

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

Dataset:

Num of genes in input gene set: 4

Total number of genes: 20834

Prediction LLR threshold: 0

The CLIME PDF output two sections:

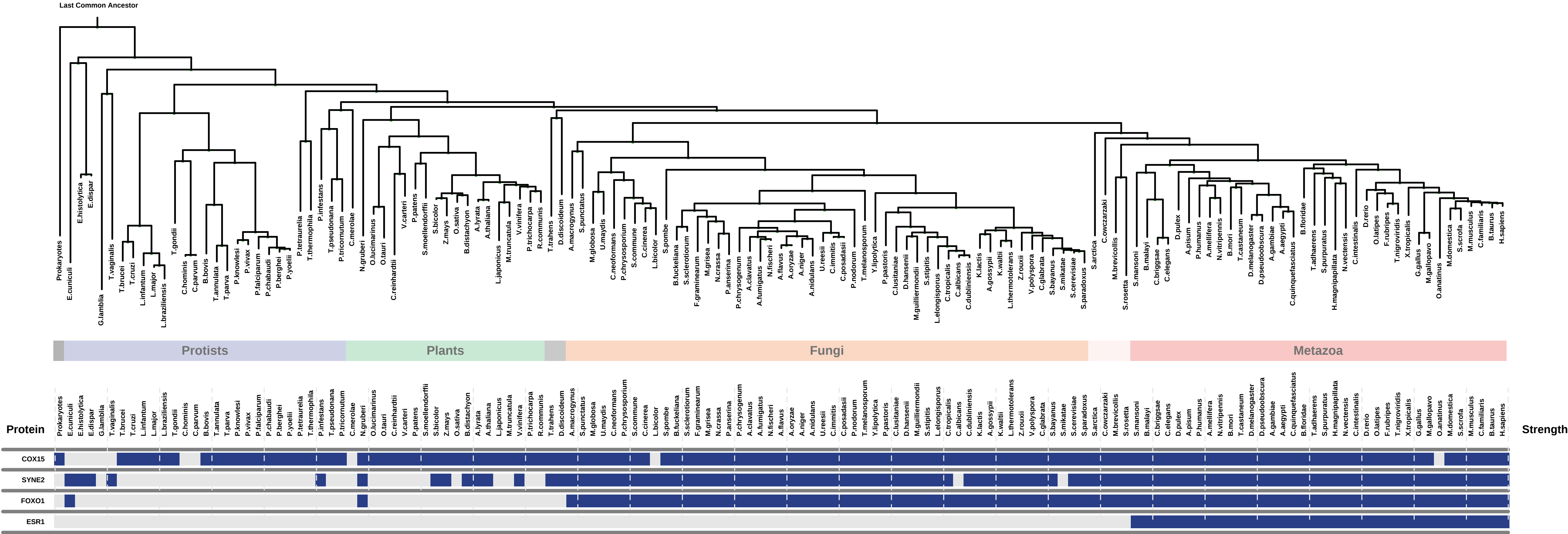
1) Overview of Evolutionarily Conserved Modules (ECMs)

- 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+

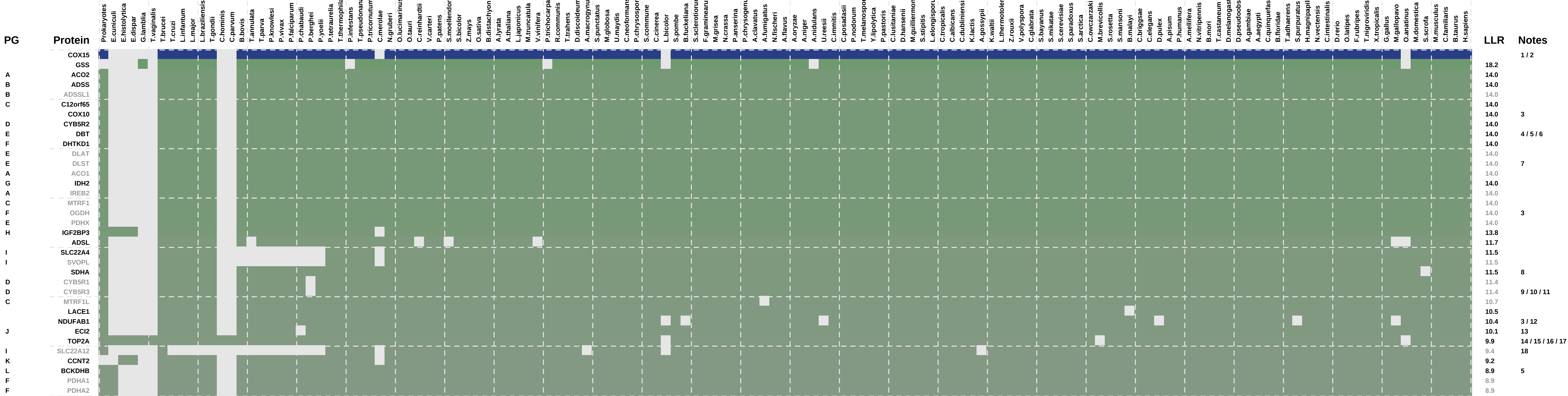
- Top panel shows the inferred evolutionary history on the predefined species tree. Branch color shows the gain event (blue) and loss events (red color, with brighter color indicating higher confidence in loss). Branches before the gain or after a loss are shown in gray.
- Bottom panel shows the input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

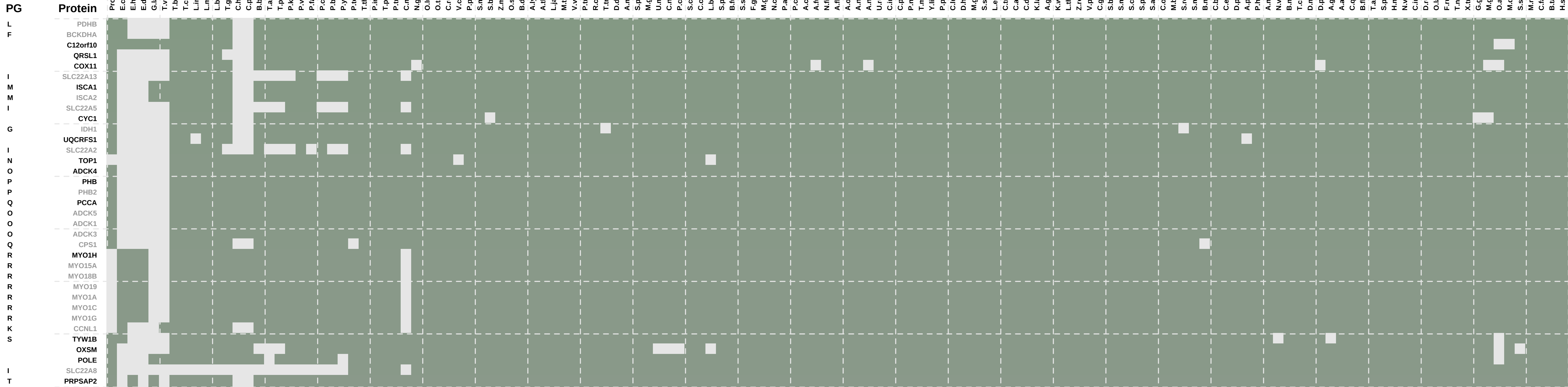


ECM 1, Gene set "mitochondrial part", Page 1

Num of ECM Genes: 1. Num of Predicted Genes: 239

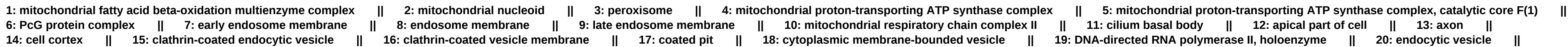
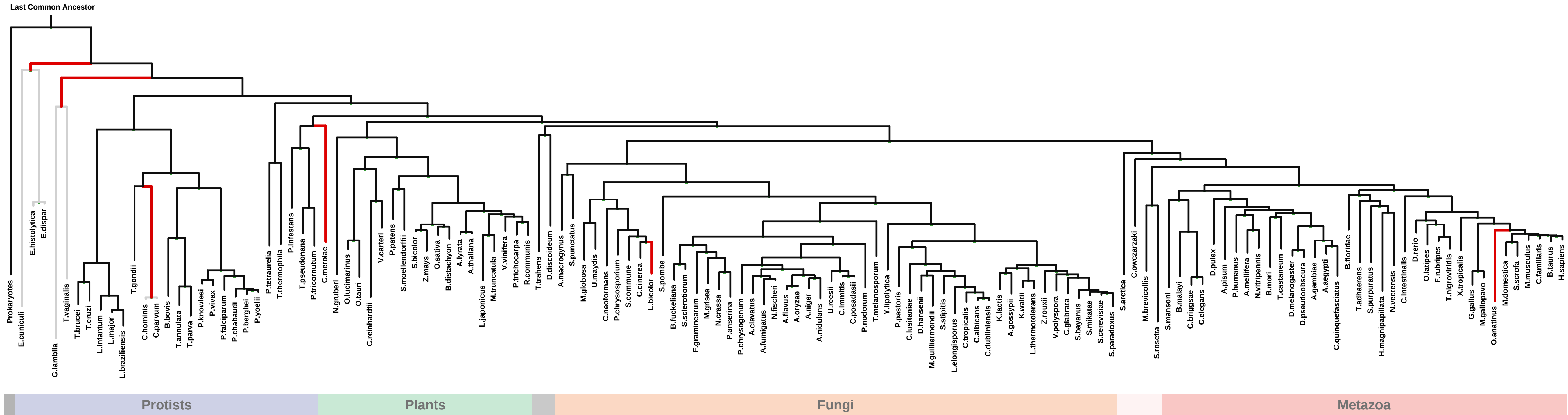


Num of ECM Genes: 1. Num of Predicted Genes: 239

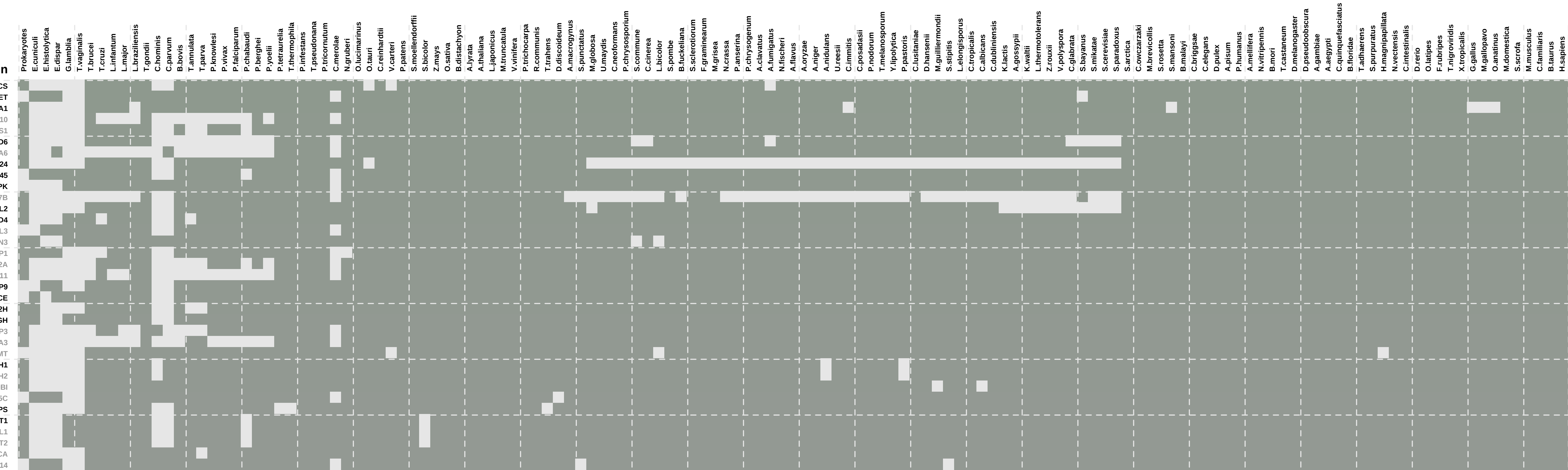


1: pyruvate dehydrogenase complex || 2: mitochondrial alpha-ketoglutarate dehydrogenase complex || 3: glutamyl-tRNA(Gln) amidotransferase complex || 4: basolateral plasma membrane || 5: brush border membrane || 6: respiratory chain || 7: peroxisomal matrix || 8: peroxisome || 9: mitochondrial respiratory chain complex III || 10: cytoplasmic mRNA processing body || 11: nuclear chromosome || 12: perikaryon || 13: replication fork protection complex || 14: mitochondrial nucleoid || 15: myosin complex || 16: stereocilium || 17: sarcomere || 18: unconventional myosin complex || 19: mitochondrial outer membrane || 20: basal plasma membrane || 21: brush border || 22: cortical actin cytoskeleton || 23: filamentous actin ||

Num of ECM Genes: 1. Num of Predicted Genes: 239

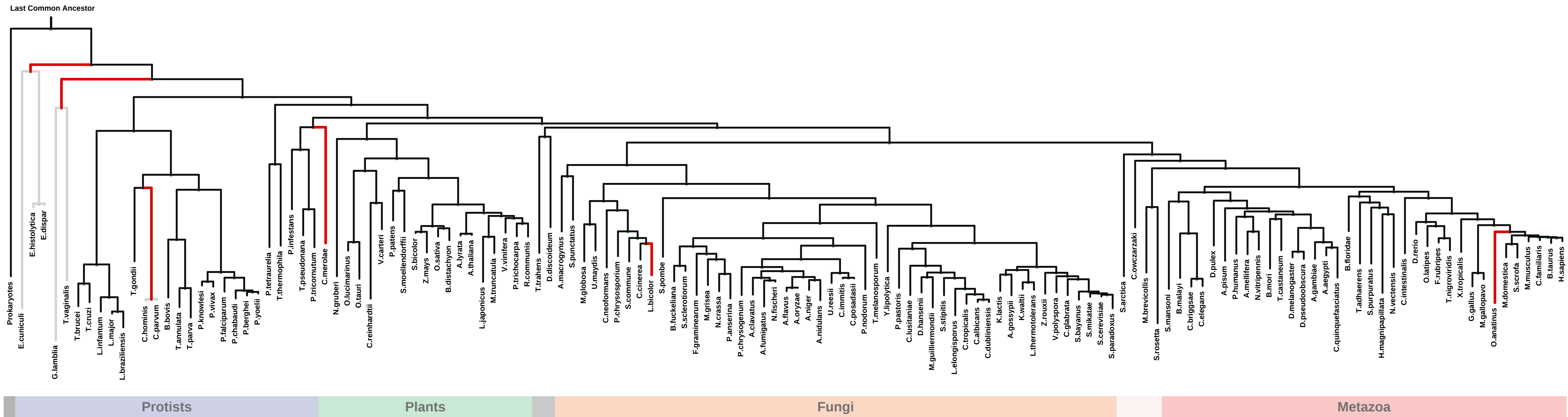


Num of ECM Genes: 1. Num of Predicted Genes: 239



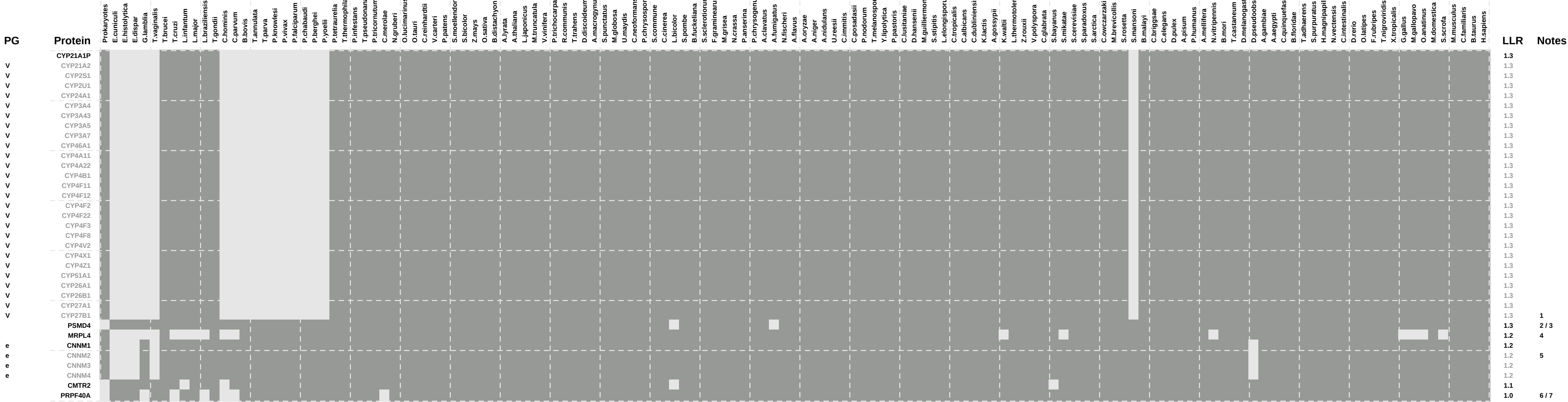
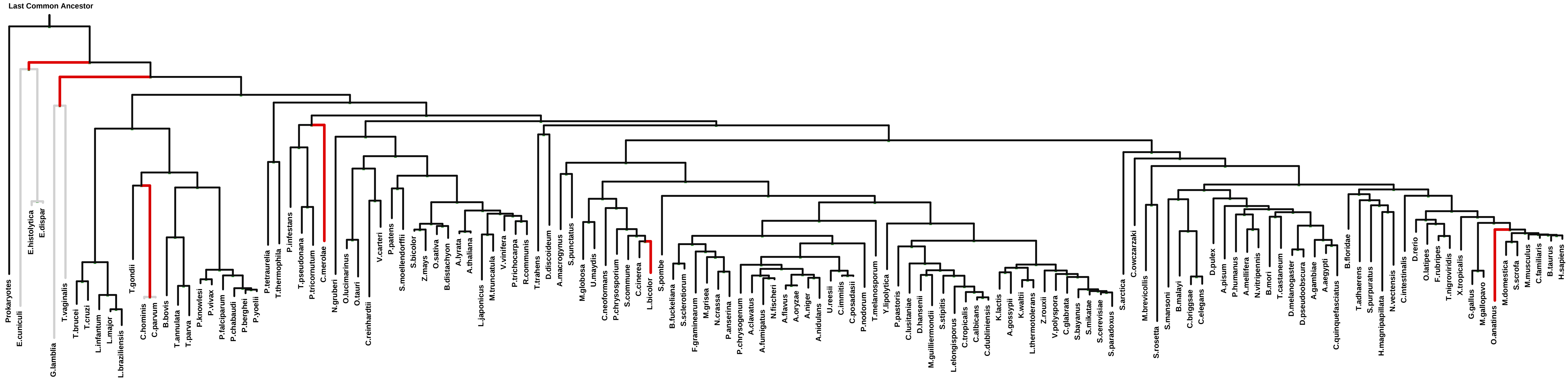
LLR	Notes
4.8	1 / 2 / 3
4.7	
4.7	
4.5	
4.4	
4.3	
4.2	4 / 5
4.2	6
4.1	
4.0	7 / 8
4.0	
4.0	9
3.8	
3.4	
3.4	
3.4	10 / 11 / 12 / 13 / 14
3.4	15 / 16 / 17 / 18
3.3	19
3.3	20
3.2	
3.2	
3.1	
3.1	
3.1	
3.0	21 / 22
3.0	
3.0	23
3.0	
2.7	24
2.6	
2.6	25 / 26
2.6	
2.6	
2.6	24 / 27 / 28 / 29

Num of ECM Genes: 1. Num of Predicted Genes: 239



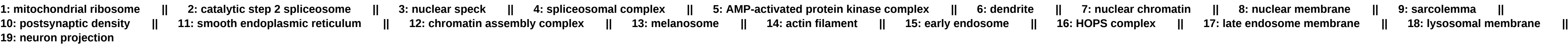
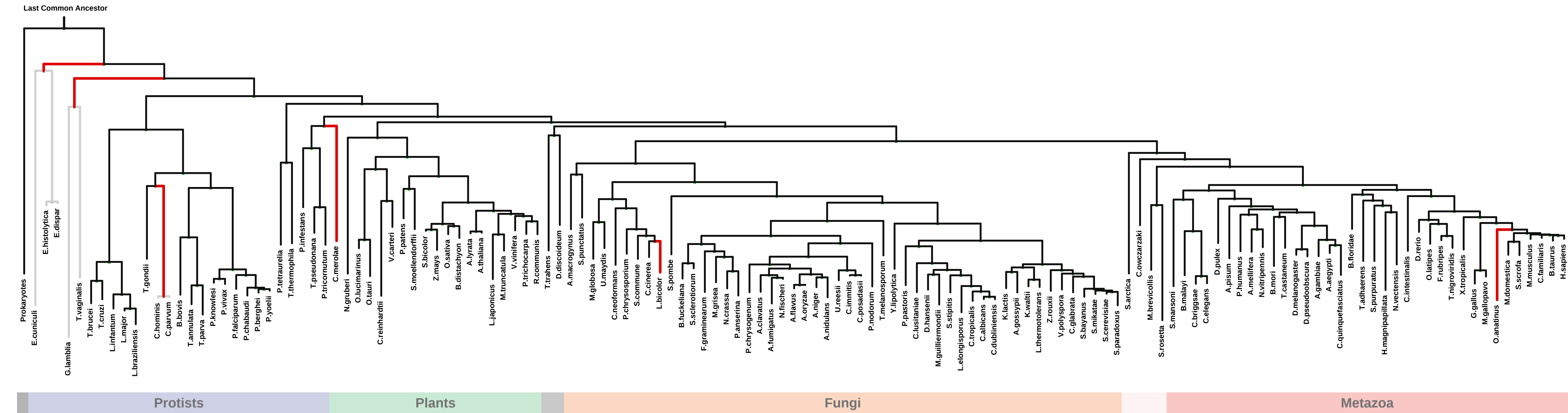
ECM 1, Gene set "mitochondrial part", Page 6

Num of ECM Genes: 1. Num of Predicted Genes: 239



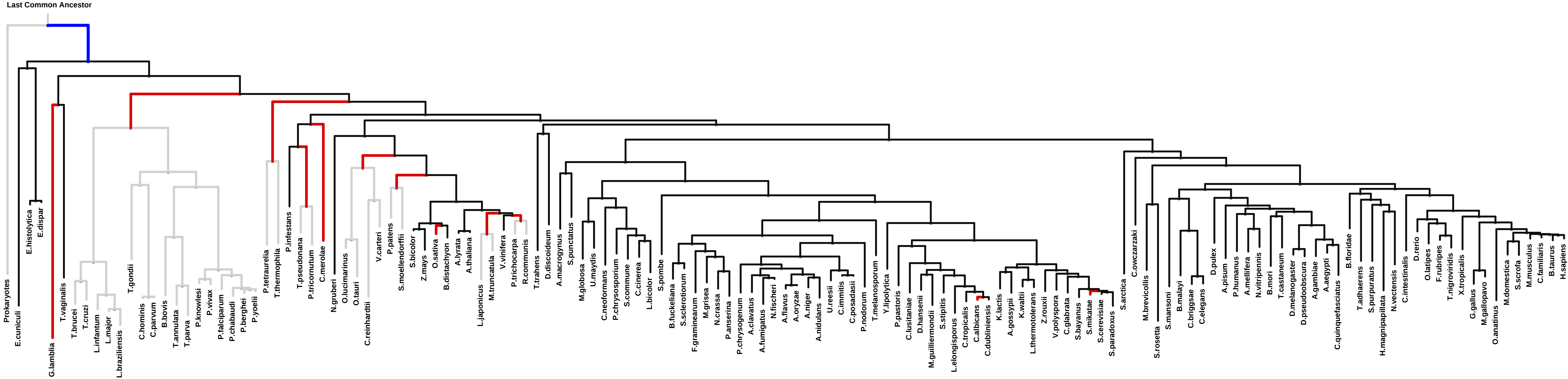
1: mitochondrial outer membrane || 2: proteasome accessory complex || 3: proteasome complex || 4: ribosome || 5: basolateral plasma membrane || 6: nuclear matrix || 7: nuclear speck

Num of ECM Genes: 1. Num of Predicted Genes: 239

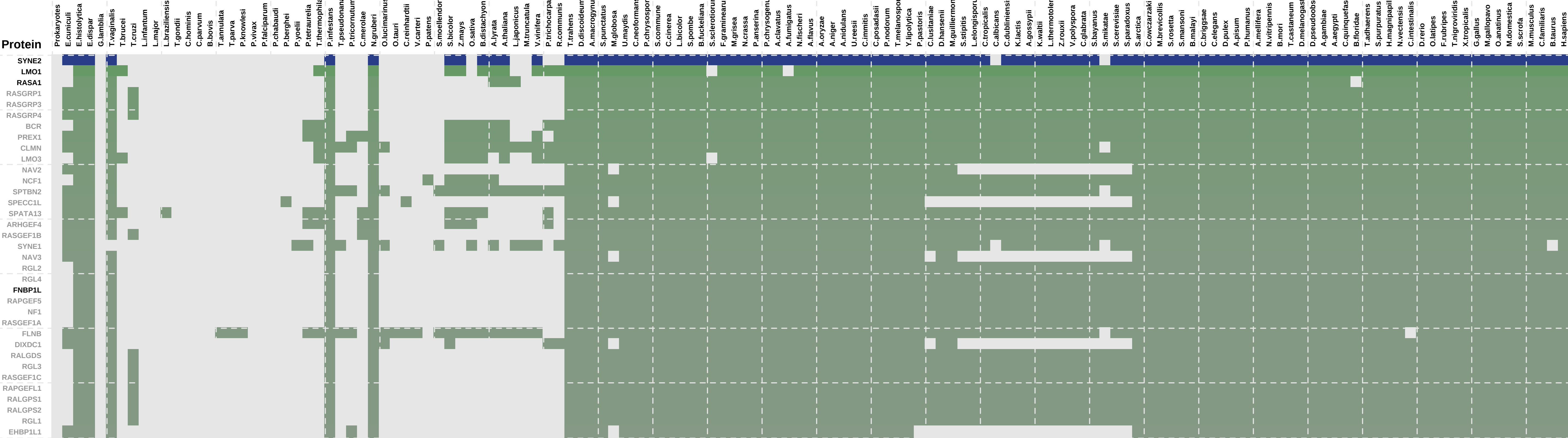


ECM 2, Gene set "mitochondrial part", Page 1

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



PG



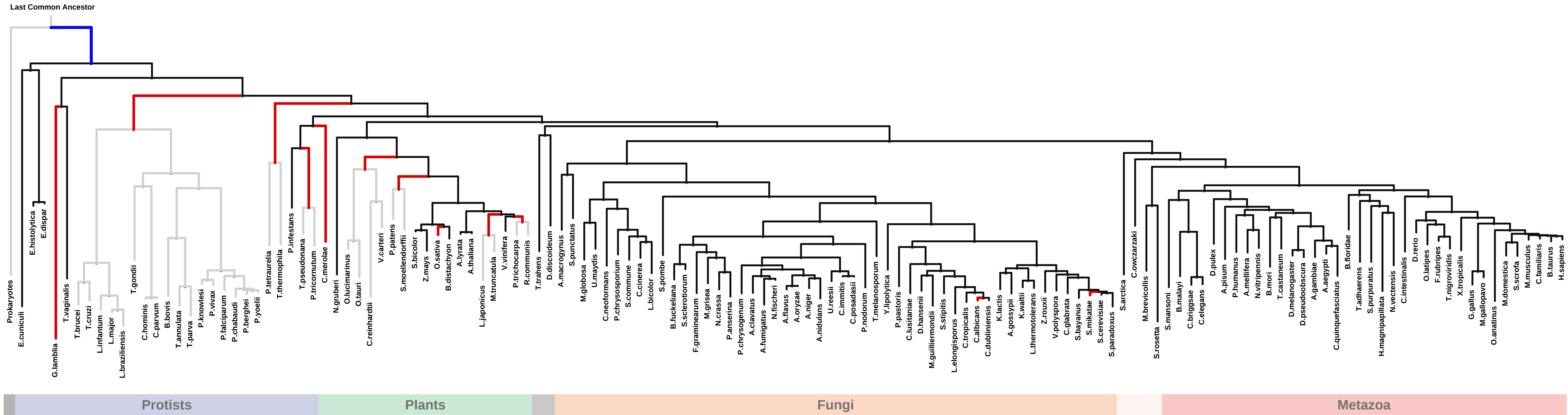
LLR

Notes

1 / 2 / 3 / 4 / 5 / 6 / 7 / 8 / 9 / 10 / 11 / 12 / 13 / 14 / 15 / 16 / 17 / 18 / 19 / 20 / 21 / 22 / 23 / 24 / 25 / 26 / 27 / 28 / 29 / 30 / 31 / 32 / 33 / 34 / 35

1: filopodium membrane 2: focal adhesion 3: lamellipodium membrane 4: mitochondrial part 5: nuclear envelope 6: nuclear lumen 7: nuclear membrane 8: nuclear outer membrane 9: sarcoplasmic reticulum 10: sarcoplasmic reticulum membrane 11: SUN-KASH complex 12: Z disc 13: intrinsic to internal side of plasma membrane 14: ruffle 15: guanyl-nucleotide exchange factor complex 16: interstitial matrix 17: NADPH oxidase complex 18: phagolysosome 19: spectrin 20: gap junction 21: spindle 22: filopodium 23: lamellipodium 24: ruffle membrane 25: early endosome 26: late endosome 27: postsynaptic membrane 28: sarcomere

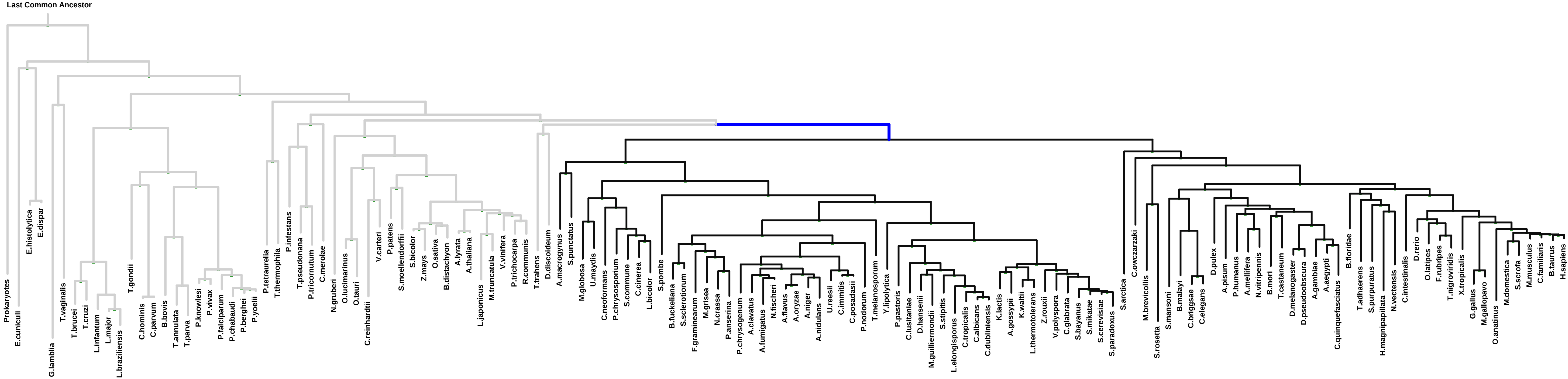
Num of ECM Genes: 1. Num of Predicted Genes: 69



1: extrinsic to membrane	2: focal adhesion	3: ruffle membrane	4: neuron projection	5: postsynaptic membrane	6: endoplasmic reticulum-Golgi intermediate compartment	7: endoplasmic reticulum-Golgi intermediate compartment membrane
8: actin cytoskeleton	9: intrinsic to internal side of plasma membrane	10: cell cortex	11: lamellipodium	12: postsynaptic density	13: ruffle	14: cuticular plate
15: spectrin	16: spectrin-associated cytoskeleton	17: contractile fiber	18: I band	19: M band	20: filopodium	21: growth cone
22: endosome	23: checkpoint clamp complex	24: cell-substrate junction	25: costamere	26: dystrophin-associated glycoprotein complex		

ECM 3, Gene set "mitochondrial part", Page 1

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



PG

Protein	FOXO1
Prokaryotes	
E.cuniculi	
E.histolytica	
E.dispar	
G.lambia	
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.berghsi	
P.yoelli	
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.ressii	
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.rossetta	
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	

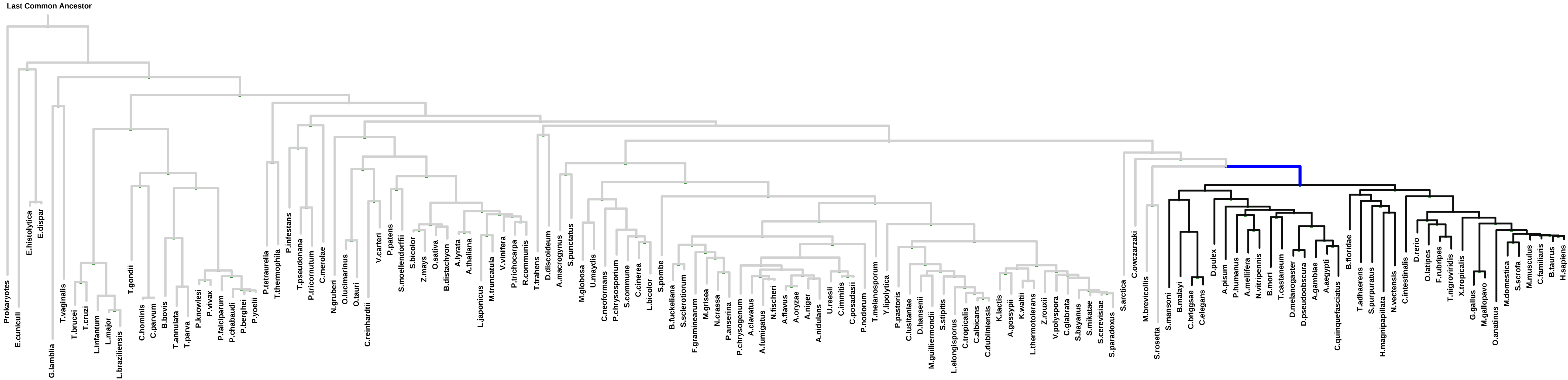
LLR Notes

1

1: mitochondrial part

ECM 4, Gene set "mitochondrial part", Page 1

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



PG

Protein	ESR1	LLR	Notes
Prokaryotes			
E.uniculi			
E.histolytica			
E.dispar			
G.lambli			
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.berghsi			
P.yoeli			
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.glabosa			
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.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: chromatin remodeling complex || 2: mitochondrial part || 3: perikaryon || 4: terminal button || 5: T-tubule

Notes

1 / 2 / 3 / 4 / 5