

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

Dataset:

Num of genes in input gene set: 5

Total number of genes: 20834

Prediction LLR threshold: 0

The CLIME PDF output two sections:

1) Overview of Evolutionarily Conserved Modules (ECMs)

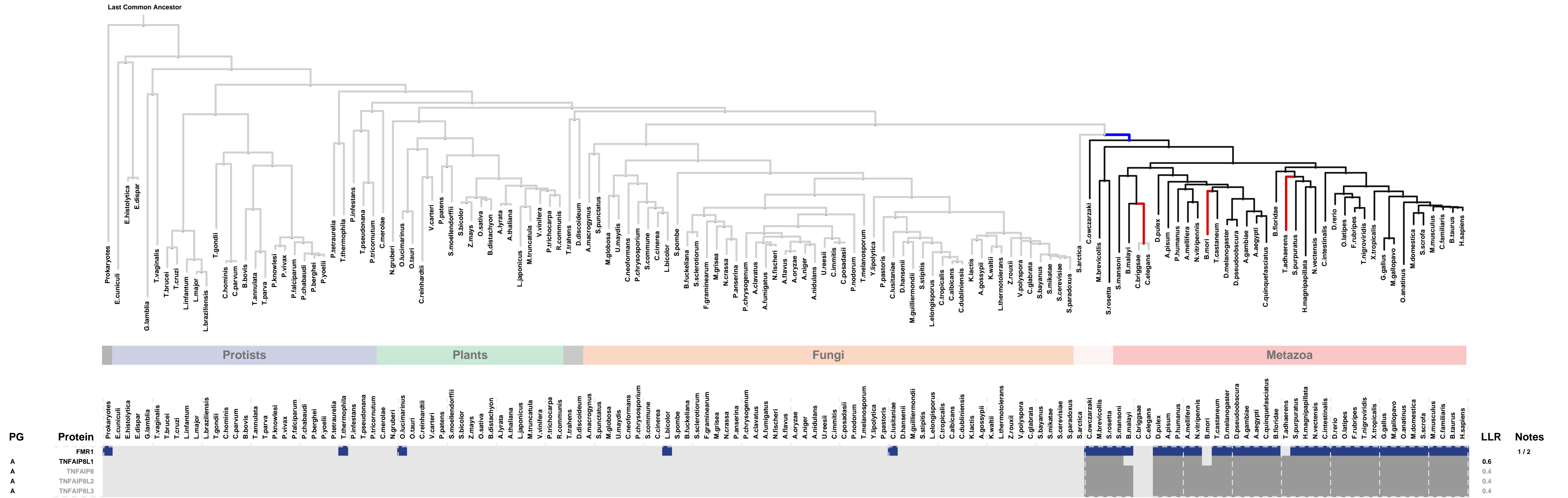
- Top panel shows the predefined species tree.
- Bottom panel shows the partition of input genes into Evolutionary Conserved Modules (ECMs), ordered by ECM strength (shown at right), and separated by horizontal lines.
- Each row show one gene, where the phylogenetic profile indicates presence (blue) 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.

ECM 2, Gene set "polysomal ribosome", Page 1

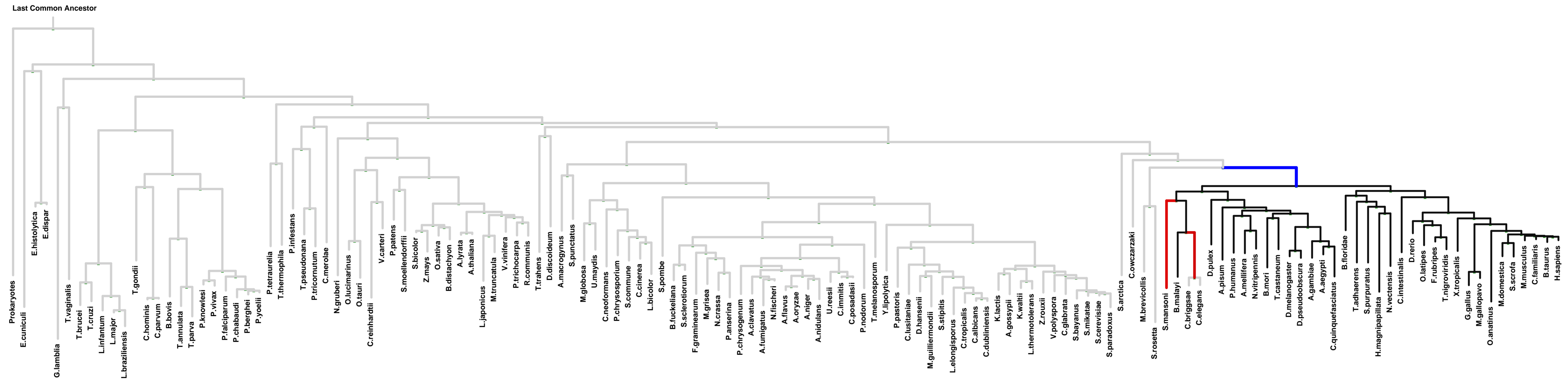
Num of ECM Genes: 1. Num of Predicted Genes: 4



1: mRNA cap binding complex || 2: polysomal ribosome

ECM 3, Gene set "polysomal ribosome", Page 1

Num of ECM Genes: 1. Num of Predicted Genes: 25



PG	Protein	LLR	Notes
A	NR0B1		1
A	INTS10	11.0	2
A	NR0B2	11.0	
	LOC728715	8.4	
	LOC728715	8.4	
	IL1RL2	5.7	
	MICALCL	3.5	
B	MBD3L1	3.5	
B	SKOR1	3.5	3
B	SKOR2	3.5	
B	SKOR2	3.5	
	VSIG8	3.5	
	TWSG1	3.3	
	AMOTL2	3.2	4 / 5 / 6
	MED24	2.7	7
	SAMSN1	2.3	8
	C1orf43	1.8	
	DCAF17	1.4	9
	FAM122A	1.3	
	CACNG5	1.1	10 / 11 / 12
C	ATP5J	1.0	13 / 14
C	AFF2	0.6	15
C	AFF3	0.6	
	SLC22A31	0.5	
	OR2L13	0.2	
	AMICA1	0.1	6

1: polysomal ribosome || 2: integrator complex || 3: dendrite || 4: cytoplasmic vesicle || 5: recycling endosome || 6: tight junction || 7: mediator complex || 8: ruffle || 9: Cul1-RING ubiquitin ligase complex || 10: alpha-amino-3-hydroxy-5-methyl-4-isoxazolepropionic acid selective glutamate receptor || 11: postsynaptic density || 12: postsynaptic membrane || 13: mitochondrial proton-transporting ATP synthase complex || 14: mitochondrial proton-transporting ATP synthase complex, coupling factor F(o) || 15: nuclear speck

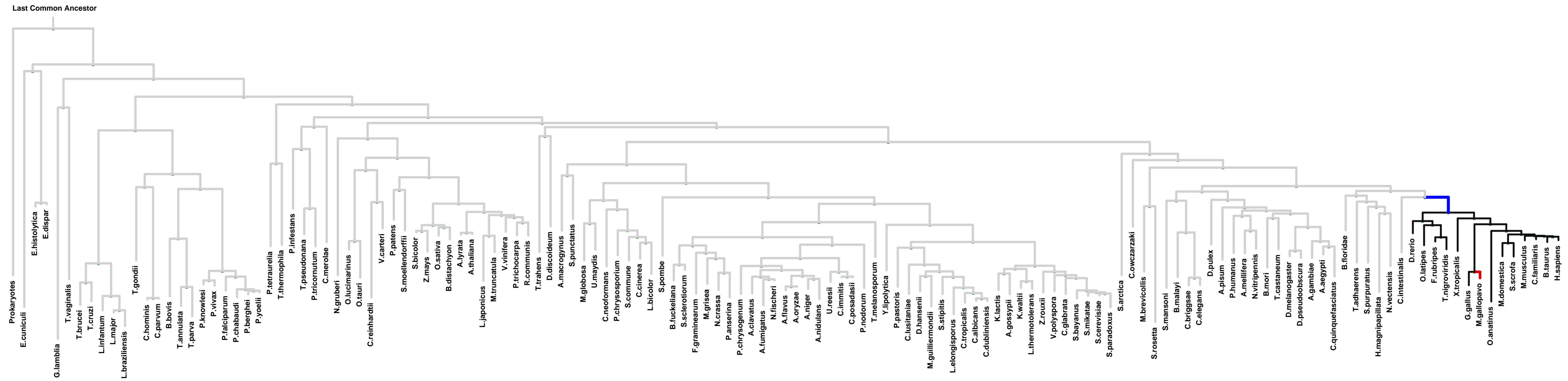
ECM 4, Gene set "polysomal ribosome", Page 1

Num of ECM Genes: 1. Num of Predicted Genes: 67

PRESENCE ——— ABSENCE ———
GAIN ——— LOSS ———

Log-likelihood Ratio Scale

0 10 20 30 40 50 60

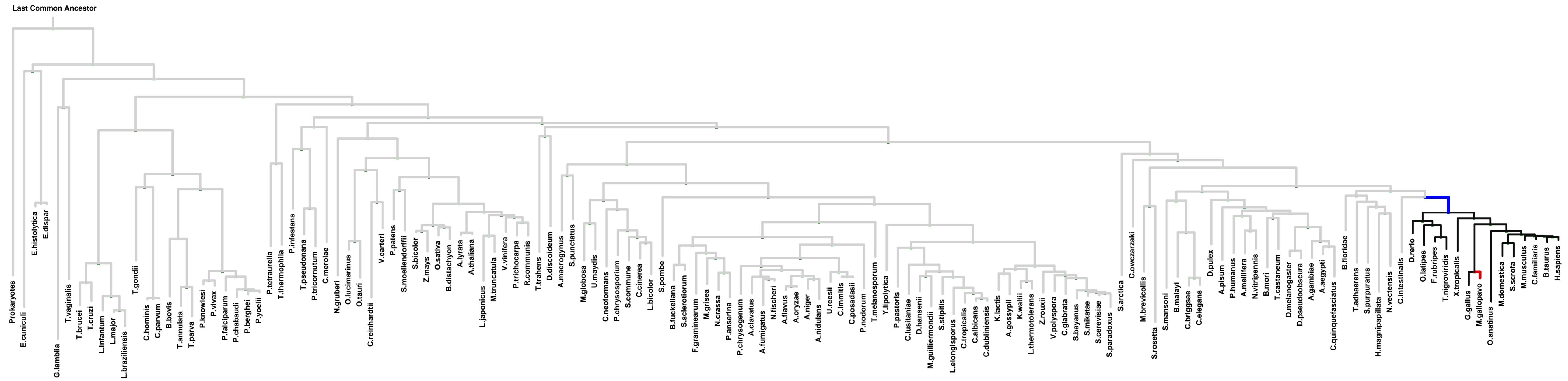


PG	Protein	LLR	Notes
	NUFIP2		
	LOC646543	5.6	1
A	C16orf11	3.5	
	MISP	3.5	
B	FAM212B	3.5	
	FAM212A	3.5	
	SMIM19	3.5	
	CCL25	3.5	
	CD7	3.5	
	DDIT3	3.5	
	EMX2	3.5	
C	ESM1	3.5	
	INSL5	3.5	
	FAM219B	3.5	
	MARVELD3	3.5	2
	RLN1	3.5	
	RLN3	3.5	
C	TMEM125	3.5	
	ZNF750	3.5	
A	MLANA	2.7	3 / 4
	CAST	2.4	
	ICAM2	2.1	5
	POMC	2.1	6 / 7 / 8
	CRH	2.1	
	PTTG1	2.1	
	C1orf174	1.6	
D	NPPA	1.6	9
	GKN2	1.6	
	C1orf168	1.6	
	NOL7	1.6	
	GLYAT	1.3	
	FANCG	1.3	10
E	KRTCAP3	1.0	
	ERMN	1.0	11 / 12 / 13 / 14
	FIBIN	1.0	

1: polysomal ribosome || 2: tight junction || 3: melanosome || 4: trans-Golgi network || 5: uropod || 6: peroxisomal matrix || 7: peroxisome || 8: secretory granule || 9: mast cell granule || 10: Fanconi anaemia nuclear complex || 11: filopodium || 12: internode region of axon || 13: myelin sheath || 14: paranode region of axon

ECM 4, Gene set "polysomal ribosome", Page 2

Num of ECM Genes: 1. Num of Predicted Genes: 67



PG	Protein	Protists	Plants	Fungi	Metazoa	LLR	Notes
E	TMEM54					1.0	
	BSN					1.0	1/2/3/4
	RAI2					0.9	
D	PTPN20A					0.9	5
	SFTPC					0.9	6/7
	PRR15					0.8	
	TNFSF10					0.8	
	NPPB					0.8	
	IFNB1					0.7	
F	IL12A					0.7	8
	IL19					0.7	
	IL24					0.7	
	ADM					0.7	
	NPB					0.7	
	LOC643802					0.7	
	FAM86C1					0.7	
	MAP6D1					0.7	9/10
	MARCKS					0.7	11/12
	EPO					0.7	
	ADM2					0.7	
G	CCDC71L					0.6	
	CCDC71					0.6	
	ALB					0.6	13/14
	RAD51AP1					0.6	
	RAET1E					0.5	15
	AKAP7					0.3	16/17/18/19
	C1orf216					0.2	
H	FAM196A					0.2	
	FAM196B					0.2	
	MS4A18					0.2	
	MS4A18					0.2	
	FOXP1					0.2	
	BRICD5					0.2	

1: dendrite || 2: microtubule cytoskeleton || 3: neuron projection terminus || 4: presynaptic active zone || 5: microtubule organizing center || 6: lamellar body || 7: multivesicular body || 8: interleukin-12 complex || 9: cis-Golgi network || 10: Golgi-associated vesicle || 11: actin cytoskeleton || 12: cell cortex || 13: basement membrane || 14: platelet alpha granule lumen || 15: MHC class I protein complex || 16: exocytic vesicle || 17: lateral plasma membrane || 18: sarcoplasmic reticulum || 19: T-tubule