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:

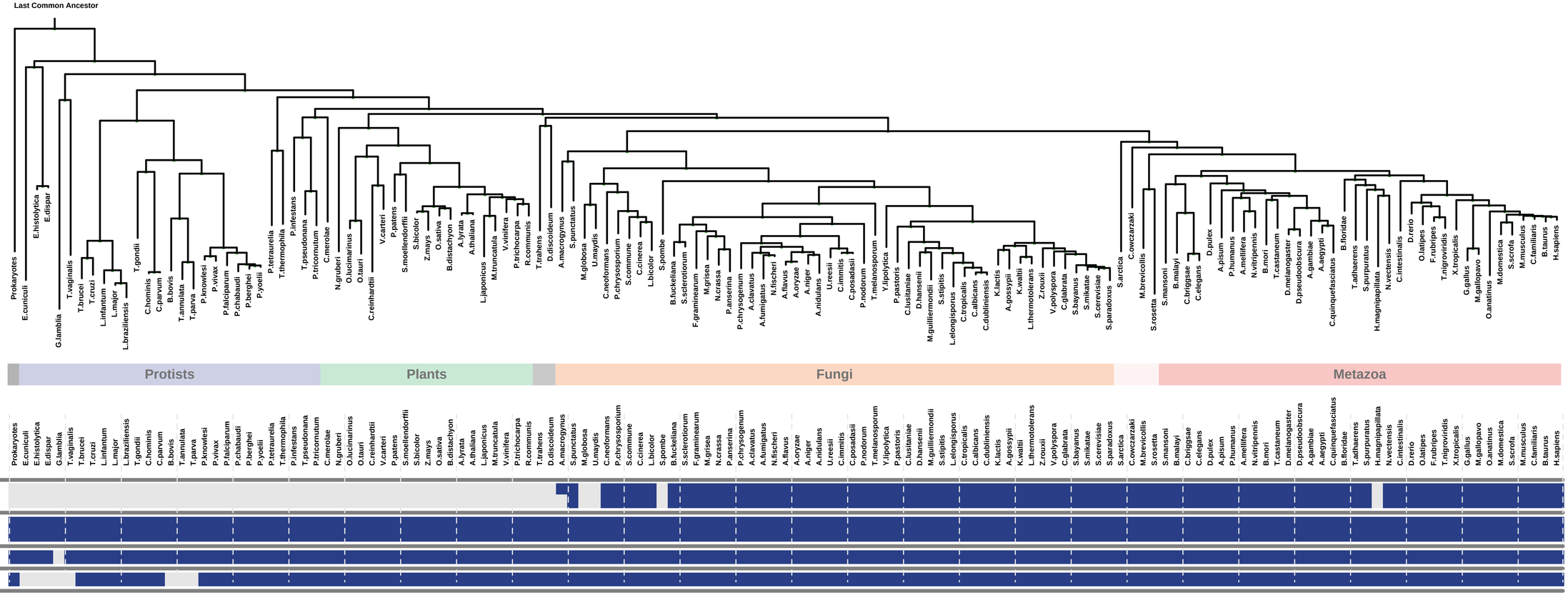
1) Overview of Evolutionarily Conserved Modules (ECMs)

- 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+

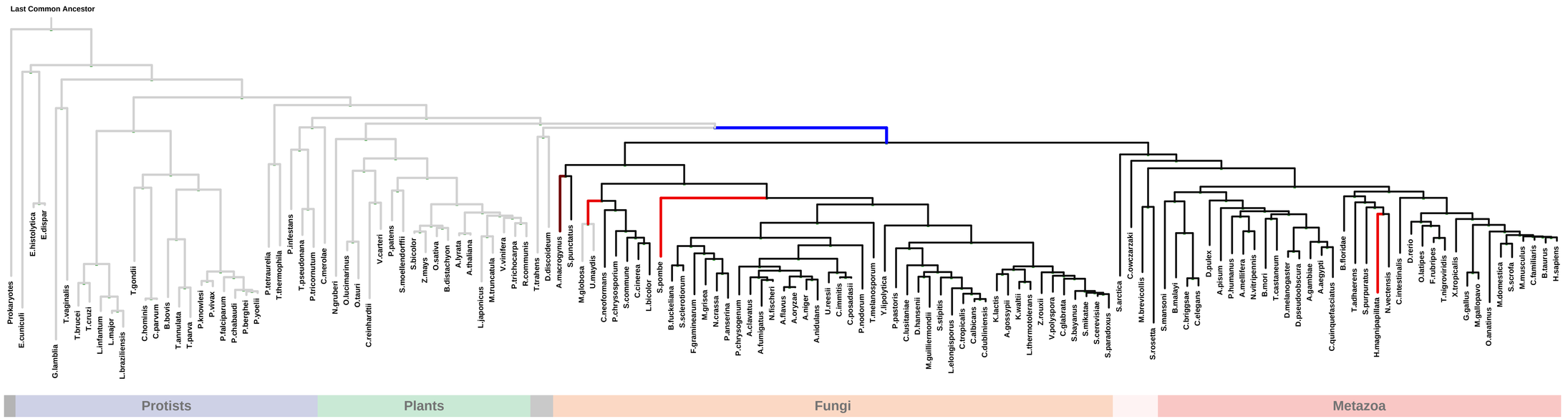
- Top panel shows the inferred evolutionary history on the predefined species tree. Branch color shows the gain event (blue) and loss events (red color, with brighter color indicating higher confidence in loss). Branches before the gain or after a loss are shown in gray.
- Bottom panel shows the input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

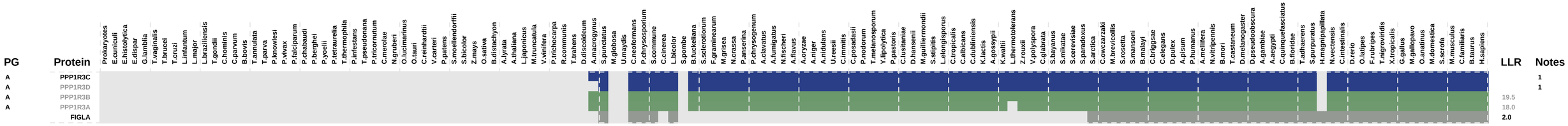
Overview of Evolutionarily Conserved Modules (ECMs)



ECM 1, Gene set "glycogen granule", Page 1

Num of ECM Genes: 2. Num of Predicted Genes: 3. ECM Strength: 2.0





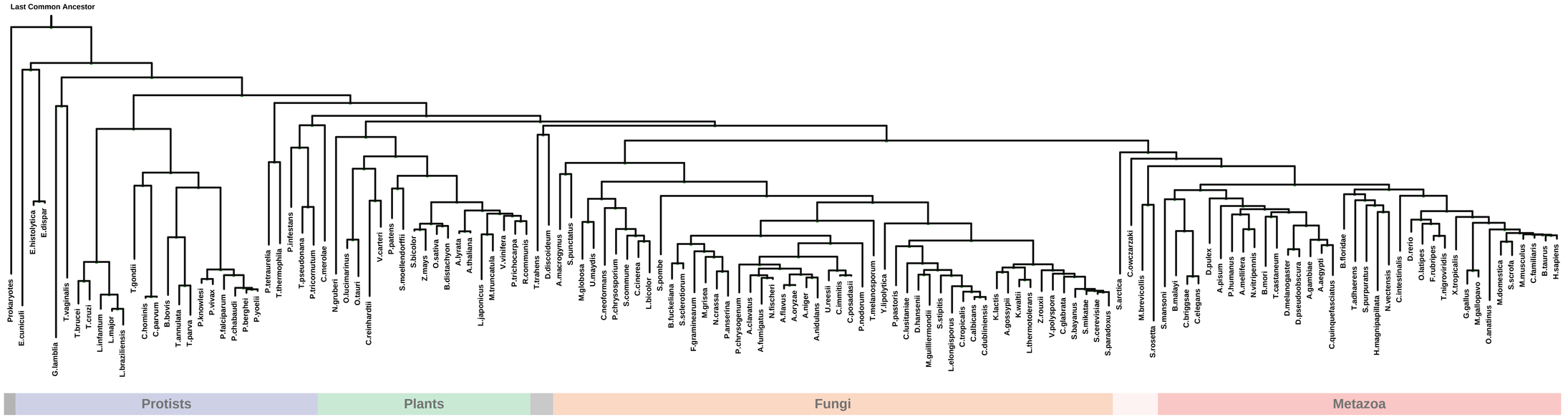
1: glycogen granule

ECM 2, Gene set "glycogen granule", Page 1

Num of ECM Genes: 2. Num of Predicted Genes: 0. ECM Strength: 0.0

PRESENCE
GAIN
ABSENCE
LOSS

Log-likelihood Ratio Scale
0 10 20 30 40 50 60

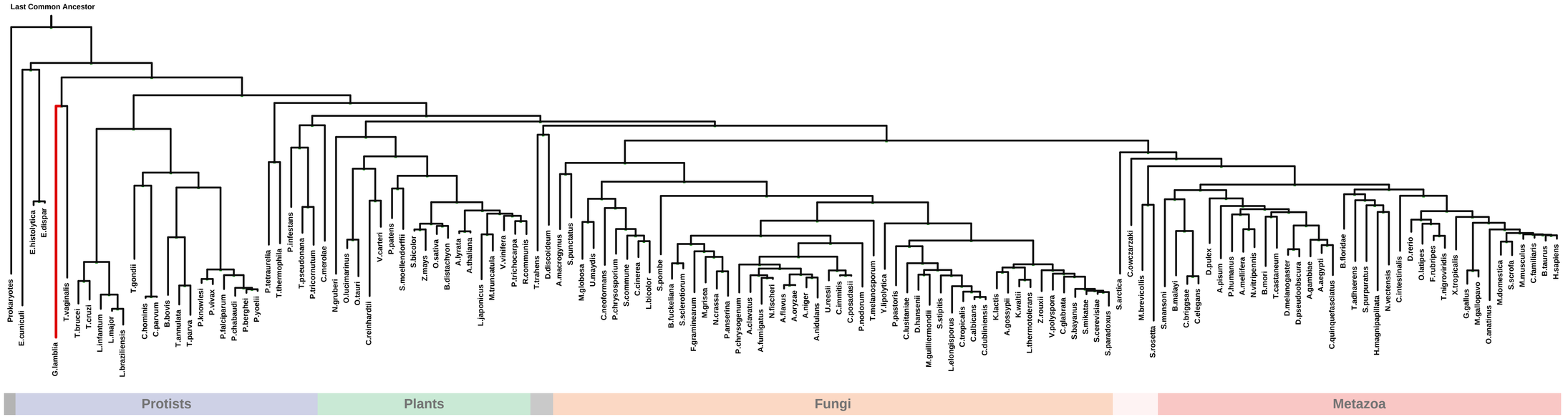


PG	Protein	LLR	Notes
A	PPP1CA		1 / 2 / 3 / 4 / 5 / 6
A	PPP1CB		2 / 3 / 5 / 6

1: dendritic spine || 2: glycogen granule || 3: MLL5-L complex || 4: perikaryon || 5: protein phosphatase type 1 complex || 6: PTW/PP1 phosphatase complex

ECM 3, Gene set "glycogen granule", Page 1

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

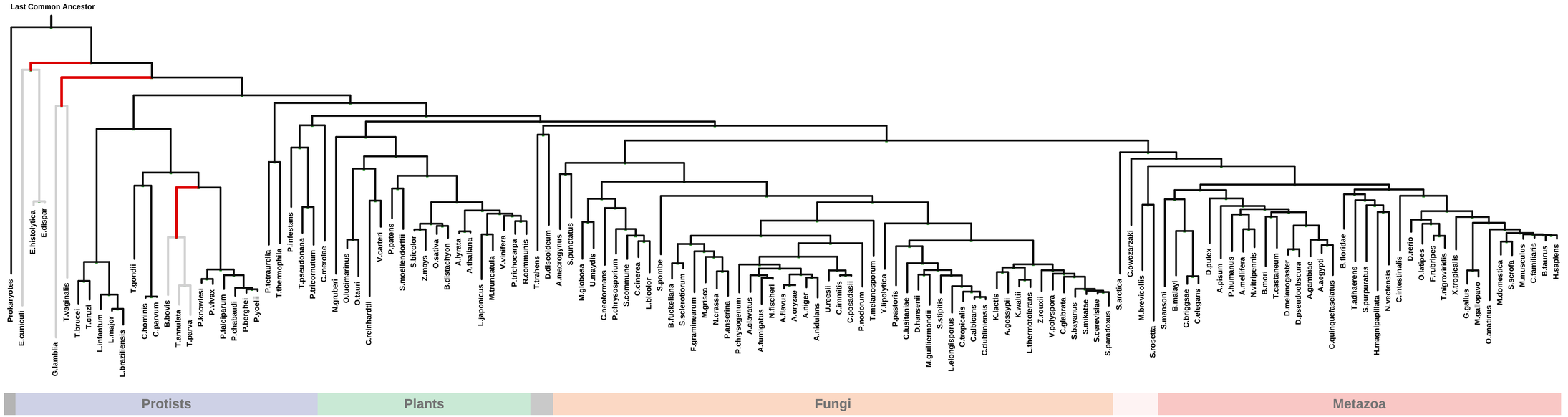


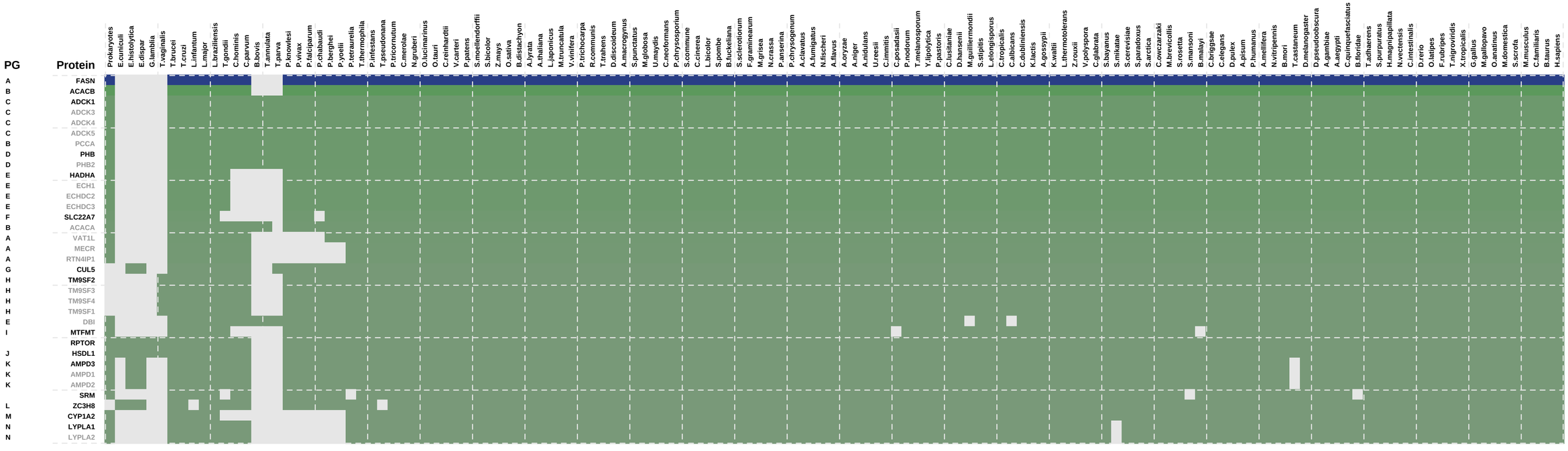
PG	Protein	LLR	Notes
	PCYT1A		1

1: glycogen granule

ECM 4, Gene set "glycogen granule", Page 1

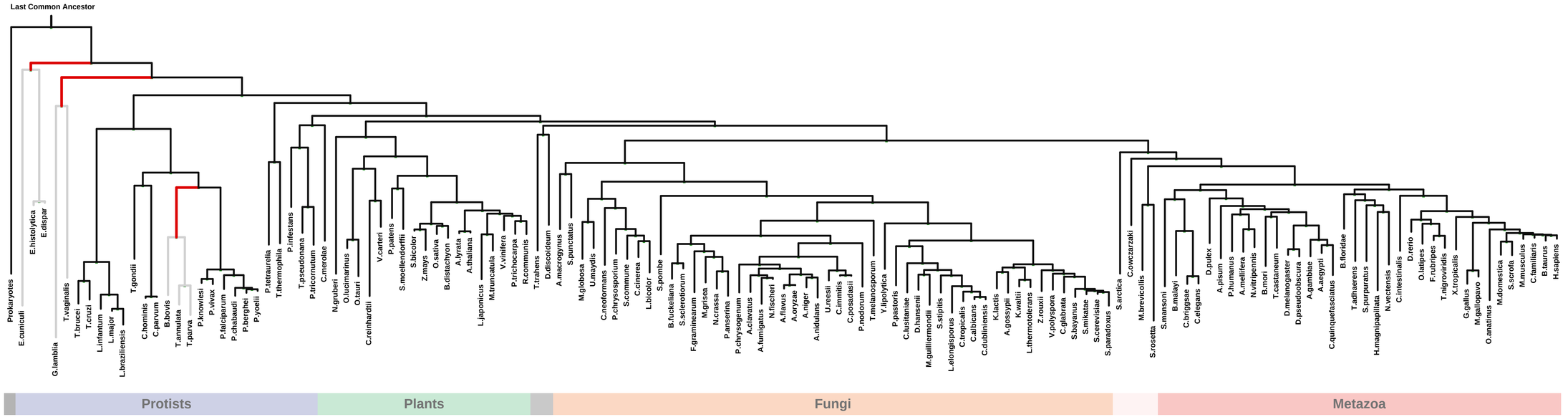
Num of ECM Genes: 1. Num of Predicted Genes: 500





ECM 4, Gene set "glycogen granule", Page 2

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

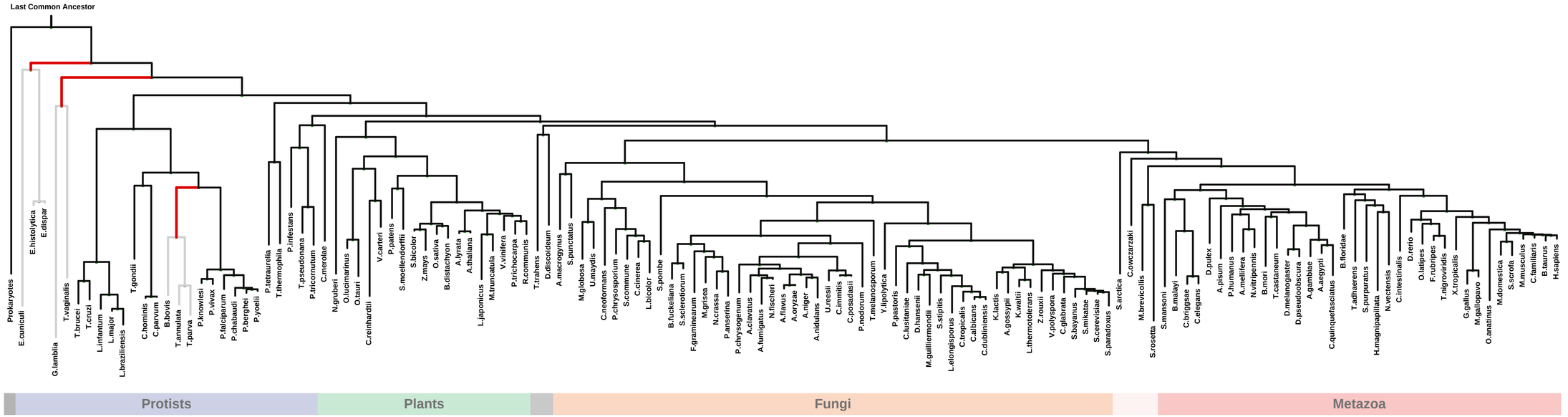


PG	Protein	LLR	Notes
N	LYPLAL1	13.8	
O	QRSL1	13.4	1
P	PINX1	13.1	2 / 3 / 4 / 5 / 6
Q	SLC25A53	13.0	
	TRMT2A	12.9	
R	GMPR	12.9	
R	GMPR2	12.9	
S	EWSR1	12.8	
T	FUBP3	12.8	
	METAP1D	12.7	
U	IBTK	12.7	
V	CNNM1	12.5	
V	CNNM2	12.5	7
V	CNNM3	12.5	
V	CNNM4	12.5	
A	VAT1	12.2	8
J	SDR16C5	11.9	
	COQ3	11.4	
W	PYCRL	11.4	
W	PYCR1	11.4	
W	PYCR2	11.4	
X	MTHFD1	11.2	
O	FAAH	11.1	9 / 10
Y	COX18	11.0	11
Z	C12orf65	10.9	
a	COX10	10.9	12
b	ADSSL1	10.9	
c	ACO1	10.9	
d	CYB5R2	10.9	
c	ACO2	10.9	
b	ADSS	10.9	
e	DBT	10.9	13 / 14 / 15
Z	MTRF1	10.9	
f	OGDH	10.9	12
f	DHTKD1	10.9	

1: glutamyl-tRNA(Gln) amidotransferase complex || 2: chromosome, telomeric region || 3: condensed chromosome kinetochore || 4: kinetochore || 5: nuclear chromosome || 6: spindle || 7: basolateral plasma membrane || 8: mitochondrial outer membrane ||
9: endomembrane system || 10: organelle membrane || 11: integral to mitochondrial inner membrane || 12: mitochondrial membrane || 13: microtubule cytoskeleton || 14: mitochondrial alpha-ketoglutarate dehydrogenase complex || 15: mitochondrial nucleoid

ECM 4, Gene set "glycogen granule", Page 3

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

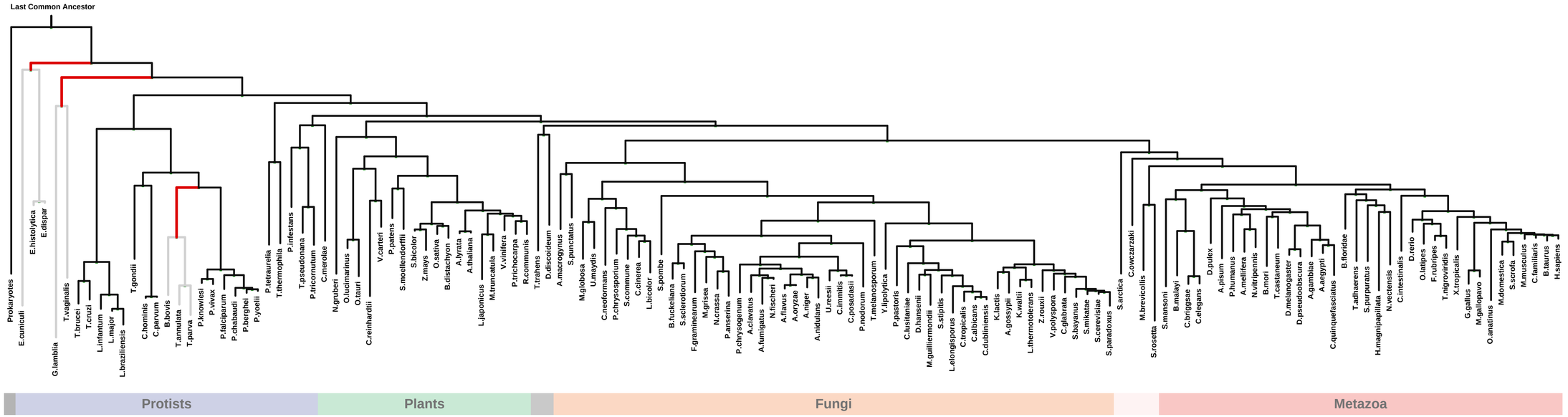


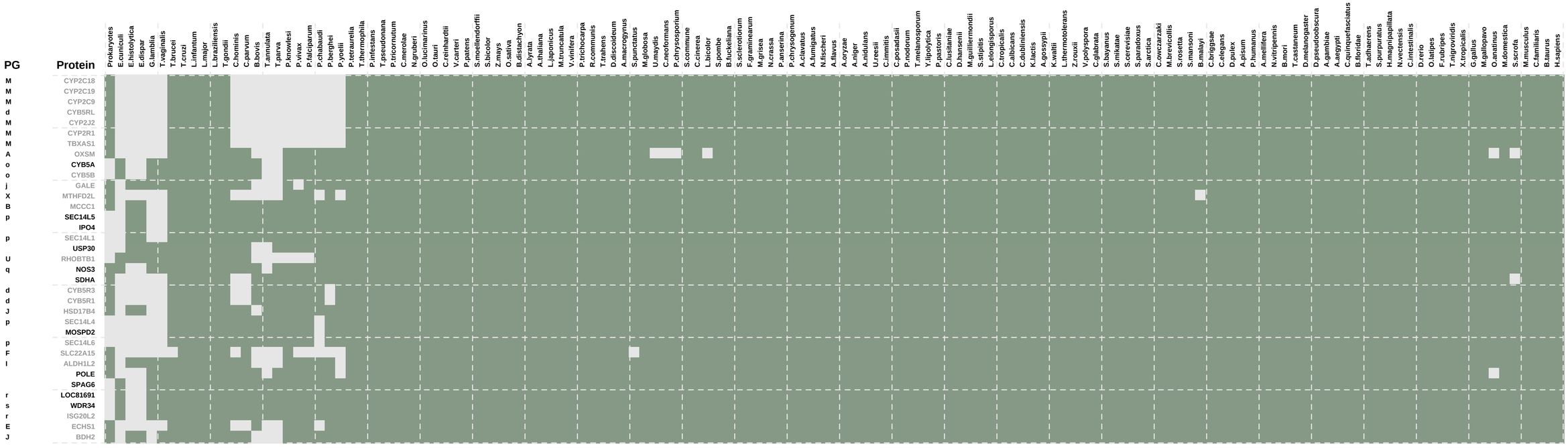
PG	Protein	LLR	Notes
e	PDHX	10.9	
e	DLAT	10.9	
e	DLST	10.9	1
g	IDH2	10.9	
c	IREB2	10.9	
	PGM3	10.8	
E	ACBD7	10.6	
	GLUL	10.5	
	COQ5	10.5	
h	PMPCA	10.5	
h	UQCRC2	10.5	2
C	ADCK2	10.3	
i	EIF2B4	10.3	3
i	EIF2B1	10.3	3 / 4
j	TGDS	10.3	
i	EIF2B2	10.3	3
	PIGB	10.2	5
R	IMPDH1	9.9	
R	IMPDH2	9.9	6
k	GLRX	9.8	
l	TMED10	9.7	7 / 8 / 9 / 10 / 11 / 12 / 13
M	CYP20A1	9.7	
M	CYP2E1	9.7	5
M	CYP39A1	9.7	
m	LDHD	9.7	
M	CYP7A1	9.7	
M	CYP7B1	9.7	
M	PTGIS	9.7	17
m	D2HGDH	9.7	
m	AGPS	9.7	6 / 18 / 19
n	PLCL2	9.6	
M	CYP2W1	9.6	
M	CYP1A1	9.6	
M	CYP2A13	9.6	
M	CYP2A7	9.6	

1: oxoglutarate dehydrogenase complex || 2: mitochondrial respiratory chain complex III || 3: eukaryotic translation initiation factor 2B complex || 4: eukaryotic translation initiation factor 2 complex || 5: intrinsic to endoplasmic reticulum membrane || 6: peroxisomal membrane || 7: cis-Golgi network || 8: COPI-coated vesicle || 9: endoplasmic reticulum-Golgi intermediate compartment || 10: endoplasmic reticulum-Golgi intermediate compartment membrane || 11: gamma-secretase complex || 12: melanosome || 13: secretory granule membrane || 14: trans-Golgi network transport vesicle || 15: transport vesicle membrane || 16: zymogen granule membrane || 17: caveola || 18: peroxisomal matrix || 19: peroxisome

ECM 4, Gene set "glycogen granule", Page 4

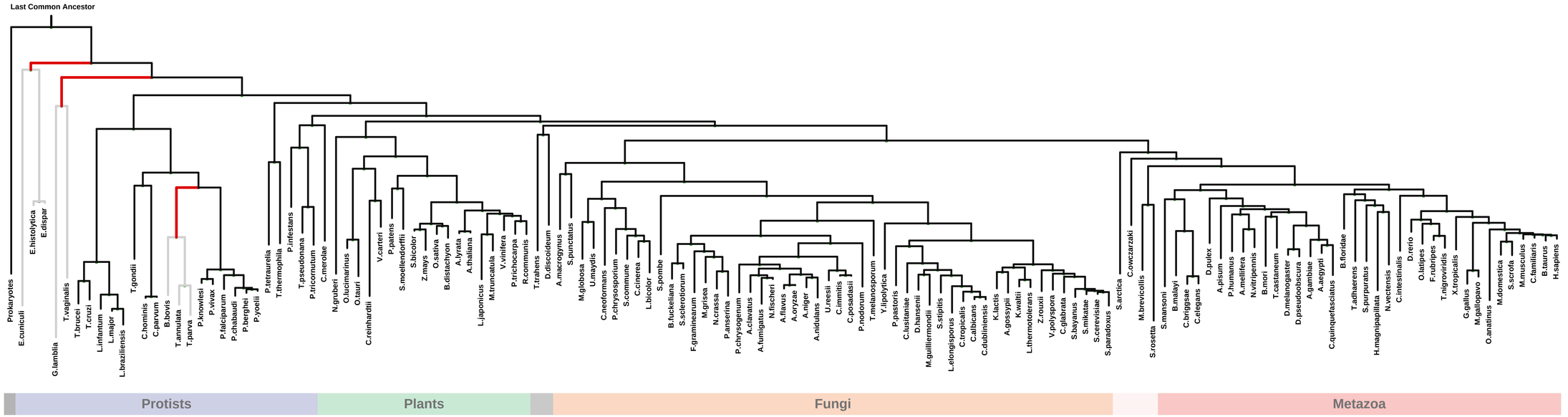
Num of ECM Genes: 1. Num of Predicted Genes: 500

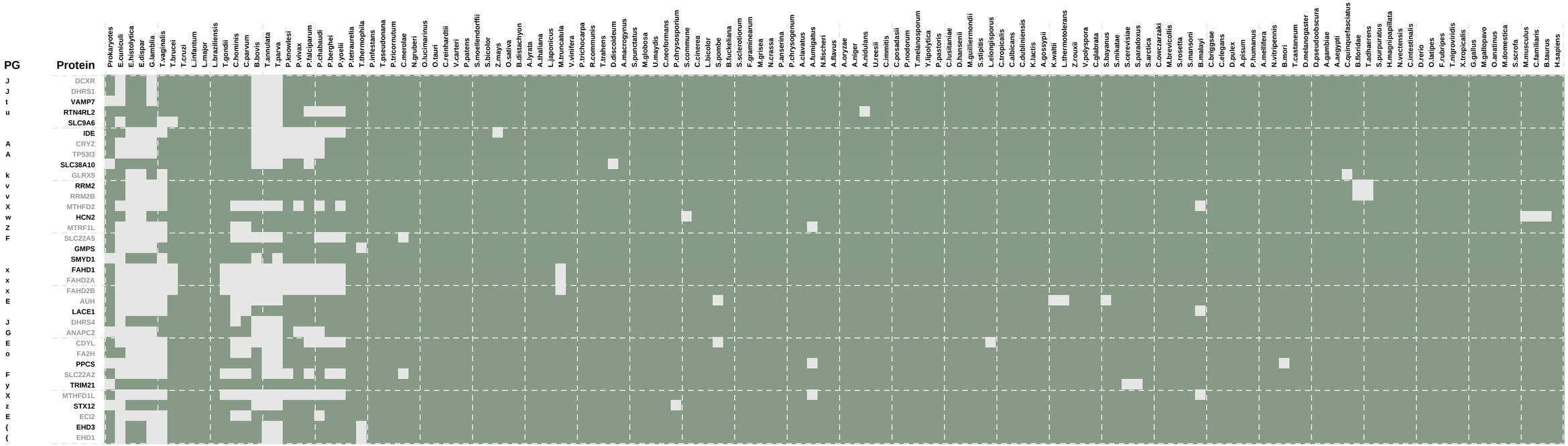




ECM 4, Gene set "glycogen granule", Page 5

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

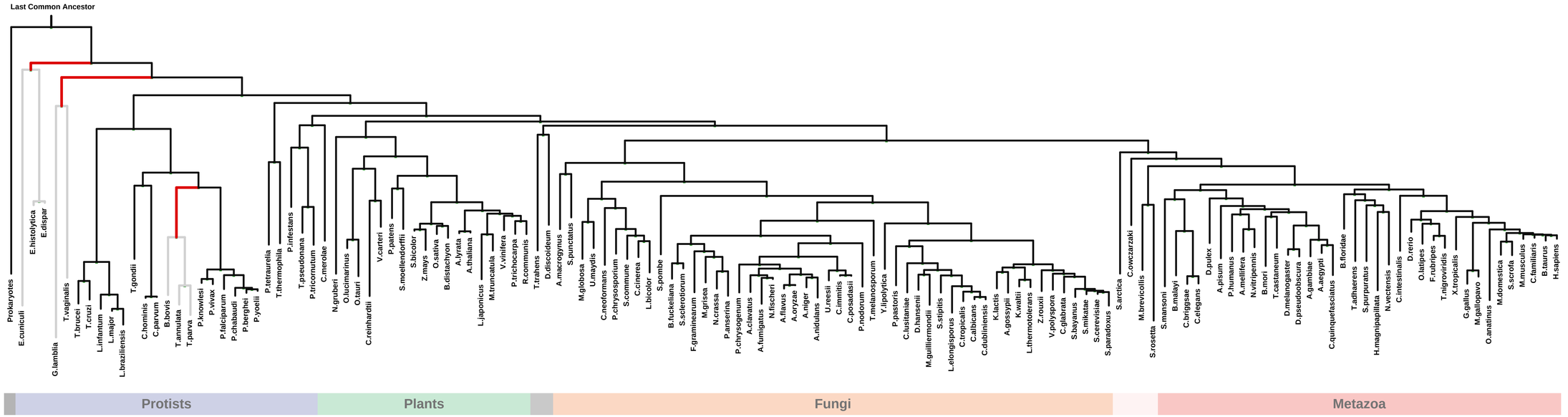


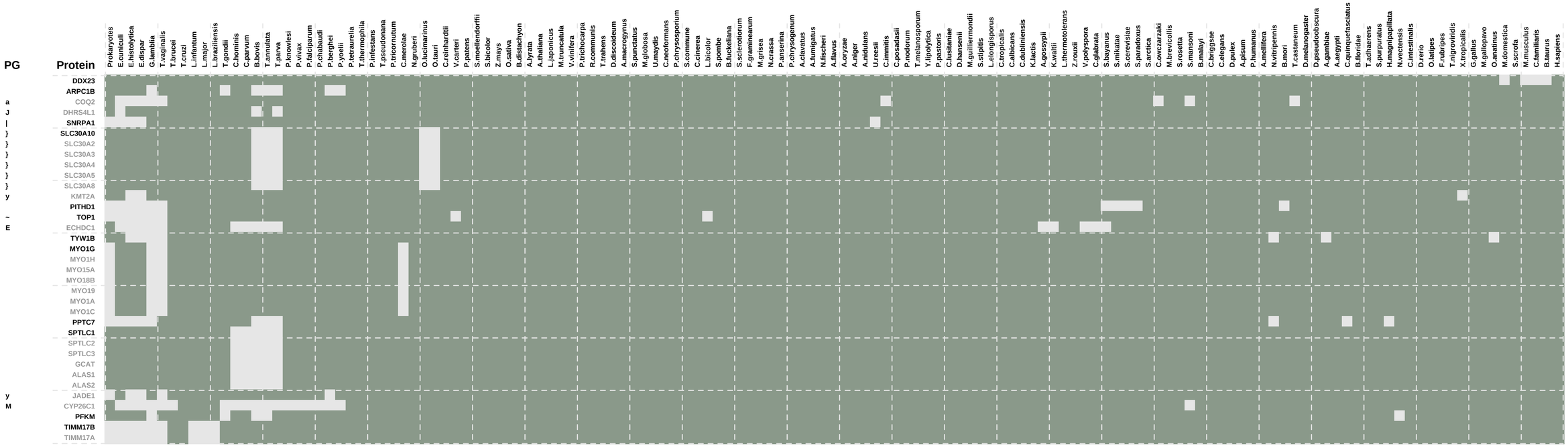


1: brush border || 2: microvillus || 3: apical part of cell || 4: late endosome membrane || 5: lysosomal membrane || 6: neuron projection || 7: phagocytic vesicle || 8: phagocytic vesicle membrane || 9: SNARE complex ||
10: synapse || 11: transport vesicle membrane || 12: anchored to plasma membrane || 13: external side of plasma membrane || 14: membrane raft || 15: early endosome membrane || 16: recycling endosome membrane || 17: cytosolic proteasome complex ||
18: peroxisomal matrix || 19: peroxisome || 20: ribonucleoside-diphosphate reductase complex || 21: axon || 22: dendritic shaft || 23: voltage-gated potassium channel complex || 24: basolateral plasma membrane || 25: brush border membrane ||

ECM 4, Gene set "glycogen granule", Page 6

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

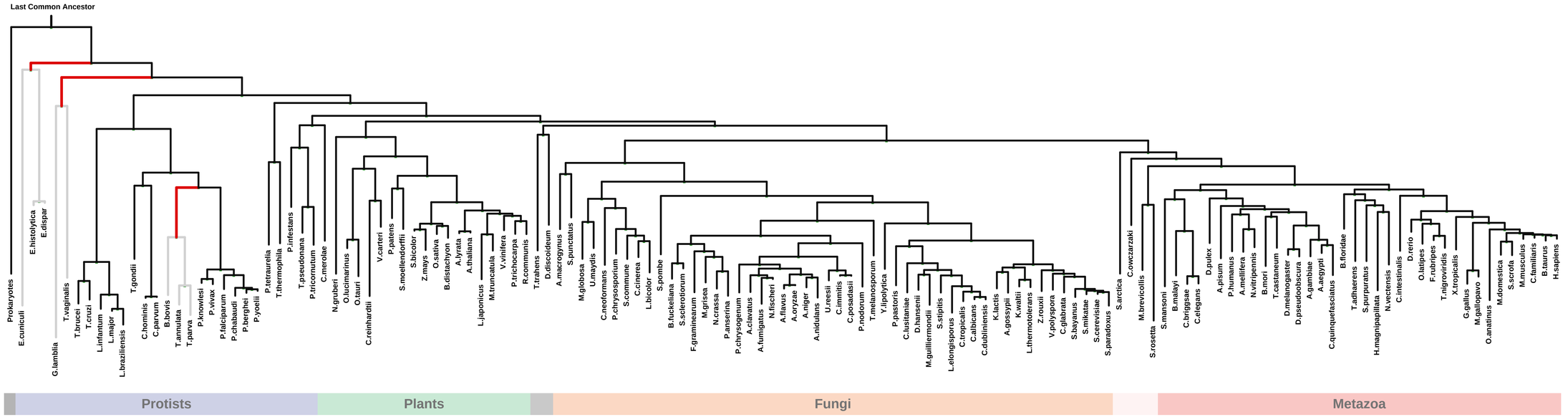




1: catalytic step 2 spliceosome || 2: U5 snRNP || 3: actin cytoskeleton || 4: Arp2/3 protein complex || 5: mitochondrial membrane || 6: small nuclear ribonucleoprotein complex || 7: spliceosomal complex || 8: U2 snRNP || 9: cytoplasmic membrane-bounded vesicle ||
10: cytoplasmic part || 11: endosome membrane || 12: late endosome || 13: lysosomal membrane || 14: endosome || 15: neuron projection || 16: synaptic vesicle || 17: synaptic vesicle membrane || 18: secretory granule ||
19: secretory granule membrane || 20: transport vesicle membrane || 21: histone methyltransferase complex || 22: MLL1 complex || 23: cytoplasmic mRNA processing body || 24: nuclear chromosome || 25: perikaryon || 26: replication fork protection complex ||

ECM 4, Gene set "glycogen granule", Page 7

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

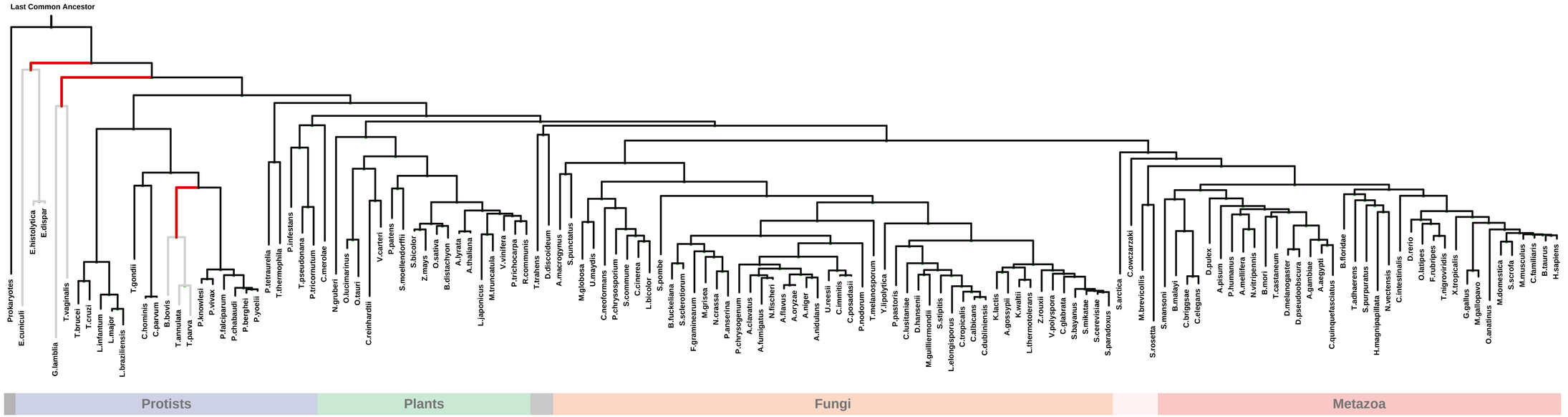


PG	Protein	LLR	Notes
{	EHD2	6.3	1 / 2
	IMMP1L	6.3	
F	SLC22A8	6.3	3
M	CYP8B1	6.3	
	CIB4	6.2	
f	PDHA2	6.2	
	PDHB	6.2	4
	BCKDHB	6.2	5
f	BCKDHA	6.2	5
f	PDHA1	6.2	
	MSMO1	6.2	
	SC5D	6.2	
	SNX30	6.1	
	SLC36A1	6.1	6
n	PLCH2	6.0	
A	ZADH2	5.9	7
	SNX7	5.9	8
	PDXP	5.9	9 / 10 / 11 / 12 / 13 / 14 / 1
	PGP	5.9	
y	KMT2D	5.9	16
F	SLC22A13	5.9	
O	FAAH2	5.9	
F	SV2C	5.9	17
	DOHH	5.8	
	TYMS	5.8	
	NME5	5.8	
n	PLCH1	5.8	18
l	DNAL1	5.7	
	UPRT	5.6	
F	SLC22A16	5.6	
w	HCN1	5.6	19 / 20
	EMC3	5.5	21
	YEATS2	5.4	22
	EIF4G2	5.4	23
y	RFPL4B	5.4	

1: endosome membrane || 2: recycling endosome membrane || 3: basolateral plasma membrane || 4: pyruvate dehydrogenase complex || 5: mitochondrial alpha-ketoglutarate dehydrogenase complex || 6: lysosomal membrane || 7: peroxisome ||
8: cytoplasmic vesicle membrane || 9: actin cytoskeleton || 10: cleavage furrow || 11: contractile ring || 12: lamellipodium || 13: lamellipodium membrane || 14: midbody || 15: ruffle membrane || 16: histone methyltransferase complex ||
17: synaptic vesicle membrane || 18: nuclear membrane || 19: axon || 20: dendrite || 21: ER membrane protein complex || 22: Ada2/Gcn5/Ada3 transcription activator complex || 23: eukaryotic translation initiation factor 4F complex

ECM 4, Gene set "glycogen granule", Page 8

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

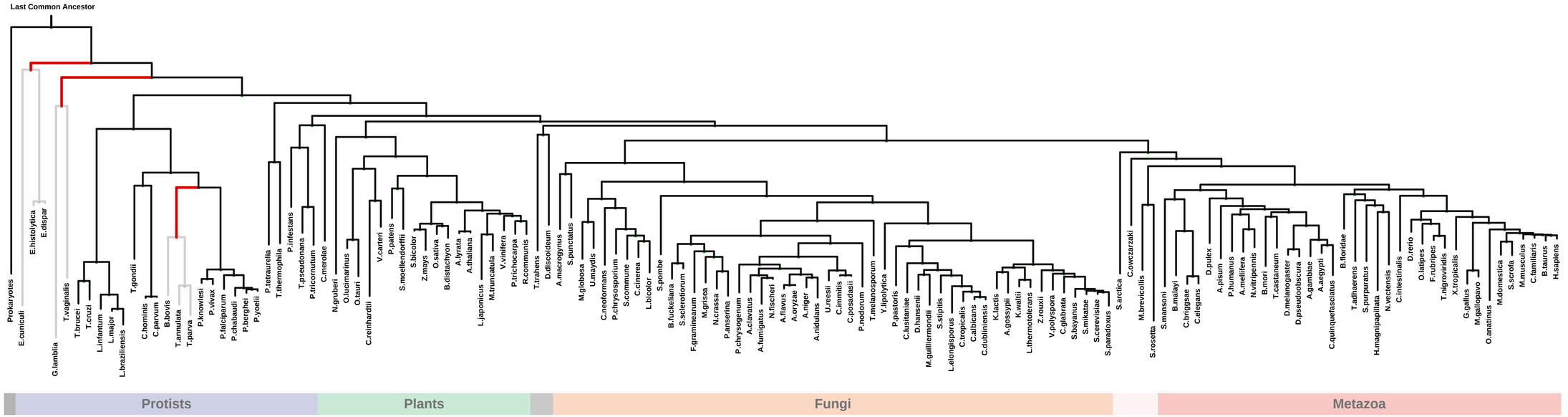


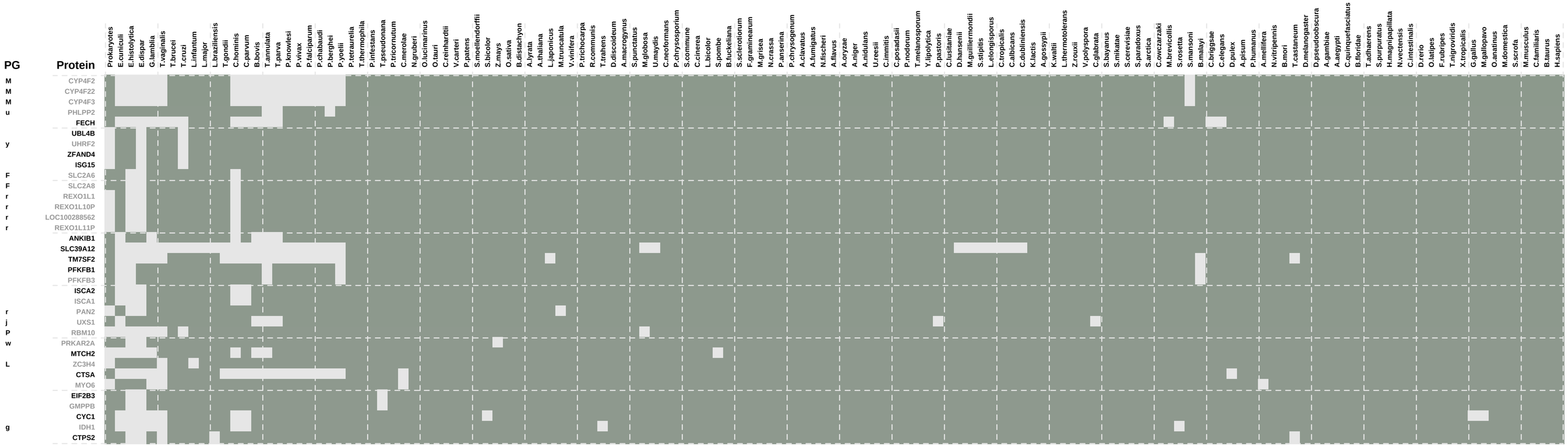
PG	Protein	LLR	Notes
M	CYP4F8	5.4	
M	CYP4V2	5.4	
M	CYP4X1	5.4	
M	CYP4Z1	5.4	
M	CYP51A1	5.4	
M	CYP27A1	5.4	
M	CYP27B1	5.4	1
M	CYP27C1	5.4	
M	CYP19A1	5.4	2 / 3 / 4
M	CYP2A6	5.4	
M	CYP11A1	5.4	5 / 6
M	CYP2B6	5.4	
M	CYP11B1	5.4	
M	CYP11B2	5.4	
M	CYP2C8	5.4	
	CYP21A1P	**5.4**	
M	CYP2D6	5.4	
M	CYP21A2	5.4	
M	CYP2F1	5.4	
M	CYP24A1	5.4	
M	CYP26A1	5.4	
M	CYP2S1	5.4	
M	CYP2U1	5.4	
M	CYP26B1	5.4	
M	CYP17A1	5.4	7
M	CYP3A4	5.4	
M	CYP3A43	5.4	
M	CYP3A5	5.4	
M	CYP3A7	5.4	
M	CYP46A1	5.4	
M	CYP4A11	5.4	
M	CYP4A22	5.4	
M	CYP4B1	5.4	
M	CYP4F11	5.4	
M	CYP4F12	5.4	

1: mitochondrial outer membrane || 2: dendritic spine || 3: synaptic vesicle || 4: terminal button || 5: mitochondrial crista || 6: perikaryon || 7: axon

ECM 4, Gene set "glycogen granule", Page 9

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

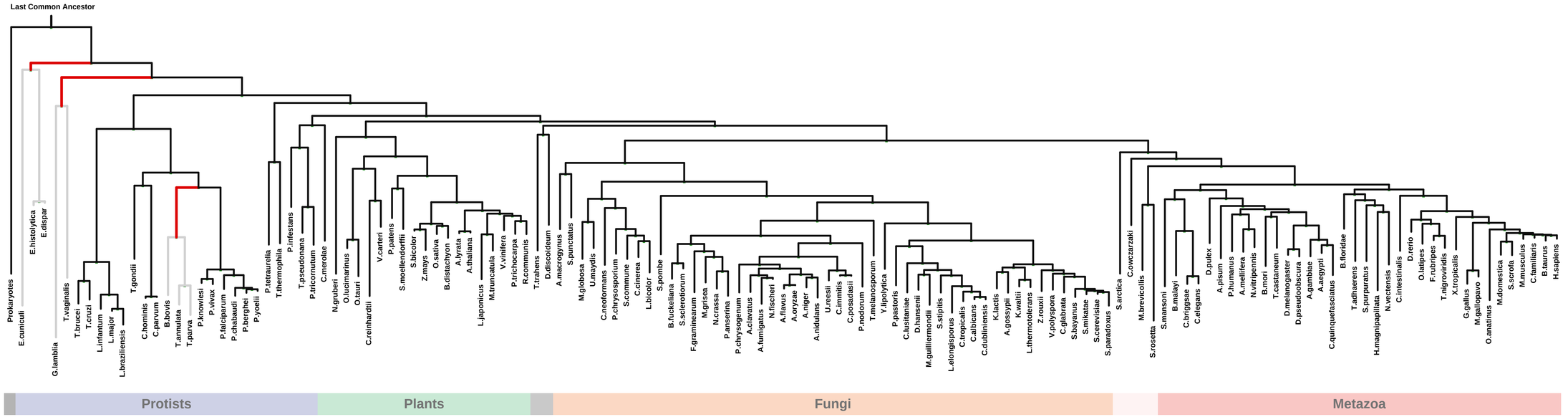


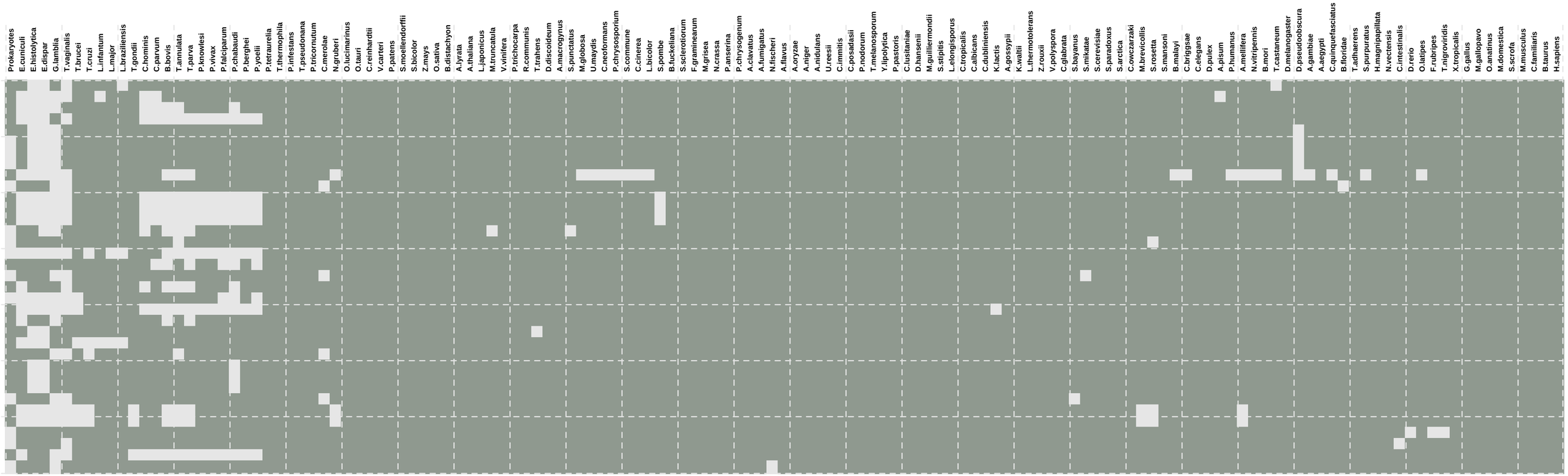


1: nuclear heterochromatin || 2: cytoplasmic vesicle membrane || 3: synaptic vesicle || 4: Golgi cisterna membrane || 5: chromatin remodeling complex || 6: cAMP-dependent protein kinase complex || 7: T-tubule || 8: lysosomal lumen ||
9: lysosome || 10: apical part of cell || 11: axon || 12: cell cortex || 13: clathrin-coated endocytic vesicle || 14: clathrin-coated vesicle membrane || 15: coated pit || 16: cytoplasmic membrane-bounded vesicle || 17: DNA-directed RNA polymerase II, holoenzyme ||
18: endocytic vesicle || 19: filamentous actin || 20: microvillus || 21: nuclear membrane || 22: ruffle || 23: ruffle membrane || 24: unconventional myosin complex || 25: eukaryotic translation initiation factor 2B complex || 26: respiratory chain ||

ECM 4, Gene set "glycogen granule", Page 10

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

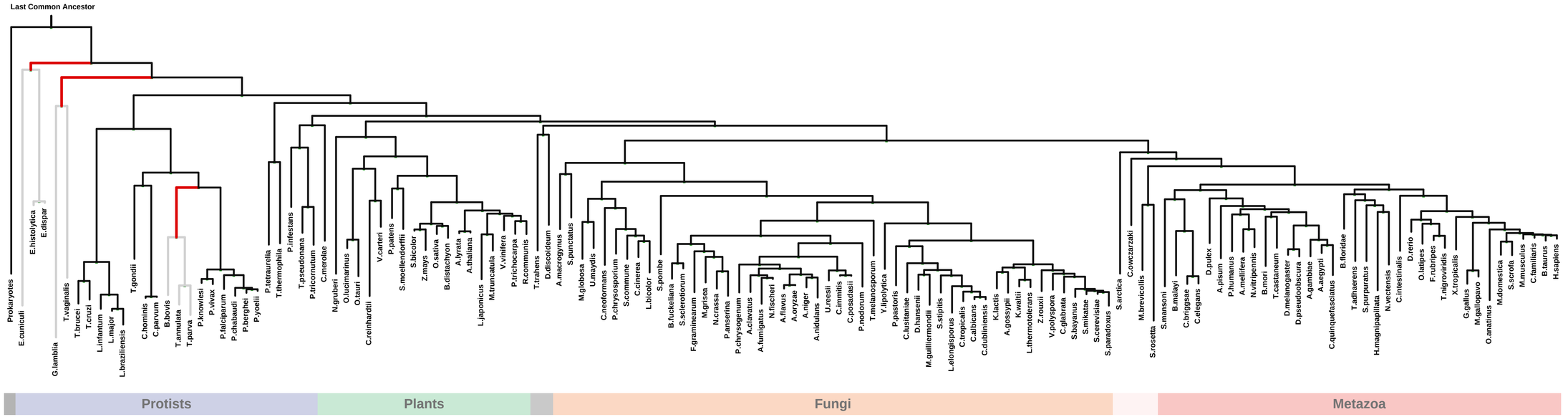




1: mitochondrial respiratory chain complex III || 2: AMP-activated protein kinase complex || 3: axolemma || 4: myosin complex || 5: smooth endoplasmic reticulum || 6: dendrite || 7: anaphase-promoting complex || 8: proteinaceous extracellular matrix || 9: cytoplasmic vesicle membrane || 10: dendritic spine || 11: synaptic vesicle || 12: synaptic vesicle membrane || 13: clathrin-coated vesicle || 14: early endosome membrane || 15: endosome || 16: trans-Golgi network || 17: nuclear envelope || 18: chromosome || 19: cytoskeletal part || 20: photoreceptor inner segment || 21: sarcolemma || 22: sarcoplasmic reticulum || 23: peroxisomal matrix || 24: peroxisome || 25: transcription factor TFIID complex || 26: actomyosin ||

ECM 4, Gene set "glycogen granule", Page 11

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

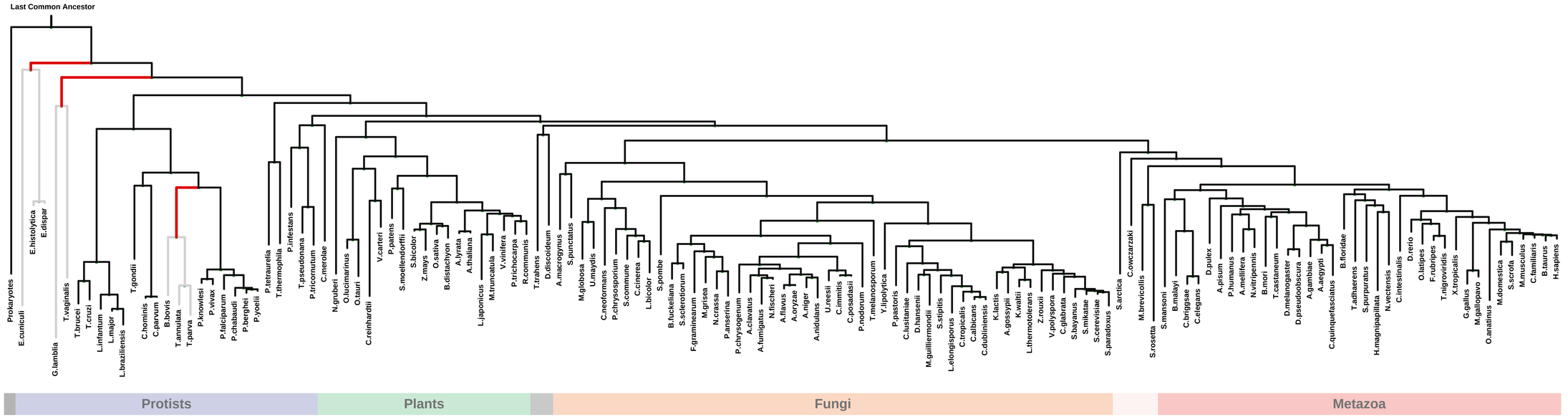


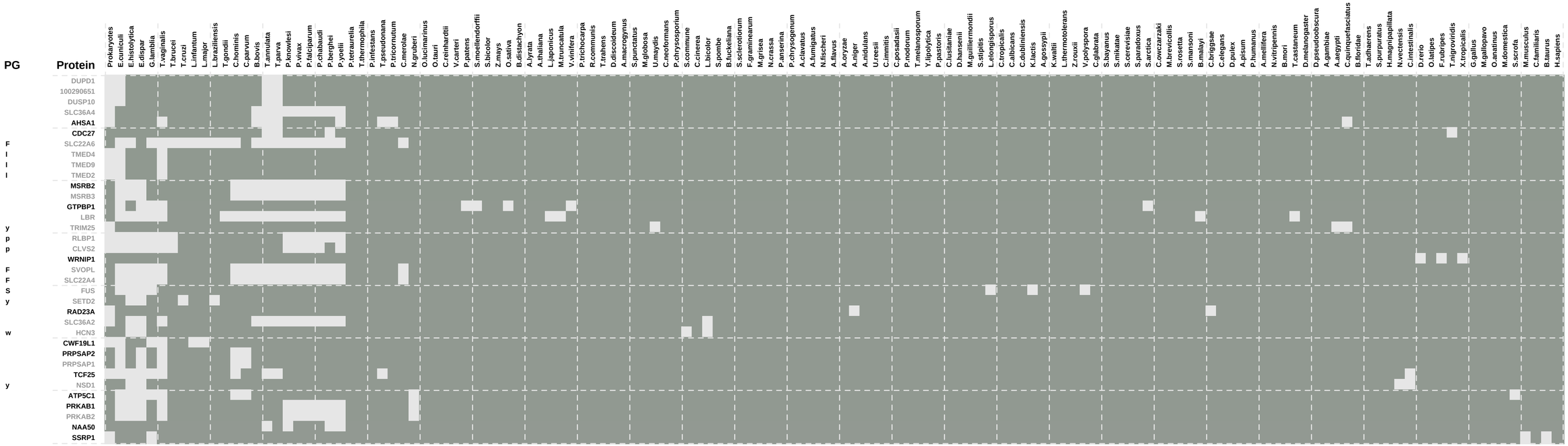
PG	Protein	LLR	Notes
s	DNAI2	4.0	1 / 2
	POLE2	**4.0**	3
	NOX5	**4.0**	
	BOLA1	**4.0**	
B	CPS1	4.0	4
F	SLC2A12	4.0	5
	IPO11	**4.0**	6
u	LRRC8C	3.9	
u	LRRTM2	3.9	7
u	SHOC2	3.9	8
u	LRRTM4	3.9	7
	DUSP14	**3.9**	
	DUSP16	3.9	9
	DUSP2	3.9	
	DUSP22	**3.9**	
	DUSP26	3.9	
	STT3A	**3.9**	10
	STT3B	3.9	10
	DUSP4	3.9	
	DUSP5	3.9	
	DUSP6	3.9	
	DUSP7	3.9	
	DUSP8	3.9	
	DUSP9	3.9	
J	CBR4	3.9	
	DUSP1	3.9	
	SSH1	3.9	11 / 12 / 13
	SSH2	3.9	
	SSH3	3.9	
	DUSP28	3.9	
	DUSP18	3.9	
	DUSP19	3.9	
	STYX	3.9	
	DUSP13	3.9	
	GNA13	**3.9**	14 / 15 / 16 / 17

1: axonemal dynein complex || 2: cilium axoneme || 3: epsilon DNA polymerase complex || 4: mitochondrial nucleoid || 5: endomembrane system || 6: nuclear pore || 7: postsynaptic membrane || 8: protein phosphatase type 1 complex || 9: cytoplasmic membrane-bounded vesicle || 10: oligosaccharyltransferase complex || 11: cleavage furrow || 12: lamellipodium || 13: midbody || 14: brush border membrane || 15: extrinsic to internal side of plasma membrane || 16: heterotrimeric G-protein complex || 17: melanosome

ECM 4, Gene set "glycogen granule", Page 12

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

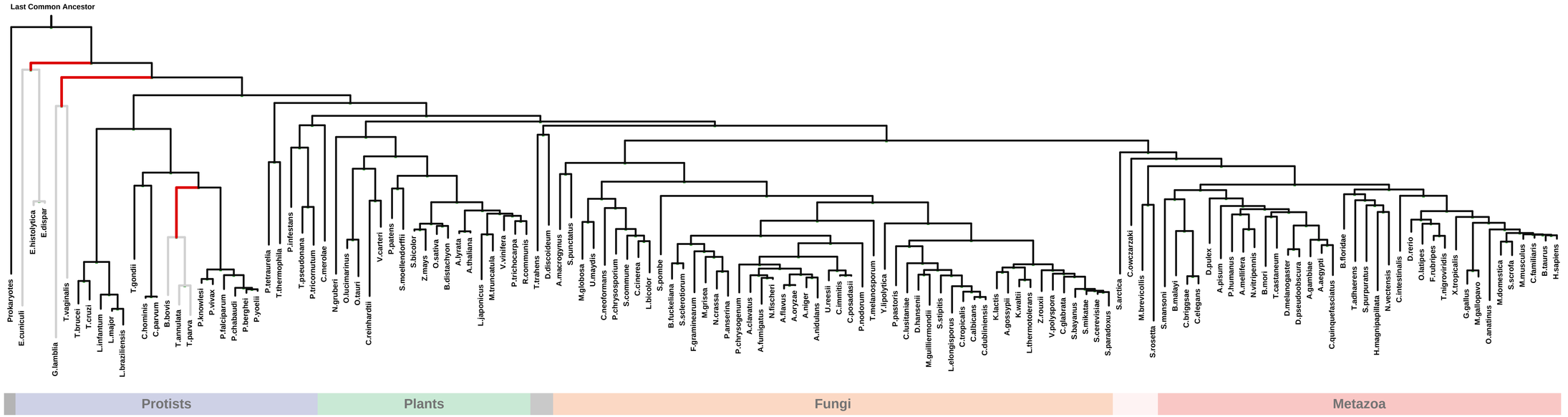




1: anaphase-promoting complex || 2: spindle || 3: spindle microtubule || 4: basolateral plasma membrane || 5: caveola || 6: endoplasmic reticulum-Golgi intermediate compartment || 7: endoplasmic reticulum-Golgi intermediate compartment membrane ||
8: trans-Golgi network transport vesicle || 9: COPI-coated vesicle || 10: COPI-coated vesicle membrane || 11: Golgi cisterna membrane || 12: zymogen granule membrane || 13: cytoplasmic exosome (RNase complex) || 14: integral to nuclear inner membrane ||
15: nuclear envelope || 16: nuclear membrane || 17: nuclear pore || 18: clathrin-coated vesicle || 19: early endosome membrane || 20: endosome || 21: trans-Golgi network || 22: chromosome || 23: proteasome complex ||

ECM 4, Gene set "glycogen granule", Page 13

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

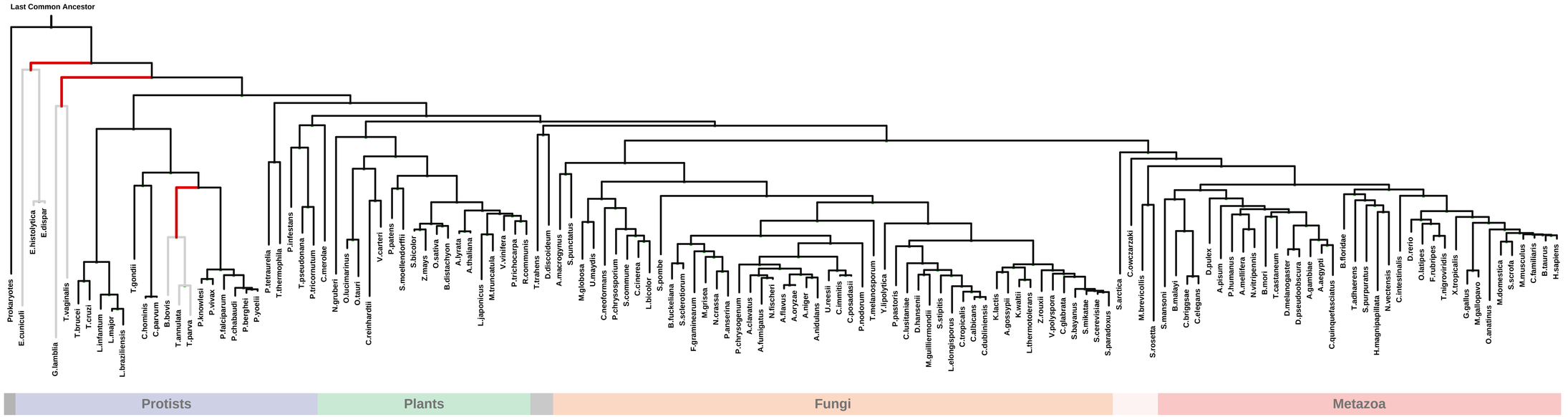


PG	Protein	LLR	Notes
	RABEPK	3.2	1 / 2
	RSL24D1P11	3.2	
Q	SLC25A25	3.0	
p	SEC14L3	3.0	
	PGRMC1	3.0	
	PGRMC2	3.0	
F	SV2A	3.0	3 / 4 / 5 / 6
	ASCC3	3.0	
	DMGDH	3.0	
B	PCCB	3.0	
	CDKL2	3.0	
}	SLC30A7	3.0	7 / 8 / 9
}	SLC30A1	3.0	10
	YEATS4	2.9	11 / 12
F	SLC22A10	2.9	
y	JADE3	2.9	13
	TBC1D9	2.9	
E	HIBCH	2.8	
	PRPF8	2.8	14 / 15 / 16
	CHD1	2.8	
	IFT88	2.8	17 / 18 / 19 / 20 / 21 / 22 /
	PFKL	2.8	26
	CERS2	2.8	27
	ABHD4	2.8	
	ZBTB8B	2.7	
	SUCLG2	2.7	
	SUCLA2	2.7	
Y	OXA1L	2.7	28 / 29 / 30
	JMJD4	2.7	
y	RNF135	2.7	
	XRN1	2.7	31
	ADH6	2.7	
J	HSD11B1L	2.6	
	SDHB	2.6	32
y	TAF3	2.6	33

1: endosome || 2: endosome membrane || 3: cell-cell junction || 4: neuromuscular junction || 5: presynaptic active zone || 6: synaptic vesicle membrane || 7: cytoplasmic membrane-bounded vesicle || 8: cytoplasmic part ||
9: vesicle || 10: T-tubule || 11: NuA4 histone acetyltransferase complex || 12: nuclear matrix || 13: histone acetyltransferase complex || 14: catalytic step 2 spliceosome || 15: nuclear speck || 16: U5 snRNP || 17: apical part of cell ||
18: centriole || 19: cilium || 20: cilium axoneme || 21: intraflagellar transport particle B || 22: microtubule basal body || 23: microtubule-based flagellum || 24: motile primary cilium || 25: photoreceptor connecting cilium || 26: 6-phosphofructokinase complex ||

ECM 4, Gene set "glycogen granule", Page 14

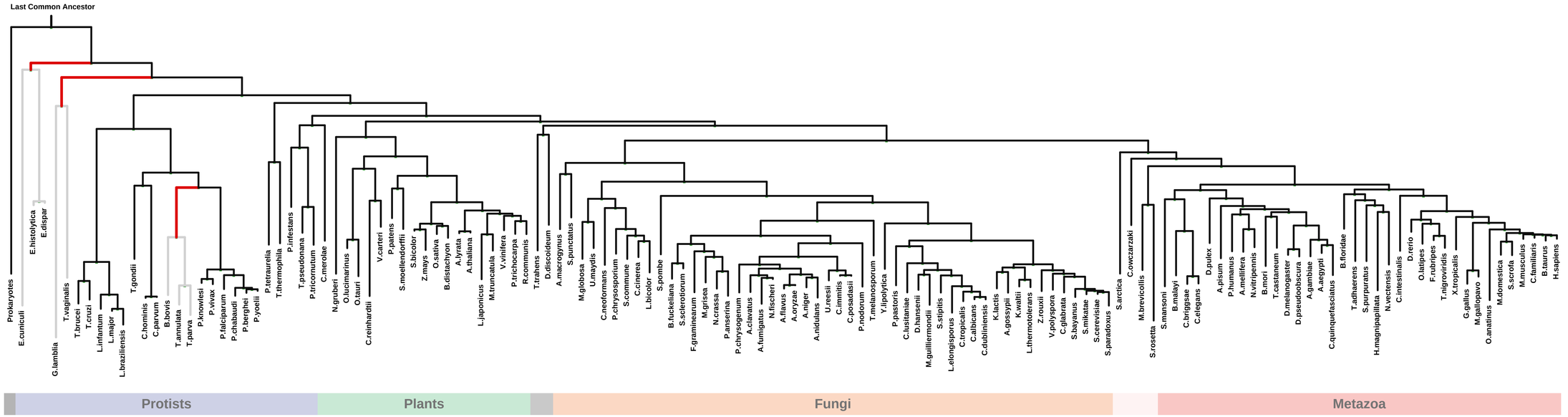
Num of ECM Genes: 1. Num of Predicted Genes: 500

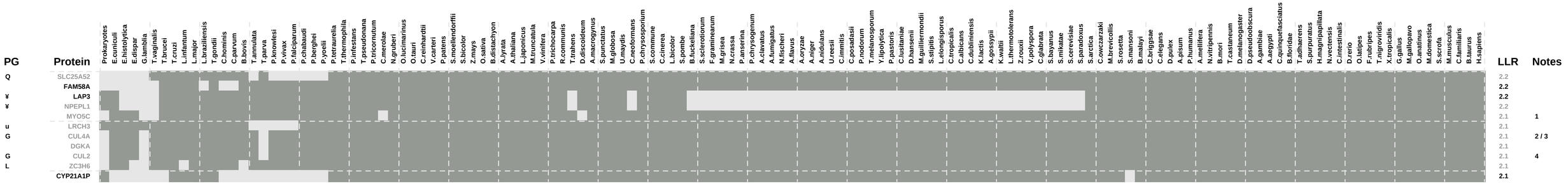


PG	Protein	LLR	Notes
	NAP1L2	2.6	1
	NAP1L4	2.6	1
	PIGA	2.6	2
U	RHOBTB2	2.6	
	UBTD1	2.6	
	UBTD2	2.6	
	MBTPS1	2.6	3 / 4
	APEX2	2.5	
	WDR74	2.5	
	CHRAC1	2.5	5 / 6
U	UACA	2.4	7 / 8
	ATP6V1H	2.4	9
	METTL2B	2.4	
	METTL8	2.4	
	METTL2A	2.4	
	PDK1	2.4	10
t	VAMP8	2.4	11 / 12 / 13 / 14 / 15 / 16
	PUS7L	2.3	
	PUS7	2.3	
u	LRRTM3	2.3	17
~	TOP1MT	2.3	18 / 19
i	UTP18	2.3	
¢	MAPRE3	2.3	20 / 21
¢	MAPRE2	2.3	22
z	STX7	2.3	12 / 13 / 16 / 23
i	TBC1D31	2.3	
	IPO7	2.3	24
£	ZNRF1	2.2	25 / 26 / 27
£	ZNRF2	2.2	13 / 28 / 29
	MAP3K5	2.2	
	ABHD5	2.2	30
/	FMO5	2.2	31
/	FMO1	2.2	3 / 31
/	FMO2	2.2	
/	FMO4	2.2	31

1: chromatin assembly complex || 2: glycosylphosphatidylinositol-N-acetylglucosaminyltransferase (GPI-GnT) complex || 3: endoplasmic reticulum lumen || 4: Golgi stack || 5: chromatin accessibility complex || 6: epsilon DNA polymerase complex ||
7: apoptosome || 8: nuclear envelope || 9: vacuolar proton-transporting V-type ATPase, V1 domain || 10: pyruvate dehydrogenase complex || 11: early endosome || 12: late endosome membrane || 13: lysosomal membrane || 14: recycling endosome ||
15: secretory granule membrane || 16: SNARE complex || 17: postsynaptic membrane || 18: mitochondrial nucleoid || 19: replication fork protection complex || 20: cytoplasmic microtubule || 21: midbody || 22: microtubule cytoskeleton ||

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





1: myosin complex || 2: Cul4A-RING ubiquitin ligase complex || 3: Cul4-RING ubiquitin ligase complex || 4: Cul2-RING ubiquitin ligase complex