

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

Dataset:

Num of genes in input gene set: 9
Total number of genes: 20834
Prediction LLR threshold: 0

The CLIME PDF output two sections:

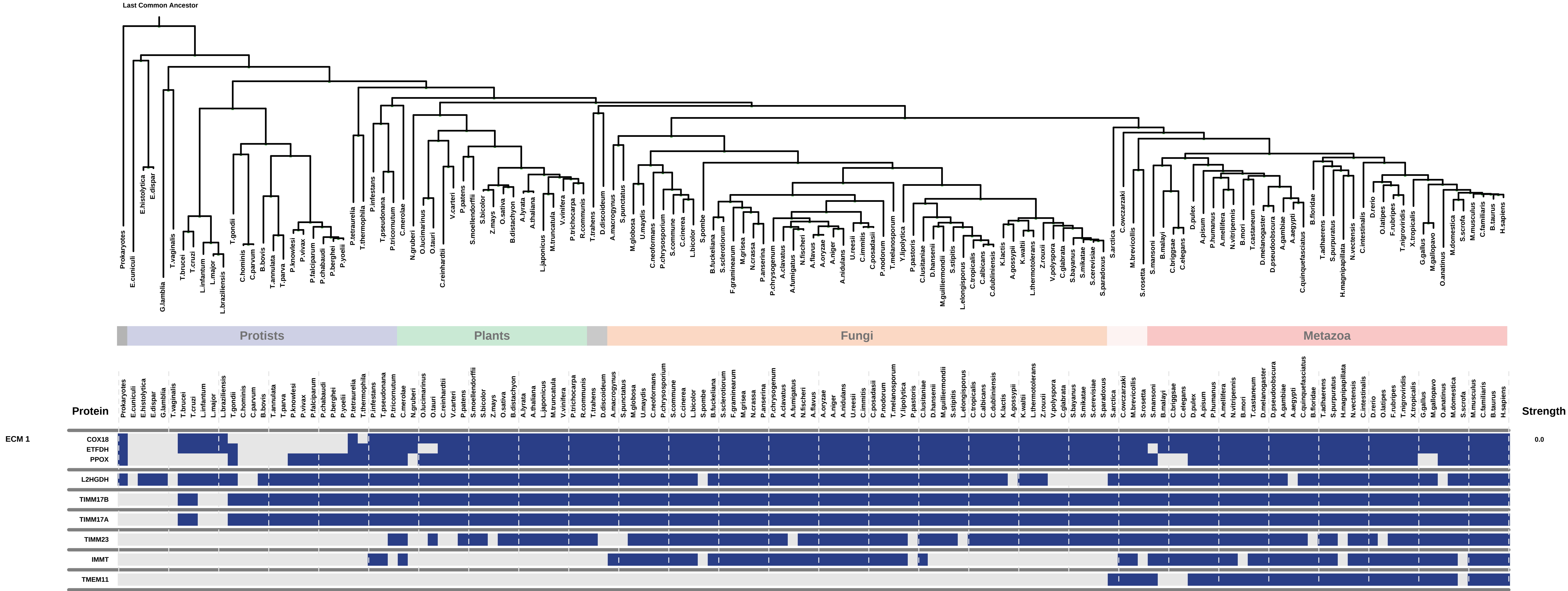
1) Overview of Evolutionarily Conserved Modules (ECMs)

- 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+

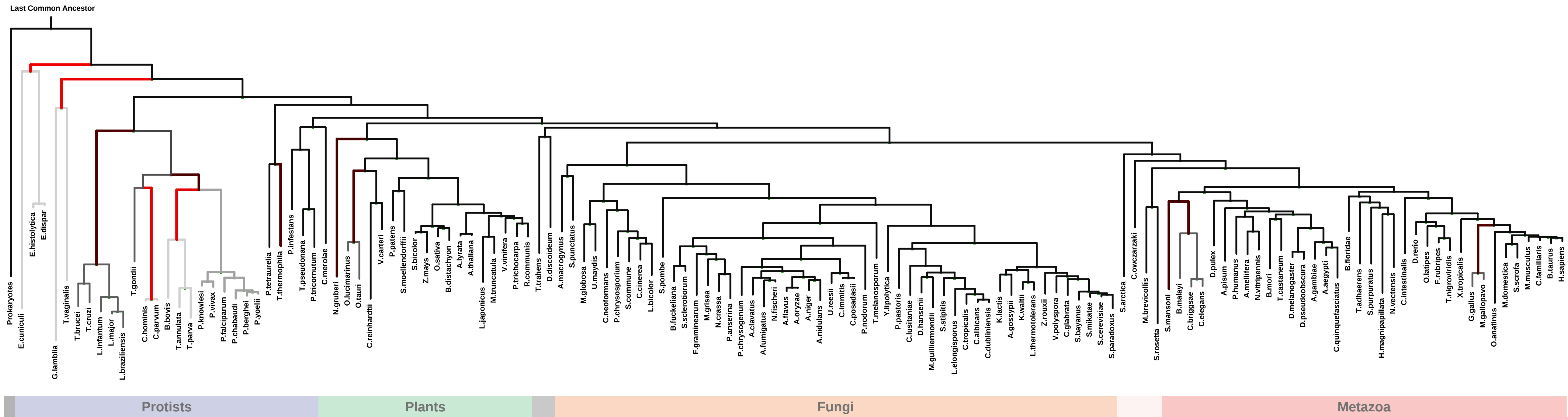
- Top panel shows the inferred evolutionary history on the predefined species tree. Branch color shows the gain event (blue) and loss events (red color, with brighter color indicating higher confidence in loss). Branches before the gain or after a loss are shown in gray.
- Bottom panel shows the input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

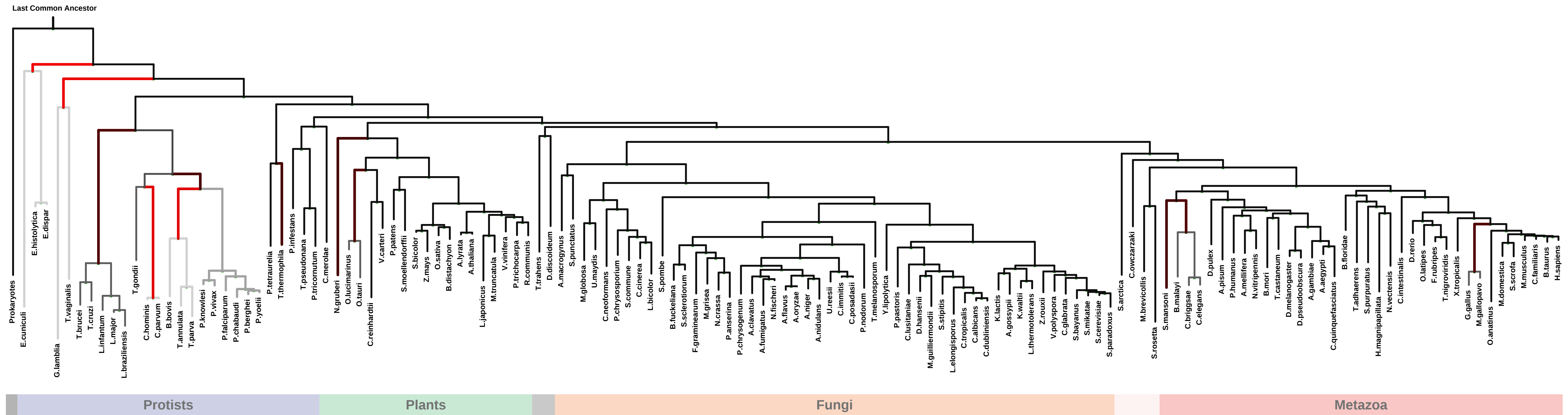
Num of ECM Genes: 3. Num of Predicted Genes: 500. ECM Strength: 0.0

[illegible]

1: integral to mitochondrial inner membrane || 2: mitochondrial membrane || 3: mitochondrial intermembrane space || 4: microtubule cytoskeleton || 5: axon || 6: dendritic spine || 7: synaptic vesicle || 8: terminal button ||
9: mitochondrial outer membrane

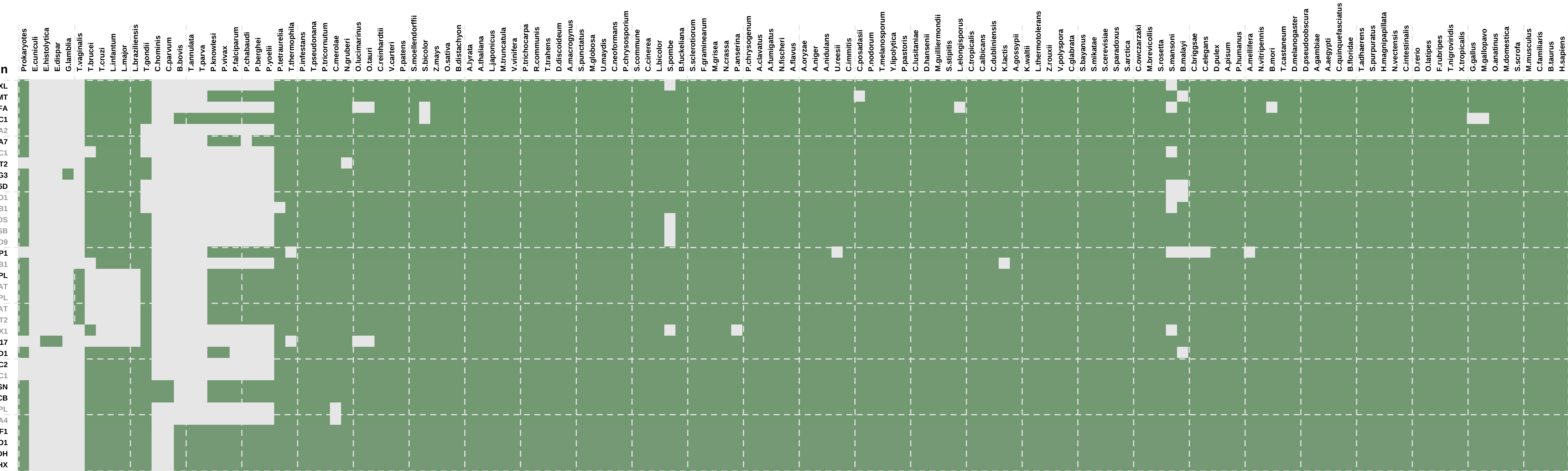
ECM 1, Gene set "integral to mitochondrial inner membrane", Page 2

Num of ECM Genes: 3. Num of Predicted Genes: 500. ECM Strength: 0.0

[illegible]

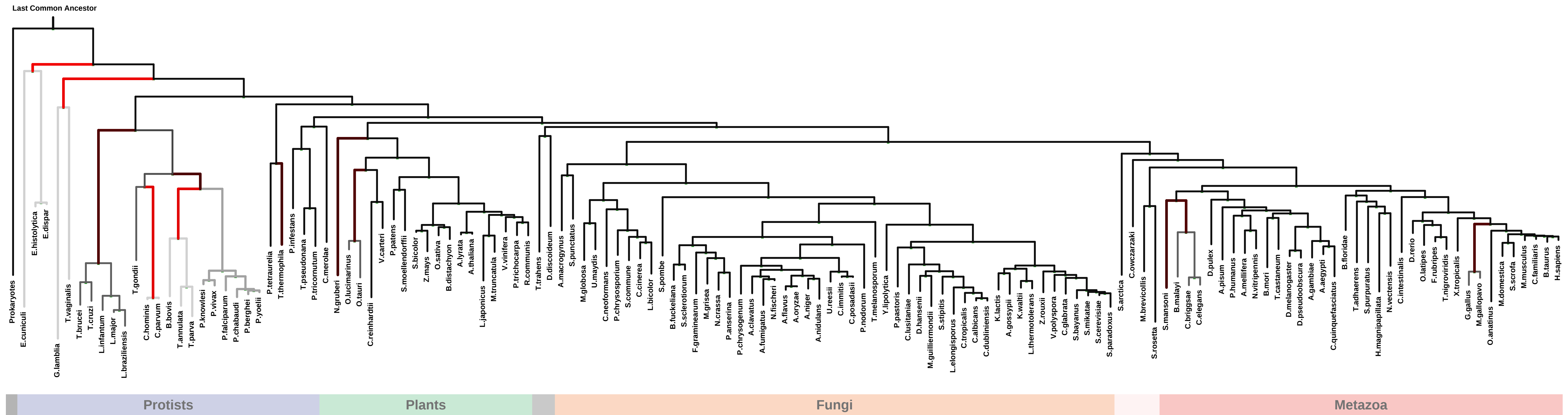
1: mitochondrial crista || 2: perikaryon || 3: axon || 4: condensed chromosome || 5: peroxisome || 6: mitochondrial fatty acid beta-oxidation multienzyme complex || 7: mitochondrial nucleoid || 8: pyruvate dehydrogenase complex || 9: peroxisomal matrix || 10: peroxisomal membrane || 11: caveola || 12: intrinsic to endoplasmic reticulum membrane

Num of ECM Genes: 3. Num of Predicted Genes: 500. ECM Strength: 0.0



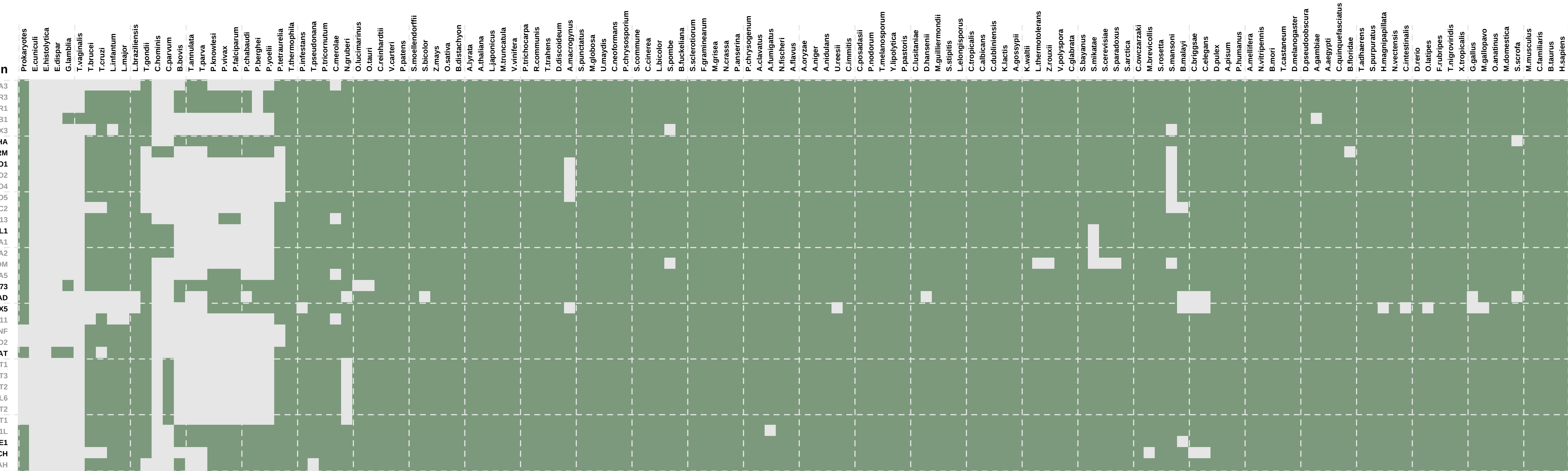
ECM 1, Gene set "integral to mitochondrial inner membrane", Page 4

Num of ECM Genes: 3. Num of Predicted Genes: 500. ECM Strength: 0.0

[illegible]

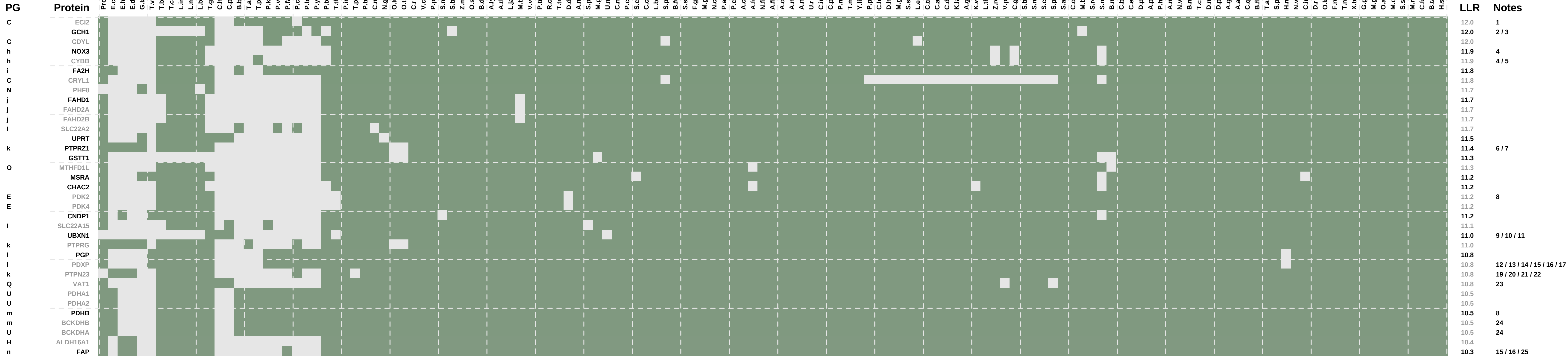
1: microtubule cytoskeleton || 2: mitochondrial alpha-ketoglutarate dehydrogenase complex || 3: mitochondrial nucleoid || 4: oxoglutarate dehydrogenase complex || 5: mitochondrial membrane || 6: mitochondrial intermembrane space ||
7: peroxisomal matrix || 8: peroxisome || 9: mitochondrial proton-transporting ATP synthase complex || 10: mitochondrial proton-transporting ATP synthase complex, catalytic core F(1) || 11: glutamyl-tRNA(Gln) amidotransferase complex ||
12: AMP-activated protein kinase complex || 13: mitochondrial respiratory chain complex ||

Num of ECM Genes: 3. Num of Predicted Genes: 500. ECM Strength: 0.0



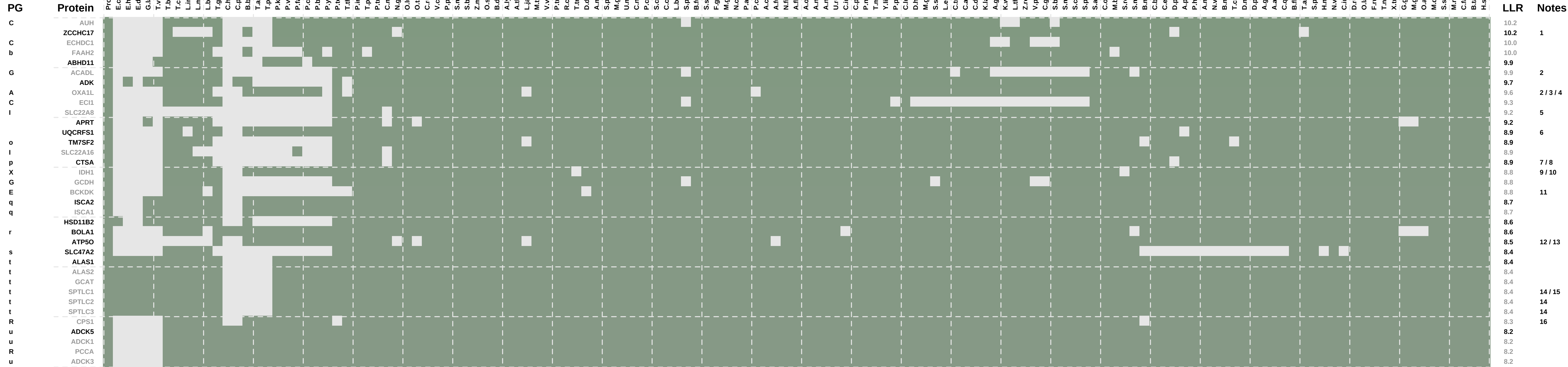
LLR	Notes
13.3	
13.3	1 / 2 / 3
13.3	
13.1	
13.0	4 / 5
13.0	6
12.9	
12.9	7 / 8
12.9	
12.9	8
12.9	8
12.9	
12.8	
12.7	
12.7	
12.7	
12.7	9 / 10
12.7	11 / 12
12.7	
12.6	
12.6	4 / 5 / 13 / 14
12.4	15
12.3	
12.3	
12.3	
12.3	2 / 16
12.3	
12.3	
12.3	
12.2	
12.1	
12.1	
12.1	17 / 18

Num of ECM Genes: 3. Num of Predicted Genes: 500. ECM Strength: 0.0



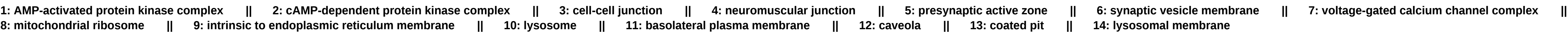
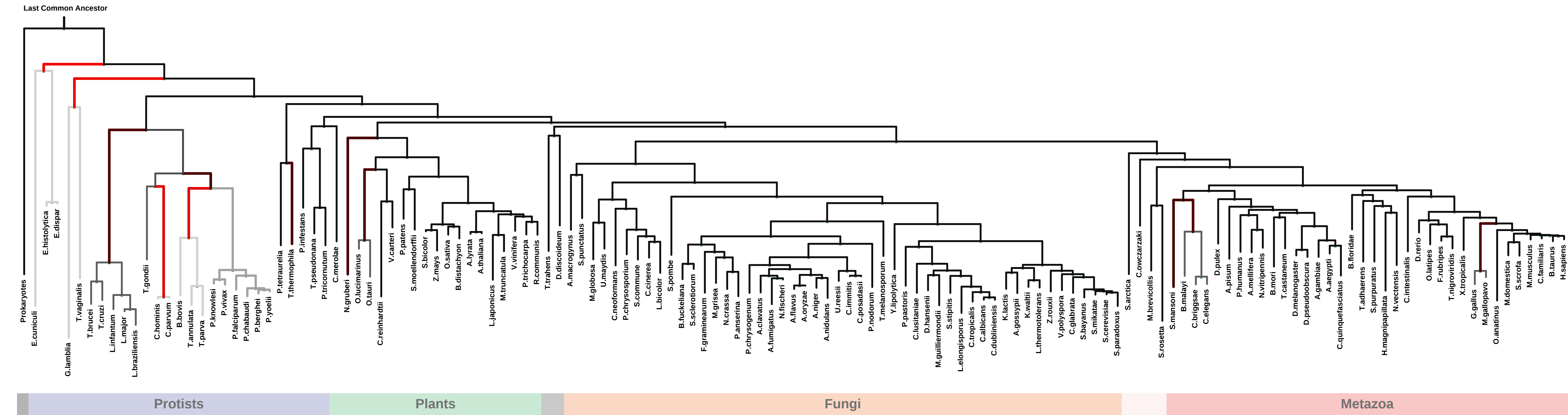
1: peroxisomal matrix || 2: cytoplasmic vesicle || 3: nuclear membrane || 4: NADPH oxidase complex || 5: phagocytic vesicle membrane || 6: perineuronal net || 7: proteinaceous extracellular matrix || 8: pyruvate dehydrogenase complex ||
9: Cdc48p-Npl4p-Ufd1p AAA ATPase complex || 10: dendrite || 11: proteasome complex || 12: actin cytoskeleton || 13: cleavage furrow || 14: contractile ring || 15: lamellipodium || 16: lamellipodium membrane || 17: midbody ||
18: ruffle membrane || 19: cilium || 20: cytoplasmic membrane-bounded vesicle || 21: endosome || 22: microtubule basal body || 23: mitochondrial outer membrane || 24: mitochondrial alpha-ketoglutarate dehydrogenase complex ||

Num of ECM Genes: 3. Num of Predicted Genes: 500. ECM Strength: 0.0

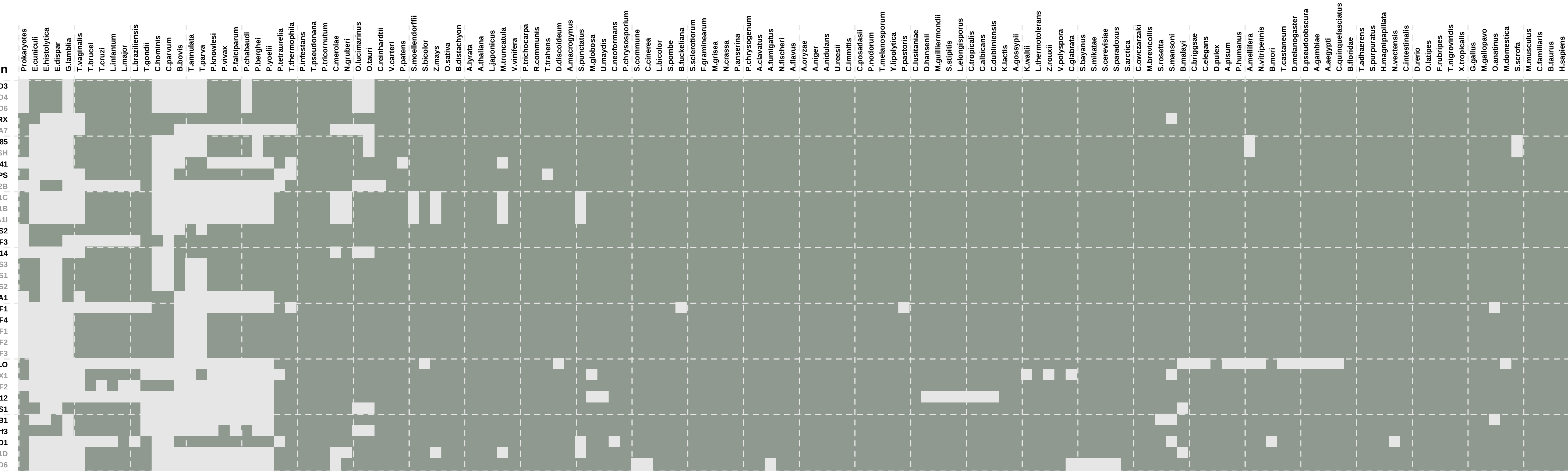


1: cytosolic large ribosomal subunit || 2: mitochondrial membrane || 3: integral to mitochondrial membrane || 4: mitochondrial respiratory chain || 5: basolateral plasma membrane || 6: mitochondrial respiratory chain complex III || 7: lysosomal lumen ||
8: lysosome || 9: peroxisomal matrix || 10: peroxisome || 11: mitochondrial alpha-ketoglutarate dehydrogenase complex || 12: mitochondrial proton-transporting ATP synthase complex || 13: mitochondrial proton-transporting ATP synthase complex, coupling factor F(o) ||
14: serine C-palmitoyltransferase complex || 15: SPOTS complex || 16: mitochondrial nucleoid

Num of ECM Genes: 3. Num of Predicted Genes: 500. ECM Strength: 0.0

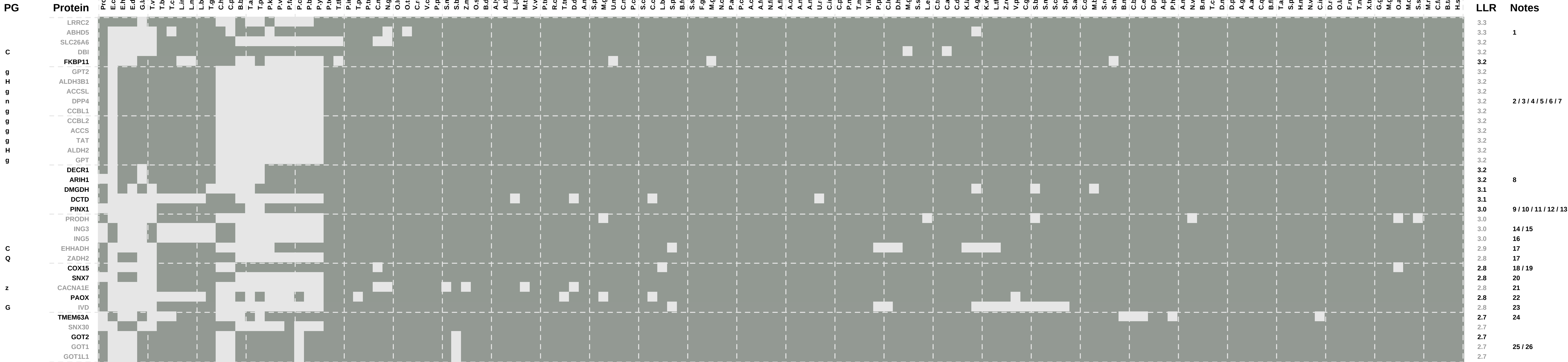


Num of ECM Genes: 3. Num of Predicted Genes: 500. ECM Strength: 0.0



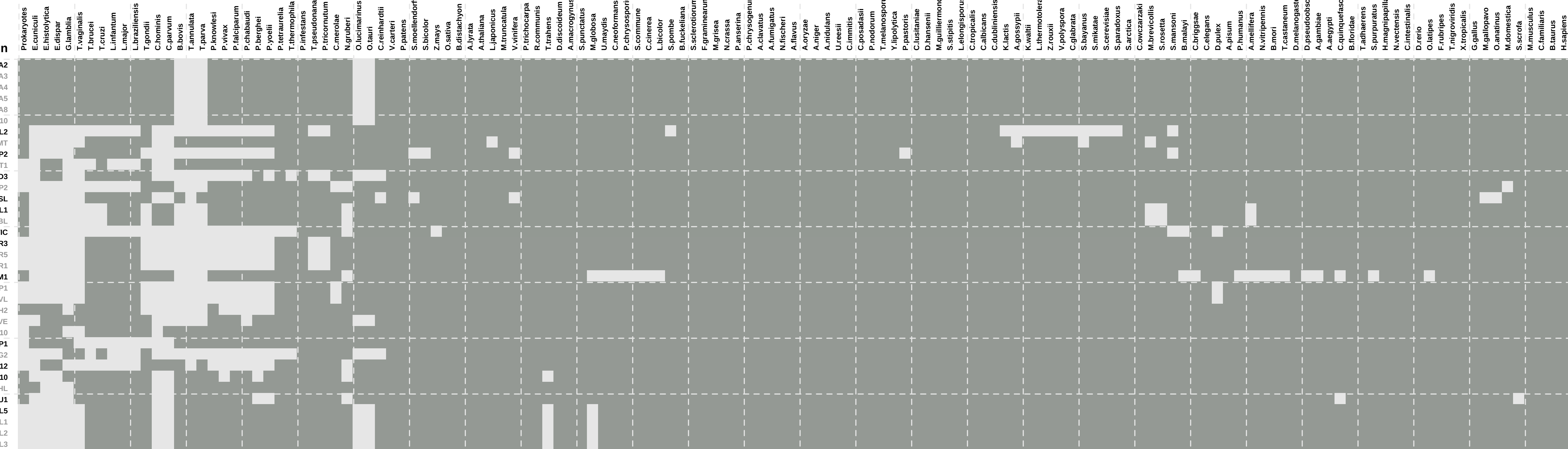
20: early endosome membrane || 21: endosome membrane || 22: late endosome membrane || 23: lysosomal membrane || 24: Cdc73/Paf1 complex || 25: autophagic vacuole membrane || 26: cytoplasmic vesicle || 27: invadopodium membrane ||

Num of ECM Genes: 3. Num of Predicted Genes: 500. ECM Strength: 0.0



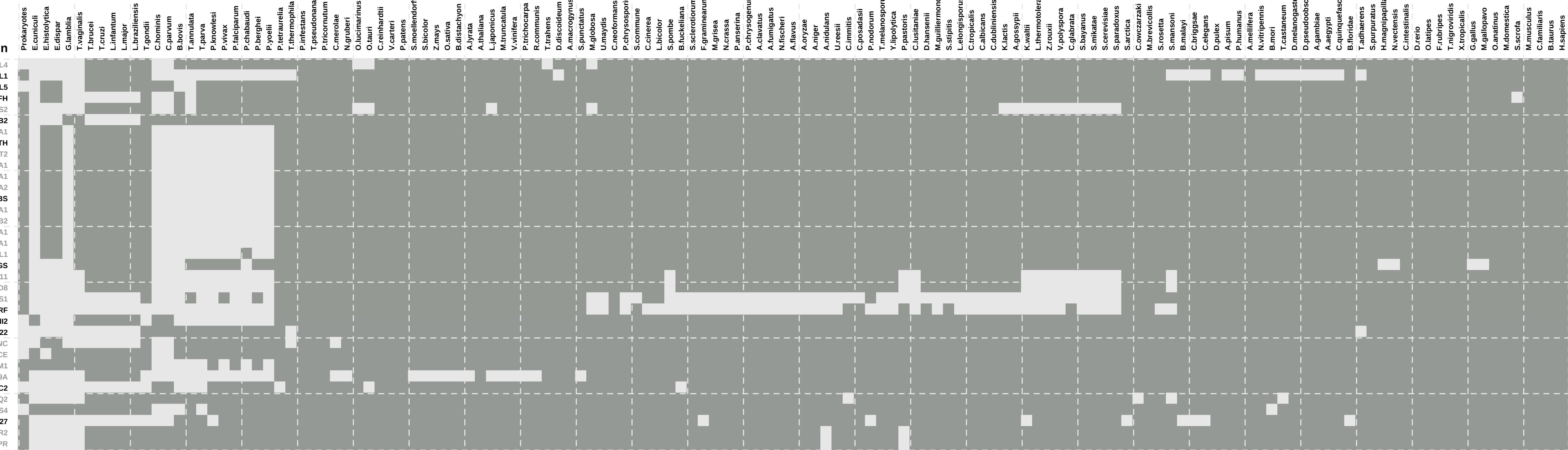
1: lipid particle || 2: endocytic vesicle || 3: intercellular canaliculus || 4: invadopodium membrane || 5: lamellipodium || 6: lamellipodium membrane || 7: membrane raft || 8: ubiquitin ligase complex || 9: chromosome, telomeric region || 10: condensed chromosome kinetochore || 11: kinetochore || 12: nuclear chromosome || 13: spindle || 14: NuA4 histone acetyltransferase complex || 15: Piccolo NuA4 histone acetyltransferase complex || 16: MOZ/MORF histone acetyltransferase complex || 17: peroxisome || 18: mitochondrial part || 19: mitochondrial respiratory chain || 20: cytoplasmic vesicle membrane || 21: voltage-gated calcium channel complex || 22: peroxisomal matrix || 23: mitochondrial membrane || 24: lysosomal membrane ||

Num of ECM Genes: 3. Num of Predicted Genes: 500. ECM Strength: 0.0

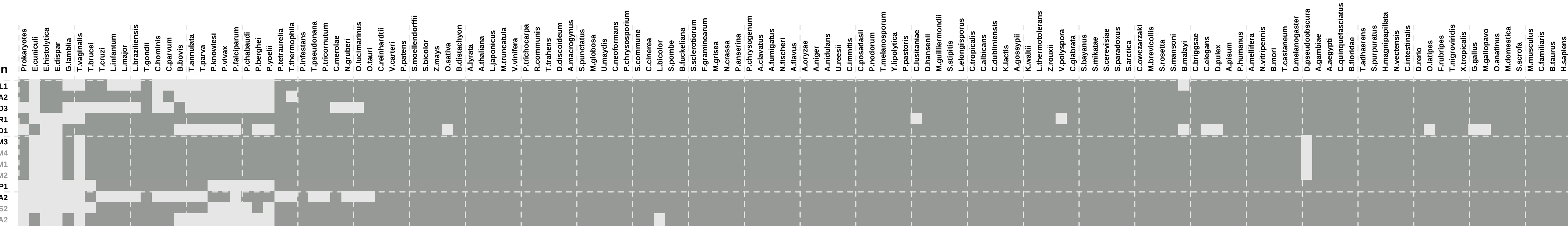


1: cytoplasmic membrane-bounded vesicle || 2: cytoplasmic part || 3: endosome membrane || 4: late endosome || 5: lysosomal membrane || 6: endosome || 7: neuron projection || 8: synaptic vesicle || 9: synaptic vesicle membrane || 10: secretory granule || 11: secretory granule membrane || 12: transport vesicle membrane || 13: peroxisome || 14: peroxisomal matrix || 15: COPI vesicle coat || 16: endoplasmic reticulum-Golgi intermediate compartment || 17: endoplasmic reticulum-Golgi intermediate compartment membrane || 18: Golgi cisterna membrane || 19: ribonucleoprotein complex || 20: cytoplasmic vesicle || 21: early endosome membrane || 22: late endosome membrane || 23: membrane raft || 24: vesicle membrane || 25: cis-Golgi network ||

Num of ECM Genes: 3. Num of Predicted Genes: 500. ECM Strength: 0.0

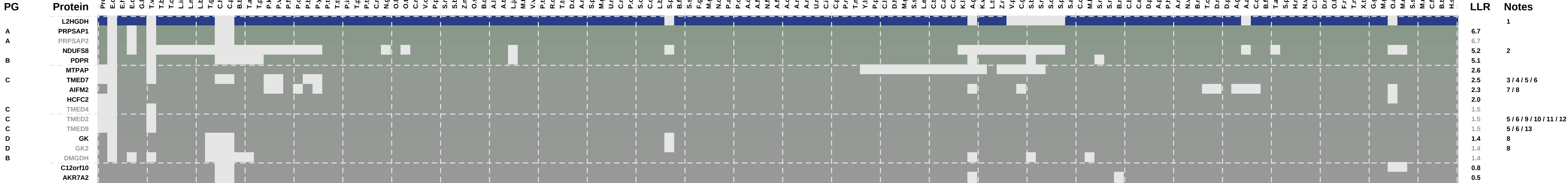


Num of ECM Genes: 3. Num of Predicted Genes: 500. ECM Strength: 0.0



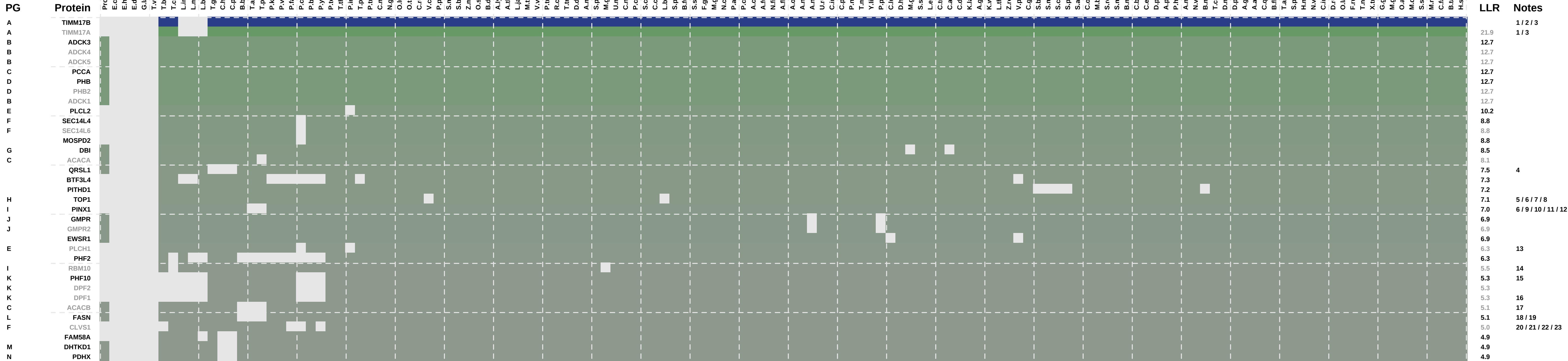
LLR	Notes
1.7	
1.7	
1.6	
1.6	
1.6	
1.5	
1.5	
1.5	
1.5	1
1.5	
1.5	2/3/4/5

Num of ECM Genes: 1. Num of Predicted Genes: 16



1: integral to mitochondrial inner membrane || 2: mitochondrial respiratory chain complex I || 3: COPI vesicle coat || 4: COPII vesicle coat || 5: endoplasmic reticulum-Golgi intermediate compartment || 6: endoplasmic reticulum-Golgi intermediate compartment membrane || 7: lipid particle || 8: mitochondrial outer membrane || 9: COPI-coated vesicle || 10: COPI-coated vesicle membrane || 11: Golgi cisterna membrane || 12: zymogen granule membrane || 13: trans-Golgi network transport vesicle

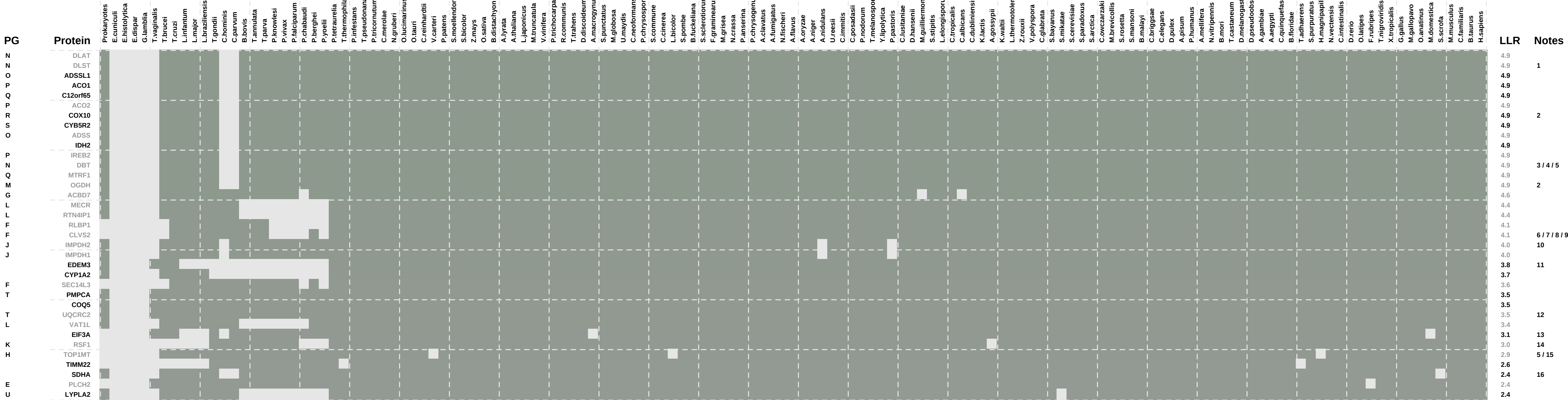
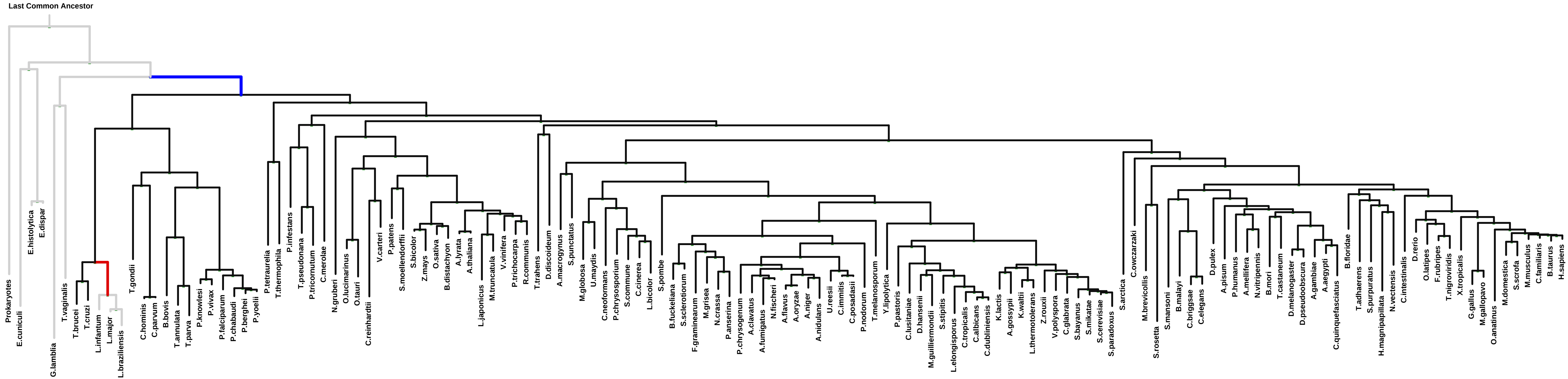
Num of ECM Genes: 1. Num of Predicted Genes: 113



1: integral to mitochondrial inner membrane || 2: microtubule cytoskeleton || 3: mitochondrial inner membrane presequence translocase complex || 4: glutamyl-tRNA(Gln) amidotransferase complex || 5: cytoplasmic mRNA processing body || 6: nuclear chromosome || 7: perikaryon || 8: replication fork protection complex || 9: chromosome, telomeric region || 10: condensed chromosome kinetochore || 11: kinetochore || 12: spindle || 13: nuclear membrane || 14: chromatin remodeling complex || 15: npBAF complex || 16: nBAF complex || 17: endomembrane system || 18: glycogen granule || 19: melanosome || 20: clathrin-coated vesicle || 21: early endosome membrane || 22: endosome || 23: trans-Golgi network

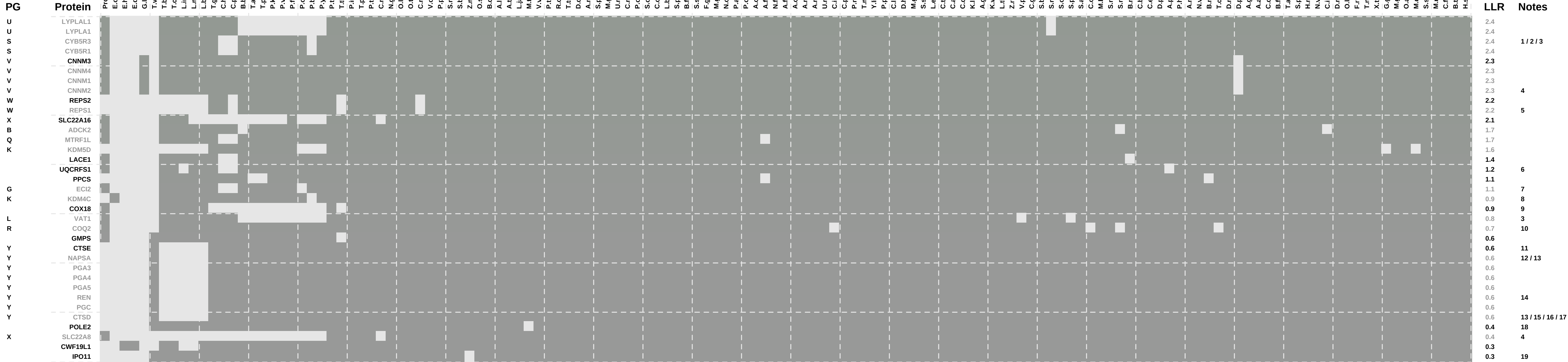
ECM 3, Gene set "integral to mitochondrial inner membrane", Page 2

Num of ECM Genes: 1. Num of Predicted Genes: 113



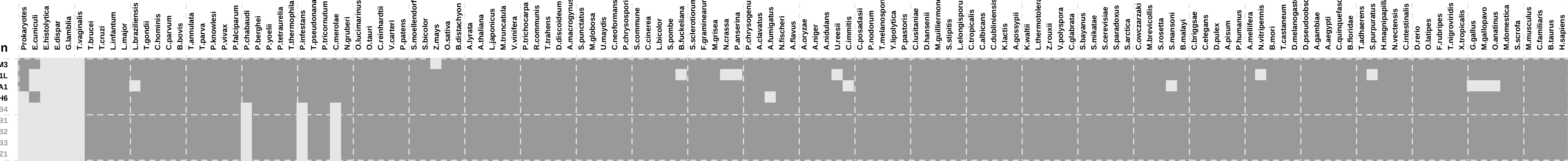
1: oxoglutarate dehydrogenase complex || 2: mitochondrial membrane || 3: microtubule cytoskeleton || 4: mitochondrial alpha-ketoglutarate dehydrogenase complex || 5: mitochondrial nucleoid || 6: clathrin-coated vesicle || 7: early endosome membrane || 8: endosome || 9: trans-Golgi network || 10: peroxisomal membrane || 11: endoplasmic reticulum lumen || 12: mitochondrial respiratory chain complex III || 13: eukaryotic translation initiation factor 3 complex || 14: RSF complex || 15: replication fork protection complex || 16: mitochondrial respiratory chain complex II

Num of ECM Genes: 1. Num of Predicted Genes: 113



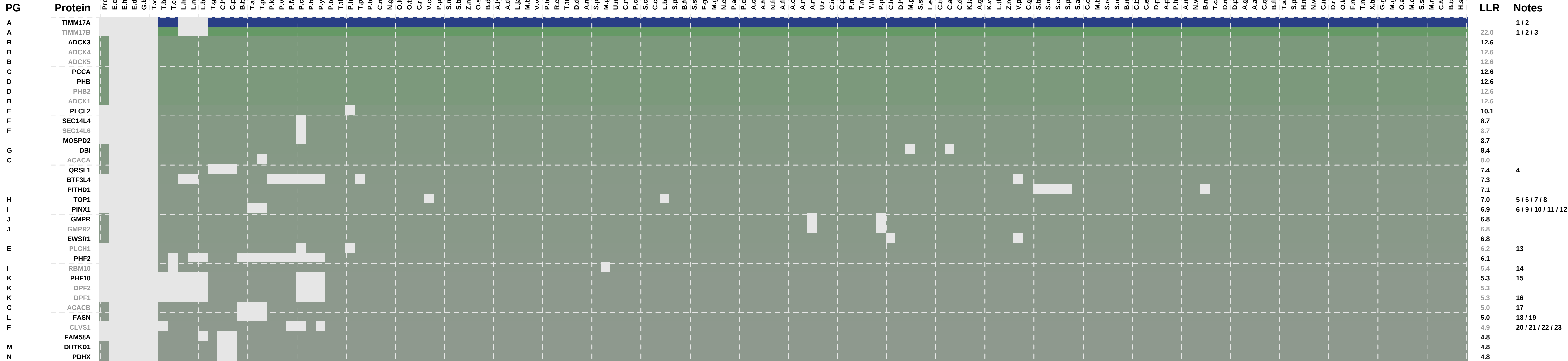
1: hemoglobin complex || 2: lipid particle || 3: mitochondrial outer membrane || 4: basolateral plasma membrane || 5: coated pit || 6: mitochondrial respiratory chain complex III || 7: peroxisomal matrix || 8: nuclear chromatin ||
9: integral to mitochondrial inner membrane || 10: mitochondrial membrane || 11: endosome || 12: alveolar lamellar body || 13: lysosome || 14: cytoplasmic part || 15: extracellular matrix || 16: lysosomal lumen || 17: melanosome ||
18: epsilon DNA polymerase complex || 19: nuclear pore

Num of ECM Genes: 1. Num of Predicted Genes: 113



1: integral to endoplasmic reticulum membrane || 2: postsynaptic density || 3: smooth endoplasmic reticulum || 4: nuclear chromatin || 5: nuclear membrane || 6: nuclear speck || 7: sarcolemma

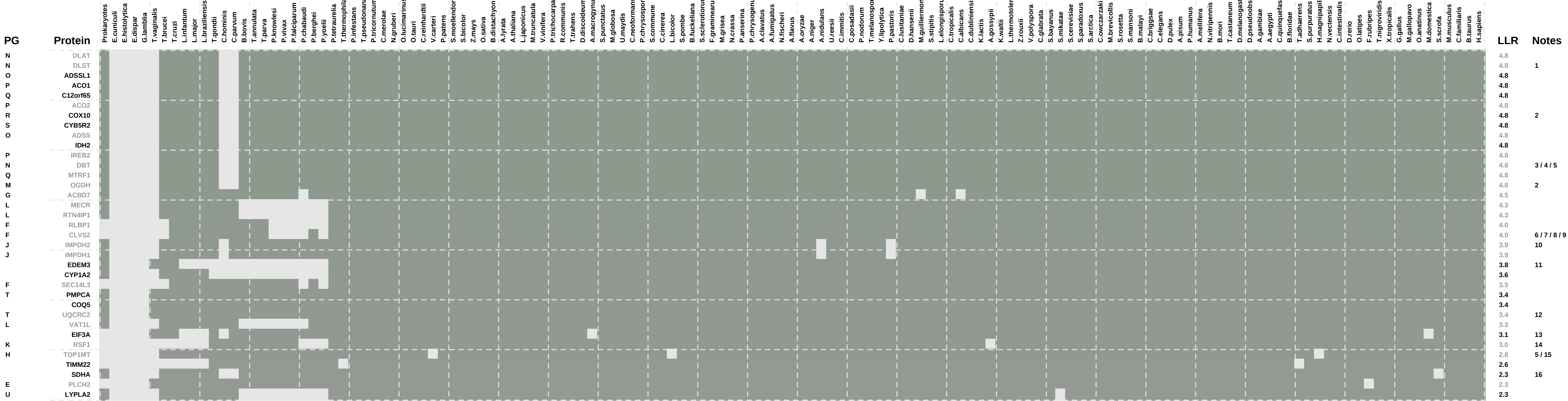
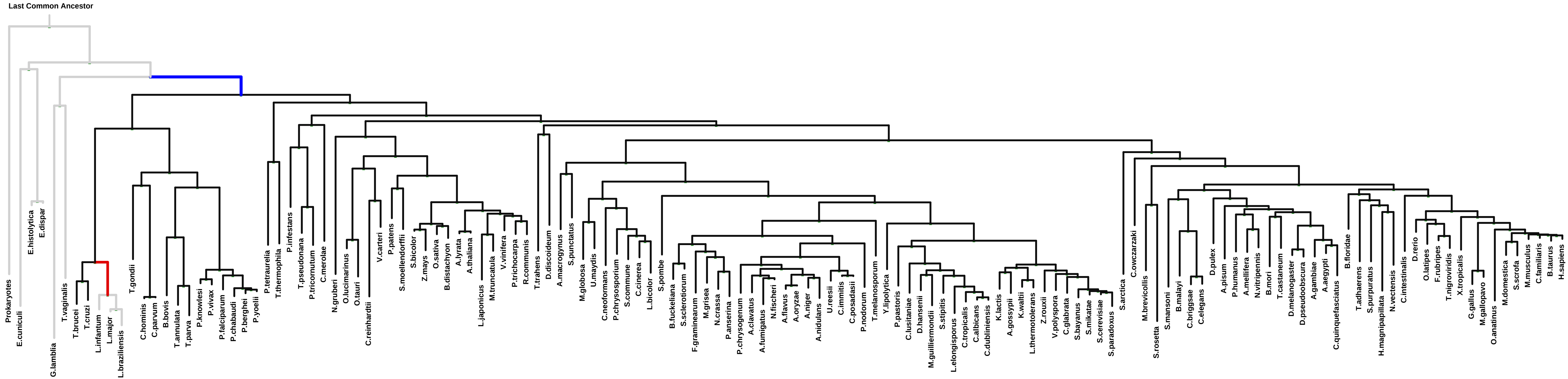
Num of ECM Genes: 1. Num of Predicted Genes: 113



1: integral to mitochondrial inner membrane || 2: mitochondrial inner membrane presequence translocase complex || 3: microtubule cytoskeleton || 4: glutamyl-tRNA(Gln) amidotransferase complex || 5: cytoplasmic mRNA processing body || 6: nuclear chromosome || 7: perikaryon || 8: replication fork protection complex || 9: chromosome, telomeric region || 10: condensed chromosome kinetochore || 11: kinetochore || 12: spindle || 13: nuclear membrane || 14: chromatin remodeling complex || 15: npBAF complex || 16: nBAF complex || 17: endomembrane system || 18: glycogen granule || 19: melanosome || 20: clathrin-coated vesicle || 21: early endosome membrane || 22: endosome || 23: trans-Golgi network

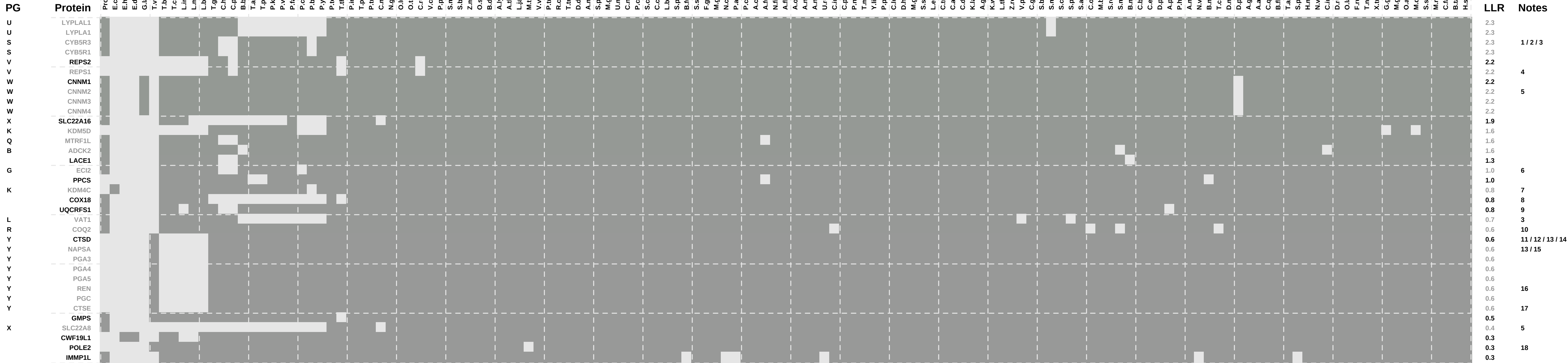
ECM 4, Gene set "integral to mitochondrial inner membrane", Page 2

Num of ECM Genes: 1. Num of Predicted Genes: 113



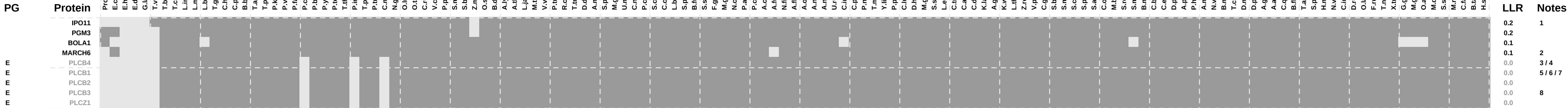
1: oxoglutarate dehydrogenase complex || 2: mitochondrial membrane || 3: microtubule cytoskeleton || 4: mitochondrial alpha-ketoglutarate dehydrogenase complex || 5: mitochondrial nucleoid || 6: clathrin-coated vesicle || 7: early endosome membrane || 8: endosome || 9: trans-Golgi network || 10: peroxisomal membrane || 11: endoplasmic reticulum lumen || 12: mitochondrial respiratory chain complex III || 13: eukaryotic translation initiation factor 3 complex || 14: RSF complex || 15: replication fork protection complex || 16: mitochondrial respiratory chain complex II

Num of ECM Genes: 1. Num of Predicted Genes: 113



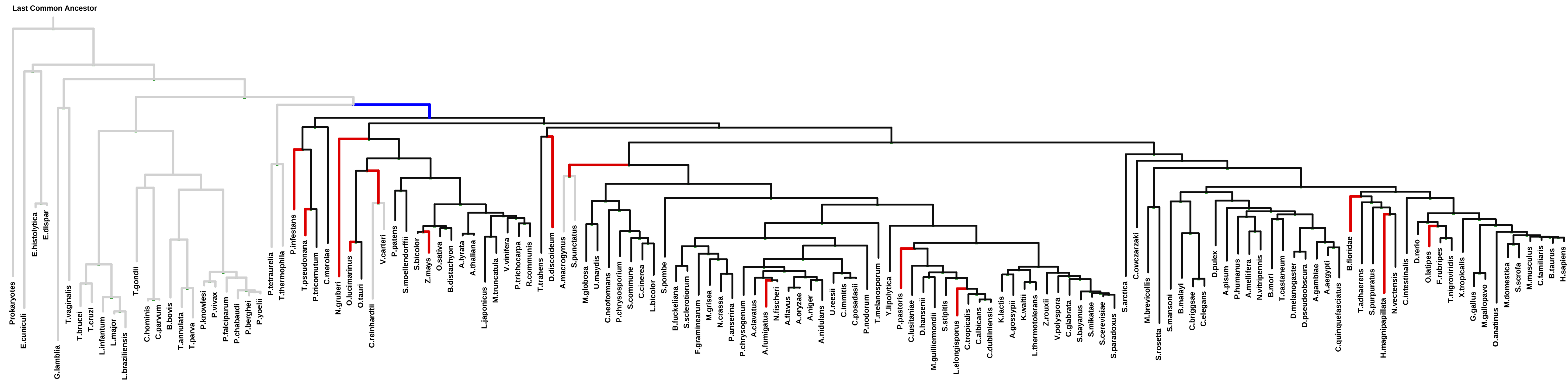
1: hemoglobin complex || 2: lipid particle || 3: mitochondrial outer membrane || 4: coated pit || 5: basolateral plasma membrane || 6: peroxisomal matrix || 7: nuclear chromatin || 8: integral to mitochondrial inner membrane || 9: mitochondrial respiratory chain complex III || 10: mitochondrial membrane || 11: extracellular matrix || 12: lysosomal lumen || 13: lysosome || 14: melanosome || 15: alveolar lamellar body || 16: cytoplasmic part || 17: endosome || 18: epsilon DNA polymerase complex

Num of ECM Genes: 1. Num of Predicted Genes: 113



ECM 5, Gene set "integral to mitochondrial inner membrane", Page 1

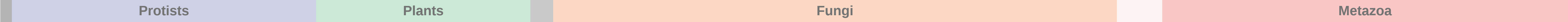
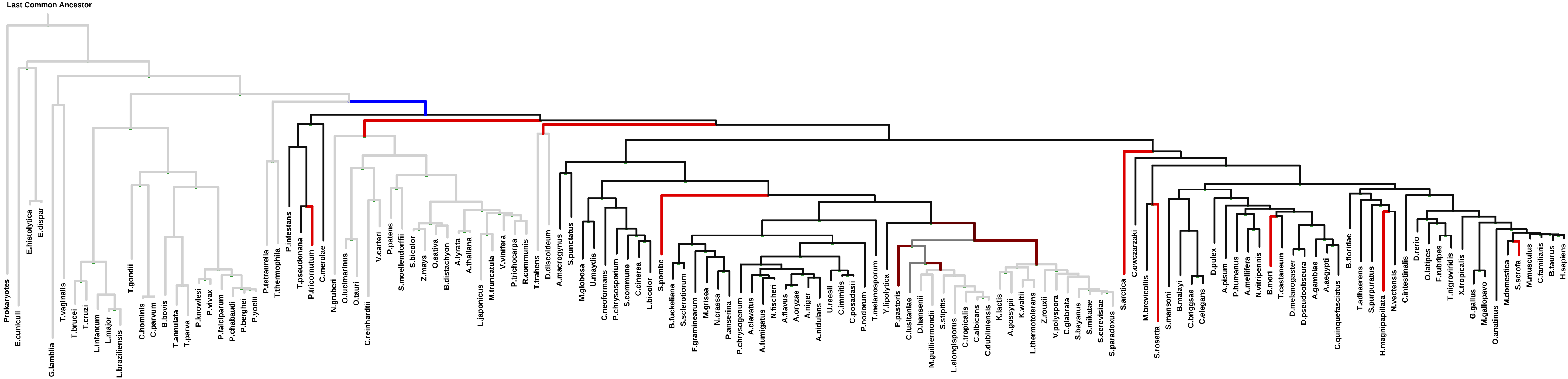
Num of ECM Genes: 1. Num of Predicted Genes: 1

[illegible]

1: integral to mitochondrial inner membrane || 2: mitochondrial inner membrane presequence translocase complex || 3: mitochondrial intermembrane space

ECM 6, Gene set "integral to mitochondrial inner membrane", Page 1

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



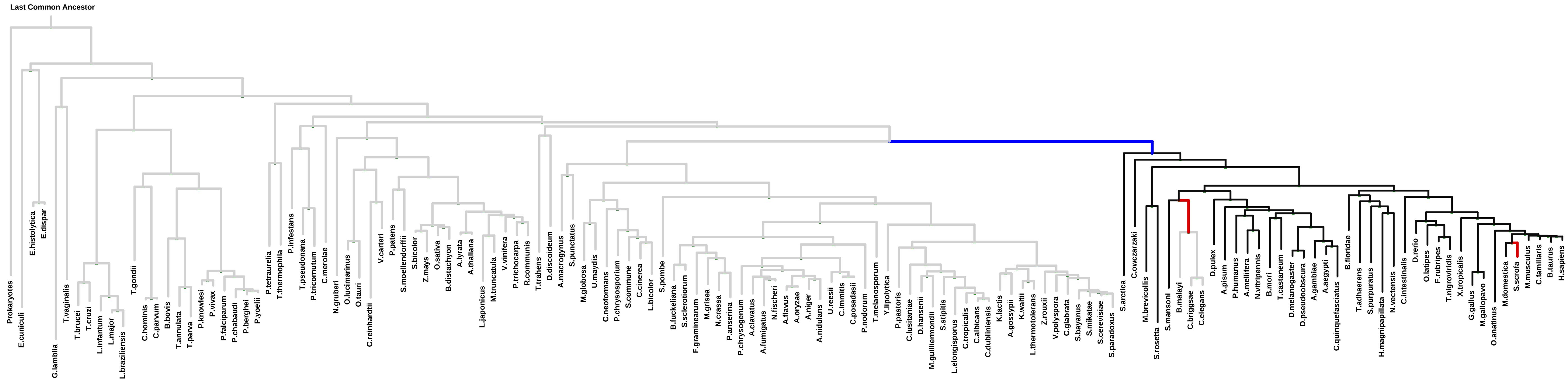
PG

Protein	IMMT	LLR	Notes
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.rosea			
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.latipes			
F.rubripes			
T.nigroviridis			
X.tropicalis			
G.gallus			
M.gallapavo			
O.anatinus			
M.domestica			
S.scrofa			
M.musculus			
C.familiaris			
B.taurus			
H.sapiens			

1: integral to mitochondrial inner membrane

ECM 7, Gene set "integral to mitochondrial inner membrane", Page 1

Num of ECM Genes: 1. Num of Predicted Genes: 2

[illegible]

1: integral to mitochondrial inner membrane || 2: chromatin || 3: chromatin assembly complex || 4: nuclear body || 5: nuclear chromatin || 6: nuclear matrix || 7: PML body || 8: replication fork || 9: transcription factor TFIID complex