

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

Dataset:

Num of genes in input gene set: 2
Total number of genes: 20834
Prediction LLR threshold: 0

The CLIME PDF output two sections:

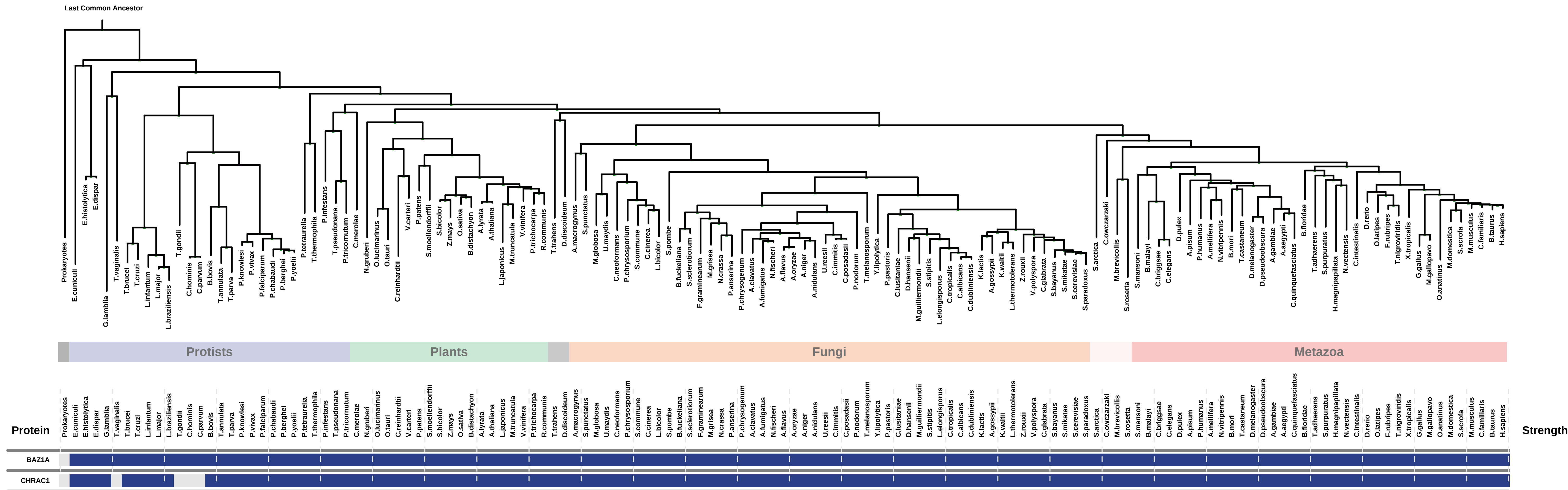
1) Overview of Evolutionarily Conserved Modules (ECMs)

- 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+

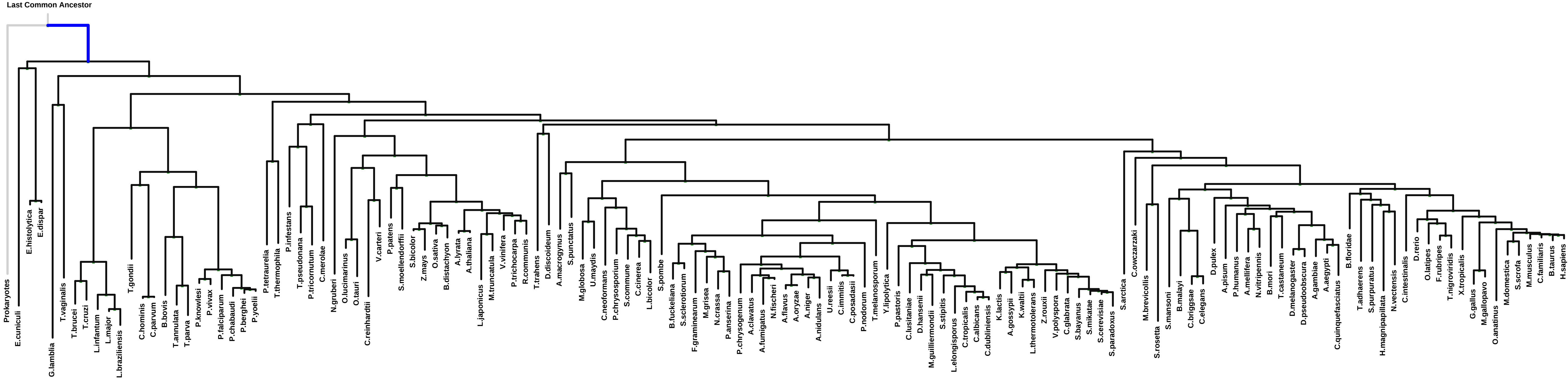
- Top panel shows the inferred evolutionary history on the predefined species tree. Branch color shows the gain event (blue) and loss events (red color, with brighter color indicating higher confidence in loss). Branches before the gain or after a loss are shown in gray.
- Bottom panel shows the input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

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



PG

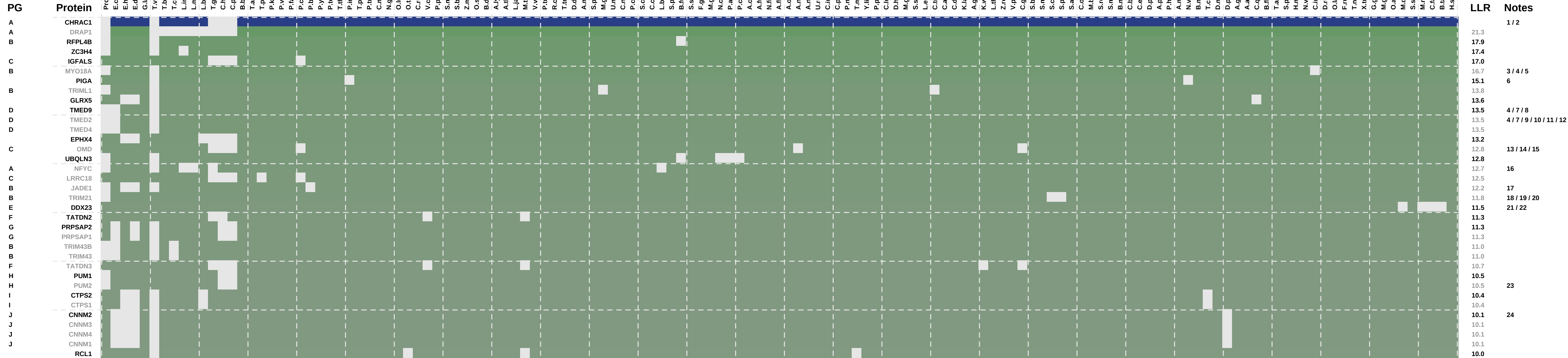
Protein	BAZ1A
Prokaryotes	
E.cuniculi	
E.histolytica	
E.dispar	
G.lamblia	
T.vaginalis	
T.brucei	
T.cruzi	
L.infantum	
L.major	
L.brazilienis	
T.gondii	
C.hominis	
C.parvum	
B.bovis	
T.annulata	
T.parva	
P.knowlesi	
P.vivax	
P.falciparum	
P.chabaudi	
P.berghiei	
P.yoelii	
P.tetraurelia	
T.thermophila	
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.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.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.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	

LLR

Notes

1: chromatin accessibility complex || 2: nuclear chromosome

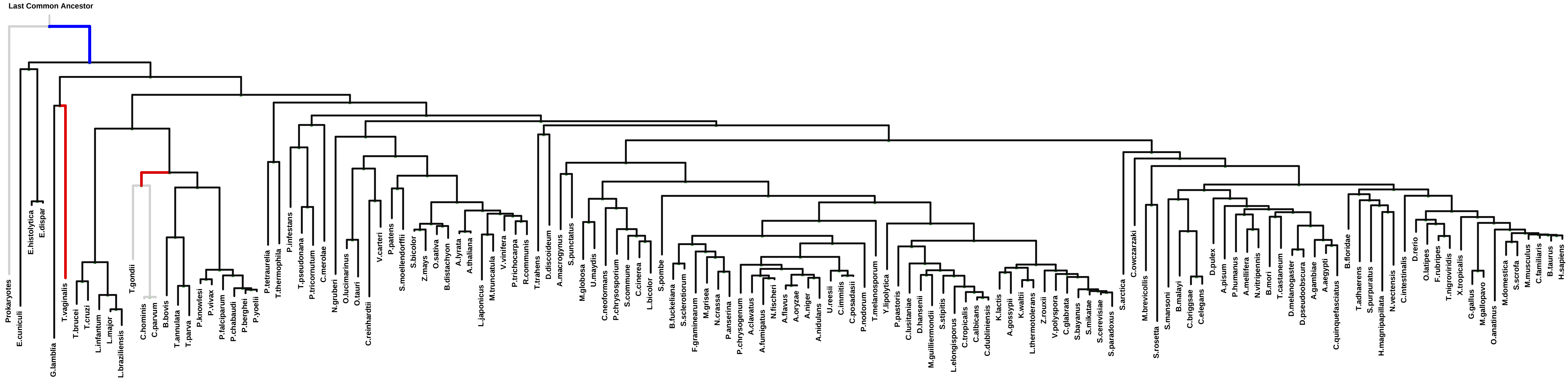
Num of ECM Genes: 1. Num of Predicted Genes: 500



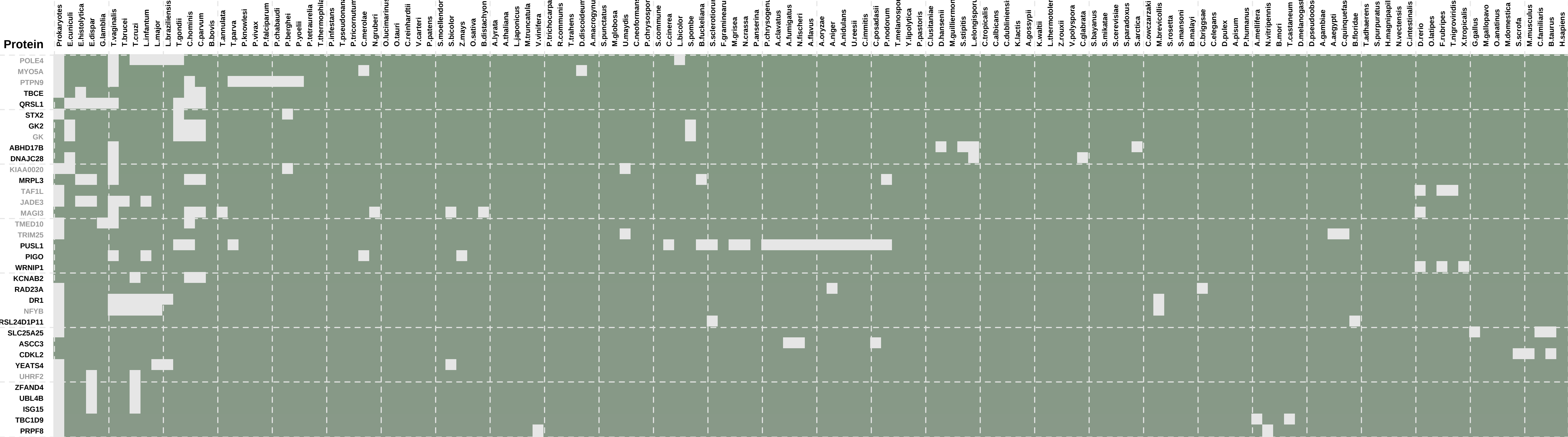
13: Golgi lumen || 14: lysosomal lumen || 15: proteinaceous extracellular matrix || 16: CCAAT-binding factor complex || 17: histone acetyltransferase complex || 18: cytoplasmic mRNA processing body || 19: ribonucleoprotein complex ||

ECM 2, Gene set "chromatin accessibility complex", Page 2

Num of ECM Genes: 1. Num of Predicted Genes: 500



PG

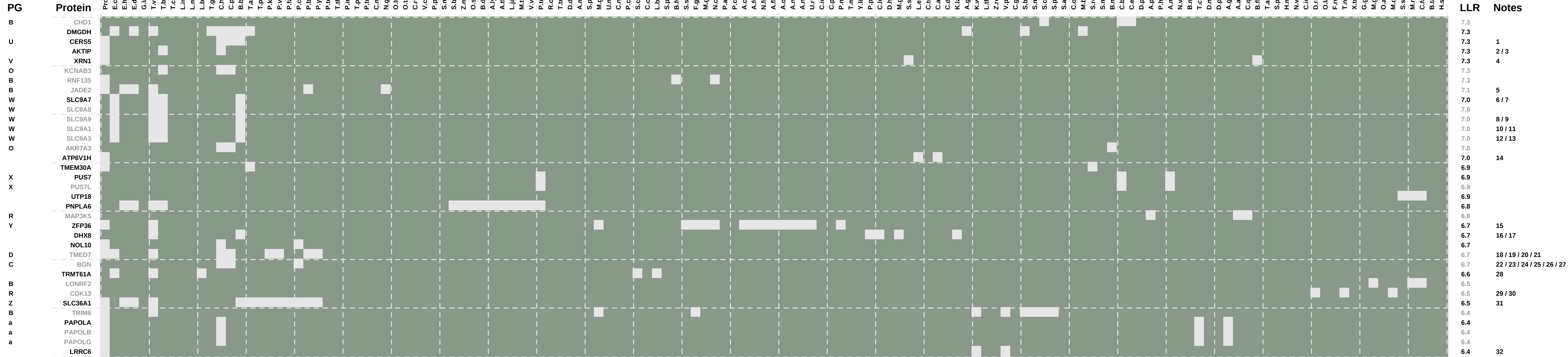


LLR

Notes

1: Ada2/Gcn5/Ada3 transcription activator complex || 2: epsilon DNA polymerase complex || 3: actomyosin || 4: growth cone || 5: insulin-responsive compartment || 6: intermediate filament || 7: melanosome || 8: microtubule plus end || 9: myosin complex || 10: neuron projection || 11: photoreceptor outer segment || 12: ruffle || 13: cytoplasmic part || 14: glutamyl-tRNA(Gln) amidotransferase complex || 15: basolateral plasma membrane || 16: cell-cell junction || 17: membrane raft || 18: midbody || 19: transport vesicle || 20: mitochondrial outer membrane || 21: mitochondrial large ribosomal subunit || 22: transcription factor TFIID complex || 23: histone acetyltransferase complex || 24: tight junction ||

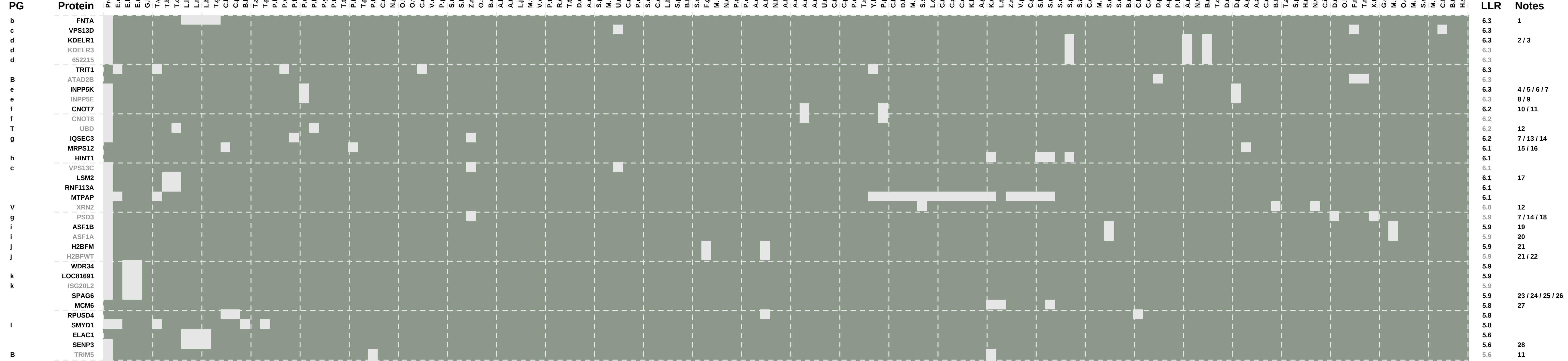
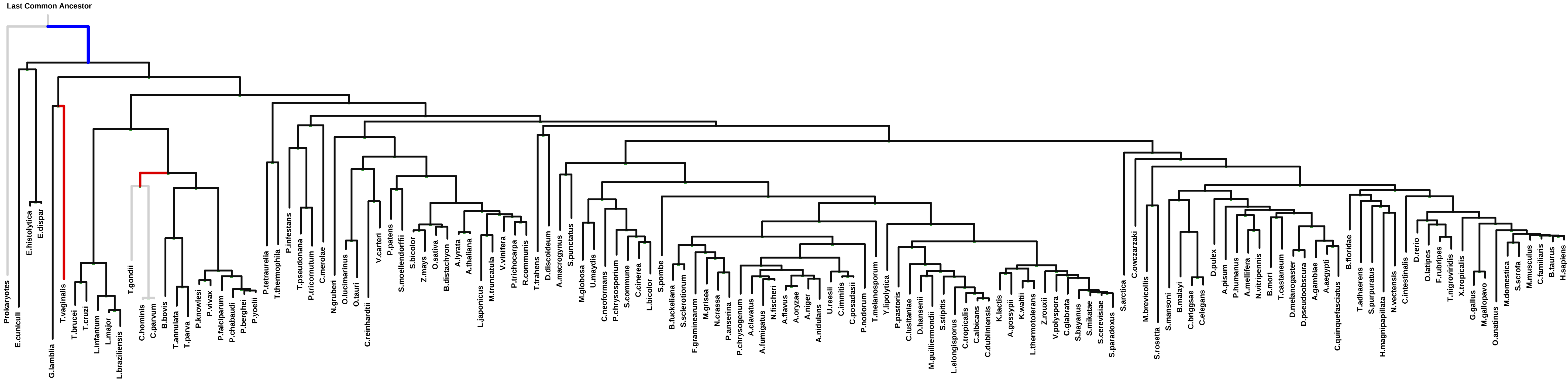
Num of ECM Genes: 1. Num of Predicted Genes: 500



16: catalytic step 2 spliceosome || 17: spliceosomal complex || 18: COPI vesicle coat || 19: COPII vesicle coat || 20: endoplasmic reticulum-Golgi intermediate compartment || 21: endoplasmic reticulum-Golgi intermediate compartment membranes

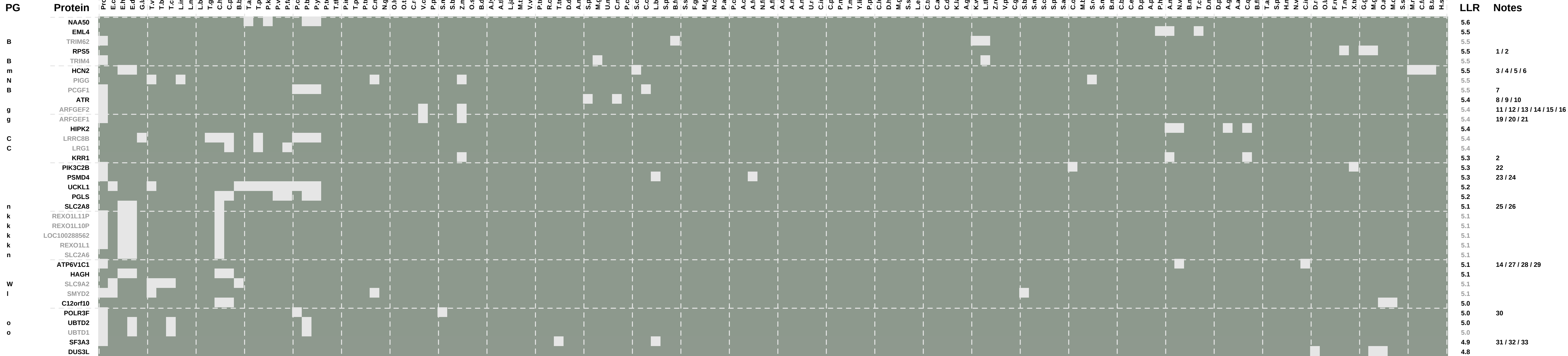
ECM 2, Gene set "chromatin accessibility complex", Page 4

Num of ECM Genes: 1. Num of Predicted Genes: 500



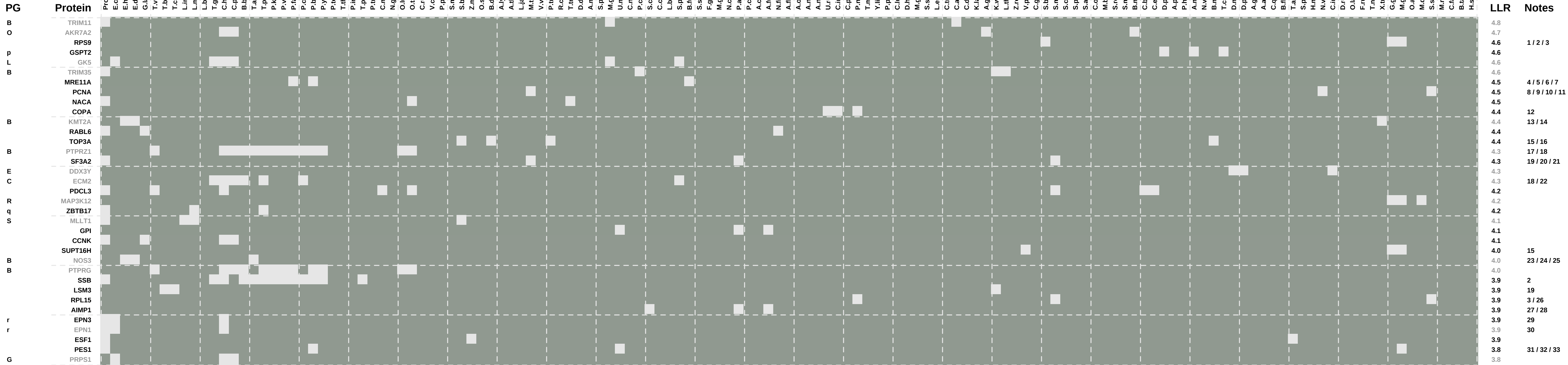
1: microtubule associated complex || 2: cis-Golgi network || 3: endoplasmic reticulum-Golgi intermediate compartment || 4: neuron projection || 5: ruffle || 6: ruffle membrane || 7: trans-Golgi network || 8: cilium axoneme ||
9: Golgi cisterna membrane || 10: CCR4-NOT complex || 11: cytoplasmic mRNA processing body || 12: aggresome || 13: inhibitory synapse || 14: postsynaptic membrane || 15: mitochondrial ribosome || 16: small ribosomal subunit ||
17: catalytic step 2 spliceosome || 18: postsynaptic density || 19: chromatin || 20: chromatin remodeling complex || 21: nucleosome || 22: nuclear membrane || 23: axoneme || 24: cilium || 25: flagellum || 26: microtubule cytoskeleton ||

Num of ECM Genes: 1. Num of Predicted Genes: 500



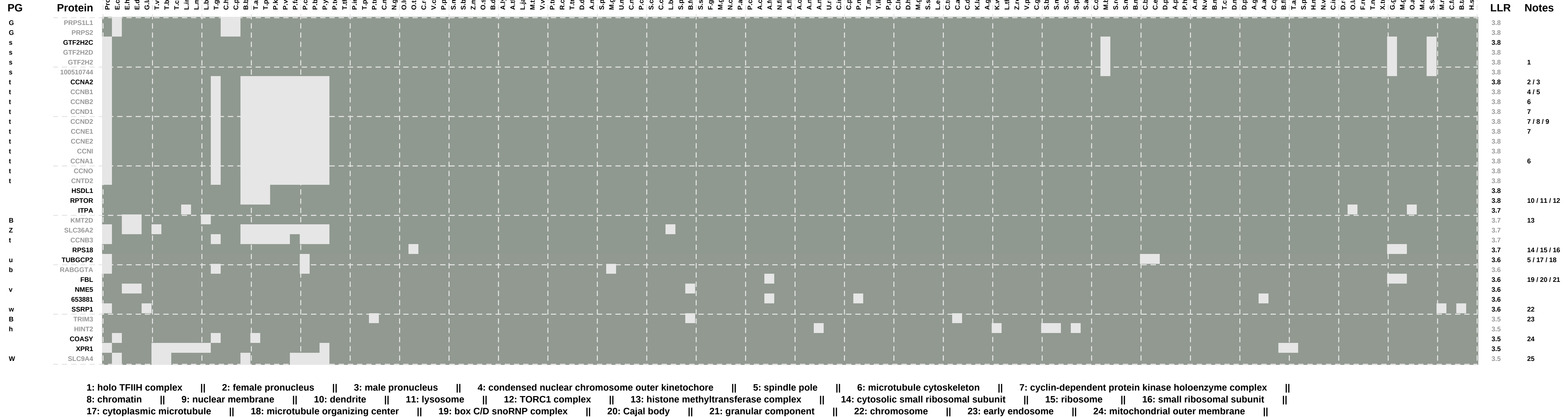
1: cytosolic small ribosomal subunit || 2: ribonucleoprotein complex || 3: axon || 4: dendritic shaft || 5: synapse || 6: voltage-gated potassium channel complex || 7: PcG protein complex || 8: chromosome || 9: PML body || 10: XY body || 11: asymmetric synapse || 12: axonemal microtubule || 13: cytoplasmic membrane-bounded vesicle || 14: cytoplasmic vesicle || 15: dendritic spine || 16: microtubule organizing center || 17: recycling endosome || 18: symmetric synapse || 19: trans-Golgi network || 20: nuclear matrix || 21: small nuclear ribonucleoprotein complex || 22: endocytic vesicle || 23: proteasome accessory complex || 24: proteasome complex || 25: cytoplasmic vesicle membrane ||

Num of ECM Genes: 1. Num of Predicted Genes: 500

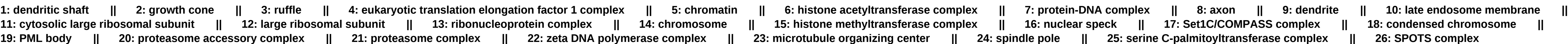
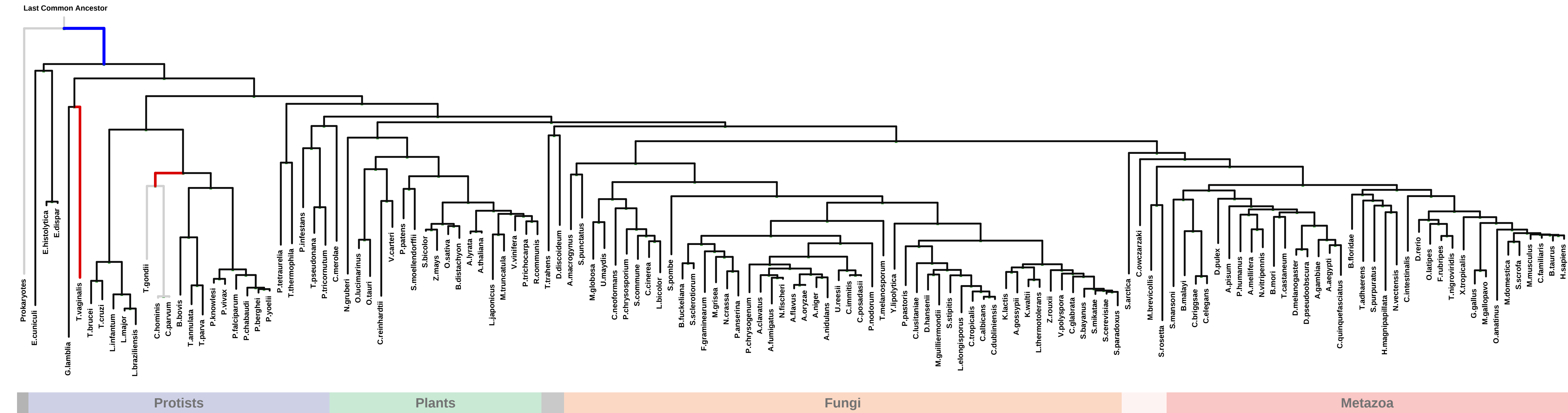


1: cytosolic small ribosomal subunit || 2: ribonucleoprotein complex || 3: ribosome || 4: chromosome, telomeric region || 5: condensed nuclear chromosome || 6: Mre11 complex || 7: nuclear chromatin || 8: DNA replication factor C complex || 9: microtubule cytoskeleton || 10: nuclear replication fork || 11: PCNA-p21 complex || 12: COPI vesicle coat || 13: histone methyltransferase complex || 14: MLL1 complex || 15: chromosome || 16: PML body || 17: perineuronal net || 18: proteinaceous extracellular matrix || 19: catalytic step 2 spliceosome || 20: small nuclear ribonucleoprotein complex || 21: spliceosomal complex || 22: interstitial matrix || 23: apical part of cell || 24: caveola || 25: endocytic vesicle membrane ||

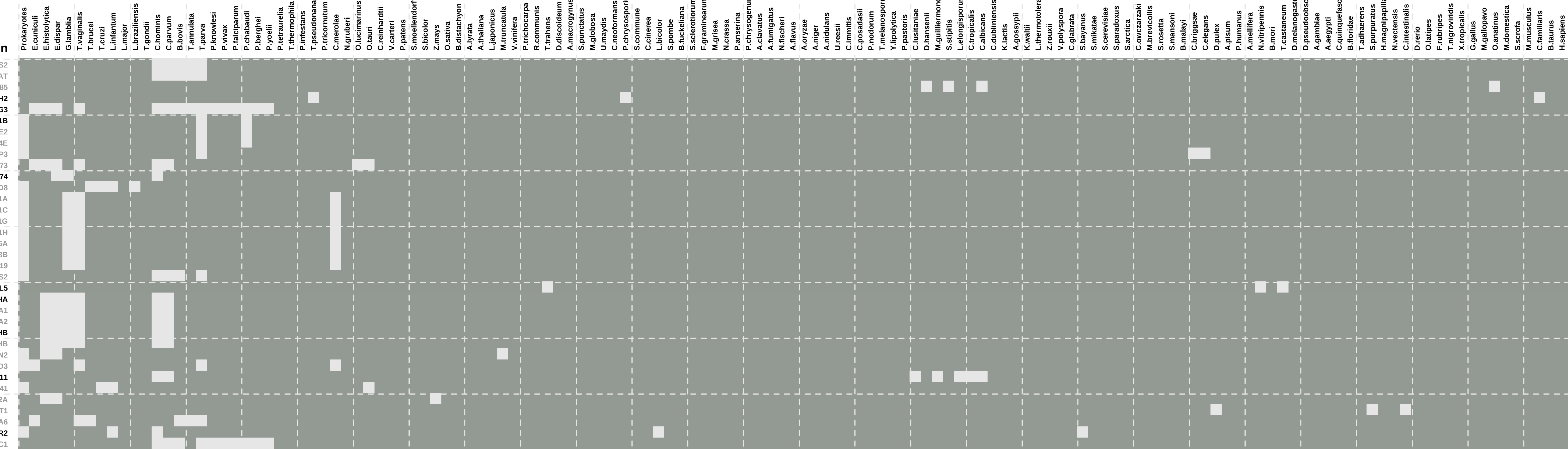
Num of ECM Genes: 1. Num of Predicted Genes: 500



Num of ECM Genes: 1. Num of Predicted Genes: 500

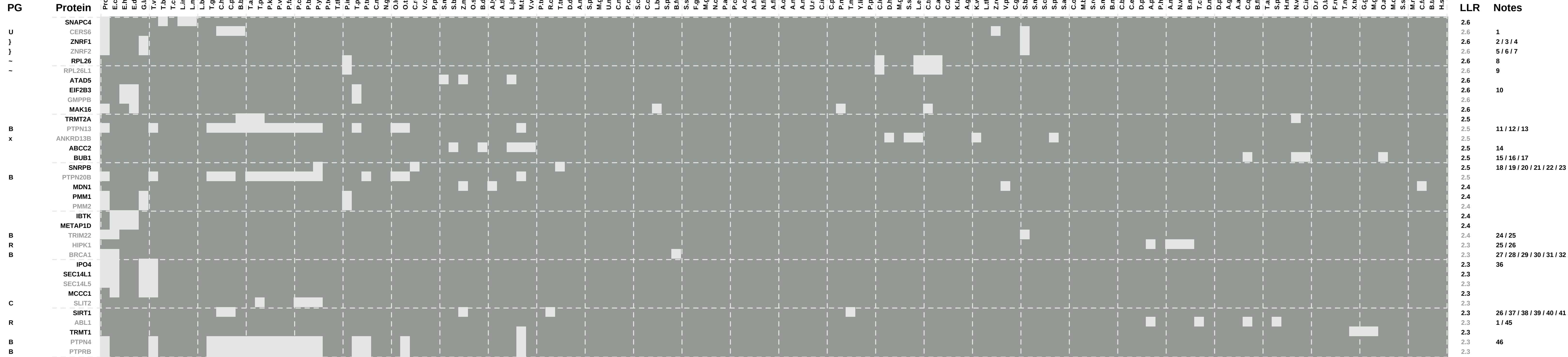


Num of ECM Genes: 1. Num of Predicted Genes: 500



1: AMP-activated protein kinase complex || 2: mRNA cap binding complex || 3: cytoplasmic mRNA processing body || 4: cytoplasmic stress granule || 5: eukaryotic translation initiation factor 4F complex || 6: RNA-induced silencing complex || 7: centriole || 8: polar microtubule || 9: spindle || 10: basal plasma membrane || 11: basolateral plasma membrane || 12: brush border || 13: cortical actin cytoskeleton || 14: filamentous actin || 15: lateral plasma membrane || 16: microvillus || 17: myosin complex || 18: nuclear pore || 19: stereocilium membrane || 20: stress fiber || 21: unconventional myosin complex || 22: stereocilium || 23: sarcomere || 24: mitochondrial outer membrane ||

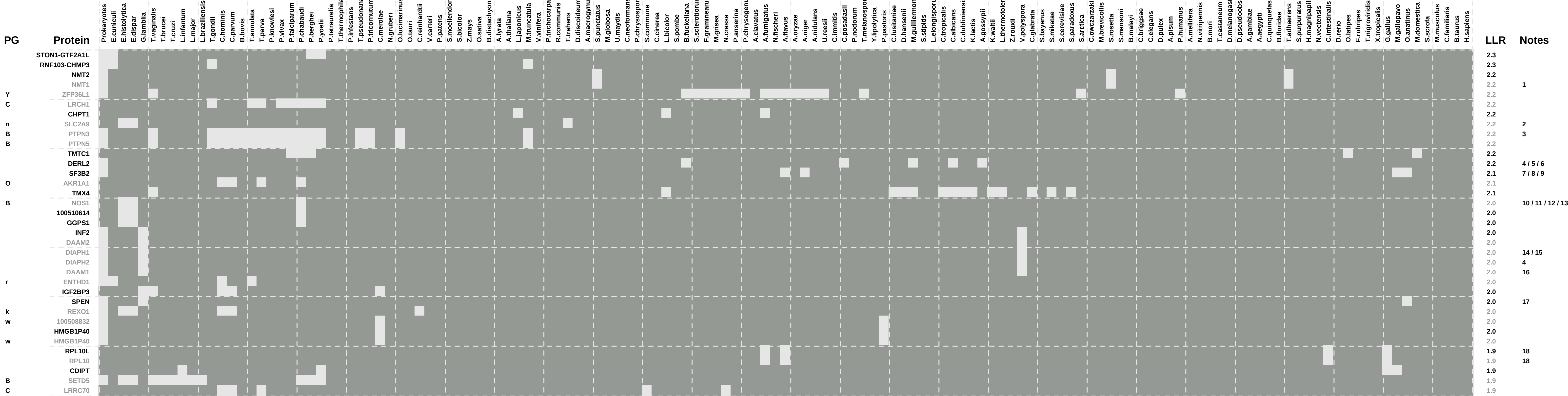
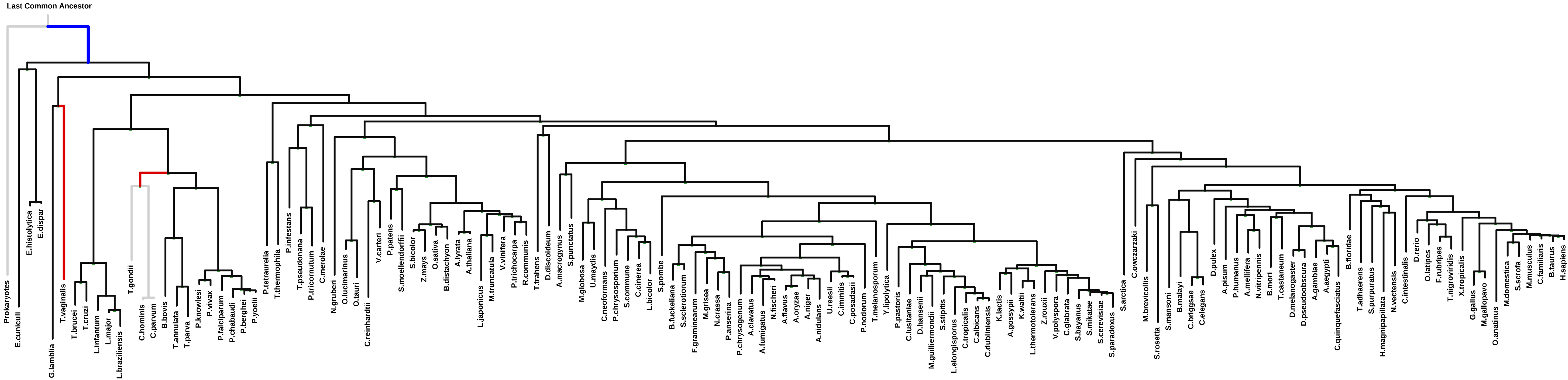
Num of ECM Genes: 1. Num of Predicted Genes: 500



1: nuclear membrane || 2: endosome || 3: lysosome || 4: synaptic vesicle membrane || 5: endosome membrane || 6: lysosomal membrane || 7: presynaptic membrane || 8: cytosolic large ribosomal subunit || 9: large ribosomal subunit ||
10: eukaryotic translation initiation factor 2B complex || 11: cell body || 12: lamellipodium || 13: neuron projection || 14: intercellular canaliculus || 15: condensed chromosome kinetochore || 16: condensed nuclear chromosome, centromeric region ||
17: kinetochore || 18: catalytic step 2 spliceosome || 19: histone pre-mRNA 3'end processing complex || 20: small nuclear ribonucleoprotein complex || 21: spliceosomal complex || 22: U12-type spliceosomal complex || 23: U7 snRNP ||

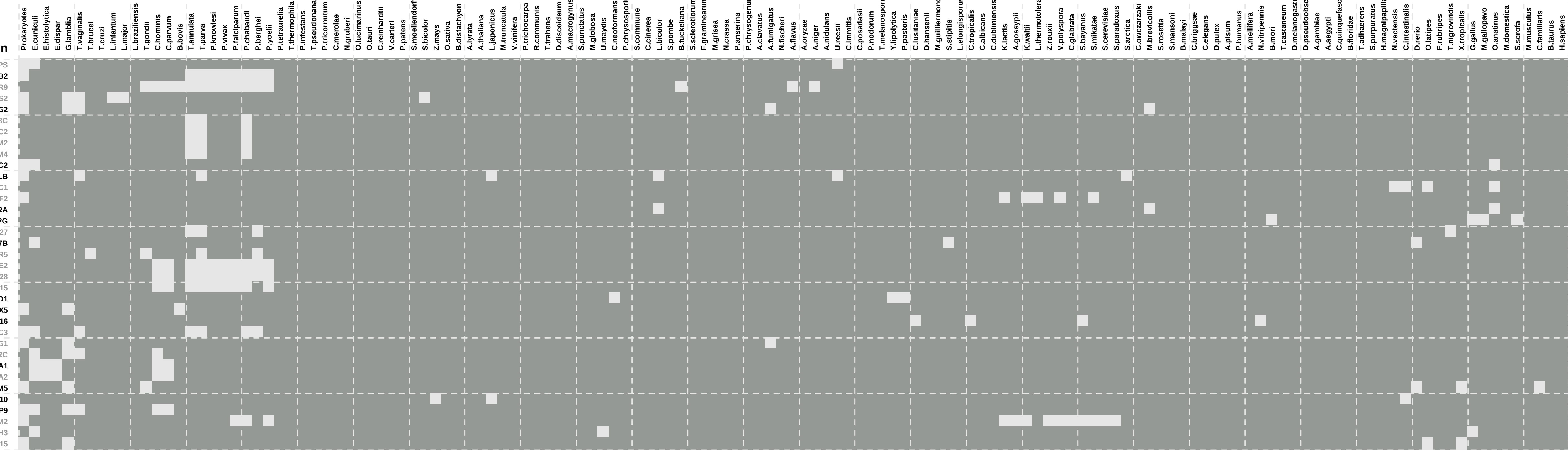
ECM 2, Gene set "chromatin accessibility complex", Page 11

Num of ECM Genes: 1. Num of Predicted Genes: 500



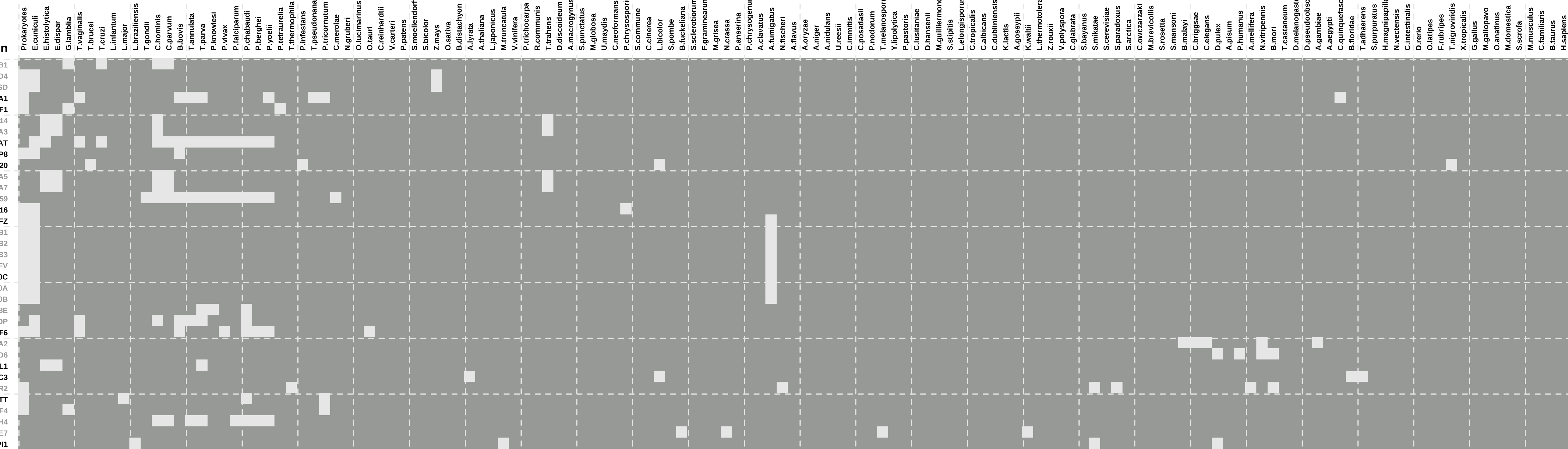
1: actin cytoskeleton || 2: nuclear envelope || 3: internal side of plasma membrane || 4: early endosome || 5: integral to endoplasmic reticulum membrane || 6: late endosome || 7: catalytic step 2 spliceosome || 8: spliceosomal complex || 9: U12-type spliceosomal complex || 10: dendritic spine || 11: photoreceptor inner segment || 12: sarcolemma || 13: sarcoplasmic reticulum || 14: mitotic spindle || 15: ruffle membrane || 16: stress fiber || 17: transcriptional repressor complex || 18: cytosolic large ribosomal subunit

Num of ECM Genes: 1. Num of Predicted Genes: 500



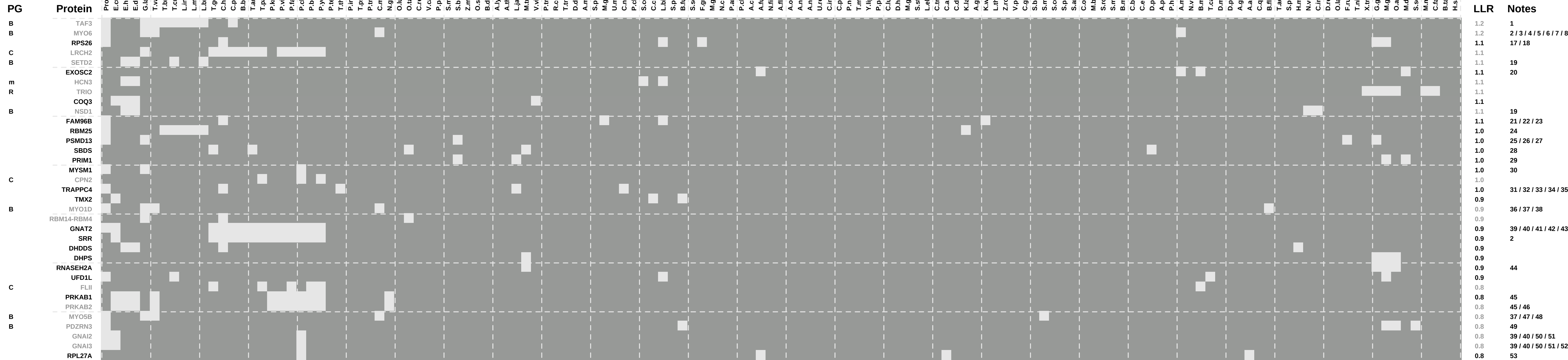
1: basolateral plasma membrane || 2: early phagosome || 3: endolysosome membrane || 4: endosome || 5: endosome membrane || 6: lysosome || 7: Ada2/Gcn5/Ada3 transcription activator complex || 8: eukaryotic translation initiation factor 4F complex || 9: protein phosphatase type 1 complex || 10: postsynaptic membrane || 11: chromosome || 12: nuclear membrane || 13: MLL1 complex || 14: nuclear body || 15: PcG protein complex || 16: PRC1 complex || 17: sex chromatin || 18: ubiquitin ligase complex || 19: centriole || 20: nuclear chromosome || 21: nucleoid || 22: synaptonemal complex || 23: DNA-directed RNA polymerase II, core complex || 24: anaphase-promoting complex || 25: spindle ||

Num of ECM Genes: 1. Num of Predicted Genes: 500



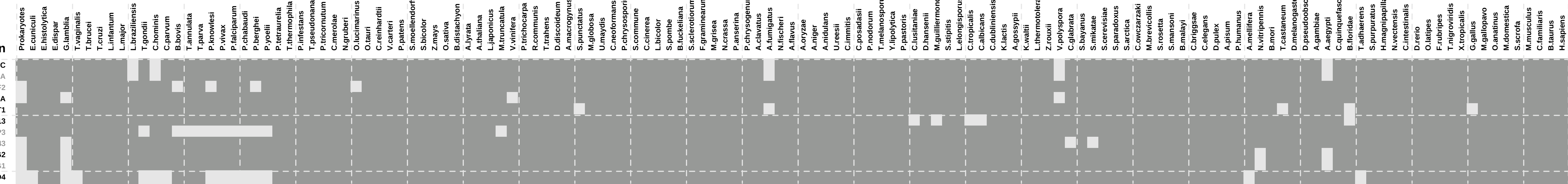
1: trans-Golgi network || 2: ruffle || 3: mRNA cleavage and polyadenylation specificity factor complex || 4: early endosome || 5: late endosome membrane || 6: lysosomal membrane || 7: recycling endosome || 8: secretory granule membrane || 9: SNARE complex || 10: cytosolic small ribosomal subunit || 11: mitochondrial nucleoid || 12: Barr body || 13: nucleosome || 14: nuclear nucleosome || 15: transcriptionally active chromatin || 16: synaptic vesicle || 17: synaptic vesicle membrane || 18: intermediate filament cytoskeleton || 19: nBAF complex || 20: npBAF complex || 21: nuclear chromatin || 22: SWI/SNF complex || 23: WINAC complex || 24: cis-Golgi network || 25: microtubule cytoskeleton || 26: PML body

Num of ECM Genes: 1. Num of Predicted Genes: 500



1: transcription factor TFIID complex || 2: apical part of cell || 3: axon || 4: cell cortex || 5: clathrin-coated endocytic vesicle || 6: clathrin-coated vesicle membrane || 7: coated pit || 8: cytoplasmic membrane-bounded vesicle || 9: DNA-directed RNA polymerase II, holoenzyme || 10: endocytic vesicle || 11: filamentous actin || 12: microvillus || 13: nuclear membrane || 14: ruffle || 15: ruffle membrane || 16: unconventional myosin complex || 17: cytosolic small ribosomal subunit || 18: small ribosomal subunit || 19: chromosome || 20: exosome (RNase complex) || 21: CIA complex || 22: MMXD complex || 23: spindle || 24: nuclear speck || 25: proteasome accessory complex || 26: proteasome complex ||

Num of ECM Genes: 1. Num of Predicted Genes: 500



1: ubiquitin ligase complex || 2: cytosolic small ribosomal subunit || 3: ribosome || 4: early endosome membrane || 5: Golgi stack || 6: membrane raft || 7: recycling endosome membrane || 8: trans-Golgi network || 9: trans-Golgi network membrane || 10: nuclear envelope || 11: COPI vesicle coat