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

Dataset:

Num of genes in input gene set: 10
Total number of genes: 20834
Prediction LLR threshold: 0

The CLIME PDF output two sections:

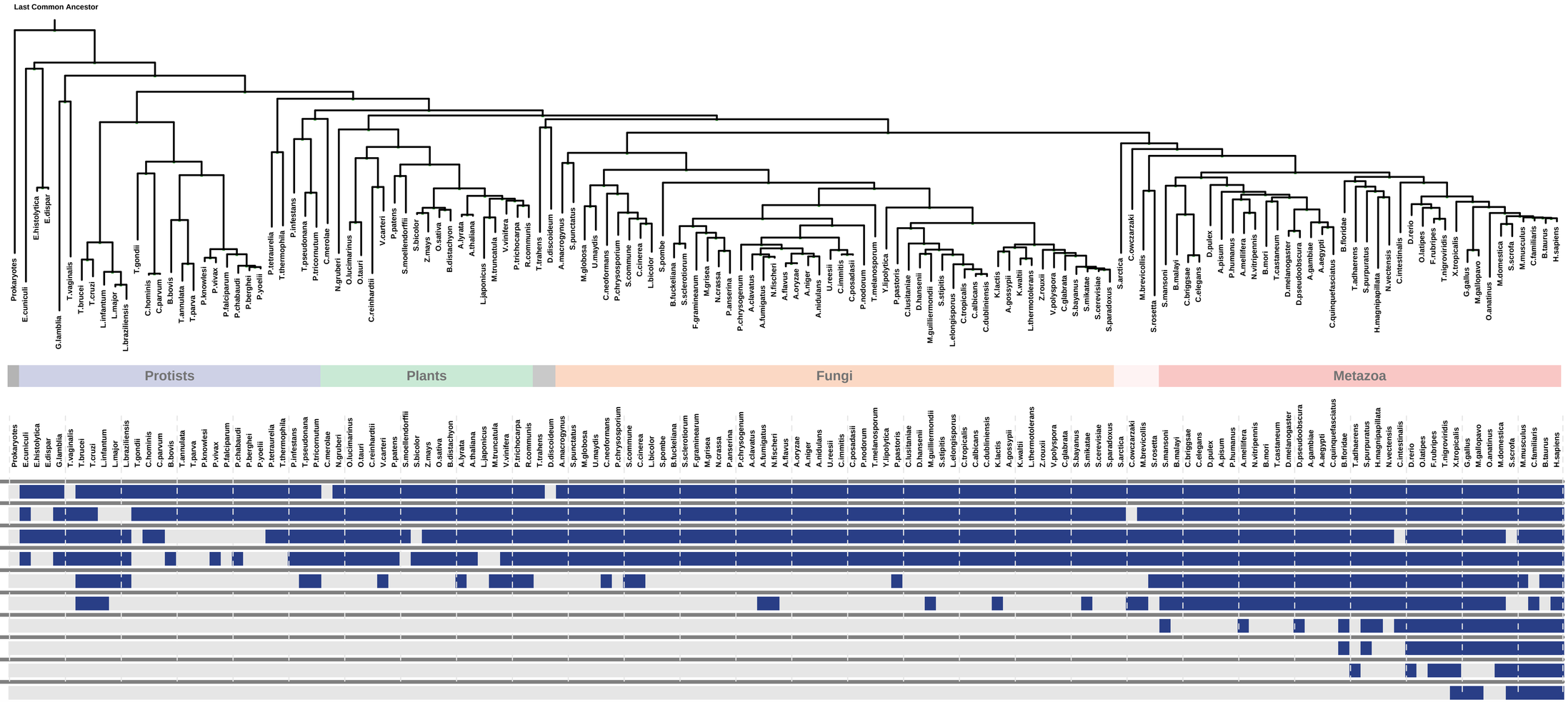
1) Overview of Evolutionarily Conserved Modules (ECMs)

- 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+

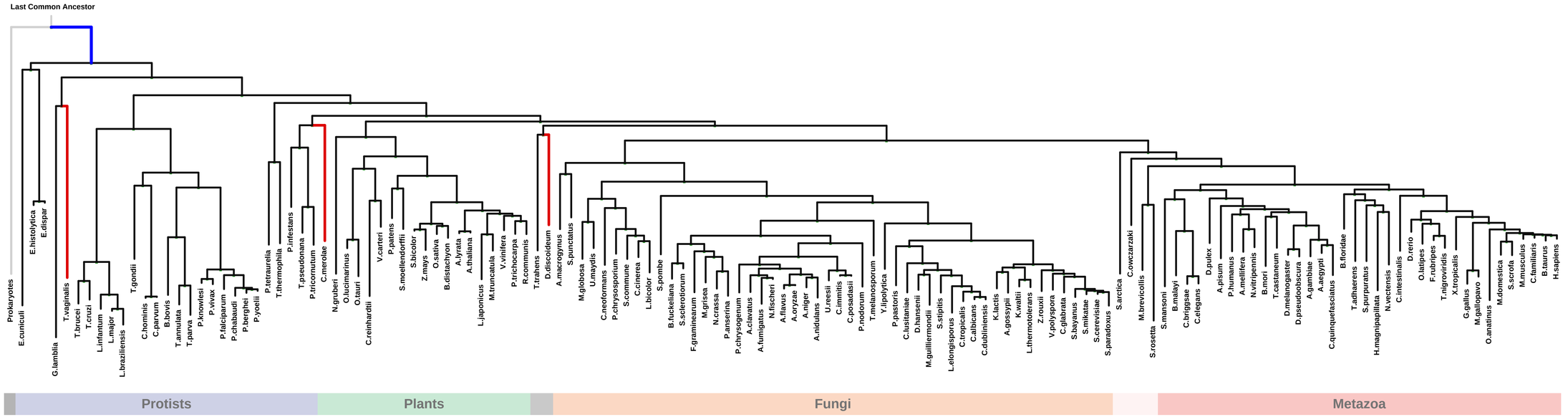
- Top panel shows the inferred evolutionary history on the predefined species tree. Branch color shows the gain event (blue) and loss events (red color, with brighter color indicating higher confidence in loss). Branches before the gain or after a loss are shown in gray.
- Bottom panel shows the input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

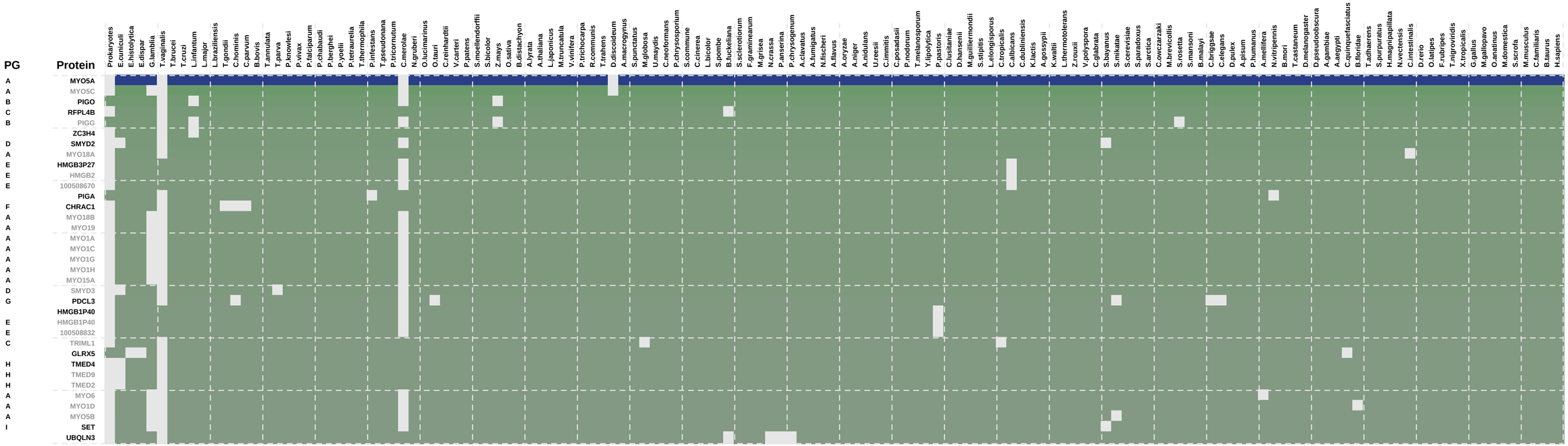
Overview of Evolutionarily Conserved Modules (ECMs)



ECM 1, Gene set "microtubule plus end", Page 1

Num of ECM Genes: 1. Num of Predicted Genes: 236

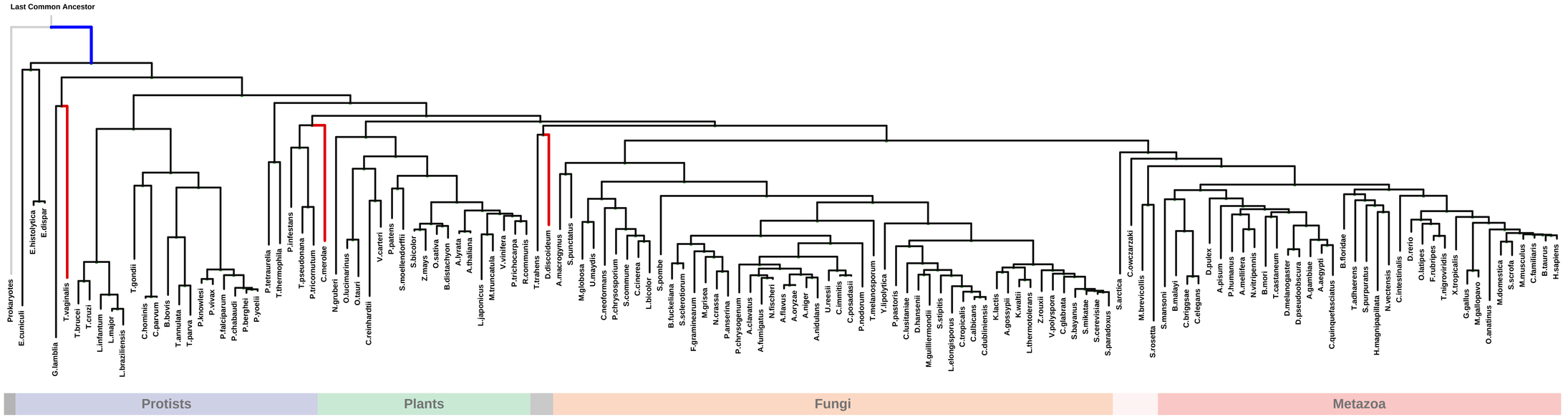




1: actomyosin || 2: growth cone || 3: insulin-responsive compartment || 4: intermediate filament || 5: melanosome || 6: microtubule plus end || 7: myosin complex || 8: neuron projection || 9: photoreceptor outer segment ||
10: ruffle || 11: endoplasmic reticulum-Golgi intermediate compartment || 12: chromosome || 13: condensed chromosome || 14: glycosylphosphatidylinositol-N-acetylglucosaminyltransferase (GPI-GnT) complex || 15: chromatin accessibility complex ||
16: epsilon DNA polymerase complex || 17: sarcomere || 18: unconventional myosin complex || 19: mitochondrial outer membrane || 20: basal plasma membrane || 21: basolateral plasma membrane || 22: brush border || 23: cortical actin cytoskeleton ||

ECM 1, Gene set "microtubule plus end", Page 2

Num of ECM Genes: 1. Num of Predicted Genes: 236

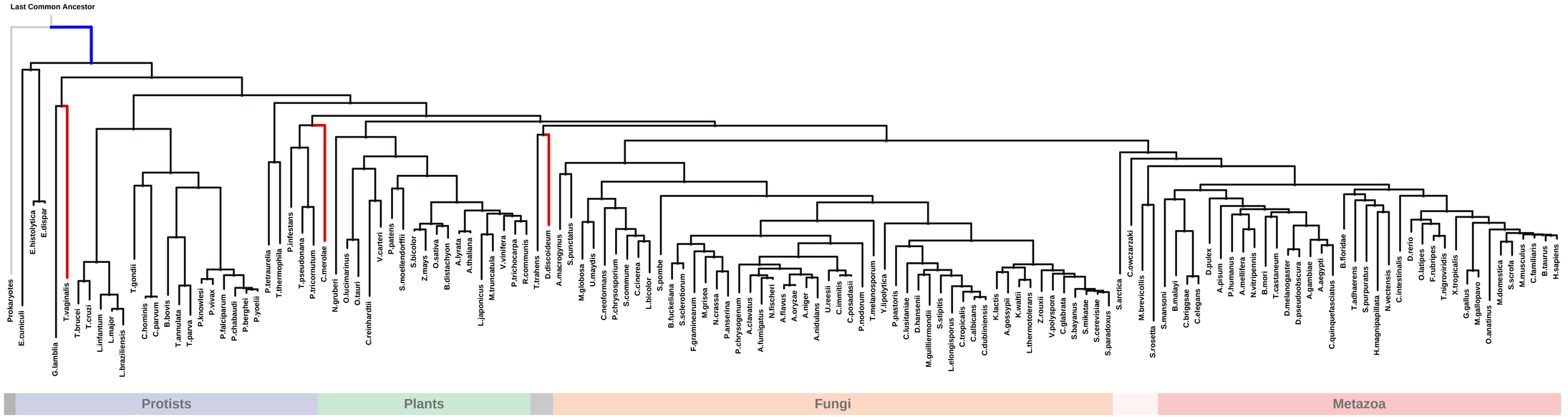


PG	Protein	LLR	Notes
J	SLC38A3	8.8	
K	JADE1	8.4	1
J	SLC38A7	8.2	2
C	TRIM21	8.0	3 / 4 / 5
L	DDX23	7.7	6 / 7
	LOC441722	7.6	
M	U2AF1	7.6	6 / 8 / 9 / 10
C	TRIM43	7.1	
C	TRIM43B	7.1	
A	MYO7B	7.0	11
E	HMGB1	7.0	12 / 13 / 14
A	MYO10	7.0	11 / 13 / 15 / 16 / 17 / 18 /
A	MYH14	6.8	2 / 11 / 20 / 21
D	UNC45B	6.8	
N	IGF2BP2	6.8	22
M	U2AF1L4	6.6	9 / 10
M	ZRSR2	6.6	23
O	CTPS1	6.6	
O	CTPS2	6.6	
J	SLC38A5	6.3	
P	CNNM2	6.3	24
P	CNNM3	6.3	
P	CNNM4	6.3	
P	CNNM1	6.3	
	RCL1	6.2	
A	MYO1B	6.2	11 / 25 / 26 / 27
J	SLC38A10	5.8	
F	NFYC	5.5	28
J	SLC38A1	5.3	2
J	SLC38A4	5.2	
	STAMBP	5.1	29 / 30
	ABHD17B	5.1	
	DNAJC28	5.1	
	KIAA0020	5.1	
J	SLC38A2	5.0	

1: histone acetyltransferase complex || 2: axon || 3: cytoplasmic mRNA processing body || 4: ribonucleoprotein complex || 5: SCF ubiquitin ligase complex || 6: catalytic step 2 spliceosome || 7: U5 snRNP || 8: Cajal body ||
9: nuclear speck || 10: spliceosomal complex || 11: myosin complex || 12: condensed chromosome || 13: neuron projection || 14: transcriptional repressor complex || 15: cell cortex || 16: filopodium membrane || 17: filopodium tip ||
18: lamellipodium || 19: ruffle || 20: growth cone || 21: stress fiber || 22: cytoskeletal part || 23: U12-type spliceosomal complex || 24: basolateral plasma membrane || 25: brush border || 26: cell periphery || 27: filopodium ||

ECM 1, Gene set "microtubule plus end", Page 3

Num of ECM Genes: 1. Num of Predicted Genes: 236

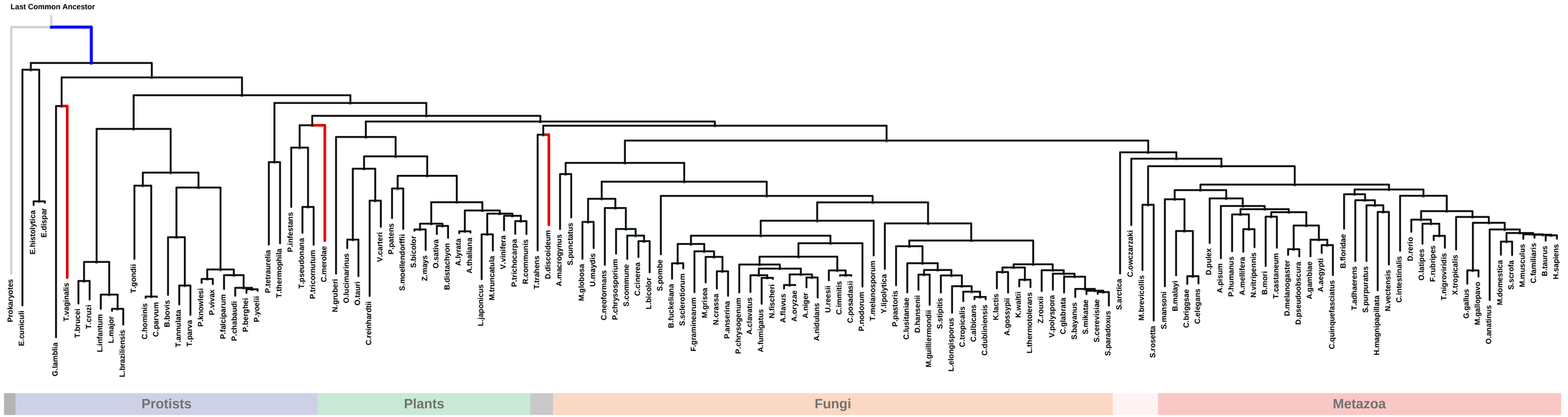


PG	Protein	LLR	Notes
Q	TAF1L	4.9	1
K	JADE3	4.9	2
R	LRRC59	4.5	3
I	NAP1L2	4.5	4
I	NAP1L4	4.5	4
C	TRIM25	4.3	
	WRNIP1	4.2	
G	PDCL2	4.2	
	RAD23A	4.1	5
S	DR1	4.0	6
S	NFYB	4.0	7
	RSL24D1P11	3.9	
	SLC25A25	3.8	
	ASCC3	3.8	
	TYMS	3.8	
T	YEATS4	3.8	8 / 9
U	CDKL2	3.7	
C	UHRF2	3.7	10
V	ISG15	3.7	
	UBL4B	3.7	
	ZFAND4	3.7	
	VPS33B	3.7	11 / 12 / 13 / 14 / 15 / 16
	PTPN9	3.7	17
	TBC1D9	3.6	
	PRPF8	3.6	18 / 19 / 20
	CHD1	3.5	
N	IGF2BP3	3.5	
W	XRN1	3.5	21
C	RNF135	3.5	
K	JADE2	3.3	2
X	SLC9A8	3.2	
X	SLC9A9	3.2	13 / 22
X	SLC9A1	3.2	23 / 24
X	SLC9A3	3.2	25 / 26
X	SLC9A7	3.2	27 / 28

1: transcription factor TFIID complex || 2: histone acetyltransferase complex || 3: mitochondrial nucleoid || 4: chromatin assembly complex || 5: proteasome complex || 6: Ada2/Gcn5/Ada3 transcription activator complex || 7: CCAAT-binding factor complex ||
8: NuA4 histone acetyltransferase complex || 9: nuclear matrix || 10: nuclear heterochromatin || 11: HOPS complex || 12: late endosome || 13: late endosome membrane || 14: lysosomal membrane || 15: lysosome || 16: platelet alpha granule ||
17: cytoplasmic part || 18: catalytic step 2 spliceosome || 19: nuclear speck || 20: U5 snRNP || 21: intermediate filament cytoskeleton || 22: recycling endosome || 23: basolateral plasma membrane || 24: membrane raft || 25: brush border ||

ECM 1, Gene set "microtubule plus end", Page 4

Num of ECM Genes: 1. Num of Predicted Genes: 236

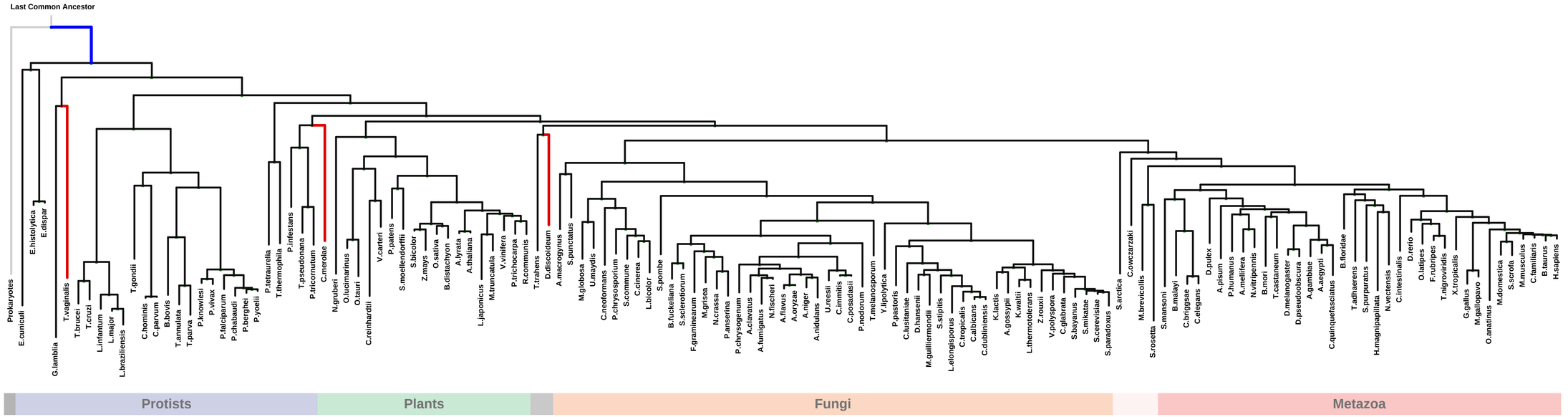


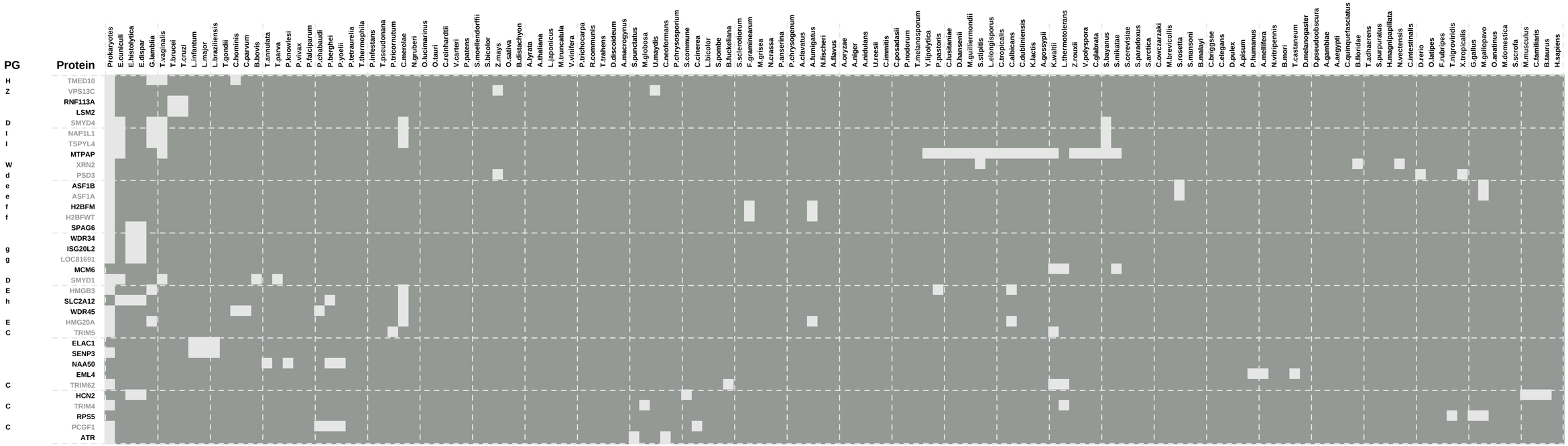
PG	Protein	LLR	Notes
	ATP6V1H	3.2	1
A	MYO7A	3.2	2 / 3 / 4 / 5 / 6 / 7 / 8 / 9 / 1
Y	PUS7L	3.1	
Y	PUS7	3.1	
	TMEM30A	3.1	
	UTP18	3.1	
U	MAP3K5	3.0	
	PNPLA6	3.0	
	ZFP36	3.0	11
	DHX8	3.0	12 / 13
F	DRAP1	2.8	
	TRMT61A	2.8	14
C	LONRF2	2.7	
J	SLC38A8	2.7	
U	CDK13	2.7	15 / 16
F	POLE4	2.7	17 / 18
J	SLC36A1	2.7	3
C	TRIM6	2.6	
	PIGK	2.6	19 / 20
	LRRC6	2.6	21
Z	VPS13D	2.5	
a	652215	2.5	
a	KDELR3	2.5	
a	KDELR1	2.5	22 / 23
b	INPP5K	2.5	24 / 25 / 26 / 27
b	INPP5E	2.5	28 / 29
	TRIT1	2.5	
Q	ATAD2B	2.5	
c	CNOT7	2.4	30 / 31
c	CNOT8	2.4	
V	UBD	2.4	32
d	IQSEC3	2.4	27 / 33 / 34
	STX2	2.4	35 / 36 / 37 / 38 / 39
J	SLC38A6	2.4	
	HINT1	2.3	

1: vacuolar proton-transporting V-type ATPase, V1 domain || 2: cell cortex || 3: lysosomal membrane || 4: melanosome || 5: myosin complex || 6: photoreceptor connecting cilium || 7: photoreceptor inner segment || 8: photoreceptor outer segment ||
9: stereocilium || 10: synapse || 11: cytoplasmic stress granule || 12: catalytic step 2 spliceosome || 13: spliceosomal complex || 14: tRNA (m1A) methyltransferase complex || 15: nuclear cyclin-dependent protein kinase holoenzyme complex ||
16: nuclear speck || 17: Ada2/Gcn5/Ada3 transcription activator complex || 18: epsilon DNA polymerase complex || 19: GPI-anchor transamidase complex || 20: integral to endoplasmic reticulum membrane || 21: cilium || 22: cis-Golgi network ||

ECM 1, Gene set "microtubule plus end", Page 5

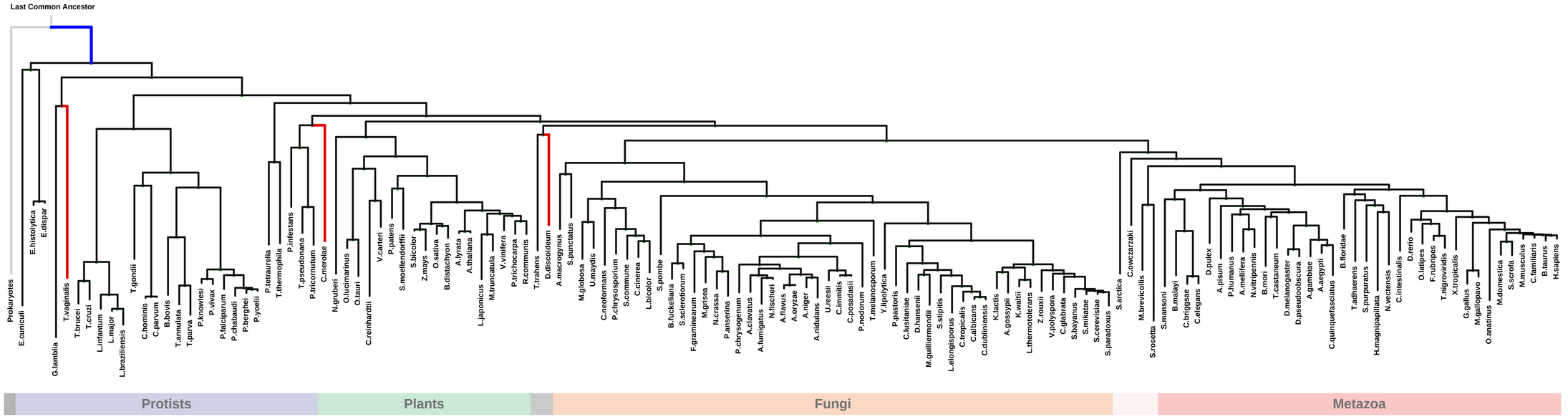
Num of ECM Genes: 1. Num of Predicted Genes: 236





ECM 1, Gene set "microtubule plus end", Page 6

Num of ECM Genes: 1. Num of Predicted Genes: 236

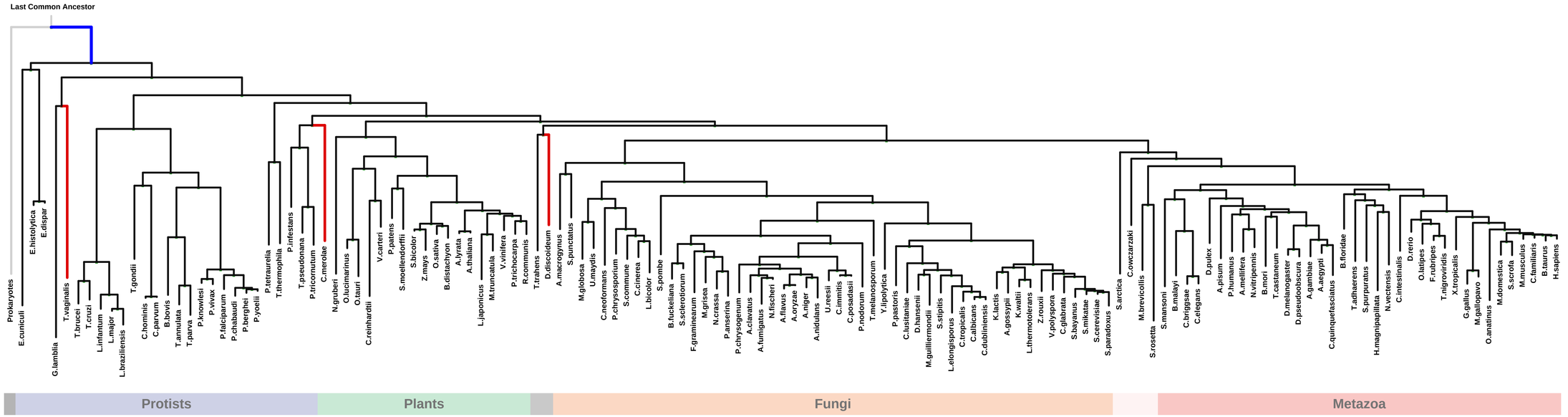


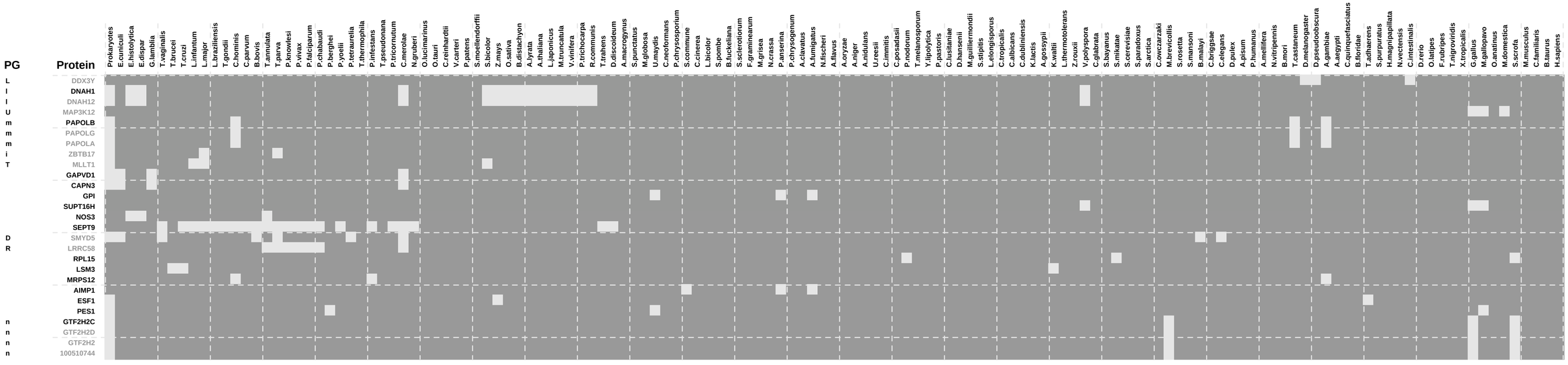
PG	Protein	LLR	Notes
d	ARFGEF2	1.6	1 / 2 / 3 / 4 / 5 / 6 / 7 / 8 / 9
d	ARFGEF1	1.6	9 / 10 / 11
	HIPK2	1.6	
	PIK3C2B	1.5	12
	KRR1	1.5	13
	PSMD4	1.5	14 / 15
h	SLC2A13	1.4	
R	LRRC30	1.4	
	UCKL1	1.4	
Z	VPS13B	1.4	
	ATP6V1C1	1.3	4 / 16 / 17 / 18
	AKTIP	1.3	19 / 20
X	SLC9A2	1.2	
i	RABEPK	1.2	21 / 22
	POLR3F	1.2	23
j	UBTD1	1.2	
j	UBTD2	1.2	
	SF3A3	1.1	24 / 25 / 26
	DUS3L	1.0	
i	KLHL9	1.0	27 / 28
C	TRIM11	1.0	
	RPS9	0.8	13 / 29 / 30
C	TRIM35	0.8	
	GSPT2	0.7	
	NOL10	0.7	
	MRE11A	0.7	31 / 32 / 33 / 34
	NACA	0.7	
	PCNA	0.7	35 / 36 / 37 / 38
	COPA	0.7	39
K	KMT2A	0.6	40 / 41
	TOP3A	0.6	42 / 43
	RABL6	0.6	
k	PRPSAP2	0.5	
k	PRPSAP1	0.5	
	SF3A2	0.5	11 / 24 / 26

1: asymmetric synapse || 2: axonemal microtubule || 3: cytoplasmic membrane-bounded vesicle || 4: cytoplasmic vesicle || 5: dendritic spine || 6: microtubule organizing center || 7: recycling endosome || 8: symmetric synapse ||
9: trans-Golgi network || 10: nuclear matrix || 11: small nuclear ribonucleoprotein complex || 12: endocytic vesicle || 13: ribonucleoprotein complex || 14: proteasome accessory complex || 15: proteasome complex || 16: apical part of cell ||
17: proton-transporting two-sector ATPase complex || 18: proton-transporting V-type ATPase, V1 domain || 19: FHF complex || 20: HOPS complex || 21: endosome || 22: endosome membrane || 23: DNA-directed RNA polymerase III complex ||

ECM 1, Gene set "microtubule plus end", Page 7

Num of ECM Genes: 1. Num of Predicted Genes: 236

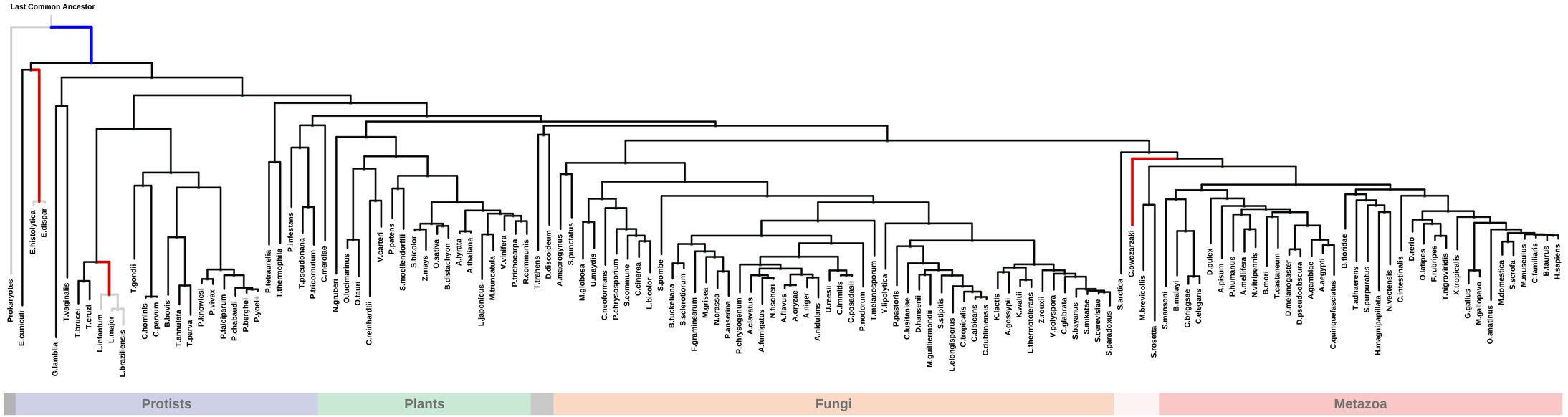




1: axonemal dynein complex || 2: cilium axoneme || 3: dynein complex || 4: endosome || 5: myofibril || 6: T-tubule || 7: Z disc || 8: chromosome || 9: apical part of cell || 10: caveola || 11: endocytic vesicle membrane ||
12: actin cytoskeleton || 13: stress fiber || 14: cytosolic large ribosomal subunit || 15: ribosome || 16: catalytic step 2 spliceosome || 17: mitochondrial ribosome || 18: small ribosomal subunit || 19: aminoacyl-tRNA synthetase multienzyme complex ||
20: transport vesicle || 21: condensed chromosome || 22: PeBoW complex || 23: preribosome, large subunit precursor || 24: holo TFIIH complex

ECM 2, Gene set "microtubule plus end", Page 1

Num of ECM Genes: 1. Num of Predicted Genes: 251

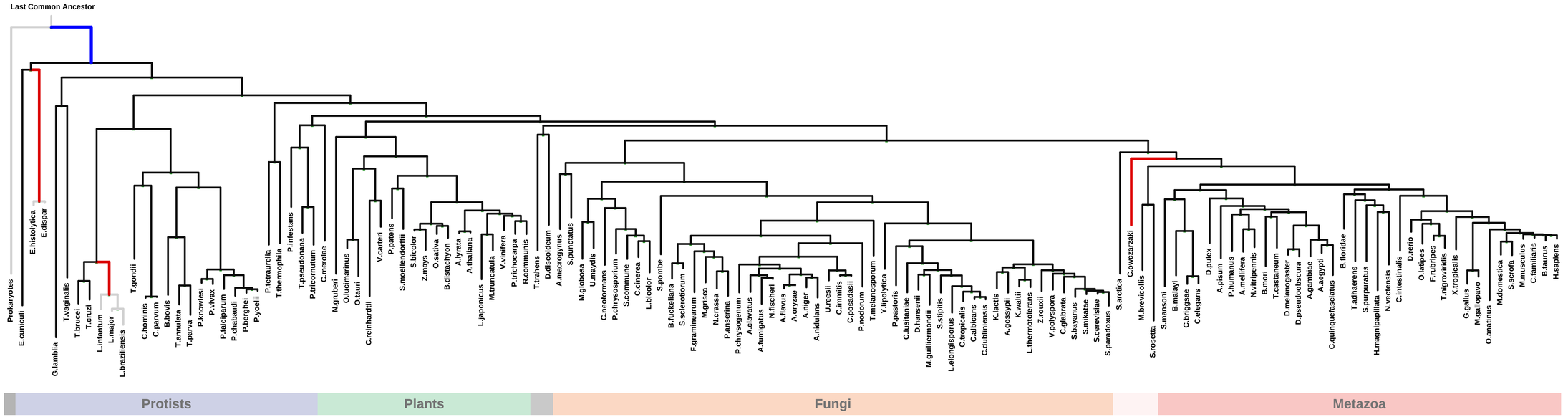


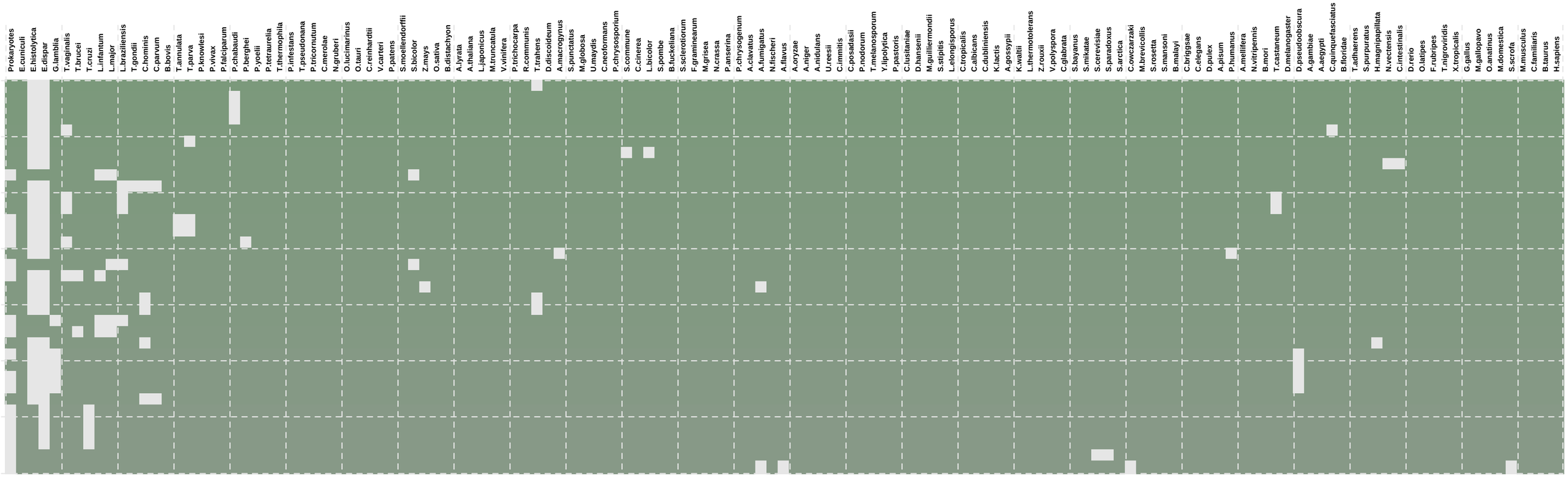
PG	Protein	LLR	Notes
A	MAPRE1		1 / 2 / 3 / 4 / 5
A	MAPRE2	25.6	6
A	MAPRE3	25.6	3 / 7
B	SETMAR	21.9	8
B	KMT2D	16.4	9
C	ISG20L2	16.4	
C	LOC81691	16.4	
	SPAG6	16.4	6 / 10 / 11 / 12
	WDR34	16.4	
	SENP3	16.3	13
	ELAC1	16.3	
D	HCN2	16.0	14 / 15 / 16 / 17
B	KMT2A	15.0	9 / 13
	RFWD3	14.7	18
E	NOS3	14.6	19 / 20 / 21
	NME5	14.1	
D	HCN1	13.9	14 / 22
B	SETD2	13.9	8
	FNTA	13.7	23
C	REXO1L11P	13.5	
C	REXO1L1	13.5	
F	SLC2A6	13.5	
F	SLC2A8	13.5	24 / 25
C	REXO1L10P	13.5	
C	LOC100288562	13.5	
B	EZH2	13.4	26 / 27
B	SETD8	13.4	8
B	SETDB1	13.4	8
B	SUV39H2	13.4	28 / 29 / 30
B	EZH1	13.4	26
	PIK3C2B	13.4	31
C	PAN2	13.3	
D	PRKAR2A	13.3	32 / 33
G	EIF2B3	13.1	34
G	GMPPB	13.1	

1: cell projection membrane || 2: cortical microtubule cytoskeleton || 3: cytoplasmic microtubule || 4: microtubule plus end || 5: spindle || 6: microtubule cytoskeleton || 7: midbody || 8: chromosome || 9: histone methyltransferase complex ||
10: axoneme || 11: cilium || 12: flagellum || 13: MLL1 complex || 14: axon || 15: dendritic shaft || 16: synapse || 17: voltage-gated potassium channel complex || 18: PML body || 19: apical part of cell || 20: caveola ||
21: endocytic vesicle membrane || 22: dendrite || 23: microtubule associated complex || 24: cytoplasmic vesicle membrane || 25: synaptic vesicle || 26: ESC/E(Z) complex || 27: pronucleus || 28: chromatin || 29: chromosome, centromeric region ||

ECM 2, Gene set "microtubule plus end", Page 2

Num of ECM Genes: 1. Num of Predicted Genes: 251

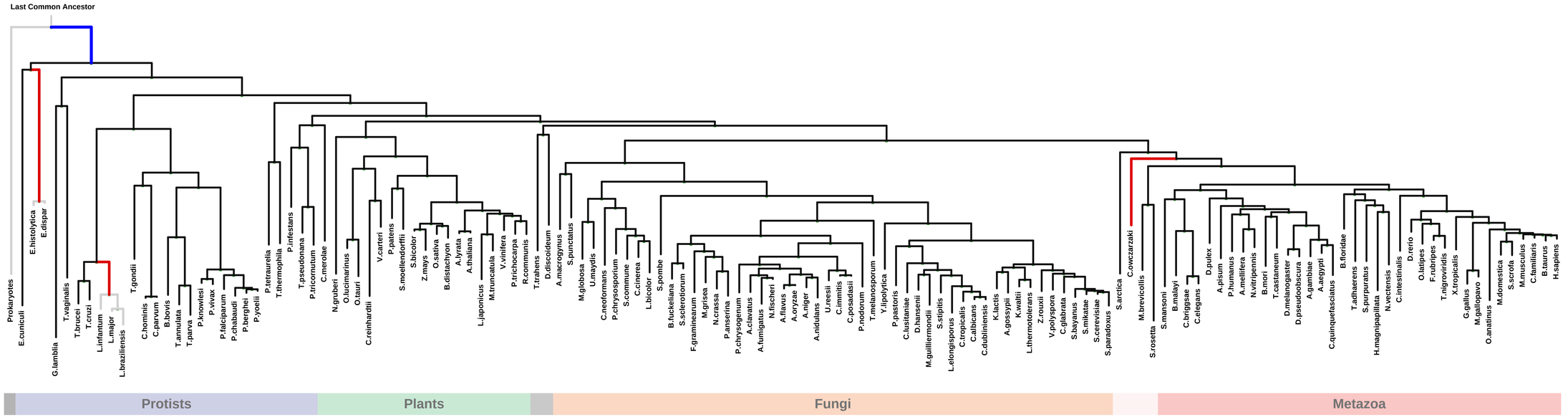


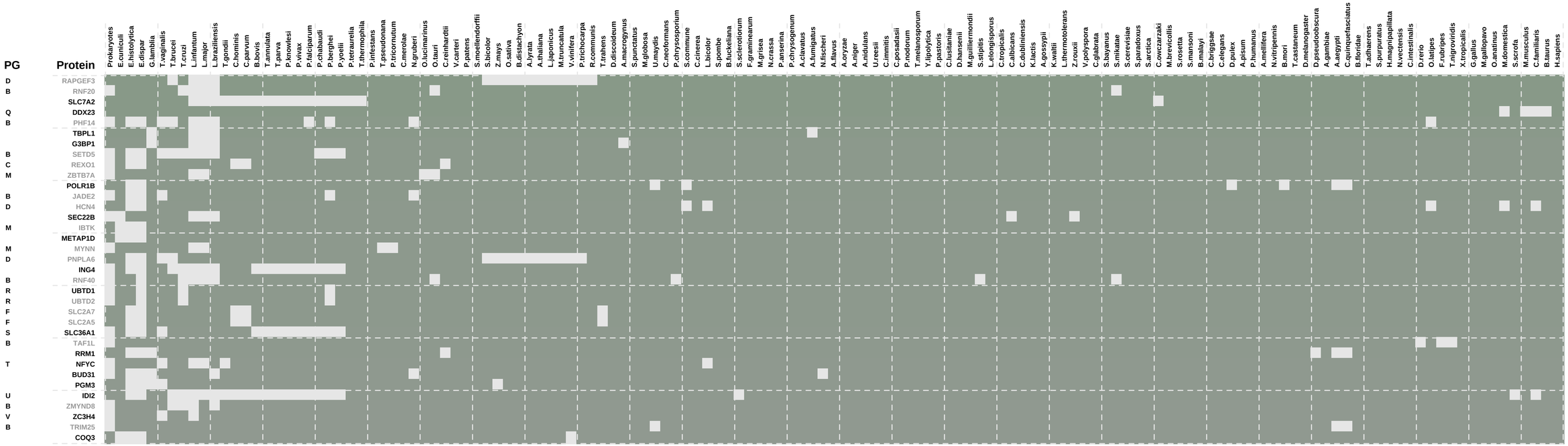


1: nuclear envelope || 2: dendritic spine || 3: photoreceptor inner segment || 4: sarcolemma || 5: sarcoplasmic reticulum || 6: chromosome || 7: mitochondrial outer membrane || 8: histone acetyltransferase complex || 9: NuA4 histone acetyltransferase complex || 10: nuclear matrix || 11: cAMP-dependent protein kinase complex || 12: membrane raft || 13: nuclear heterochromatin || 14: cytoplasmic mRNA processing body || 15: ribonucleoprotein complex || 16: SCF ubiquitin ligase complex

ECM 2, Gene set "microtubule plus end", Page 3

Num of ECM Genes: 1. Num of Predicted Genes: 251

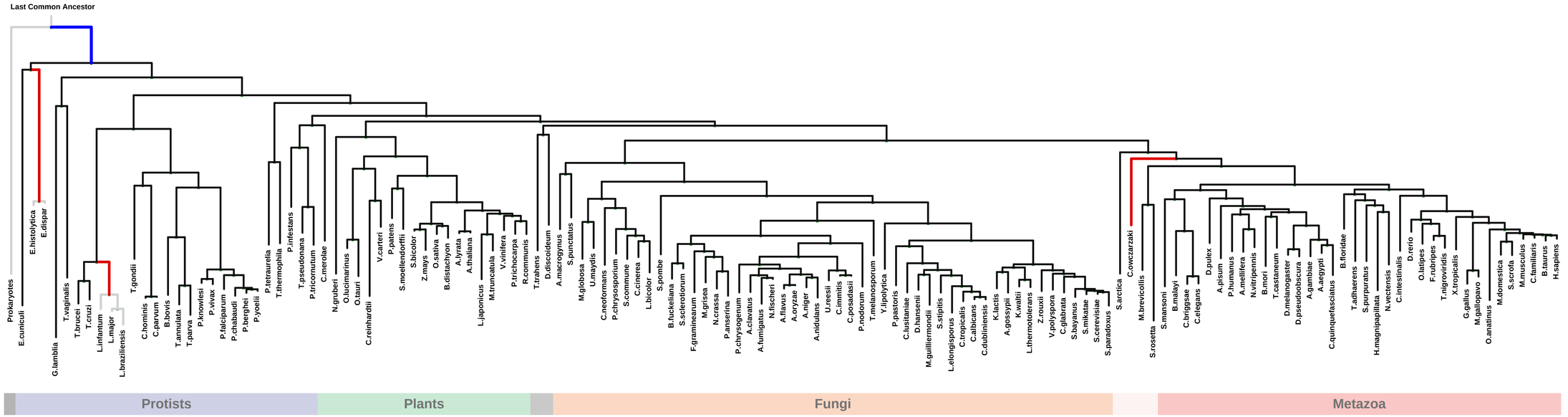




1: cAMP-dependent protein kinase complex || 2: endomembrane system || 3: HULC complex || 4: ubiquitin ligase complex || 5: catalytic step 2 spliceosome || 6: U5 snRNP || 7: transcription factor TFIIA complex || 8: DNA-directed RNA polymerase I complex || 9: histone acetyltransferase complex || 10: terminal button || 11: endoplasmic reticulum-Golgi intermediate compartment || 12: endoplasmic reticulum-Golgi intermediate compartment membrane || 13: melanosome || 14: neuron projection || 15: lysosomal membrane || 16: transcription factor TFIID complex || 17: ribonucleoside-diphosphate reductase complex || 18: CCAAT-binding factor complex || 19: peroxisome

ECM 2, Gene set "microtubule plus end", Page 4

Num of ECM Genes: 1. Num of Predicted Genes: 251

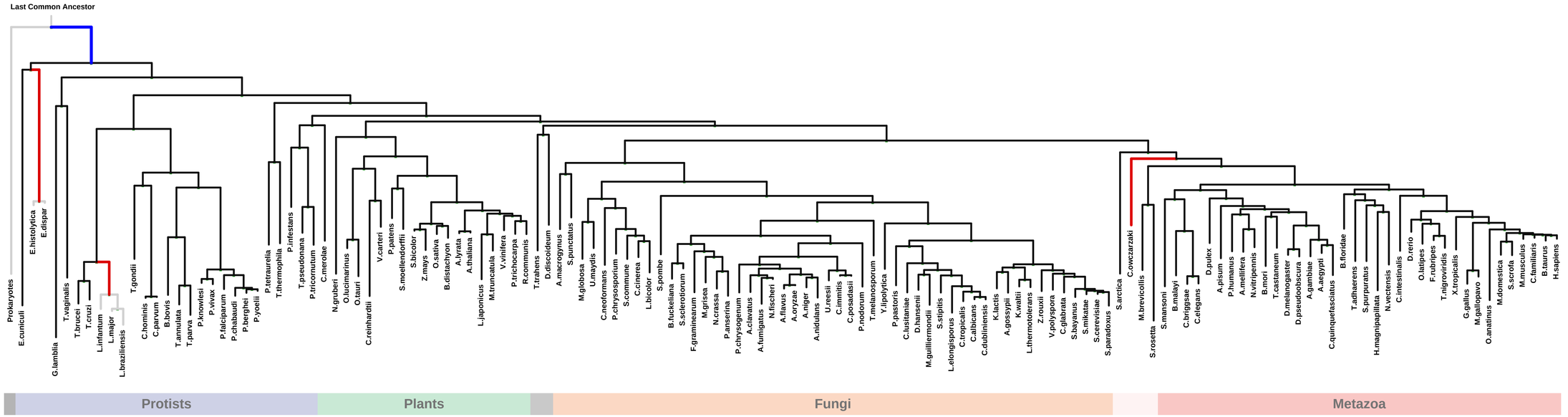


PG	Protein	LLR	Notes
T	POLE4	3.9	1 / 2
	ARHGAP22	3.8	
	WRNIP1	3.8	
	RAD23A	3.7	3
F	SLC2A13	3.6	
	RSL24D1P11	3.6	
	SLC25A25	3.5	
	ASCC3	3.4	
W	CDKL2	3.4	
B	MLLT10	3.3	
	TBC1D9	3.3	
I	MLLT3	3.2	
	CCDC94	3.2	
H	GLRX	3.2	
	PRPF8	3.2	4 / 5 / 6
K	SUOX	3.2	7
X	SHMT1	3.2	
X	SHMT2	3.2	7 / 8 / 9
L	CHD1	3.2	
Y	XRN1	3.1	10
B	RNF135	3.1	
K	FADS3	3.0	
K	FADS1	3.0	
K	FADS2	3.0	
	ATP6V1H	2.8	11
Z	TBCE	2.8	
a	PUS7L	2.7	
a	PUS7	2.7	
	TMEM30A	2.7	
	UTP18	2.7	
	MAK16	2.7	
b	DNAH1	2.7	12 / 13 / 14
b	DNAH12	2.7	13 / 14
c	FDX1L	2.7	
c	FDX1	2.7	15

1: Ada2/Gcn5/Ada3 transcription activator complex || 2: epsilon DNA polymerase complex || 3: proteasome complex || 4: catalytic step 2 spliceosome || 5: nuclear speck || 6: U5 snRNP || 7: mitochondrial intermembrane space || 8: microtubule cytoskeleton || 9: mitochondrial nucleoid || 10: intermediate filament cytoskeleton || 11: vacuolar proton-transporting V-type ATPase, V1 domain || 12: axonemal dynein complex || 13: cilium axoneme || 14: dynein complex || 15: mitochondrial crista

ECM 2, Gene set "microtubule plus end", Page 5

Num of ECM Genes: 1. Num of Predicted Genes: 251

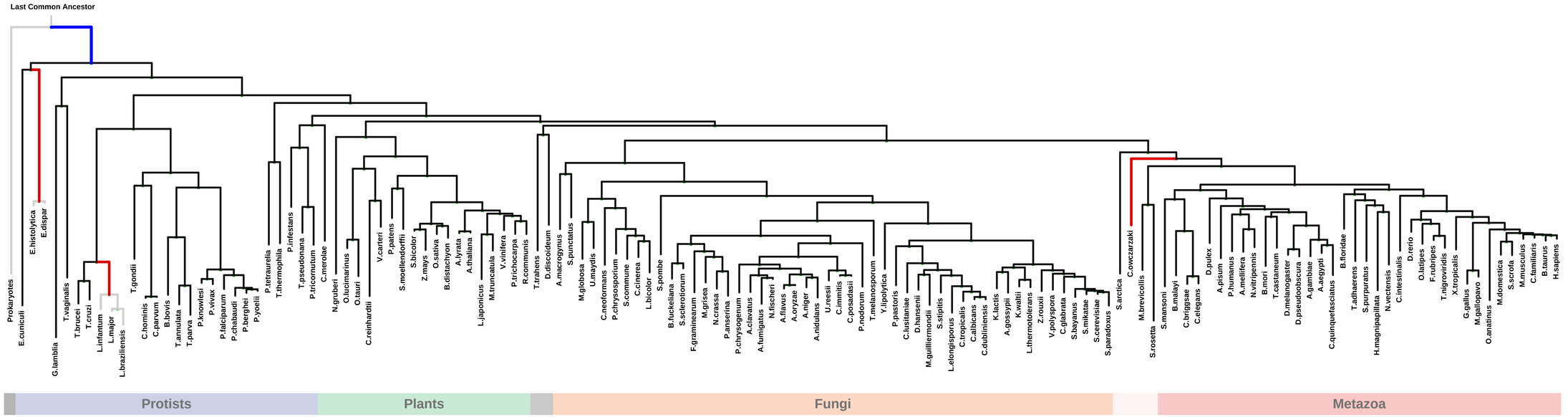


PG	Protein	LLR	Notes
W	MAP3K5	2.6	
	ITPA	2.6	
M	GZF1	2.4	
I	YEATS2	2.4	1
B	LONRF2	2.4	
M	ZNF768	2.4	2
W	CDK13	2.3	3 / 4
	RBM25	2.3	4
d	VPS13D	2.2	
	LRRC6	2.2	5
M	ZBTB17	2.2	
B	SETDB2	2.2	6
O	HAGHL	2.2	
e	KDELR1	2.2	7 / 8
e	652215	2.2	
e	KDELR3	2.2	
D	PNPLA7	2.1	9 / 10 / 11
B	ATAD2B	2.1	
f	INPP5K	2.1	12 / 13 / 14 / 15
f	INPP5E	2.1	16 / 17
B	SETD1A	2.1	4 / 6 / 18 / 19
g	CNOT7	2.0	20 / 21
g	CNOT8	2.0	
P	UBD	2.0	22
S	SLC36A2	2.0	
h	IQSEC3	2.0	15 / 23 / 24
b	DYNC2H1	2.0	16 / 25 / 26 / 27
	STX2	2.0	28 / 29 / 30 / 31 / 32
	HINT1	1.9	
d	VPS13C	1.9	
	RNF113A	1.9	
	LSM2	1.9	33
	100291851	1.9	
Y	XRN2	1.8	22
h	PSD3	1.8	15 / 24 / 34

1: Ada2/Gcn5/Ada3 transcription activator complex || 2: DNA-directed RNA polymerase II, core complex || 3: nuclear cyclin-dependent protein kinase holoenzyme complex || 4: nuclear speck || 5: cilium || 6: chromosome || 7: cis-Golgi network ||
8: endoplasmic reticulum-Golgi intermediate compartment || 9: lysosomal membrane || 10: mitochondrial membrane || 11: nuclear membrane || 12: neuron projection || 13: ruffle || 14: ruffle membrane || 15: trans-Golgi network ||
16: cilium axoneme || 17: Golgi cisterna membrane || 18: histone methyltransferase complex || 19: Set1C/COMPASS complex || 20: CCR4-NOT complex || 21: cytoplasmic mRNA processing body || 22: aggresome || 23: inhibitory synapse ||

ECM 2, Gene set "microtubule plus end", Page 6

Num of ECM Genes: 1. Num of Predicted Genes: 251

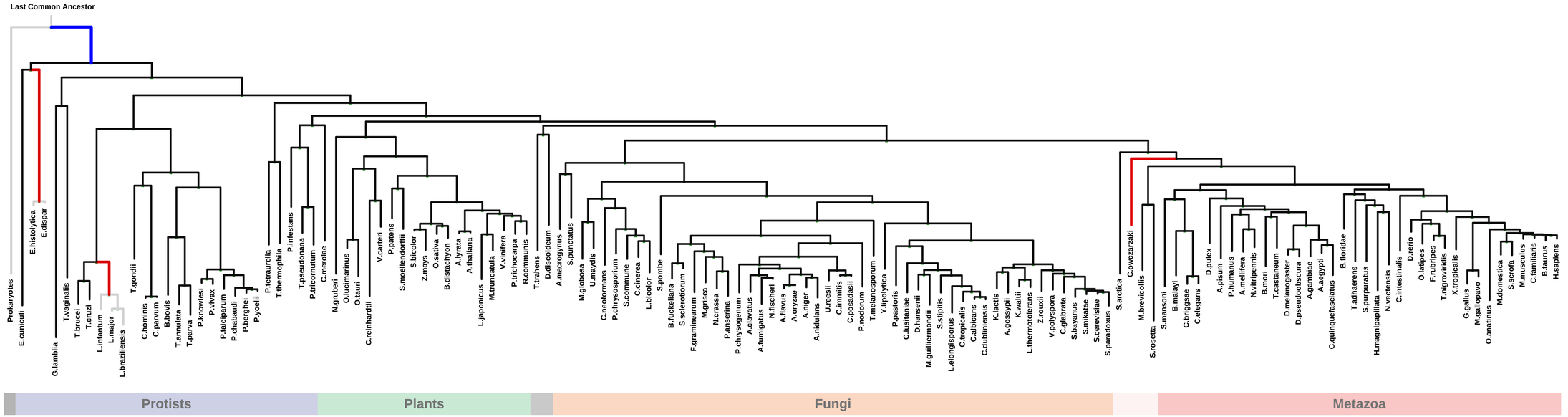


PG	Protein	LLR	Notes
i	ASF1B	1.7	1
i	ASF1A	1.7	2
j	H2BFM	1.7	3
j	H2BFWT	1.7	3 / 4
	MCM6	1.6	5
B	RFPL4B	1.6	
M	ZBTB41	1.6	
B	TRIM5	1.4	6
	NAA50	1.4	
	EML4	1.4	
B	TRIM62	1.3	
	RPS5	1.3	7 / 8
B	TRIM4	1.3	
B	PCGF1	1.3	9
	RANGAP1	1.3	4 / 10 / 11 / 12 / 13
	ATR	1.2	14 / 15 / 16
k	RRM2B	1.2	17
k	RRM2	1.2	17
	HIPK2	1.2	
h	ARFGEF1	1.2	18 / 19 / 20
h	ARFGEF2	1.2	20 / 21 / 22 / 23 / 24 / 25 /
	HSD11B2	1.2	
	UTY	1.2	
	KRR1	1.1	8
	PSMD4	1.1	29 / 30
	RNF121	1.0	
U	IDI1	1.0	31
	ATP6V1C1	0.9	24 / 32 / 33 / 34
	AKTIP	0.9	35 / 36
l	GPD1	0.9	37
l	GPD1L	0.9	37
	TRAPPC2	0.8	
	POLR3F	0.8	38
	CDIPT	0.8	
	WDR74	0.7	

1: chromatin || 2: chromatin remodeling complex || 3: nucleosome || 4: nuclear membrane || 5: MCM complex || 6: cytoplasmic mRNA processing body || 7: cytosolic small ribosomal subunit || 8: ribonucleoprotein complex ||
9: PcG protein complex || 10: condensed chromosome kinetochore || 11: kinetochore || 12: nuclear pore || 13: spindle pole || 14: chromosome || 15: PML body || 16: XY body || 17: ribonucleoside-diphosphate reductase complex ||
18: nuclear matrix || 19: small nuclear ribonucleoprotein complex || 20: trans-Golgi network || 21: asymmetric synapse || 22: axonemal microtubule || 23: cytoplasmic membrane-bounded vesicle || 24: cytoplasmic vesicle || 25: dendritic spine ||

ECM 2, Gene set "microtubule plus end", Page 7

Num of ECM Genes: 1. Num of Predicted Genes: 251

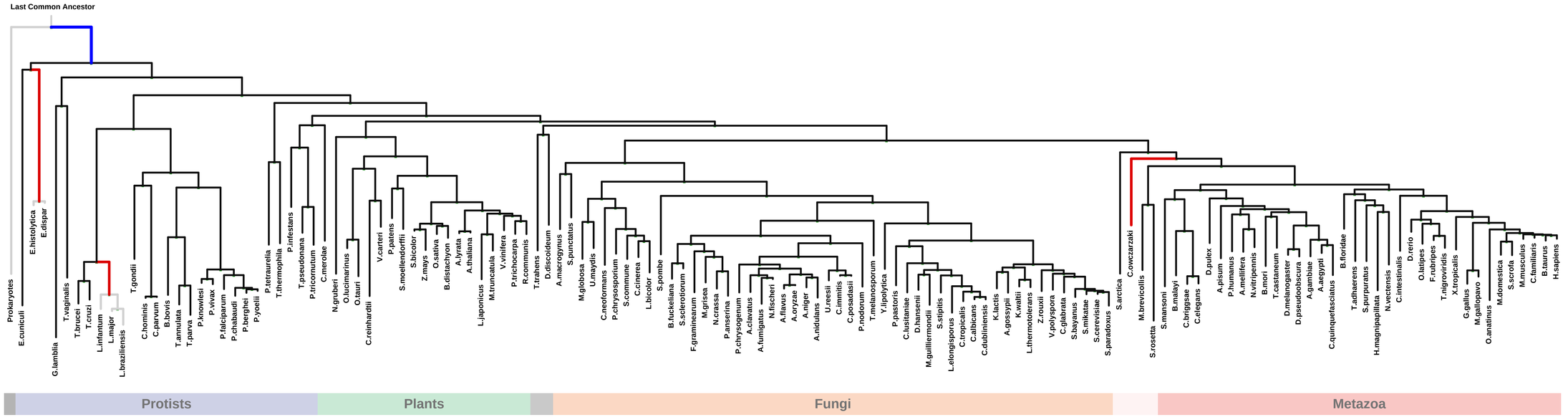


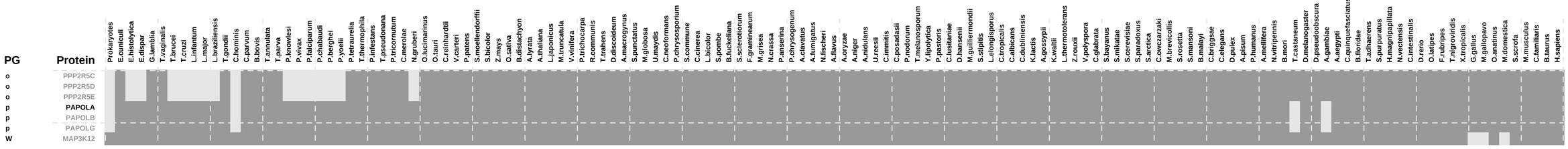
PG	Protein	LLR	Notes
	NCOA7	0.7	
m	CNNM1	0.7	
m	CNNM2	0.7	1
m	CNNM3	0.7	
m	CNNM4	0.7	
	DUS3L	0.7	
	SF3A3	0.7	2 / 3 / 4
V	ZC3H6	0.7	
	POLA2	0.6	5
B	TRIM11	0.6	
M	ZBTB48	0.6	
M	ZBTB8A	0.5	
	IPO7	0.5	6
	NUP155	0.5	6 / 7 / 8
M	ZBTB14	0.4	
Z	CEP350	0.4	9
	RPS9	0.4	10 / 11 / 12
	GSPT2	0.4	
B	TRIM35	0.4	
	NOL10	0.3	
	MRE11A	0.3	13 / 14 / 15 / 16
	PCNA	0.3	17 / 18 / 19 / 20
	NACA	0.3	
	MYO18A	0.3	21 / 22 / 23
	COPA	0.3	24
	TOP3A	0.2	25 / 26
n	BIRC3	0.2	
n	BIRC2	0.2	27 / 28
	MRPL3	0.2	29
	RABL6	0.2	
	SF3A2	0.2	2 / 4 / 30
Q	DDX3Y	0.1	
	AGAP3	0.0	31
o	PPP2R5A	0.0	32 / 33 / 34
o	PPP2R5B	0.0	34

1: basolateral plasma membrane || 2: catalytic step 2 spliceosome || 3: nuclear speck || 4: spliceosomal complex || 5: alpha DNA polymerase:primase complex || 6: nuclear pore || 7: nuclear envelope || 8: nuclear membrane ||
9: spindle || 10: cytosolic small ribosomal subunit || 11: ribonucleoprotein complex || 12: ribosome || 13: chromosome, telomeric region || 14: condensed nuclear chromosome || 15: Mre11 complex || 16: nuclear chromatin ||
17: DNA replication factor C complex || 18: microtubule cytoskeleton || 19: nuclear replication fork || 20: PCNA-p21 complex || 21: actomyosin || 22: endoplasmic reticulum-Golgi intermediate compartment || 23: myosin complex ||

ECM 2, Gene set "microtubule plus end", Page 8

Num of ECM Genes: 1. Num of Predicted Genes: 251

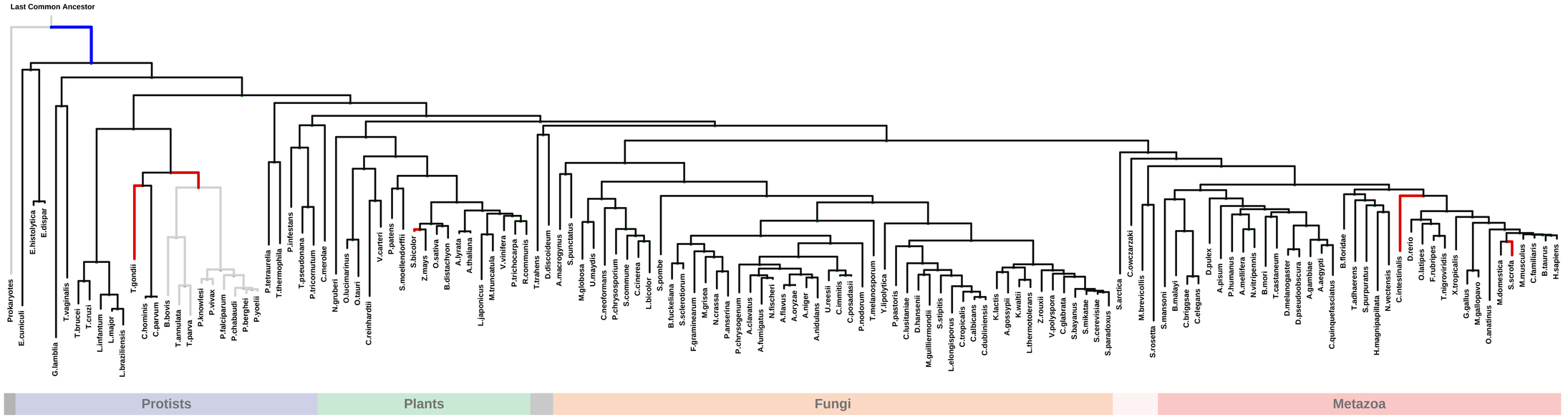




1: chromosome, centromeric region || 2: protein phosphatase type 2A complex

ECM 3, Gene set "microtubule plus end", Page 1

Num of ECM Genes: 1. Num of Predicted Genes: 109

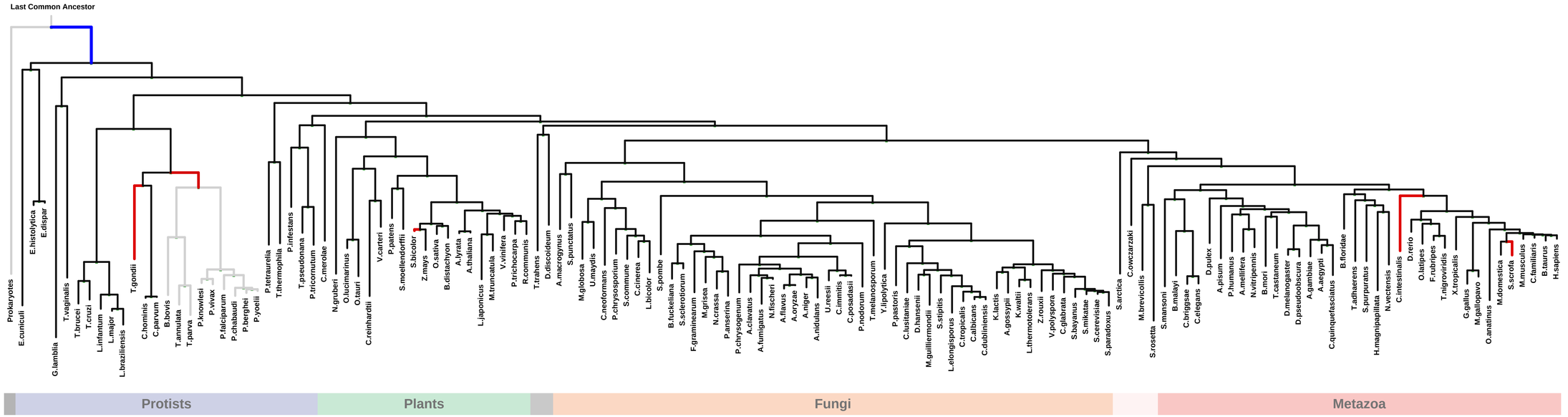


PG	Protein	LLR	Notes
	CKAP5		1 / 2 / 3 / 4
A	CCNA1	15.5	2
A	CCNA2	15.5	5 / 6
A	CCNB1	15.5	4 / 7
A	CCNB2	15.5	2
A	CCND1	15.5	8
A	CCND2	15.5	8 / 9 / 10
A	CCNE1	15.5	8
A	CCNE2	15.5	
A	CCNI	15.5	
A	CCNO	15.5	
A	CNTD2	15.5	
A	CCNB3	15.4	
B	LRCH1	12.8	
	CLIP3	12.4	11 / 12 / 13 / 14 / 15 / 16
B	RTN4R	10.2	17
	ISCU	8.9	
	STX2	8.1	13 / 18 / 19 / 20 / 21
B	LRRC30	7.6	
C	YEATS4	7.4	22 / 23
	CDKL2	7.4	
D	ME1	7.3	
D	ME2	7.3	
D	ME3	7.3	
E	RRP1B	7.0	24
E	RRP1	7.0	24
	RFT1	6.8	
F	UTP18	6.7	
B	NRROS	6.4	
	SLC36A4	6.0	
G	SSB	5.9	25
A	CCND3	5.7	8
G	LARP6	5.7	25
	UGP2	5.7	
B	FLII	5.3	

1: gamma-tubulin complex || 2: microtubule cytoskeleton || 3: microtubule plus end || 4: spindle pole || 5: female pronucleus || 6: male pronucleus || 7: condensed nuclear chromosome outer kinetochore || 8: cyclin-dependent protein kinase holoenzyme complex || 9: chromatin || 10: nuclear membrane || 11: early endosome membrane || 12: Golgi stack || 13: membrane raft || 14: recycling endosome membrane || 15: trans-Golgi network || 16: trans-Golgi network membrane || 17: anchored to membrane || 18: basolateral plasma membrane || 19: cell-cell junction || 20: midbody || 21: transport vesicle || 22: NuA4 histone acetyltransferase complex || 23: nuclear matrix || 24: preribosome, small subunit precursor || 25: ribonucleoprotein complex

ECM 3, Gene set "microtubule plus end", Page 2

Num of ECM Genes: 1. Num of Predicted Genes: 109

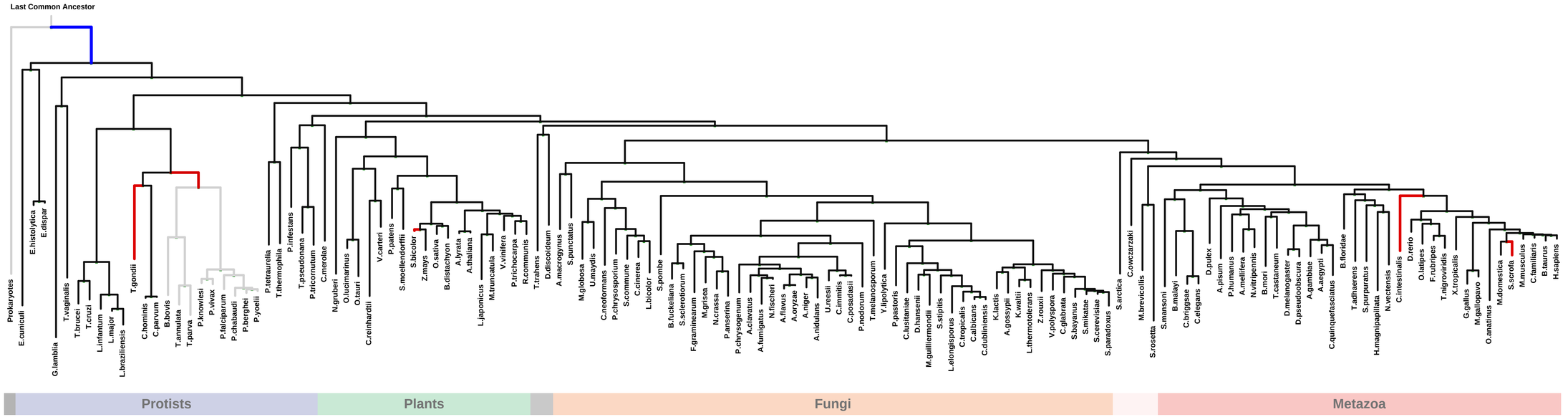


PG	Protein	LLR	Notes
	ATP6V1C1	5.0	1 / 2 / 3 / 4
	CDC16	4.8	5 / 6 / 7
B	LRRC4	4.3	8
	PCNA	4.3	9 / 10 / 11 / 12
	MYO18A	4.3	13 / 14 / 15
F	TBC1D31	4.3	
	TOP3A	4.2	16 / 17
	RHOBTB2	4.2	
H	DDX3Y	4.2	
C	MLLT1	4.0	
	RPL15	3.8	18 / 19
I	GTF2H2D	3.7	
I	GTF2H2	3.7	20
I	GTF2H2C	3.7	
I	100510744	3.7	
A	CCNI2	3.6	
	METTL21A	3.2	
	HCN1	3.2	21 / 22
	RPL13A	3.1	18 / 23 / 24
J	HIST4H4	3.1	
J	HIST1H4A	3.1	
J	HIST1H4B	3.1	
J	HIST1H4C	3.1	
J	HIST1H4D	3.1	
J	HIST1H4E	3.1	
J	HIST1H4F	3.1	
J	HIST1H4G	3.1	25 / 26
J	HIST1H4H	3.1	
J	HIST1H4I	3.1	
J	HIST1H4J	3.1	
J	HIST1H4K	3.1	
J	HIST1H4L	3.1	
J	HIST2H4A	3.1	
J	HIST2H4B	3.1	25 / 26
	YIPF5	3.0	27 / 28 / 29

1: apical part of cell || 2: cytoplasmic vesicle || 3: proton-transporting two-sector ATPase complex || 4: proton-transporting V-type ATPase, V1 domain || 5: anaphase-promoting complex || 6: spindle || 7: spindle microtubule || 8: postsynaptic membrane || 9: DNA replication factor C complex || 10: microtubule cytoskeleton || 11: nuclear replication fork || 12: PCNA-p21 complex || 13: actomyosin || 14: endoplasmic reticulum-Golgi intermediate compartment || 15: myosin complex || 16: chromosome || 17: PML body || 18: cytosolic large ribosomal subunit || 19: ribosome || 20: holo TFIIH complex || 21: axon || 22: dendrite || 23: large ribosomal subunit || 24: ribonucleoprotein complex || 25: actin cytoskeleton ||

ECM 3, Gene set "microtubule plus end", Page 3

Num of ECM Genes: 1. Num of Predicted Genes: 109

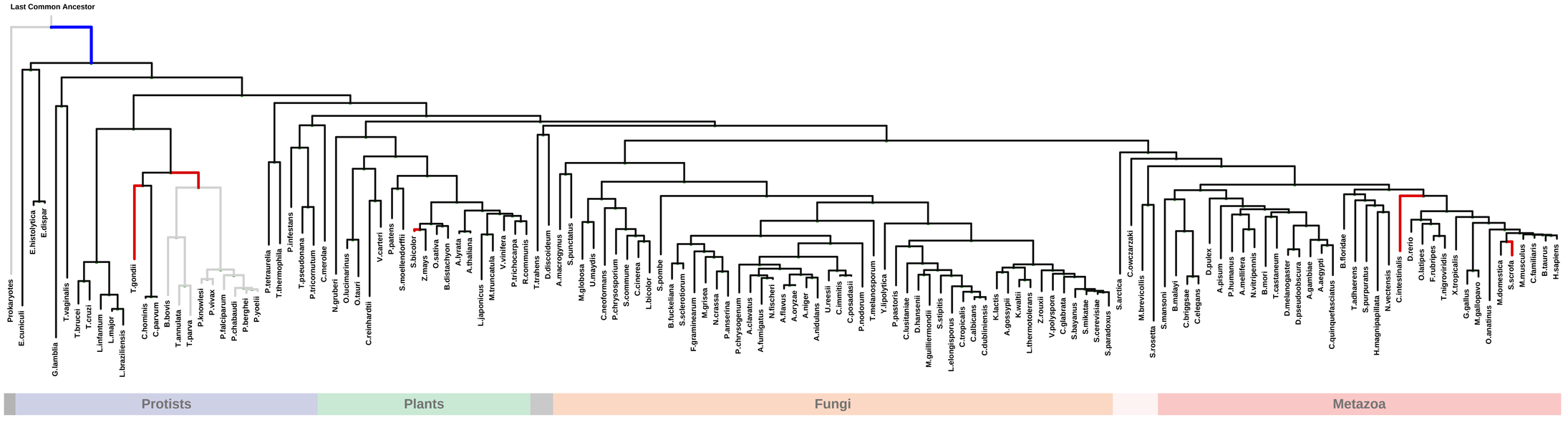


PG	Protein	LLR	Notes
	ABHD17A	3.0	
	FEM1C	3.0	
	REV3L	2.9	1 / 2
K	FNTA	2.8	3
L	SBF1	2.6	
L	SBF2	2.6	4
	GSPT1	2.6	
	ARPC1B	2.5	5 / 6
B	TLR5	2.5	
	PAN3	2.4	
	PLS3	2.3	
	ABCC2	2.3	7
M	ERGIC1	2.3	8 / 9
M	ERGIC2	2.3	9
M	ERGIC3	2.3	9
	BUB1	2.3	10 / 11 / 12
K	RABGGTA	2.2	
	COASY	2.1	13
B	LRRC4B	2.1	14
N	RPL10	1.8	15
N	RPL10L	1.8	15
	NAA50	1.8	
H	DDX23	1.7	16 / 17
O	WHSC1	1.6	1 / 18
	POLR2G	1.6	19
	NAT10	1.4	
	651921	1.4	
	GAA	1.4	20 / 21
	BBS4	1.1	22 / 23 / 24 / 25 / 26 / 27 /
	TMTC3	1.1	
	PRIM1	0.9	30
O	NSD1	0.9	1
	STAMBP	0.9	31 / 32
	PSMD13	0.9	33 / 34 / 35
	PDZRN3	0.7	36

1: chromosome || 2: zeta DNA polymerase complex || 3: microtubule associated complex || 4: vacuolar membrane || 5: actin cytoskeleton || 6: Arp2/3 protein complex || 7: intercellular canaliculus || 8: endoplasmic reticulum-Golgi intermediate compartment ||
9: endoplasmic reticulum-Golgi intermediate compartment membrane || 10: condensed chromosome kinetochore || 11: condensed nuclear chromosome, centromeric region || 12: kinetochore || 13: mitochondrial outer membrane || 14: presynaptic membrane ||
15: cytosolic large ribosomal subunit || 16: catalytic step 2 spliceosome || 17: U5 snRNP || 18: nuclear membrane || 19: DNA-directed RNA polymerase II, core complex || 20: lysosomal membrane || 21: lysosome || 22: BBSome ||

ECM 3, Gene set "microtubule plus end", Page 4

Num of ECM Genes: 1. Num of Predicted Genes: 109

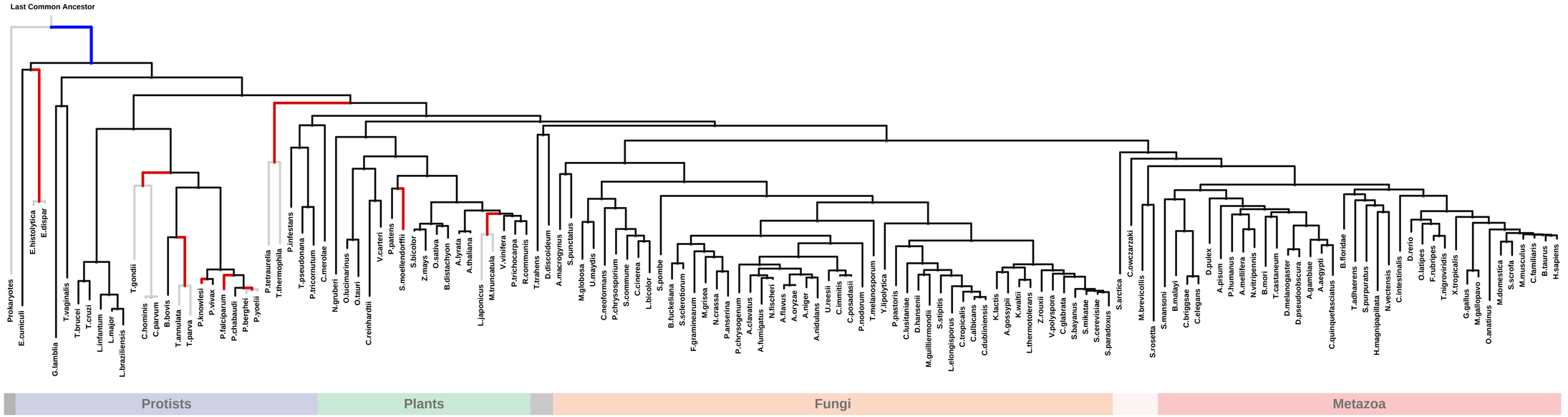


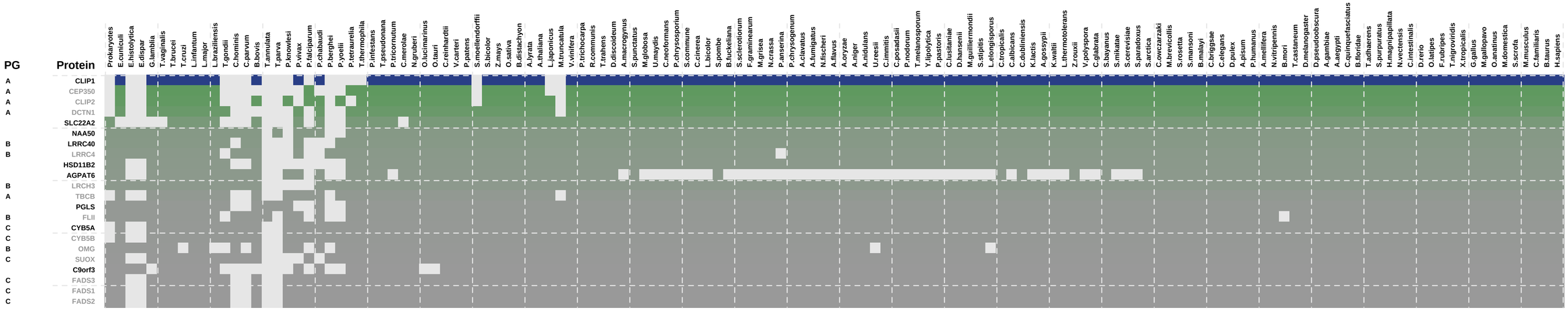
PG	Protein	LLR	Notes
	DTYMK	0.5	
	100510065	0.4	
	SNF8	0.1	1
B	LRRTM3	0.1	2
	PPP2R1B	0.0	

1: late endosome membrane || 2: postsynaptic membrane

ECM 4, Gene set "microtubule plus end", Page 1

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

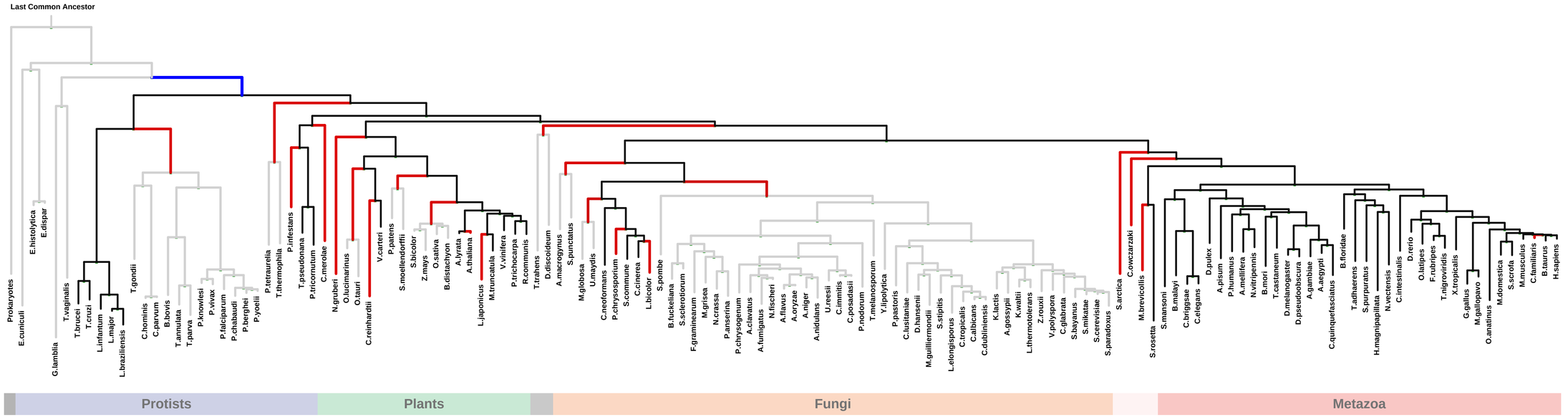


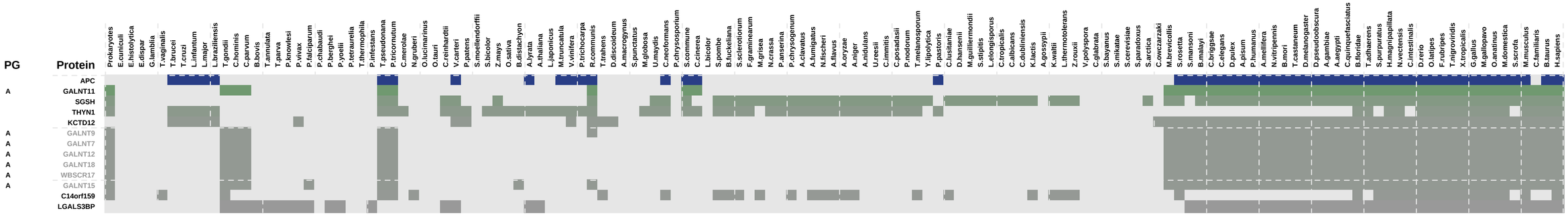


1: cytoplasmic microtubule || 2: cytoplasmic vesicle membrane || 3: endosome || 4: intermediate filament || 5: kinetochore || 6: microtubule cytoskeleton || 7: microtubule plus end || 8: ruffle || 9: spindle || 10: microtubule associated complex ||
11: cell leading edge || 12: cytoplasmic dynein complex || 13: spindle pole || 14: postsynaptic membrane || 15: mitochondrial outer membrane || 16: anchored to membrane || 17: mitochondrial intermembrane space

ECM 5, Gene set "microtubule plus end", Page 1

Num of ECM Genes: 1. Num of Predicted Genes: 12

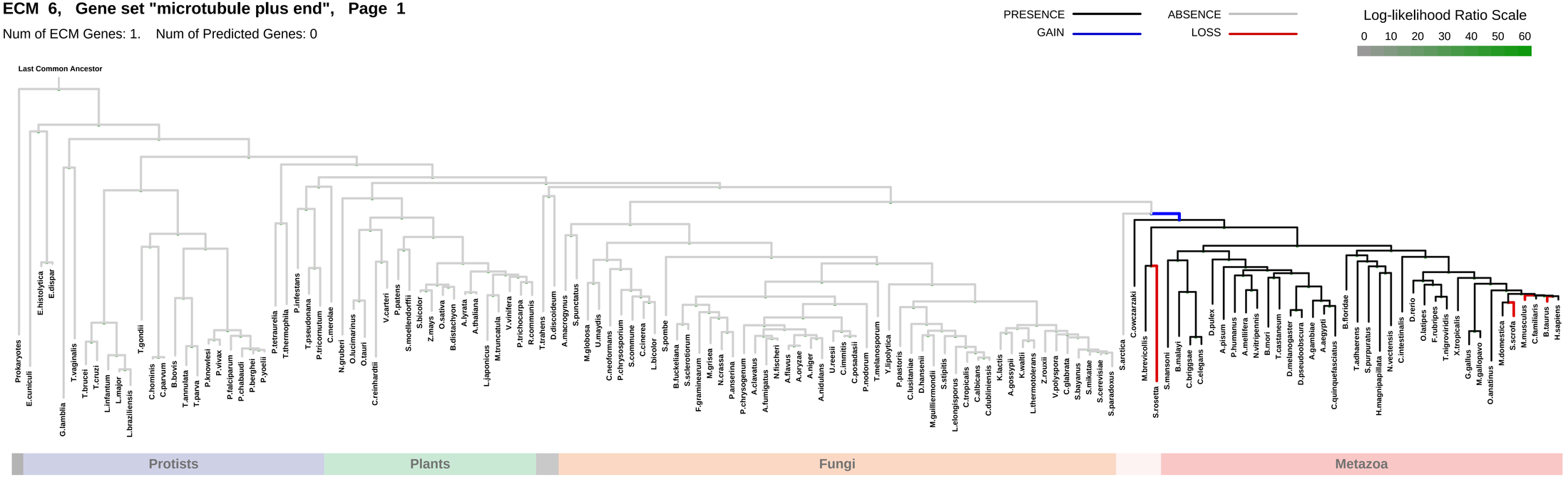




1: axonal growth cone || 2: beta-catenin destruction complex || 3: cell-cell adherens junction || 4: cytoplasmic microtubule || 5: kinetochore || 6: lamellipodium || 7: lateral plasma membrane || 8: microtubule plus end || 9: ruffle membrane ||
10: synapse || 11: tight junction || 12: lysosomal lumen || 13: postsynaptic membrane || 14: presynaptic membrane || 15: receptor complex || 16: transport vesicle || 17: extracellular matrix || 18: proteinaceous extracellular matrix

ECM 6, Gene set "microtubule plus end", Page 1

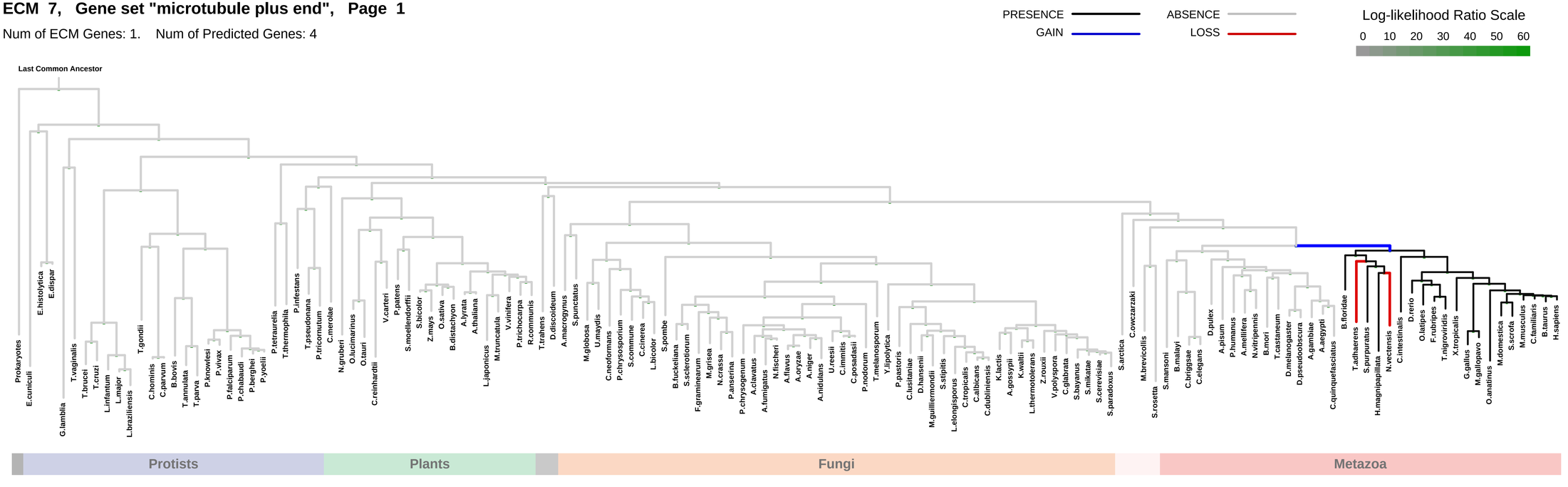
Num of ECM Genes: 1. Num of Predicted Genes: 0



1: actin cytoskeleton || 2: axon || 3: axon part || 4: basal plasma membrane || 5: basement membrane || 6: cell cortex || 7: cell leading edge || 8: cytoplasmic membrane-bounded vesicle || 9: H zone || 10: hemidesmosome ||
11: intermediate filament || 12: intermediate filament cytoskeleton || 13: microtubule cytoskeleton || 14: microtubule plus end || 15: nuclear envelope || 16: Z disc

ECM 7, Gene set "microtubule plus end", Page 1

Num of ECM Genes: 1. Num of Predicted Genes: 4

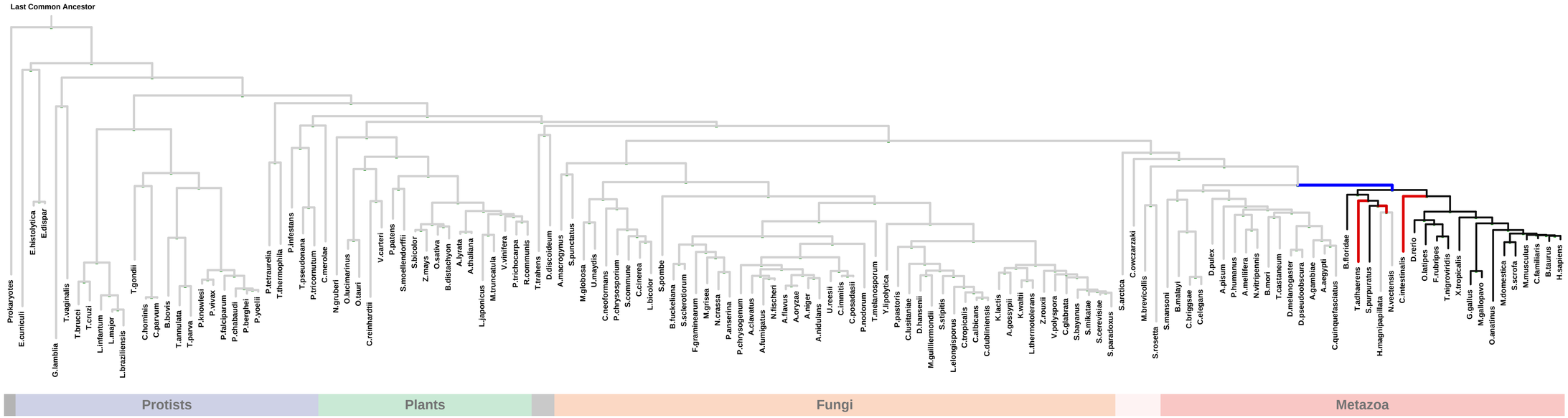


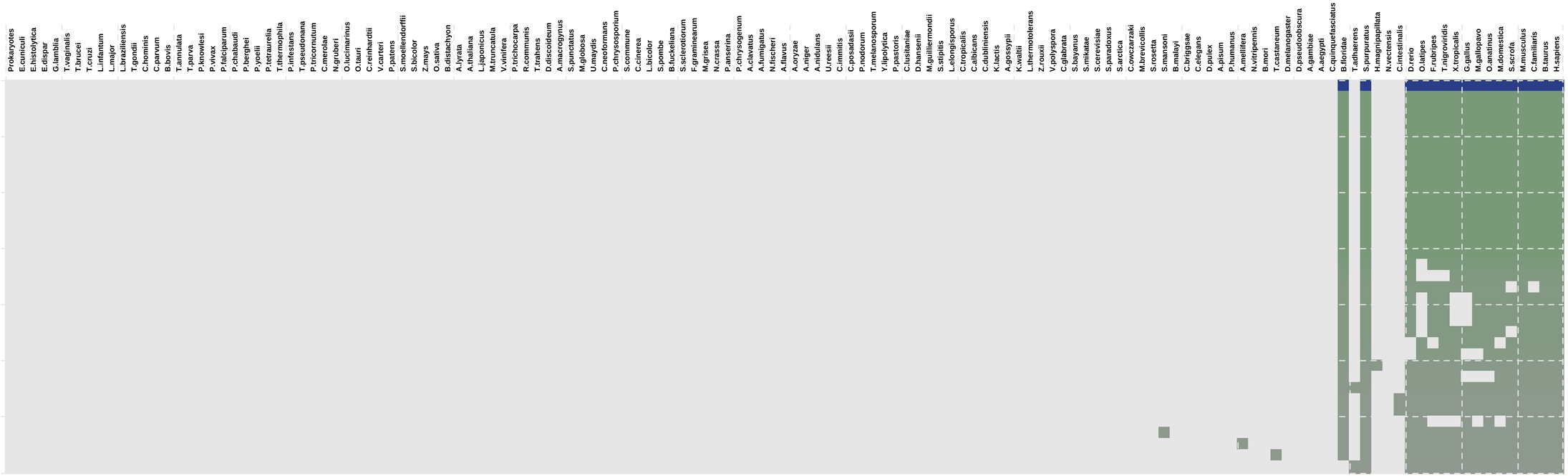
PG	Protein	LLR	Notes
	MLPH		1 / 2 / 3 / 4
	IMPG1	6.3	5
	NXPE1	1.2	
	SLAIN1	1.2	
	IRF6	0.7	

1: cortical actin cytoskeleton || 2: microtubule organizing center || 3: microtubule plus end || 4: stress fiber || 5: proteinaceous extracellular matrix

ECM 8, Gene set "microtubule plus end", Page 1

Num of ECM Genes: 1. Num of Predicted Genes: 54

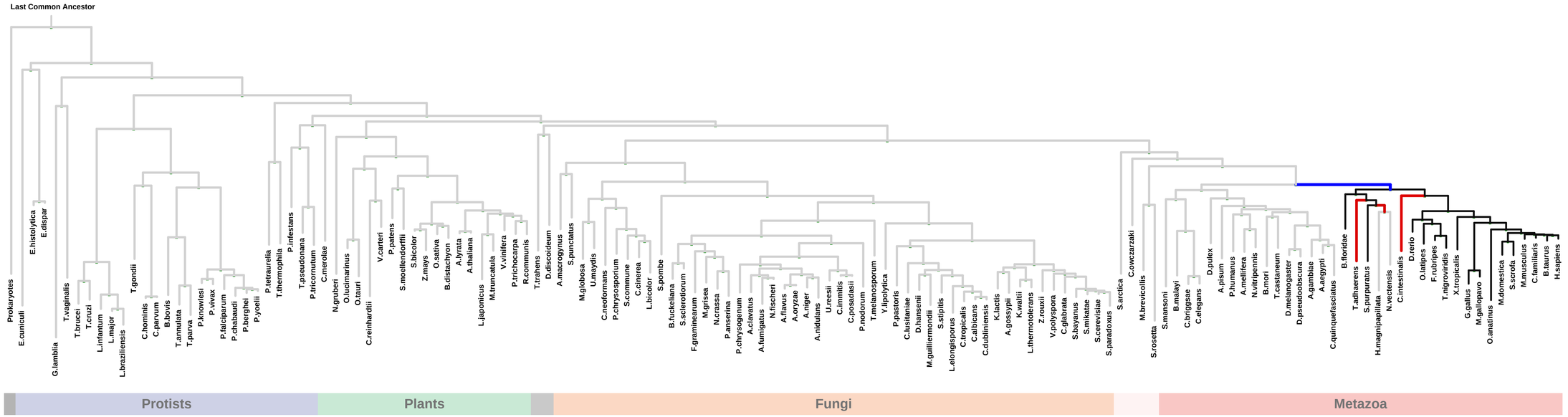


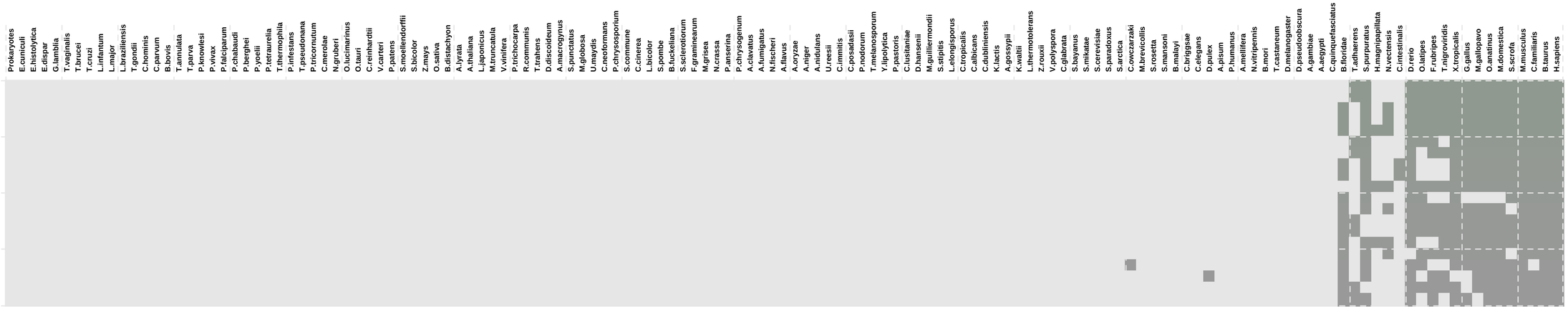


1: microtubule cytoskeleton || 2: microtubule plus end || 3: cytoplasmic membrane-bounded vesicle || 4: CD40 receptor complex || 5: internal side of plasma membrane || 6: mitochondrial intermembrane space || 7: Cajal body ||
8: small nuclear ribonucleoprotein complex || 9: spliceosomal complex || 10: endoplasmic reticulum lumen || 11: endosome || 12: Golgi lumen || 13: cytoplasmic vesicle membrane || 14: endoplasmic reticulum-Golgi intermediate compartment ||
15: BLOC-1 complex || 16: transport vesicle || 17: HAUS complex || 18: spindle || 19: high-density lipoprotein particle || 20: chromatin || 21: Fanconi anaemia nuclear complex || 22: chromosome, centromeric region || 23: proteinaceous extracellular matrix ||

ECM 8, Gene set "microtubule plus end", Page 2

Num of ECM Genes: 1. Num of Predicted Genes: 54



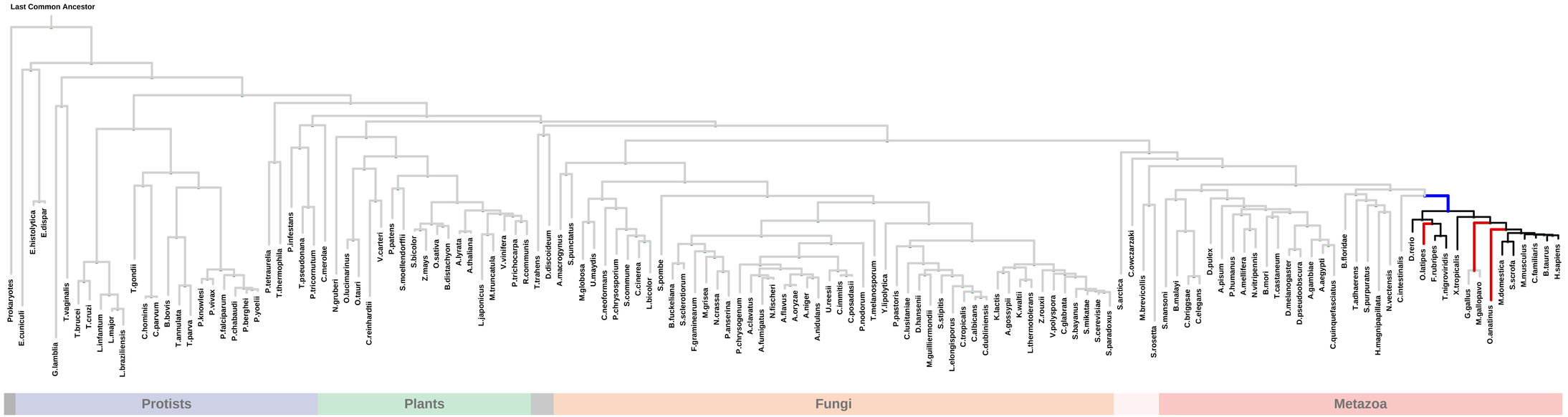


PG	Protein	LLR	Notes
	HBQ1	4.3	1
H	GPBP1	4.3	
	TNFSF15	4.0	
	OR8J3	4.0	
E	PRRT1	3.8	
	MTIF3	2.9	
	CCDC125	2.4	2
	C9orf9	2.1	
	SIRPD	2.1	
	BCL2L1	1.9	3 / 4 / 5
	PNMA5	1.5	
	RD3	1.4	
	SYNC	1.1	6 / 7 / 8 / 9
	OR52W1	1.1	
	MEI1	0.8	
	FAM181A	0.7	
	TMEM251	0.5	
G	SAA1	0.1	10
	CARD18	0.1	
	CCDC73	0.1	

1: hemoglobin complex || 2: intermediate filament cytoskeleton || 3: Bcl-2 family protein complex || 4: mitochondrial outer membrane || 5: nuclear membrane || 6: intermediate filament || 7: neuromuscular junction || 8: sarcolemma || 9: Z disc || 10: high-density lipoprotein particle

ECM 9, Gene set "microtubule plus end", Page 1

Num of ECM Genes: 1. Num of Predicted Genes: 52

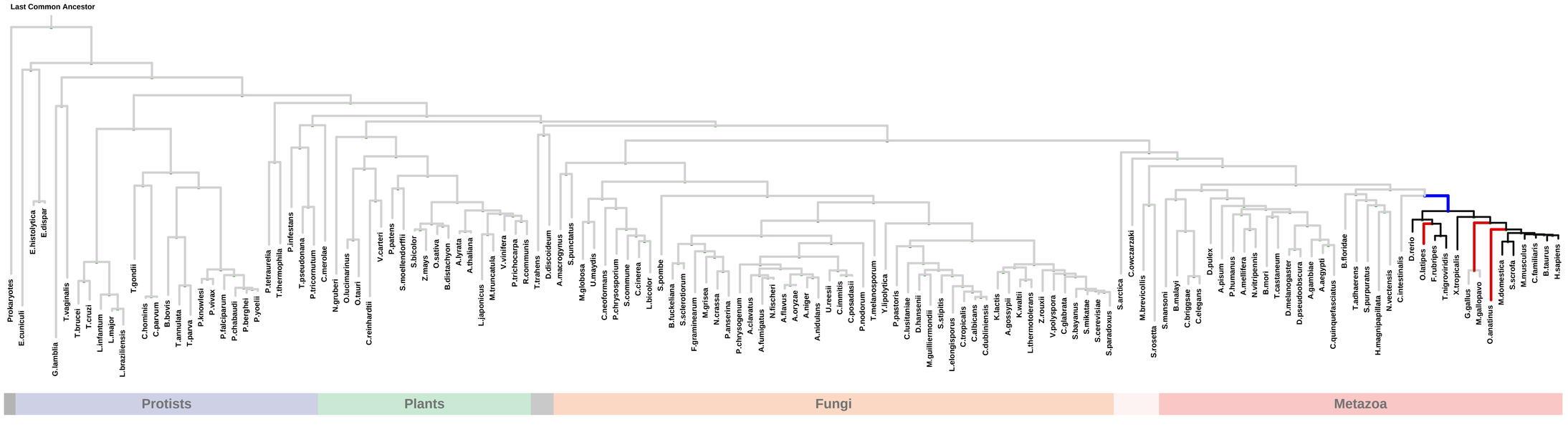


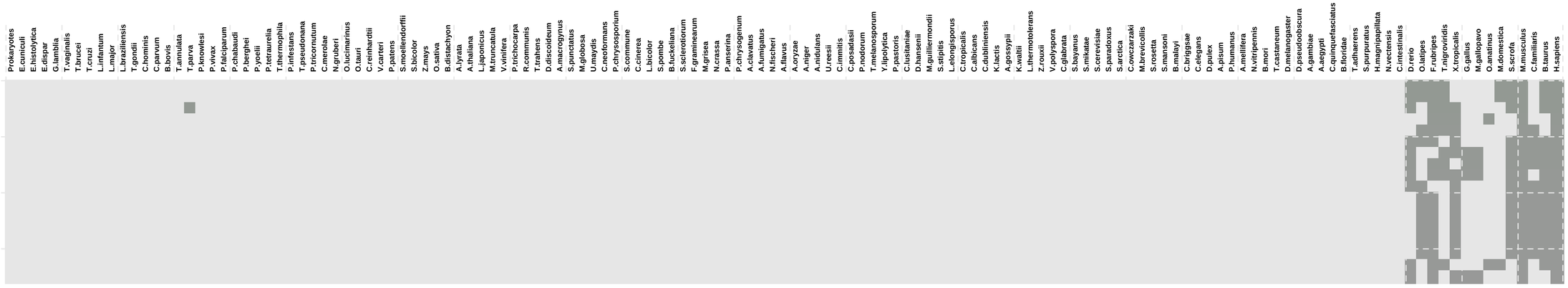
PG	Protein	LLR	Notes
	SPAG5		1 / 2 / 3 / 4 / 5 / 6
	LOC646543	7.2	
	C1orf210	7.2	
	C11orf53	6.8	
	TMEM71	6.8	
A	CAMK2N2	5.8	
	C1orf51	5.8	
	NDUFA3	5.8	7
	NPW	5.8	
A	CAMK2N1	5.8	8 / 9
	C19orf26	5.6	
	DEXI	5.5	
	SMIM10	5.4	
	SYCN	5.4	10 / 11
	SMIM1	5.4	
	MARVELD1	5.1	
	PYDC1	5.1	12
	C1orf172	4.3	
	PRRT3	4.3	
	APOF	4.1	13 / 14
	MGP	4.0	15 / 16
	REP15	4.0	17
	SPACA4	3.6	18 / 19
B	LOC100294020	3.6	
B	LOC100294020	3.6	
	BCL2L12	3.5	
	C2orf80	3.5	
	TCTA	3.3	
	ECM1	3.3	15 / 16
	MLIP	3.2	20 / 21 / 22
	C1orf226	3.2	
	CD58	3.1	19
C	LOC100129626	3.0	
C	TOMM5	3.0	23
C	100510530	3.0	

1: condensed chromosome kinetochore || 2: kinetochore || 3: microtubule plus end || 4: mitotic spindle || 5: spindle microtubule || 6: spindle pole || 7: mitochondrial respiratory chain complex I || 8: postsynaptic density ||
9: postsynaptic membrane || 10: secretory granule membrane || 11: transport vesicle membrane || 12: IkappaB kinase complex || 13: high-density lipoprotein particle || 14: low-density lipoprotein particle || 15: extracellular matrix ||
16: proteinaceous extracellular matrix || 17: early endosome membrane || 18: acrosomal vesicle || 19: anchored to membrane || 20: nuclear envelope || 21: nuclear lumen || 22: PML body || 23: mitochondrial outer membrane translocase complex

ECM 9, Gene set "microtubule plus end", Page 2

Num of ECM Genes: 1. Num of Predicted Genes: 52



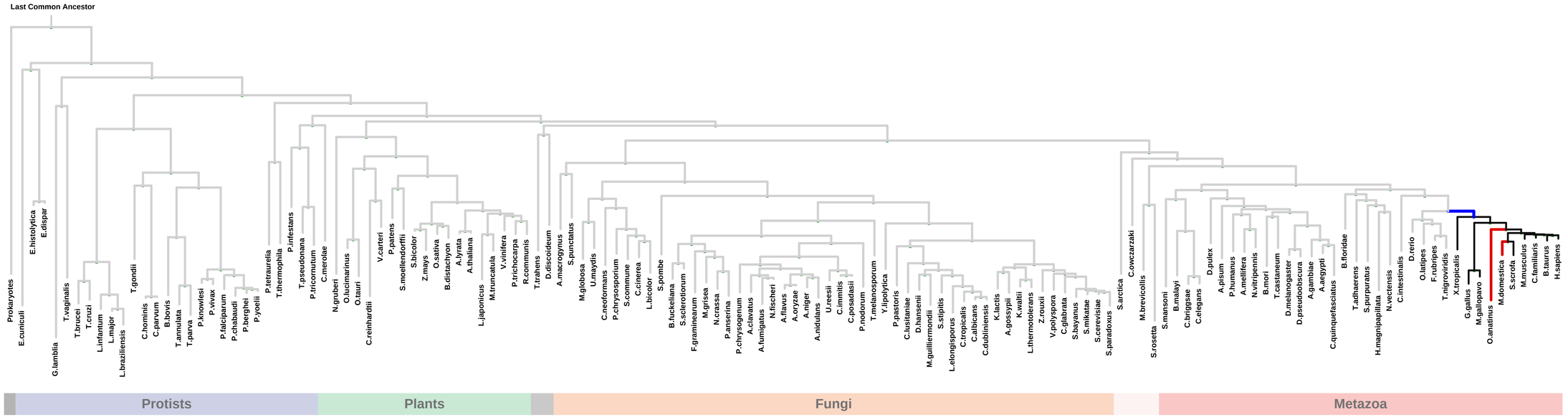


PG	Protein	LLR	Notes
	C19orf67	2.5	
	C19orf67	2.5	
	TMEM202	2.4	
	C1orf127	2.2	
	LOC728056	1.9	
	OMP	1.8	1
	CENPW	1.6	2 / 3 / 4 / 5
	LOC100128160	1.6	
	SYCE3	1.2	6 / 7
	LOC649201	1.1	
D	FAM197Y5	1.0	
D	FAM197Y6	1.0	
D	FAM197Y7	1.0	
D	FAM197Y8	1.0	
D	FAM197Y9	1.0	
D	FAM197Y4	1.0	
	VGF	1.0	8 / 9 / 10 / 11
	SLX4IP	0.6	

1: axon || 2: chromosome, centromeric region || 3: condensed chromosome kinetochore || 4: kinetochore || 5: nuclear matrix || 6: central element || 7: chromosome || 8: cytoplasmic vesicle || 9: neuron projection ||
10: secretory granule membrane || 11: transport vesicle

ECM 10, Gene set "microtubule plus end", Page 1

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



PG	Protein	LLR	Notes
	KNSTRN		1 / 2 / 3 / 4 / 5
	C20orf173	8.9	
	C9orf129	8.9	
	CCDC107	8.9	
	FAM64A	8.9	
A	LOC100507035	7.8	
	IL9	7.0	
	AC010731.4	7.0	
	EVI2B	6.0	
	SELPLG	6.0	
	C2orf72	6.0	
	C9orf152	4.2	
	COX8C	4.2	
	UTS2B	4.1	
	C18orf42	1.2	
	C11orf52	0.3	
	LNP1	0.3	
A	GOLGA6L10	0.3	
A	GOLGA6L3	0.3	
	PTMS	0.3	
A	GOLGA6L9	0.3	
	IL4	0.3	6

1: condensed chromosome kinetochore || 2: kinetochore || 3: microtubule plus end || 4: mitotic spindle || 5: spindle pole || 6: external side of plasma membrane