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

Dataset:

Num of genes in input gene set: 2
Total number of genes: 20834
Prediction LLR threshold: 0

The CLIME PDF output two sections:

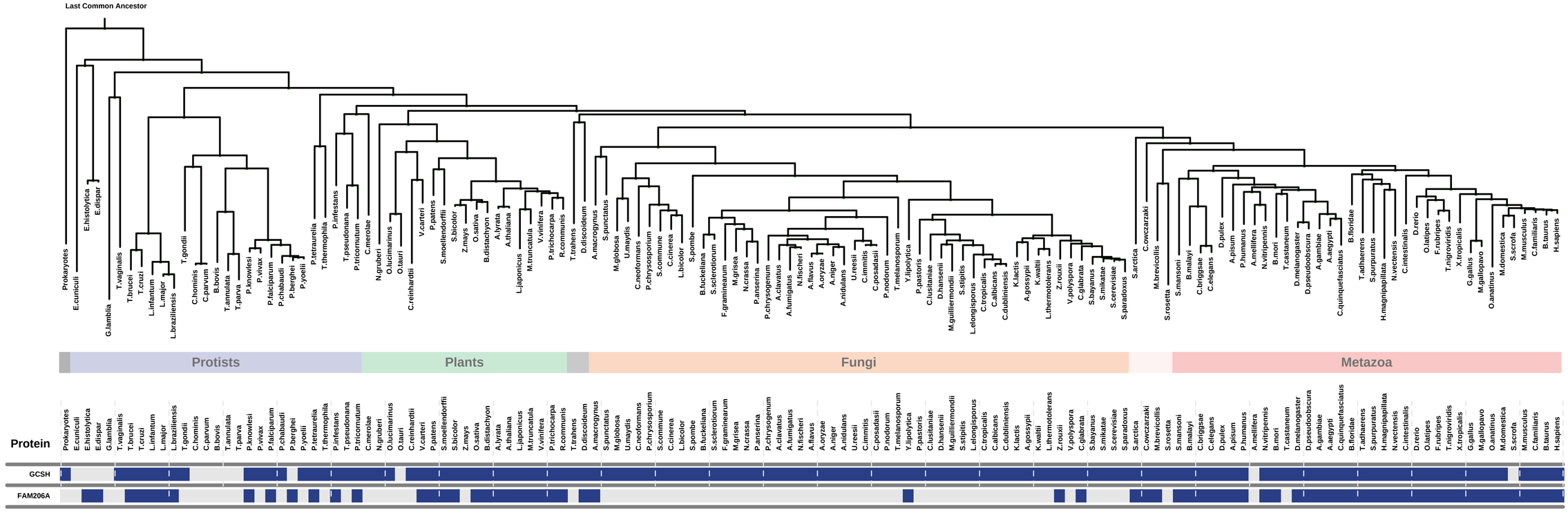
1) Overview of Evolutionarily Conserved Modules (ECMs)

- 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+

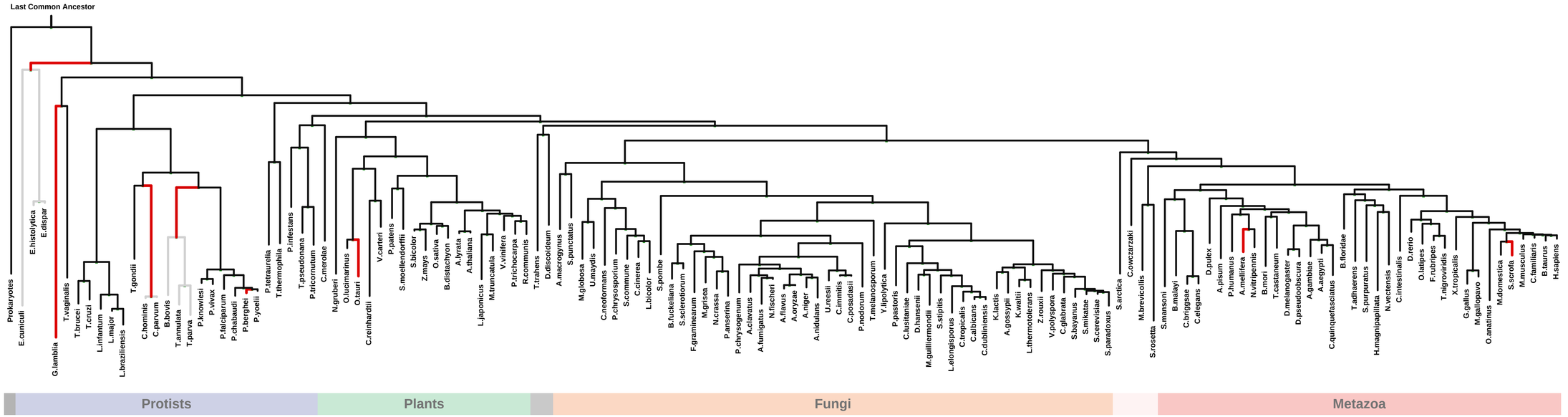
- Top panel shows the inferred evolutionary history on the predefined species tree. Branch color shows the gain event (blue) and loss events (red color, with brighter color indicating higher confidence in loss). Branches before the gain or after a loss are shown in gray.
- Bottom panel shows the input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

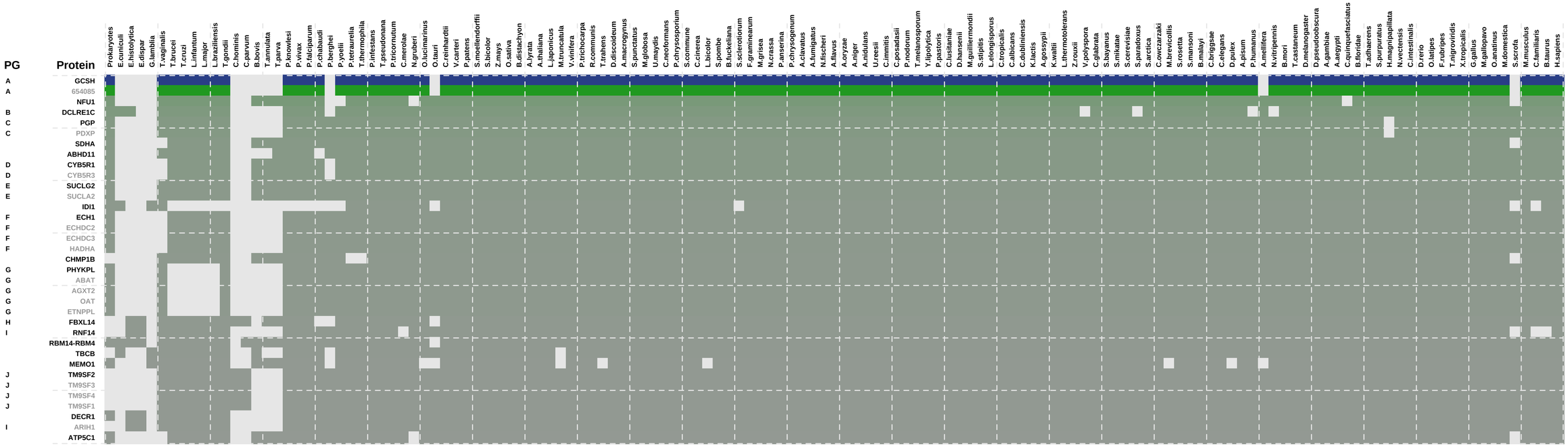
Overview of Evolutionarily Conserved Modules (ECMs)



ECM 1, Gene set "glycine cleavage complex", Page 1

Num of ECM Genes: 1. Num of Predicted Genes: 69

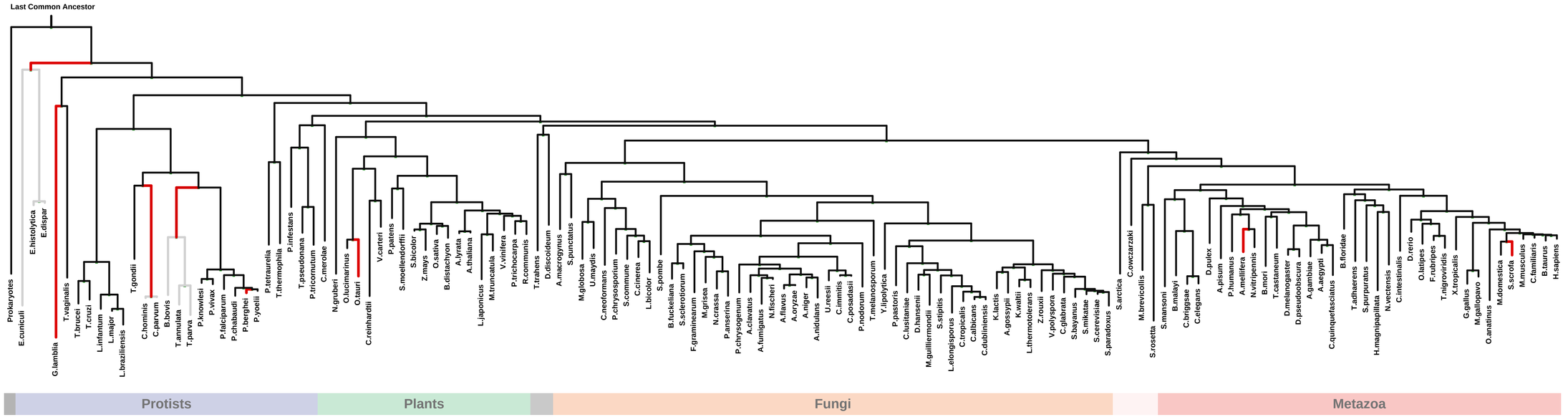




1: glycine cleavage complex || 2: actin cytoskeleton || 3: cleavage furrow || 4: contractile ring || 5: lamellipodium || 6: lamellipodium membrane || 7: midbody || 8: ruffle membrane || 9: mitochondrial respiratory chain complex II ||
10: hemoglobin complex || 11: lipid particle || 12: mitochondrial outer membrane || 13: peroxisome || 14: mitochondrial fatty acid beta-oxidation multienzyme complex || 15: mitochondrial nucleoid || 16: late endosome membrane ||
17: microtubule cytoskeleton || 18: endosome || 19: endosome membrane || 20: autophagic vacuole membrane || 21: cytoplasmic vesicle || 22: lysosomal membrane || 23: ubiquitin ligase complex || 24: mitochondrial proton-transporting ATP synthase complex ||

ECM 1, Gene set "glycine cleavage complex", Page 2

Num of ECM Genes: 1. Num of Predicted Genes: 69



PG	Protein	LLR	Notes
	GTPBP3	2.5	
K	FGD4	2.4	1 / 2 / 3 / 4
K	FGD6	2.4	3 / 4
K	FGD3	2.4	3 / 4
E	ACLY	2.3	5
	LINGO1	2.2	
B	DCLRE1B	2.2	6
	MTHFD1	2.1	
	ARPC1B	1.9	1 / 7
	SLC25A51	1.7	
K	HGS	1.7	8 / 9 / 10 / 11 / 12
L	LRRC2	1.7	
M	ALAS1	1.5	
M	SPTLC1	1.5	13 / 14
M	SPTLC2	1.5	13
M	SPTLC3	1.5	13
M	ALAS2	1.5	
M	GCAT	1.5	
	MTFMT	1.4	
	HAGHL	1.2	
N	MSRB2	1.1	
N	MSRB3	1.1	
	CYCS	1.1	15 / 16 / 17
	LCMT2	1.1	
H	FBXL2	1.0	
I	RNF144A	0.9	
	CERS3	0.6	18
	100506332	0.6	
	TMTC3	0.6	
O	ISCA1	0.5	
O	ISCA2	0.5	
L	LRRC10B	0.4	
	SDR16C5	0.3	
	ARCN1	0.0	19 / 20
	CCNK	0.0	

1: actin cytoskeleton || 2: filopodium || 3: lamellipodium || 4: ruffle || 5: citrate lyase complex || 6: chromosome, telomeric region || 7: Arp2/3 protein complex || 8: early endosome || 9: early endosome membrane || 10: endosome ||
11: multivesicular body membrane || 12: secretory granule || 13: serine C-palmitoyltransferase complex || 14: SPOTS complex || 15: mitochondrial intermembrane space || 16: protein phosphatase type 2A complex || 17: respiratory chain ||
18: nuclear membrane || 19: clathrin adaptor complex || 20: COPI vesicle coat

ECM 2, Gene set "glycine cleavage complex", Page 1

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