

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:

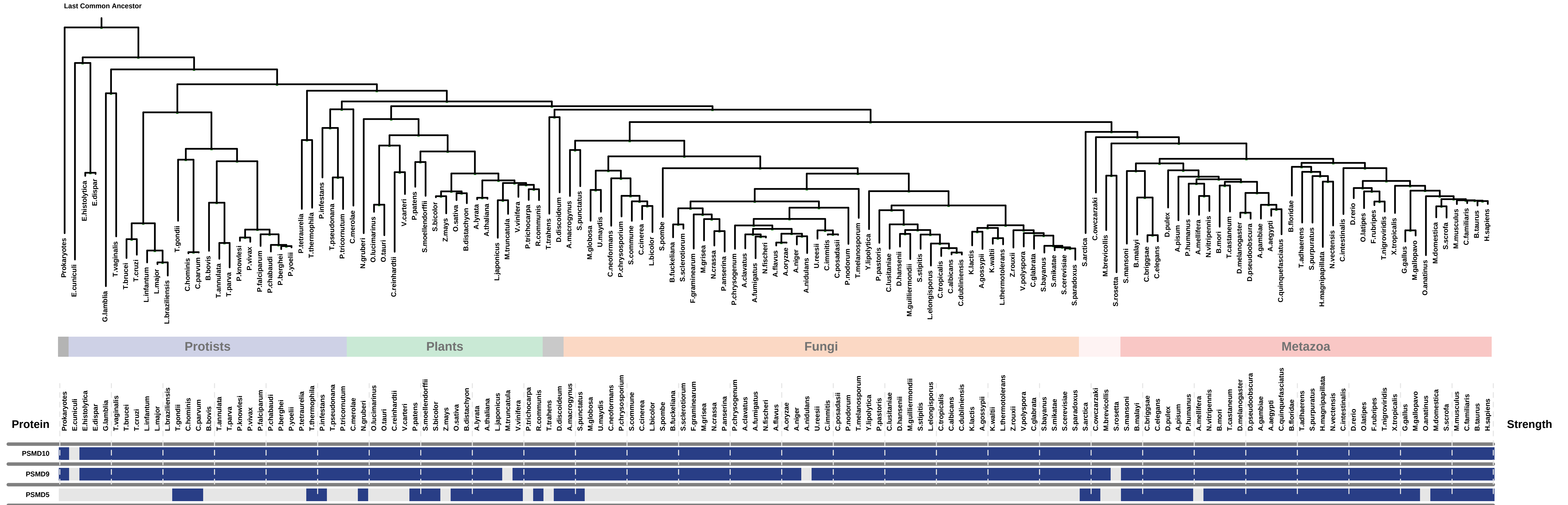
1) Overview of Evolutionarily Conserved Modules (ECMs)

- 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+

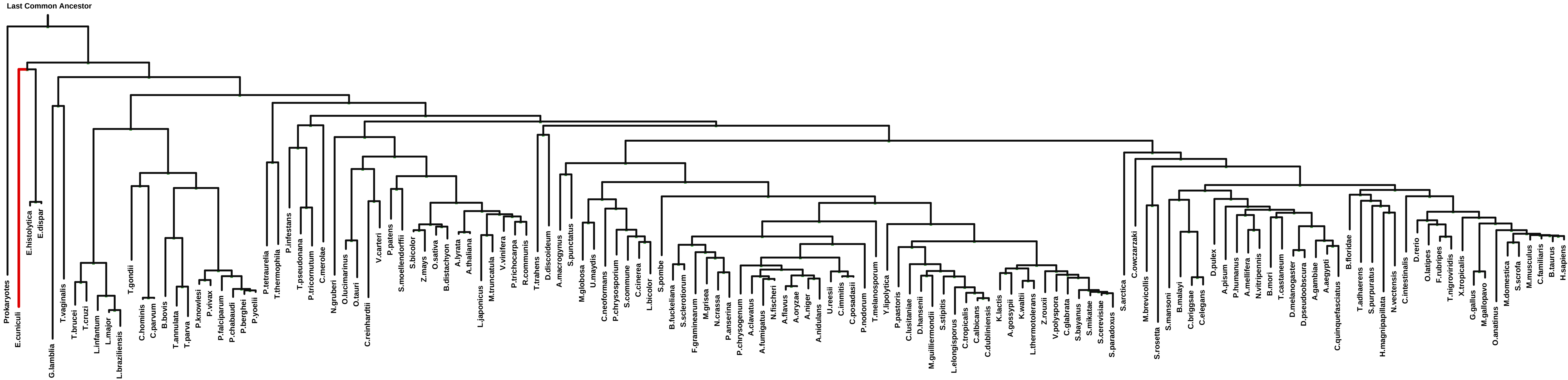
- Top panel shows the inferred evolutionary history on the predefined species tree. Branch color shows the gain event (blue) and loss events (red color, with brighter color indicating higher confidence in loss). Branches before the gain or after a loss are shown in gray.
- Bottom panel shows the input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

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



PG

Protein	PSMD10
Prokaryotes	
E.cuniculi	
E.histolytica	
E.dispar	
G.lamblia	
T.vaginalis	
T.brucei	
T.cruzi	
L.infantum	
L.major	
L.brazilienis	
T.gondii	
C.hominis	
C.parvum	
B.bovis	
T.annulata	
T.parva	
P.knowlesi	
P.vivax	
P.falciparum	
P.chabaudi	
P.berghiei	
P.yoelii	
P.tetraurelia	
T.thermophila	
P.infestans	
T.pseudonana	
P.tricornutum	
C.merolae	
N.gruberi	
O.lucimarinus	
O.auri	
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.tuckeliana	
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.sarctica	
Cowczarzaki	
M.brevicollis	
S.rosetta	
S.mansoni	
B.malayii	
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.erio	
O.laetipes	
F.rubripes	
T.nigroviridis	
X.tropicalis	
G.gallus	
M.gallopavo	
O.anatinus	
M.domestica	
S.scrofa	
M.musculus	
C.familiaris	
B.taurus	
H.sapiens	

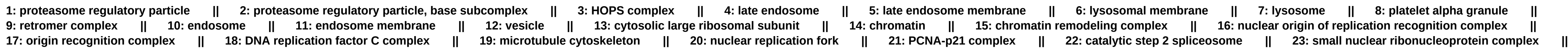
LLR

Notes

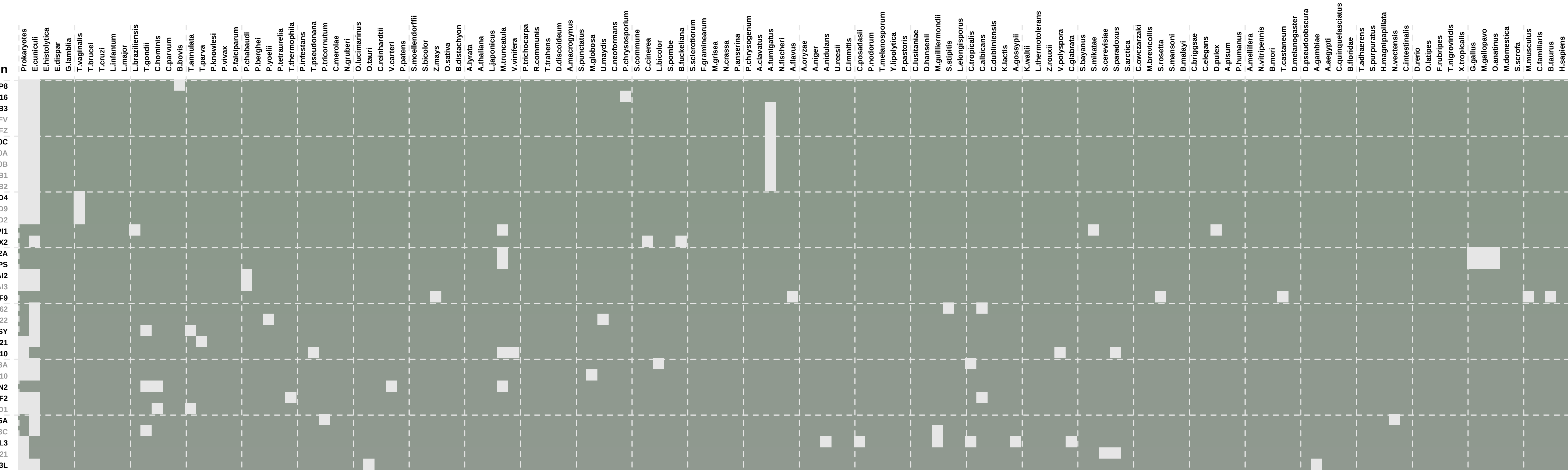
1 / 2 / 3 / 4 / 5

1: actin cytoskeleton || 2: intermediate filament cytoskeleton || 3: proteasome complex || 4: proteasome regulatory particle || 5: proteasome regulatory particle, base subcomplex

Num of ECM Genes: 1. Num of Predicted Genes: 277



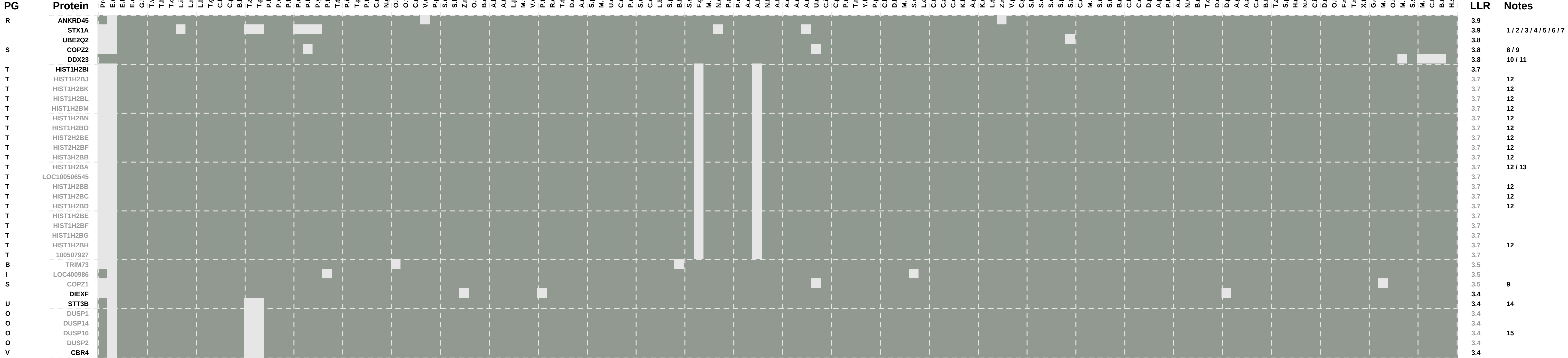
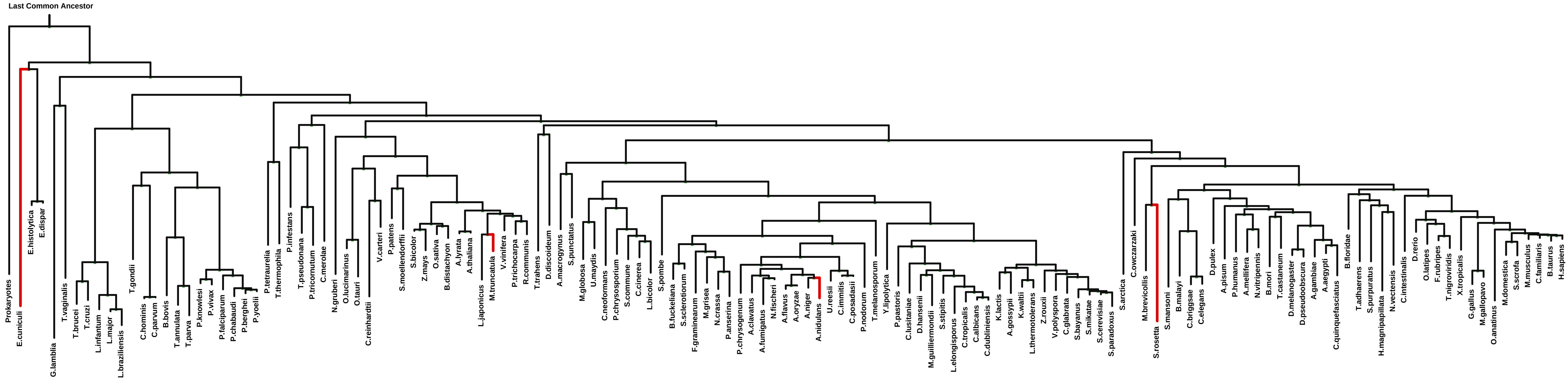
Num of ECM Genes: 1. Num of Predicted Genes: 277



1: early endosome || 2: late endosome membrane || 3: lysosomal membrane || 4: recycling endosome || 5: secretory granule membrane || 6: SNARE complex || 7: nucleosome || 8: Barr body || 9: nuclear nucleosome || 10: transcriptionally active chromatin || 11: endoplasmic reticulum-Golgi intermediate compartment || 12: endoplasmic reticulum-Golgi intermediate compartment membrane || 13: trans-Golgi network transport vesicle || 14: COPI-coated vesicle || 15: COPI-coated vesicle membrane || 16: Golgi cisterna membrane || 17: zymogen granule membrane || 18: ribonuclease H2 complex || 19: extrinsic to internal side of plasma membrane || 20: heterotrimeric G-protein complex || 21: membrane raft ||

ECM 2, Gene set "proteasome regulatory particle, base subcomplex", Page 3

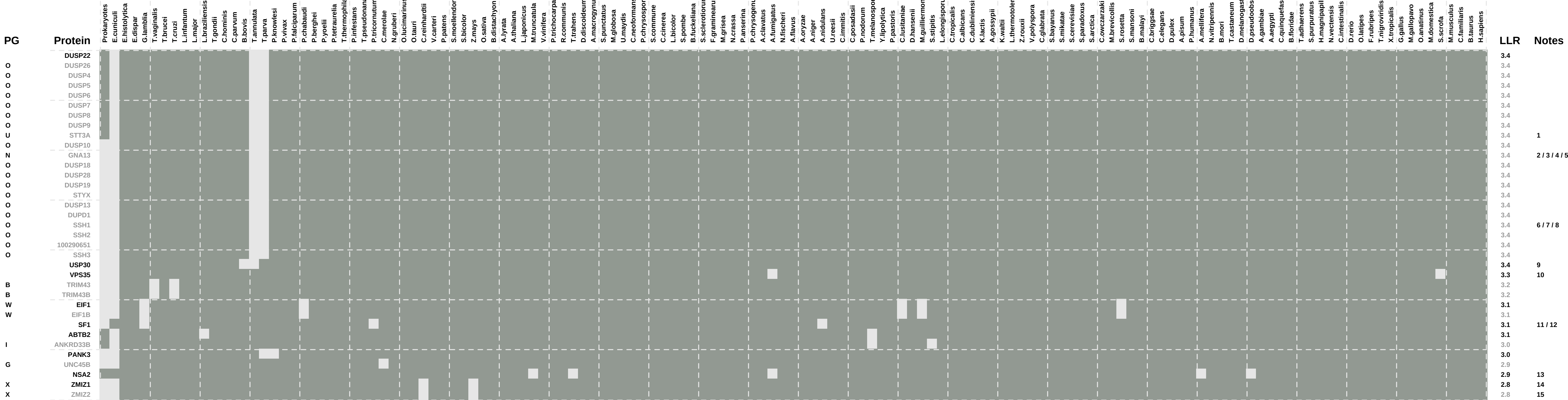
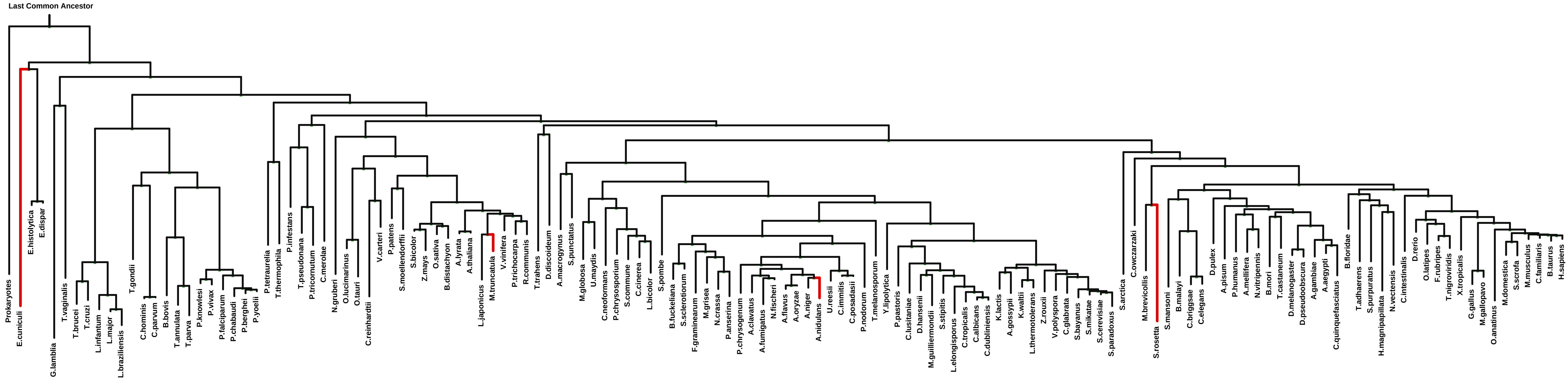
Num of ECM Genes: 1. Num of Predicted Genes: 277



1: actomyosin || 2: neuron projection || 3: secretory granule || 4: SNARE complex || 5: synaptic vesicle membrane || 6: synaptobrevin 2-SNAP-25-syntaxin-1a complex || 7: synaptobrevin 2-SNAP-25-syntaxin-1a-complexin I complex || 8: cis-Golgi network || 9: COPI vesicle coat || 10: catalytic step 2 spliceosome || 11: U5 snRNP || 12: nucleosome || 13: extrinsic to plasma membrane || 14: oligosaccharyltransferase complex || 15: cytoplasmic membrane-bounded vesicle

ECM 2, Gene set "proteasome regulatory particle, base subcomplex", Page 4

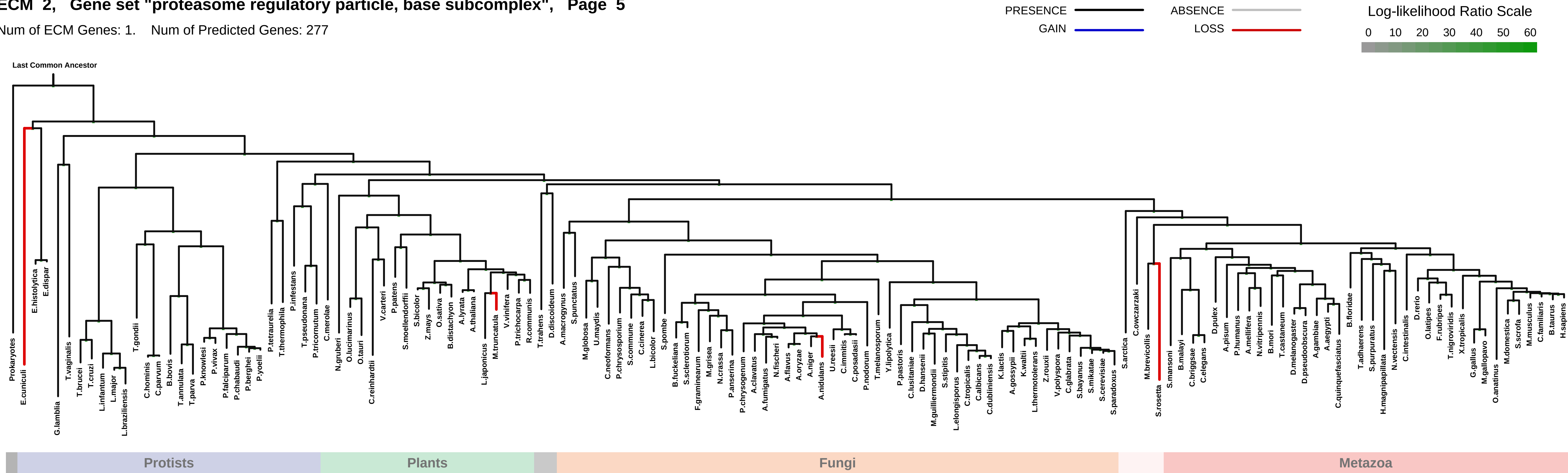
Num of ECM Genes: 1. Num of Predicted Genes: 277



1: oligosaccharyltransferase complex || 2: brush border membrane || 3: extrinsic to internal side of plasma membrane || 4: heterotrimeric G-protein complex || 5: melanosome || 6: cleavage furrow || 7: lamellipodium || 8: midbody || 9: mitochondrial outer membrane || 10: endosome || 11: ribosome || 12: spliceosomal complex || 13: ribonucleoprotein complex || 14: nuclear speck || 15: nuclear replication fork

ECM 2, Gene set "proteasome regulatory particle, base subcomplex", Page 5

Num of ECM Genes: 1. Num of Predicted Genes: 277

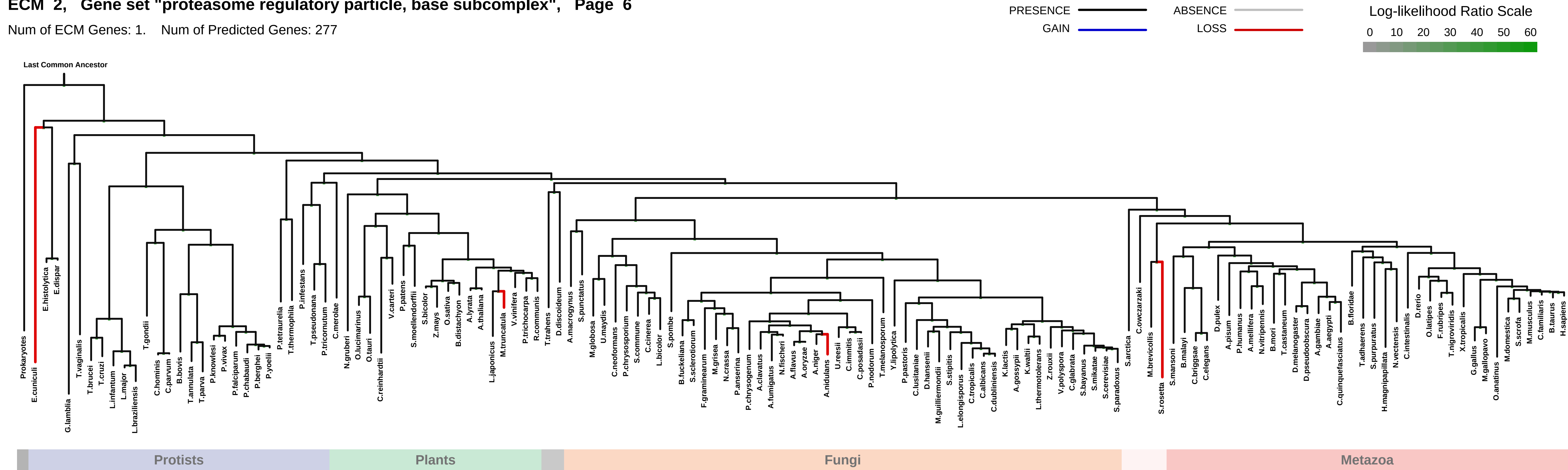


	PG	Protein	Prokaryotes E.cuniculi E.histolytica E.dispar G.lamblia T.vaginalis T.brucei T.cruzi L.infantum L.major L.braziliensis T.gondii C.hominis C.parvum B.bovis T.amulata T.parva P.knowlesi P.vivax P.falciparum P.chabaudi P.berghei P.yoelli P.tetraulera T.thermophila P.intestans T.pseudomana P.tricornutum C.merlae N.gruberi O.lucimarinus O.tauri C.reinhardtii V.carteri P.patens S.moellendorff 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.neofomanis P.chrysosporium S.commune C.chinea 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.reesli C.immitis C.posadasii P.nodorum T.melanosporeum Y.lipolytica P.pastoris C.lutitiae D.hansenii M.guilliermondii S.stipitis L.elongisporum 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.cowczaraki M.brevicollis S.rosea S.mansoni B.malayi C.briggsae C.elegans D.pulex A.pisum P.humanus A.meliffera N.viripennis B.mori T.castaneum D.melanogaster D.pseudoobscura A.gambiae A.aegypti C.quinqfascia B.floridae T.adhaerens S.purpuratus H.magnipapilio N.vectensis C.intestinalis D.rerio O.latipes F.ruripes T.nigrovirdidis X.tropicalis G.gallus M.gallopavo O.anatinus M.domestica S.scrofa M.musculus C.familiaris B.taurus H.sapiens	LLR	Notes
X		PIAS1		2.8	1
X		PIAS2		2.8	1 / 2
X		PIAS3		2.8	3 / 4
X		PIAS4		2.8	2 / 5
		100294376		2.7	
Y		SLC25A5		2.6	6 / 7
Y		SLC25A6		2.6	8
A		CHMP2A		2.6	9
Z		EIF2A		2.6	10
Z		EIF3B		2.6	11
V		DECR2		2.6	12
		PRMT8		2.6	
		ITSN2		2.6	
		CHKA		2.6	
		RBM15B		2.6	
a		SF3B3		2.6	13 / 14 / 15 / 16
Y		SLC25A1		2.6	
Y		SLC25A10		2.6	
Y		SLC25A11		2.6	
Y		SLC25A12		2.6	
Y		SLC25A13		2.6	
Y		SLC25A14		2.6	
Y		SLC25A15		2.6	
b		TNPO1		2.6	17
b		TNPO2		2.6	17
Y		SLC25A16		2.6	
Y		SLC25A17		2.6	
Y		SLC25A18		2.6	12 / 18 / 19
Y		SLC25A19		2.6	
Y		SLC25A2		2.6	
Y		SLC25A20		2.6	
Y		SLC25A21		2.6	
Y		SLC25A22		2.6	
Y		SLC25A26		2.6	
Y		SLC25A28		2.6	

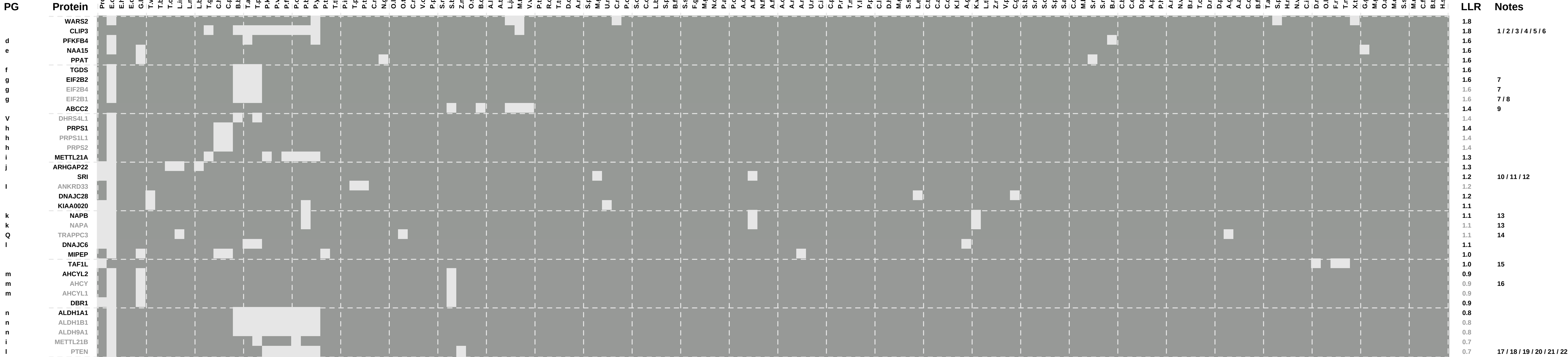
1: nuclear speck || 2: PML body || 3: dendrite || 4: synapse || 5: nuclear matrix || 6: mitochondrial nucleoid || 7: MMXD complex || 8: mitochondrial inner membrane presequence translocase complex || 9: late endosome membrane || 10: eukaryotic translation initiation factor 2 complex || 11: eukaryotic translation initiation factor 3 complex || 12: peroxisome || 13: catalytic step 2 spliceosome || 14: small nuclear ribonucleoprotein complex || 15: spliceosomal complex || 16: U12-type spliceosomal complex || 17: nuclear pore || 18: integral to peroxisomal membrane || 19: peroxisomal membrane

ECM 2, Gene set "proteasome regulatory particle, base subcomplex", Page 6

Num of ECM Genes: 1. Num of Predicted Genes: 277

[illegible]

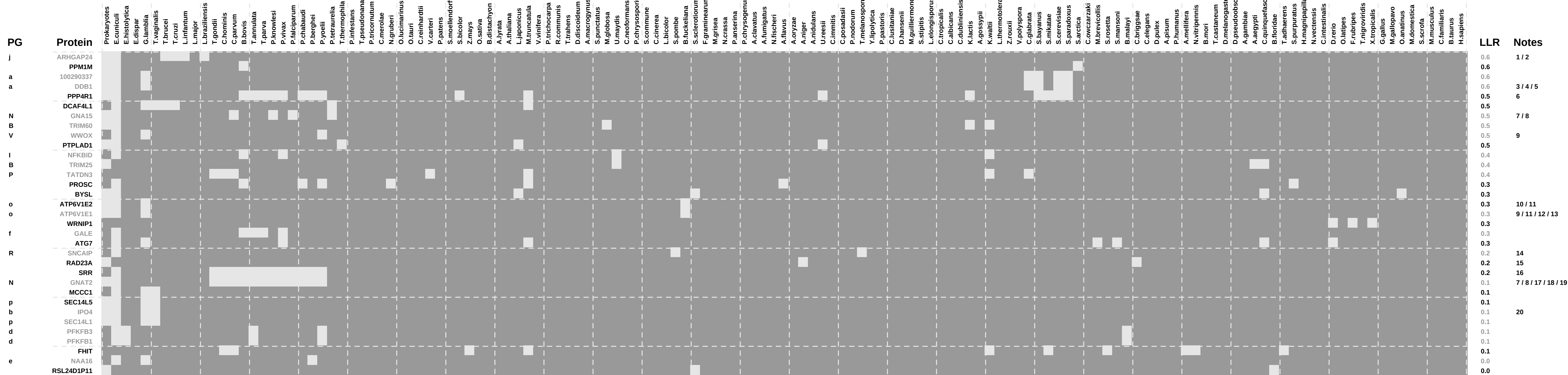
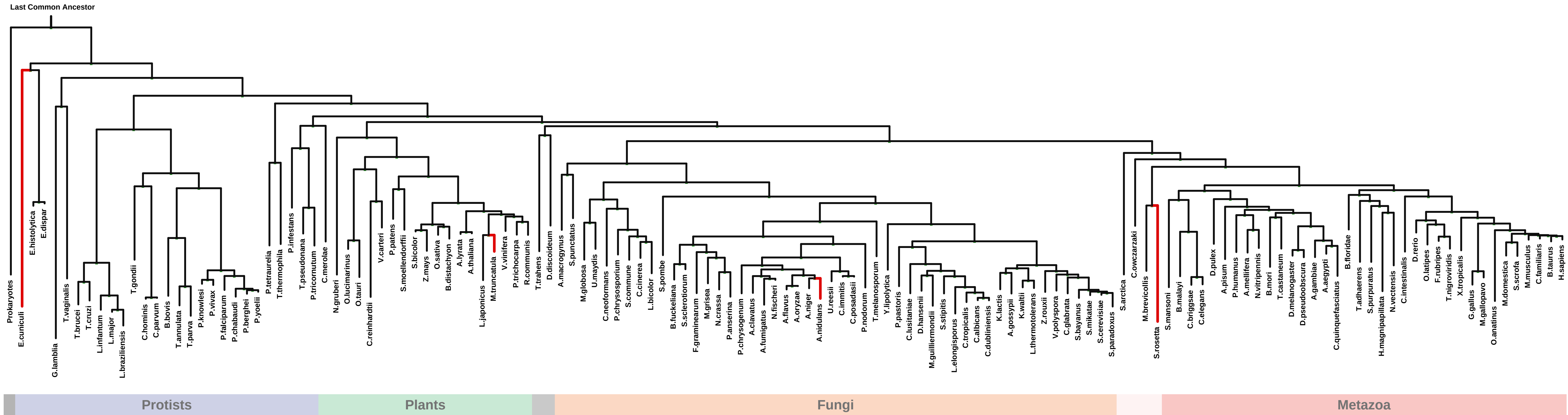
Num of ECM Genes: 1. Num of Predicted Genes: 277



1: early endosome membrane || 2: Golgi stack || 3: membrane raft || 4: recycling endosome membrane || 5: trans-Golgi network || 6: trans-Golgi network membrane || 7: eukaryotic translation initiation factor 2B complex || 8: eukaryotic translation initiation factor 2 complex || 9: intercellular canaliculus || 10: sarcoplasmic reticulum membrane || 11: vesicle || 12: Z disc || 13: synaptobrevin 2-SNAP-25-syntaxin-1a complex || 14: TRAPP complex || 15: transcription factor TFIID complex || 16: melanosome || 17: cell projection || 18: internal side of plasma membrane || 19: myelin sheath adaxonal region || 20: neuron projection || 21: PML body || 22: Schmidt-Lanterman incisure

ECM 2, Gene set "proteasome regulatory particle, base subcomplex", Page 8

Num of ECM Genes: 1. Num of Predicted Genes: 277



1: cell projection || 2: focal adhesion || 3: Cul4A-RING ubiquitin ligase complex || 4: Cul4B-RING ubiquitin ligase complex || 5: Cul4-RING ubiquitin ligase complex || 6: protein phosphatase 4 complex || 7: extrinsic to internal side of plasma membrane || 8: heterotrimeric G-protein complex || 9: microvillus || 10: acrosomal vesicle || 11: proton-transporting two-sector ATPase complex, catalytic domain || 12: endosome || 13: proton-transporting two-sector ATPase complex || 14: presynaptic membrane || 15: proteasome complex || 16: apical part of cell || 17: photoreceptor inner segment || 18: photoreceptor outer segment || 19: photoreceptor outer segment membrane || 20: nuclear pore

ECM 3, Gene set "proteasome regulatory particle, base subcomplex", Page 1

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

