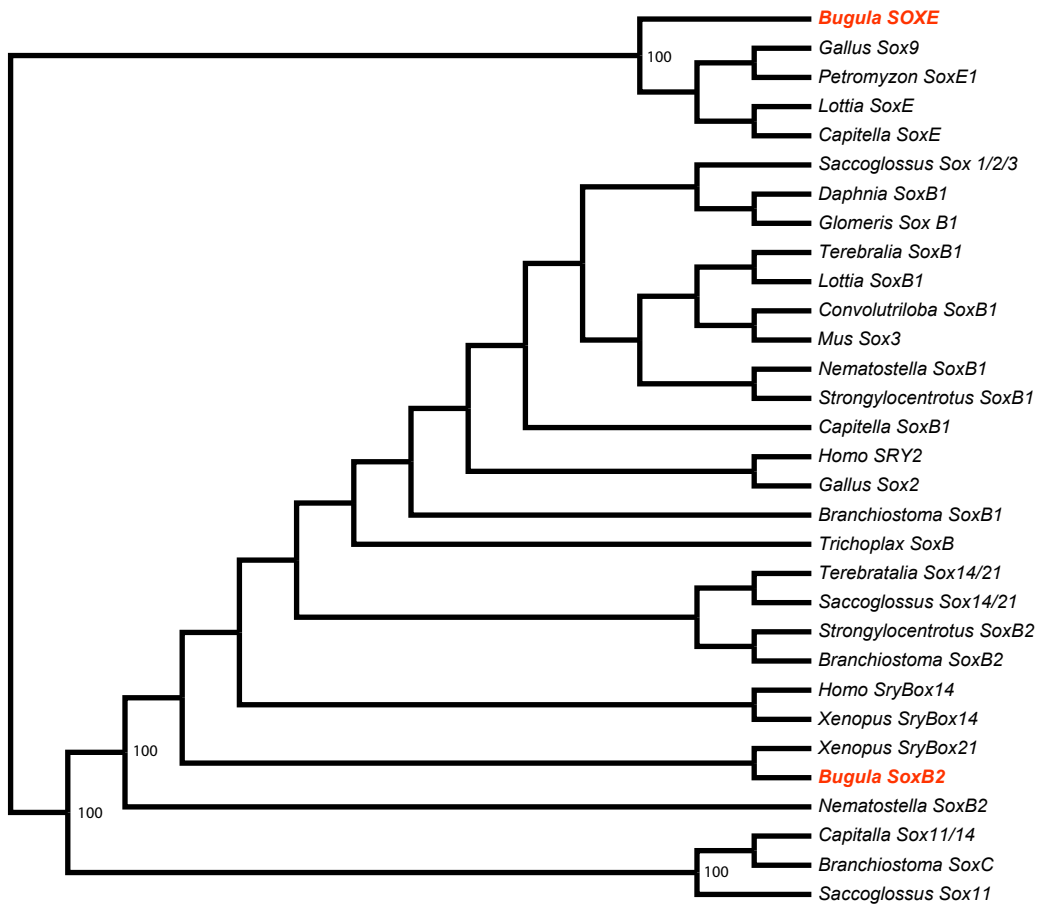


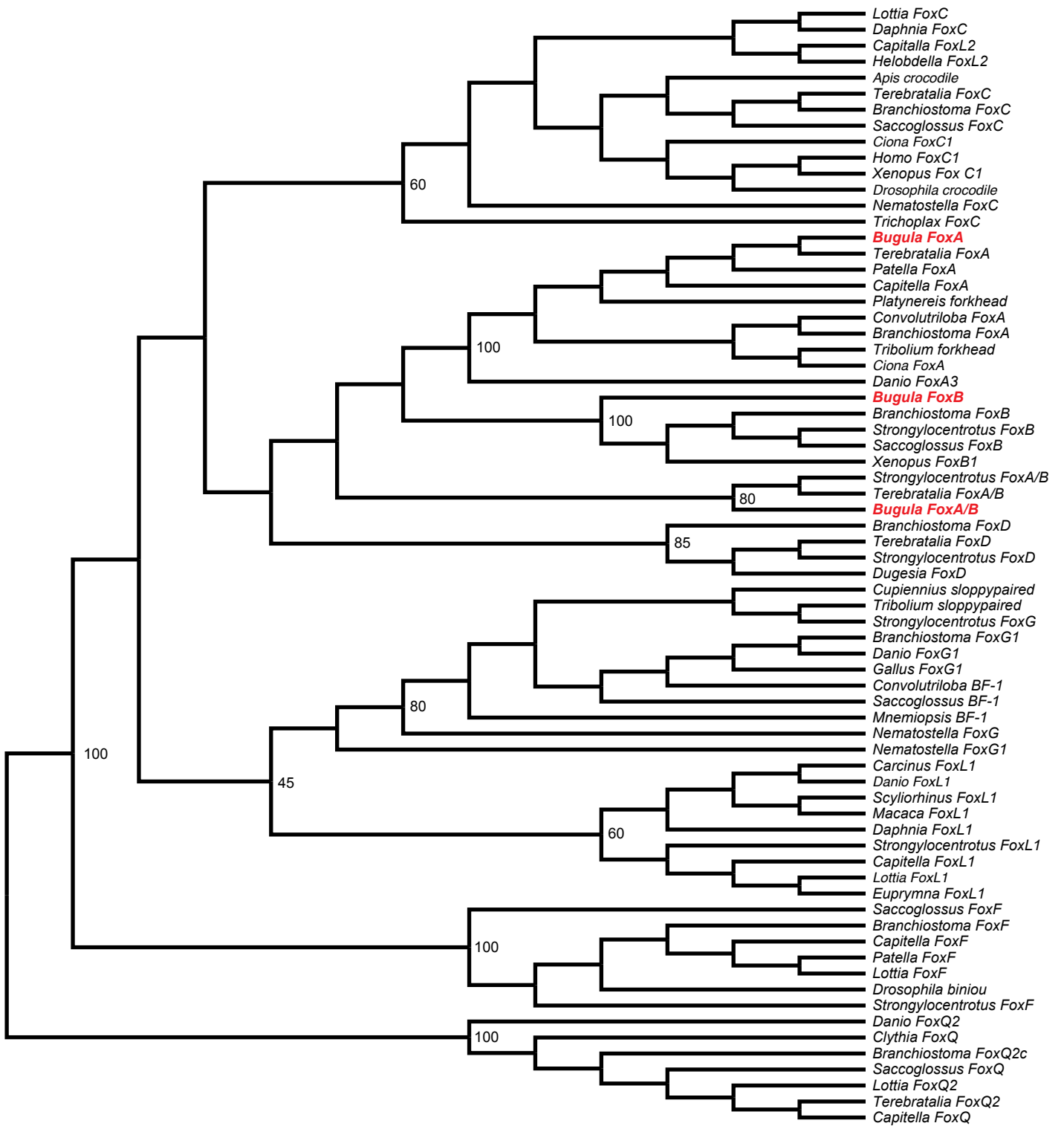
## Additional Files

**Table 1: Degenerate Primer Sequences**

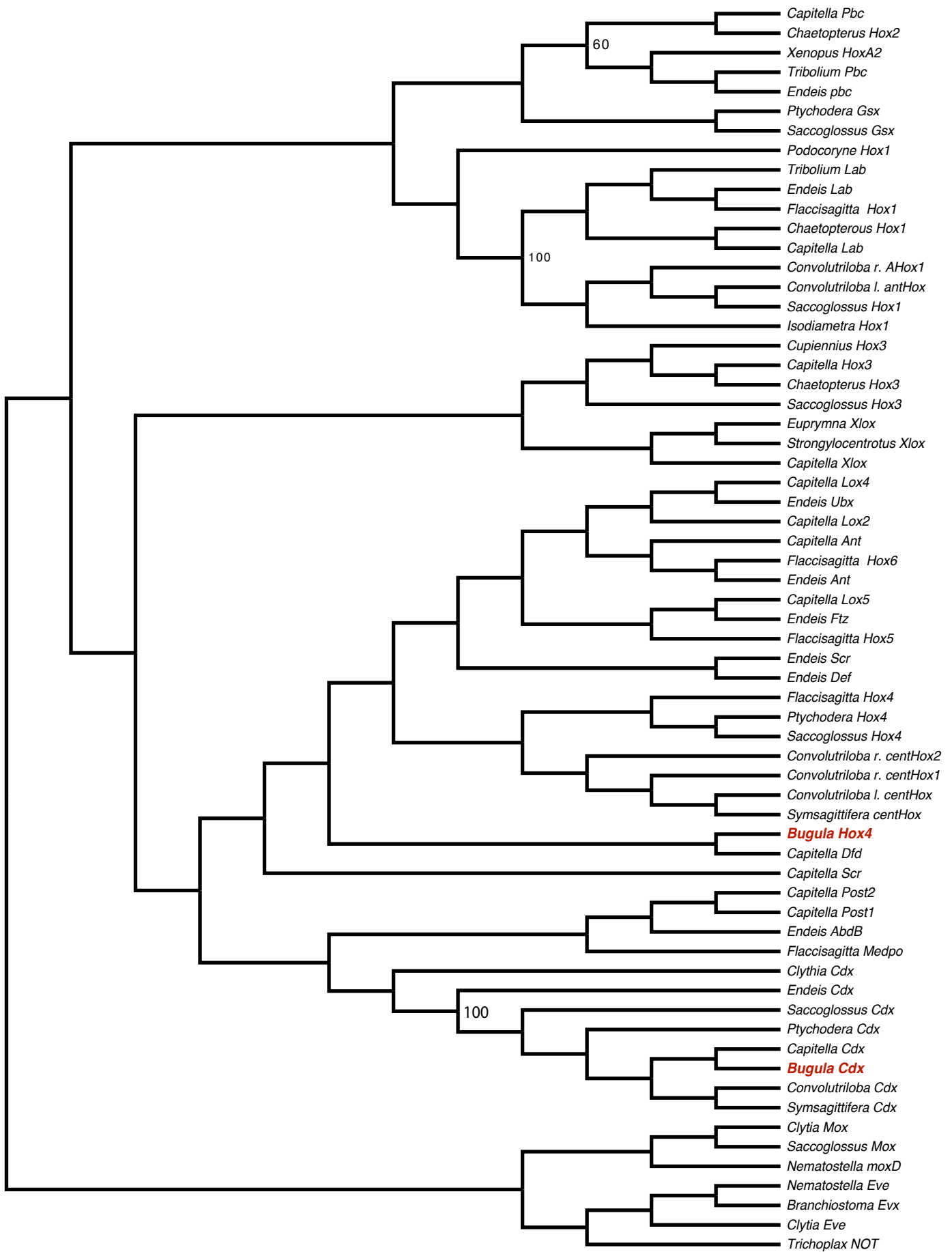
Gene	Primer F1	Primer F2	Primer R1	Primer R2
<b>Cdx/caudal</b>	5' - AARACNMGNACNAARGAYAARTA - 3'	5' - GAYAARTAYMGNGTNGTNTA - 3'	5' - TTNCKYTCYTTNGCNCKNCKRRTT - 3'	5' - TTNGCNCKNCKRRTTYTGRAACCA - 3'
<b>forkhead</b>	5' - AARCCNCCNTAYWSNTAYAT - 3'	5' - TAYATHWSNYTNATHACNATG - 3'	5' - TARCANCCRTTYTCRAACAT - 3'	5' - CCRTTYTCRAACATRTTNCC - 3'
<b>GATA</b>	5' - GARTGYGTNAAYTYGGNGC - 3'	5' - GGNCAYTAYTNTGYAAYGC - 3'	5' - GGYTTNCKYTTNCKNGTYTG - 3'	5' - GTYGDATNCCYTCYTTYTTTCAT - 3'
<b>WNT</b>	5' - ATGAAYTICAYAAYAAYGA - 3'	5' - TGYAARTGYCAYGGIGTIWSIGG - 3'	5' - RCARCACCARTGRAAITRCA - 3'	



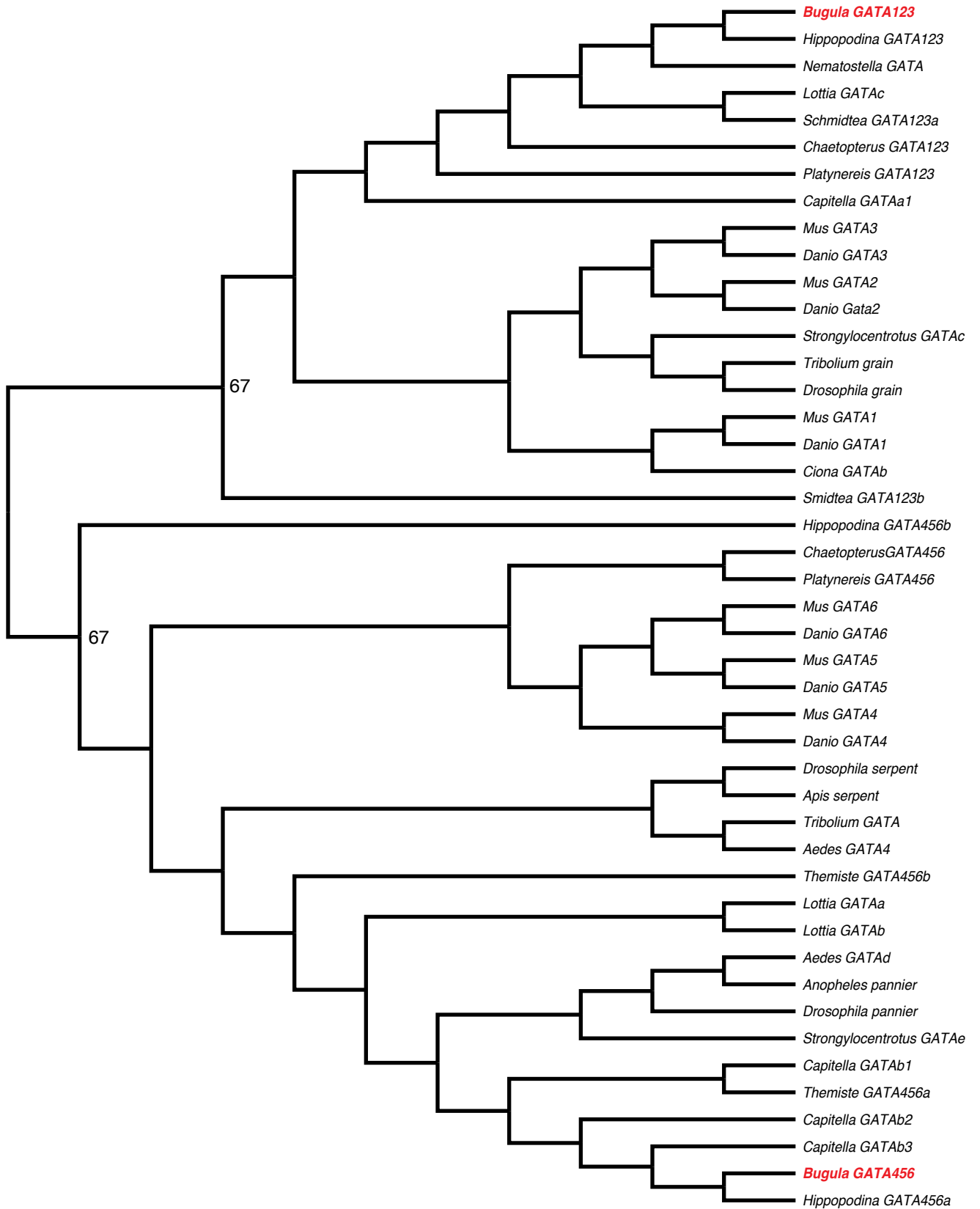
**Figure 1: Maximum Likelihood phylogenetic orthology assignment of Sox genes. (3000 bootstrap replicates)**



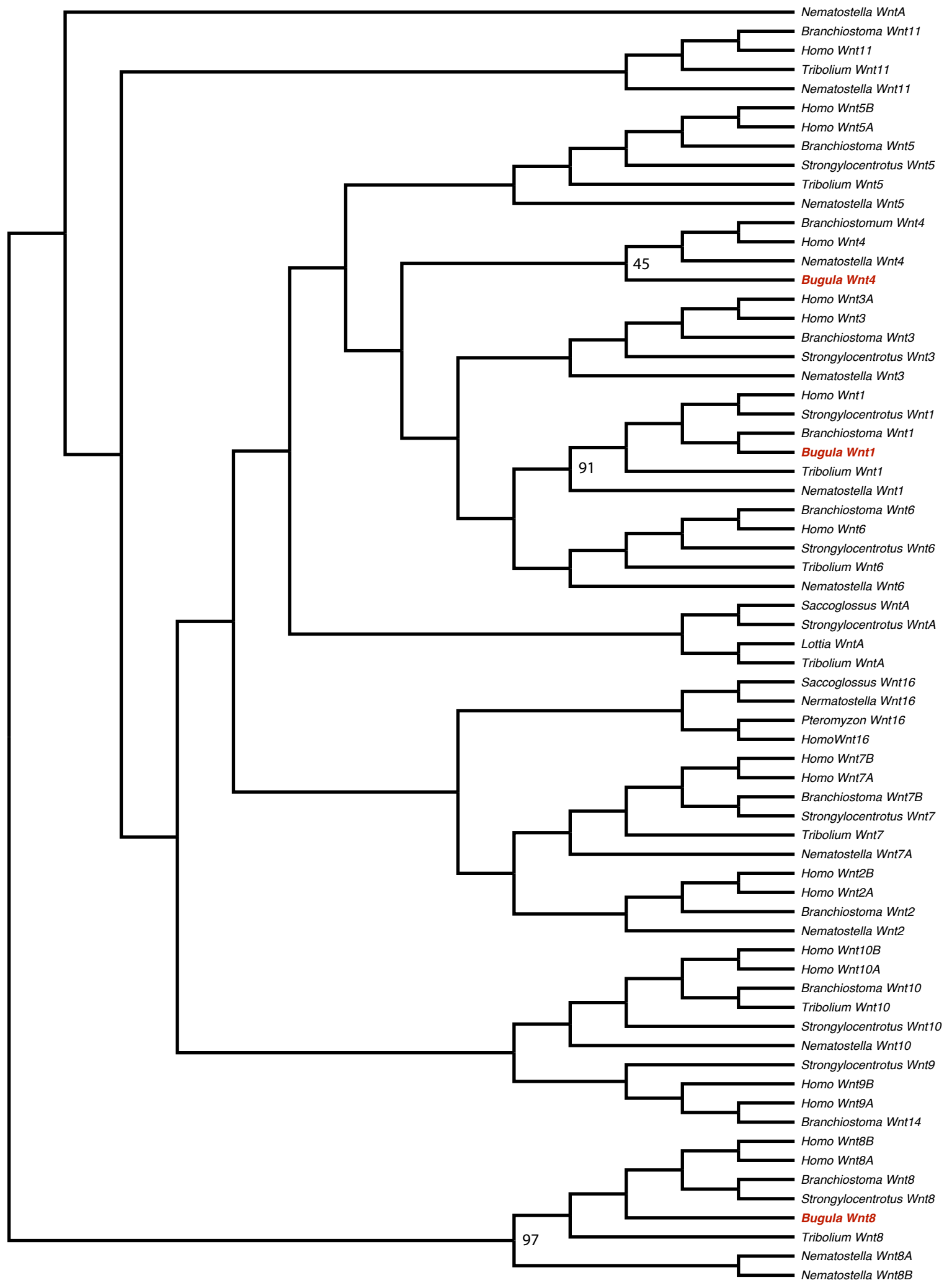
**Figure 2: Maximum Likelihood phylogenetic orthology assignment of Fox genes. (2000 bootstrap replicates)**



**Figure 3: Maximum Likelihood phylogenetic orthology assignment of *Hox/ParaHox* genes. (2000 bootstrap replicates)**



**Figure 4: Maximum Likelihood phylogenetic orthology assignment of GATA genes. (3000 bootstrap replicates)**



**Figure 5: Maximum Likelihood phylogenetic orthology assignment of *WNT* genes. (1000 bootstrap replicates)**