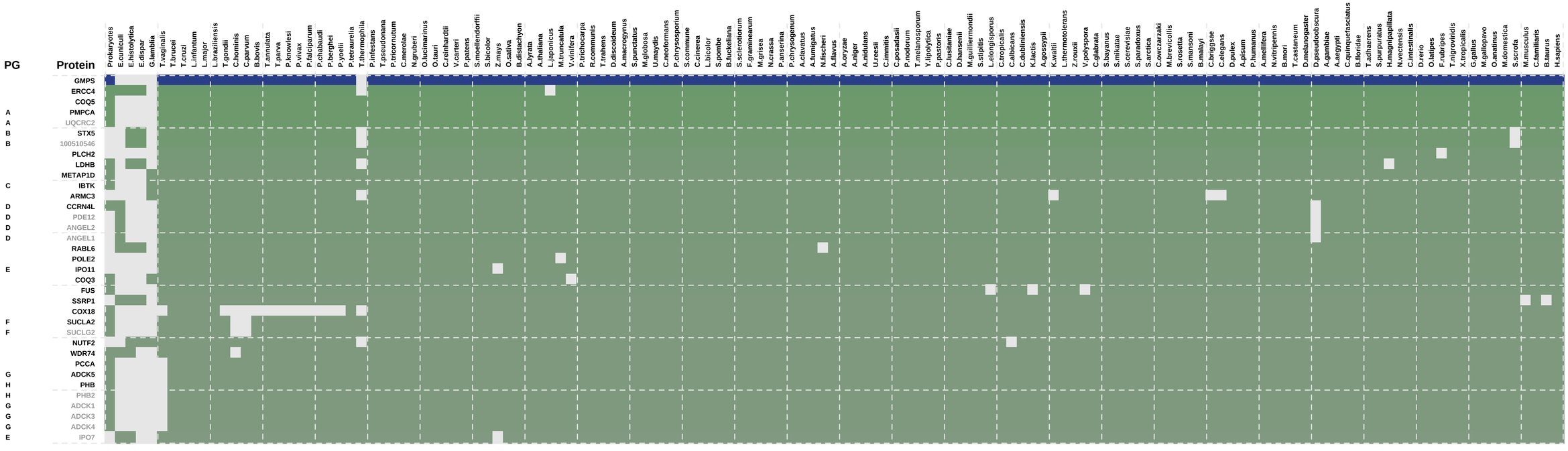




ECM 6, Gene set "Drug metabolism - other enzymes", Page 1

Num of ECM Genes: 1. Num of Predicted Genes: 100

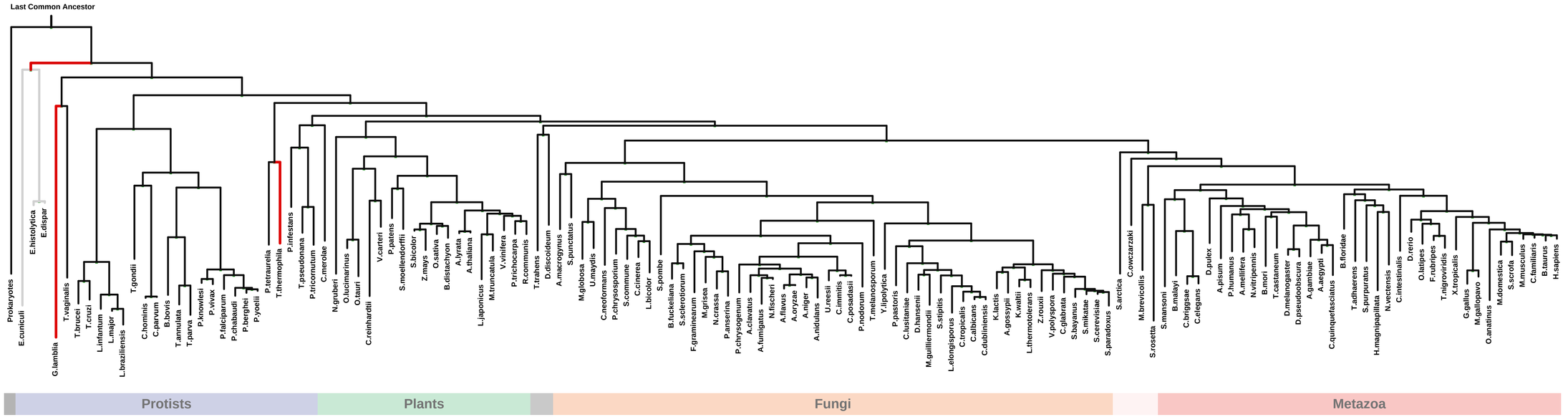


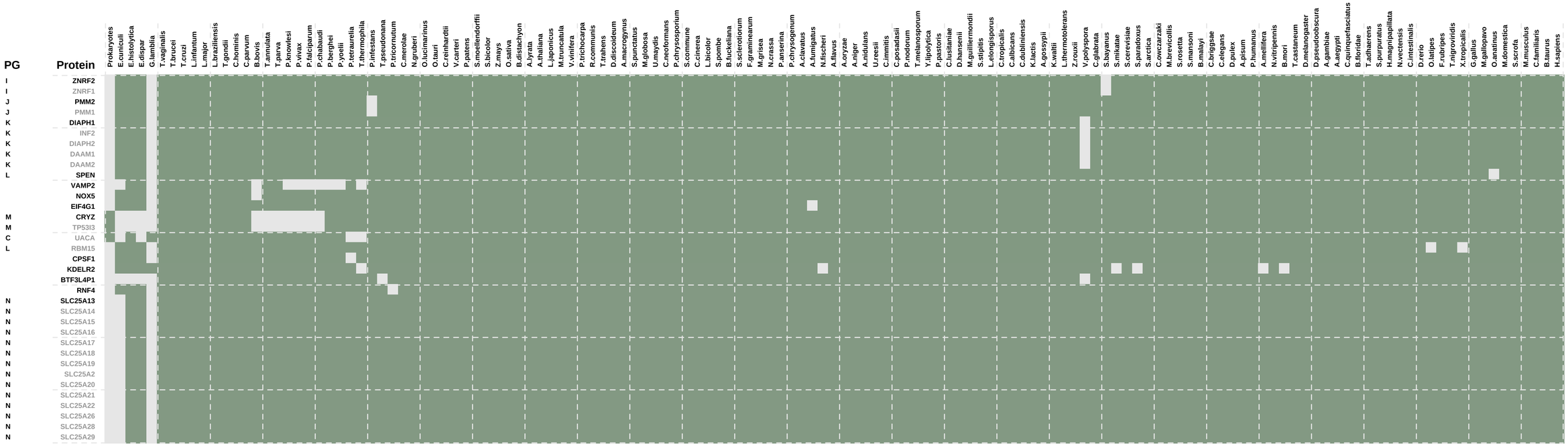


1: Drug metabolism - other enzymes || 2: Purine metabolism || 3: Nucleotide excision repair || 4: Ubiquinone and other terpenoid-quinone biosynthesis || 5: Oxidative phosphorylation || 6: SNARE interactions in vesicular transport || 7: Propanoate metabolism || 8: Citrate cycle (TCA cycle) || 9: Glyoxylate and dicarboxylate metabolism || 10: Valine, leucine and isoleucine degradation

ECM 6, Gene set "Drug metabolism - other enzymes", Page 2

Num of ECM Genes: 1. Num of Predicted Genes: 100

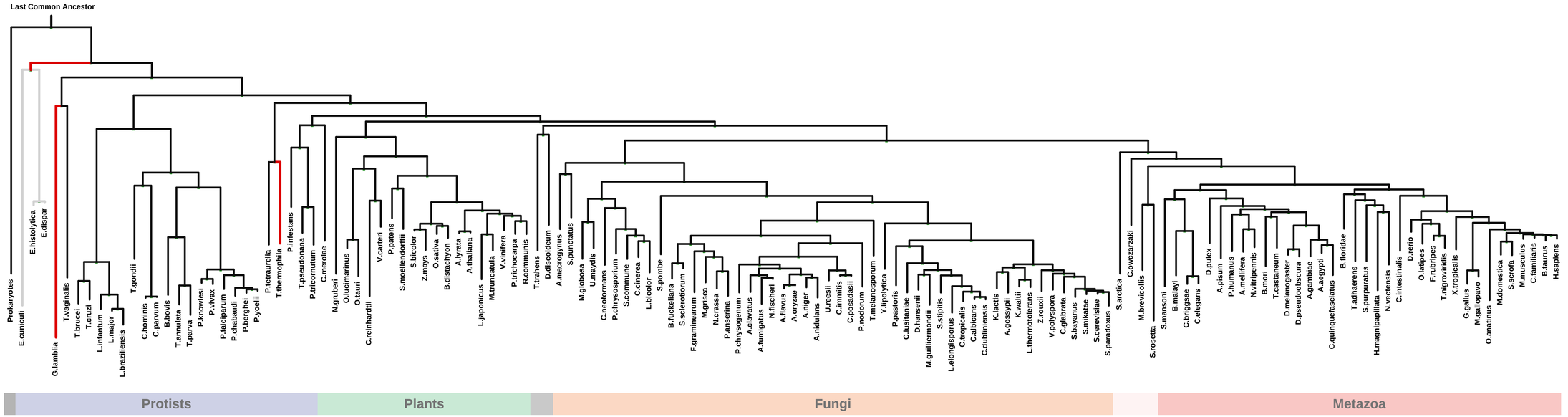




1: Fructose and mannose metabolism || 2: Amino sugar and nucleotide sugar metabolism || 3: Regulation of actin cytoskeleton || 4: Focal adhesion || 5: SNARE interactions in vesicular transport || 6: RNA transport || 7: p53 signaling pathway || 8: mRNA surveillance pathway || 9: Peroxisome

ECM 6, Gene set "Drug metabolism - other enzymes", Page 3

Num of ECM Genes: 1. Num of Predicted Genes: 100

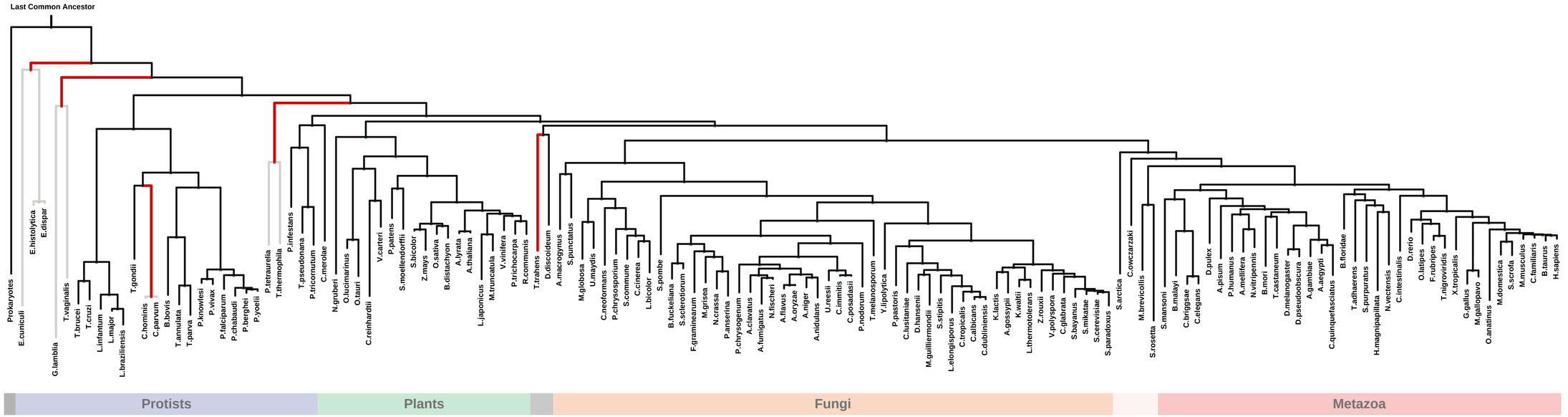


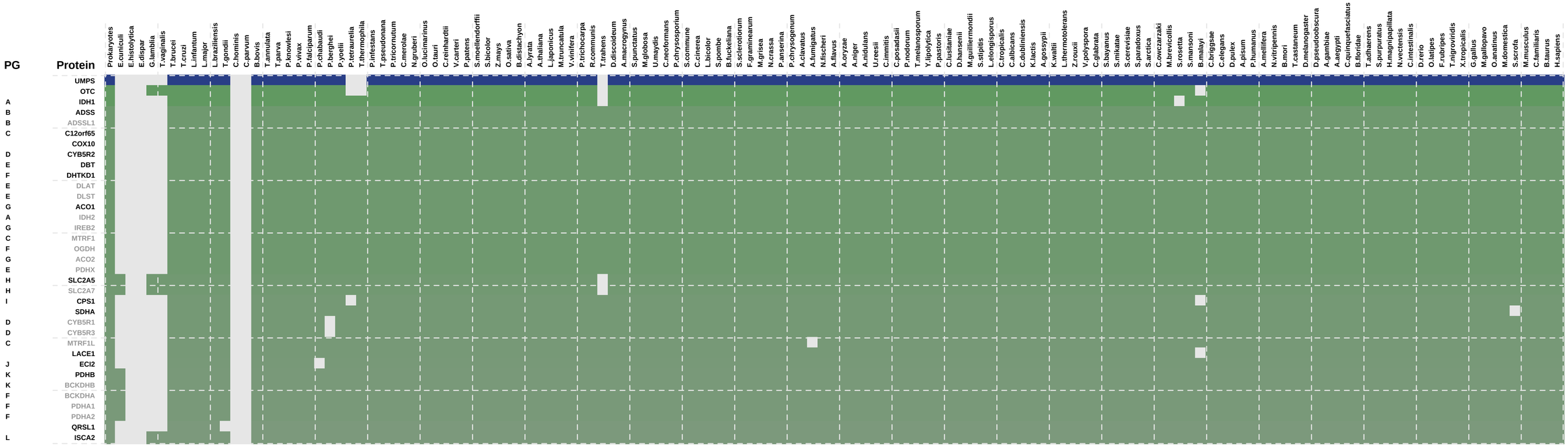
PG	Protein	LLR	Notes
N	SLC25A3	9.3	
N	SLC25A30	9.3	
N	SLC25A31	9.3	
N	SLC25A32	9.3	
N	SLC25A33	9.3	
N	SLC25A34	9.3	
N	SLC25A36	9.3	
N	SLC25A37	9.3	
N	SLC25A38	9.3	
N	SLC25A39	9.3	
N	SLC25A4	9.3	
N	SLC25A40	9.3	
N	SLC25A41	9.3	
N	SLC25A42	9.3	
N	SLC25A43	9.3	
N	SLC25A44	9.3	
N	SLC25A45	9.3	
N	SLC25A48	9.3	
N	SLC25A5	9.3	
N	SLC25A6	9.3	
	CHMP2A	**9.3**	1
	ITSN2	**9.3**	
	CHKA	**9.3**	2
O	**EIF2A**	**9.3**	
	PRMT8	**9.3**	
E	TNPO1	9.3	
E	TNPO2	9.3	
O	EIF3B	9.3	3
L	RBM15B	9.3	
N	UCP1	9.3	
N	UCP2	9.3	

1: Endocytosis || 2: Glycerophospholipid metabolism || 3: RNA transport

ECM 7, Gene set "Drug metabolism - other enzymes", Page 1

Num of ECM Genes: 1. Num of Predicted Genes: 100

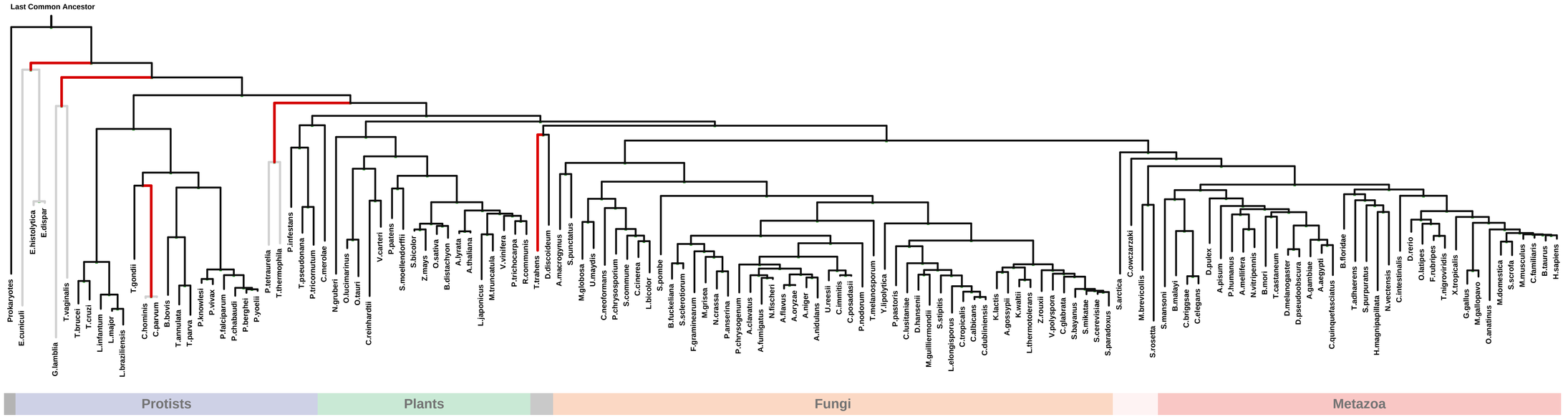


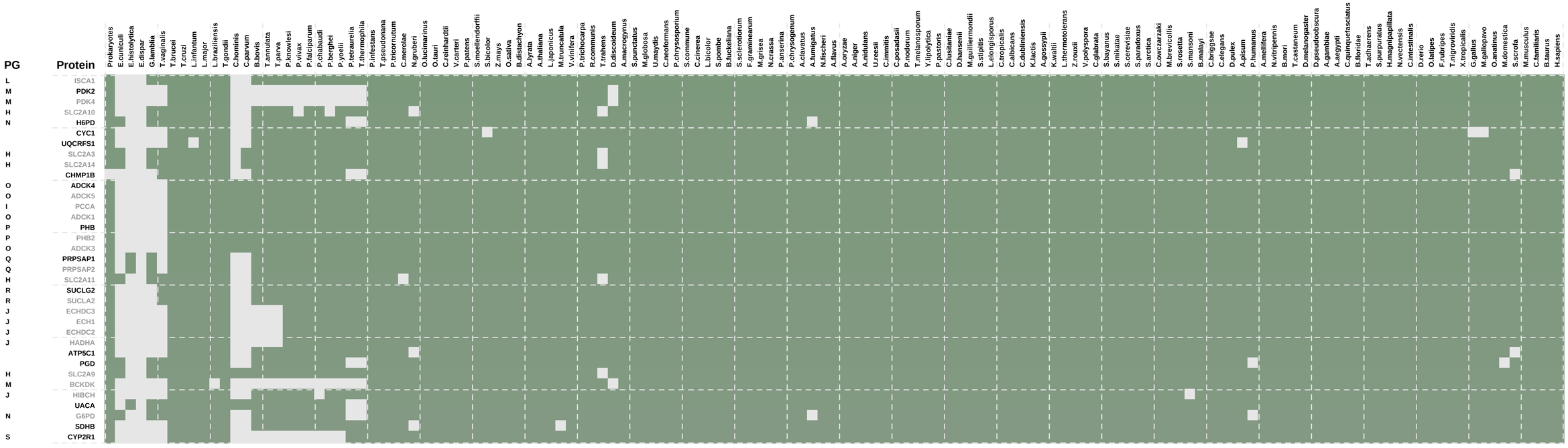


1: Drug metabolism - other enzymes || 2: Pyrimidine metabolism || 3: Arginine and proline metabolism || 4: Glutathione metabolism || 5: Citrate cycle (TCA cycle) || 6: Peroxisome || 7: Alanine, aspartate and glutamate metabolism ||
8: Purine metabolism || 9: Porphyrin and chlorophyll metabolism || 10: Oxidative phosphorylation || 11: Amino sugar and nucleotide sugar metabolism || 12: Valine, leucine and isoleucine degradation || 13: Pyruvate metabolism || 14: Glycolysis / Gluconeogenesis ||
15: Lysine degradation || 16: Glyoxylate and dicarboxylate metabolism || 17: Tryptophan metabolism || 18: Nitrogen metabolism || 19: Fatty acid metabolism

ECM 7, Gene set "Drug metabolism - other enzymes", Page 2

Num of ECM Genes: 1. Num of Predicted Genes: 100

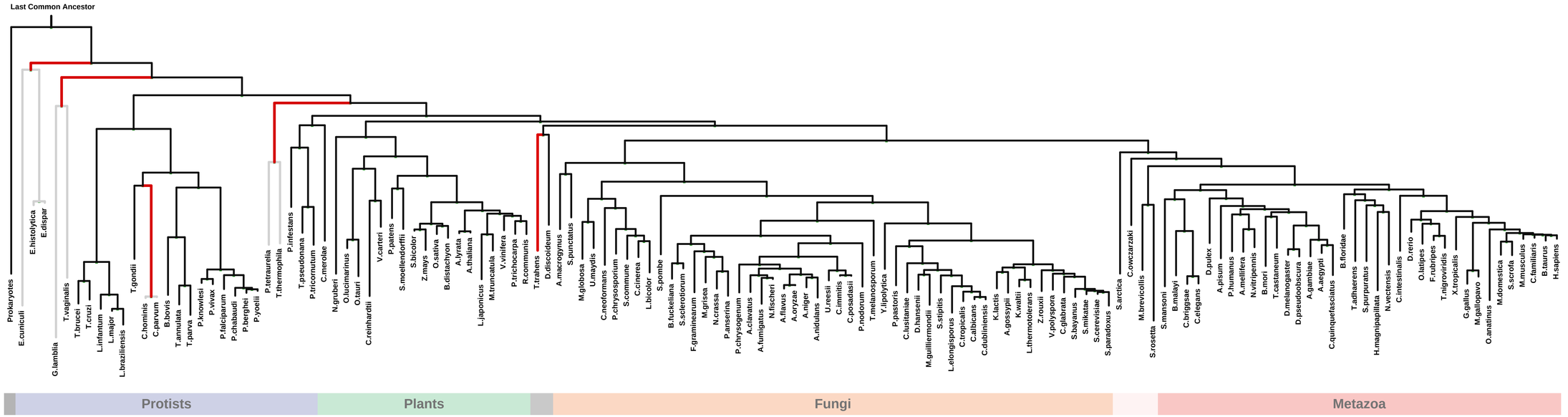


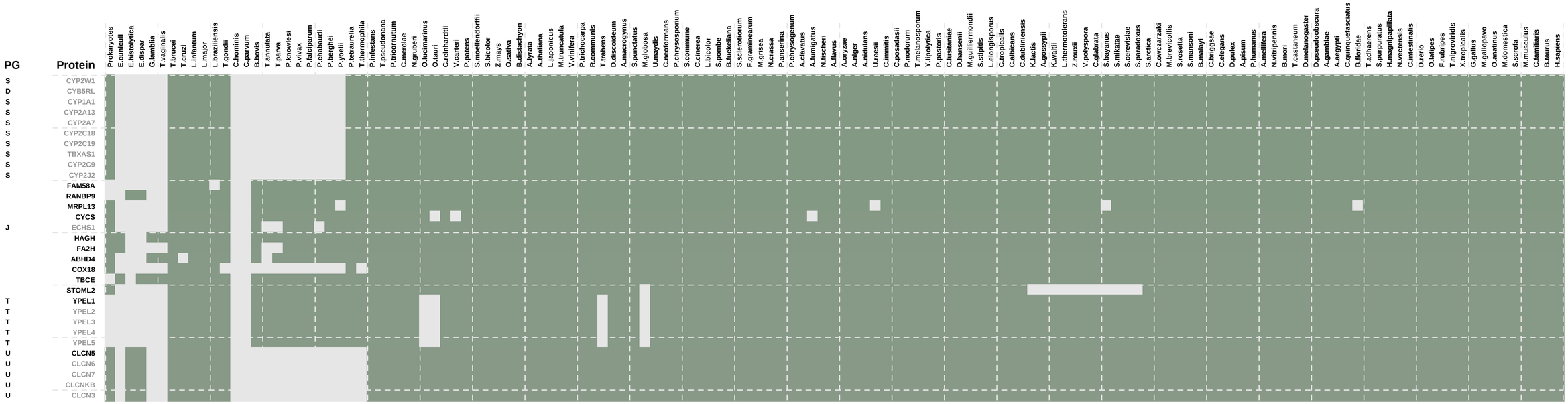


1: Pentose phosphate pathway || 2: Oxidative phosphorylation || 3: Endocytosis || 4: Glyoxylate and dicarboxylate metabolism || 5: Propanoate metabolism || 6: Valine, leucine and isoleucine degradation || 7: Citrate cycle (TCA cycle) ||
8: Peroxisome || 9: Glutathione metabolism || 10: beta-Alanine metabolism || 11: Steroid biosynthesis

ECM 7, Gene set "Drug metabolism - other enzymes", Page 3

Num of ECM Genes: 1. Num of Predicted Genes: 100

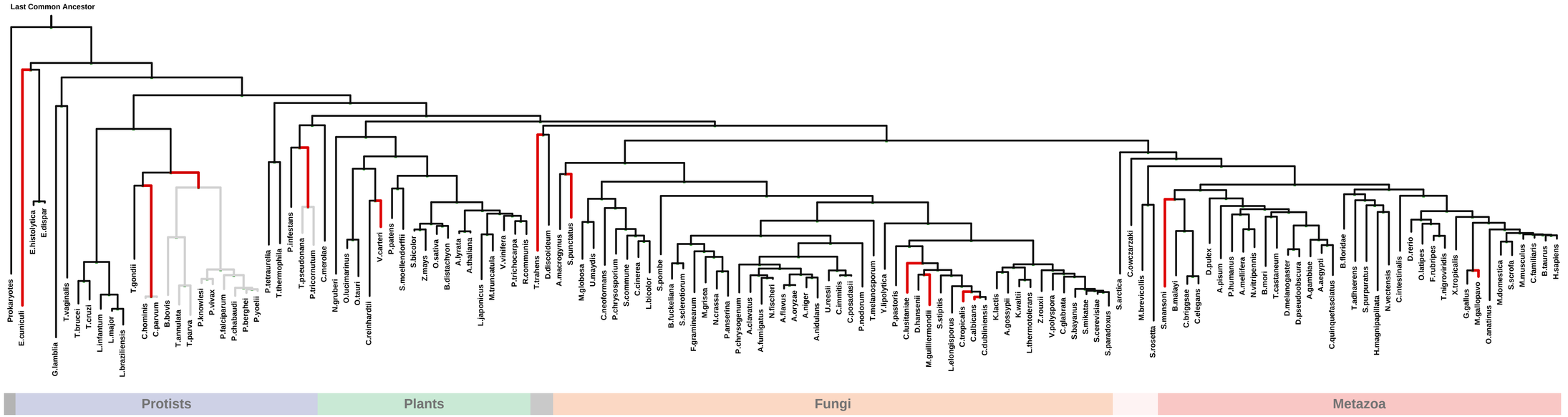




1: Arachidonic acid metabolism || 2: Linoleic acid metabolism || 3: Ribosome || 4: p53 signaling pathway || 5: Apoptosis || 6: Pyruvate metabolism

ECM 8, Gene set "Drug metabolism - other enzymes", Page 1

Num of ECM Genes: 1. Num of Predicted Genes: 5

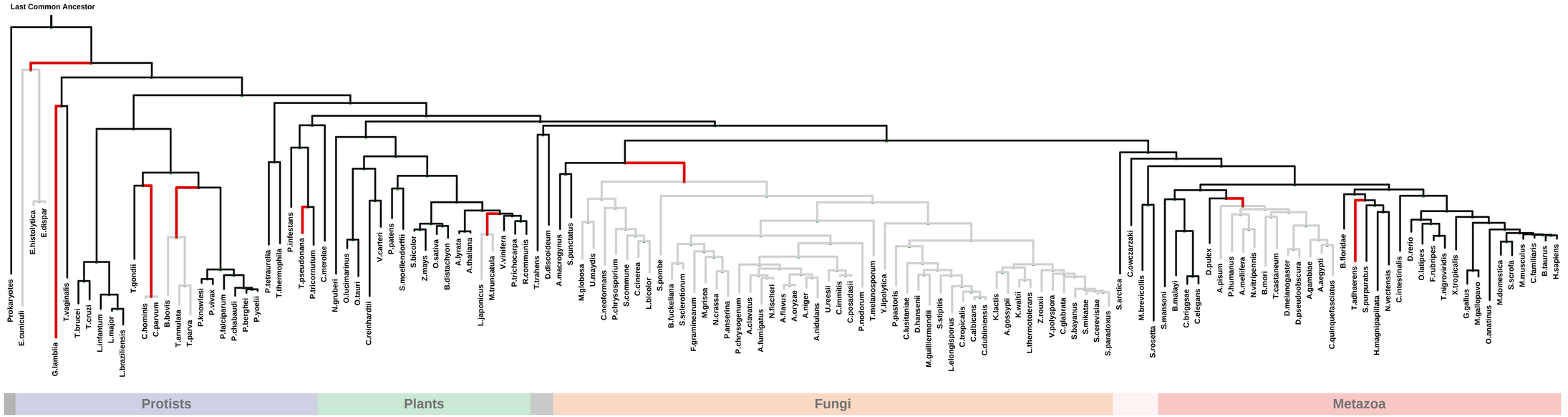


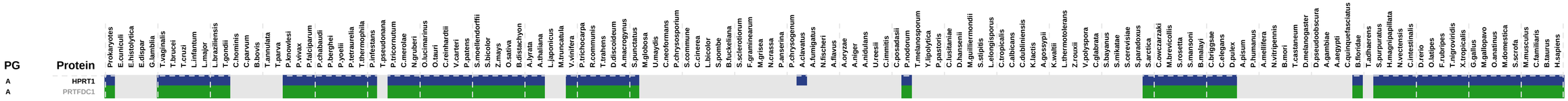
PG	Protein	LLR	Notes
	CDA		1 / 2
	RPS11	8.9	3
	RPS13	5.3	3
A	RPL22	1.2	3
A	RPL22L1	1.2	3
	RPL35	1.1	3

1: Drug metabolism - other enzymes || 2: Pyrimidine metabolism || 3: Ribosome

ECM 9, Gene set "Drug metabolism - other enzymes", Page 1

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

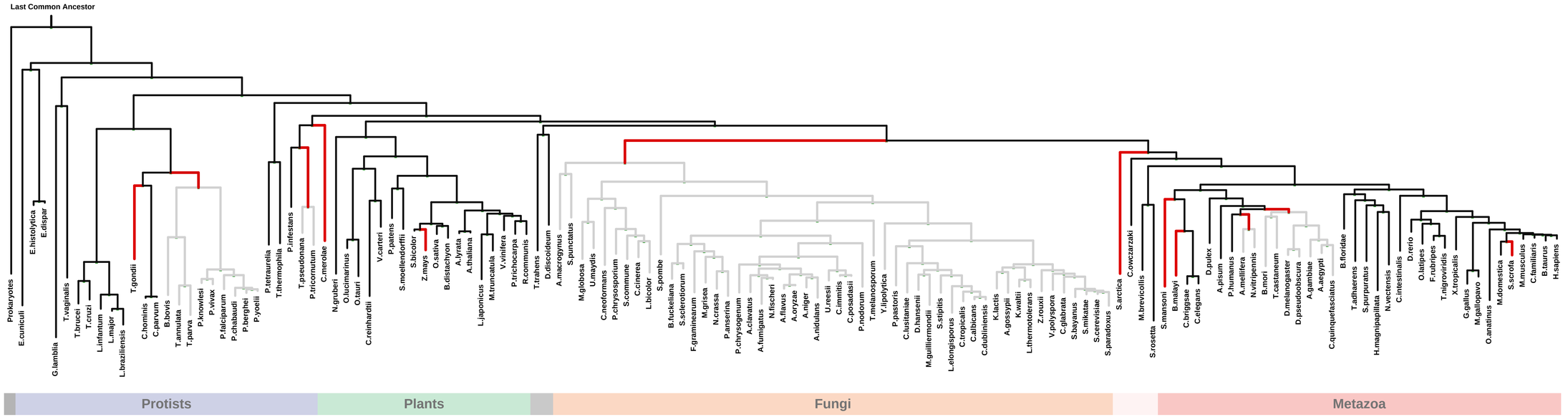




1: Drug metabolism - other enzymes || 2: Purine metabolism

ECM 10, Gene set "Drug metabolism - other enzymes", Page 1

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

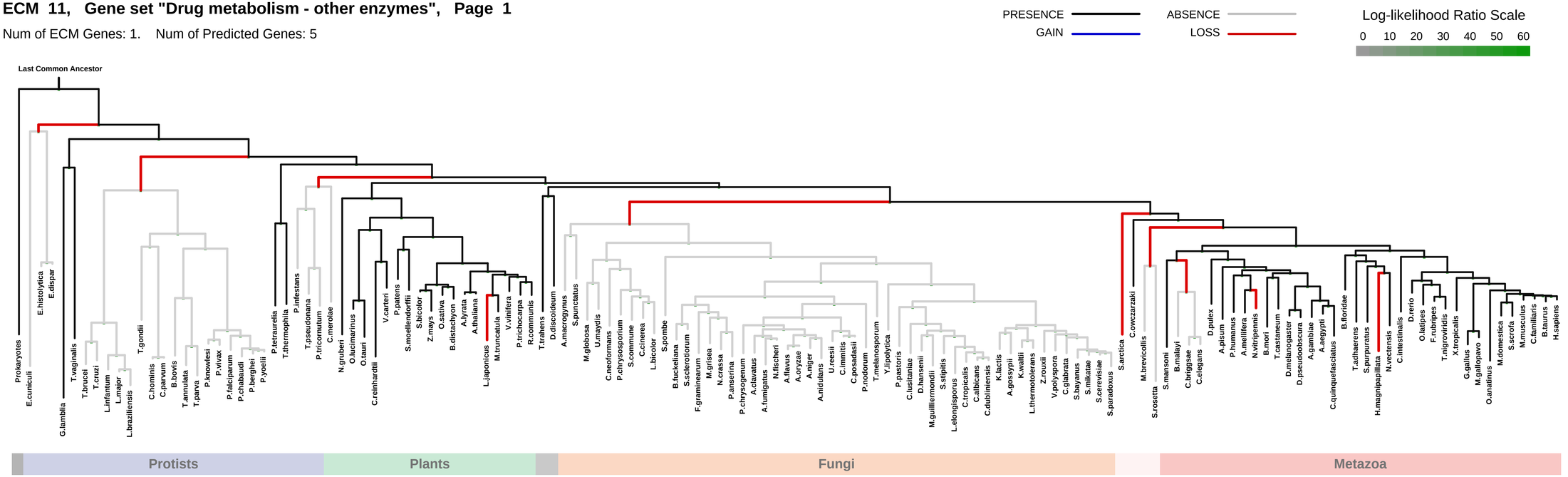


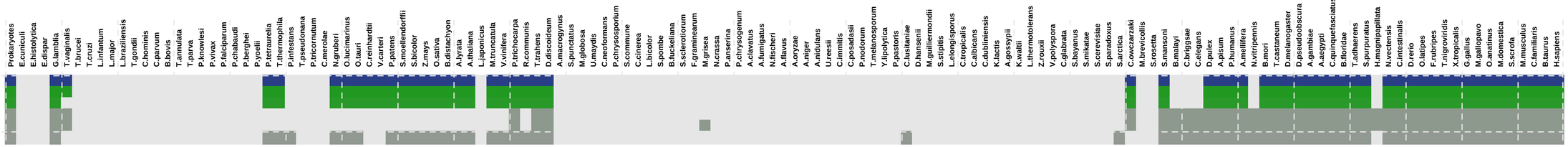
PG	Protein	LLR	Notes
	TK1		1 / 2
	SLC38A8	0.8	

1: Drug metabolism - other enzymes || 2: Pyrimidine metabolism

ECM 11, Gene set "Drug metabolism - other enzymes", Page 1

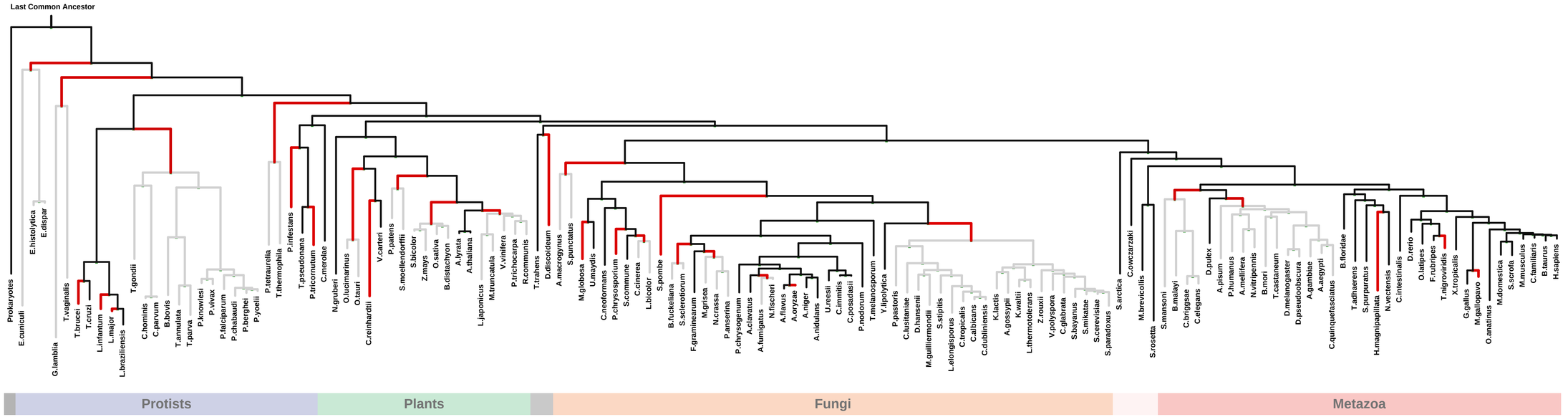
Num of ECM Genes: 1. Num of Predicted Genes: 5

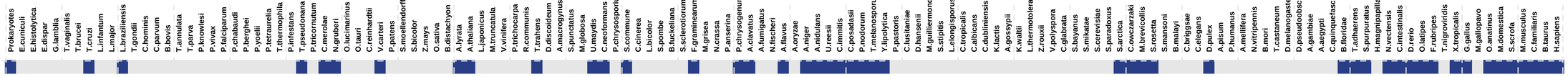




ECM 12, Gene set "Drug metabolism - other enzymes", Page 1

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

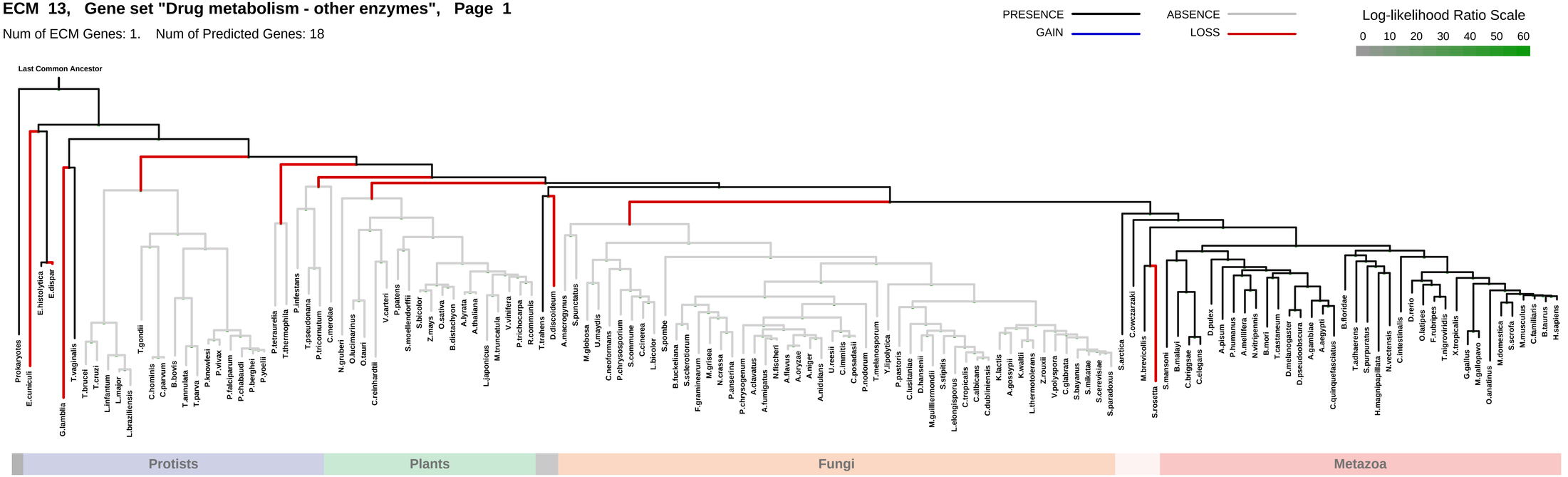


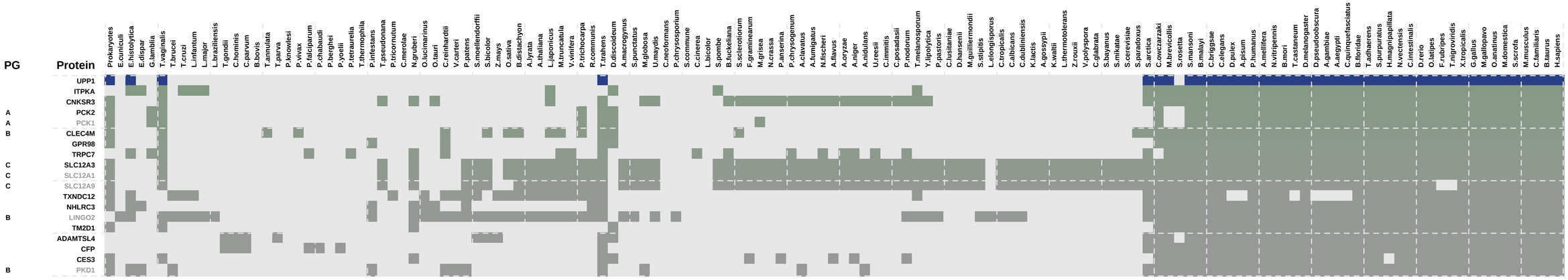


1: Drug metabolism - other enzymes

ECM 13, Gene set "Drug metabolism - other enzymes", Page 1

Num of ECM Genes: 1. Num of Predicted Genes: 18

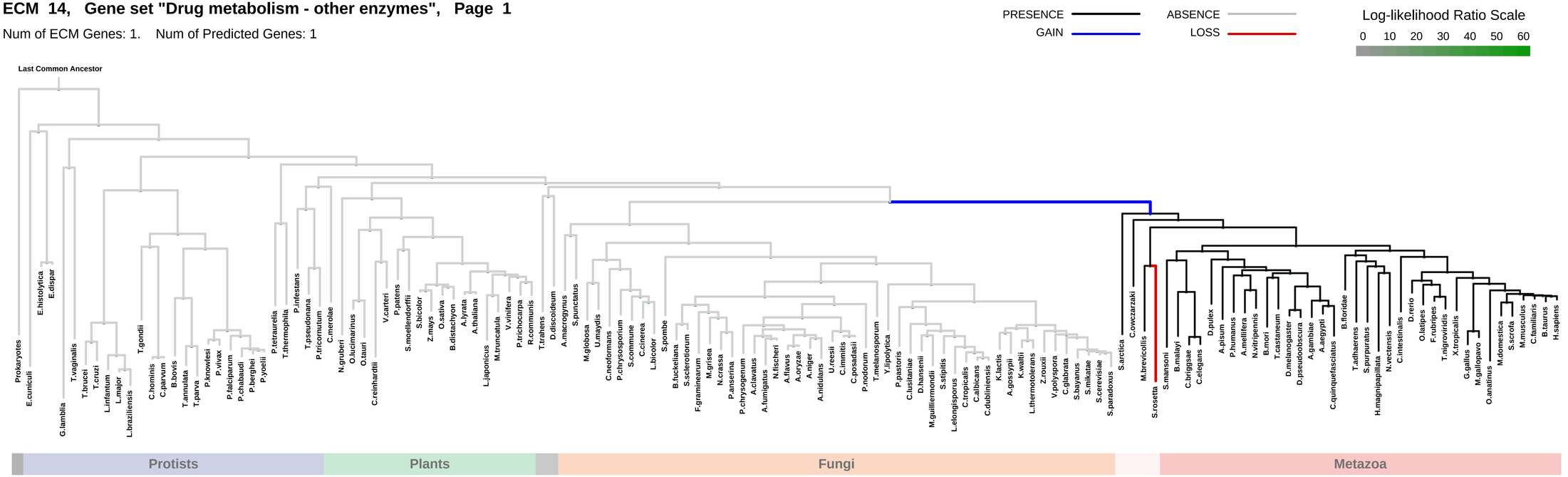




1: Drug metabolism - other enzymes || 2: Pyrimidine metabolism || 3: Inositol phosphate metabolism || 4: Pyruvate metabolism || 5: Glycolysis / Gluconeogenesis || 6: Citrate cycle (TCA cycle) || 7: Phagosome || 8: Glutathione metabolism

ECM 14, Gene set "Drug metabolism - other enzymes", Page 1

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

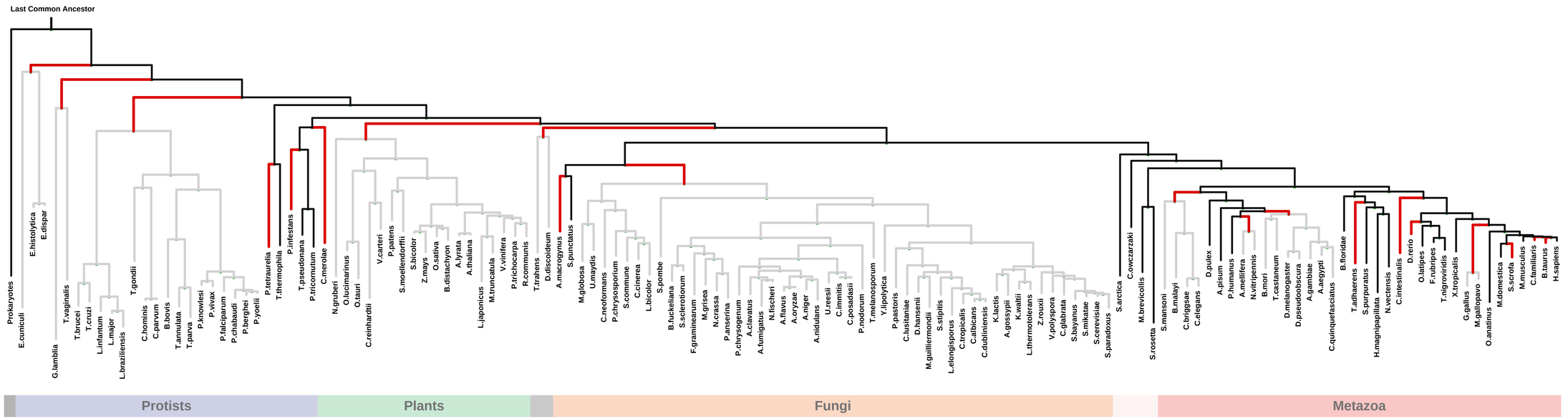


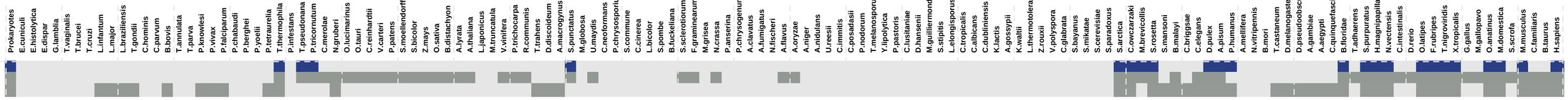
PG	Protein	LLR	Notes
	UPP2		1 / 2
	MXD3	5.3	

1: Drug metabolism - other enzymes || 2: Pyrimidine metabolism

ECM 15, Gene set "Drug metabolism - other enzymes", Page 1

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





1: Drug metabolism - other enzymes || 2: Pyrimidine metabolism || 3: Retinol metabolism