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

Dataset:

Num of genes in input gene set: 13
Total number of genes: 20834
Prediction LLR threshold: 0

The CLIME PDF output two sections:

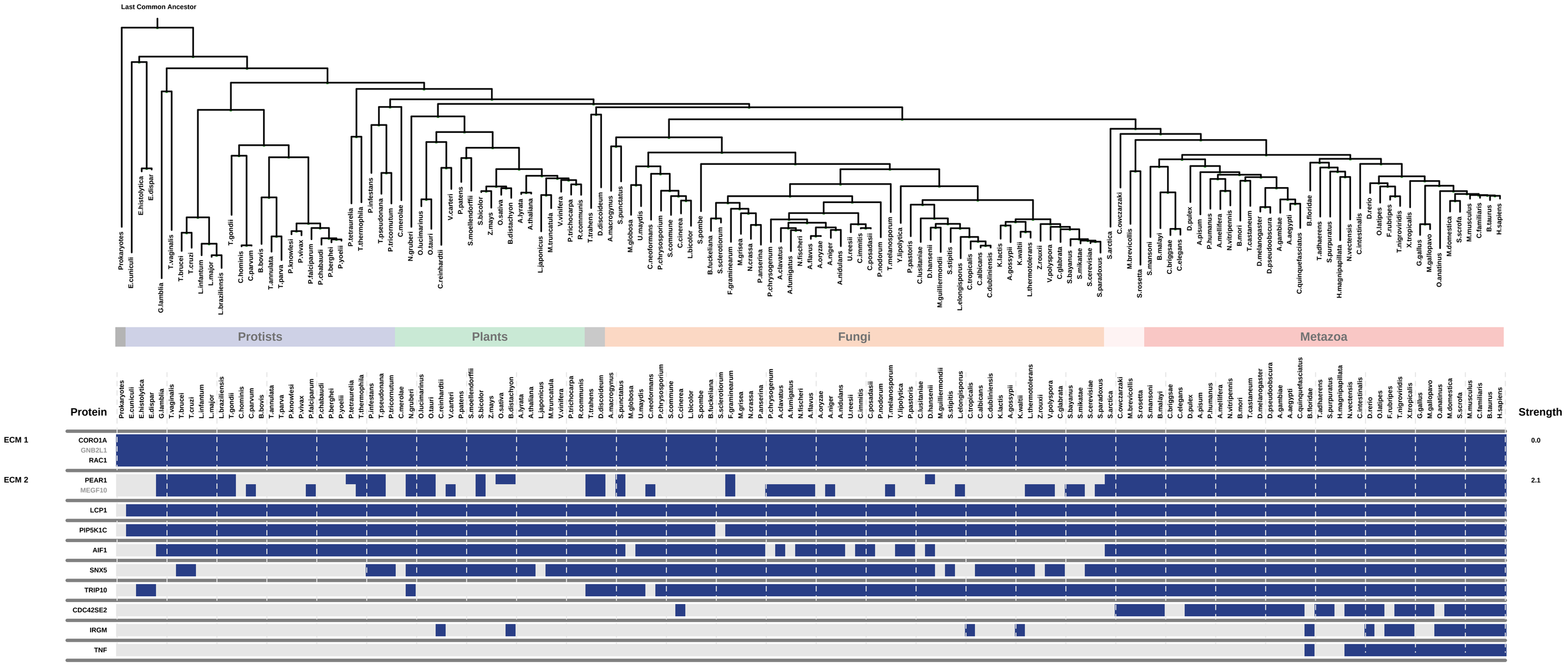
1) Overview of Evolutionarily Conserved Modules (ECMs)

- 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)

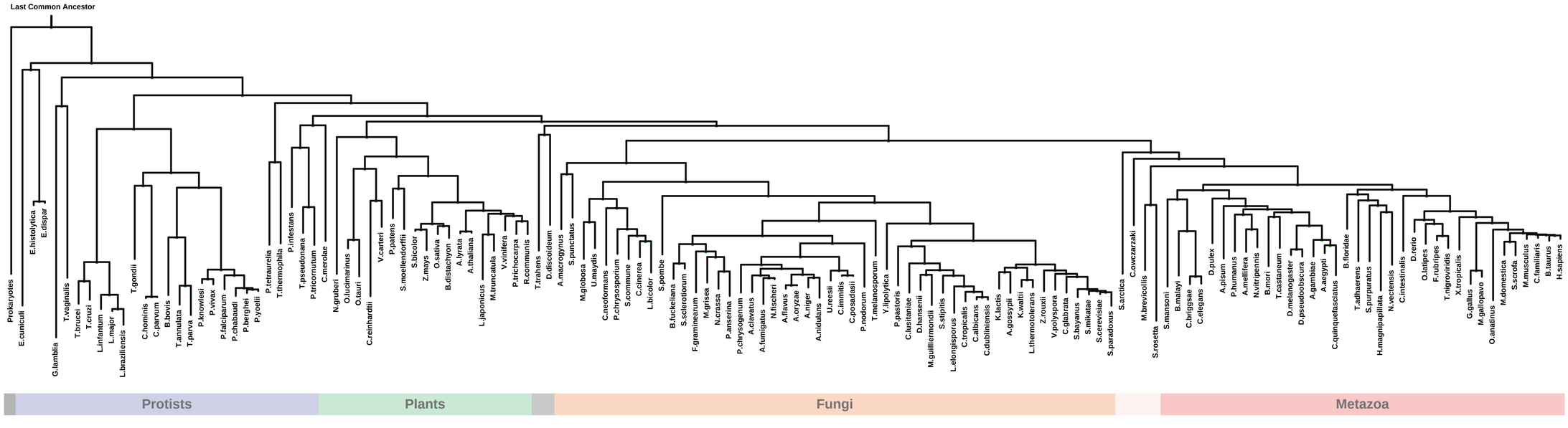


ECM 1, Gene set "phagocytic cup", Page 1

Num of ECM Genes: 3. 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	COROA		1 / 2 / 3 / 4 / 5 / 6 / 7
A	GNB2L1		5 / 8 / 9 / 10 / 11
	RAC1		4 / 5 / 12 / 13 / 14

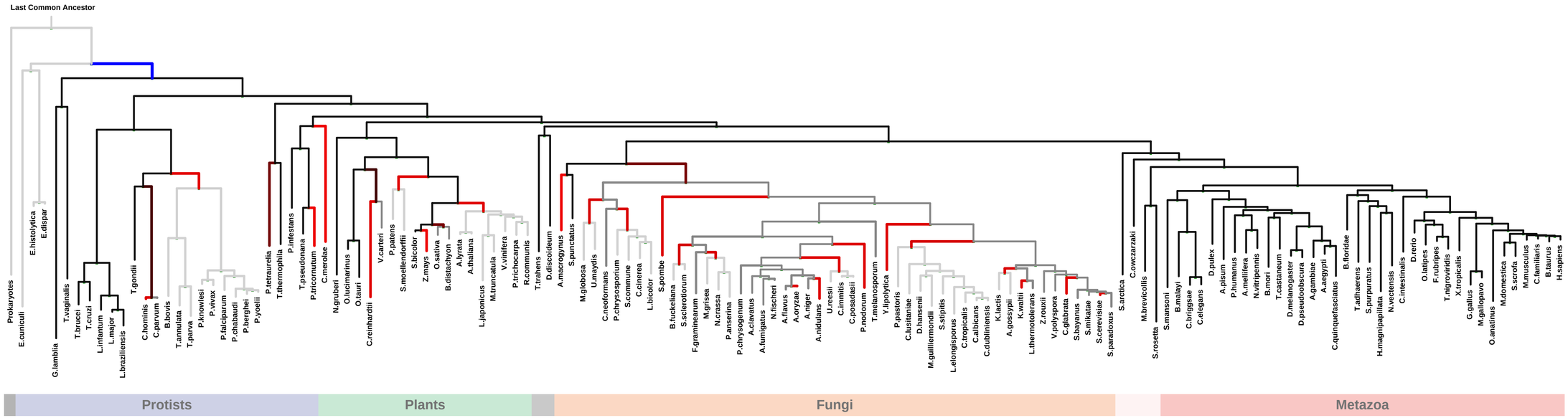
1: actin filament || 2: cortical actin cytoskeleton || 3: immunological synapse || 4: lamellipodium || 5: phagocytic cup || 6: phagocytic vesicle || 7: phagocytic vesicle membrane || 8: dendrite || 9: midbody || 10: perikaryon || 11: small ribosomal subunit || 12: extrinsic to plasma membrane || 13: melanosome || 14: ruffle membrane

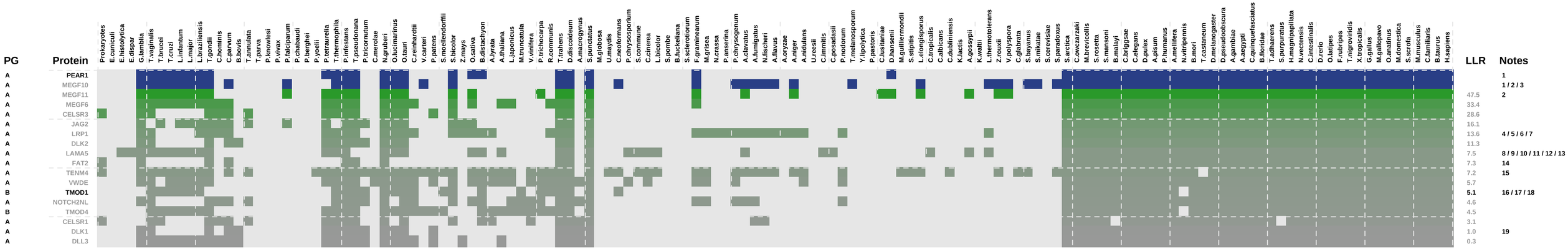
ECM 2, Gene set "phagocytic cup", Page 1

Num of ECM Genes: 2. Num of Predicted Genes: 16. ECM Strength: 2.1

PRESENCE — GAIN — ABSENCE — LOSS

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





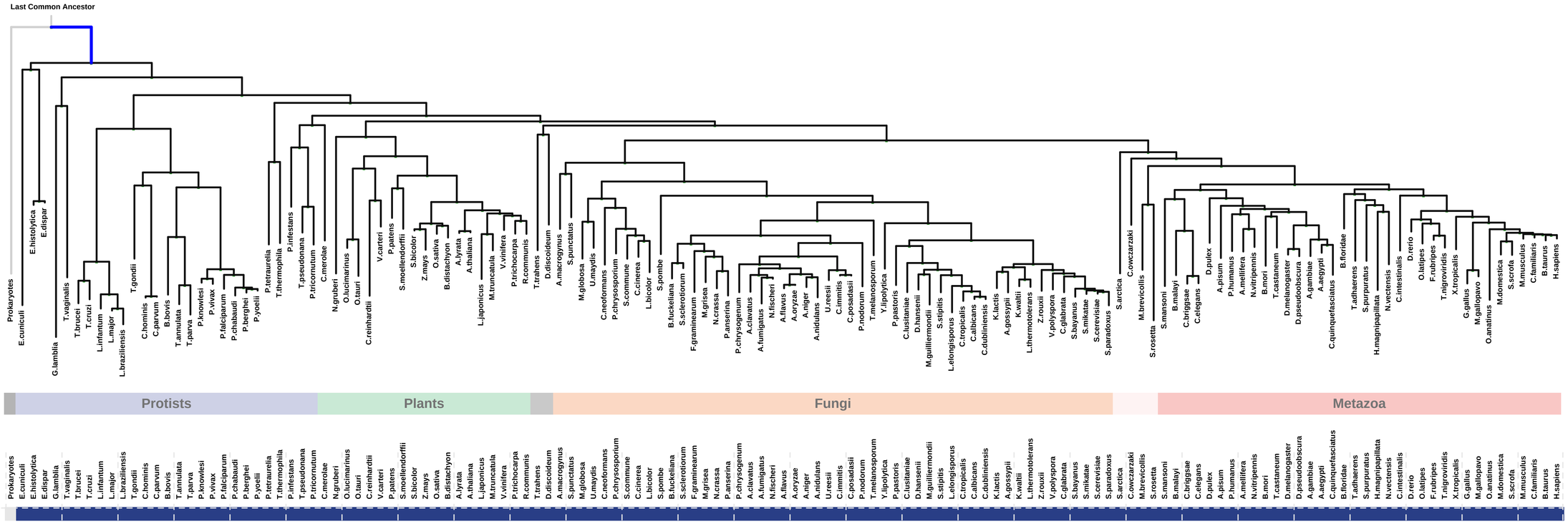
1: phagocytic cup || 2: basolateral plasma membrane || 3: cell projection || 4: clathrin-coated vesicle || 5: coated pit || 6: dendrite || 7: endosome || 8: basal lamina || 9: basement membrane || 10: extracellular matrix ||
11: laminin-1 complex || 12: laminin-10 complex || 13: laminin-11 complex || 14: cell-cell adherens junction || 15: neuron projection || 16: cortical cytoskeleton || 17: myofibril || 18: signalosome || 19: external side of plasma membrane

ECM 3, Gene set "phagocytic cup", Page 1

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

PRESENCE — GAIN — ABSENCE — LOSS

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



PG	Protein	LLR	Notes
	LCP1		1 / 2 / 3 / 4

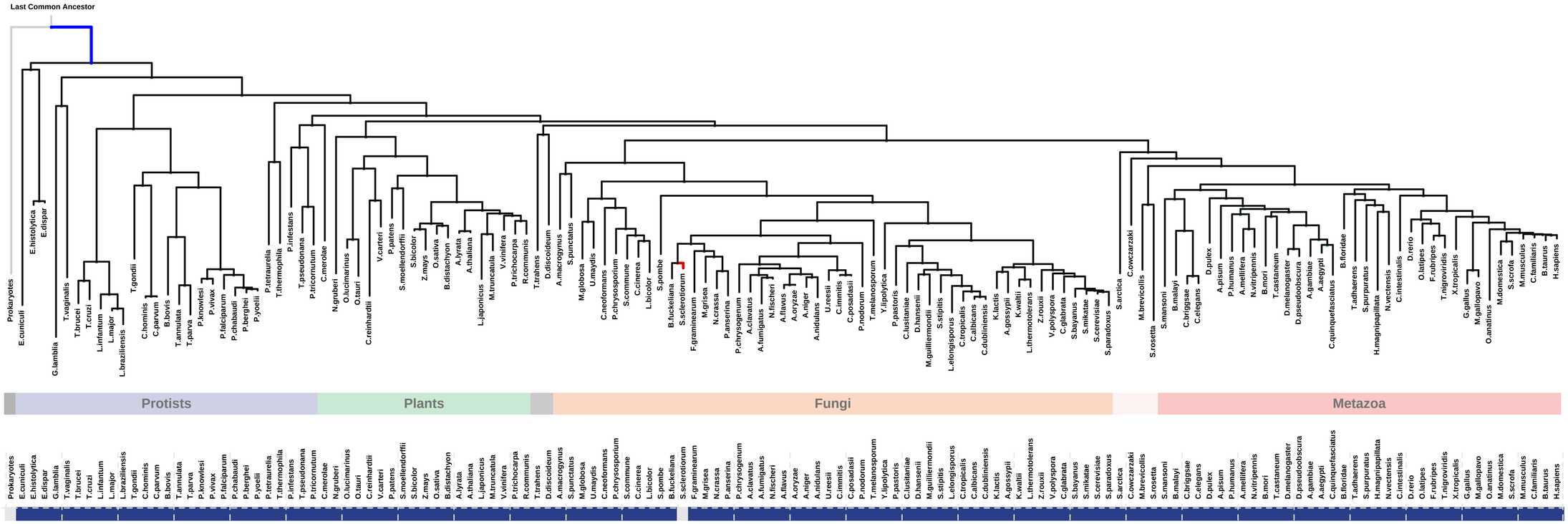
1: actin cytoskeleton || 2: actin filament || 3: phagocytic cup || 4: ruffle membrane

ECM 4, Gene set "phagocytic cup", Page 1

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

PRESENCE — GAIN — ABSENCE — LOSS

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



PG	Protein	LLR	Notes
	PIP5K1C		1 / 2 / 3 / 4 / 5

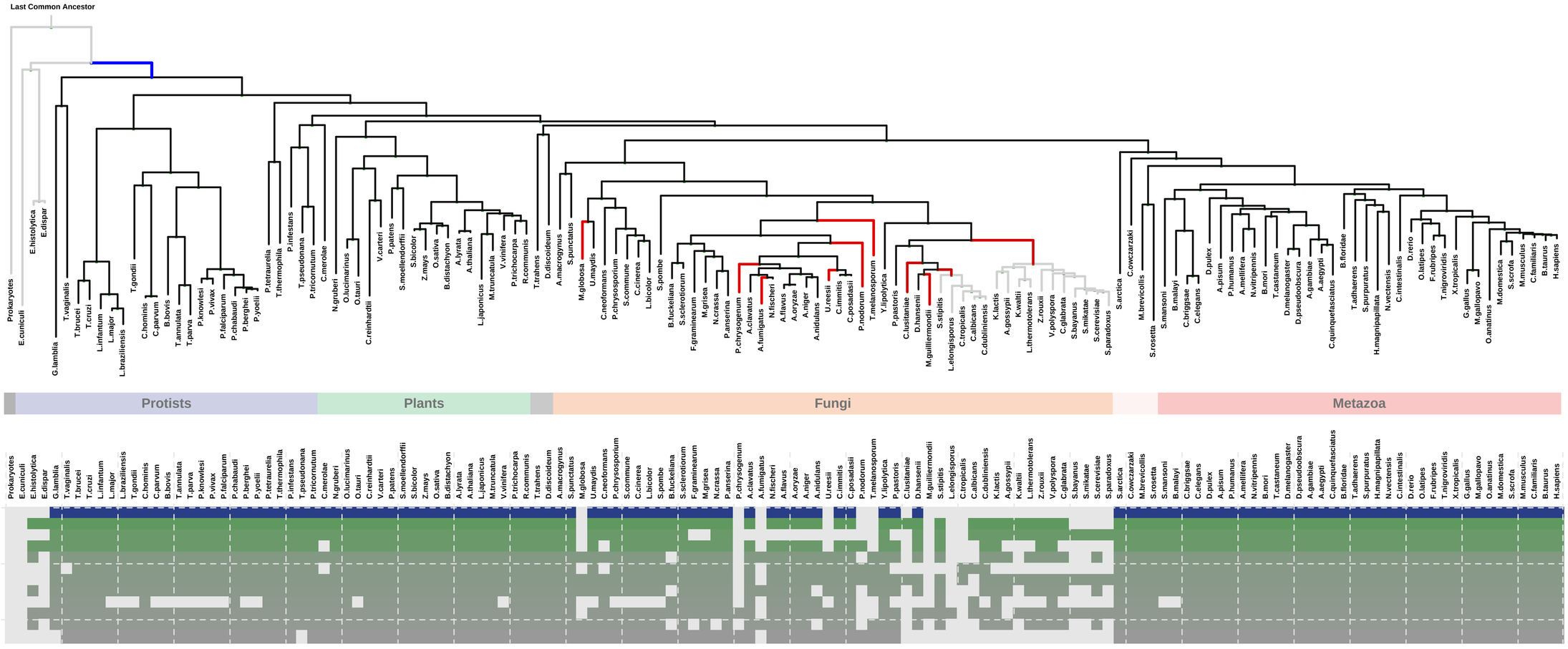
1: endomembrane system || 2: focal adhesion || 3: phagocytic cup || 4: ruffle membrane || 5: uropod

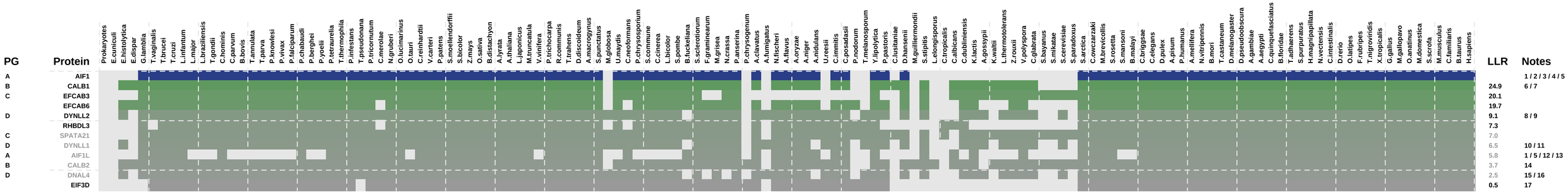
ECM 5, Gene set "phagocytic cup", Page 1

Num of ECM Genes: 1. Num of Predicted Genes: 11

PRESENCE — GAIN — ABSENCE — LOSS

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





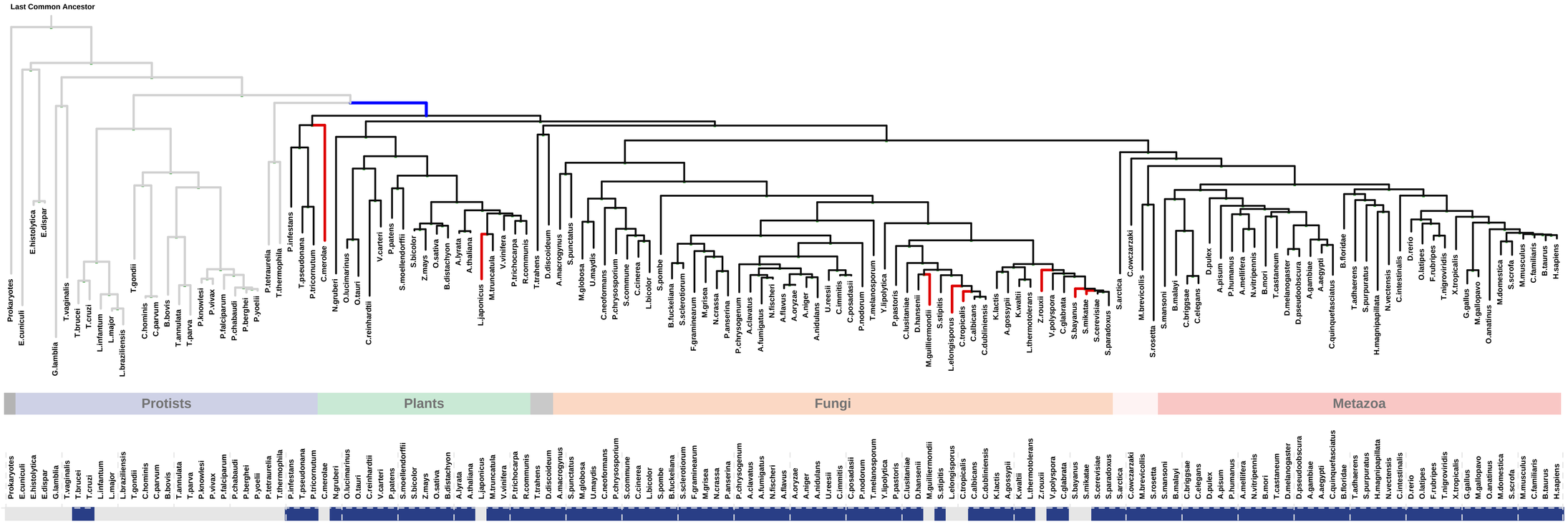
1: actin filament || 2: lamellipodium || 3: perikaryon || 4: phagocytic cup || 5: ruffle membrane || 6: axon || 7: dendrite || 8: dynein complex || 9: myosin complex || 10: cytoplasmic dynein complex || 11: signalosome ||
12: actin cytoskeleton || 13: focal adhesion || 14: gap junction || 15: axonemal dynein complex || 16: cilium axoneme || 17: eukaryotic translation initiation factor 3 complex

ECM 6, Gene set "phagocytic cup", Page 1

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

PRESENCE — GAIN — ABSENCE — LOSS

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



PG	Protein	LLR	Notes
	SNX5		1 / 2 / 3 / 4 / 5 / 6

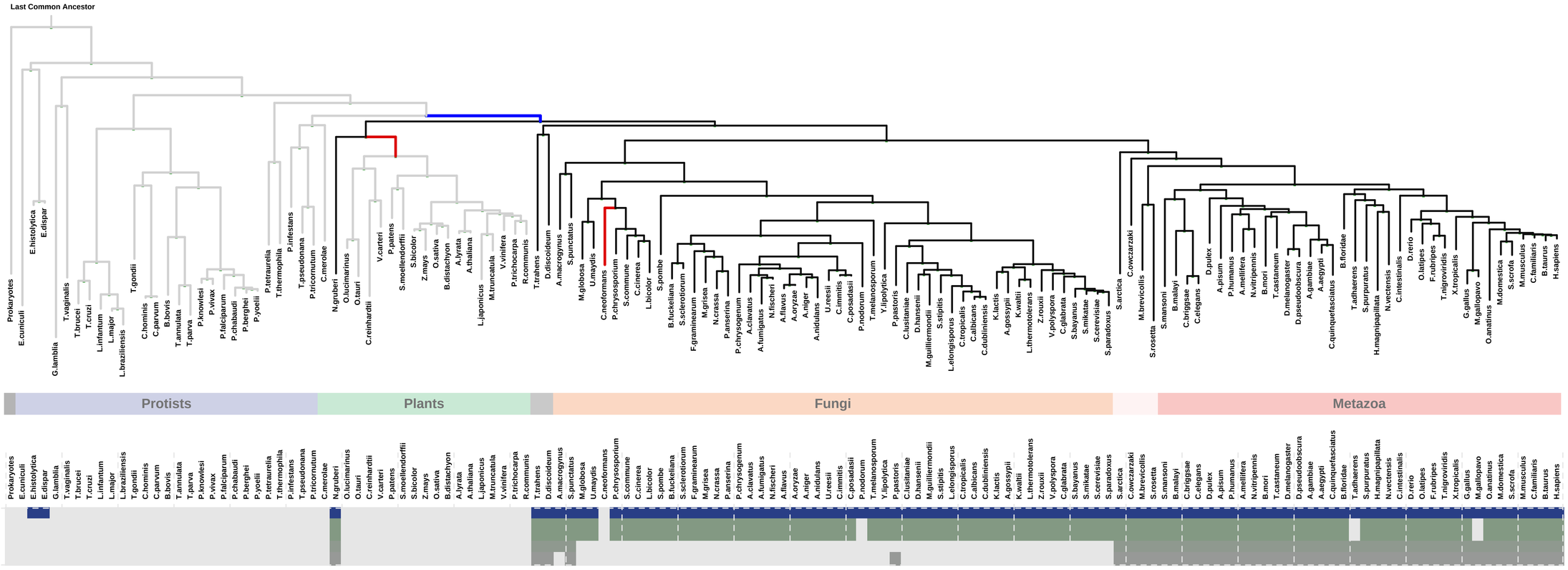
1: cytoplasmic vesicle membrane || 2: early endosome membrane || 3: extrinsic to endosome membrane || 4: extrinsic to internal side of plasma membrane || 5: phagocytic cup || 6: ruffle

ECM 7, Gene set "phagocytic cup", Page 1

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

PRESENCE — GAIN — ABSENCE — LOSS

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



PG	Protein	LLR	Notes
	TRIP10		1 / 2 / 3 / 4
A	NXF2	9.3	
A	NXF2B	9.3	5 / 6
	FRMD5	4.3	7
	BCAR3	1.0	

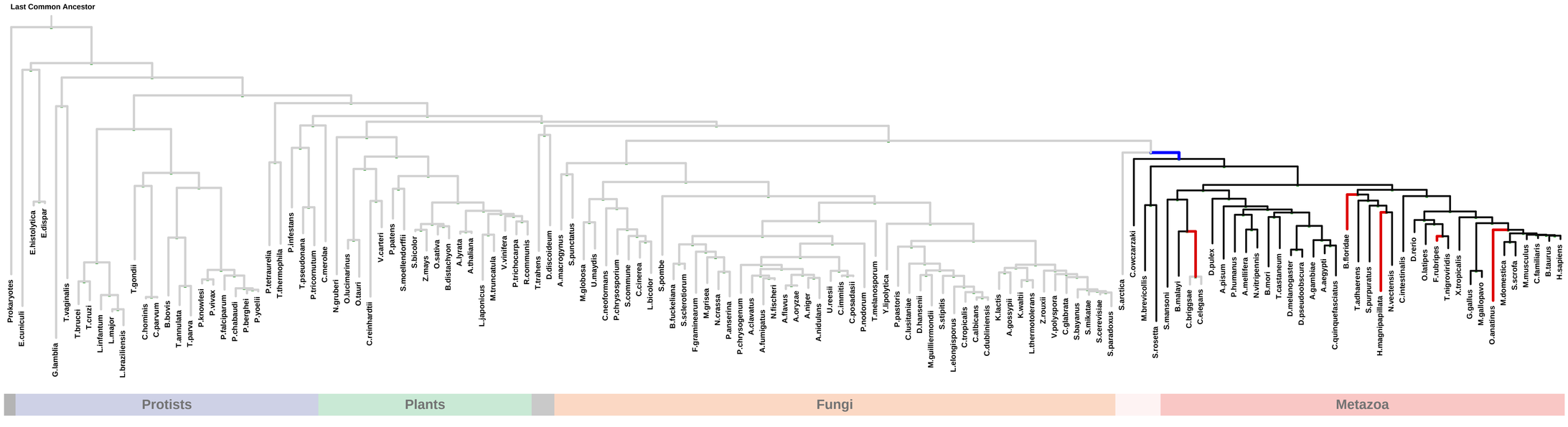
1: cell cortex || 2: cell projection || 3: lysosome || 4: phagocytic cup || 5: actin cytoskeleton || 6: nuclear RNA export factor complex || 7: extrinsic to membrane

ECM 8, Gene set "phagocytic cup", Page 1

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

PRESENCE — GAIN — ABSENCE — LOSS

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



PG	Protein	LLR	Notes
A	CDC42SE2		1 / 2
A	CDC42SE1	12.5	
	WBP11	9.0	3
	UBN1	3.7	4 / 5
	TMEM170A	2.6	

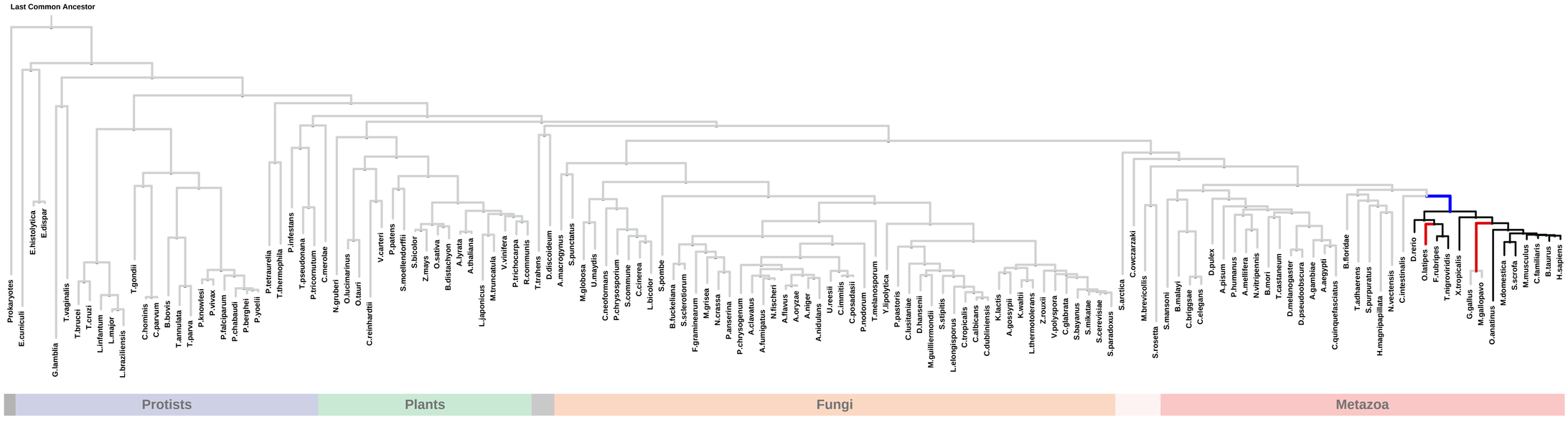
1: cell projection || 2: phagocytic cup || 3: nuclear speck || 4: PML body || 5: tight junction

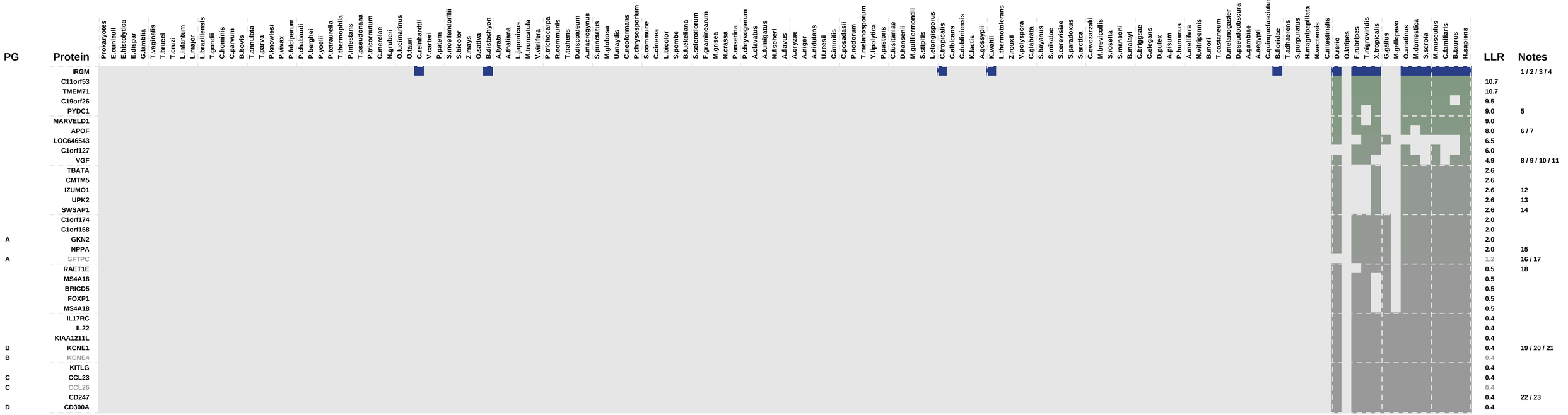
ECM 9, Gene set "phagocytic cup", Page 1

Num of ECM Genes: 1. Num of Predicted Genes: 63

PRESENCE — GAIN — ABSENCE — LOSS

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





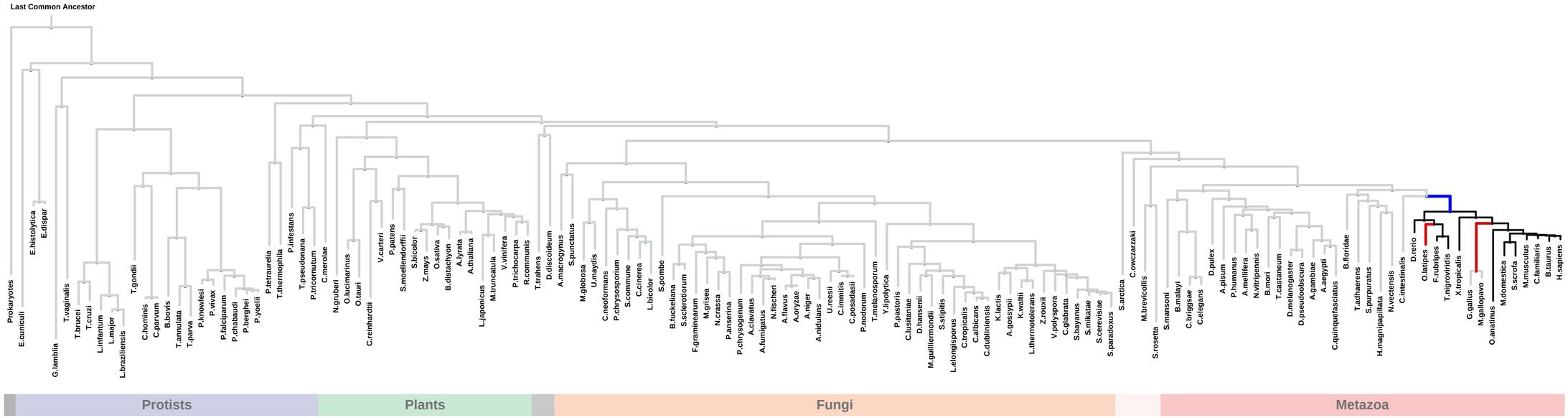
1: autophagic vacuole membrane || 2: cell projection || 3: phagocytic cup || 4: phagocytic vesicle membrane || 5: IkappaB kinase complex || 6: high-density lipoprotein particle || 7: low-density lipoprotein particle || 8: cytoplasmic vesicle || 9: neuron projection || 10: secretory granule membrane || 11: transport vesicle || 12: acrosomal membrane || 13: integral to endoplasmic reticulum membrane || 14: Shu complex || 15: mast cell granule || 16: lamellar body || 17: multivesicular body || 18: MHC class I protein complex || 19: lysosome || 20: voltage-gated potassium channel complex || 21: Z disc || 22: alpha-beta T cell receptor complex || 23: T cell receptor complex

ECM 9, Gene set "phagocytic cup", Page 2

Num of ECM Genes: 1. Num of Predicted Genes: 63

PRESENCE — GAIN — ABSENCE — LOSS

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



PG	Protein	LLR	Notes
D	CD300LD	0.4	
	CD3D	0.4	1 / 2
	AKAP12	0.4	3
	RCSD1	0.4	4
	CCSER2	0.4	
	SLAMF8	0.4	
	SPOCK2	0.4	5
	TAC1	0.4	6
	TMEM108	0.4	
D	FCAMR	0.4	
D	TREML4	0.4	
	ARMCX5	0.4	
	C2orf40	0.4	7
C	XCL1	0.4	
C	XCL2	0.4	
	100508317	0.4	
	OTOS	0.4	
	TINF2	0.4	8 / 9 / 10
	PROCA1	0.4	
	C14orf28	0.4	
	APOM	0.4	11 / 12 / 13 / 14
	TUSC5	0.4	
	CXorf21	0.4	
	RHBDD3	0.4	
	VN1R4	0.4	15
E	C11orf84	0.4	
E	C11orf95	0.4	
	SYNE4	0.4	
	AKAP7	0.3	16 / 17 / 18 / 19

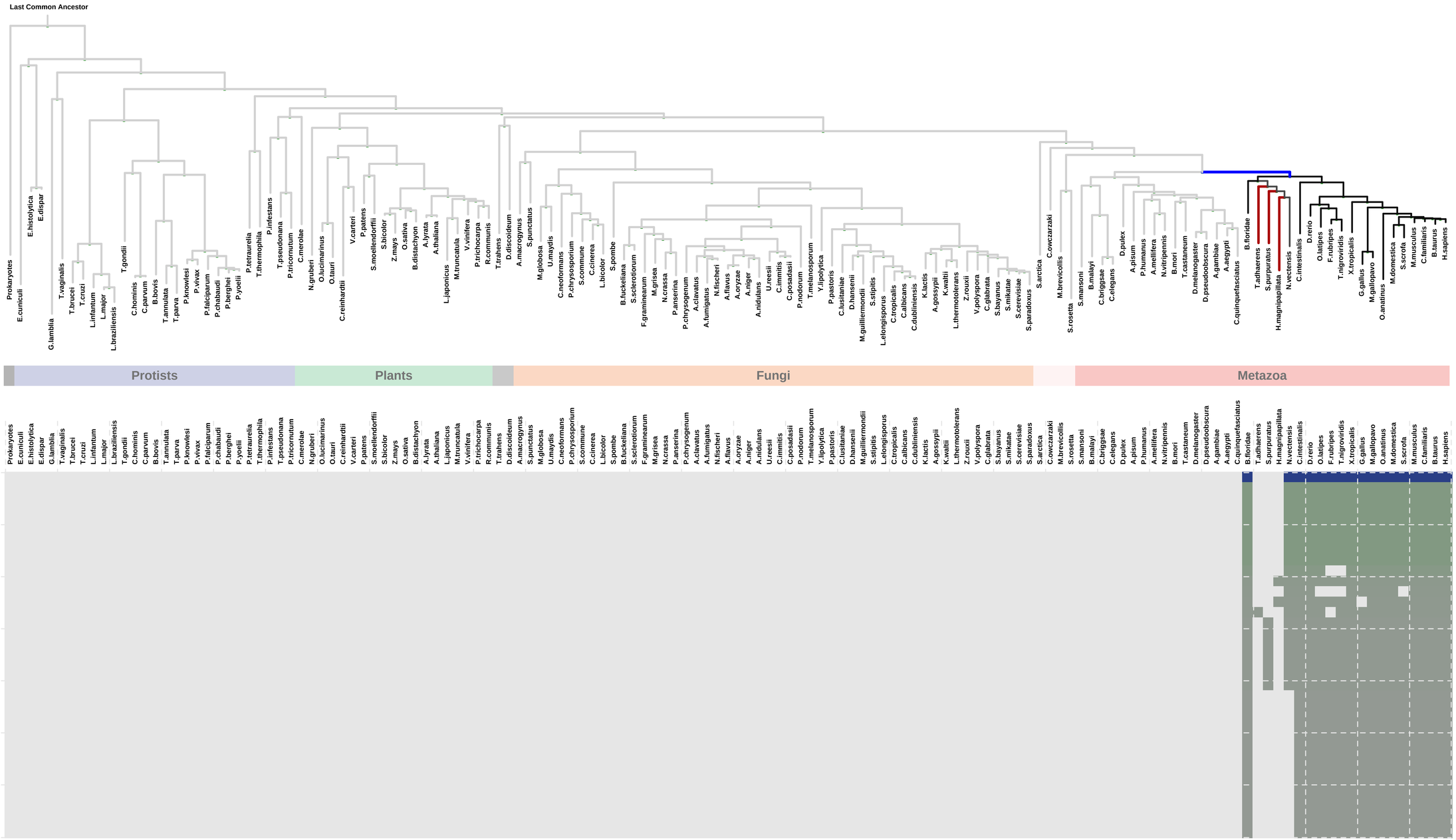
1: alpha-beta T cell receptor complex || 2: T cell receptor complex || 3: cell cortex || 4: actin filament || 5: proteinaceous extracellular matrix || 6: axon || 7: transport vesicle || 8: chromosome, telomeric region || 9: nuclear matrix ||
10: nuclear telomere cap complex || 11: high-density lipoprotein particle || 12: low-density lipoprotein particle || 13: spherical high-density lipoprotein particle || 14: very-low-density lipoprotein particle || 15: actin cytoskeleton || 16: exocytic vesicle ||
17: lateral plasma membrane || 18: sarcoplasmic reticulum || 19: T-tubule

ECM 10, Gene set "phagocytic cup", Page 1

Num of ECM Genes: 1. Num of Predicted Genes: 70

PRESENCE — GAIN — ABSENCE — LOSS

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



PG	Protein	LLR	Notes
A	TNF		1 / 2 / 3 / 4
B	CKAP2	10.0	5 / 6 / 7
B	CKAP2L	10.0	
	FAM134B	10.0	8
C	KCNMB4	10.0	9
A	LTA	10.0	
D	LYVE1	10.0	
	TMEM102	10.0	
	TRAF3IP2	10.0	
	KIAA0753	7.8	
	TOR1AIP2	5.3	10
	CCDC14	4.5	
	FAM199X	4.3	
	SPIDR	4.2	
	MTBP	3.2	
D	HAPLN1	3.2	11 / 12
	TMEM168	3.2	13
	TNIP3	3.2	
	WBP1L	3.2	
	MAS1L	3.2	
	ZP3	3.2	11 / 12 / 14 / 15 / 16 / 17
E	IL17RA	2.7	
E	IL17RD	2.7	
C	KCNMB1	2.7	9
C	KCNMB3	2.7	9
F	CRYBA4	2.7	
F	CRYBB2	2.7	
F	CRYBB3	2.7	
	KIAA1549	2.7	
	LECT1	2.7	18
	EDAR	2.7	19
G	EMID1	2.7	20
G	COL26A1	2.7	20 / 21
H	BTN3A1	2.7	
I	PRRG1	2.7	

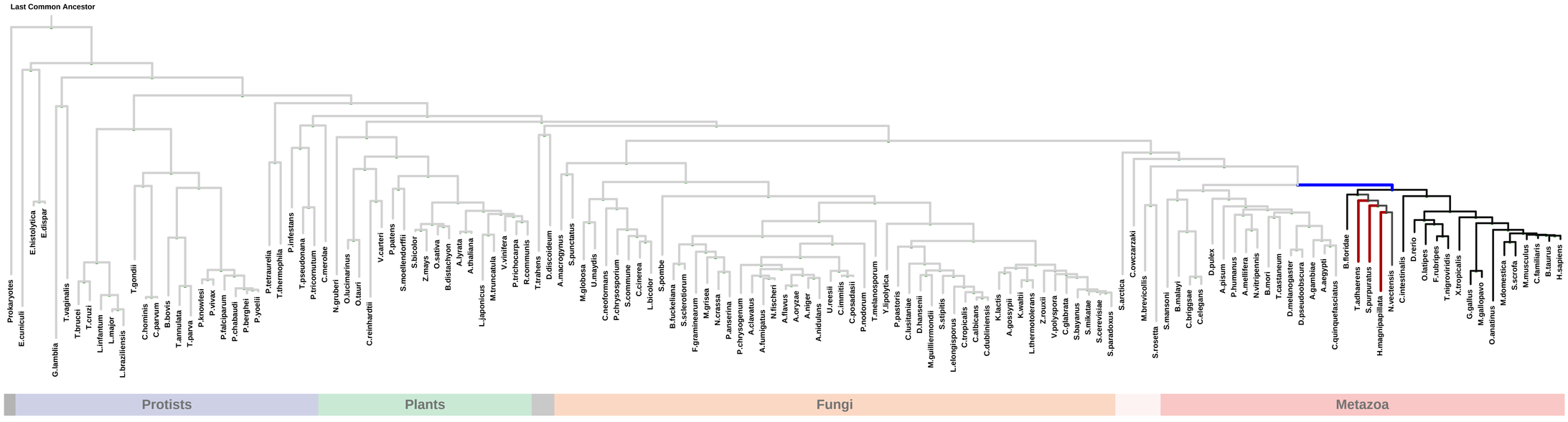
1: external side of plasma membrane || 2: membrane raft || 3: phagocytic cup || 4: recycling endosome || 5: cytoplasmic microtubule || 6: microtubule cytoskeleton || 7: spindle pole || 8: cis-Golgi network || 9: voltage-gated potassium channel complex || 10: nuclear membrane || 11: extracellular matrix || 12: proteinaceous extracellular matrix || 13: transport vesicle || 14: acrosomal vesicle || 15: multivesicular body || 16: outer acrosomal membrane || 17: secretory granule || 18: endomembrane system || 19: apical part of cell || 20: collagen || 21: endoplasmic reticulum lumen

ECM 10, Gene set "phagocytic cup", Page 2

Num of ECM Genes: 1. Num of Predicted Genes: 70

PRESENCE — GAIN — ABSENCE — LOSS

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



PG	Protein	LLR	Notes
I	PRRG2	2.7	
I	PRRG3	2.7	
J	PTGER1	2.7	
K	STC1	2.7	
K	STC2	2.7	
	CLDN7	2.7	1 / 2
F	CRYBA2	2.7	
	TMEM178A	2.7	
	HOMEZ	2.7	
	IFFO2	2.7	
	IGFBP6	2.7	
H	TRIM14	2.7	
H	TRIM16L	2.7	
H	TRIM69	2.7	3
	WISP1	2.7	
	ZNF365	2.7	4
	IL17F	2.7	
	KNOP1	2.4	
	AKAP14	2.4	5
	PRR14L	1.6	
	FAM167A	0.8	
H	TRIM16	0.8	6
L	NT5C1A	0.8	
L	NT5C1B	0.8	
	GCHFR	0.8	7 / 8 / 9
	MAML3	0.8	3
	NRSN1	0.8	10 / 11 / 12 / 13
J	TBXA2R	0.8	14
C	KCNMB2	0.8	15
	NDP	0.8	16
	SLC48A1	0.7	17 / 18
	CLPS	0.6	
	SAMD9L	0.4	
	SEPN1	0.4	
	MACC1	0.2	

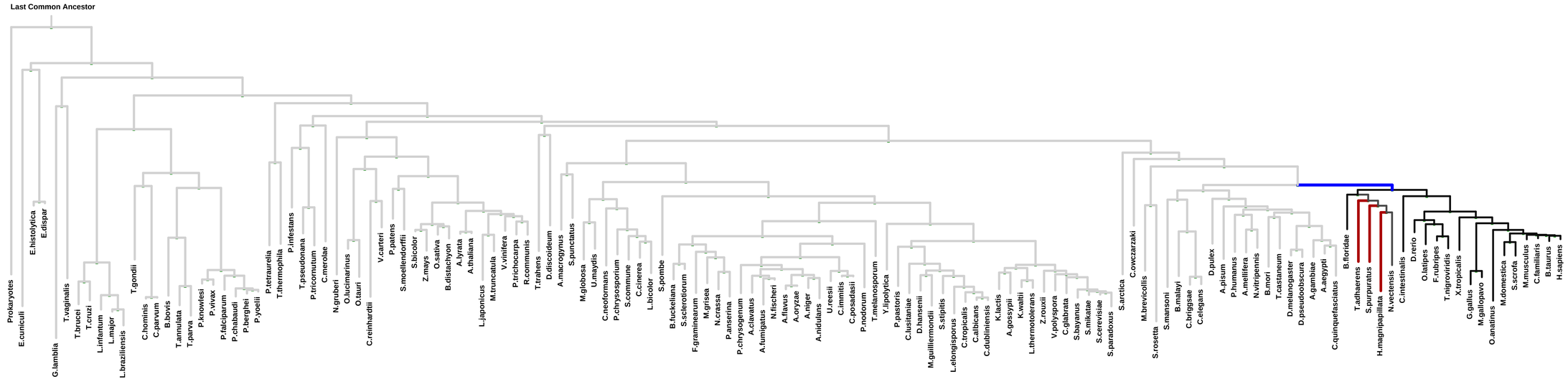
1: lateral plasma membrane || 2: tight junction || 3: nuclear speck || 4: microtubule organizing center || 5: microtubule-based flagellum part || 6: PML body || 7: dendrite || 8: melanosome || 9: nuclear membrane || 10: cytoplasmic membrane-bounded vesicle || 11: growth cone || 12: neuron projection || 13: transport vesicle || 14: acrosomal vesicle || 15: voltage-gated potassium channel complex || 16: extracellular matrix || 17: endosome membrane || 18: lysosomal membrane

ECM 10, Gene set "phagocytic cup", Page 3

Num of ECM Genes: 1. Num of Predicted Genes: 70

PRESENCE — GAIN — ABSENCE — LOSS

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



PG	Protein	LLR	Notes
	TMEM220	0.0	