

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

Dataset:

Num of genes in input gene set: 8

Total number of genes: 20834

Prediction LLR threshold: 0

The CLIME PDF output two sections:

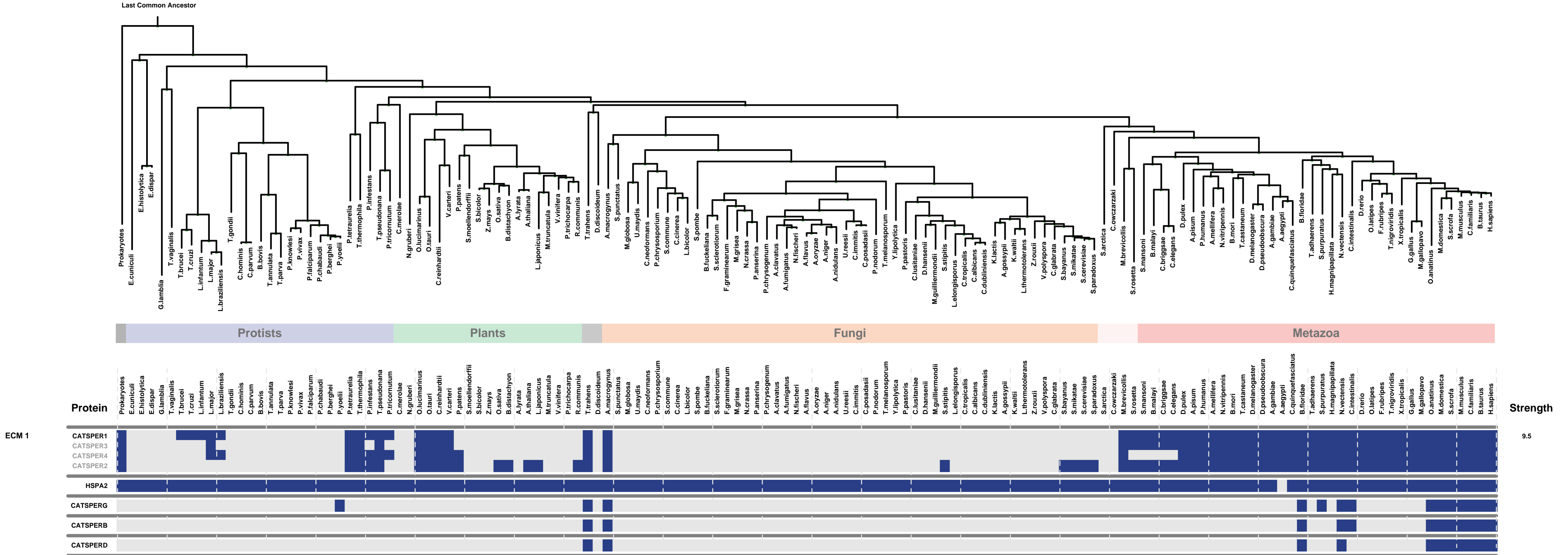
1) Overview of Evolutionarily Conserved Modules (ECMs)

- 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+

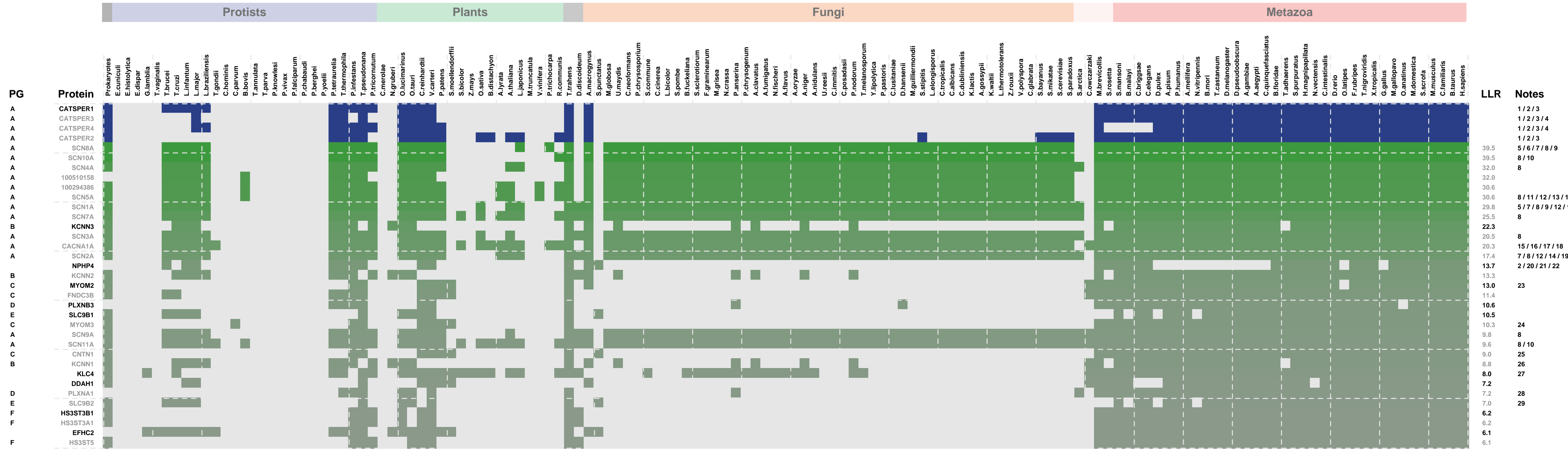
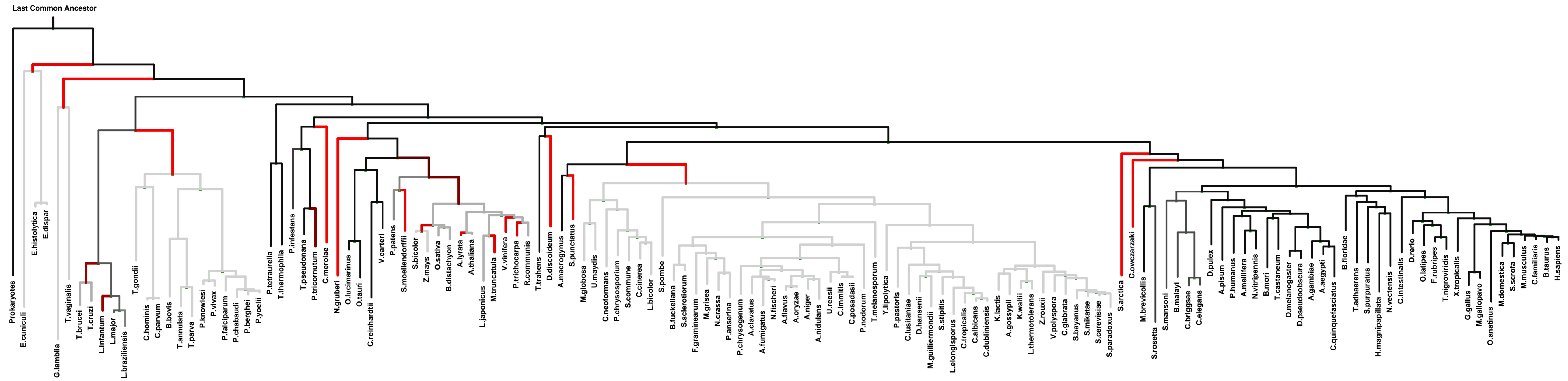
- Top panel shows the inferred evolutionary history on the predefined species tree. Branch color shows the gain event (blue) and loss events (red color, with brighter color indicating higher confidence in loss). Branches before the gain or after a loss are shown in gray.
- Bottom panel shows the input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

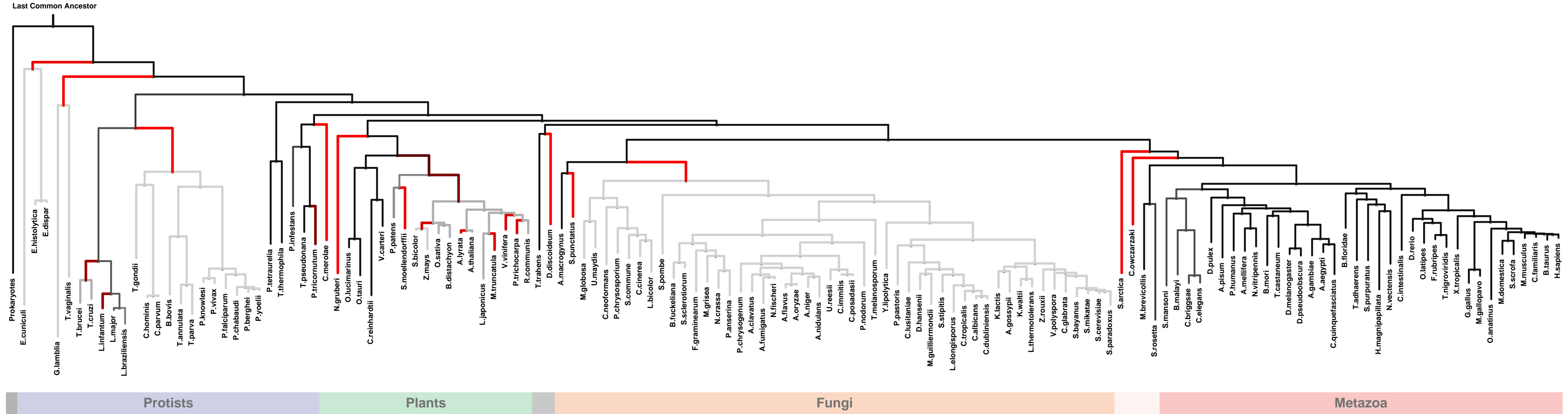
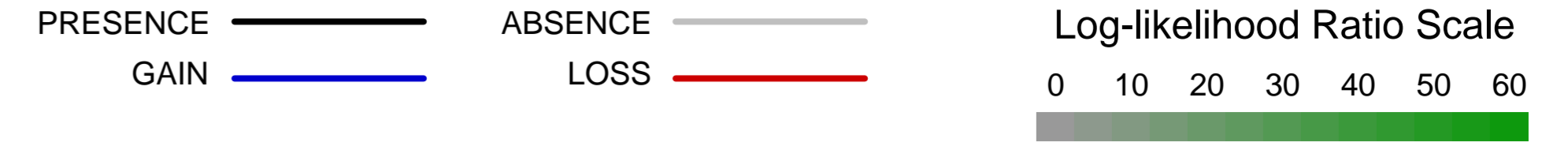
Num of ECM Genes: 4. Num of Predicted Genes: 53. ECM Strength: 9.5



1: CatSper complex || 2: cilium || 3: flagellum membrane || 4: acrosomal vesicle || 5: axon initial segment || 6: cytoplasmic membrane-bounded vesicle || 7: node of Ranvier || 8: voltage-gated sodium channel complex || 9: Z disc || 10: C-fiber || 11: caveola || 12: intercalated disc || 13: sarcolemma || 14: T-tubule || 15: cell projection || 16: dendrite || 17: perikaryon || 18: voltage-gated calcium channel complex || 19: axon || 20: cell-cell junction || 21: microtubule basal body || 22: tight junction || 23: myosin filament || 24: M band || 25: anchored to membrane || 26: voltage-gated potassium channel complex || 27: kinesin complex || 28: semaphorin receptor complex ||

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

Num of ECM Genes: 4. Num of Predicted Genes: 53. ECM Strength: 9.5

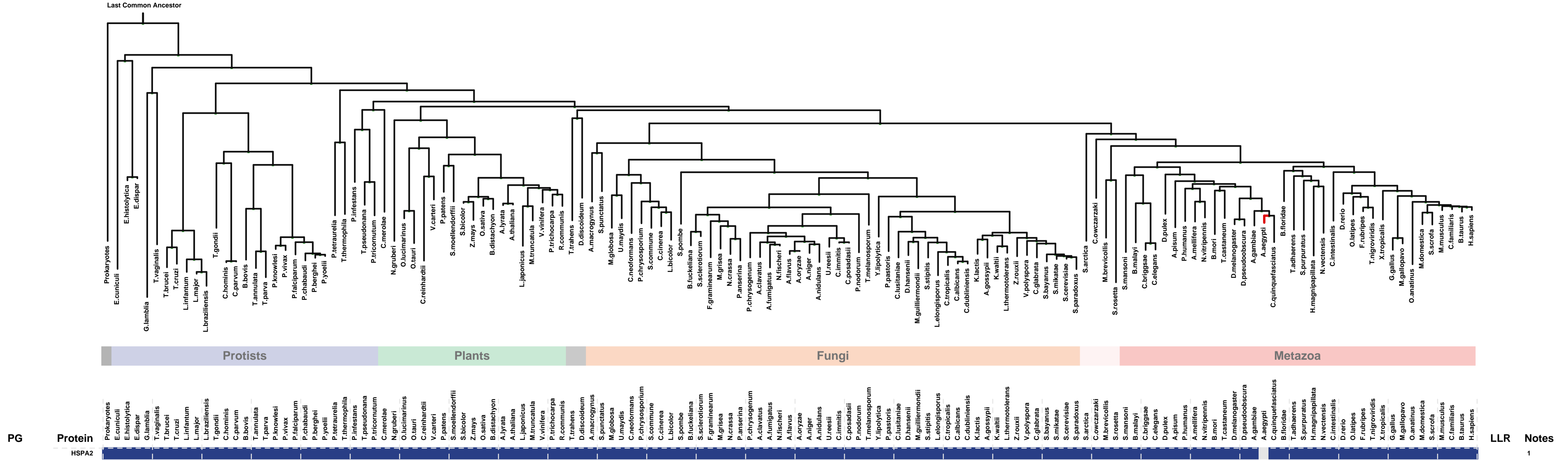


PG	Protein	Prokaryotes	Protists	Plants	Fungi	Metazoa	LLR	Notes
G	ZC2HC1B						5.1	
H	B9D1						3.9	1 / 2 / 3 / 4
I	CEP104						3.6	5
I	CKB						3.1	
I	CKM						3.1	
I	CKMT1A						3.1	
I	CKMT1B						3.1	
I	CKMT2						3.1	
A	NALCN						2.9	
H	MKS1						2.8	3 / 4
A	CACNA1G						2.7	6
D	PLXNB1						2.3	7
	TPPP3						1.9	
	CEP19						1.8	5 / 8
C	KIFAP3						1.1	9 / 10 / 11
G	MYBPC3						0.9	12 / 13 / 14
H	ZC2HC1A						0.7	
C	B9D2						0.5	2 / 3 / 4
C	FNDC3A						0.3	15 / 16
	PRTG						0.2	
	INPP4A						0.2	
	SLC18A3						0.0	17 / 18 / 19 / 20 / 21

1: ciliary transition zone || 2: cilium axoneme || 3: microtubule basal body || 4: TCTN-B9D complex || 5: centriole || 6: voltage-gated calcium channel complex || 7: semaphorin receptor complex || 8: spindle pole || 9: condensed nuclear chromosome ||
 10: kinesin II complex || 11: spindle microtubule || 12: A band || 13: sarcomere || 14: striated muscle myosin thick filament || 15: acrosomal vesicle || 16: vesicle membrane || 17: AP-1 adaptor complex || 18: AP-2 adaptor complex ||
 19: axon terminus || 20: clathrin-sculpted acetylcholine transport vesicle membrane || 21: synaptic vesicle

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

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



1: CatSper complex

LLR Notes

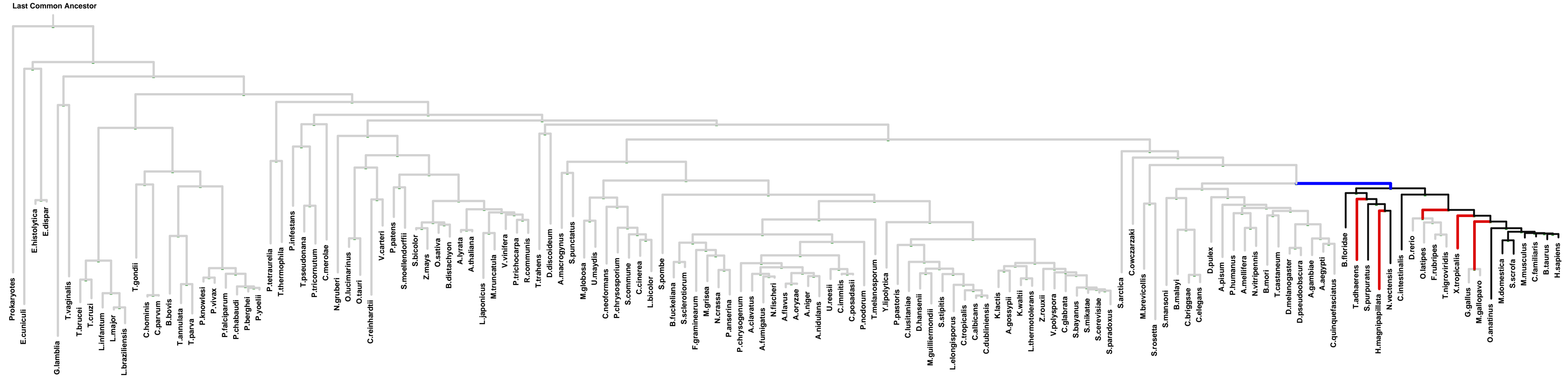
ECM 3, Gene set "CatSper complex", Page 1

Num of ECM Genes: 1. Num of Predicted Genes: 29

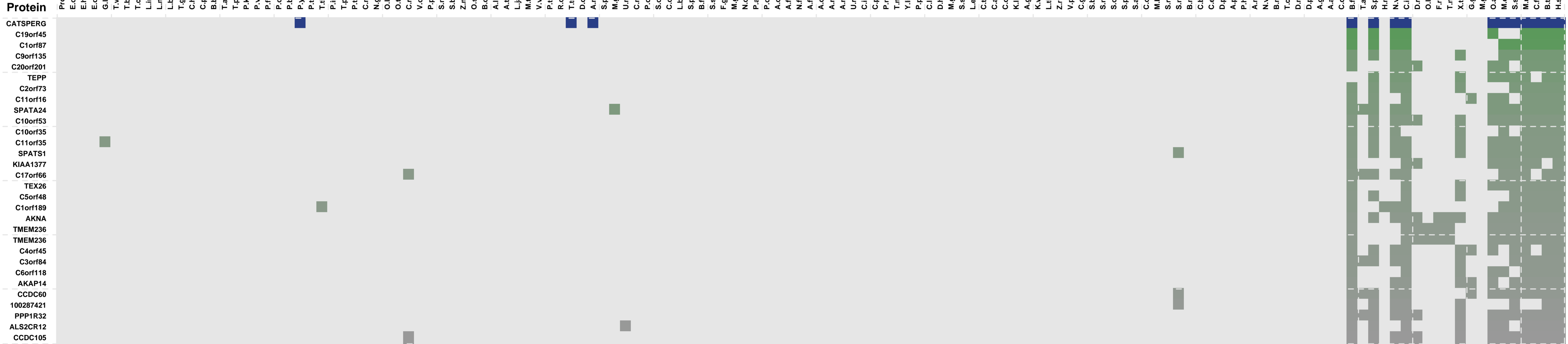
PRESENCE ———— ABSENCE ————
GAIN ———— LOSS ————

Log-likelihood Ratio Scale

0 10 20 30 40 50 60



PG



1: CatSper complex || 2: microtubule-based flagellum part

LLR Notes

1
26.7
25.8
15.0
14.3
14.1
12.3
11.6
9.2
8.9
8.7
8.7
7.7
7.7
6.9
6.8
6.6
6.5
5.3
4.7
4.7
4.6
4.5
4.3
3.3
2.8
1.6
1.3
0.4
0.0

2

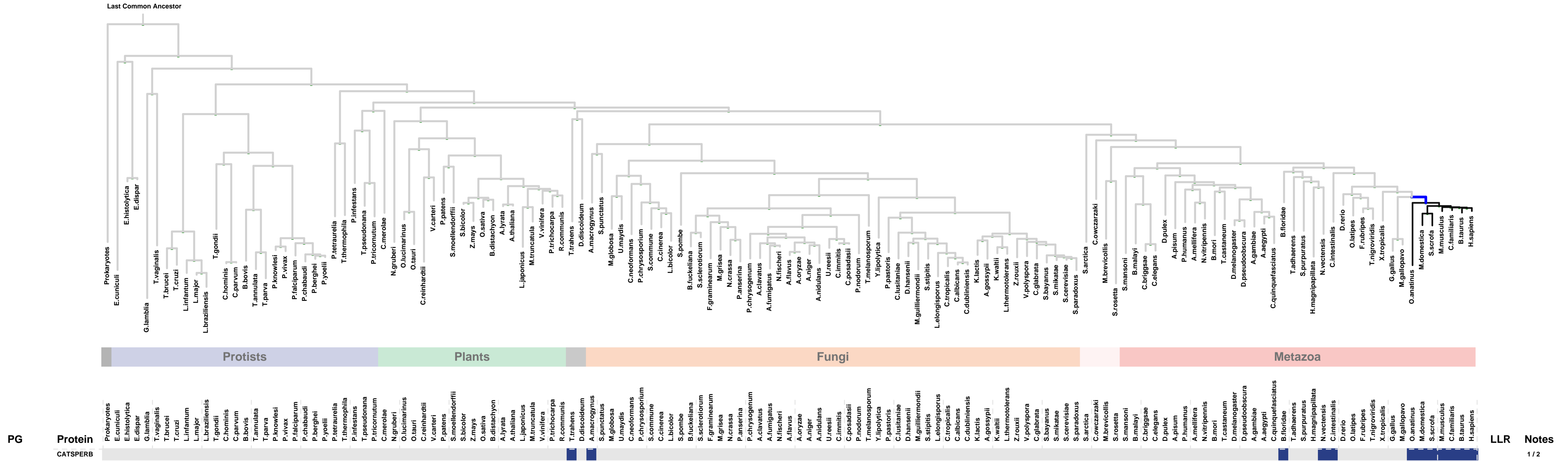
ECM 4, Gene set "CatSper complex", Page 1

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

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

Log-likelihood Ratio Scale

0 10 20 30 40 50 60



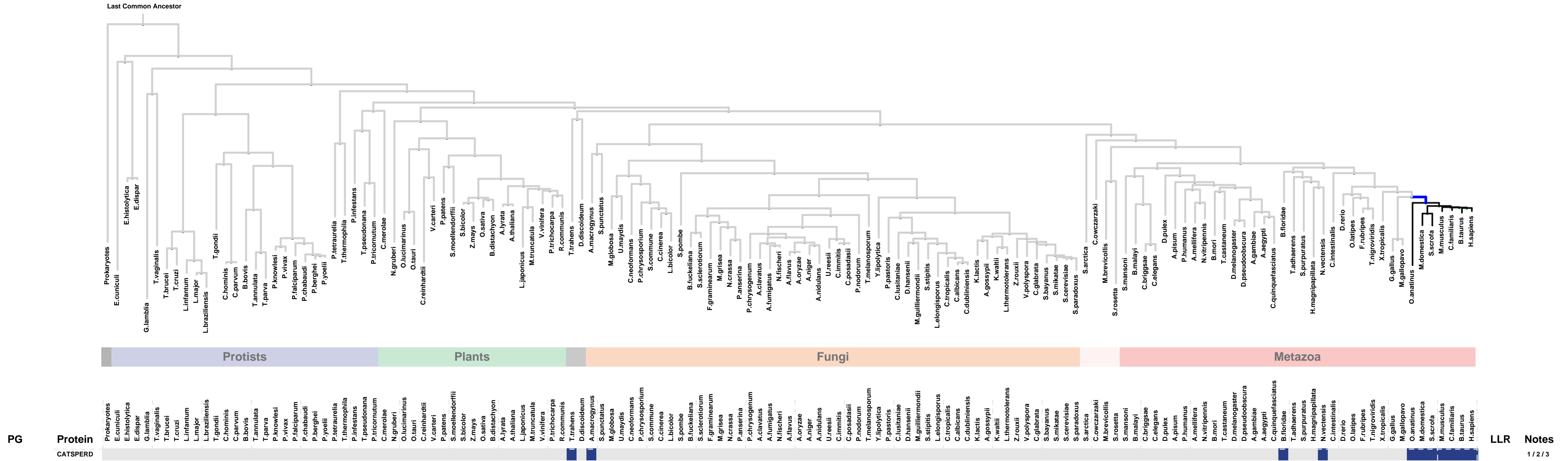
ECM 5, Gene set "CatSper complex", Page 1

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

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

Log-likelihood Ratio Scale

0 10 20 30 40 50 60



1: CatSper complex || 2: cilium || 3: flagellar membrane