

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

Dataset:

Num of genes in input gene set: 3

Total number of genes: 20834

Prediction LLR threshold: 0

The CLIME PDF output two sections:

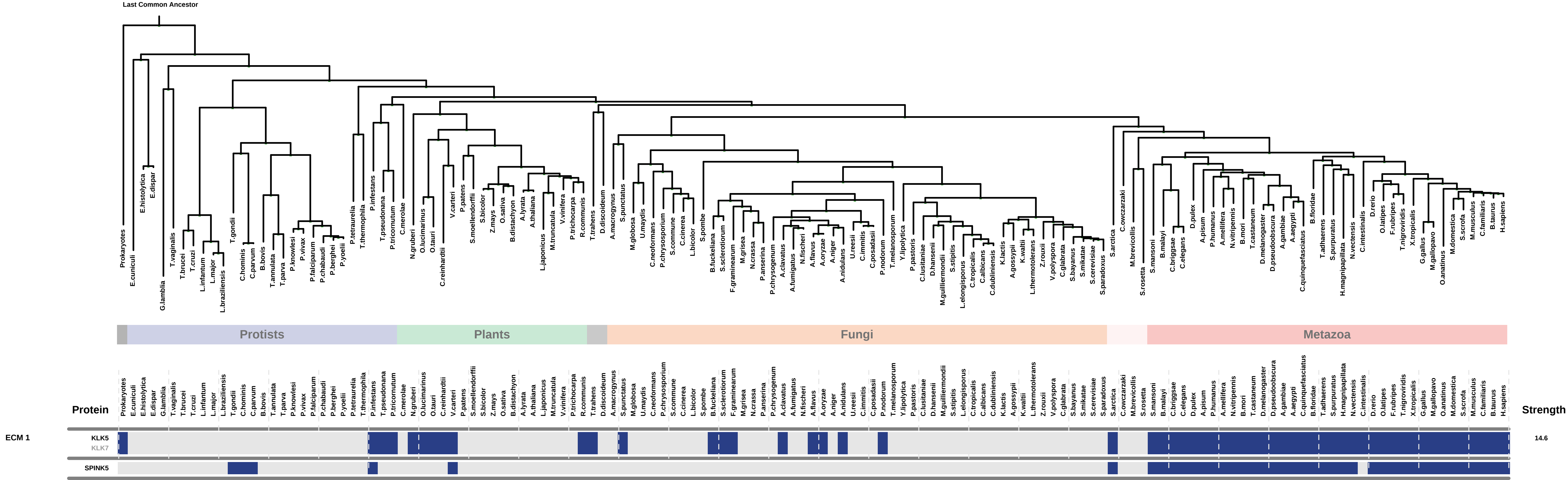
1) Overview of Evolutionarily Conserved Modules (ECMs)

- 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+

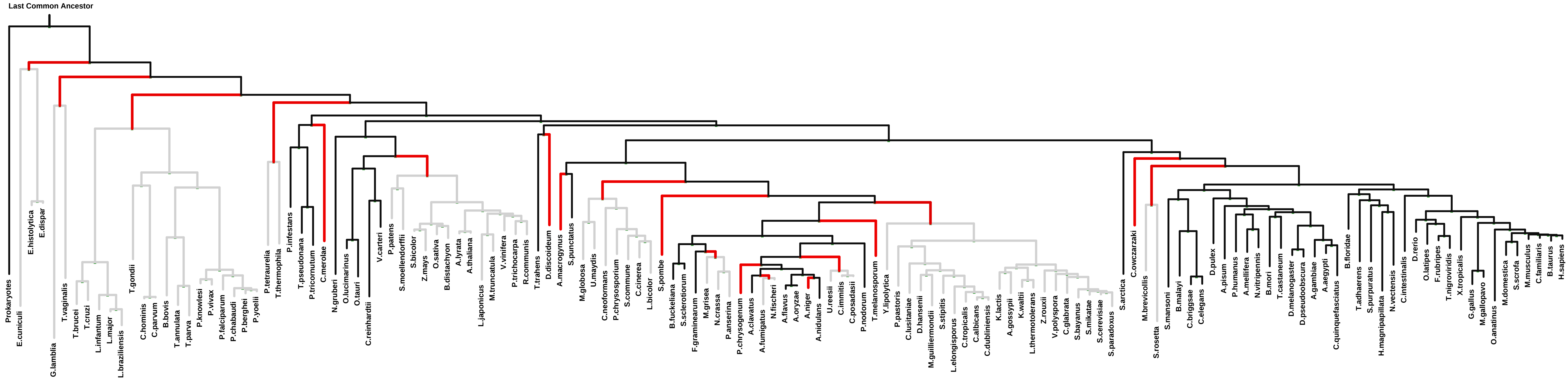
- Top panel shows the inferred evolutionary history on the predefined species tree. Branch color shows the gain event (blue) and loss events (red color, with brighter color indicating higher confidence in loss). Branches before the gain or after a loss are shown in gray.
- Bottom panel shows the input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

Num of ECM Genes: 2. Num of Predicted Genes: 168. ECM Strength: 14.6



PG	Protein	LLR	Notes
A	KLK5		1
A	KLK7		1
A	CELA3A	98.8	
A	CMA1	98.8	
A	CTSG	98.8	2
A	KLK10	98.8	2 / 3
A	KLK12	98.8	
A	KLK6	98.8	
A	KLK8	98.8	
A	LOC100505597	98.8	
A	PRSS45	98.8	
A	PRSS56	98.8	
A	PRSS57	98.8	
A	TMPRSS11A	98.8	
A	TMPRSS3	98.8	
A	TPSG1	98.8	
A	GZMK	98.8	
A	GZMM	98.8	
A	KLK1	98.8	
A	ACR	98.8	4 / 5
A	KLK11	98.8	
A	CELA3B	98.8	
A	KLK13	98.8	3
A	KLK14	98.8	
A	KLK15	98.8	
A	CFD	98.8	6
A	CELA1	98.8	
A	CTRB1	98.8	
A	OVCH2	98.8	
A	PRSS2	98.8	2
A	PRSS22	98.8	
A	PRSS27	98.8	
A	PRSS3	98.8	
A	PRSS41	98.8	7 / 8
A	PRSS42	98.8	

1: epidermal lamellar body || 2: extracellular matrix || 3: secretory granule || 4: acrosomal matrix || 5: Golgi-associated vesicle || 6: platelet alpha granule lumen || 7: anchored to membrane || 8: intracellular organelle

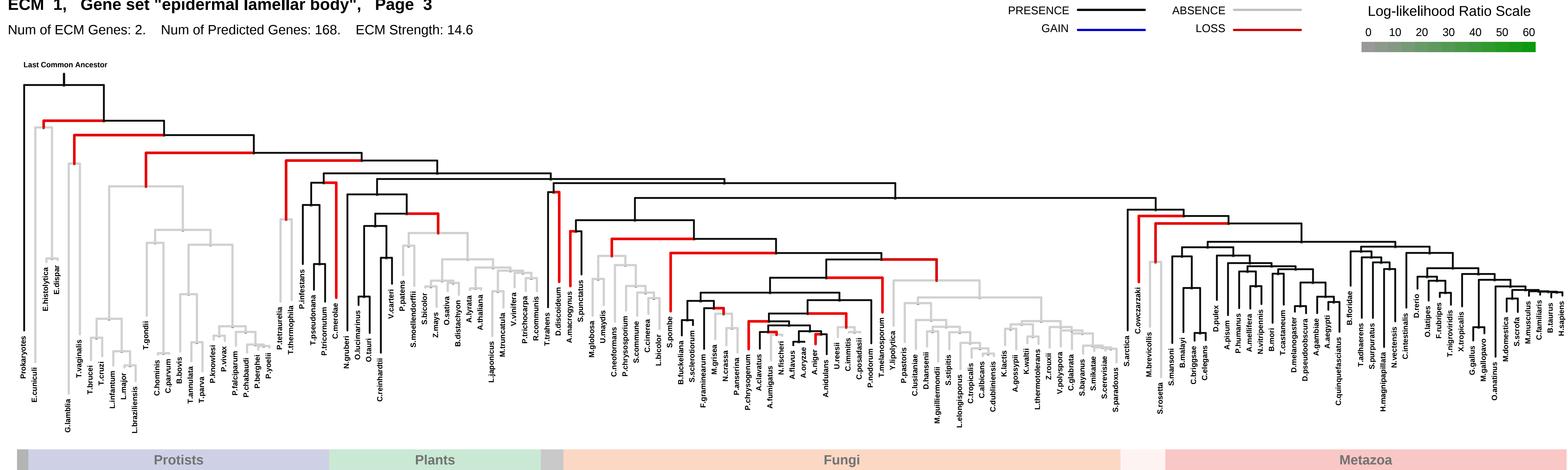
Num of ECM Genes: 2. Num of Predicted Genes: 168. ECM Strength: 14.6



Notes

ECM 1, Gene set "epidermal lamellar body", Page 3

Num of ECM Genes: 2. Num of Predicted Genes: 168. ECM Strength: 14.6

[illegible]

1: secretory granule || 2: anchored to membrane || 3: basolateral plasma membrane || 4: extrinsic to plasma membrane || 5: endoplasmic reticulum lumen || 6: Golgi lumen || 7: cytoplasmic vesicle || 8: dendrite || 9: synaptic cleft || 10: terminal button || 11: proteinaceous extracellular matrix || 12: platelet alpha granule lumen || 13: apical part of cell || 14: extracellular matrix || 15: synapse || 16: intrinsic to external side of plasma membrane || 17: extrinsic to external side of plasma membrane || 18: brush border || 19: spherical high-density lipoprotein particle

Num of ECM Genes: 2. Num of Predicted Genes: 168. ECM Strength: 14.6



1: cytoplasmic mRNA processing body || 2: cytoplasmic stress granule || 3: brush border membrane || 4: axon || 5: brush border || 6: dendrite || 7: neuron projection terminus || 8: synapse || 9: synaptic vesicle || 10: early endosome || 11: endosome || 12: external side of plasma membrane || 13: vesicle || 14: Weibel-Palade body || 15: cytoplasmic vesicle membrane || 16: endoplasmic reticulum lumen || 17: dendrite cytoplasm || 18: perikaryon || 19: postsynaptic membrane || 20: terminal button || 21: polysome || 22: CRD-mediated mRNA stability complex || 23: histone pre-mRNA 3'end processing complex || 24: ribonucleoprotein complex || 25: U12-type spliceosomal complex || 26: mitochondrial small ribosomal subunit || 27: basolateral plasma membrane || 28: dendritic spine || 29: fibril || 30: intermediate filament || 31: melanosome || 32: dystrophin-associated glycoprotein complex || 33: microvillus

Num of ECM Genes: 1. Num of Predicted Genes: 9



1: cell cortex || 2: epidermal lamellar body || 3: basement membrane || 4: secretory granule || 5: transcriptional repressor complex