

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

Dataset:

Num of genes in input gene set: 2
Total number of genes: 20834
Prediction LLR threshold: 0

The CLIME PDF output two sections:

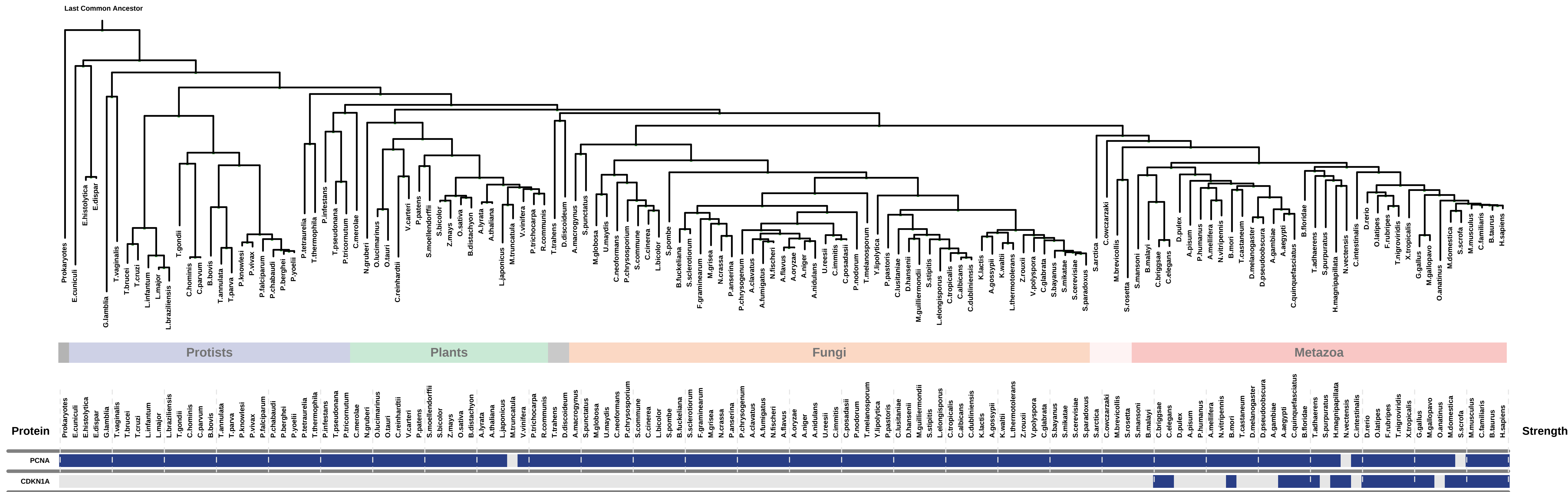
1) Overview of Evolutionarily Conserved Modules (ECMs)

- 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 $E < 1e-3$).

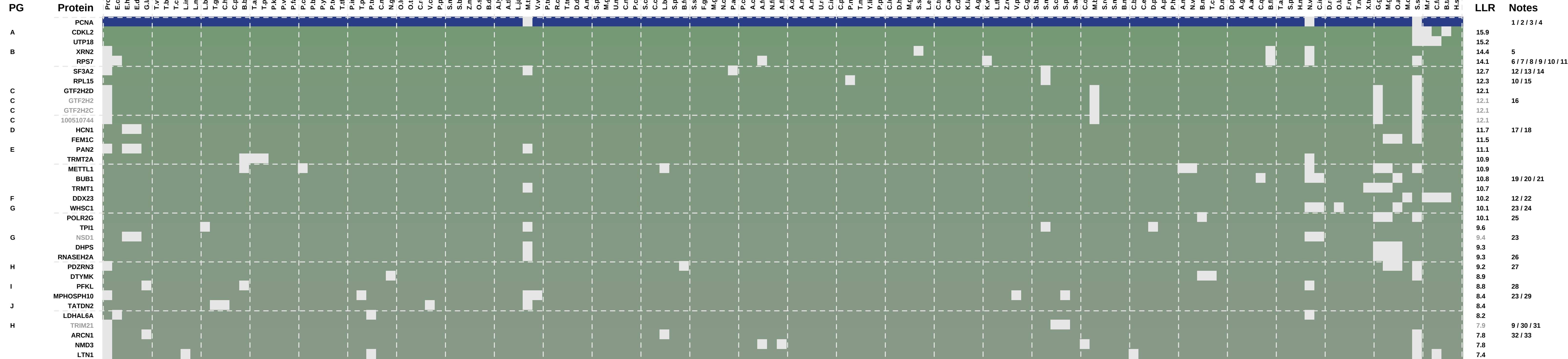
2) Details of each ECM and its expansion ECM+

- 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)



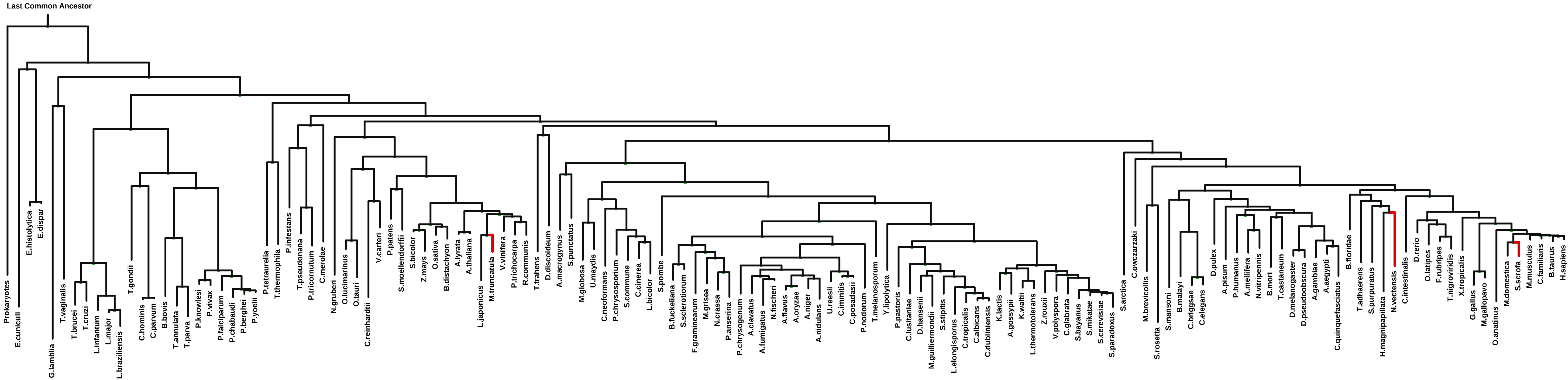
Num of ECM Genes: 1. Num of Predicted Genes: 172



1: DNA replication factor C complex || 2: microtubule cytoskeleton || 3: nuclear replication fork || 4: PCNA-p21 complex || 5: aggresome || 6: 90S preribosome || 7: cytosolic small ribosomal subunit || 8: microtubule organizing center || 9: ribonucleoprotein complex || 10: ribosome || 11: small-subunit processome || 12: catalytic step 2 spliceosome || 13: small nuclear ribonucleoprotein complex || 14: spliceosomal complex || 15: cytosolic large ribosomal subunit || 16: holo TFIIF complex || 17: axon || 18: dendrite || 19: condensed chromosome kinetochore || 20: condensed nuclear chromosome, centromeric region || 21: kinetochore || 22: U5 snRNP || 23: chromosome || 24: nuclear membrane ||

ECM 1, Gene set "PCNA-p21 complex", Page 2

Num of ECM Genes: 1. Num of Predicted Genes: 172

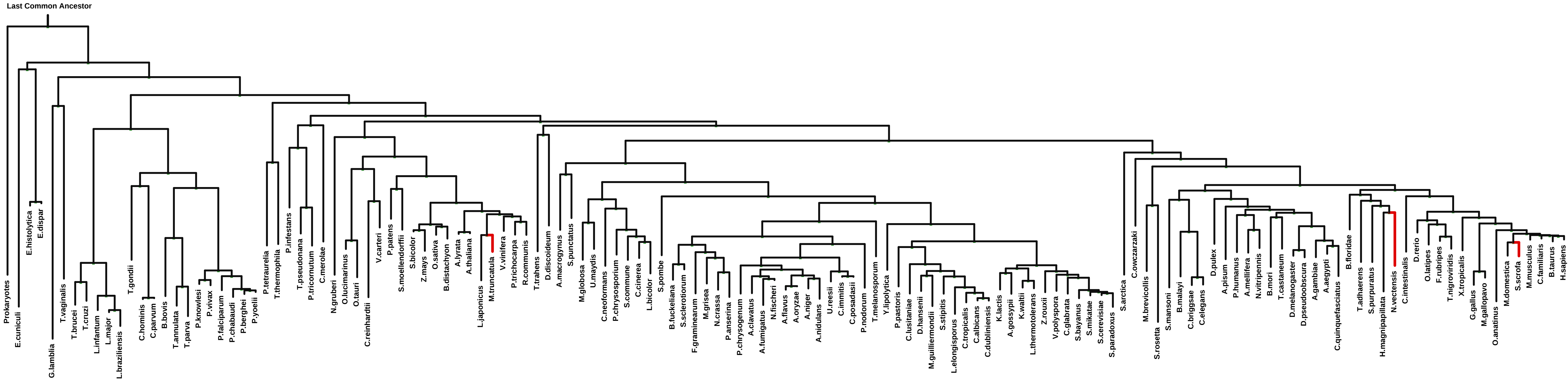


PG	Protein	Protists	Plants	Fungi	Metazoa	LLR	Notes
K	RNF103-CHMP3					7.3	
	VPS35					7.2	1
	RPL13					7.1	2 / 3
	NSA2					6.8	4
	EMG1					6.7	
	RCL1					6.2	
	EP300					6.1	5 / 6 / 7
	SBDS					6.0	8
	PCID2					5.9	
	RER1					5.9	9
L	CLIP3					5.7	10 / 11 / 12 / 13 / 14 / 15
	ABCC2					5.3	16
	ISCU					5.1	
	RPS14					5.1	17
	TAF1L					5.1	
	PSMD9					4.9	18
	TRIM25					4.8	19 / 20
	TATDN3					4.3	
	WRNIP1					4.3	
	RAD23A					4.2	
M	RSL24D1P11					4.1	21
	SLC25A25					3.9	
	ASCC3					3.8	
	YEATS4					3.8	
	UHRF2					3.7	22 / 23
	ZFAND4					3.7	24
	ISG15					3.7	
	UBL4B					3.7	
	VPS33B					3.7	
	TBC1D9					3.7	25 / 26 / 27 / 28 / 29 / 30
I	PFKM					3.6	
	PRPF8					3.6	31
	CHD1					3.5	32 / 33 / 34
	XRN1					3.5	
	RNF135					3.4	35
						3.4	
						3.4	
						3.4	
						3.4	
						3.4	

1: endosome || 2: cytosolic large ribosomal subunit || 3: cytosolic ribosome || 4: ribonucleoprotein complex || 5: chromatin || 6: histone acetyltransferase complex || 7: protein-DNA complex || 8: spindle pole || 9: integral to Golgi membrane || 10: early endosome membrane || 11: Golgi stack || 12: membrane raft || 13: recycling endosome membrane || 14: trans-Golgi network || 15: trans-Golgi network membrane || 16: intercellular canaliculus || 17: cytosolic small ribosomal subunit || 18: transcription factor TFIID complex || 19: proteasome regulatory particle || 20: proteasome regulatory particle, base subcomplex || 21: proteasome complex || 22: NuA4 histone acetyltransferase complex || 23: nuclear matrix || 24: nuclear heterochromatin ||

ECM 1, Gene set "PCNA-p21 complex", Page 3

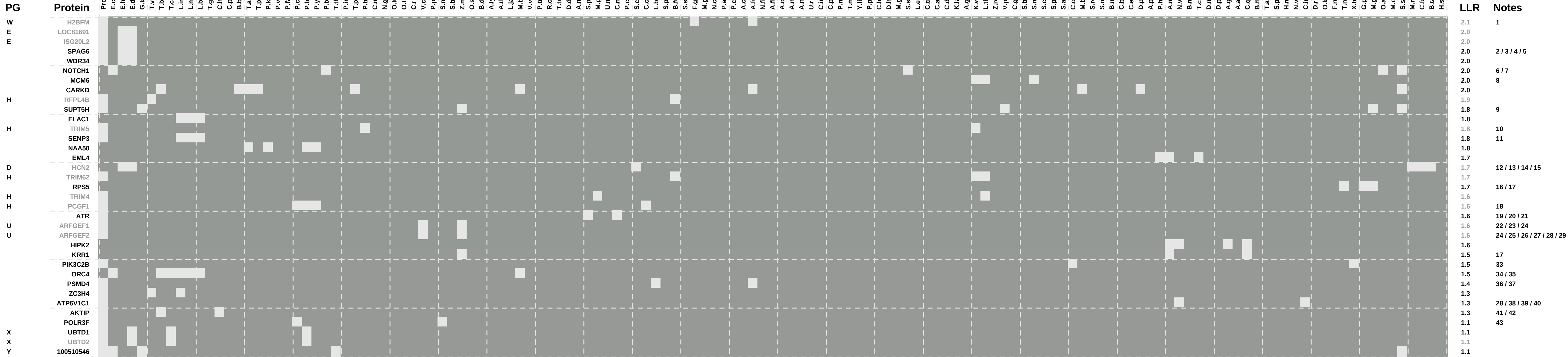
Num of ECM Genes: 1. Num of Predicted Genes: 172



PG		Protein		Protists		Plants		Fungi		Metazoa		LLR	Notes
O O A P P P H A L K	LOC100507699	ATP6V1H										3.2	1
		PUS7										3.1	
		PUS7L										3.1	
		TMEM30A										3.1	2 / 3 / 4 / 5
		MAP3K5										3.0	
		VPS26A										2.9	
		VPS26B										2.9	4
		LONR2										2.7	
		CDK13										2.7	
		CLIP4										2.6	6 / 7
Q Q Q R K S S T N U	LOC100507699	LRR6										2.6	
		KDEL1										2.5	8
		652215										2.5	
		KDEL3										2.5	
		VPS13D										2.5	11 / 12
		ATAD2B										2.5	
		INPP5E										2.4	
		INPP5K										2.4	13 / 14 / 15 / 16
		CNOT7										2.4	
		CNOT8										2.4	
R	LOC100507699	UBD										2.4	19
		IQSEC3										2.3	
		ERCC3										2.3	
		STX2										2.3	22 / 23
		HINT1										2.3	
		VPS13C										2.3	
		RNF113A										2.2	24 / 25 / 26 / 27 / 28
		LSM2										2.2	
		RPLP2										2.1	
		PSD3										2.1	30
U V V W	LOC100507699	ASF1A										2.1	
		ASF1B										2.1	16 / 21 / 31
		ZNF622										2.1	
		H2BFWT										2.1	32
												2.1	
												2.1	
												2.1	33
												2.1	
												2.1	
												2.1	34 / 35

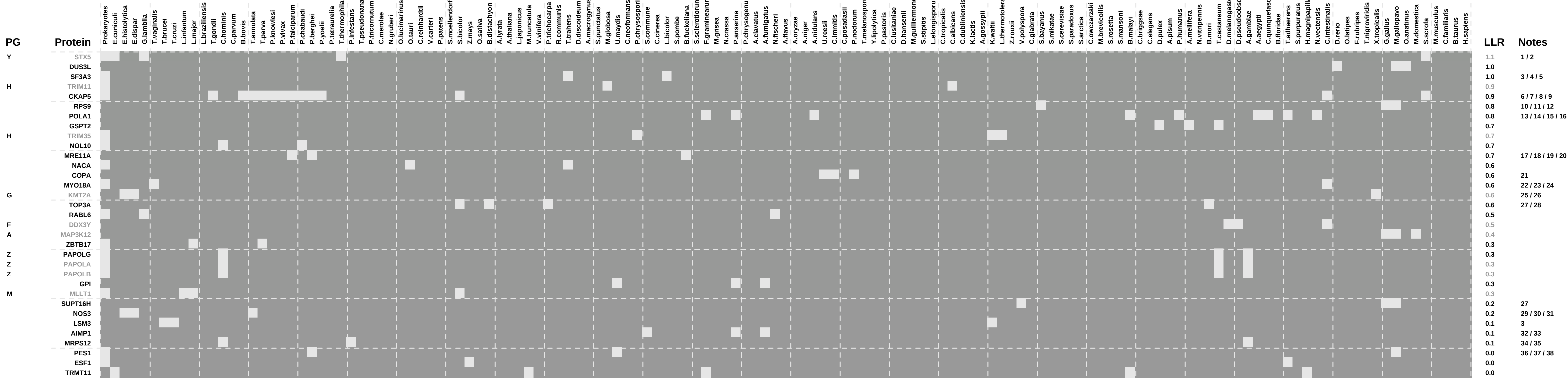
1: vacuolar proton-transporting V-type ATPase, V1 domain 2: endosome 3: endosome membrane 4: retromer complex 5: vesicle 6: nuclear cyclin-dependent protein kinase holoenzyme complex 7: nuclear speck 8: cilium 9: cis-Golgi network 10: endoplasmic reticulum-Golgi intermediate compartment 11: cilium axoneme 12: Golgi cisterna membrane 13: neuron projection 14: ruffle 15: ruffle membrane 16: trans-Golgi network 17: CCR4-NOT complex 18: cytoplasmic mRNA processing body 19: aggresome 20: inhibitory synapse 21: postsynaptic membrane 22: holo TFIIF complex 23: SSL2-core TFIIF complex 24: basolateral plasma membrane

Num of ECM Genes: 1. Num of Predicted Genes: 172



1: nucleosome || 2: axoneme || 3: cilium || 4: flagellum || 5: microtubule cytoskeleton || 6: acrosomal vesicle || 7: MAML1-RBP-Jkappa- ICN1 complex || 8: MCM complex || 9: DSIF complex || 10: cytoplasmic mRNA processing body ||
 11: MLL1 complex || 12: axon || 13: dendritic shaft || 14: synapse || 15: voltage-gated potassium channel complex || 16: cytosolic small ribosomal subunit || 17: ribonucleoprotein complex || 18: PcG protein complex || 19: chromosome ||
 20: PML body || 21: XY body || 22: nuclear matrix || 23: small nuclear ribonucleoprotein complex || 24: trans-Golgi network || 25: asymmetric synapse || 26: axonemal microtubule || 27: cytoplasmic membrane-bounded vesicle ||

Num of ECM Genes: 1. Num of Predicted Genes: 172

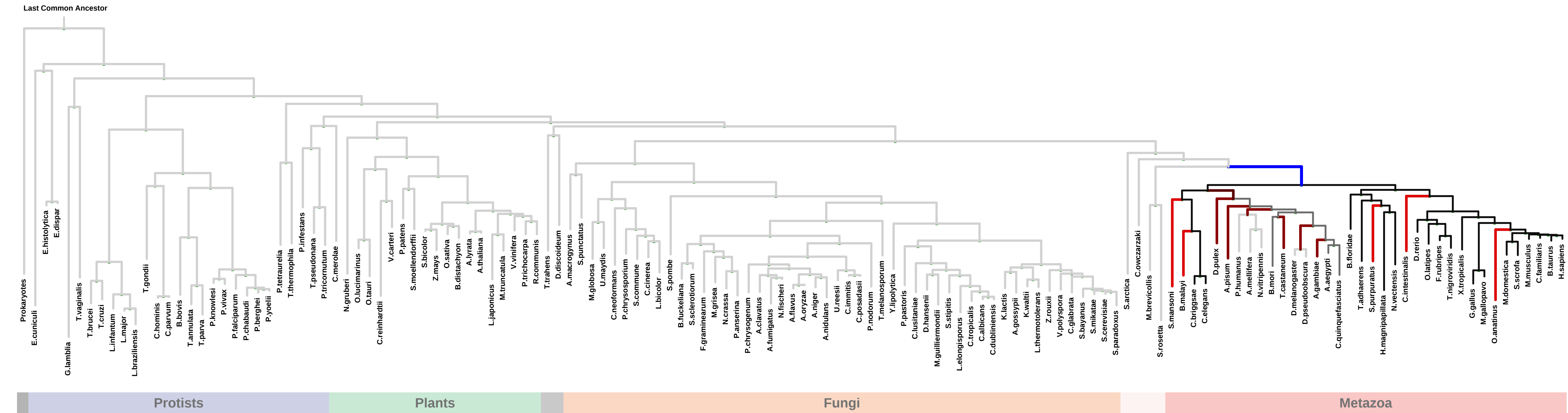


1: endoplasmic reticulum-Golgi intermediate compartment membrane || 2: SNARE complex || 3: catalytic step 2 spliceosome || 4: nuclear speck || 5: spliceosomal complex || 6: gamma-tubulin complex || 7: microtubule cytoskeleton || 8: microtubule plus end || 9: spindle pole || 10: cytosolic small ribosomal subunit || 11: ribonucleoprotein complex || 12: ribosome || 13: alpha DNA polymerase:primase complex || 14: chromatin || 15: nuclear envelope || 16: nuclear matrix || 17: chromosome, telomeric region || 18: condensed nuclear chromosome || 19: Mre11 complex || 20: nuclear chromatin || 21: COPI vesicle coat || 22: actomyosin || 23: endoplasmic reticulum-Golgi intermediate compartment || 24: myosin complex || 25: histone methyltransferase complex || 26: MLL1 complex || 27: chromosome || 28: PML body || 29: apical part of cell || 30: caveola || 31: endocytic vesicle membrane || 32: aminoacyl-tRNA synthetase multienzyme complex || 33: transport vesicle || 34: mitochondrial ribosome || 35: small ribosomal subunit || 36: condensed chromosome || 37: PeBoW complex || 38: peribosome, large subunit precursor

Num of ECM Genes: 1. Num of Predicted Genes: 97



Num of ECM Genes: 1. Num of Predicted Genes: 97



ECM 2, Gene set "PCNA-p21 complex", Page 3

Num of ECM Genes: 1. Num of Predicted Genes: 97



PG		Protein		Protists		Plants		Fungi		Metazoa		LLR	Notes
J	FCGR3B											2.2	1
	STOX2											2.0	
B	TMEM200A											1.9	
	OR2L8											1.6	
D	FAM162B											1.6	
	LILRA3											1.6	
	LYSMD2											1.5	
	NDNF											1.5	2
	THAP10											1.5	
	LAPTM4B											1.4	3
B	OR51D1											1.3	
B	OR13D1											1.1	
	ND6											1.1	4
N	TIMP2											0.9	5
N	TIMP3											0.9	2 / 5
N	TIMP4											0.9	6
	XK											0.9	
M	C18orf63											0.8	
	CD164											0.6	7 / 8 / 9 / 10
	FAM65A											0.6	
	TMEM169											0.6	
B	OR5AP2											0.5	
	NDUFA1											0.5	4 / 11
	FADD											0.5	12 / 13 / 14 / 15 / 16
K	GLCC1											0.4	
	LYSMD4											0.4	
	NDUFB4											0.2	4
F	CACNG4											0.0	17 / 18 / 19

1: anchored to membrane || 2: extracellular matrix || 3: endomembrane system || 4: mitochondrial respiratory chain complex I || 5: basement membrane || 6: sarcomere || 7: endosome || 8: endosome membrane || 9: lysosomal membrane || 10: lysosome || 11: mitochondrial membrane || 12: CD95 death-inducing signaling complex || 13: cell body || 14: death-inducing signaling complex || 15: membrane raft || 16: neuron projection || 17: alpha-amino-3-hydroxy-5-methyl-4-isoxazolepropionic acid selective glutamate receptor complex || 18: endocytic vesicle membrane || 19: voltage-gated calcium channel complex