

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

Dataset:

Num of genes in input gene set: 1
Total number of genes: 20834
Prediction LLR threshold: 0

The CLIME PDF output two sections:

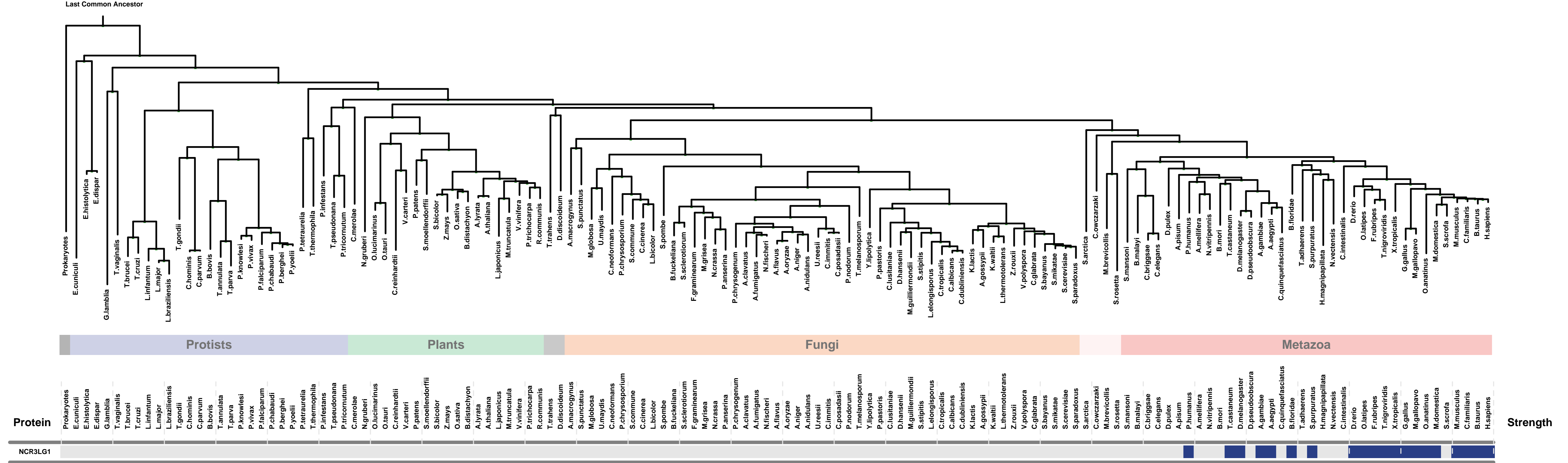
1) Overview of Evolutionarily Conserved Modules (ECMs)

- 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+

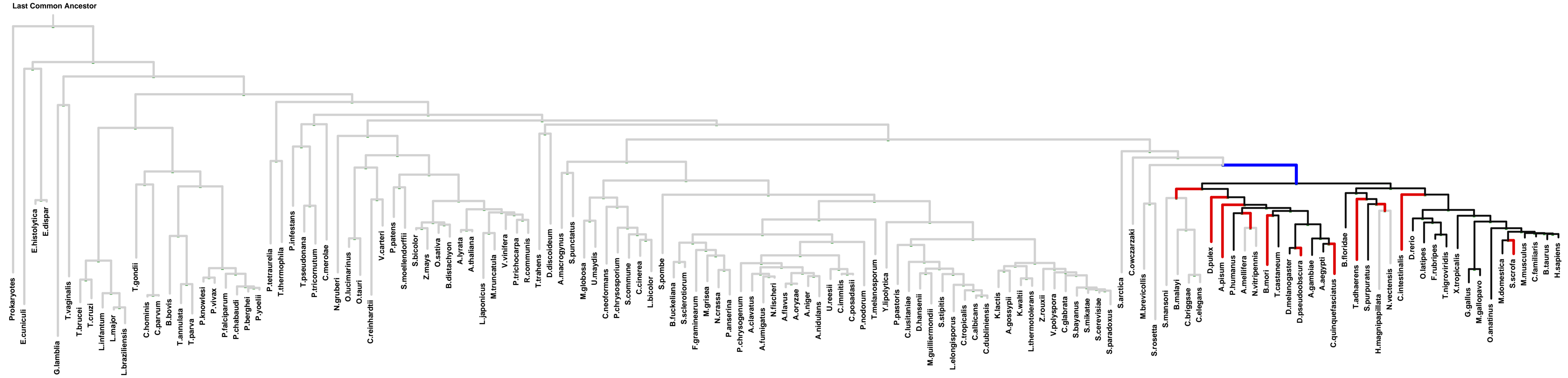
- Top panel shows the inferred evolutionary history on the predefined species tree. Branch color shows the gain event (blue) and loss events (red color, with brighter color indicating higher confidence in loss). Branches before the gain or after a loss are shown in gray.
- Bottom panel shows the input 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 "viral capsid", Page 1

Num of ECM Genes: 1. Num of Predicted Genes: 118

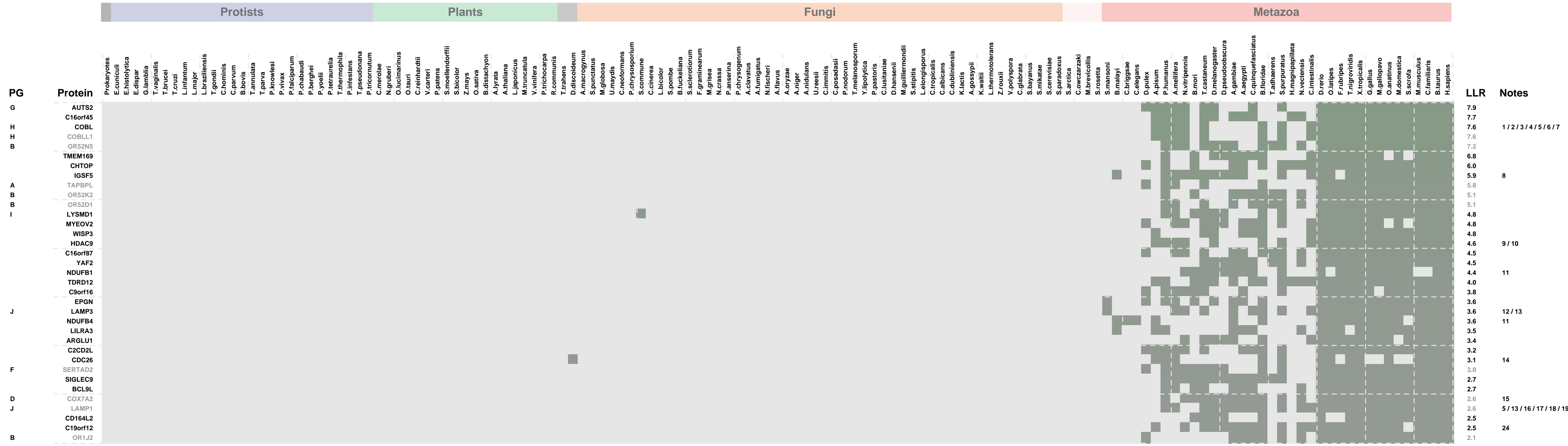
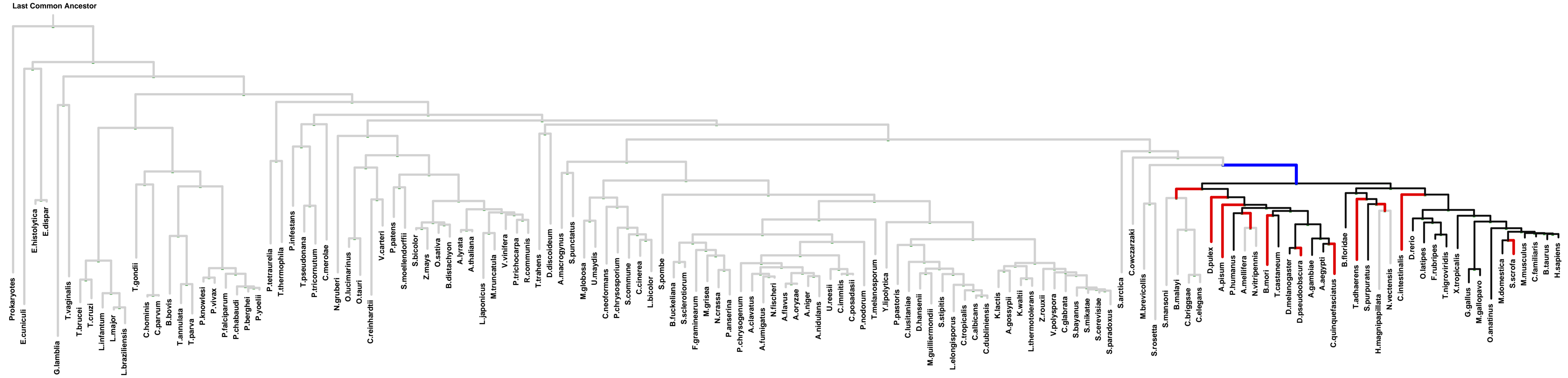


PG	Protein	Prokaryotes	Protists	Plants	Fungi	Metazoa	LLR	Notes
A	NCR3LG1							1
B	OR10T2						30.0	2
	TMEM123						25.1	3 / 4 / 5 / 6
	AKAP6						23.5	7
	FNDC5						19.8	8 / 9
C	GFRA2						18.8	10
	ND6						18.3	11 / 12
	EBI3						18.2	13 / 14 / 15
	SHARPIN						18.1	16
	MFF						16.7	17
	DAPL1						14.5	18 / 19 / 20 / 21
	TMEM60						14.1	22 / 23
	SAYSD1						14.1	24
D	COX7A1						13.6	25
E	VEGFA						13.1	8 / 9
	RASSF10						12.7	2 / 8 / 9
	EPPK1						12.6	2 / 8 / 9
	ITFG3						12.1	
	FIGF						11.9	
E	MED9						11.7	19
	BTNL8						11.4	24
A	CDCA4						11.2	
F	COX16						11.0	
	GFRA1						10.5	25
C	GFRA3						10.4	8 / 9
	MIA						10.4	2 / 8 / 9
	USHBP1						10.4	
	C16orf89						10.0	
C	GFAL						9.3	
	CCDC127						9.3	
	FANCC						9.0	
	FJX1						9.0	26 / 27
	HSF2BP						8.9	
	FBXO5						8.6	
	HAVCR2						8.5	28

1: viral capsid || 2: external side of plasma membrane || 3: calcium channel complex || 4: nuclear envelope || 5: nuclear outer membrane || 6: sarcoplasmic reticulum || 7: peroxisomal membrane || 8: anchored to membrane || 9: extrinsic to membrane || 10: mitochondrial respiratory chain complex I || 11: LUBAC complex || 12: postsynaptic density || 13: integral to mitochondrial membrane || 14: mitochondrial outer membrane || 15: peroxisome || 16: cytoplasmic vesicle membrane || 17: mitochondrial respiratory chain || 18: basement membrane || 19: platelet alpha granule lumen || 20: proteinaceous extracellular matrix || 21: secretory granule || 22: microtubule organizing center || 23: spindle pole || 24: mediator complex ||

ECM 1, Gene set "viral capsid", Page 2

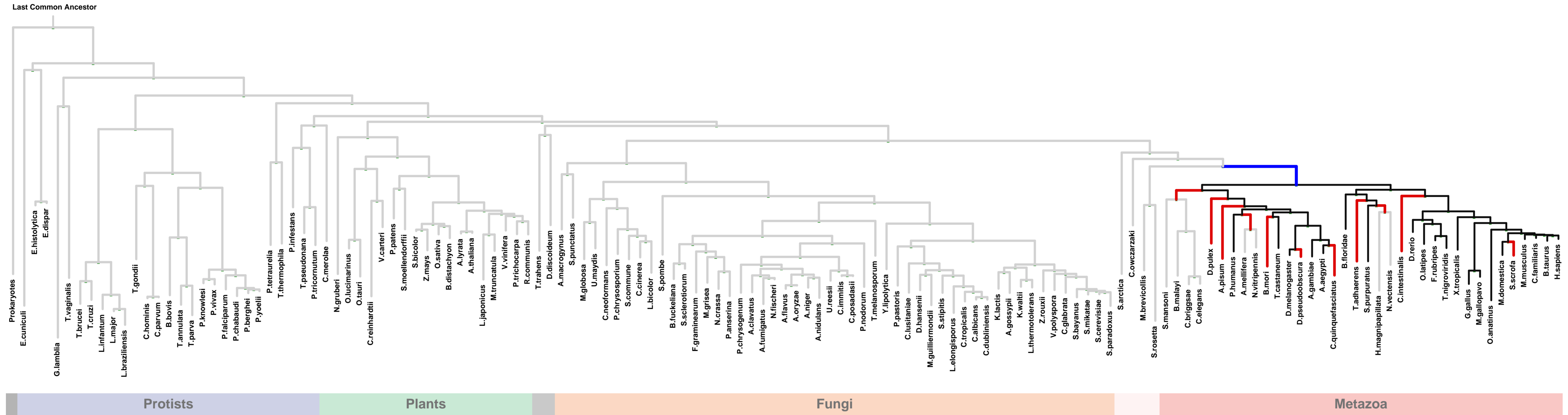
Num of ECM Genes: 1. Num of Predicted Genes: 118



1: actin filament || 2: axon || 3: axonal growth cone || 4: cell cortex || 5: dendrite || 6: dendritic growth cone || 7: ruffle || 8: tight junction || 9: histone deacetylase complex || 10: histone methyltransferase complex || 11: mitochondrial respiratory chain complex I || 12: alveolar lamellar body membrane || 13: lysosomal membrane || 14: anaphase-promoting complex || 15: mitochondrial respiratory chain || 16: endosome membrane || 17: external side of plasma membrane || 18: lamellar body || 19: late endosome || 20: lysosome || 21: melanosome || 22: multivesicular body || 23: sarcolemma || 24: mitochondrial membrane

ECM 1, Gene set "viral capsid", Page 3

Num of ECM Genes: 1. Num of Predicted Genes: 118

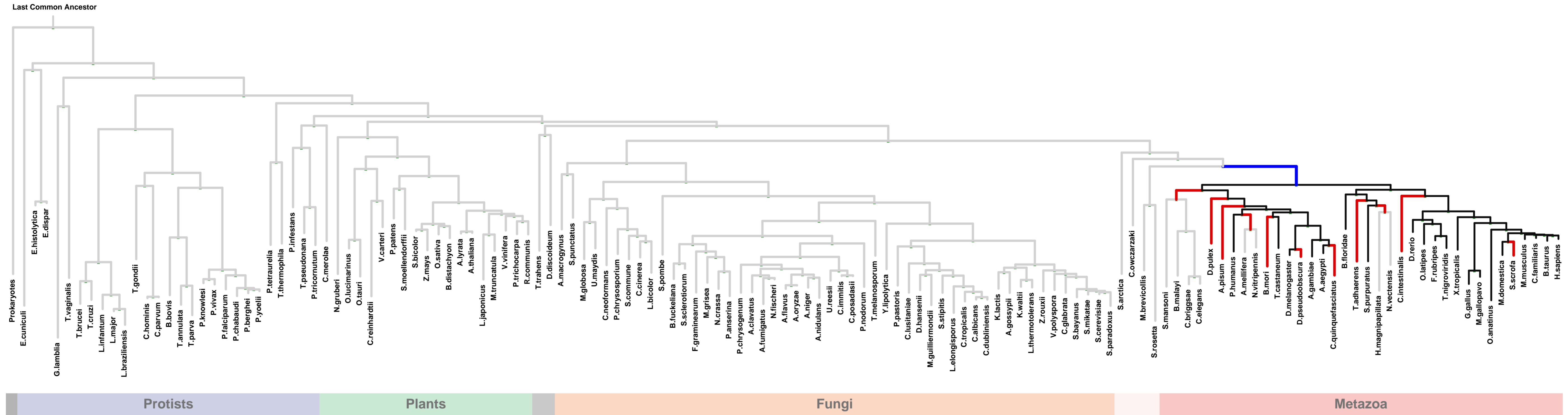


PG	Protein	Protists	Plants	Fungi	Metazoa	LLR	Notes
K	C6orf203					2.1	
	NINJ1					2.0	
K	NINJ2					2.0	
	ZNF185					2.0	1
L	GLYATL2					1.9	
	LYRM9					1.8	
L	TMEM198					1.7	
	GKAP1					1.7	
L	TMEM25					1.5	
	ITM2B					1.5	2 / 3 / 4
L	ITM2C					1.5	5 / 6
	ITM2A					1.5	
M	FANCA					1.4	7
	PGLYRP4					1.3	
M	CBLN1					1.2	8
	GEMIN4					1.2	9 / 10 / 11
M	SLAIN2					1.2	12 / 13
	FAM198B					1.2	
M	NTF3					1.2	14
	NTF4					1.2	15
M	IFITM1					1.2	
	IFITM2					1.2	
M	DIABLO					1.2	16 / 17 / 18
	BDNF					1.2	14
O	TMEM91					1.2	
	FAM133B					1.2	
O	FAM171A1					1.2	
	WHAMM					1.2	19 / 20
M	FAM171A2					1.2	
	FAM171B					1.2	
G	NGF					1.2	
	FBRSL1					1.2	15 / 21 / 22
G	CD226					1.2	
	C5orf15					1.1	23
	CPLX1					0.9	8 / 24 / 25

1: focal adhesion || 2: endosome membrane || 3: Golgi-associated vesicle membrane || 4: integral to organelle membrane || 5: lysosomal membrane || 6: lysosome || 7: Fanconi anaemia nuclear complex || 8: synapse || 9: Cajal body || 10: small nuclear ribonucleoprotein complex || 11: spliceosomal complex || 12: microtubule cytoskeleton || 13: microtubule plus end || 14: cytoplasmic membrane-bounded vesicle || 15: endoplasmic reticulum lumen || 16: CD40 receptor complex || 17: internal side of plasma membrane || 18: mitochondrial intermembrane space || 19: cytoplasmic vesicle membrane || 20: endoplasmic reticulum-Golgi intermediate compartment || 21: endosome || 22: Golgi lumen || 23: membrane raft ||

ECM 1, Gene set "viral capsid", Page 4

Num of ECM Genes: 1. Num of Predicted Genes: 118



PG	Protein	Prokaryotes	Protists	Plants	Fungi	Metazoa	LLR	Notes
B	OR6B2						0.8	
B	OR6B3						0.8	
	PLEKHN1						0.7	
	PAGR1						0.7	1
	OPTN						0.6	2/3
I	LYSMD2						0.6	
	MYF6						0.6	
	NDUFA1						0.5	4/5
	RD3						0.4	
	ZHX2						0.4	
P	GADD45B						0.3	
P	GADD45A						0.3	
	EPN2						0.2	
	FAM193B						0.0	

1: histone methyltransferase complex || 2: cytoplasmic membrane-bounded vesicle || 3: trans-Golgi network || 4: mitochondrial membrane || 5: mitochondrial respiratory chain complex I