

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

Dataset:

Num of genes in input gene set: 6
Total number of genes: 20834
Prediction LLR threshold: 0

The CLIME PDF output two sections:

1) Overview of Evolutionarily Conserved Modules (ECMs)

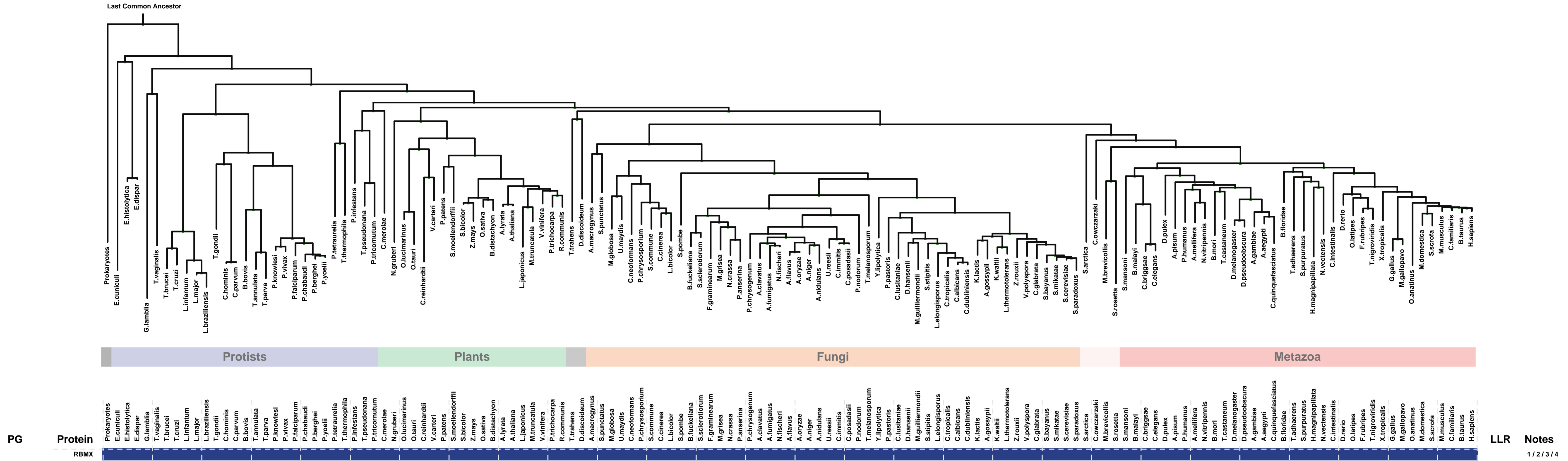
- Top panel shows the predefined species tree.
- Bottom panel shows the partition of input genes into Evolutionary Conserved Modules (ECMs), ordered by ECM strength (shown at right), and separated by horizontal lines.
- Each row show one gene, where the phylogenetic profile indicates presence (blue) 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.

ECM 1, Gene set "extracellular vesicular exosome", Page 1

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

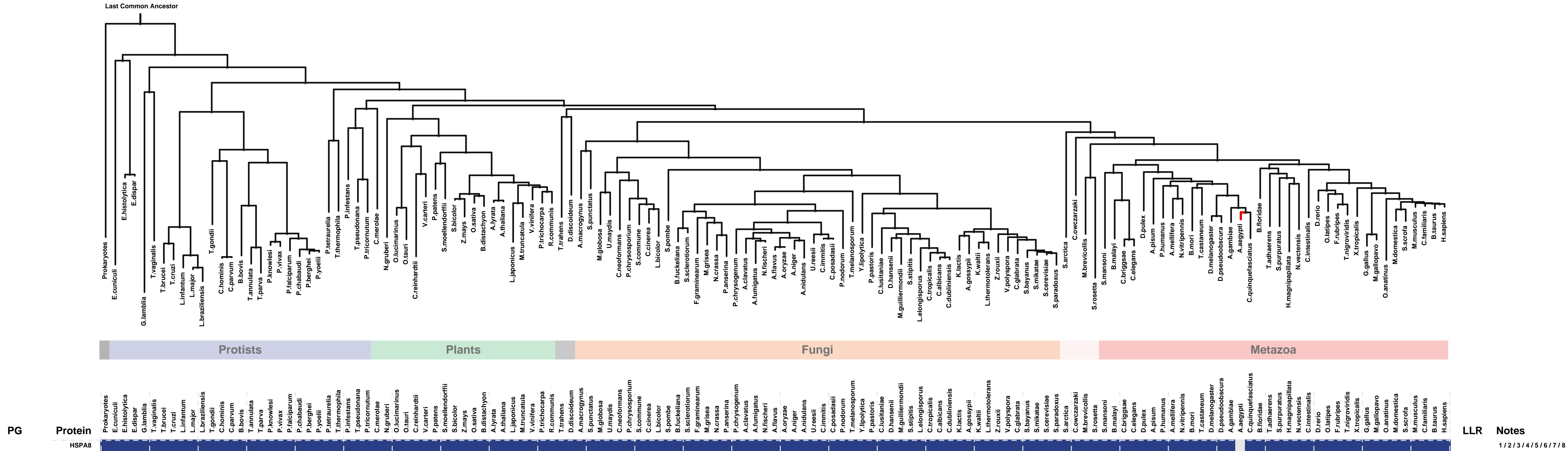


PG	Protein	LLR	Notes
	Prokaryotes		
	E.cuniculi		
	E.histolytica		
	E.dispar		
	G.lamblia		
	T.vaginalis		
	T.brucei		
	T.cruzi		
	L.infantum		
	L.major		
	L.braziliensis		
	T.gondii		
	C.hominis		
	C.parvum		
	B.bovis		
	T.annulata		
	T.parva		
	P.knowlesi		
	P.vivax		
	P.falciparum		
	P.chabaudi		
	P.berghoi		
	P.yoelii		
	P.tetraurelia		
	T.thermophila		
	P.infestans		
	T.pseudonana		
	P.tricornutum		
	C.merolae		
	N.gruberi		
	O.lucimarinus		
	O.tauri		
	C.reinhardtii		
	V.carteri		
	P.patens		
	S.moellendorffii		
	S.bicolor		
	Z.mays		
	O.sativa		
	B.distachyon		
	A.lyrata		
	A.thaliana		
	L.japonicus		
	M.truncatula		
	V.vinifera		
	P.trichocarpa		
	R.communis		
	T.trahens		
	D.discoidium		
	A.macrogynus		
	S.punctatus		
	M.globosa		
	U.maydis		
	C.neoformans		
	P.chrysosporium		
	S.commune		
	C.cinerea		
	L.bicolor		
	S.pombe		
	B.fuckeliana		
	S.sclerotiorum		
	F.graminearum		
	M.grisea		
	N.crassa		
	P.anserina		
	P.chrysogenum		
	A.clavatus		
	A.fumigatus		
	N.fischeri		
	A.flavus		
	A.oryzae		
	A.niger		
	A.nidulans		
	U.reezii		
	C.immitis		
	C.posadasii		
	P.nodorum		
	T.melanosporium		
	Y.lipolytica		
	P.pastoris		
	C.lusitanae		
	D.hansenii		
	M.guilliermondii		
	S.stiptitis		
	L.elongisporus		
	C.tropicalis		
	C.albicans		
	C.dubliniensis		
	K.lactis		
	A.gossypii		
	K.waltii		
	L.thermotolerans		
	Z.rouxii		
	V.polyspora		
	C.glabrata		
	S.bayanus		
	S.mikatae		
	S.cerevisiae		
	S.paradoxus		
	S.arctica		
	Cowczarzaki		
	M.brevicollis		
	S.rosetta		
	S.mansoni		
	B.malayi		
	C.briggsae		
	C.elegans		
	D.pulex		
	A.pisum		
	P.humanus		
	A.mellifera		
	N.vitripennis		
	B.mori		
	T.castaneum		
	D.melanogaster		
	D.pseudoobscura		
	A.gambiae		
	A.aegypti		
	C.quinquefasciatus		
	B.floridae		
	T.adhaerens		
	S.purpuratus		
	H.magnipapillata		
	N.vectensis		
	C.intestinalis		
	D.rerio		
	O.laipes		
	F.rubripes		
	T.nigroviridis		
	X.tropicalis		
	G.gallus		
	M.gallopavo		
	O.anatinus		
	M.domestica		
	S.scrofa		
	M.musculus		
	C.familiaris		
	B.taurus		
	H.sapiens		

1: catalytic step 2 spliceosome || 2: extracellular vesicular exosome || 3: nuclear euchromatin || 4: supraspliceosomal complex

ECM 2, Gene set "extracellular vesicular exosome", Page 1

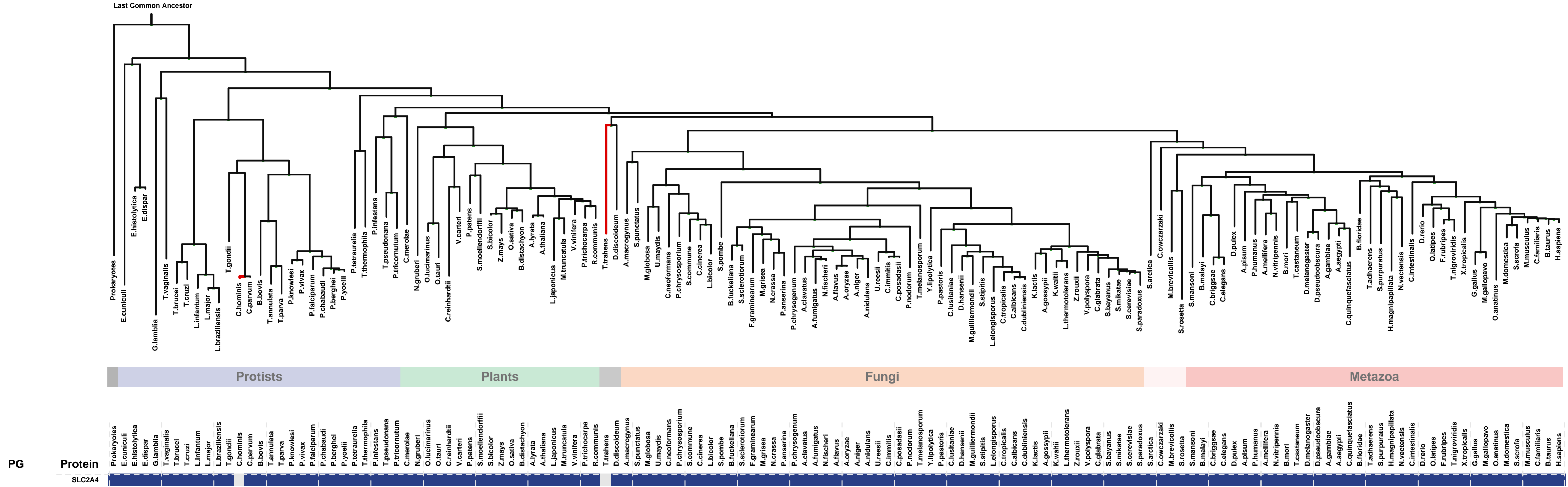
Num of ECM Genes: 1. Num of Predicted Genes: 0



1: clathrin-sculpted gamma-aminobutyric acid transport vesicle membrane || 2: extracellular vesicular exosome || 3: melanosome || 4: neuron projection || 5: Prp19 complex || 6: ribonucleoprotein complex || 7: spliceosomal complex || 8: synaptic vesicle

ECM 3, Gene set "extracellular vesicular exosome", Page 1

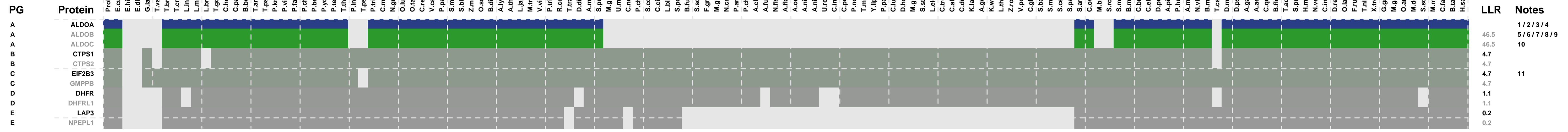
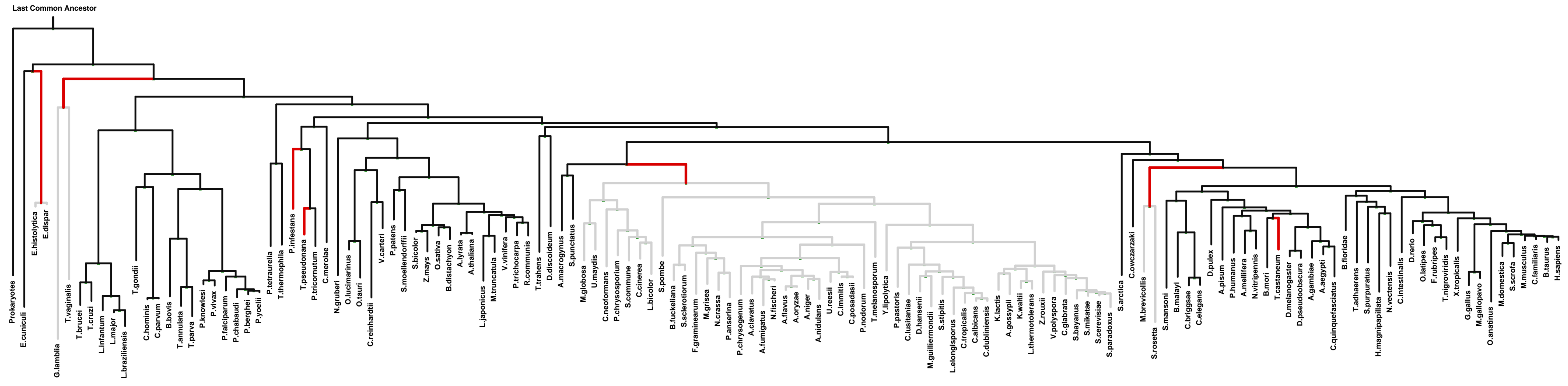
Num of ECM Genes: 1. Num of Predicted Genes: 0



1: clathrin-coated vesicle || 2: coated pit || 3: external side of plasma membrane || 4: extracellular vesicular exosome || 5: insulin-responsive compartment || 6: multivesicular body || 7: sarcolemma || 8: trans-Golgi network transport vesicle || 9: vesicle membrane

ECM 4, Gene set "extracellular vesicular exosome", Page 3

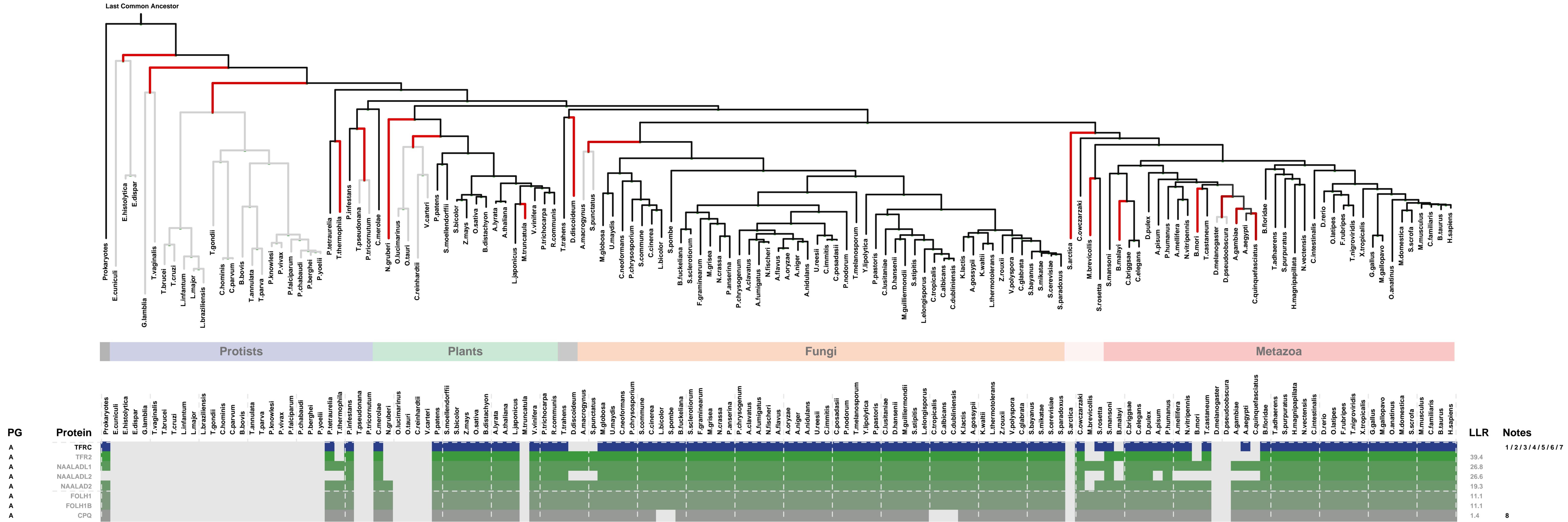
Num of ECM Genes: 1. Num of Predicted Genes: 10



1: actin cytoskeleton || 2: extracellular vesicular exosome || 3: I band || 4: platelet alpha granule lumen || 5: centriolar satellite || 6: lysosome || 7: microtubule organizing center || 8: rough endoplasmic reticulum membrane || 9: smooth endoplasmic reticulum membrane || 10: axon || 11: eukaryotic translation initiation factor 2B complex

ECM 5, Gene set "extracellular vesicular exosome", Page 3

Num of ECM Genes: 1. Num of Predicted Genes: 7

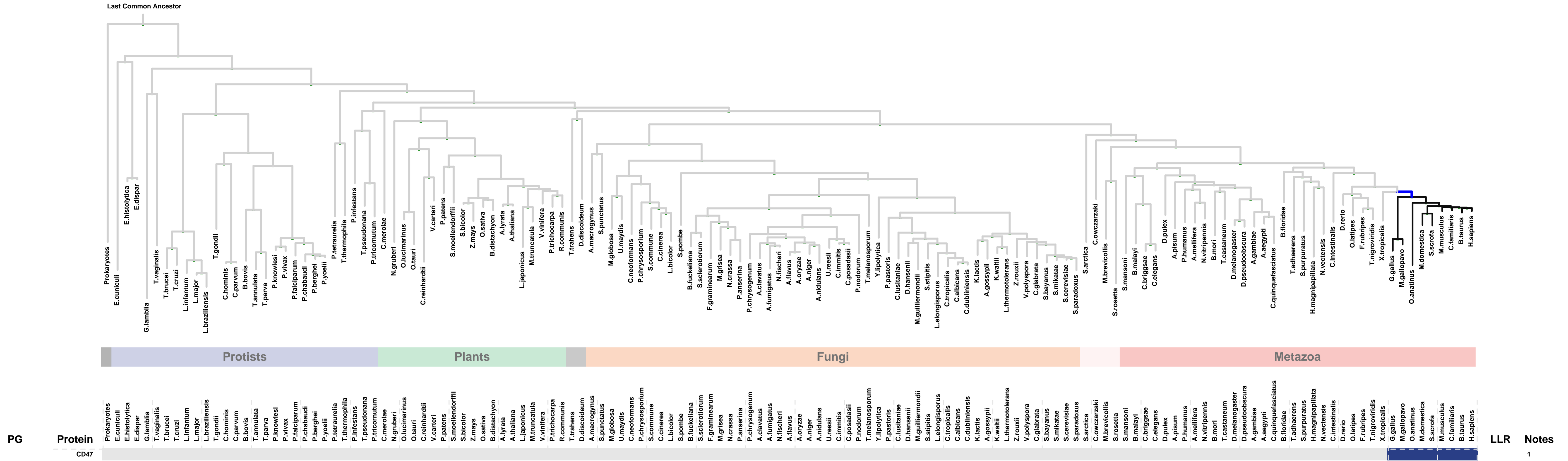


1: coated pit || 2: cytoplasmic membrane-bounded vesicle || 3: endosome || 4: external side of plasma membrane || 5: extracellular vesicular exosome || 6: melanosome || 7: recycling endosome membrane || 8: lysosome

Protein	LLR	Notes
TFRC	39.4	1 2 3 4 5 6 7
TFR2	26.8	
NAALADL1	26.6	
NAALADL2	19.3	
FOLH1	11.1	
FOLH1B	11.1	
CPQ	1.4	8

ECM 6, Gene set "extracellular vesicular exosome", Page 1

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



1: extracellular vesicular exosome