

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

Dataset:

Num of genes in input gene set: 6
Total number of genes: 20834
Prediction LLR threshold: 0

The CLIME PDF output two sections:

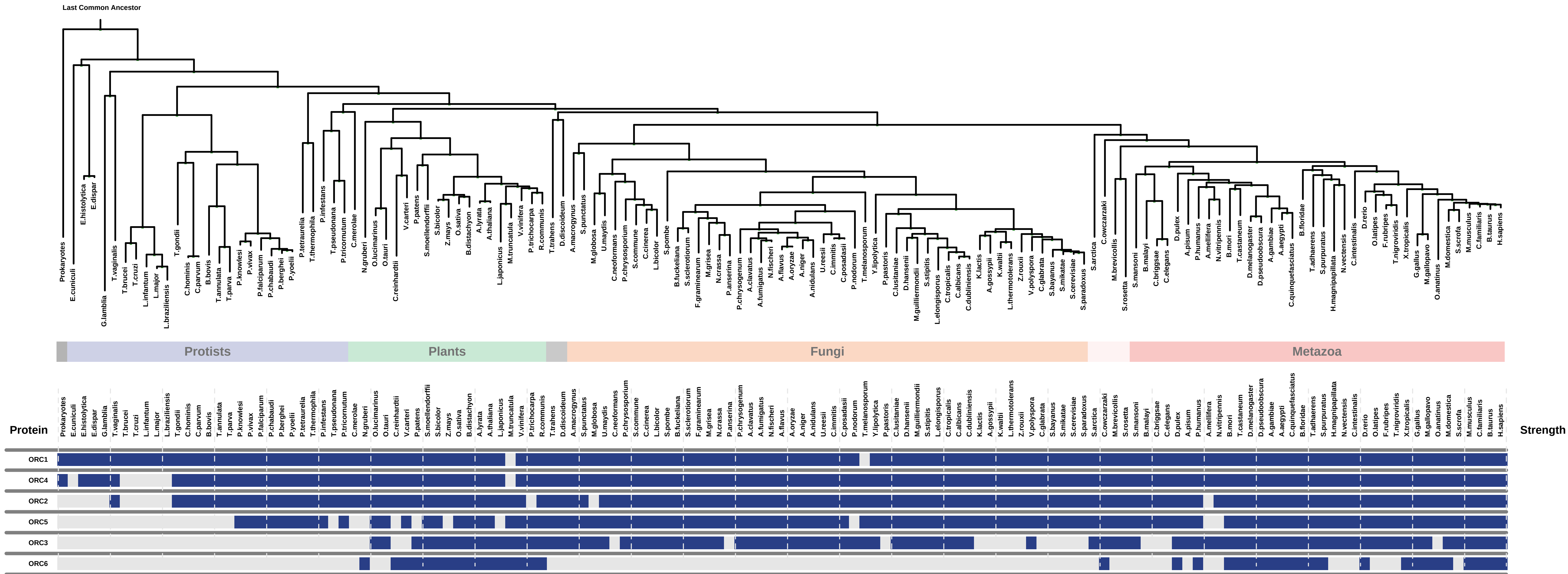
1) Overview of Evolutionarily Conserved Modules (ECMs)

- 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+

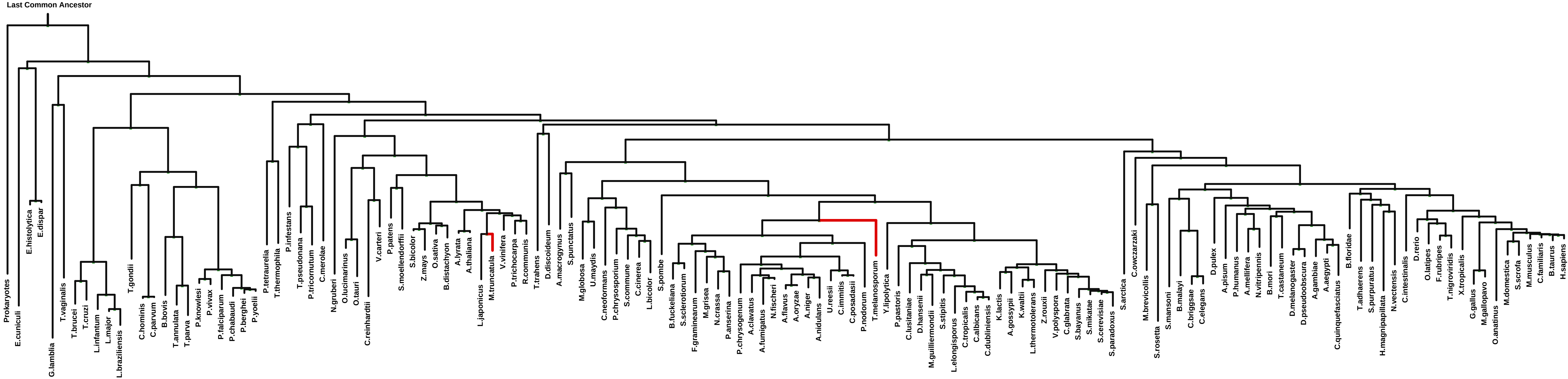
- Top panel shows the inferred evolutionary history on the predefined species tree. Branch color shows the gain event (blue) and loss events (red color, with brighter color indicating higher confidence in loss). Branches before the gain or after a loss are shown in gray.
- Bottom panel shows the input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

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



PG

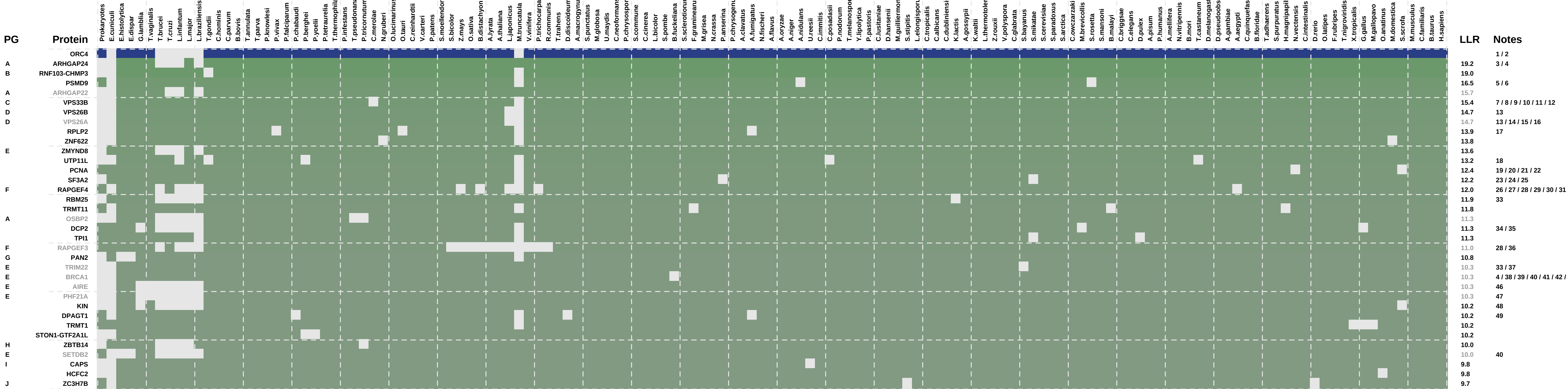
Protein	Pt	Pr	E	E	G	T	T	T	T	L	L	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T
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1: nuclear origin of replication recognition complex || 2: origin recognition complex

LLR Notes

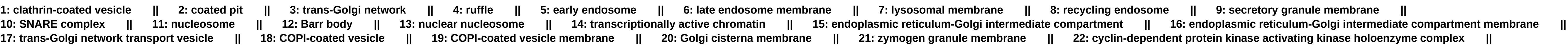
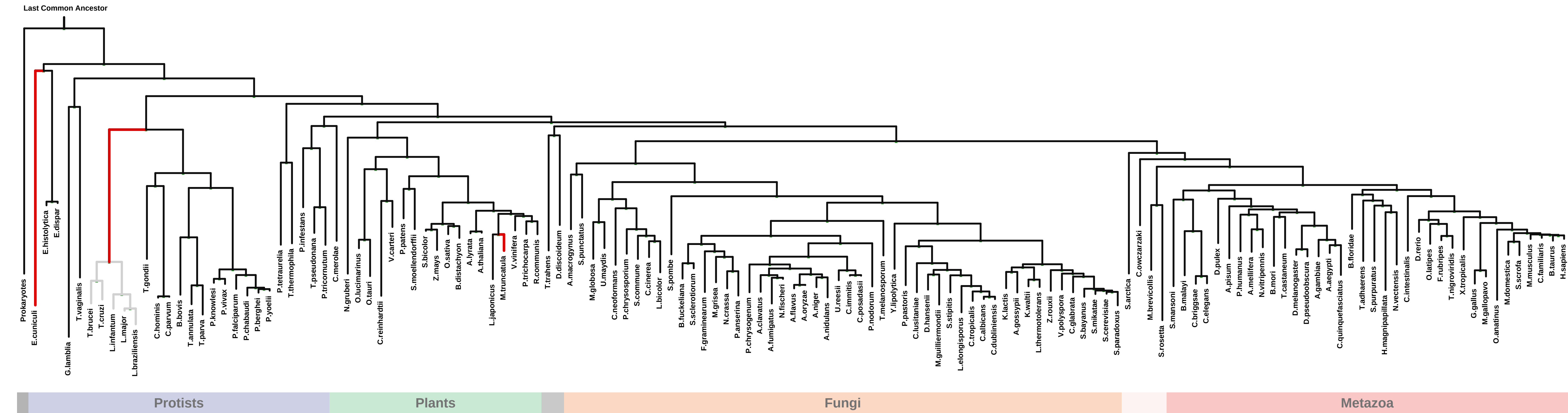
ECM 2, Gene set "origin recognition complex", Page 1

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



1: nuclear origin of replication recognition complex || 2: origin recognition complex || 3: cell projection || 4: focal adhesion || 5: proteasome regulatory particle || 6: proteasome regulatory particle, base subcomplex || 7: HOPS complex ||
8: late endosome || 9: late endosome membrane || 10: lysosomal membrane || 11: lysosome || 12: platelet alpha granule || 13: retromer complex || 14: endosome || 15: endosome membrane || 16: vesicle || 17: cytosolic large ribosomal subunit ||
18: small-subunit processome || 19: DNA replication factor C complex || 20: microtubule cytoskeleton || 21: nuclear replication fork || 22: PCNA-p21 complex || 23: catalytic step 2 spliceosome || 24: small nuclear ribonucleoprotein complex ||

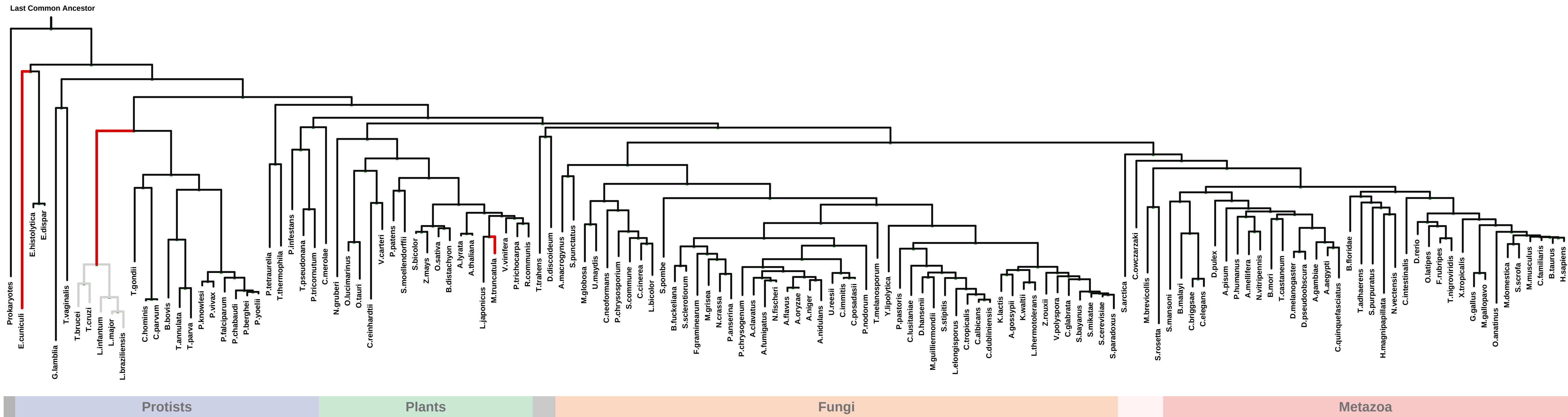
Num of ECM Genes: 1. Num of Predicted Genes: 500



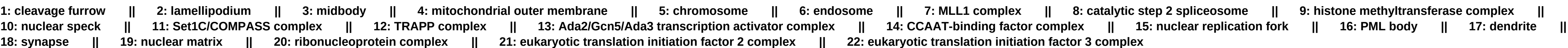
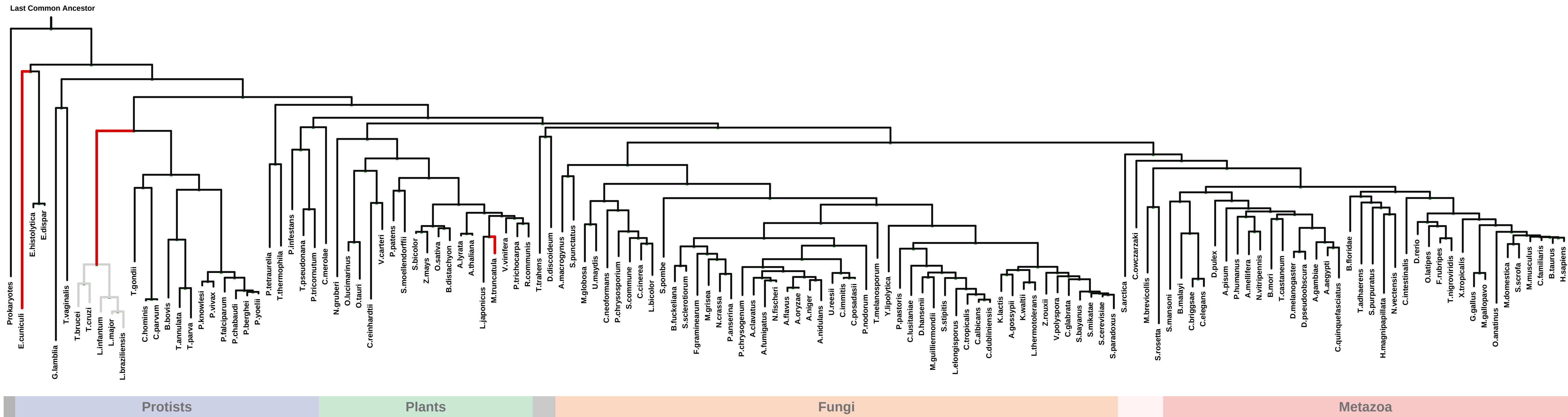
Num of ECM Genes: 1. Num of Predicted Genes: 500



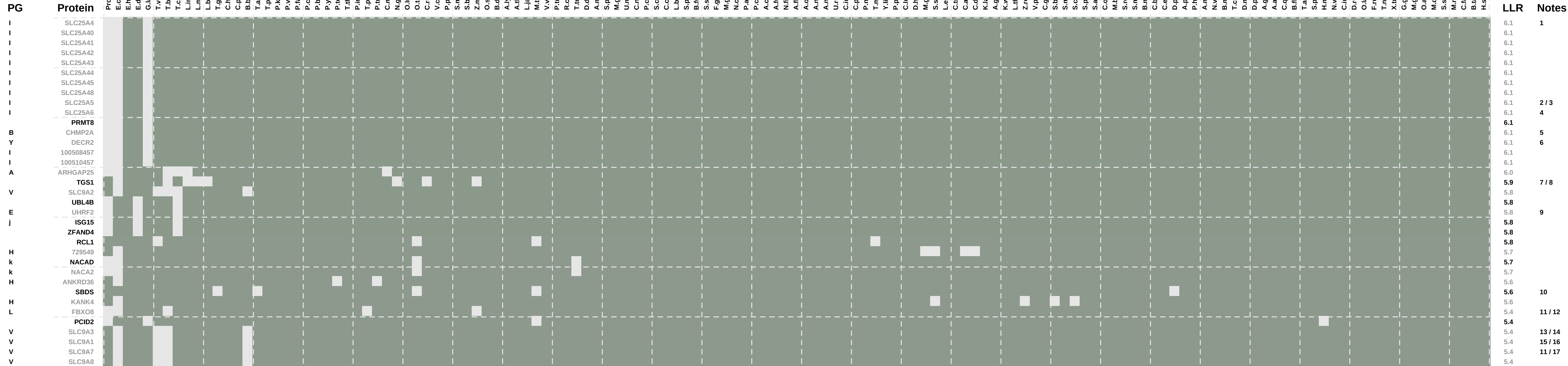
Num of ECM Genes: 1. Num of Predicted Genes: 500



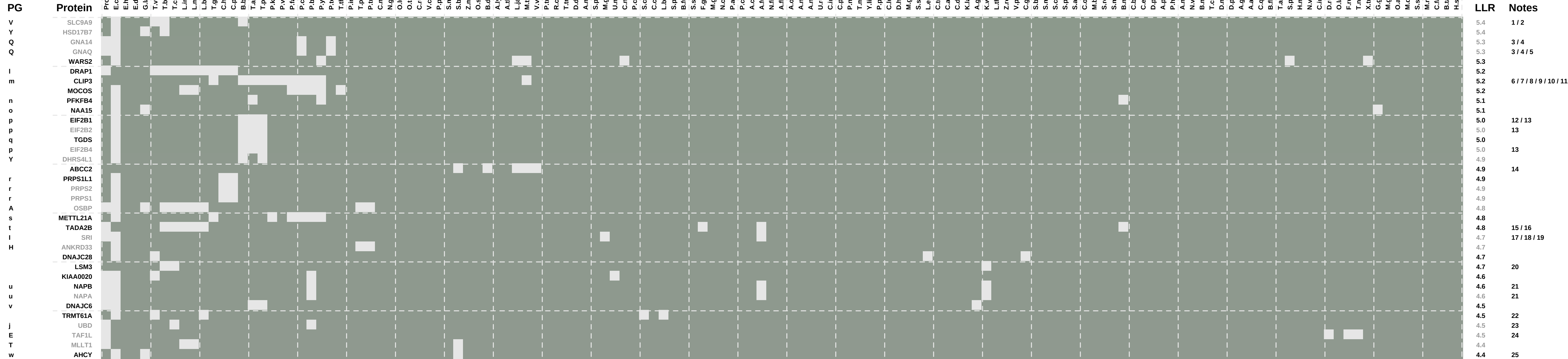
Num of ECM Genes: 1. Num of Predicted Genes: 500



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

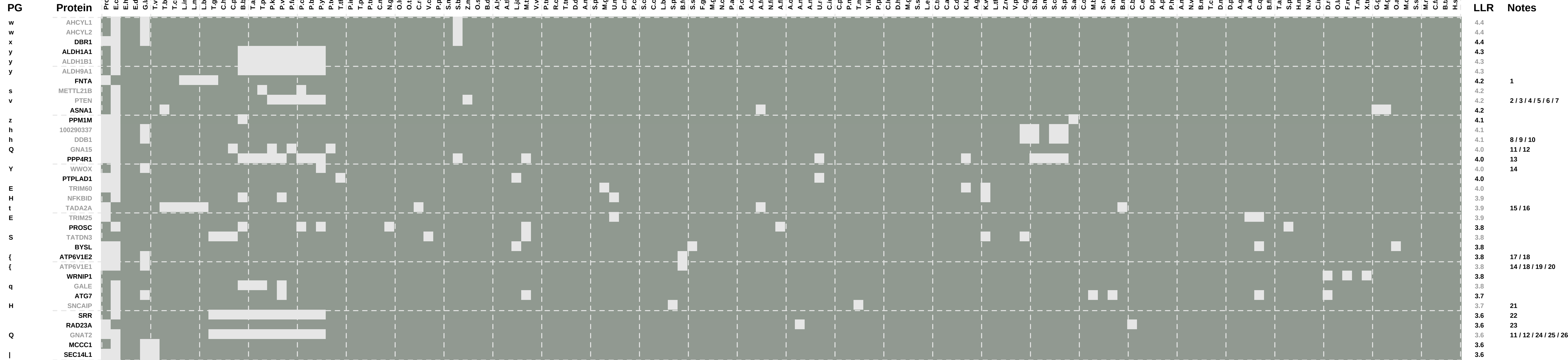


Num of ECM Genes: 1. Num of Predicted Genes: 500



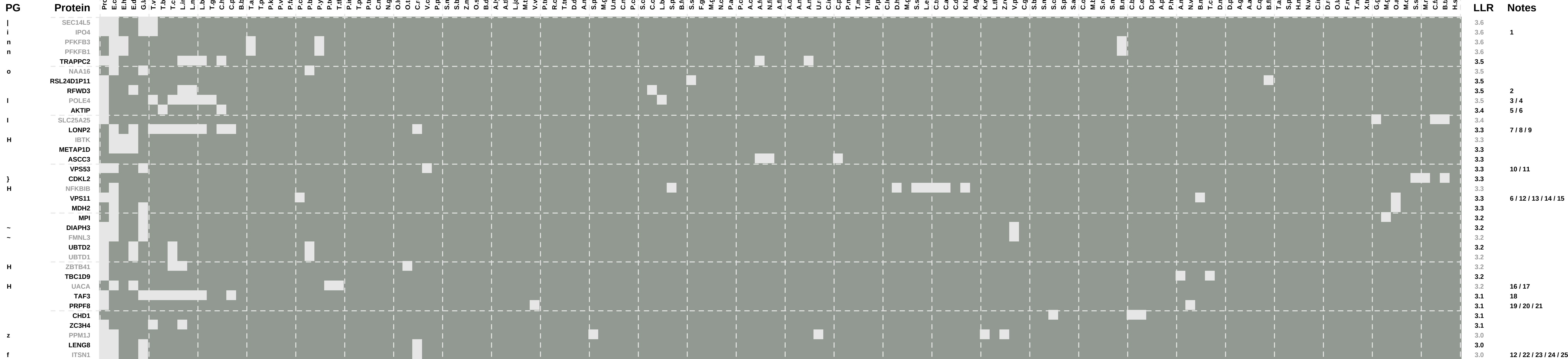
1: late endosome membrane || 2: recycling endosome || 3: extrinsic to internal side of plasma membrane || 4: heterotrimeric G-protein complex || 5: nuclear membrane || 6: early endosome membrane || 7: Golgi stack || 8: membrane raft ||
9: recycling endosome membrane || 10: trans-Golgi network || 11: trans-Golgi network membrane || 12: eukaryotic translation initiation factor 2 complex || 13: eukaryotic translation initiation factor 2B complex || 14: intercellular canaliculus ||
15: SAGA-type complex || 16: STAGA complex || 17: sarcoplasmic reticulum membrane || 18: vesicle || 19: Z disc || 20: catalytic step 2 spliceosome || 21: synaptobrevin 2-SNAP-25-syntaxin-1a complex || 22: tRNA (m1A) methyltransferase complex ||

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



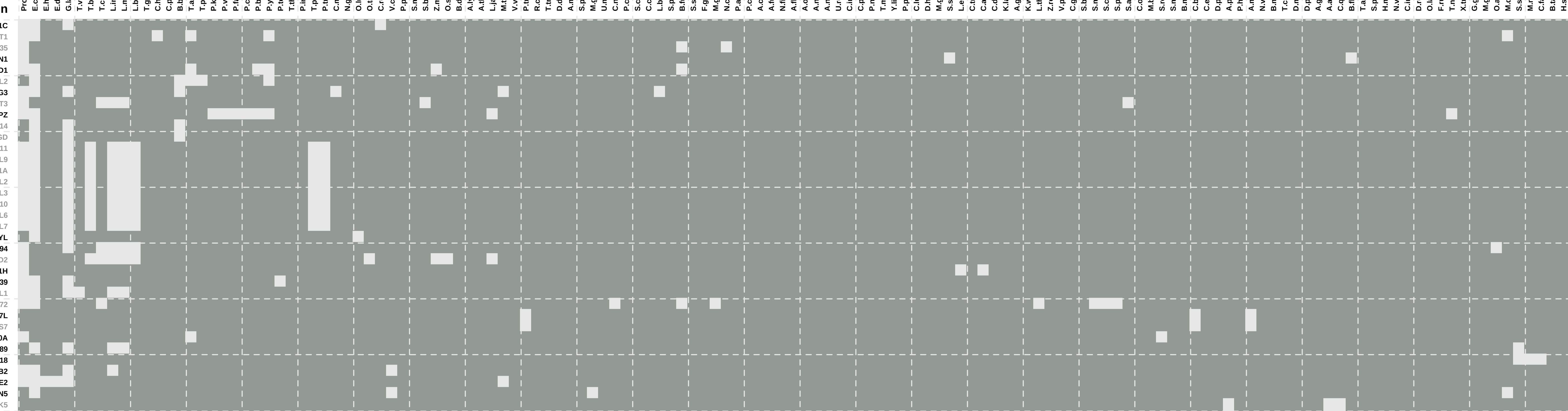
1: microtubule associated complex || 2: cell projection || 3: internal side of plasma membrane || 4: myelin sheath adaxonal region || 5: neuron projection || 6: PML body || 7: Schmidt-Lanterman incisure || 8: Cul4A-RING ubiquitin ligase complex || 9: Cul4B-RING ubiquitin ligase complex || 10: Cul4-RING ubiquitin ligase complex || 11: extrinsic to internal side of plasma membrane || 12: heterotrimeric G-protein complex || 13: protein phosphatase 4 complex || 14: microvillus || 15: chromosome || 16: PCAF complex || 17: acrosomal vesicle || 18: proton-transporting two-sector ATPase complex, catalytic domain || 19: endosome || 20: proton-transporting two-sector ATPase complex || 21: presynaptic membrane || 22: apical part of cell ||

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



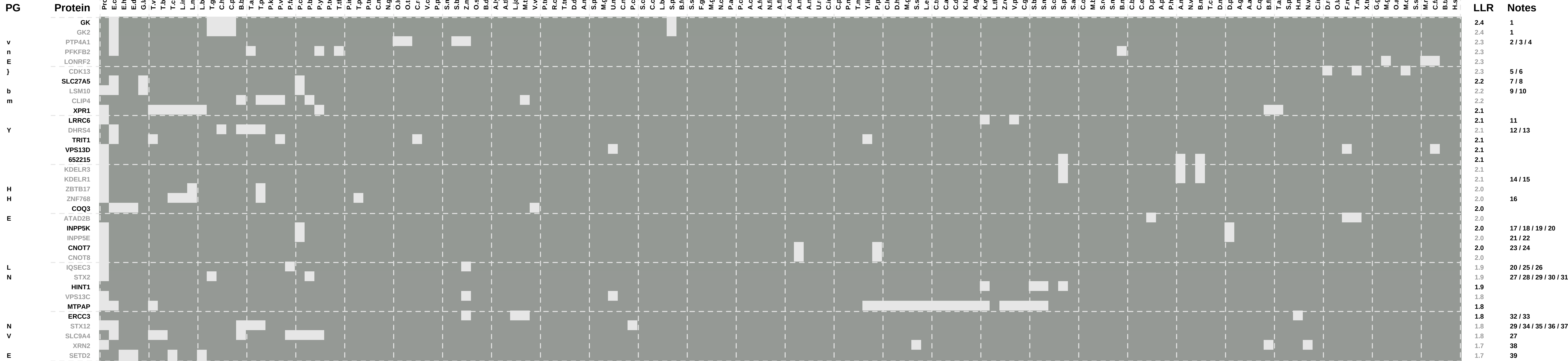
1: nuclear pore || 2: PML body || 3: Ada2/Gcn5/Ada3 transcription activator complex || 4: epsilon DNA polymerase complex || 5: FHF complex || 6: HOPS complex || 7: nucleoid || 8: peroxisomal matrix || 9: peroxisome || 10: endosome membrane || 11: GARP complex || 12: endocytic vesicle || 13: endosome || 14: late endosome membrane || 15: lysosomal membrane || 16: apoptosome || 17: nuclear envelope || 18: transcription factor TFIID complex || 19: catalytic step 2 spliceosome || 20: nuclear speck || 21: U5 snRNP || 22: coated pit || 23: lamellipodium || 24: neuron projection || 25: synapse

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



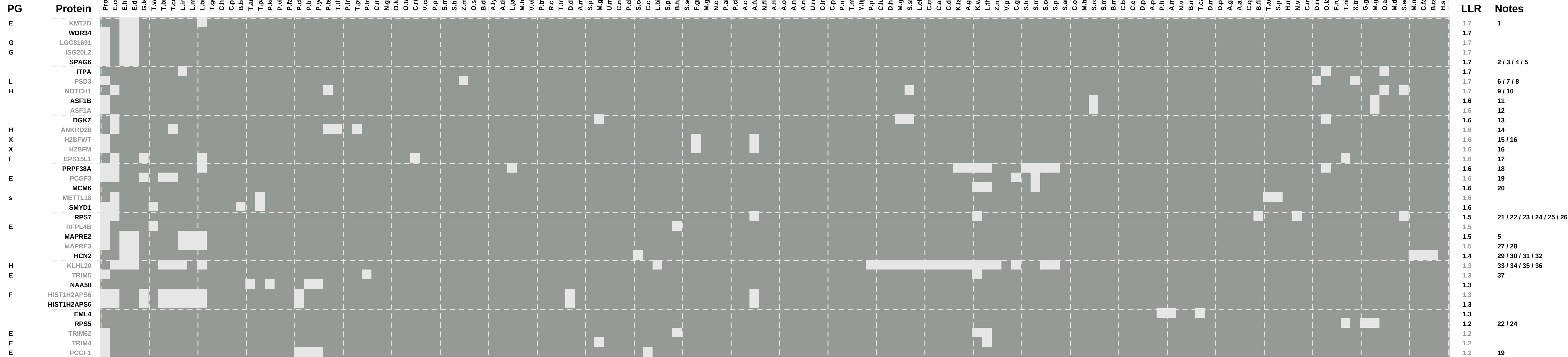
LLR	Notes
3.0	1 / 2
3.0	3
3.0	
3.0	4
2.9	
2.9	
2.9	
2.9	
2.9	
2.8	
2.8	
2.8	5 / 6
2.8	
2.8	
2.8	
2.8	
2.8	
2.8	
2.7	7
2.7	
2.7	
2.7	8 / 9
2.7	
2.6	
2.6	
2.6	
2.6	10
2.5	11
2.5	12

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



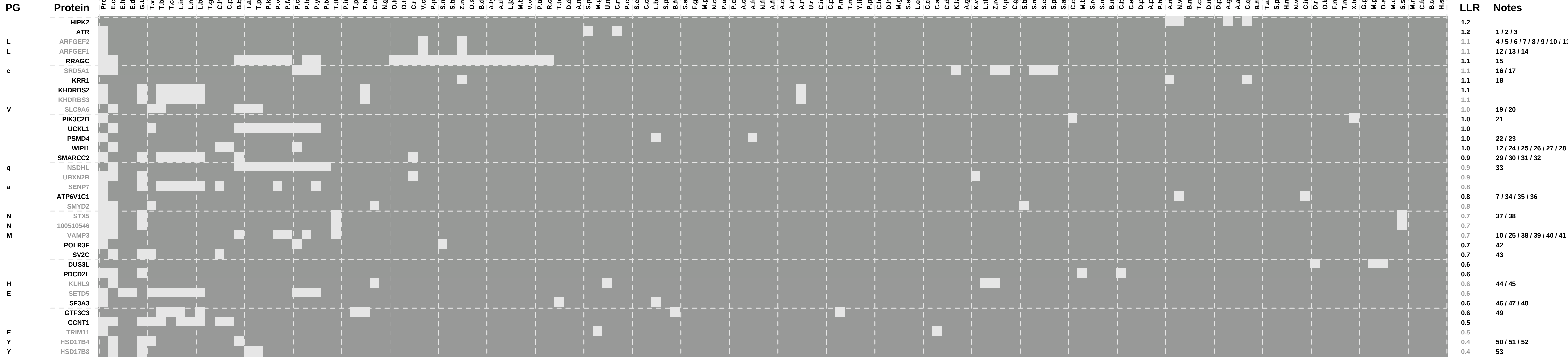
1: mitochondrial outer membrane || 2: early endosome || 3: internal side of plasma membrane || 4: spindle || 5: nuclear cyclin-dependent protein kinase holoenzyme complex || 6: nuclear speck || 7: basal plasma membrane || 8: integral to endoplasmic reticulum membrane ||
9: Cajal body || 10: U7 snRNP || 11: cilium || 12: peroxisomal membrane || 13: peroxisome || 14: cis-Golgi network || 15: endoplasmic reticulum-Golgi intermediate compartment || 16: DNA-directed RNA polymerase II, core complex ||
17: neuron projection || 18: ruffle || 19: ruffle membrane || 20: trans-Golgi network || 21: cilium axoneme || 22: Golgi cisterna membrane || 23: CCR4-NOT complex || 24: cytoplasmic mRNA processing body || 25: inhibitory synapse ||

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



1: histone methyltransferase complex || 2: axoneme || 3: cilium || 4: flagellum || 5: microtubule cytoskeleton || 6: postsynaptic density || 7: postsynaptic membrane || 8: trans-Golgi network || 9: acrosomal vesicle ||
10: MAML1-RBP-Jkappa-ICN1 complex || 11: chromatin || 12: chromatin remodeling complex || 13: lamellipodium || 14: actin filament || 15: nuclear membrane || 16: nucleosome || 17: coated pit || 18: spliceosomal complex ||
19: PcG protein complex || 20: MCM complex || 21: 90S preribosome || 22: cytosolic small ribosomal subunit || 23: microtubule organizing center || 24: ribonucleoprotein complex || 25: ribosome || 26: small-subunit processome ||

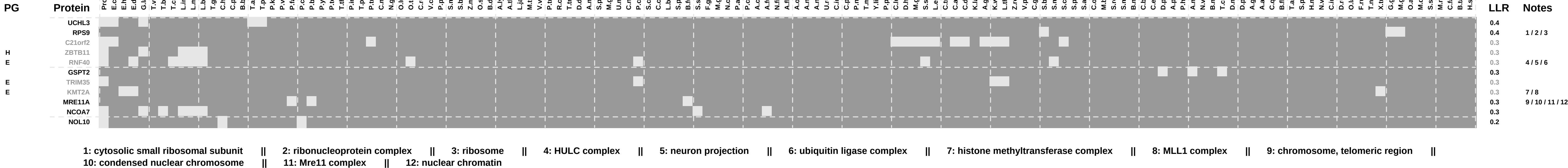
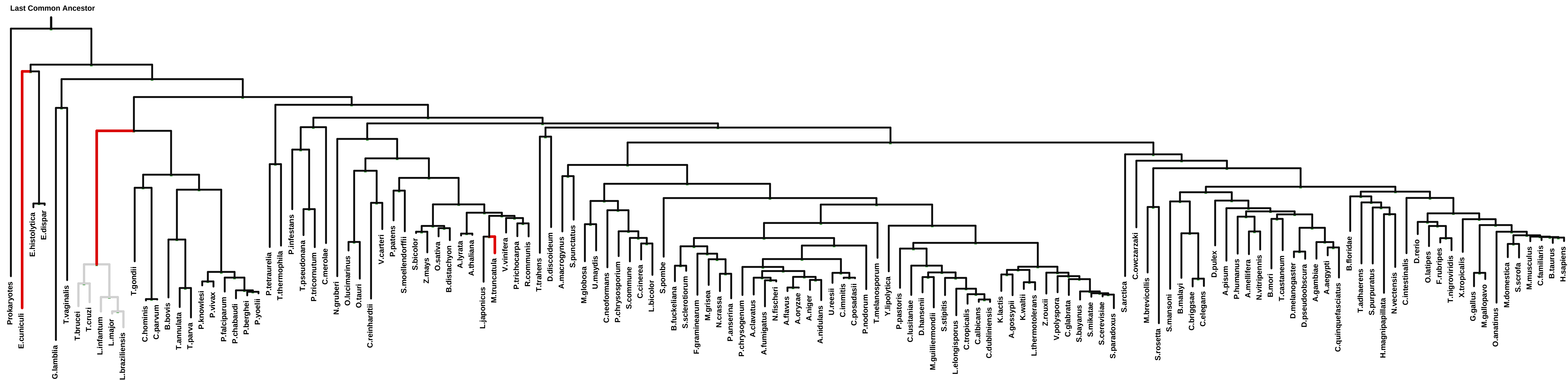
Num of ECM Genes: 1. Num of Predicted Genes: 500



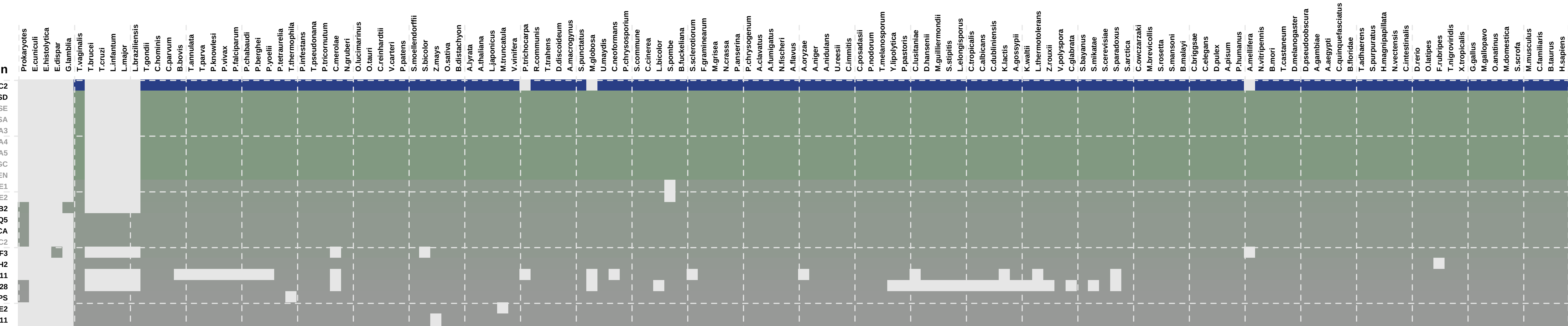
1: chromosome || 2: PML body || 3: XY body || 4: asymmetric synapse || 5: axonemal microtubule || 6: cytoplasmic membrane-bounded vesicle || 7: cytoplasmic vesicle || 8: dendritic spine || 9: microtubule organizing center || 10: recycling endosome || 11: symmetric synapse || 12: trans-Golgi network || 13: nuclear matrix || 14: small nuclear ribonucleoprotein complex || 15: lysosome || 16: cell body fiber || 17: myelin sheath || 18: ribonucleoprotein complex || 19: early endosome membrane || 20: recycling endosome membrane || 21: endocytic vesicle || 22: proteasome accessory complex || 23: proteasome complex || 24: autophagic vacuole membrane || 25: clathrin-coated vesicle || 26: endosome membrane ||

ECM 2, Gene set "origin recognition complex", Page 15

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

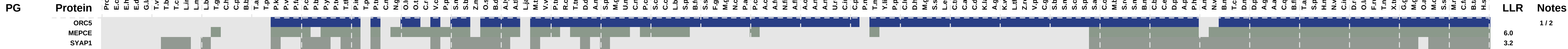


Num of ECM Genes: 1. Num of Predicted Genes: 21



1: condensed chromosome inner kinetochore || 2: heterochromatin || 3: nuclear origin of replication recognition complex || 4: origin recognition complex || 5: extracellular matrix || 6: lysosomal lumen || 7: lysosome || 8: melanosome || 9: endosome || 10: alveolar lamellar body || 11: cytoplasmic part || 12: cytoplasmic vesicle membrane || 13: trans-Golgi network || 14: chromosome || 15: mitochondrial respiratory chain complex III || 16: Cajal body || 17: nuclear speck || 18: spliceosomal complex || 19: epsilon DNA polymerase complex || 20: nuclear pore

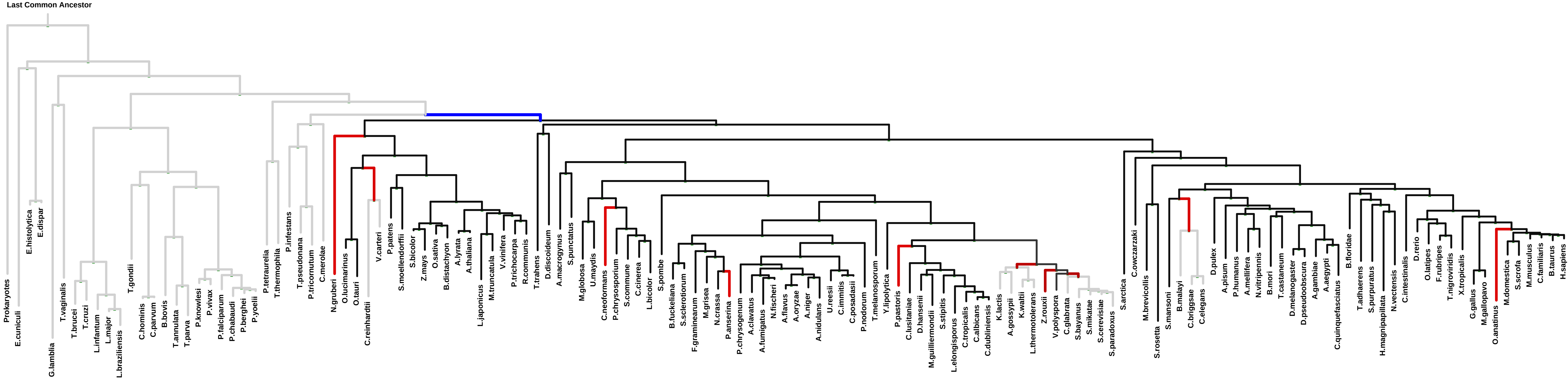
Num of ECM Genes: 1. Num of Predicted Genes: 2



1 / 2

ECM 5, Gene set "origin recognition complex", Page 1

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



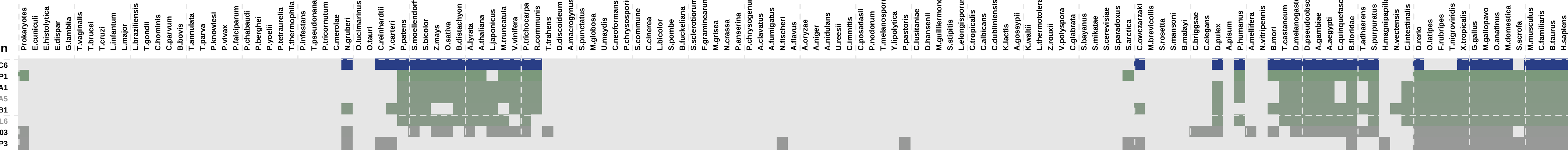
PG

Protein	ORC3
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. annulata	
T. parva	
P. knowlesi	
P. vivax	
P. falciparum	
P. chabaudi	
P. berghei	
P. yoelii	
P. tetraurelia	
T. thermophila	
P. infestans	
T. pseudonana	
P. tricornutum	
C. merolae	
N. gruberi	
O. lucimarinus	
O. tauri	
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. arctica	
Cowczarzaki	
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	

LLR Notes

1: nuclear origin of replication recognition complex || 2: origin recognition complex

Num of ECM Genes: 1. Num of Predicted Genes: 7



LLR	Not
	1 / 2
12.3	3
8.2	4
8.2	4
7.7	
7.2	4
1.2	
0.5	5 / 6