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

Dataset:

Num of genes in input gene set: 8
Total number of genes: 20834
Prediction LLR threshold: 0

The CLIME PDF output two sections:

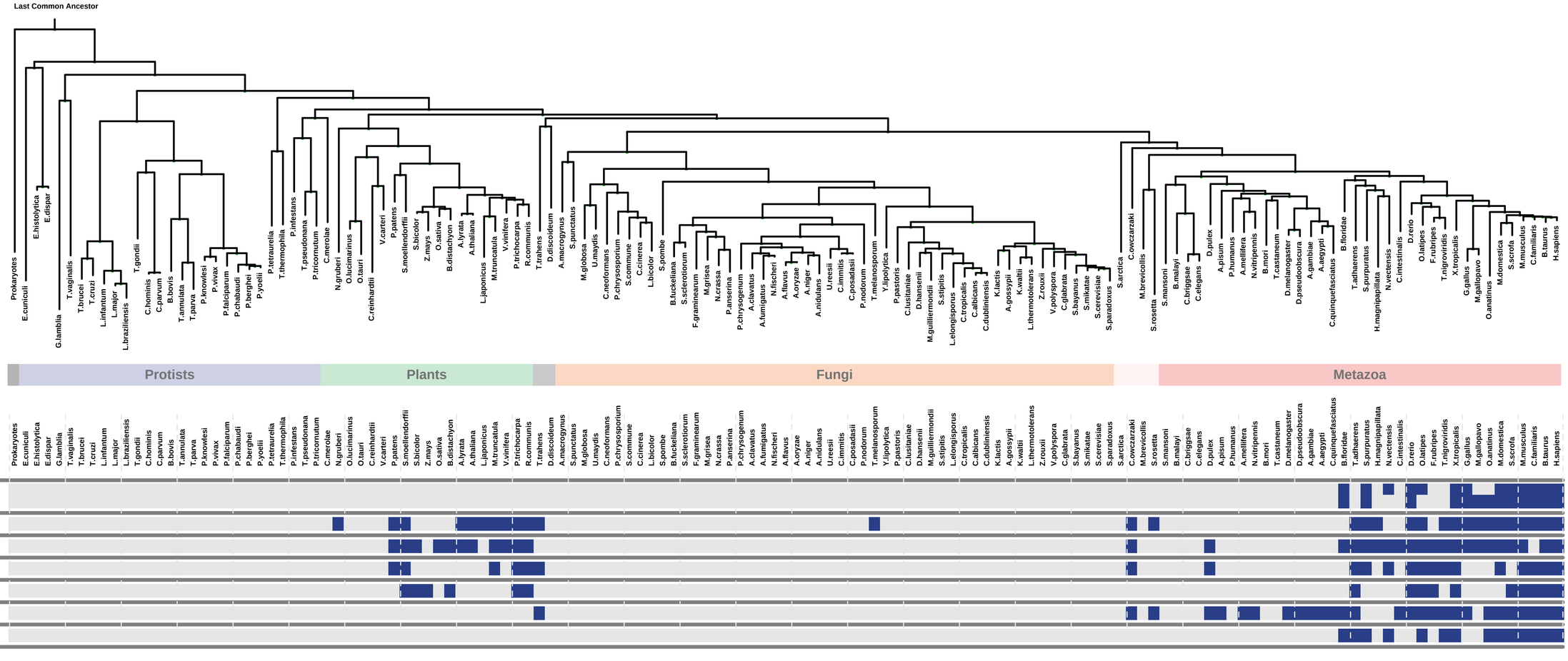
1) Overview of Evolutionarily Conserved Modules (ECMs)

- 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)

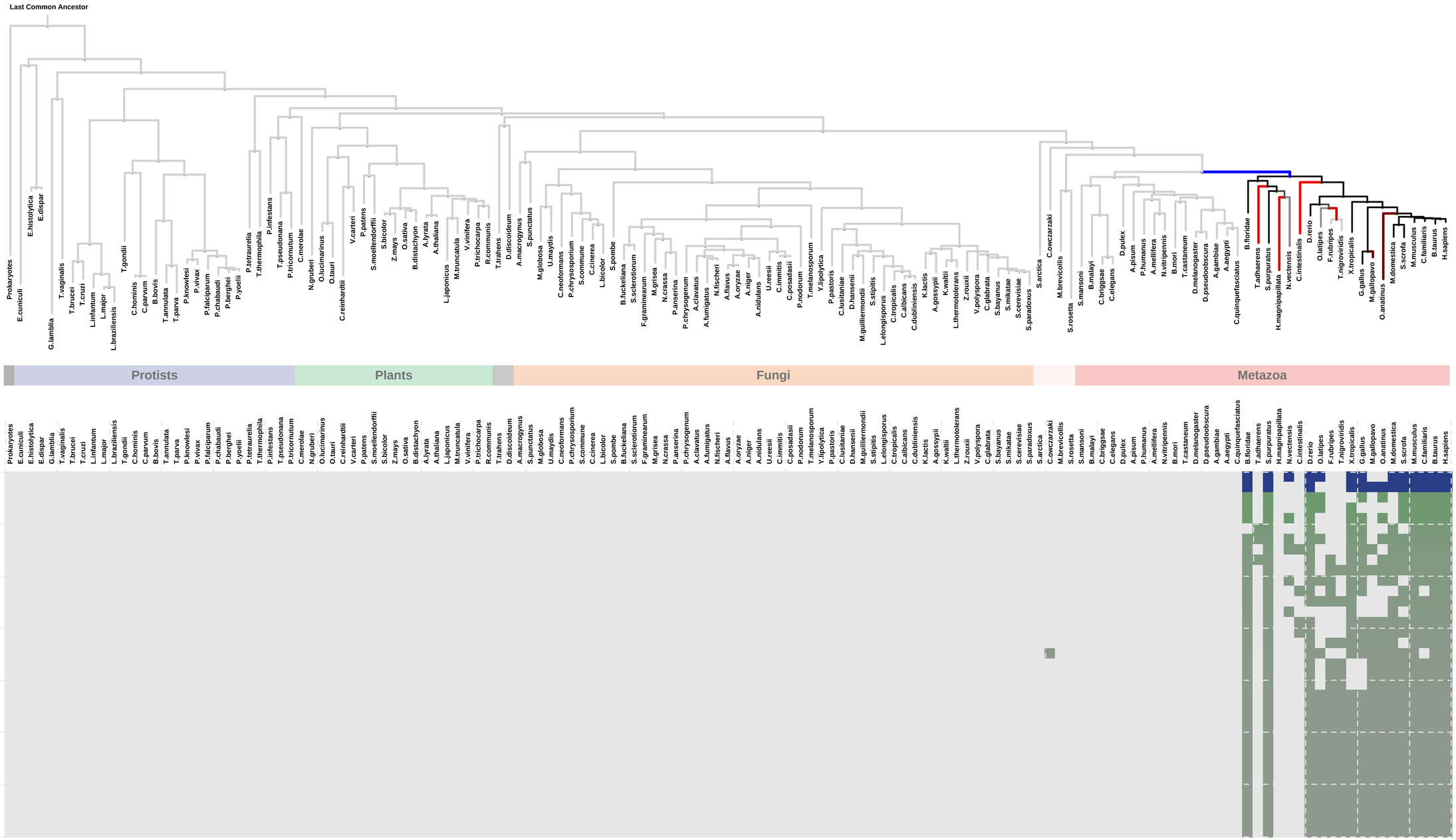


ECM 1, Gene set "HAUS complex", Page 1

Num of ECM Genes: 2. Num of Predicted Genes: 63. ECM Strength: 0.0

PRESENCE — GAIN — ABSENCE — LOSS

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



PG	Protein	LLR	Notes
	HAUS8		1 / 2
	HAUS2		1 / 3
	AKIP1	18.3	
	PNMA5	17.9	
	FSIP1	17.1	
	C14orf80	13.1	
	FANCE	12.1	4
	FBXL8	10.2	
	CCDC73	9.7	
	BLOC1S5	9.5	5 / 6
	CASC5	9.1	7 / 8
	C11orf88	8.9	
	GPS2	8.4	9
	C10orf35	8.0	
	C9orf9	6.7	
	SIRPD	6.7	
	FANCC	6.7	4 / 10
	TMEM251	6.5	
A	SAA2-SAA4	6.4	
A	SAA4	6.4	11
A	SAA2	6.4	11
	GEMIN4	5.3	12 / 13 / 14
B	FAM171A2	5.3	
C	IFITM1	5.3	
C	IFITM2	5.3	
B	FAM171B	5.3	
D	NGF	5.3	15 / 16 / 17
D	NTF3	5.3	18
D	NTF4	5.3	15
	FAM198B	5.3	
D	BDNF	5.3	18
	DIABLO	5.3	19 / 20 / 21
	FAM133B	5.3	
B	FAM171A1	5.3	
	SLAIN2	5.3	22 / 23

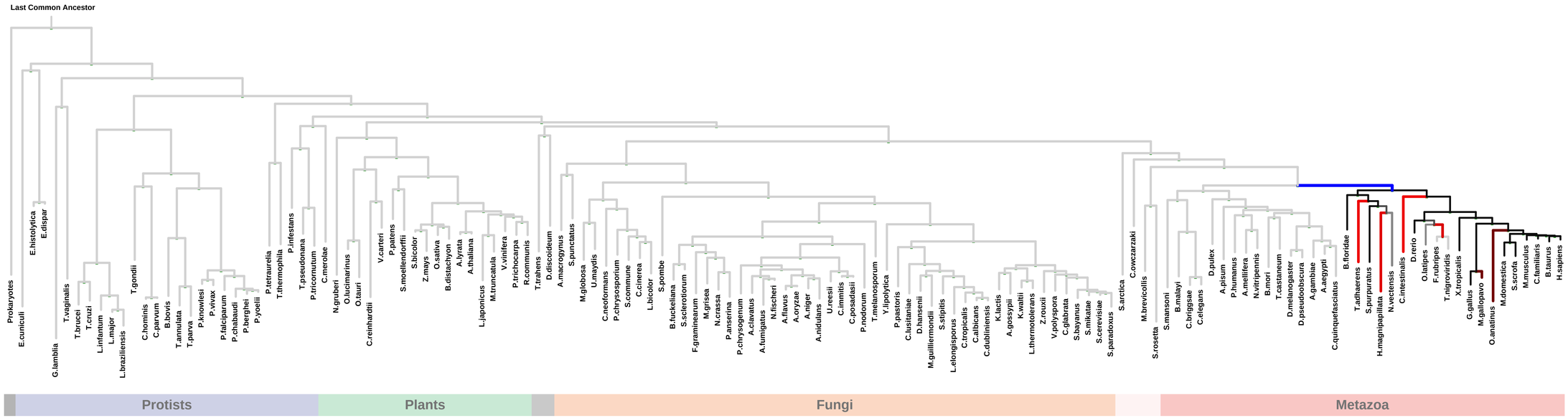
1: HAUS complex || 2: spindle pole || 3: spindle || 4: Fanconi anaemia nuclear complex || 5: BLOC-1 complex || 6: transport vesicle || 7: acrosomal vesicle || 8: condensed chromosome kinetochore || 9: transcriptional repressor complex ||
10: chromatin || 11: high-density lipoprotein particle || 12: Cajal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

ECM 1, Gene set "HAUS complex", Page 2

Num of ECM Genes: 2. Num of Predicted Genes: 63. ECM Strength: 0.0

PRESENCE — GAIN — ABSENCE — LOSS

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



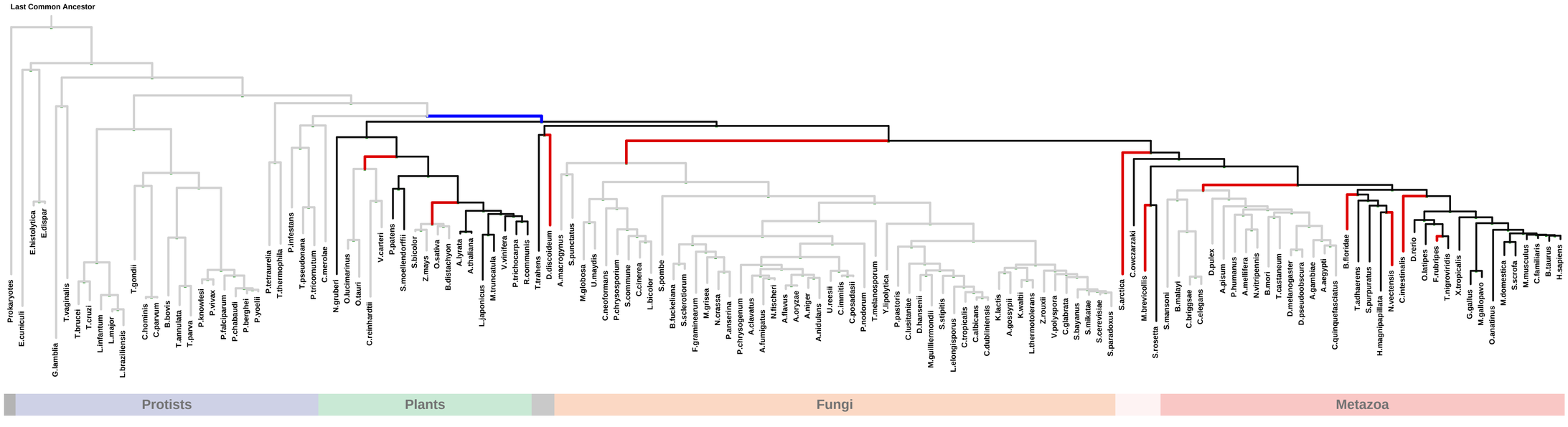
1: cytoplasmic vesicle membrane || 2: endoplasmic reticulum-Golgi intermediate compartment || 3: endomembrane system || 4: gamma-tubulin ring complex || 5: spindle || 6: chromosome, centromeric region || 7: anchored to external side of plasma membrane || 8: sarcolemma || 9: sarcoplasmic reticulum || 10: endosome || 11: integral to organelle membrane || 12: proteinaceous extracellular matrix

ECM 2, Gene set "HAUS complex", Page 1

Num of ECM Genes: 1. Num of Predicted Genes: 5

PRESENCE — GAIN — ABSENCE — LOSS

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



PG	Protein	LLR	Notes
	HAUS1		1 / 2
A	BPIFB2	19.8	
A	BPIFB4	7.3	
	COMMD1	4.5	3
	HAUS4	3.5	1 / 4
	C9orf72	1.1	

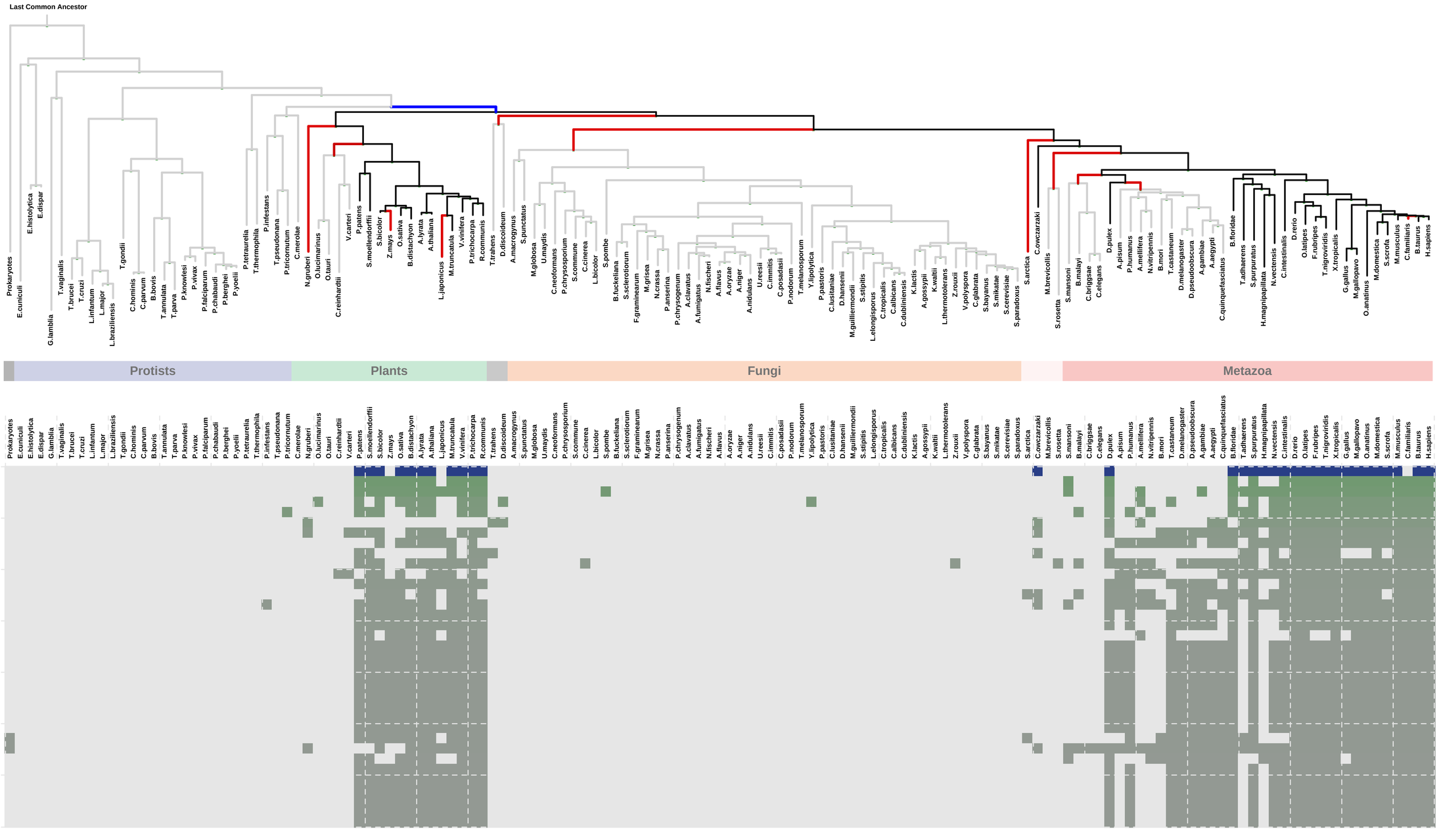
1: HAUS complex || 2: spindle pole || 3: Cul2-RING ubiquitin ligase complex || 4: spindle

ECM 3, Gene set "HAUS complex", Page 1

Num of ECM Genes: 1. Num of Predicted Genes: 49

PRESENCE — GAIN — ABSENCE — LOSS

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



PG	Protein	LLR	Notes
	HAUS3		1 / 2
	TMEM45A	17.1	
	100287665	15.7	
	FBXO7	11.9	3
A	YY1AP1	11.3	
	BCAS4	8.7	
	NUB1	6.3	
B	ZMYM1	6.2	
	HAUS4	5.4	1 / 2
A	GON4L	5.1	
B	ZNF862	4.9	
C	ST8SIA6	4.7	4
	DDA1	4.4	
	RBM48	4.2	
C	ST8SIA1	4.2	4
C	ST8SIA5	4.2	4
	PDCD7	3.2	5
C	ST6GALNAC5	2.9	4
C	ST3GAL1	2.9	4 / 6
C	ST3GAL2	2.9	4 / 6
C	ST3GAL3	2.9	4 / 6
C	ST3GAL4	2.9	4 / 6
C	ST6GAL1	2.9	4 / 6
C	ST6GAL2	2.9	4 / 6
C	ST6GALNAC2	2.9	4
C	ST6GALNAC3	2.9	4
	GDAP1	2.9	7
	CPAMD8	2.8	
	SAAL1	2.4	
C	ST6GALNAC6	2.4	4
C	ST6GALNAC1	2.4	4
C	ST8SIA2	2.4	4
C	ST8SIA3	2.4	4
C	ST8SIA4	2.4	4
C	ST3GAL5	2.4	4

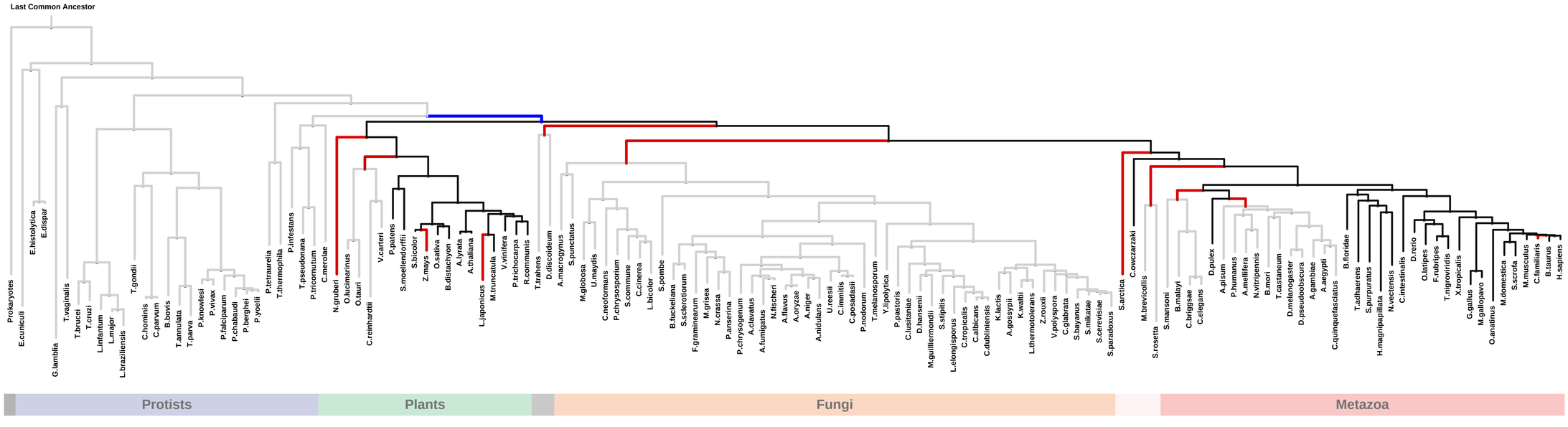
1: HAUS complex || 2: spindle || 3: ubiquitin ligase complex || 4: integral to Golgi membrane || 5: U12-type spliceosomal complex || 6: Golgi cisterna membrane || 7: integral to mitochondrial outer membrane

ECM 3, Gene set "HAUS complex", Page 2

Num of ECM Genes: 1. Num of Predicted Genes: 49

PRESENCE — GAIN — ABSENCE — LOSS

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



PG	Protein	LLR	Notes
D	FOLR2	2.2	1
D	FOLR3	2.2	2
D	FOLR4	2.2	
D	FOLR1	2.2	1
	UNC93B1	2.2	3 / 4 / 5
	SIAH3	2.0	
	TMEM230	1.9	
	TMEM8B	1.3	
E	CLEC2A	1.0	
	TMEM259	1.0	
C	ST3GAL6	1.0	6
E	CLEC17A	0.7	
	EAF2	0.5	7
	ZNF385B	0.5	
C	ST6GALNAC4	0.0	6

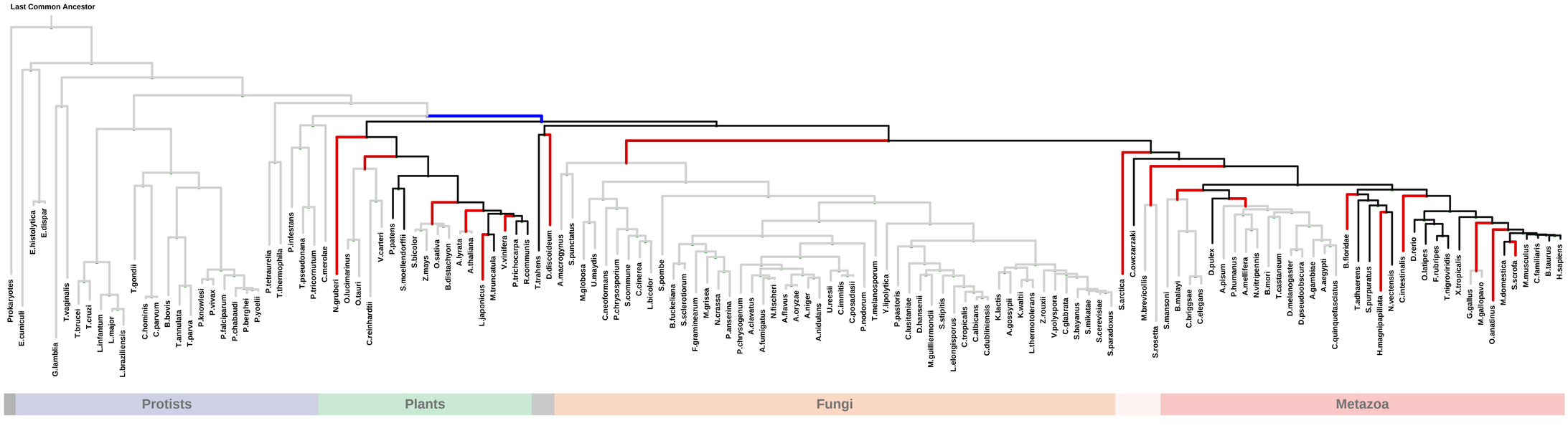
1: anchored to membrane || 2: extrinsic to membrane || 3: early phagosome || 4: endosome || 5: lysosome || 6: integral to Golgi membrane || 7: nuclear speck

ECM 4, Gene set "HAUS complex", Page 1

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

PRESENCE — GAIN — ABSENCE — LOSS

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



PG	Protein	LLR	Notes
	HAUS4		1 / 2
	BPIFB2	30.8	
	SDHAF1	21.3	
	TEX11	16.4	3
	C1orf109	1.9	
	BCAS4	0.9	
	C9orf72	0.8	
	NCDN	0.4	4 / 5

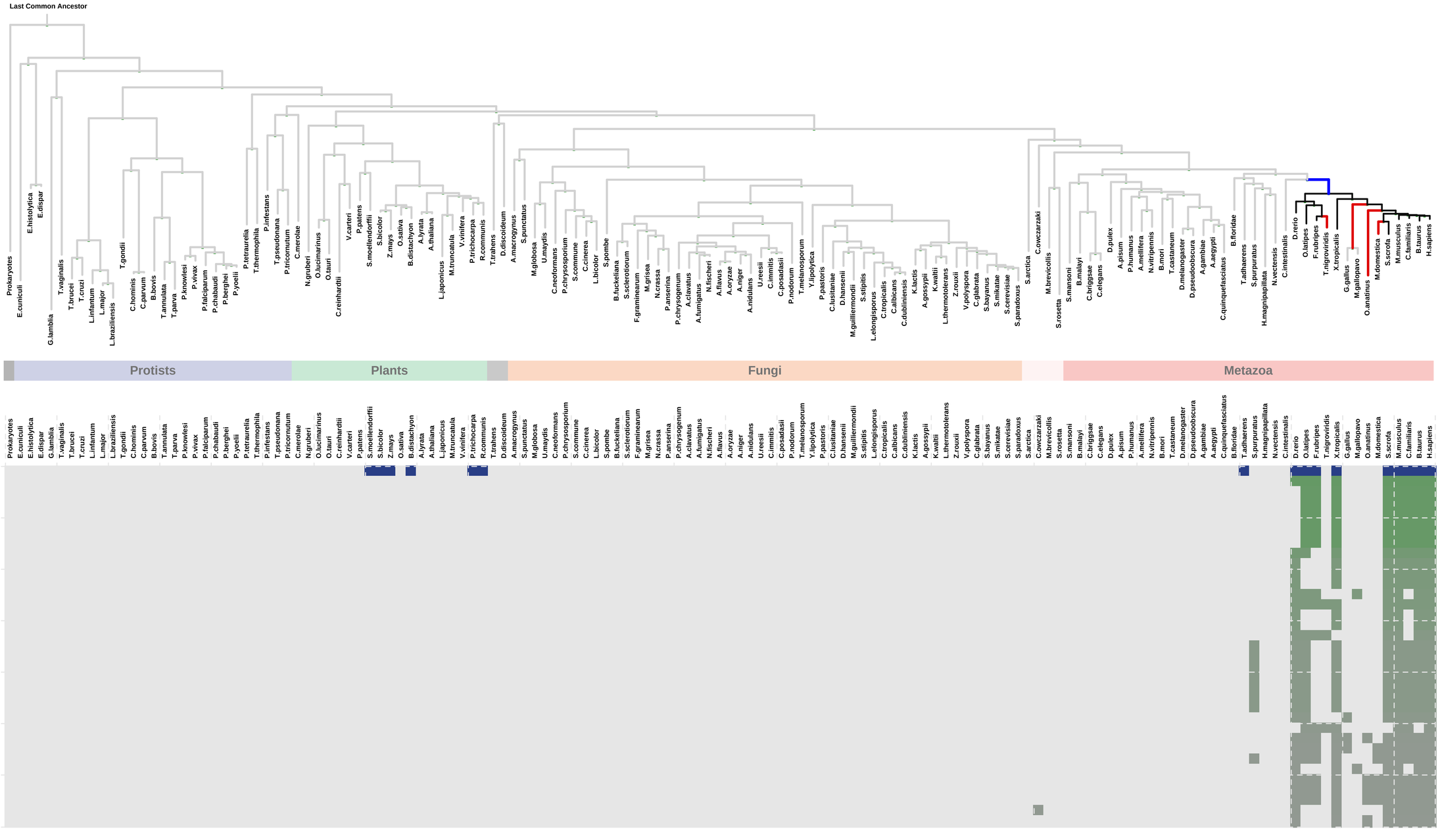
1: HAUS complex || 2: spindle || 3: central element || 4: axon || 5: dendrite

ECM 5, Gene set "HAUS complex", Page 1

Num of ECM Genes: 1. Num of Predicted Genes: 83

PRESENCE — GAIN — ABSENCE — LOSS

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



PG	Protein	LLR	Notes
	HAUS5		1 / 2
	OMP	22.2	3
A	FAM197Y5	21.4	
A	FAM197Y6	21.4	
A	FAM197Y7	21.4	
A	FAM197Y8	21.4	
A	FAM197Y9	21.4	
A	FAM197Y4	21.4	
B	LOC649201	16.0	
	SMIM10	12.5	
	SMIM1	12.5	
	SYCN	12.5	4 / 5
	TMEM221	11.6	
	CD58	11.4	6
	C2orf80	10.6	
	BCL2L12	10.6	
	NPFF	8.1	
B	PNMA3	6.8	
B	PNMA6A	6.8	
B	PNMA6C	6.8	
B	PNMA6D	6.8	
B	LOC649238	6.8	
B	MOAP1	6.8	
B	100287500	6.8	
	NMS	5.4	
	LOC728056	4.7	
	MAP9	3.7	2
	GOLM1	3.5	
	SNAPC2	3.5	
	SLN	3.3	7 / 8
	CD33	3.3	9
	VN1R2	3.3	
	TCAP	3.3	10 / 11
	C19orf66	3.3	
	TMEM218	3.1	

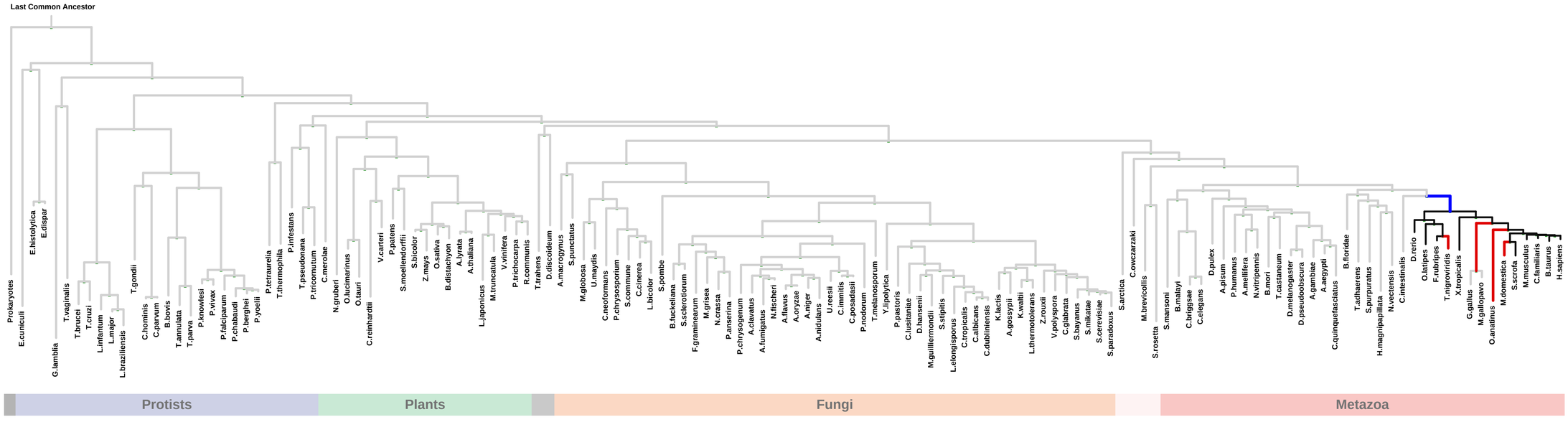
1: HAUS complex || 2: spindle || 3: axon || 4: secretory granule membrane || 5: transport vesicle membrane || 6: anchored to membrane || 7: sarcoplasmic reticulum || 8: sarcoplasmic reticulum membrane || 9: external side of plasma membrane || 10: I band || 11: Z disc

ECM 5, Gene set "HAUS complex", Page 2

Num of ECM Genes: 1. Num of Predicted Genes: 83

PRESENCE — GAIN — ABSENCE — LOSS

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



PG	Protein	LLR	Notes
C	100505680	2.5	
	SLX4IP	2.4	
D	NBPF12	2.3	
D	LOC100506032	2.3	
D	NBPF1	2.3	
D	NBPF11	2.3	
D	NBPF14	2.3	
D	NBPF15	2.3	
D	NBPF16	2.3	
D	NBPF24	2.3	
D	NBPF3	2.3	
D	NBPF4	2.3	
D	NBPF5P	2.3	
D	NBPF6	2.3	
D	NBPF7	2.3	
D	NBPF9	2.3	
	C10orf54	2.3	
	TMEM87A	2.2	
	CLDND2	2.1	
	649887	2.1	
	RAD54B	2.0	
	TCOF1	2.0	
	SLC51B	2.0	
	NPW	1.9	
	C1orf51	1.9	
	NDUFA3	1.9	1
E	CAMK2N1	1.9	2 / 3
E	CAMK2N2	1.9	
	APOL1	1.9	4 / 5 / 6
	IL6	1.6	7 / 8
	SGOL2	1.5	9 / 10 / 11
	DEXI	1.3	
	HMGN3	1.3	12
	MARVELD1	1.1	
	PYDC1	1.1	13

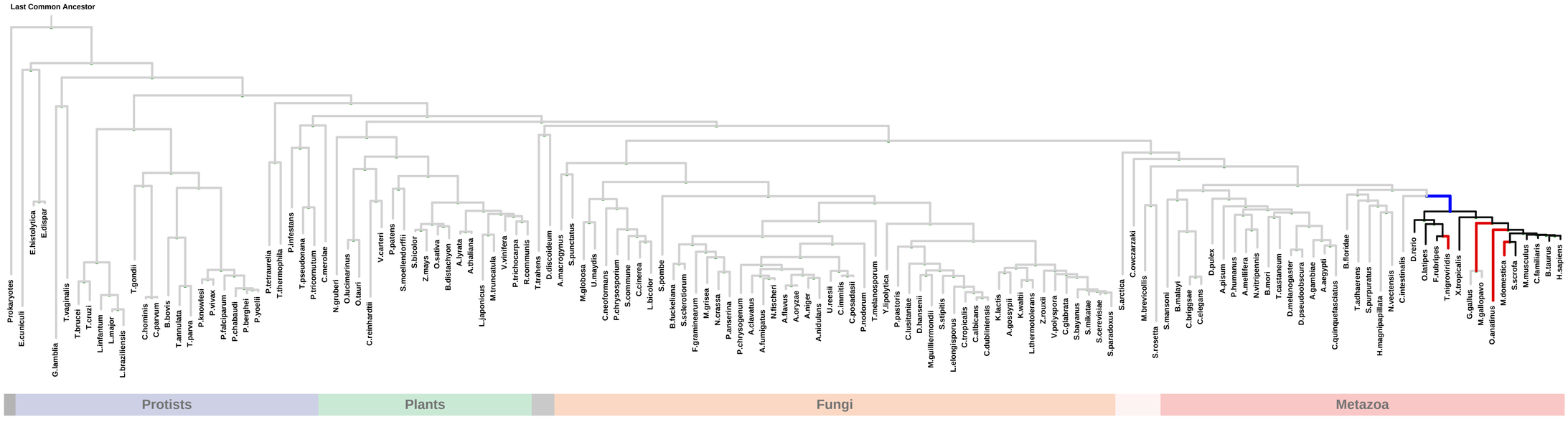
1: mitochondrial respiratory chain complex I || 2: postsynaptic density || 3: postsynaptic membrane || 4: high-density lipoprotein particle || 5: intrinsic to membrane || 6: very-low-density lipoprotein particle || 7: external side of plasma membrane || 8: interleukin-6 receptor complex || 9: chromosome, centromeric region || 10: condensed chromosome kinetochore || 11: mitotic cohesin complex || 12: chromatin || 13: IkappaB kinase complex

ECM 5, Gene set "HAUS complex", Page 3

Num of ECM Genes: 1. Num of Predicted Genes: 83

PRESENCE — GAIN — ABSENCE — LOSS

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



PG	Protein	LLR	Notes
	LOC390638	1.0	
C	LOC441736	1.0	
	FLJ38723	1.0	
	UCMA	0.9	1 / 2
F	TOMM5	0.8	3
F	LOC100129626	0.8	
F	100510530	0.8	
G	PLGLB1	0.7	
G	PLGLB2	0.7	
	TRIQK	0.7	
	TEX12	0.4	4
	APOF	0.2	5 / 6
	C12orf75	0.2	
	REP15	0.1	7

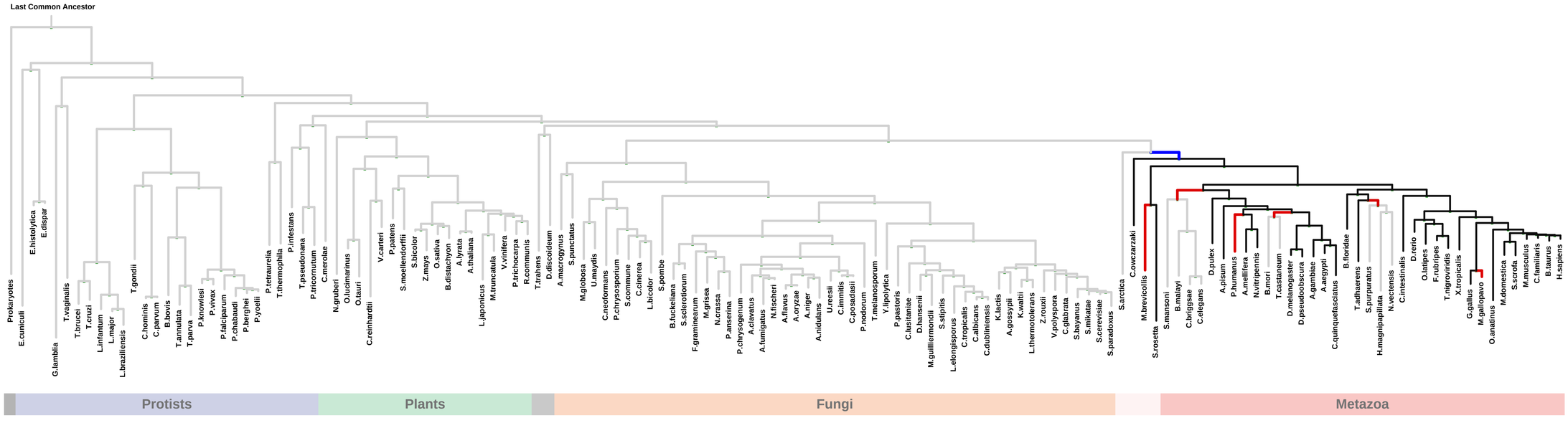
1: aggresome || 2: proteinaceous extracellular matrix || 3: mitochondrial outer membrane translocase complex || 4: synaptonemal complex || 5: high-density lipoprotein particle || 6: low-density lipoprotein particle || 7: early endosome membrane

ECM 6, Gene set "HAUS complex", Page 1

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

PRESENCE — GAIN — ABSENCE — LOSS

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



PG	Protein	LLR	Notes
	HAUS6		1 / 2
	AGTRAP	11.2	3
	NRM	0.8	4 / 5

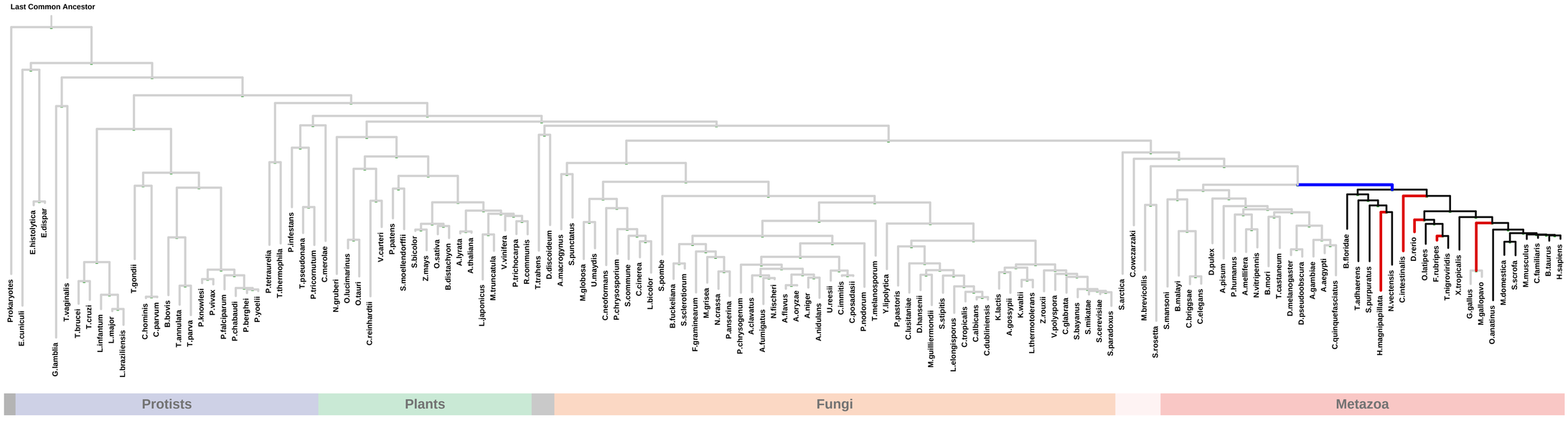
1: HAUS complex || 2: spindle || 3: cytoplasmic vesicle membrane || 4: nuclear envelope || 5: nuclear inner membrane

ECM 7, Gene set "HAUS complex", Page 1

Num of ECM Genes: 1. Num of Predicted Genes: 10

PRESENCE — GAIN — ABSENCE — LOSS

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



PG	Protein	LLR	Notes
	HAUS7		1 / 2
	MEDAG	7.7	
	C12orf63	6.5	
	C12orf63	6.5	
	CENPQ	5.9	3
	MAP10	4.8	
	C19orf55	4.2	
	C7orf43	3.9	
	C10orf35	3.4	
	FANCE	1.8	4
	FAM181A	0.4	

1: HAUS complex || 2: spindle || 3: chromosome, centromeric region || 4: Fanconi anaemia nuclear complex