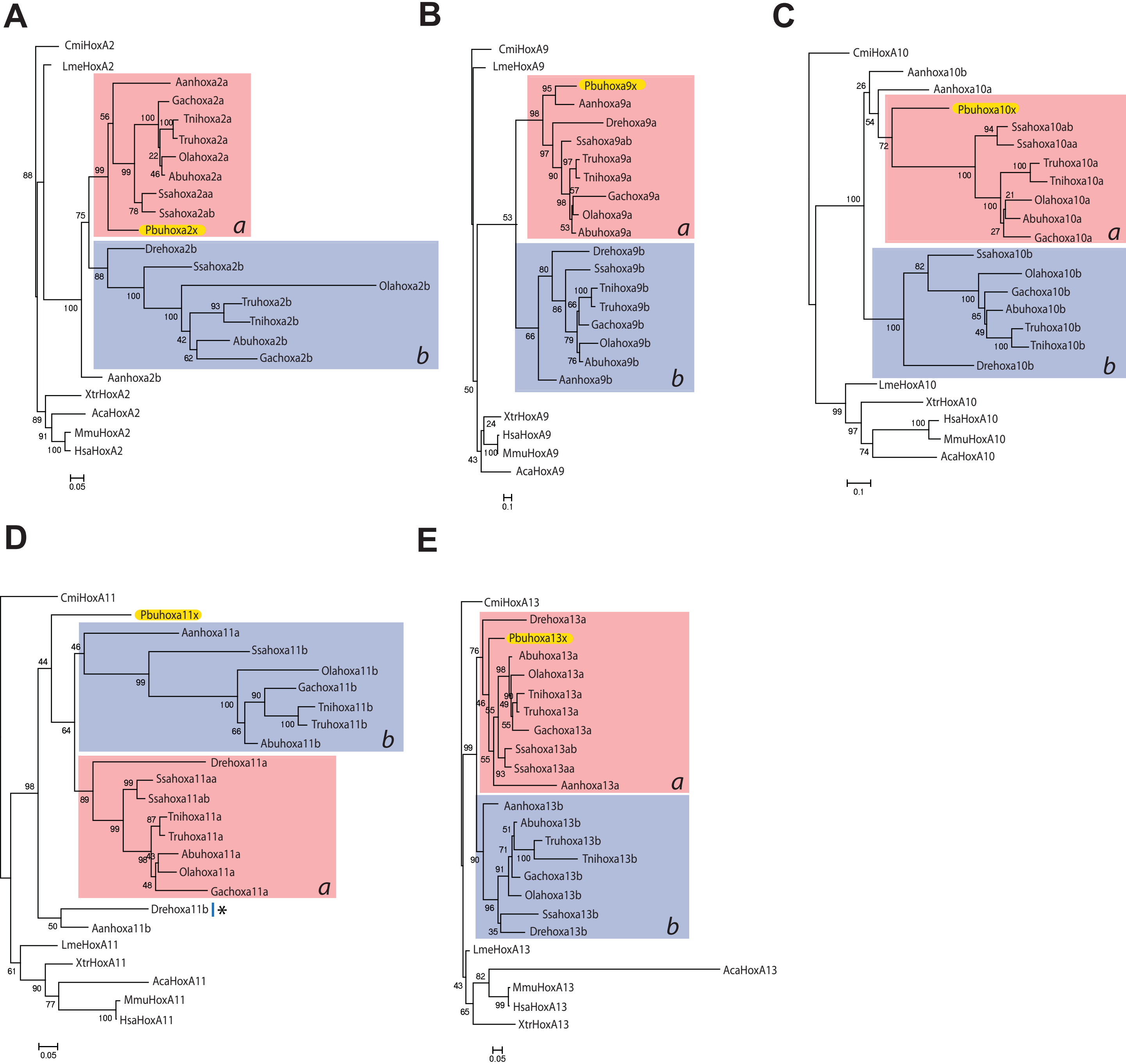
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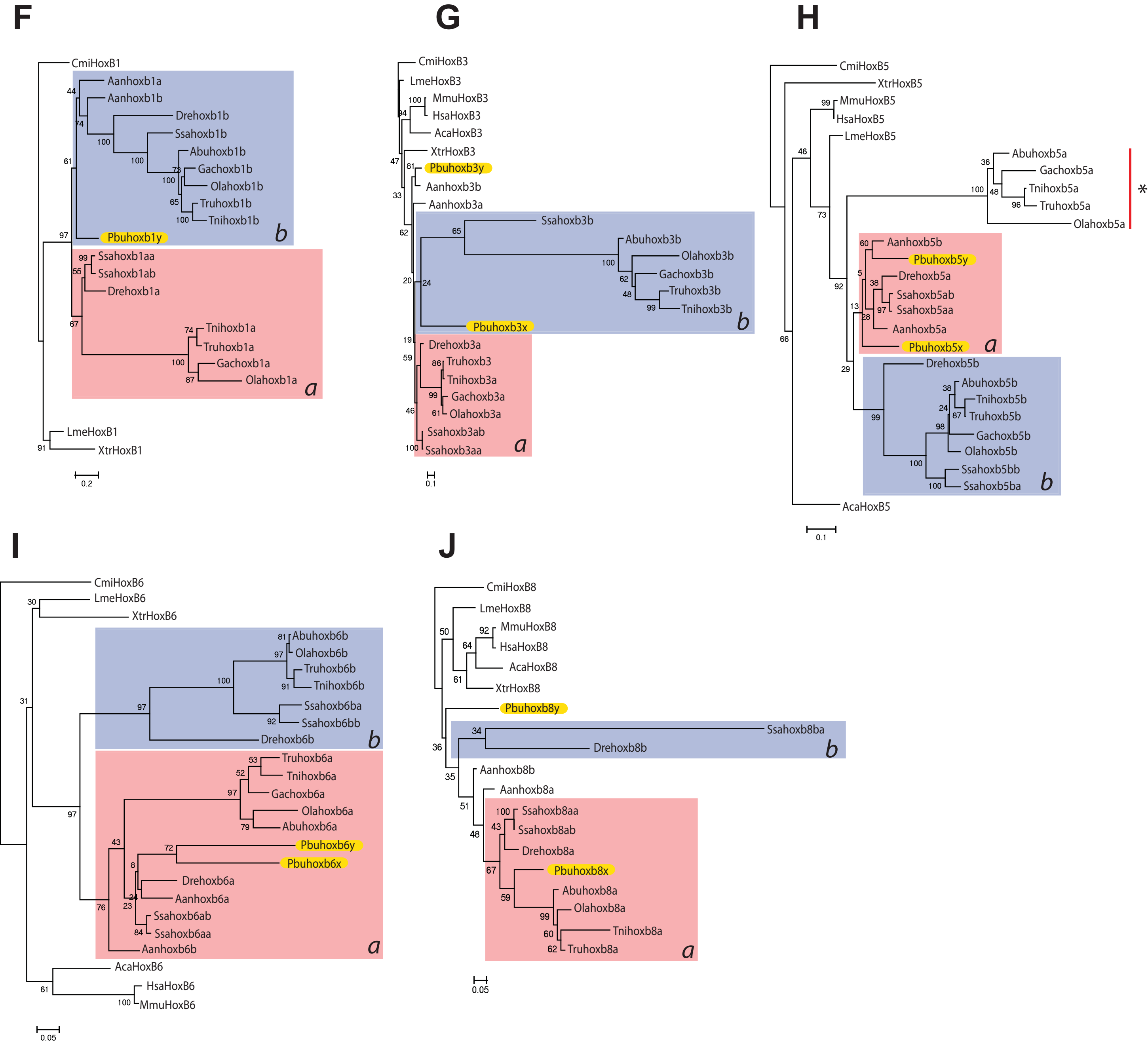
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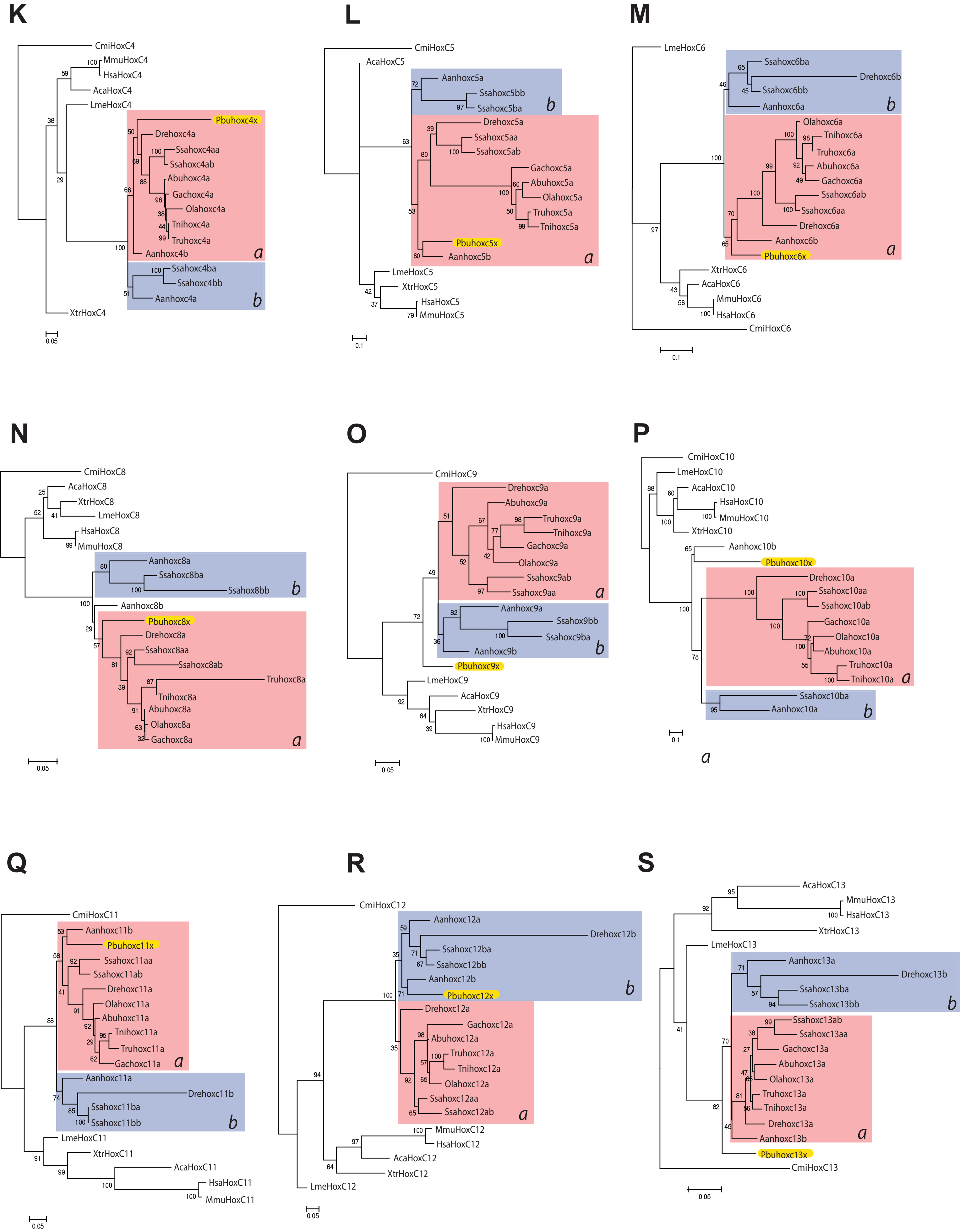
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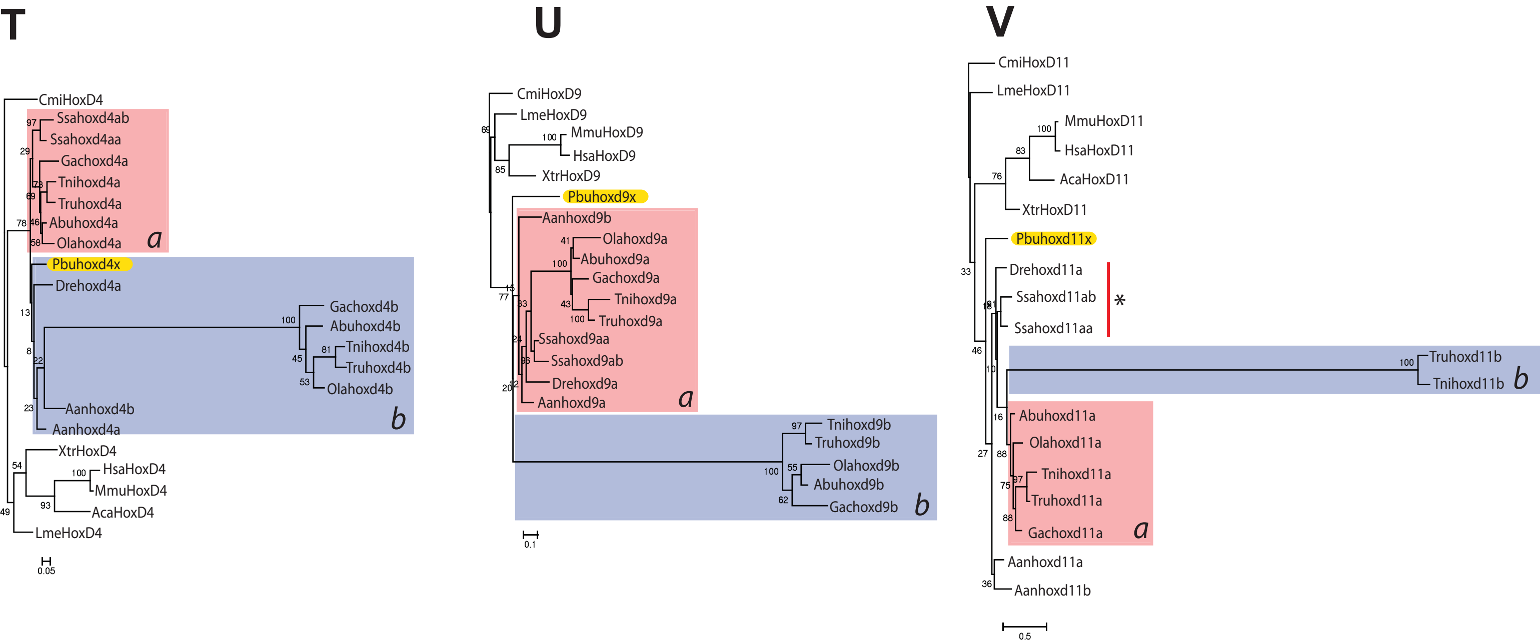
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Truhoxd4b
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Aanhoxd4b
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b
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MmuHoxD4
AcaHoxD4
LmeHoxD4
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13
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54
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Aanhoxd11b
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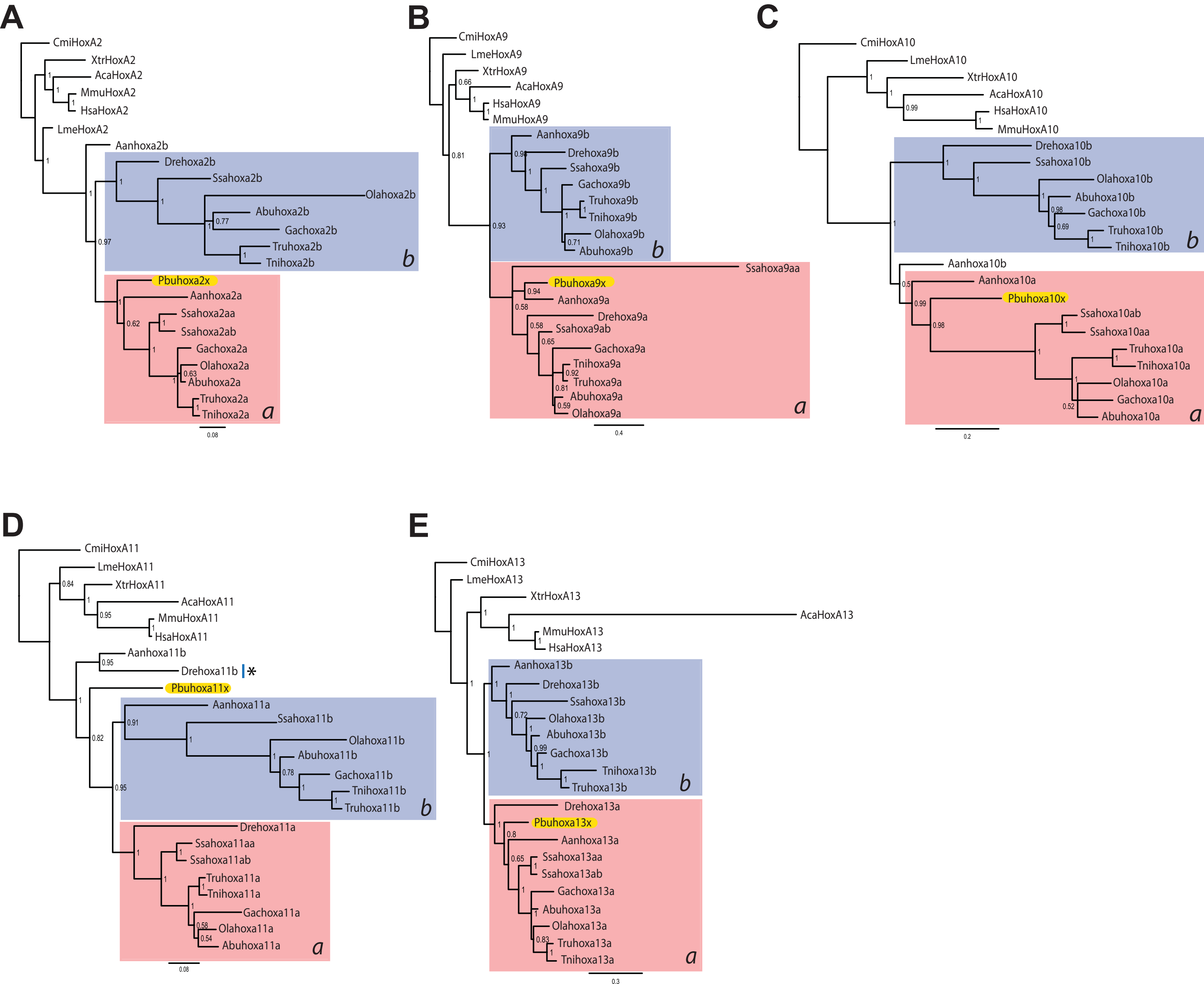
76
33
18
91
46
10
100
16
27
88
97
75
88
36
0.5

Figure S1: Maximum likelihood *Hox* gene genealogies.

Maximum-Likelihood trees were built using with the program RAxML using the LG amino acid substitution model with gamma and invariant parameters and 1000 bootstrap replicates. Trees are shown for each orthology informative *Hox* gene family for which a *Pantodon* sequence was found. A: *HoxA2*, B: *HoxA9*, C: *HoxA10*, D: *HoxA11*, E: *HoxA13* F: *HoxB1*, G: *HoxB3*, H: *HoxB5*, I: *HoxB6*, J: *HoxB8* K: *HoxC4*, L: *HoxC5*, M: *HoxC6*, N: *HoxC8*, O: *HoxC9*, P: *HoxC10*, Q: *HoxC11*, R: *HoxC12*, S: *HoxC13*, T: *HoxD4*, U: *HoxD9*, V: *HoxD1*. The red boxes demarcate the post-TGD ‘a’ clades, while blue boxes mark is the post-TGD ‘b’ clades. Each clade is delineated at the most highly supported node inclusive of all clupeocephalan teleost ‘a’ or ‘b’ genes and the *Pantodon* gene where applicable, and may or may not include *Anguilla* sequences. Atypically paraphyletic clupeocephalan post-TGD ‘a’ or ‘b’ clades are demarcated with an asterisk (*). Bootstrap support values are shown above each node. *Pantodon* sequences are displayed in bold and highlighted in yellow. Species names are abbreviated are as follows. Cmi: *Callorhinchus milii*, Lme: *Latimeria menadoensis*, Xtr: *Xenopus tropicalis*, Aca: *Anolis caroliensis*, Mmu: *Mus musculus*, Hsa: *Homo sapiens*, Aan: *Anguilla anguilla*, Pbu: *Pantodon buchholzi*, Dre: *Danio rerio*, Ssa: *Salmo salar*, Ola: *Oryzias latipes*, Gac: *Gasterosteus aculeatus*, Abu: *Astatotilapia burtoni*, Tru: *Takifugu rubripes*, Tni: *Tetraodon nigroviridis*.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Olahoxa9b
Abuhoxa9b
b
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Pbuhoxa9x
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Gachoxa10b
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b
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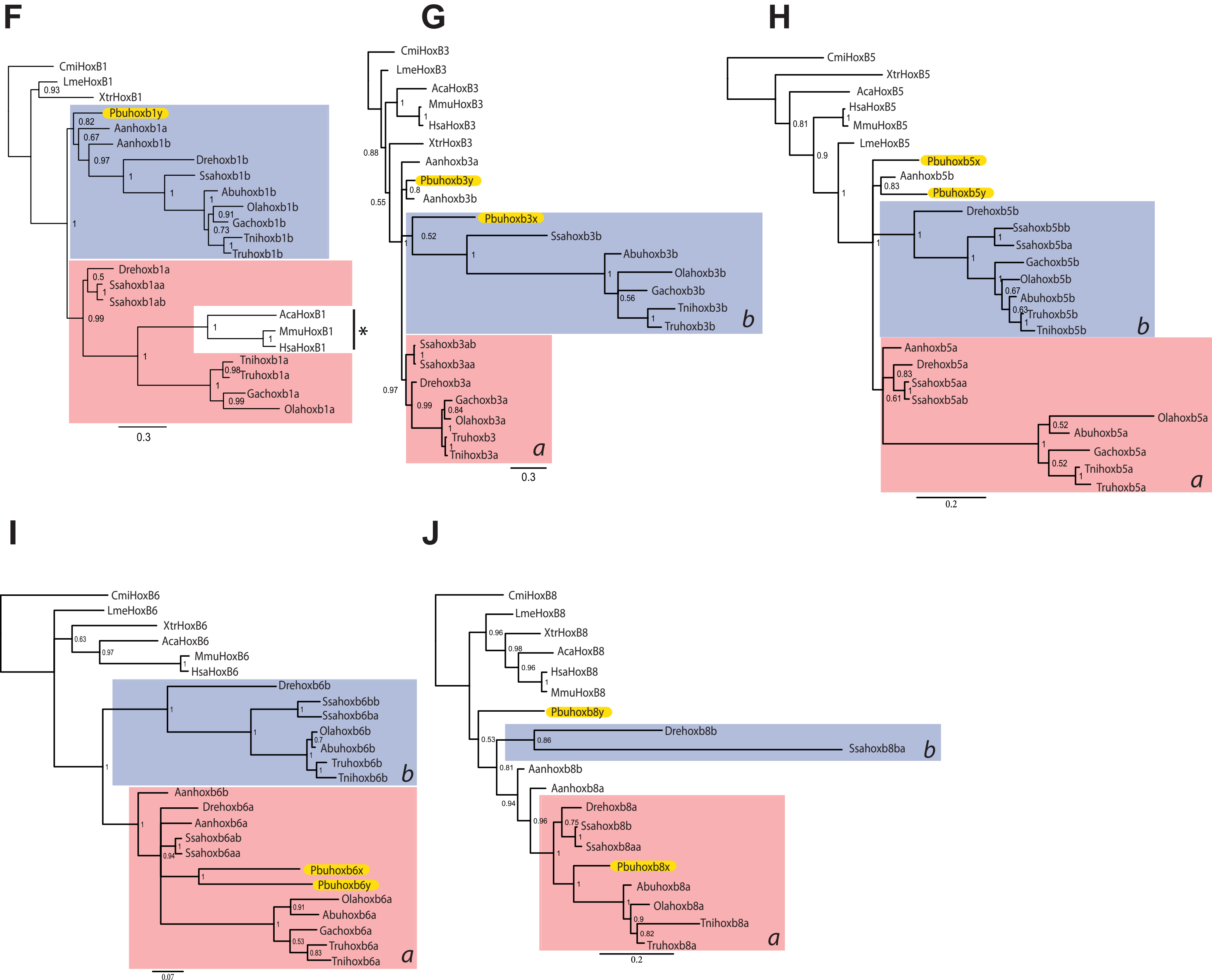
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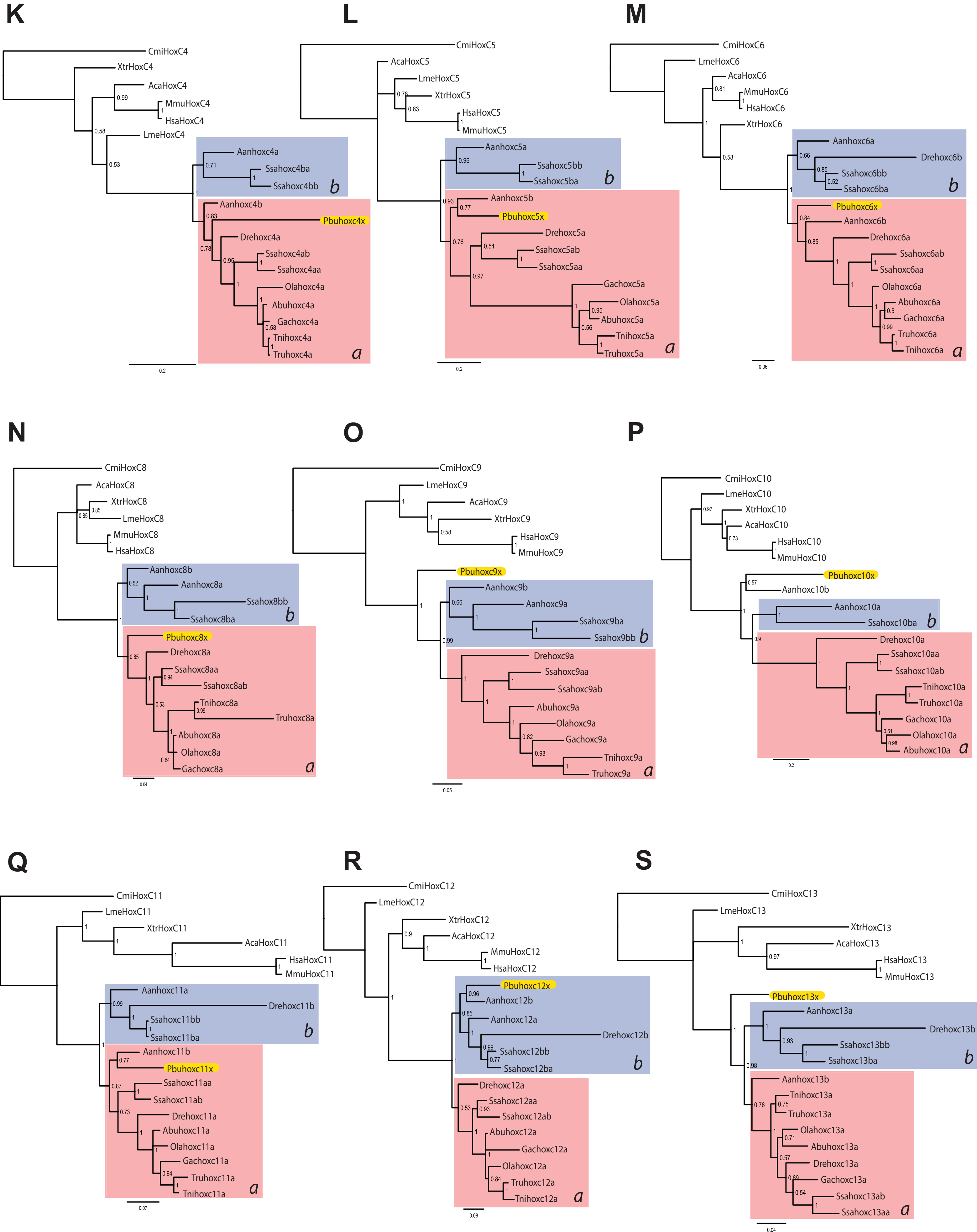
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1
XtrHoxC6
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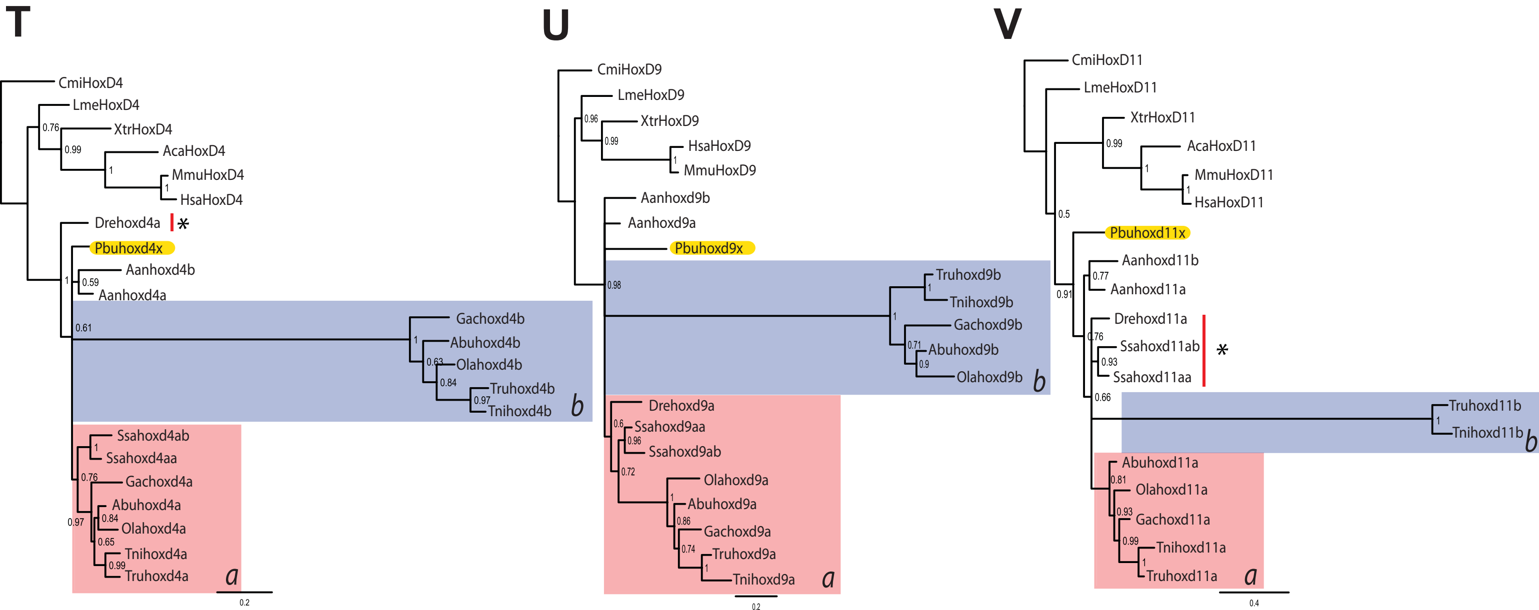
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Gachoxd4b
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Truhoxd4b
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Pbuhoxd11x
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a
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Figure S2: Bayesian *Hox* gene genealogies.

Bayesian trees were built using with the program mrbayes using the WAG amino acid substitution model with gamma and invariant parameters and run over 1000000 generations. Trees are shown for each orthology informative *Hox* gene family for which a *Pantodon* sequence was found. A: *HoxA2*, B: *HoxA9*, C: *HoxA10*, D: *HoxA11*, E: *HoxA13* F: *HoxB1*, G: *HoxB3*, H: *HoxB5*, I: *HoxB6*, J: *HoxB8* K: *HoxC4*, L: *HoxC5*, M: *HoxC6*, N: *HoxC8*, O: *HoxC9*, P: *HoxC10*, Q: *HoxC11*, R: *HoxC12*, S: *HoxC13*, T: *HoxD4*, U: *HoxD9*, V: *HoxD1*. The red boxes demarcate the post-TGD ‘a’ clades, while blue boxes mark is the post-TGD ‘b’ clades. Each clade is delineated at the most highly supported node inclusive of all clupeocephalan teleost ‘a’ or ‘b’ genes and the *Pantodon* gene where applicable, and may or may not include *Anguilla* sequences. Atypically paraphyletic clupeocephalan post-TGD ‘a’ or ‘b’ clades are demarcated with an asterisk (*). Posterior probabilities are shown above each node. *Pantodon* sequences are displayed in bold and highlighted in yellow. Species names are abbreviated are as follows. Cmi: *Callorhinchus milii*, Lme: *Latimeria menadoensis*, Xtr: *Xenopus tropicalis*, Aca: *Anolis caroliensis*, Mmu: *Mus musculus*, Hsa: *Homo sapiens*, Aan: *Anguilla anguilla*, Pbu: *Pantodon buchholzi*, Dre: *Danio rerio*, Ssa: *Salmo salar*, Ola: *Oryzias latipes*, Gac: *Gasterosteus aculeatus*, Abu: *Astatotilapia burtoni*, Tru: *Takifugu rubripes*, Tni: *Tetraodon nigroviridis*.