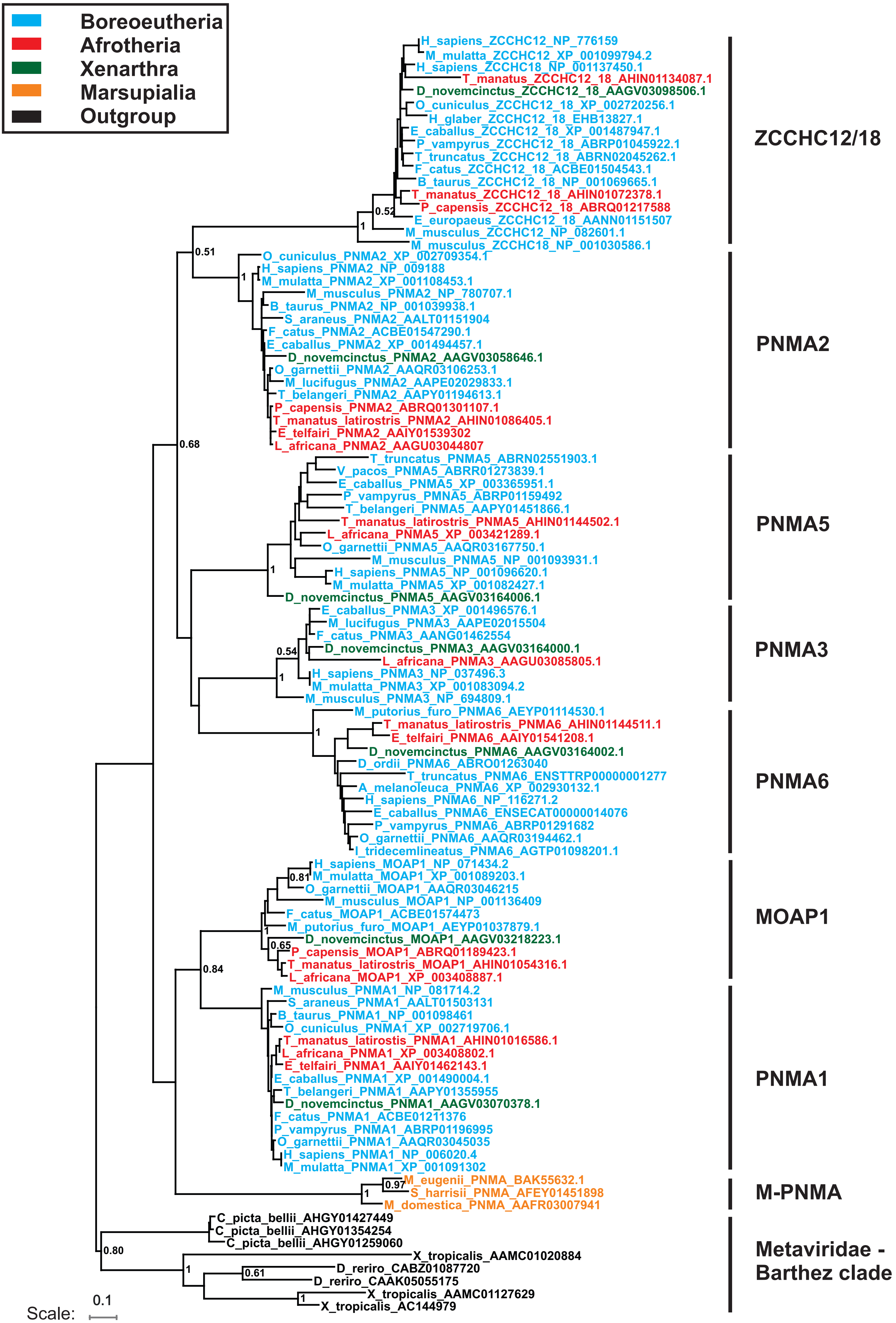
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Metaviridae - Barthez clade
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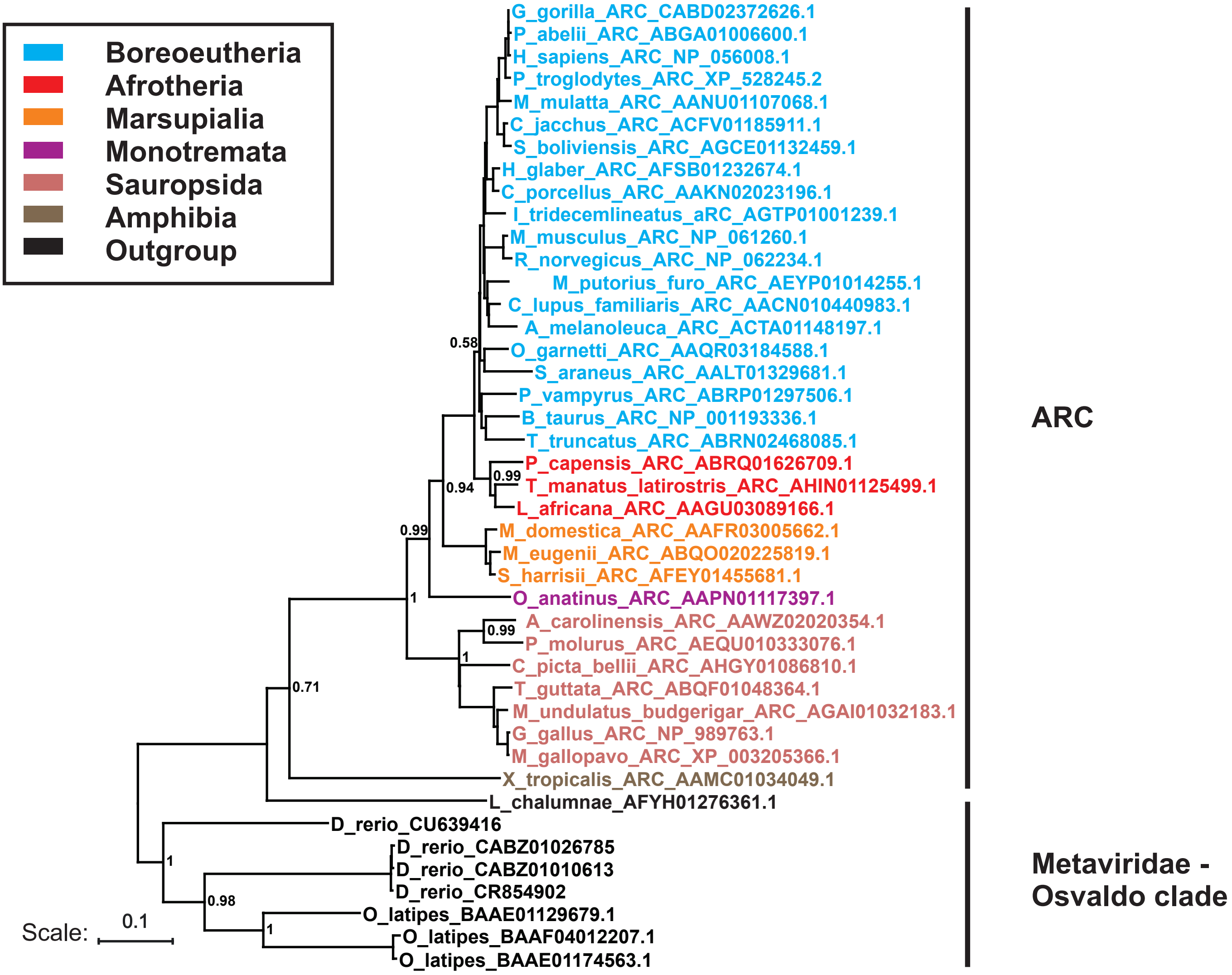
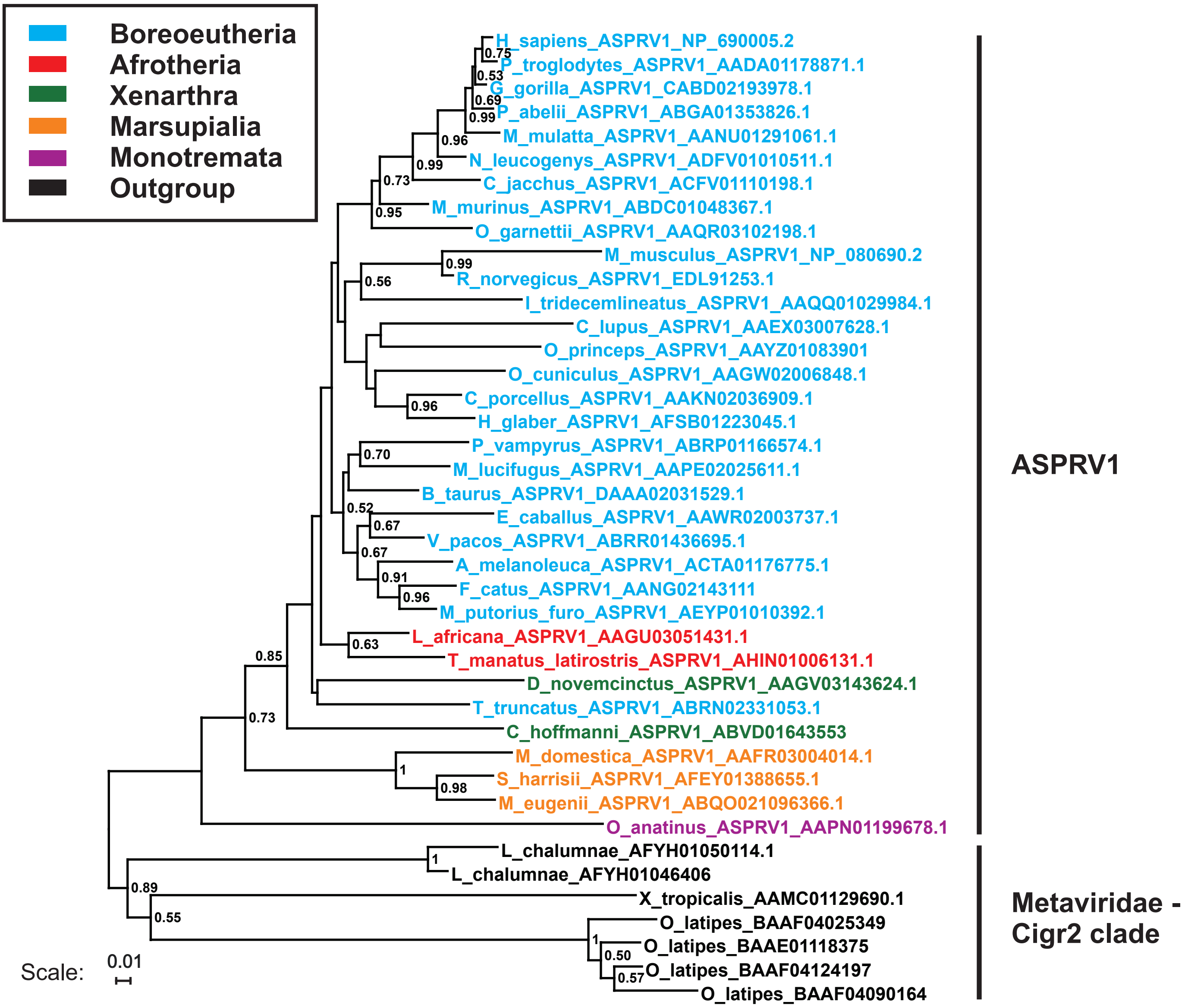
Scale:

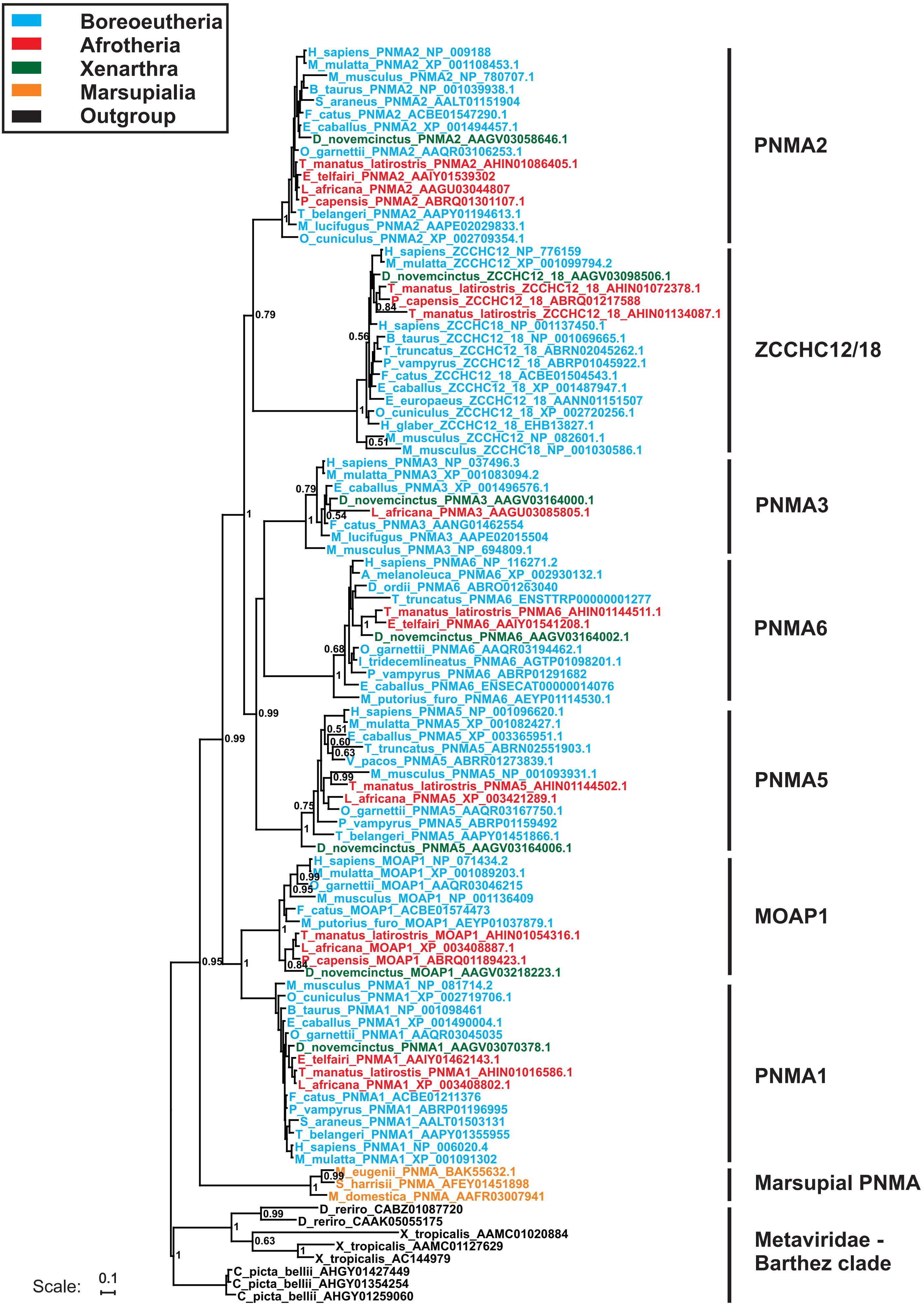
Supplementary Figure S1. ML phylogeny of the PNMA gene family. The maximum likelihood phylogenetic tree was inferred from the capsid part of the gag domain by PhyML 3.0 program under a Poisson+G4 model. Reliability for the internal branches was assessed using 100 bootstrap replications. Bootstrap support values larger than 0.5 are shown. The scale bar corresponds to 0.1 substitutions per site. Capsid part of the gag domain from diverse vertebrate Barthez retroelements was used to root this tree. PNMAL1, PNMAL2 and CCDC8 sequences were omitted from the alignment because they only retain the matrix part of the gag domain.



Supplementary Figure S2. NJ phylogeny of the ARC genes. The rooted neighbor-joining tree was inferred by MEGA 5.0 program under a *p*-distance+pairwise deletion model from the gag domain. Reliability for the internal branches was assessed using the 10000 bootstrap replications. Bootstrap support values larger than 0.5 are shown. The scale bar corresponds to 0.1 substitutions per site. Gag domains from diverse vertebrate Osvaldo retroelements were used to root this tree.



Supplementary Figure S3. NJ phylogeny of the ASPRV1 genes. The rooted neighbor-joining tree was inferred by MEGA 5.0 program under a *p*-distance+pairwise deletion model from the protease domain. Reliability for the internal branches was assessed using the 10000 bootstrap replications. Bootstrap support values larger than 0.5 are shown. The scale bar corresponds to 0.01 substitutions per site. Protease domains from diverse vertebrate Cigr2 retroelements were used to root this tree.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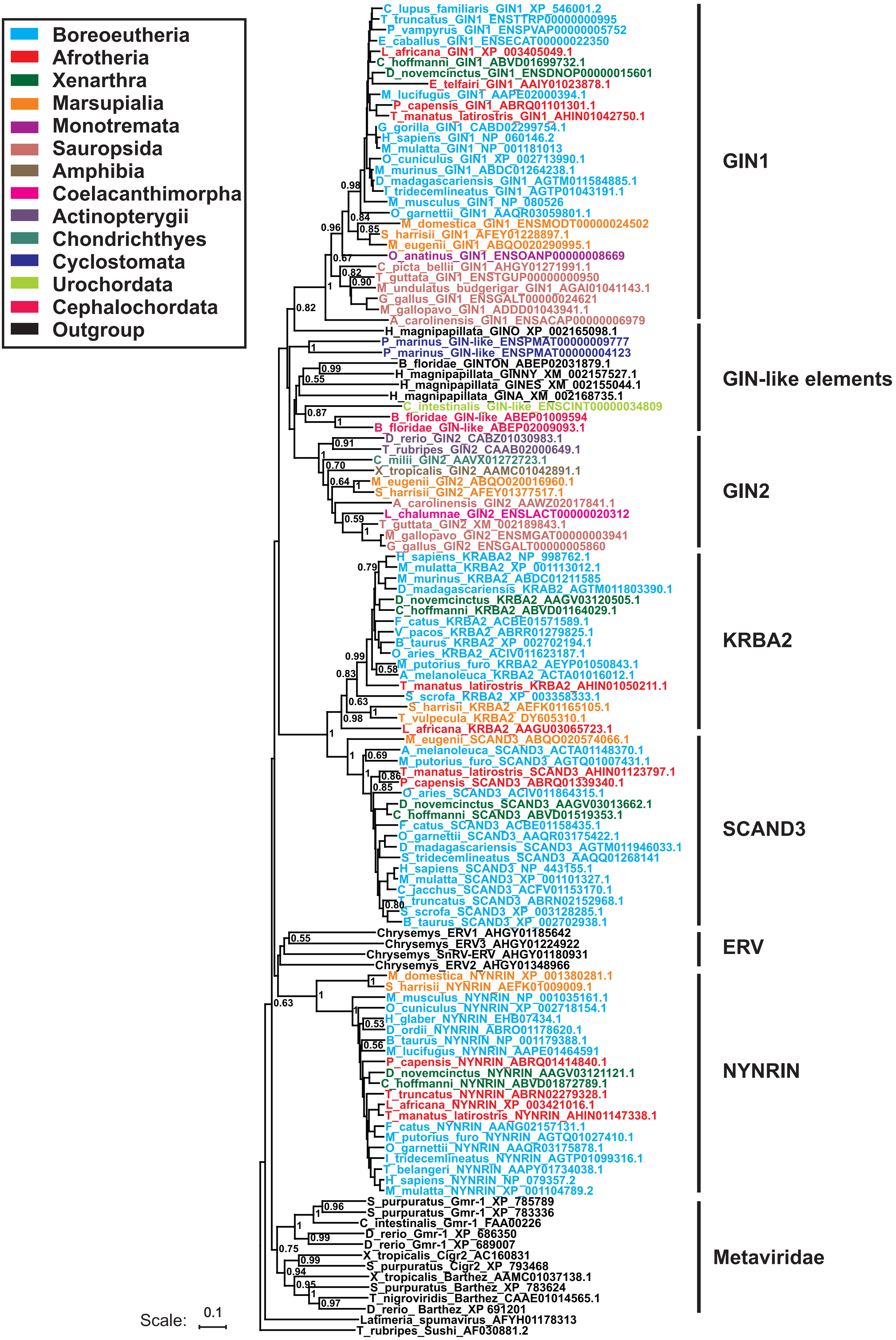
Metaviridae - Barthez clade
Scale:
0.1

Supplementary Figure S4. Bayesian phylogeny of the PNMA gene family. This tree was inferred from the capsid part of the gag domain by MrBayes 3 program under a JTT+G4 model. Only posterior probabilities larger than 0.5 are shown. The scale bar corresponds to 0.1 substitutions per site. Capsid part of the gag domain from diverse vertebrate Barthez retroelements was used to root this tree. PNMAL1, PNMAL2 and CCDC8 sequences were omitted from the alignment because they only retain the matrix part of the gag domain.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🟩 Xenarthra
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🟫 Amphibia
🟥 Coelacanthimorpha
🟪 Actinopterygii
🟩 Chondrichthyes
🟦 Cyclostomata
🟩 Urochordata
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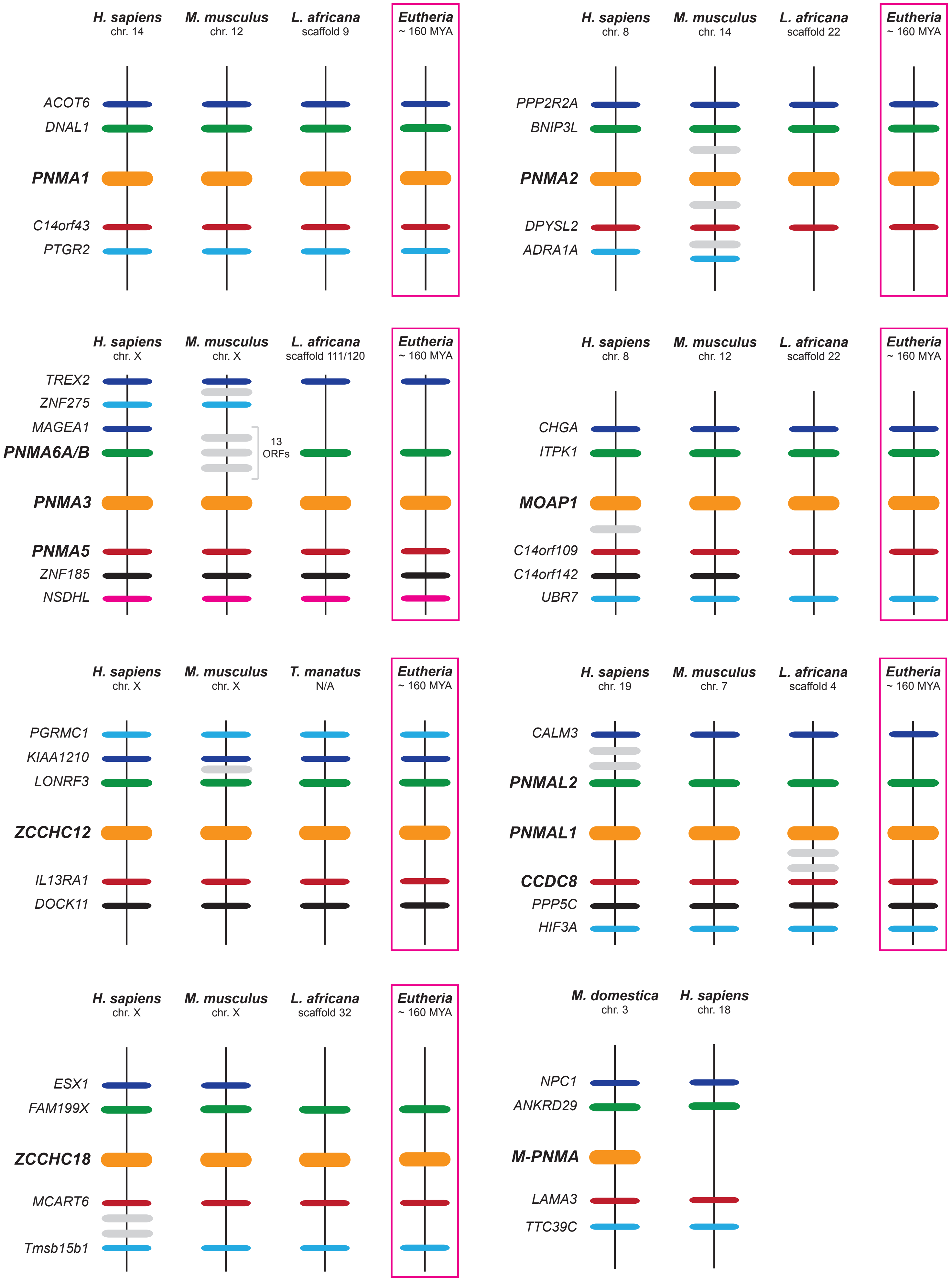
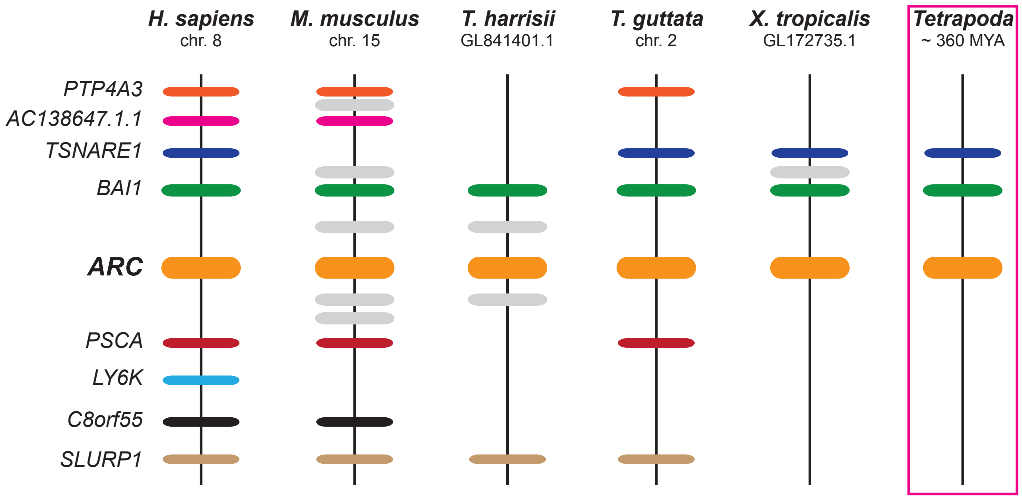
Scale:
0.1

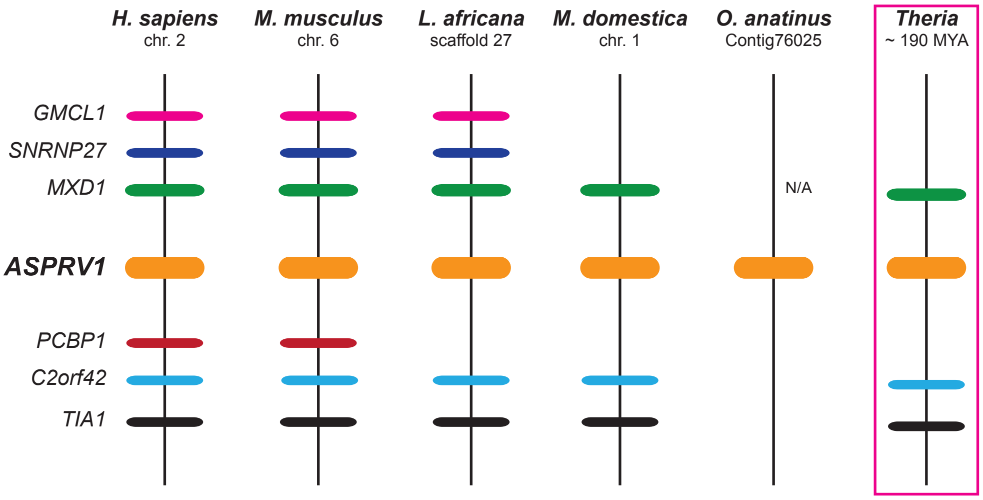
Supplementary Figure S5. NJ phylogeny of the integrase-derived RDDGs. The rooted neighbor-joining tree was inferred by MEGA 5.0 program under a *p*-distance+pairwise deletion model from the integrase domain. Reliability for the internal branches was assessed using the 10000 bootstrap replications. Bootstrap support values larger than 0.5 are shown. The scale bar corresponds to 0.1 substitutions per site. Integrase domains from diverse deuterostome Metaviridae and ERV retroelements were used to root this tree.


H. sapiens
chr. 14
M. musculus
chr. 12
L. africana
scaffold 9
Eutheria
~ 160 MYA
ACOT6
DNAL1
PNMA1
C14orf43
PTGR2
H. sapiens
chr. 8
M. musculus
chr. 14
L. africana
scaffold 22
Eutheria
~ 160 MYA
PPP2R2A
BNIP3L
PNMA2
DPYSL2
ADRA1A
H. sapiens
chr. X
M. musculus
chr. X
L. africana
scaffold 111/120
Eutheria
~ 160 MYA
TREX2
ZNF275
MAGEA1
PNMA6A/B
PNMA3
PNMA5
ZNF185
NSDHL
13
ORFs
H. sapiens
chr. 8
M. musculus
chr. 12
L. africana
scaffold 22
Eutheria
~ 160 MYA
CHGA
ITPK1
MOAP1
C14orf109
C14orf142
UBR7
H. sapiens
chr. X
M. musculus
chr. X
T. manatus
N/A
Eutheria
~ 160 MYA
PGRMC1
KIAA1210
LONRF3
ZCCHC12
IL13RA1
DOCK11
H. sapiens
chr. 19
M. musculus
chr. 7
L. africana
scaffold 4
Eutheria
~ 160 MYA
CALM3
PNMAL2
PNMAL1
CCDC8
PPP5C
HIF3A
H. sapiens
chr. X
M. musculus
chr. X
L. africana
scaffold 32
Eutheria
~ 160 MYA
ESX1
FAM199X
ZCCHC18
MCART6
Tmsb15b1
M. domestica
chr. 3
H. sapiens
chr. 18
NPC1
ANKRD29
M-PNMA
LAMA3
TTC39C

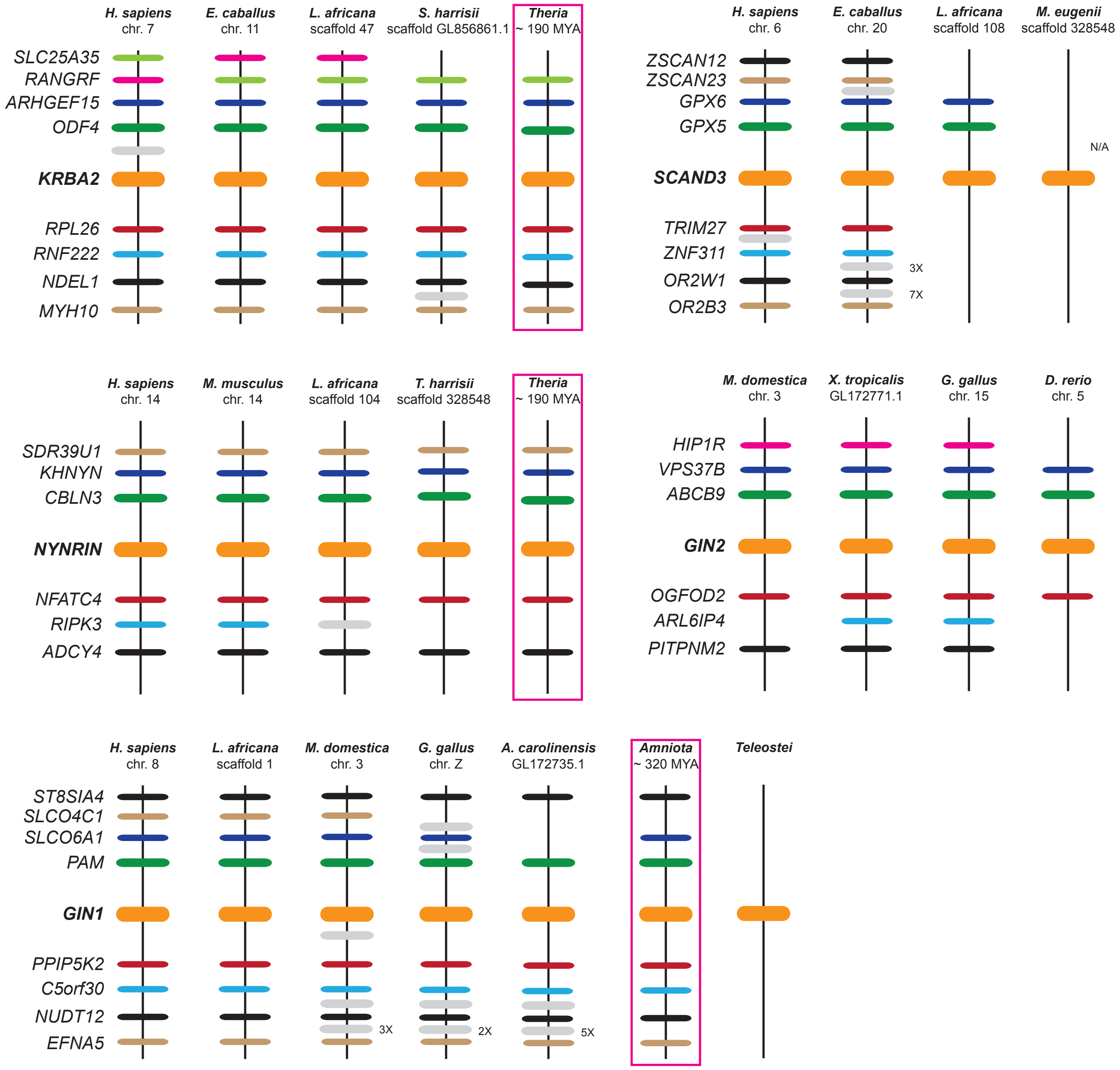
Supplementary Figure S6. Conserved synteny in the PNMA family of RDDGs. Chromosomal regions carrying all RDDGs in the species considered in this analysis were compared, and neighbouring genes with conserved synteny were identified. Horizontal lines denote orthologous relationships. Each RDDG gene is represented in bold as a horizontal orange line on the chromosome. Neighbouring genes that are in synteny are shown with a schematic indication of their distance (not to scale). The ancestral states of the RDDG chromosomal positions were reconstructed from a comparison of syntenic positions between multiple mammalian lineages.



Supplementary Figure S7. Conserved synteny of the ARC gene. Chromosomal regions carrying ARC gene in the species considered in this analysis were compared, and neighbouring genes with conserved synteny were identified. Horizontal lines denote orthologous relationships. ARC gene is represented in bold as an horizontal orange line on the chromosome. Neighbouring genes that are in synteny are shown with a schematic indication of their distance (not to scale). The ancestral state of the ARC gene chromosomal position was reconstructed from a comparison of syntenic positions between multiple tetrapod lineages.



Supplementary Figure S8. Conserved synteny of the ASPRV1 gene. Chromosomal regions carrying ASPRV1 gene in the species considered in this analysis were compared, and neighbouring genes with conserved synteny were identified. Horizontal lines denote orthologous relationships. ASPRV1 gene is represented in bold as an horizontal orange line on the chromosome. Neighbouring genes that are in synteny are shown with a schematic indication of their distance (not to scale). The ancestral state of the ASPRV1 gene chromosomal position was reconstructed from a comparison of syntenic positions between multiple mammalian lineages.



Supplementary Figure S9. Conserved synteny in the integrase-derived RDDGs. Chromosomal regions carrying all RDDGs in the species considered in this analysis were compared, and neighbouring genes with conserved synteny were identified. Horizontal lines denote orthologous relationships. Each RDDG gene is represented in bold as a horizontal orange line on the chromosome. Neighbouring genes that are in synteny are shown with a schematic indication of their distance (not to scale). The ancestral states of the RDDG chromosomal positions were reconstructed from a comparison of syntenic positions between multiple mammalian or sauropsid lineages.