

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)

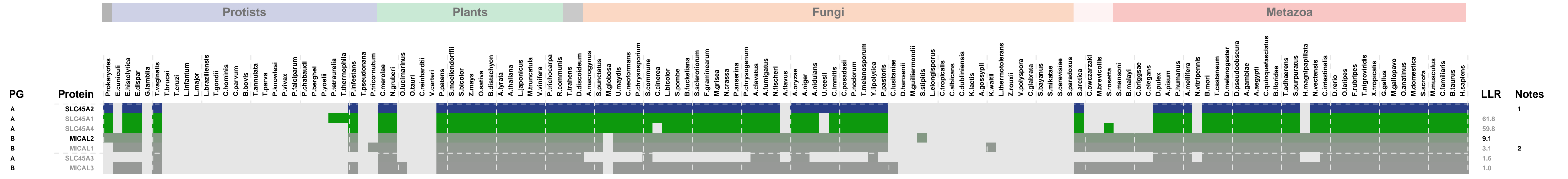
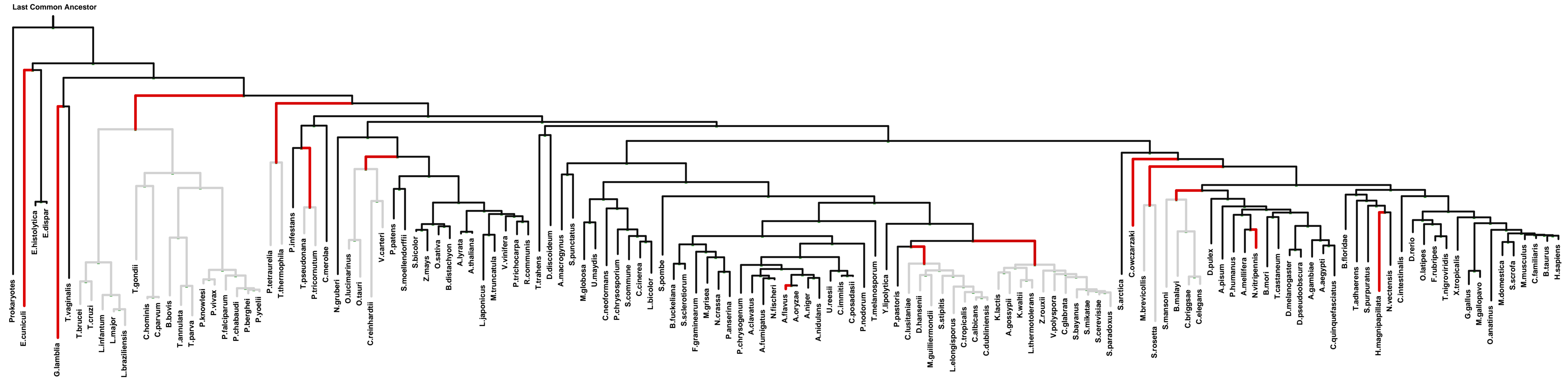
- Top panel shows the predefined species tree.
- Bottom panel shows the partition of input genes into Evolutionary Conserved Modules (ECMs), ordered by ECM strength (shown at right), and separated by horizontal lines.
- Each row show one gene, where the phylogenetic profile indicates presence (blue)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

ECM 1, Gene set "melanosome membrane", Page 1

Num of ECM Genes: 1. Num of Predicted Genes: 6

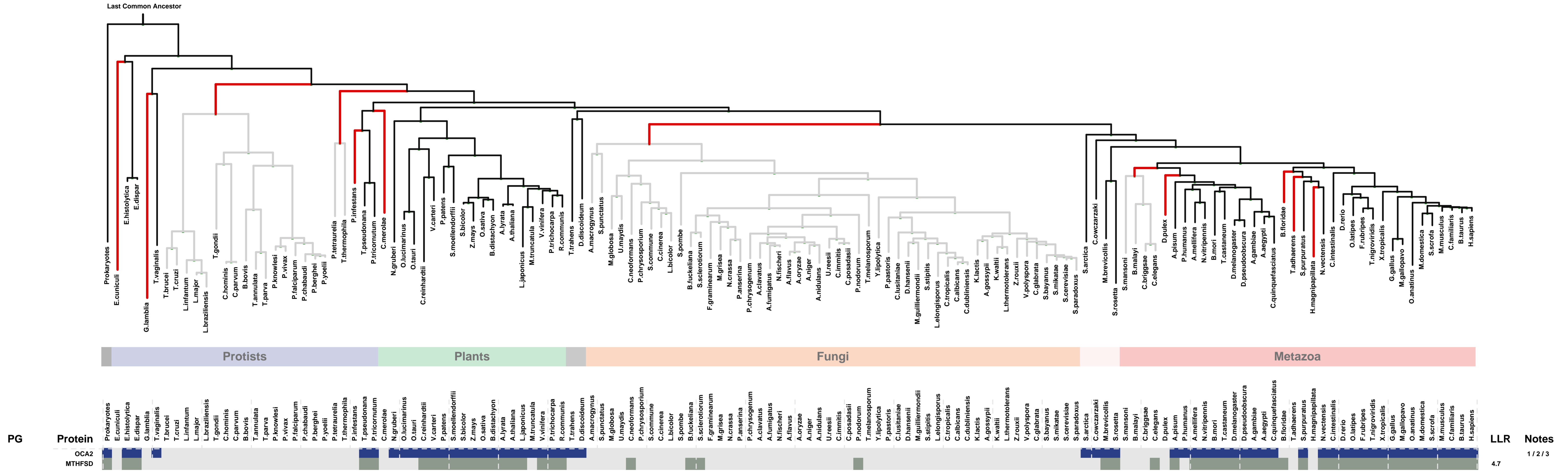


1: melanosome membrane || 2: intermediate filament

PG	Protein	LLR	Notes
A	SLC45A2	61.8	1
A	SLC45A1	59.8	
A	SLC45A4	9.1	
B	MICAL2	3.1	2
B	MICAL1	1.6	
A	SLC45A3	1.0	
B	MICAL3		

ECM 2, Gene set "melanosome membrane", Page 1

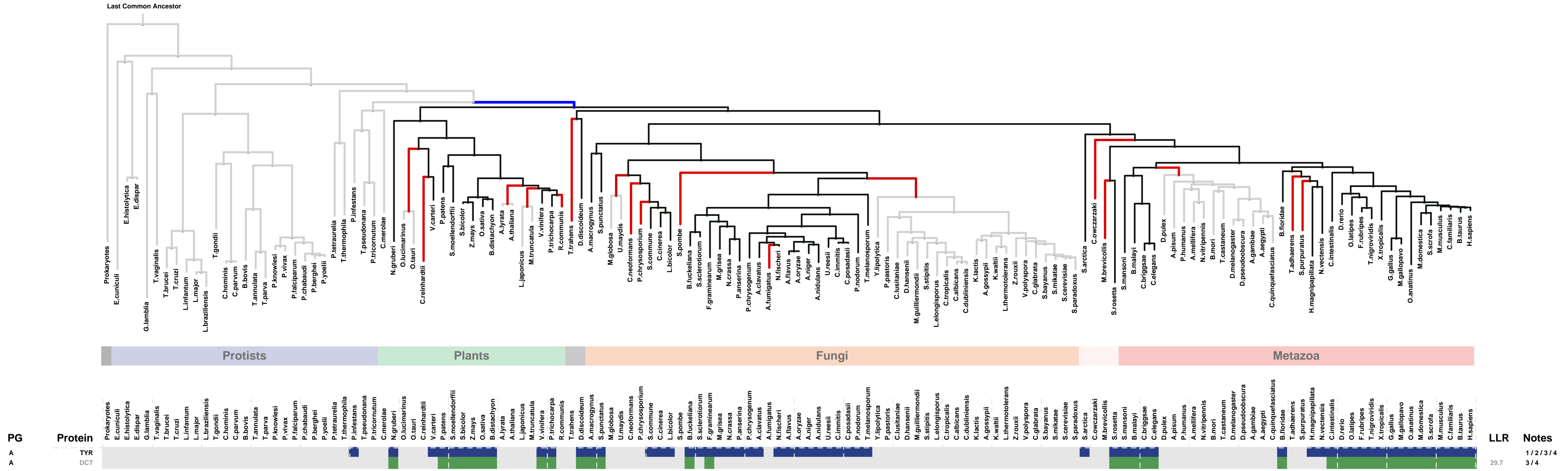
Num of ECM Genes: 1. Num of Predicted Genes: 1



1: endosome membrane || 2: lysosomal membrane || 3: melanosome membrane

ECM 3, Gene set "melanosome membrane", Page 1

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

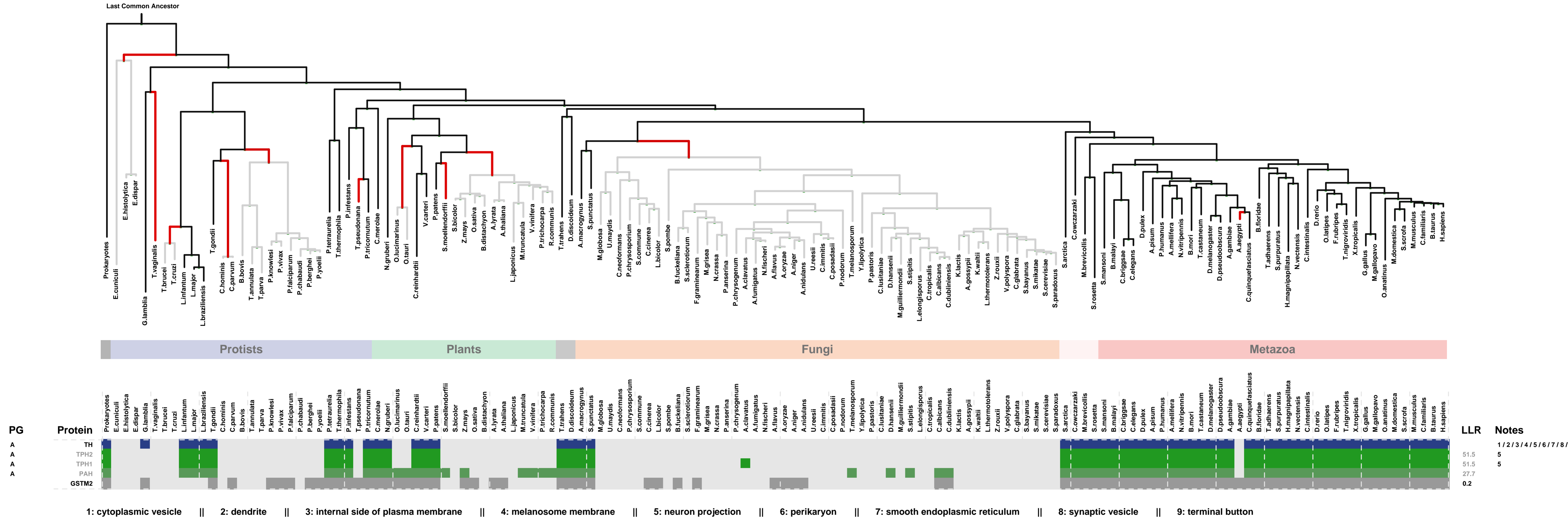


1: Golgi-associated vesicle || 2: lysosome || 3: melanosome || 4: melanosome membrane

LLR 29.7 Notes 1/2/3/4 3/4

ECM 4, Gene set "melanosome membrane", Page 1

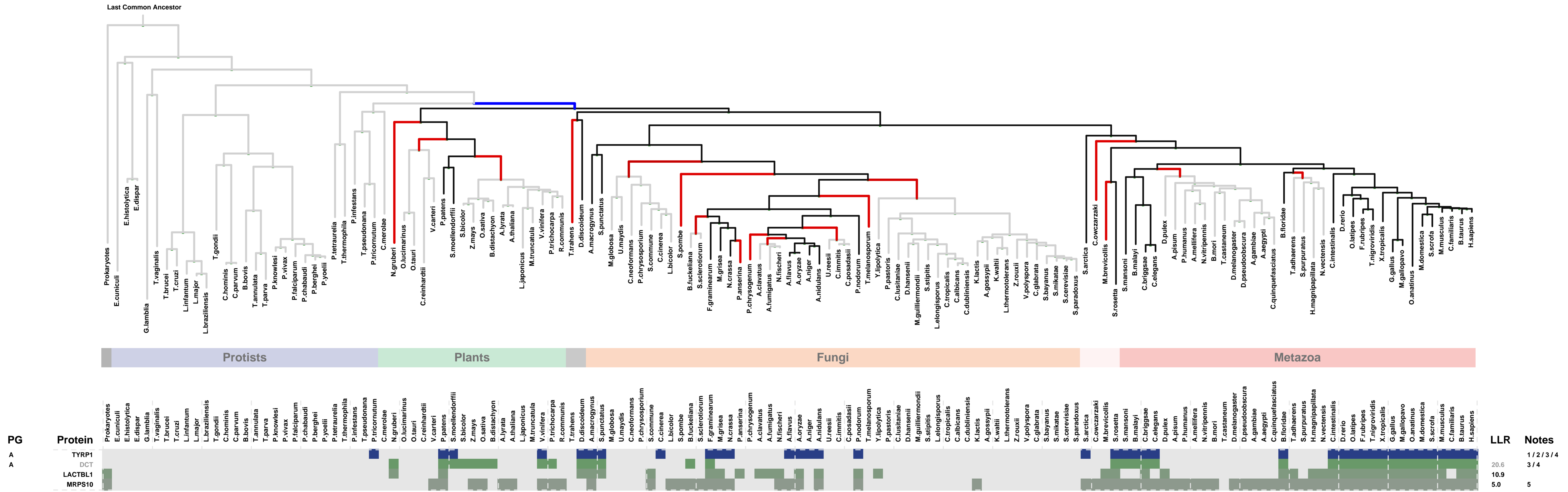
Num of ECM Genes: 1. Num of Predicted Genes: 4



PG	TH	TPH2	TPH1	PAH	GSTM2	LLR	Notes
A	51.5	51.5	51.5	27.7	0.2	5	1/2/3/4/5/6/7/8/9
A	51.5	51.5	51.5	27.7	0.2	5	1/2/3/4/5/6/7/8/9
A	51.5	51.5	51.5	27.7	0.2	5	1/2/3/4/5/6/7/8/9
A	51.5	51.5	51.5	27.7	0.2	5	1/2/3/4/5/6/7/8/9

ECM 5, Gene set "melanosome membrane", Page 1

Num of ECM Genes: 1. Num of Predicted Genes: 3

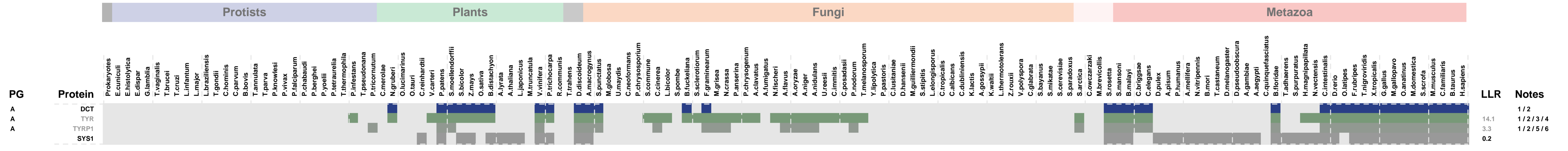
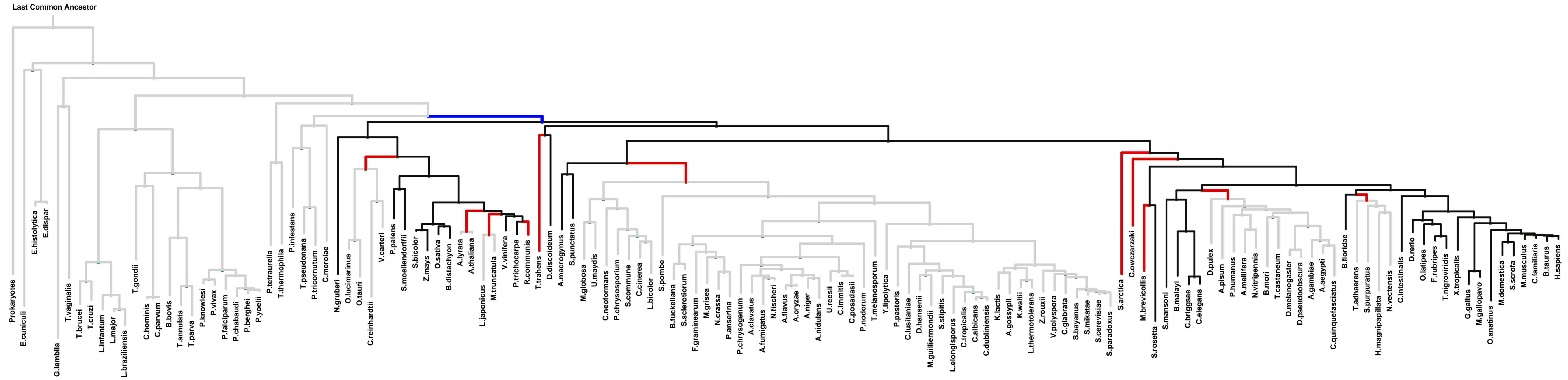


1: clathrin-coated endocytic vesicle membrane || 2: endosome membrane || 3: melanosome || 4: melanosome membrane || 5: ribosome

Protein	LLR	Notes
TYRP1	20.6	1/2/3/4
DCT	10.9	3/4
LACTBL1	10.9	
MRPS10	5.0	5

ECM 6, Gene set "melanosome membrane", Page 1

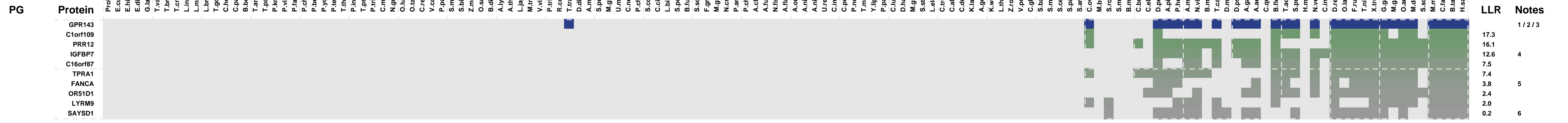
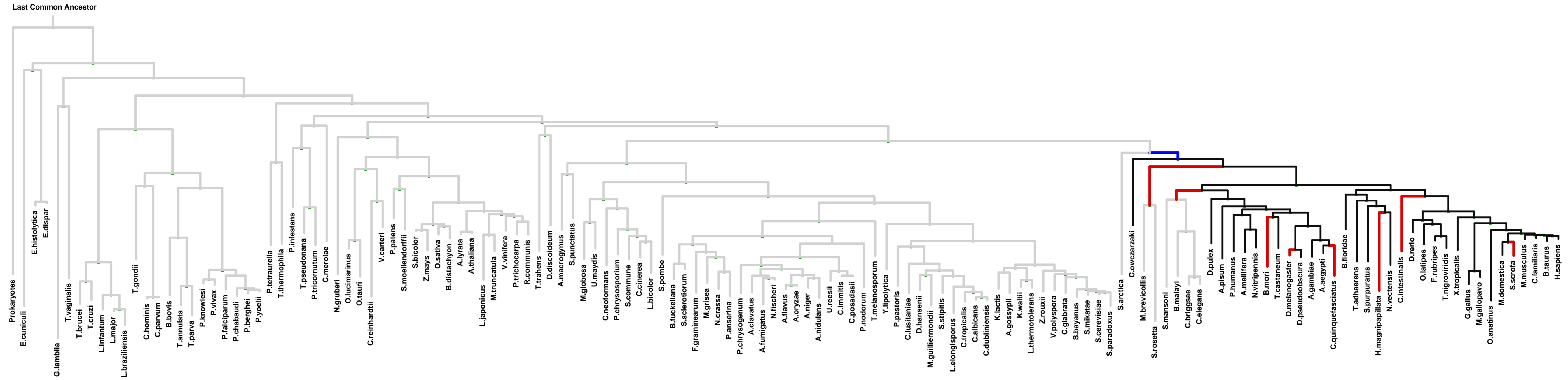
Num of ECM Genes: 1. Num of Predicted Genes: 3



1: melanosome || 2: melanosome membrane || 3: Golgi-associated vesicle || 4: lysosome || 5: clathrin-coated endocytic vesicle membrane || 6: endosome membrane

ECM 7, Gene set "melanosome membrane", Page 1

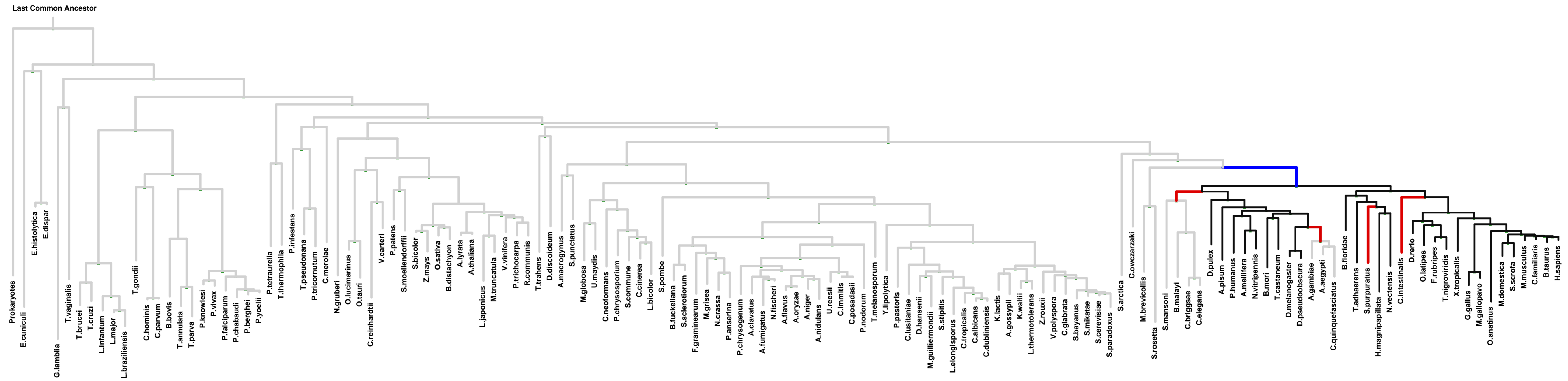
Num of ECM Genes: 1. Num of Predicted Genes: 9



1: lysosomal membrane || 2: melanosome || 3: melanosome membrane || 4: extracellular matrix || 5: Fanconi anaemia nuclear complex || 6: cytoplasmic vesicle membrane

ECM 8, Gene set "melanosome membrane", Page 1

Num of ECM Genes: 1. Num of Predicted Genes: 38

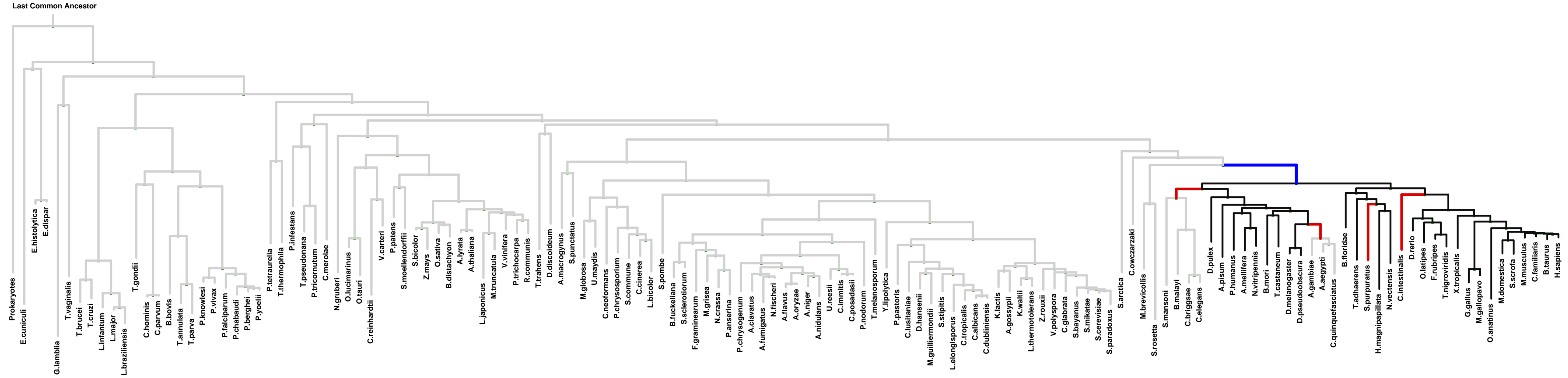


PG	Protein	Protists	Plants	Fungi	Metazoa	LLR	Notes
A	DTNBP1					17.3	1/2/3/4/5/6/7/8/9/10
	LAPTM4B					14.6	14
	CCDC64B					11.2	
	TNFSF13B					10.9	15
	SOST					10.4	
B	FAM122C					8.6	16
	DFFA					7.6	17/18
	CIDEA					7.6	16
	DFFB					7.6	17/19
	CIDEC					7.4	
C	OR10G3					7.3	14
	LAPTM4A					7.0	20
	TMEM173					6.0	
	AUTS2					5.9	
	SERTAD2					5.6	
D	TMEM130					5.5	
	ZC3H13					4.4	21
	FANCA					4.1	22
	LYPD6B					4.1	
	LYPD6					3.8	23
E	FBXO5					3.8	24
	TJAP1					3.6	25
	MED9					3.1	26
	PLA2G3					2.7	
	DAND5					2.6	
E	CD164L2					2.1	14/27/28
	CDC42EP4					1.7	
	BAG4					1.7	29/30
	NPM1					1.6	
	HAVCR2					1.5	
E	CD96					1.5	
	NPM3					1.4	25
	MED15					1.4	31
	LAG3					1.3	32/33
ATN1							

1: axon || 2: axon part || 3: BLOC-1 complex || 4: dendritic spine || 5: endosome membrane || 6: growth cone || 7: melanosome membrane || 8: neuron projection || 9: postsynaptic density || 10: postsynaptic membrane || 11: sarcolemma || 12: sarcoplasm || 13: synaptic vesicle membrane || 14: endomembrane system || 15: extracellular matrix || 16: nuclear chromatin || 17: lipid particle || 18: mitochondrial envelope || 19: focal adhesion || 20: mitochondrial outer membrane || 21: Fanconi anaemia nuclear complex || 22: anchored to membrane || 23: spindle || 24: tight junction || 25: mediator complex || 26: centriole || 27: actin cytoskeleton || 28: microtubule cytoskeleton ||

ECM 8, Gene set "melanosome membrane", Page 2

Num of ECM Genes: 1. Num of Predicted Genes: 38



PG	Protein	Species	LLR	Notes
	INIP	Prokaryotes		
	OR10H1	E. cuniculi		
	OR10H2	E. histolytica		
	CIDEB	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. berghei		
		P. yoelii		
		P. tetraurelia		
		T. thermophila		
		P. infestans		
		T. pseudonana		
		P. ricornutum		
		C. merolae		
		N. gruberi		
		O. lucimarinus		
		O. lauri		
		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. discoideum		
		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. reesii		
		C. immitis		
		C. posadasii		
		P. nodorum		
		T. melanosporum		
		Y. lipolytica		
		P. pastoris		
		C. lusitanae		
		D. hansenii		
		M. guilliermondii		
		S. stipitidis		
		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		
		C. owczarzaki		
		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. latipes		
		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: SOSS complex