

## **Supplementary Materials**

**Additional File 2: Phylogenetic trees and their branches**

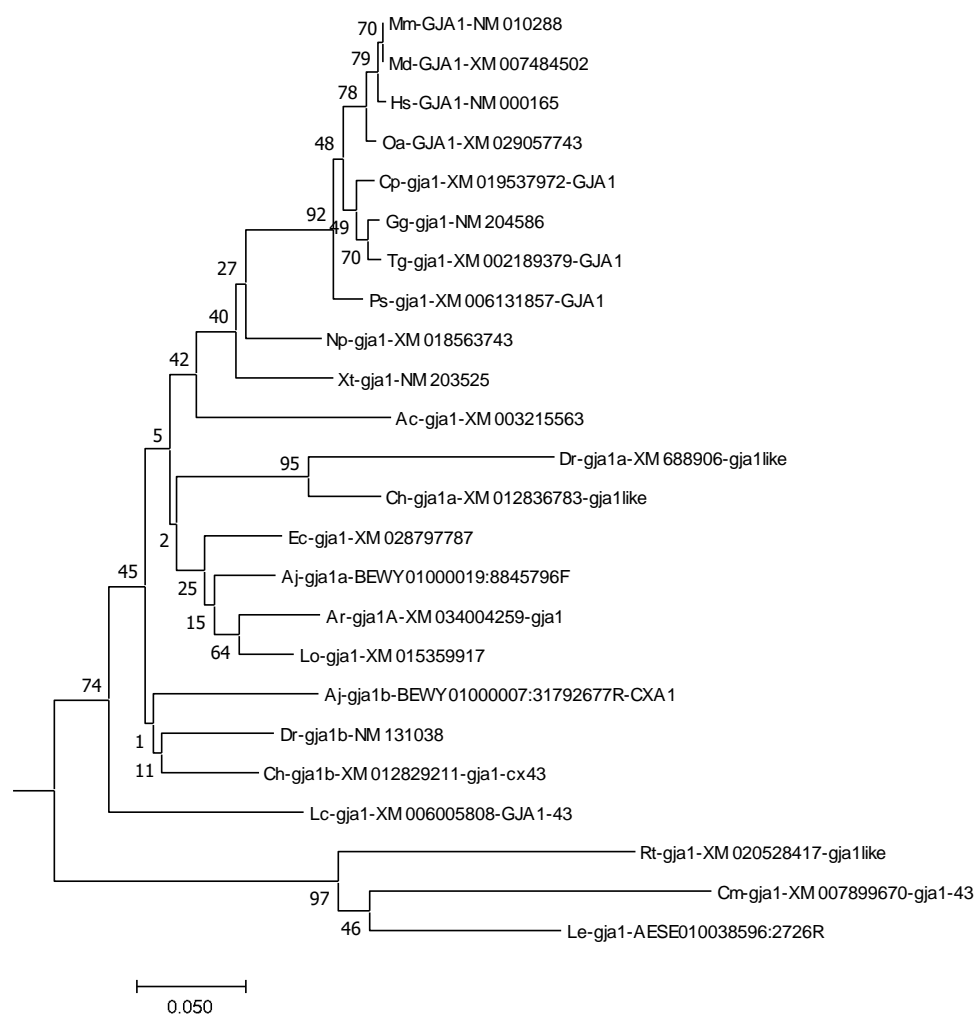
**Supplementary Figures S44 - S71**

**Mikalsen, SO; í Kongsstovu, S; Tausen, M.**

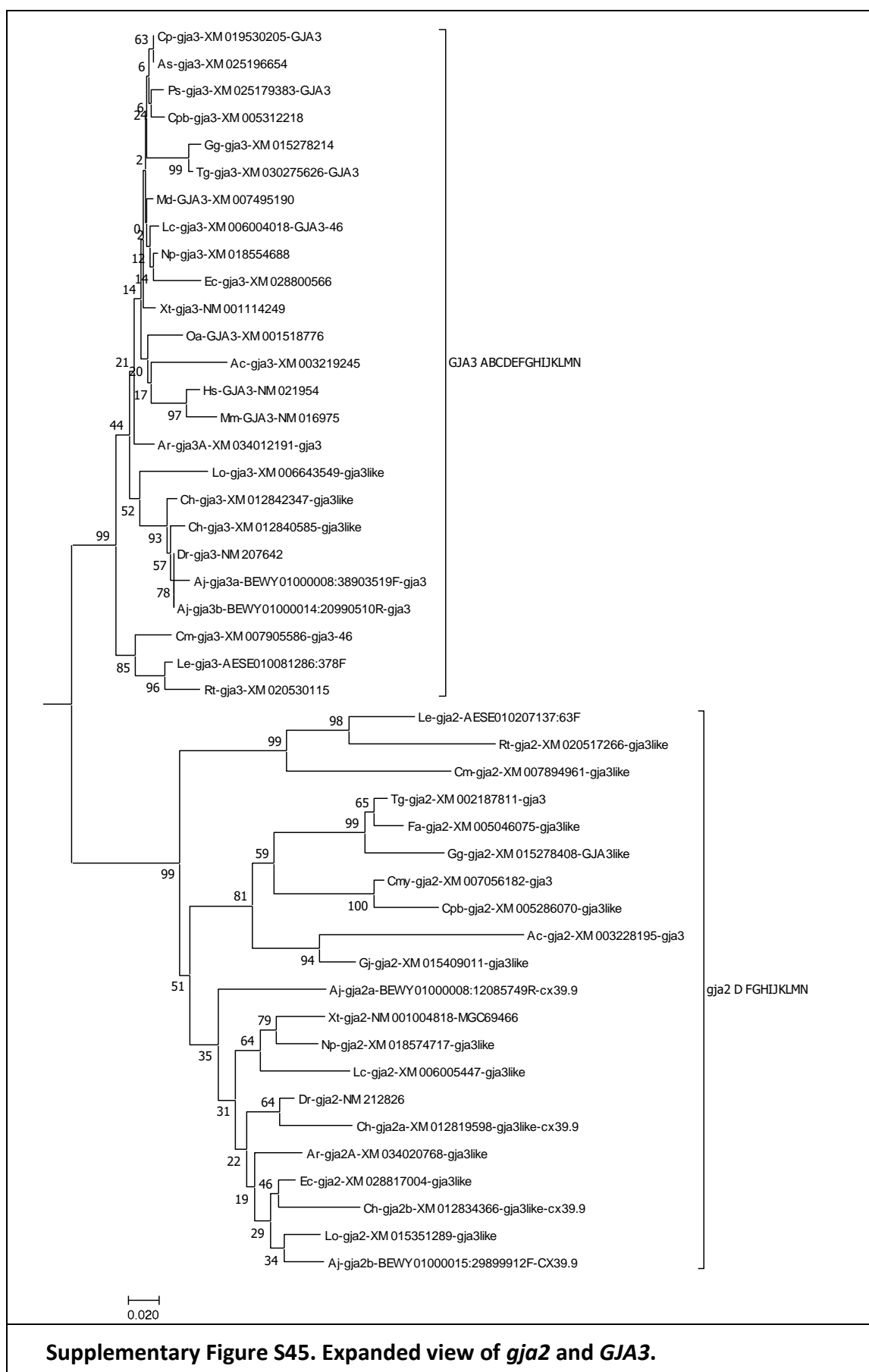
**Connexins during 500 million years – from cyclostomes to mammals**

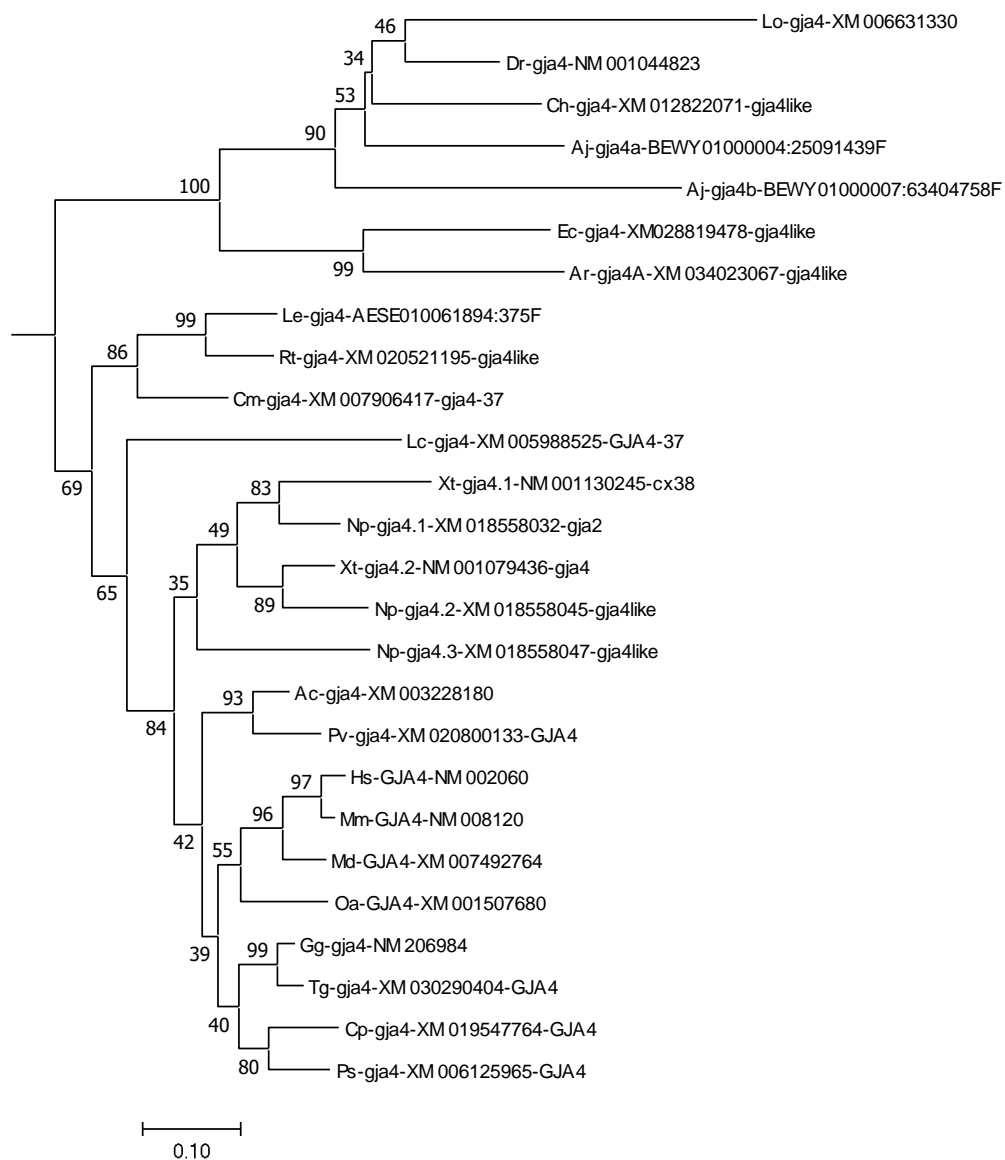
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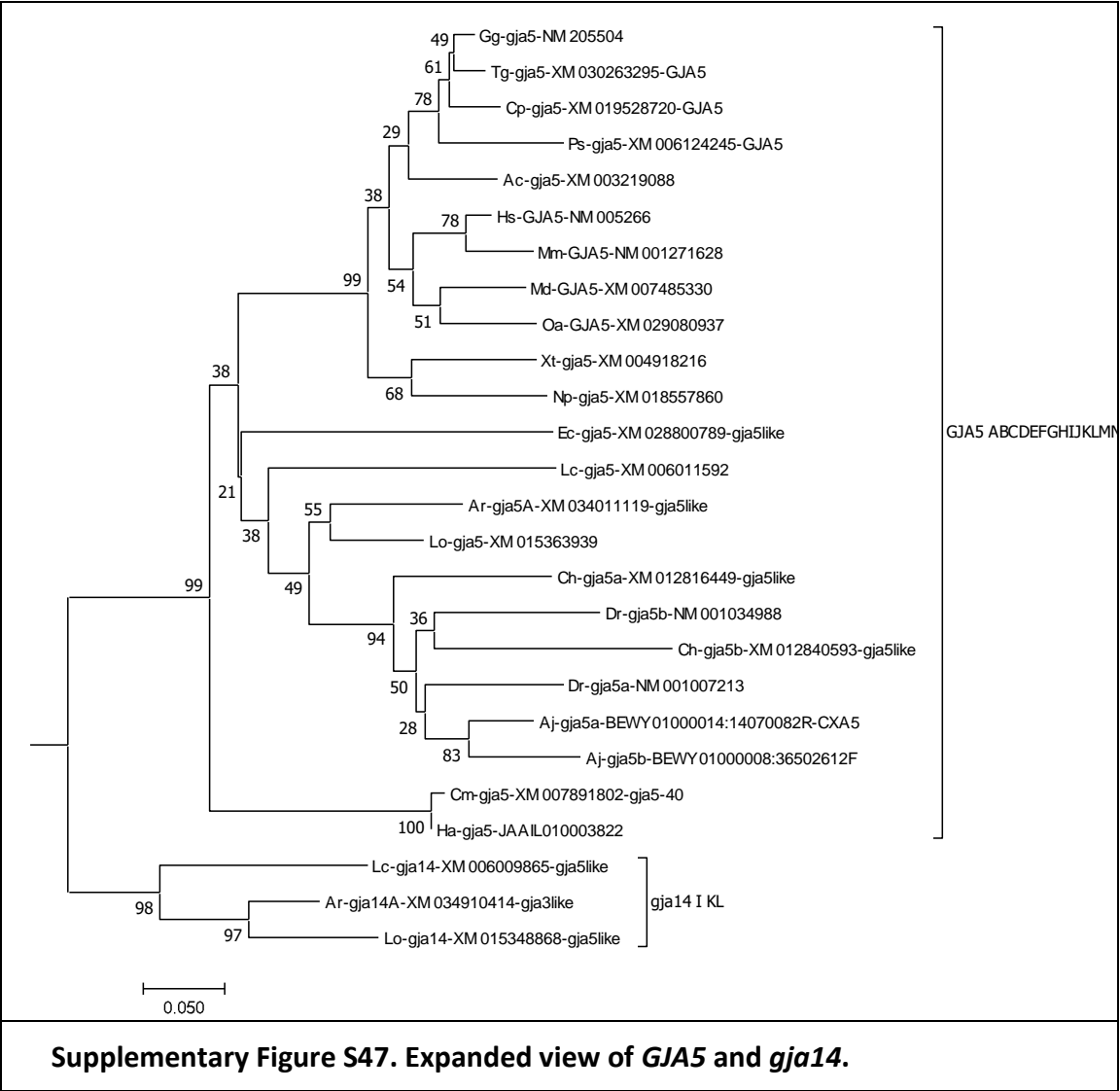


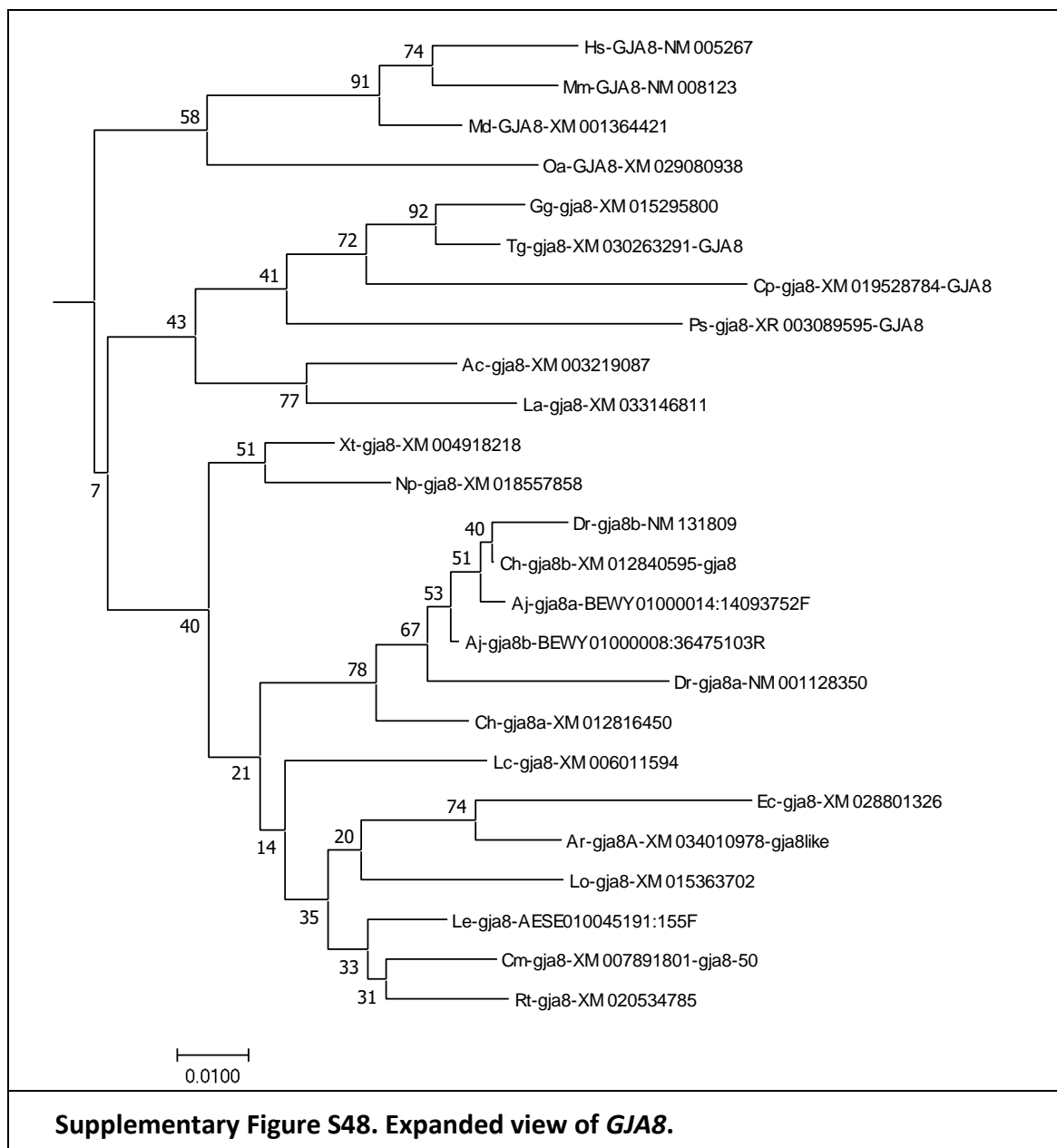
**Supplementary Figure S44. Expanded view of *GJA1*.**

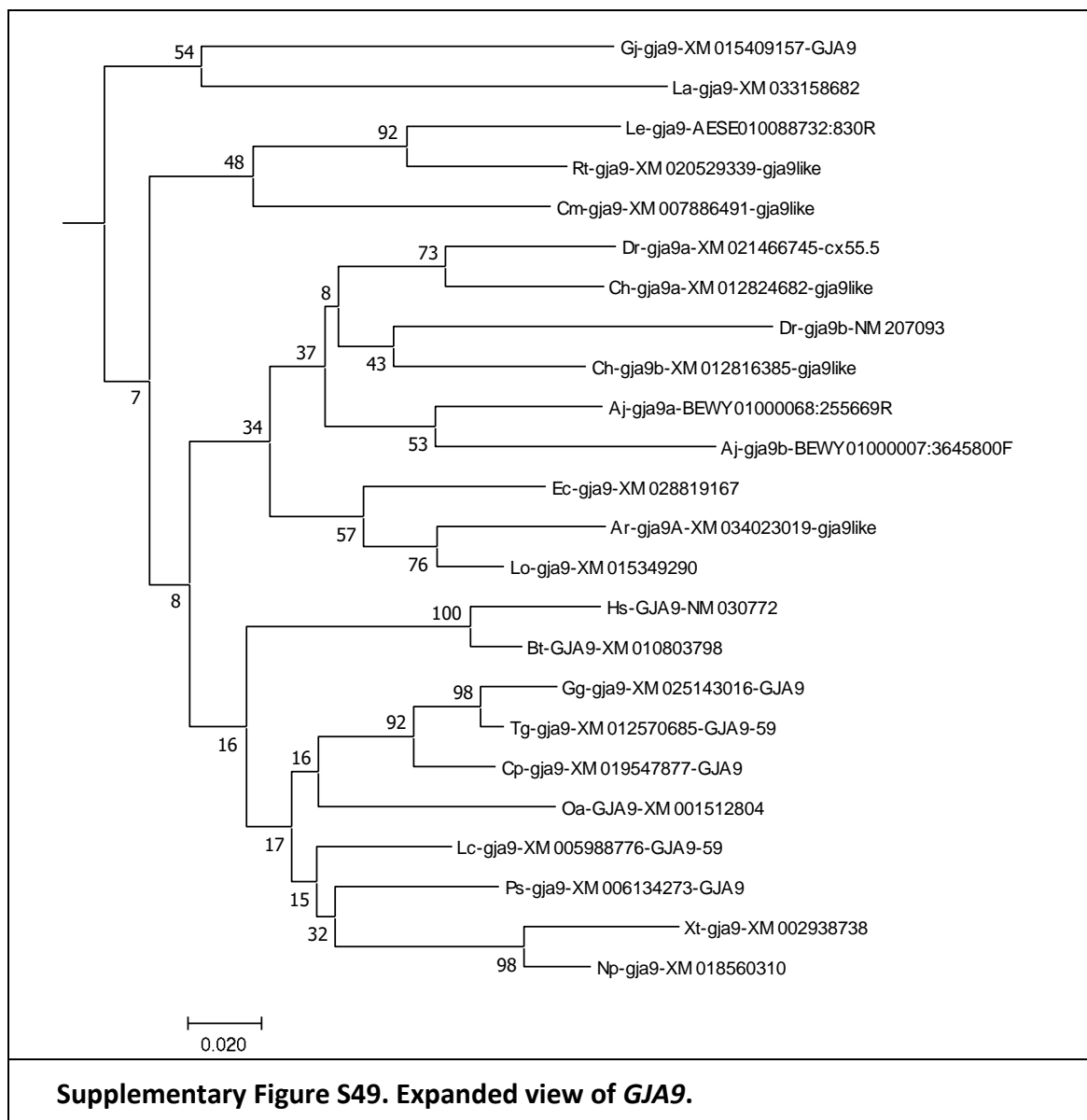




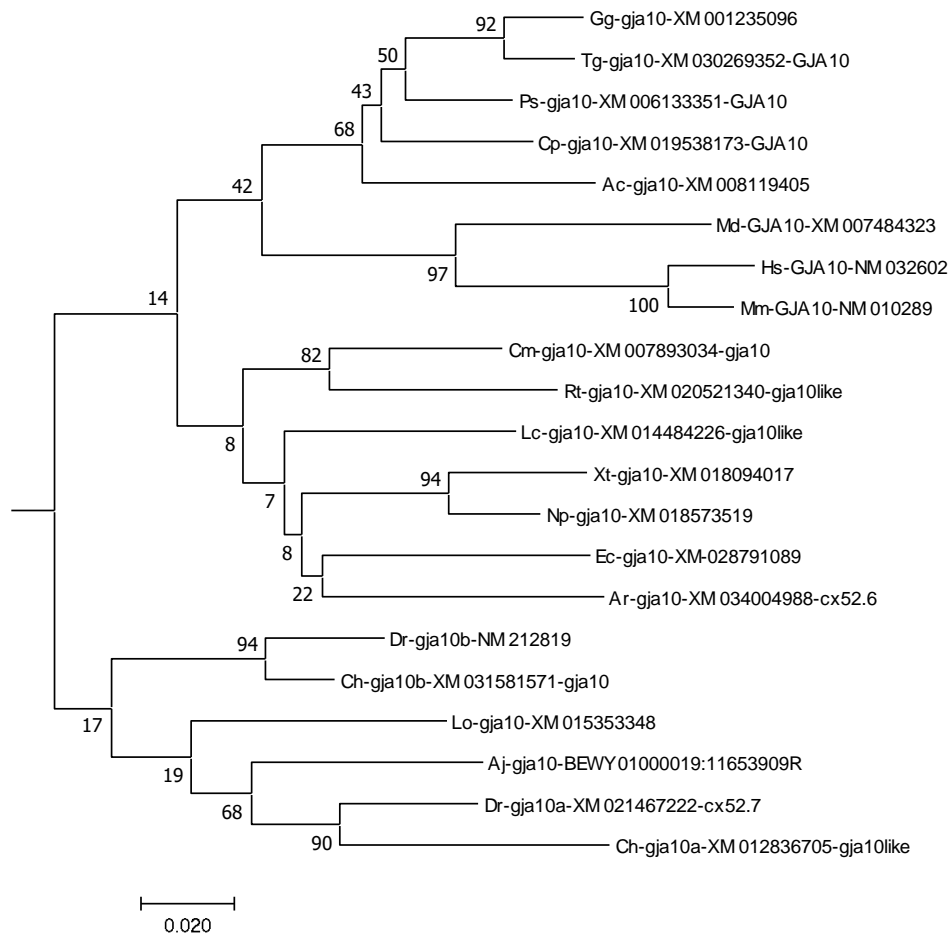
**Supplementary Figure S46. Expanded view of *GJA4*.**



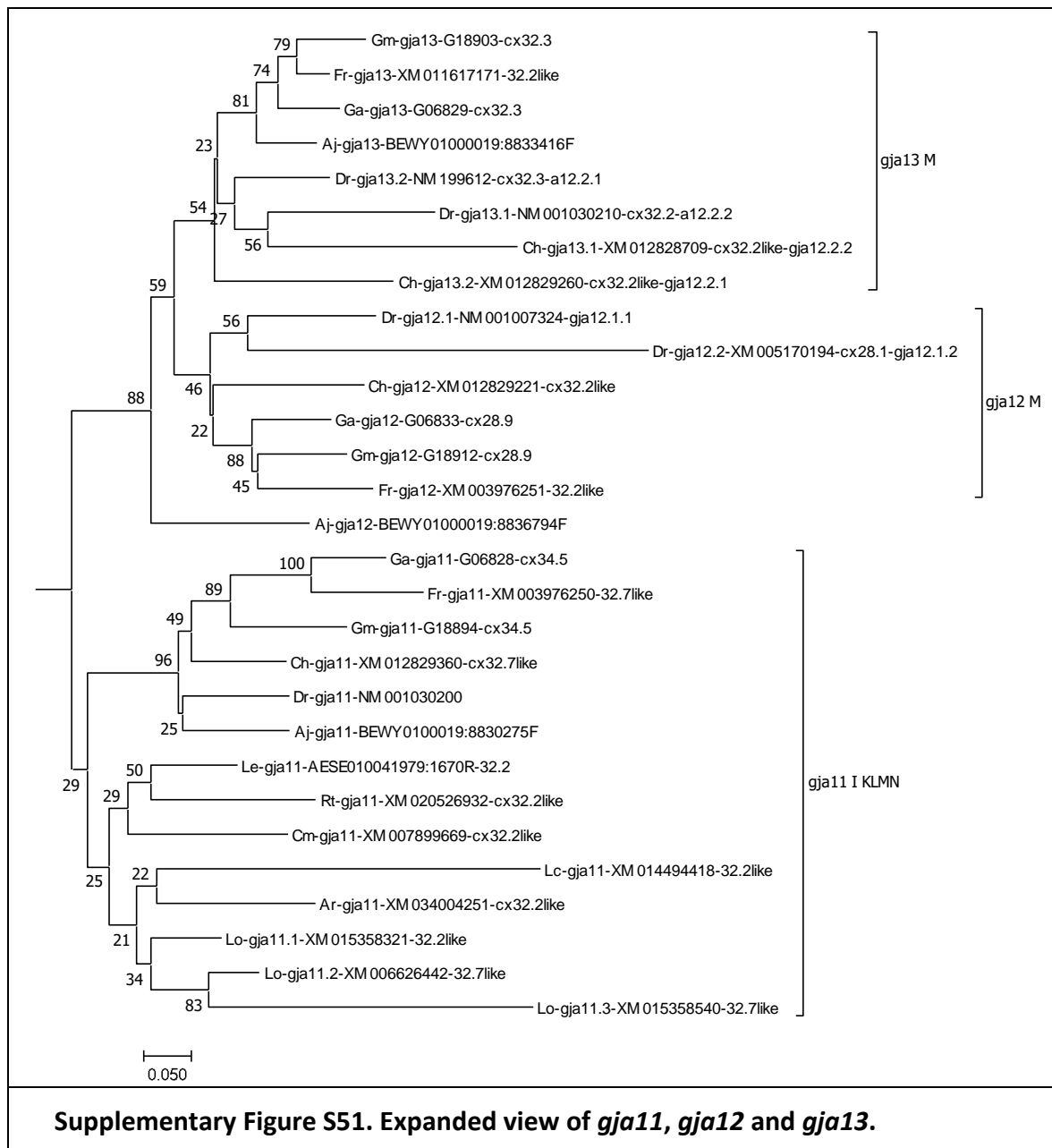


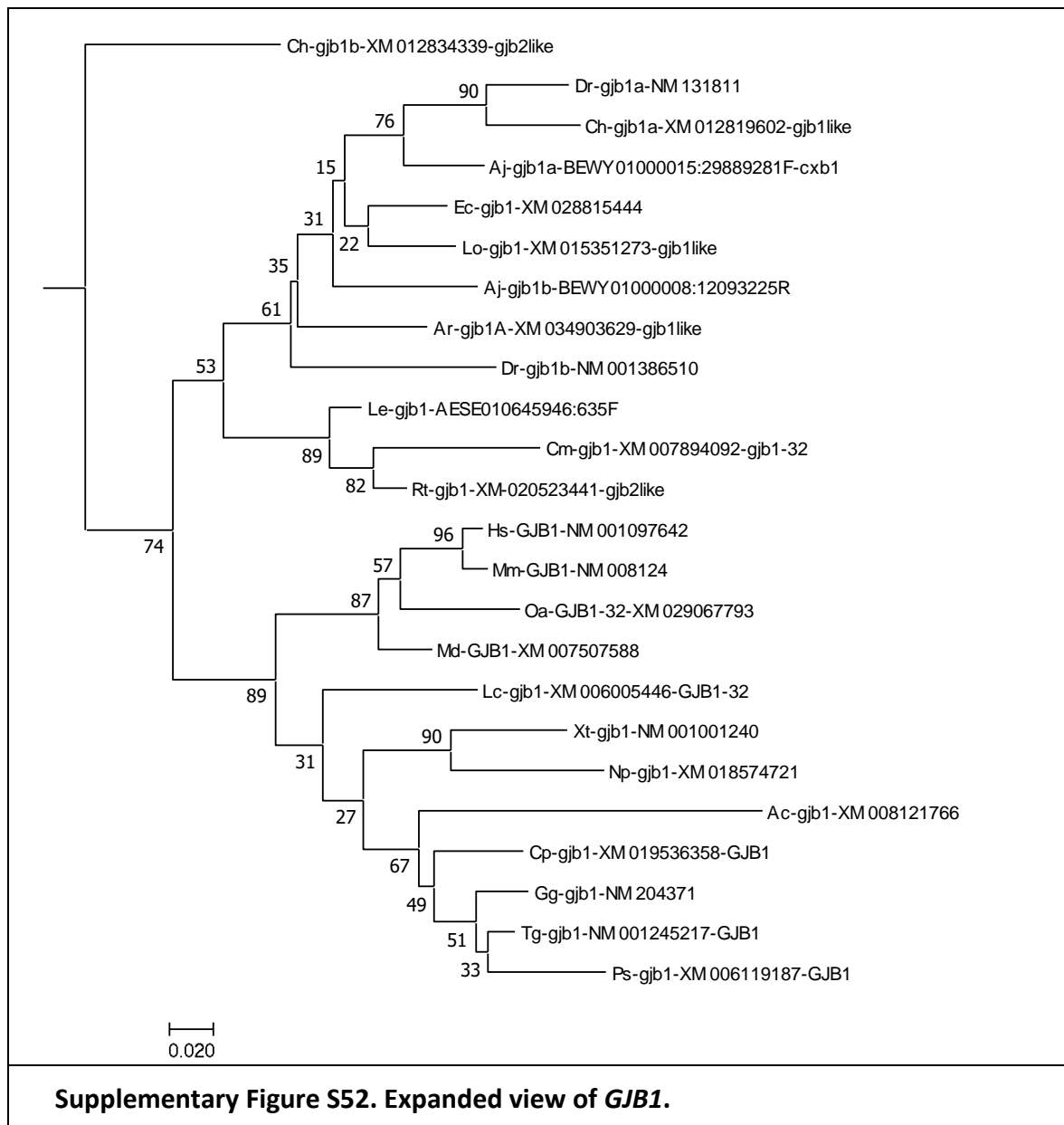


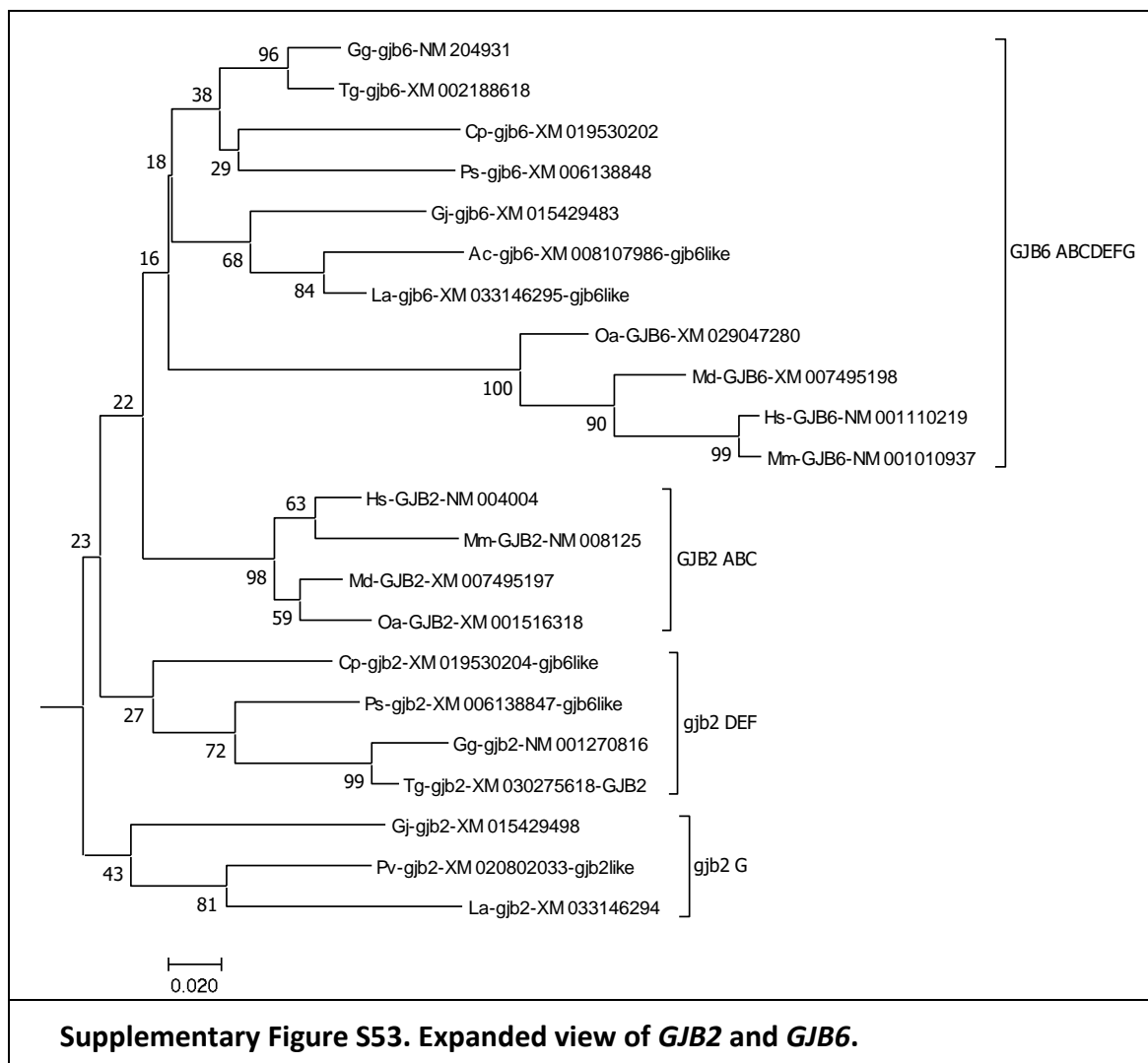


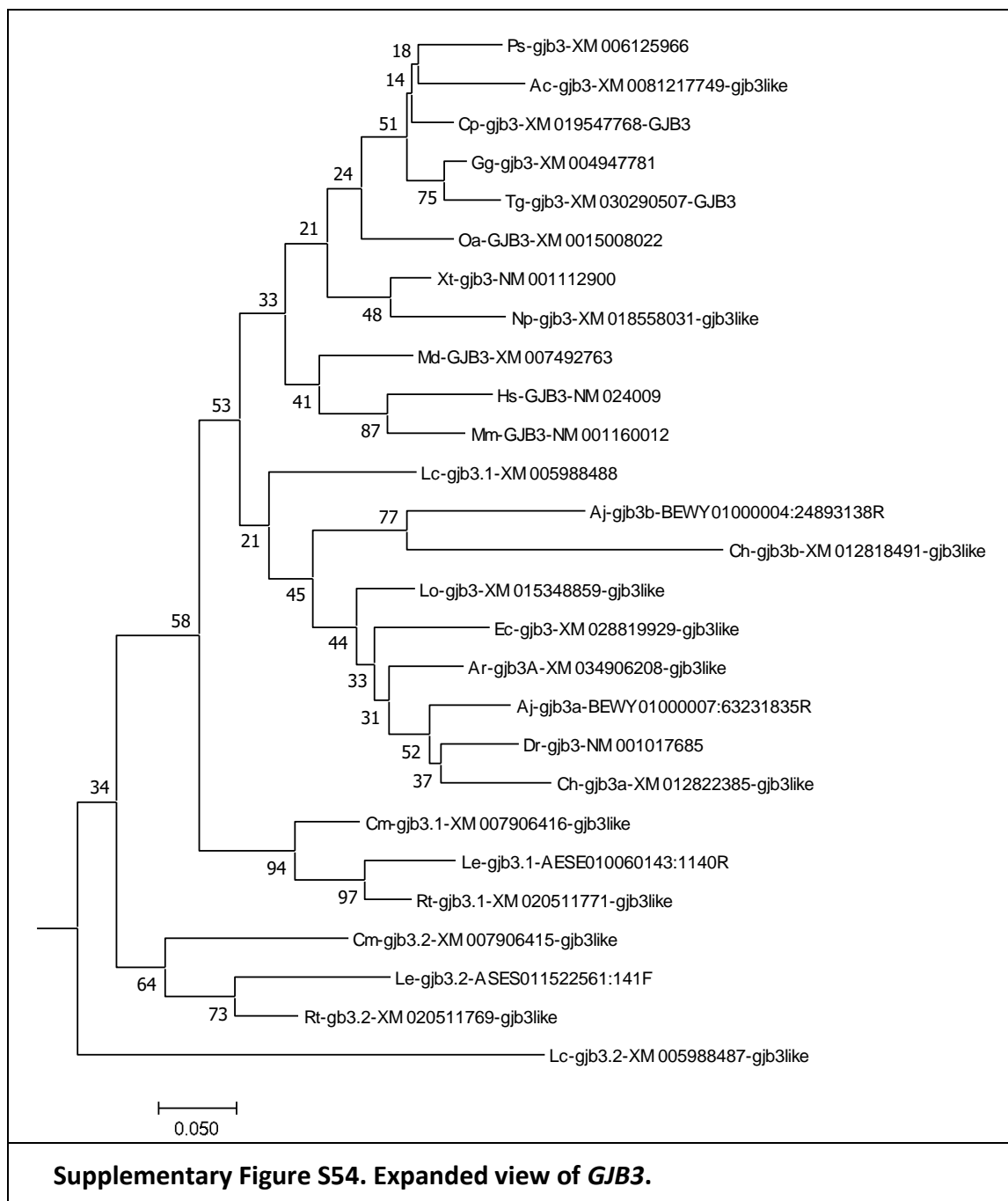


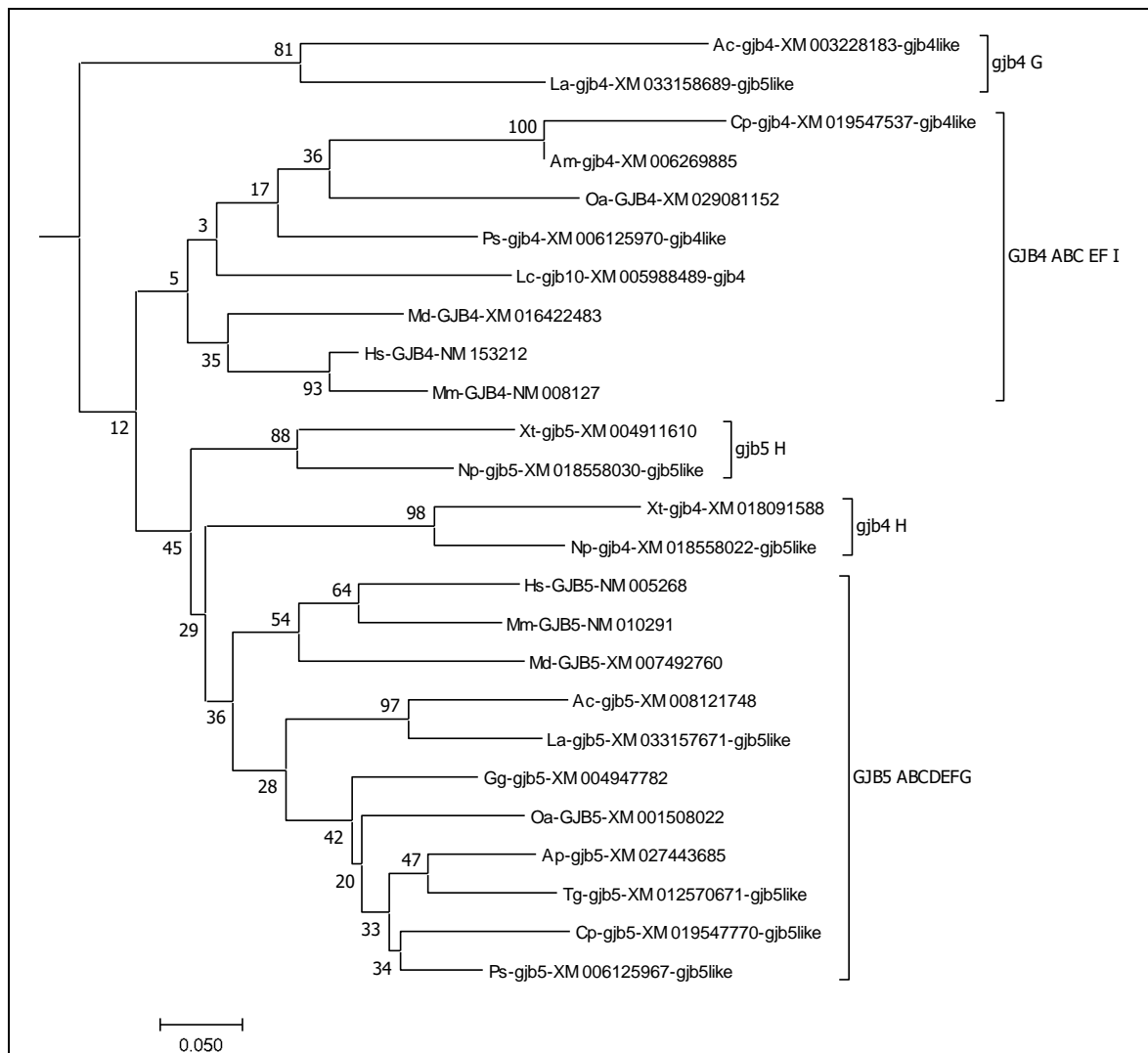
**Supplementary Figure S50. Expanded view of *GJA10*.**





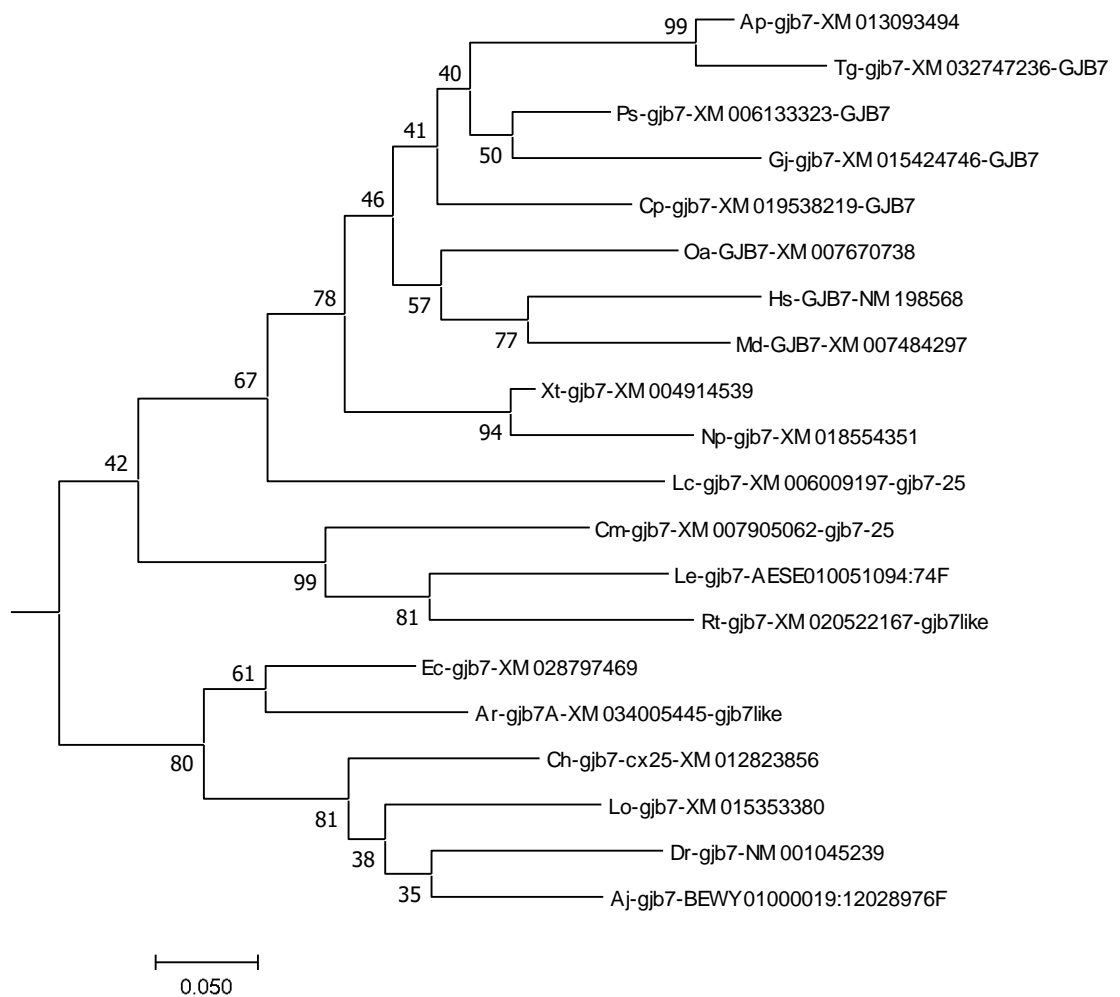




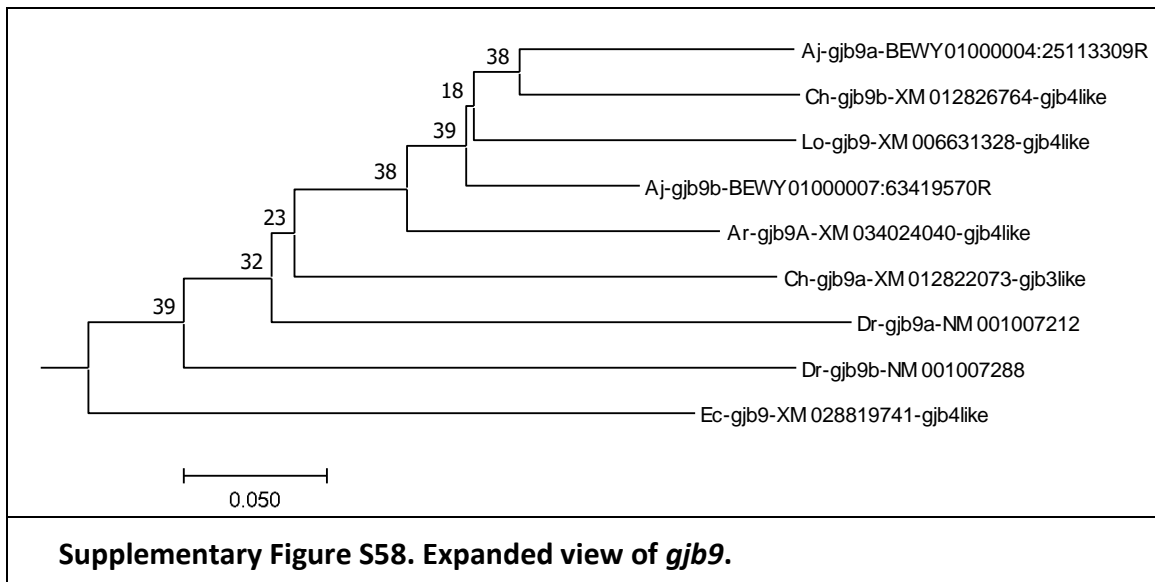
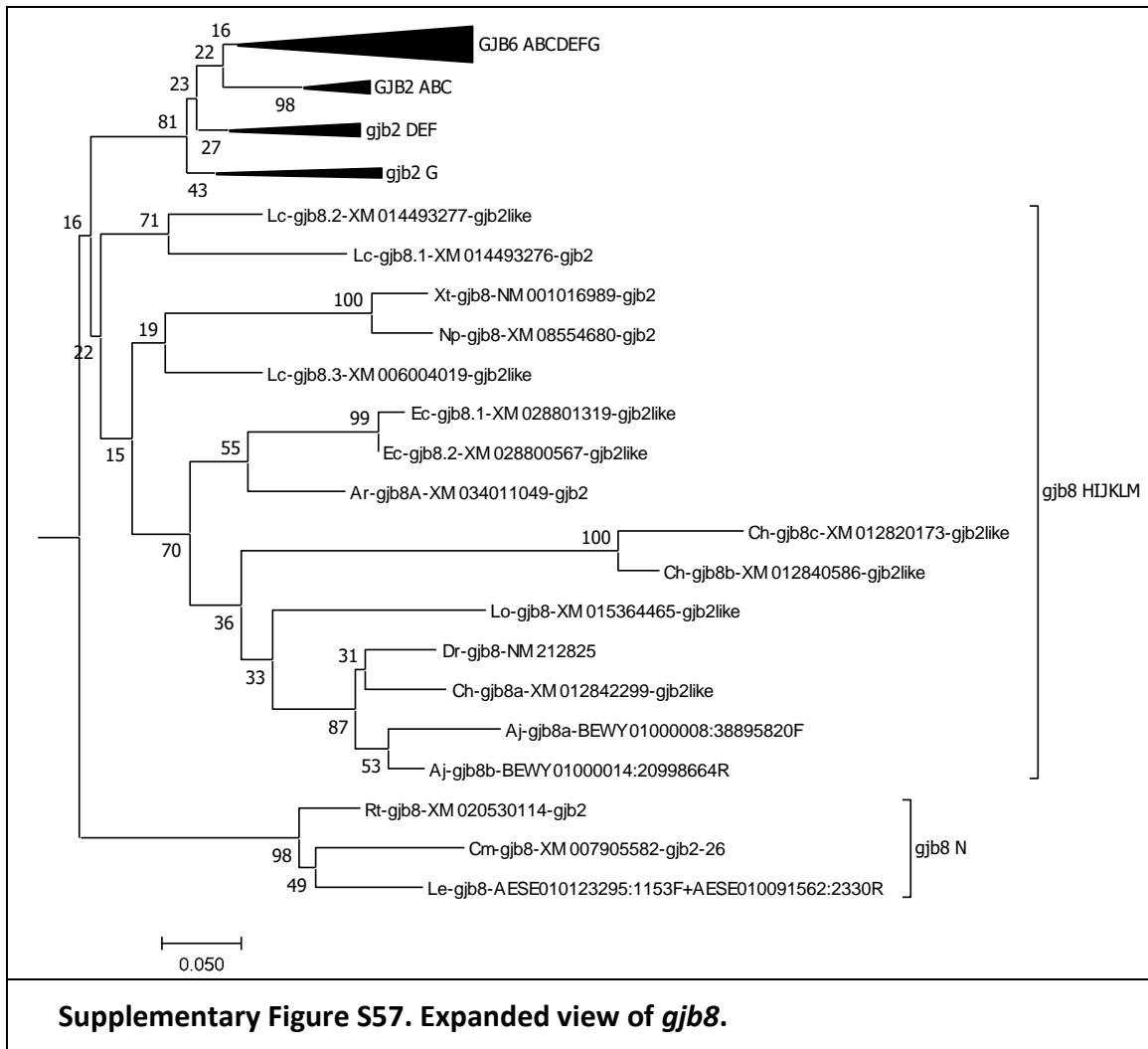


### Supplementary Figure S55. Expanded view of *GJB4* and *GJB5*.

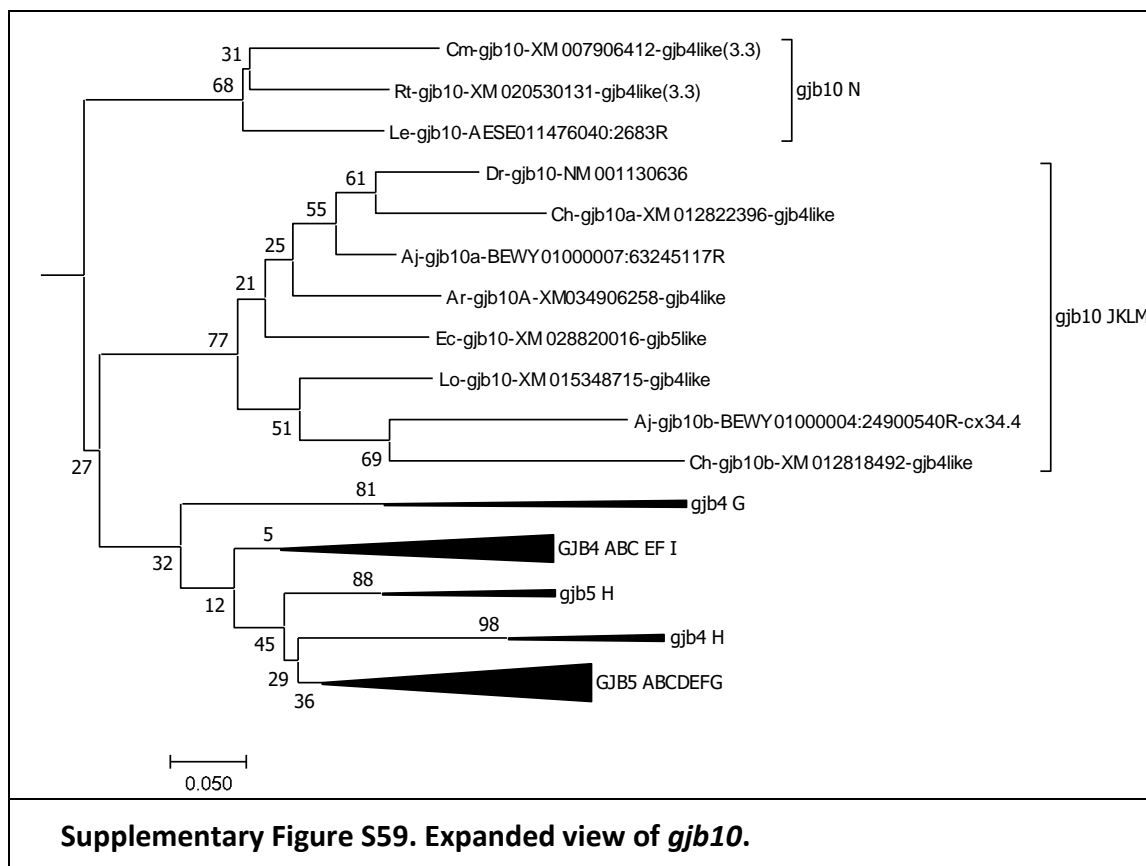
Note that Lc-*gjb10*-XM\_005988489 in some models and when lower gamma value was used, either located together with chondrichthyan *gjb10*, with the larger *GJB3* orthogroup, or as a singleton. Further note that the amphibian sequences indicated by *gjb5* H and *gjb4* H tended to inverse their location depending on whether the model was run with amino acids or nucleotides. We have here used the same names on the *Xenopus* sequences as in GenBank, but synteny considerations suggests that the names should be reversed, *i.e.*, *Xenopus* XM\_004911610 should be named *gjb4* and XM\_018091588 should be named *gjb5* (see text), and similarly for the *Nanorana* sequences.



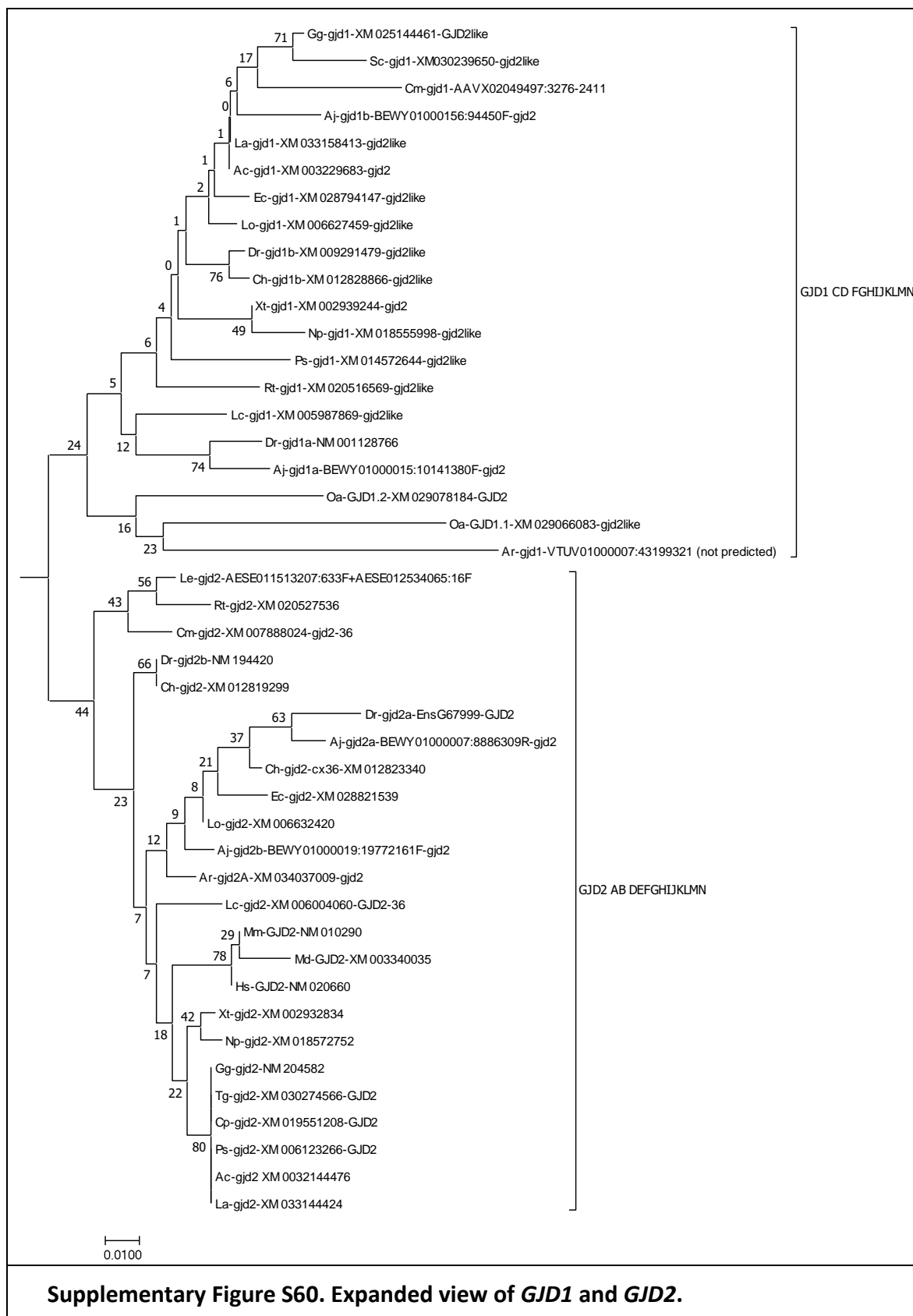
**Supplementary Figure S56. Expanded view of *GJB7*.**

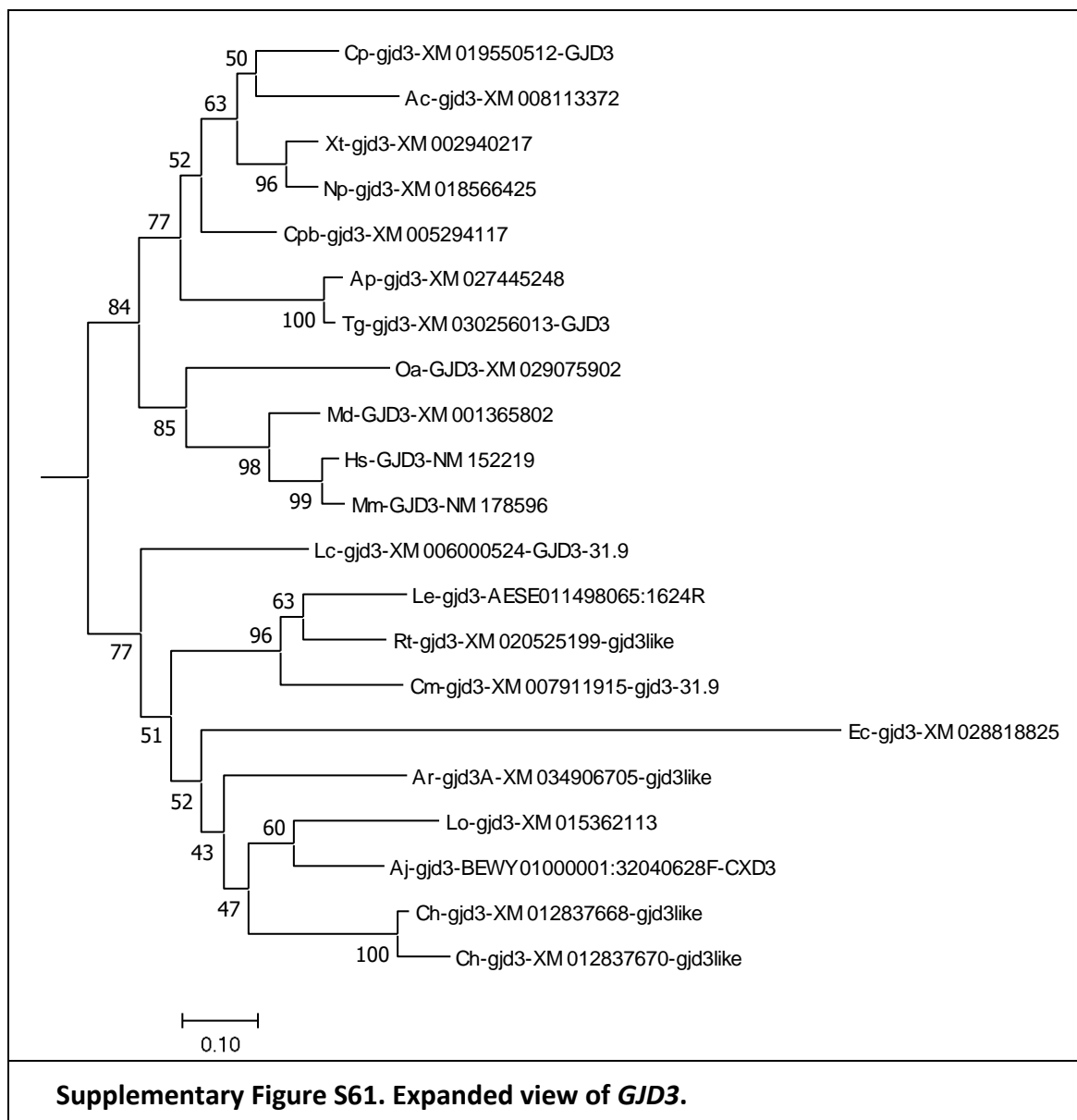


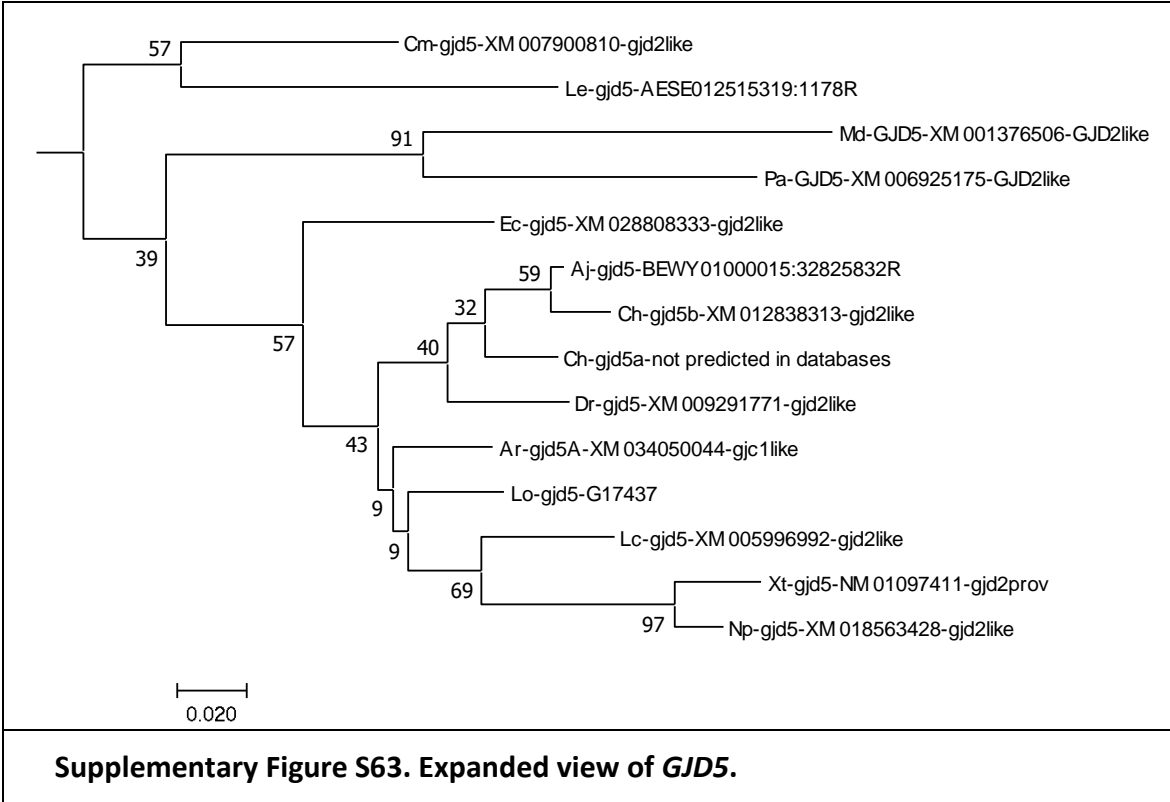
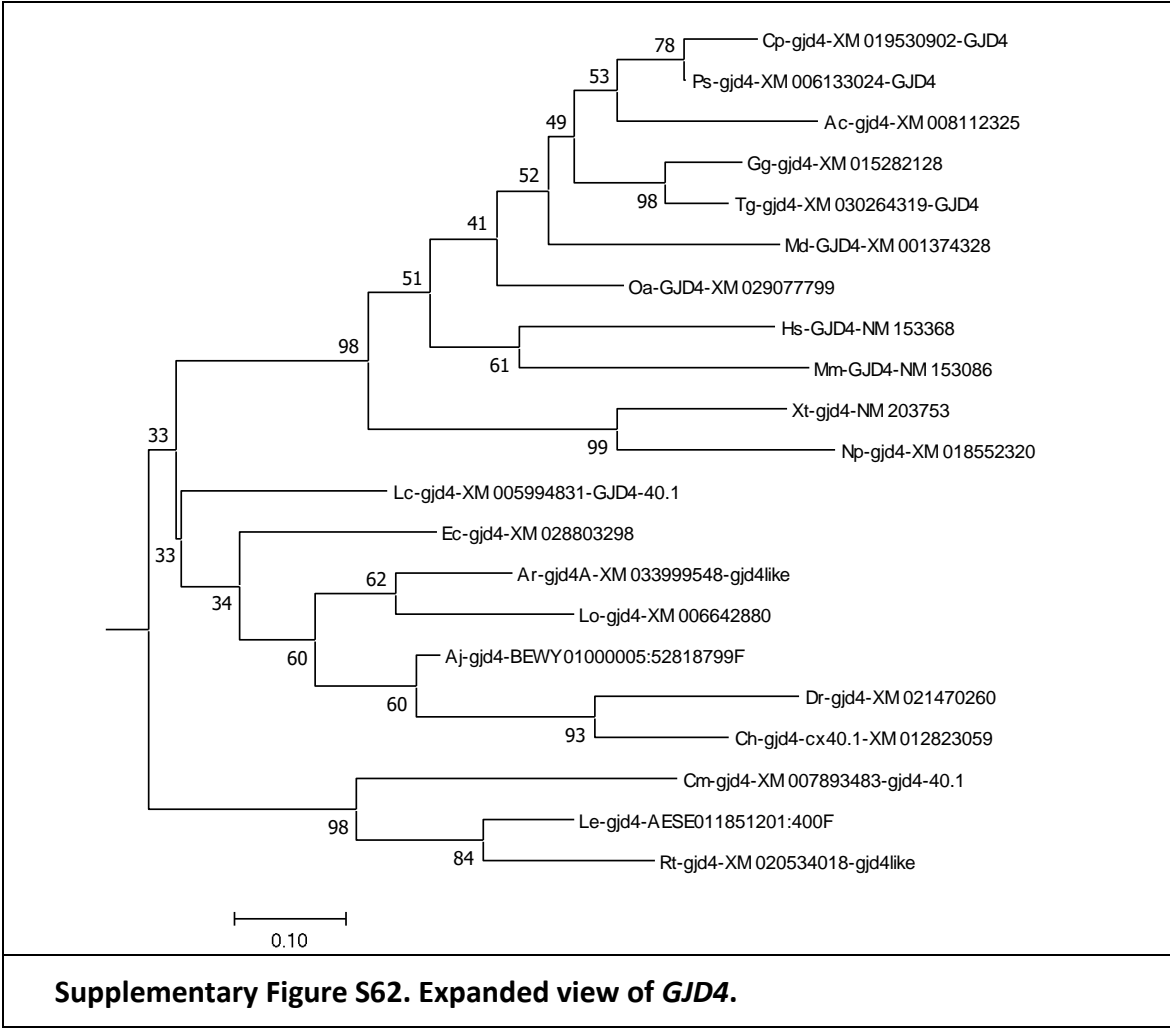


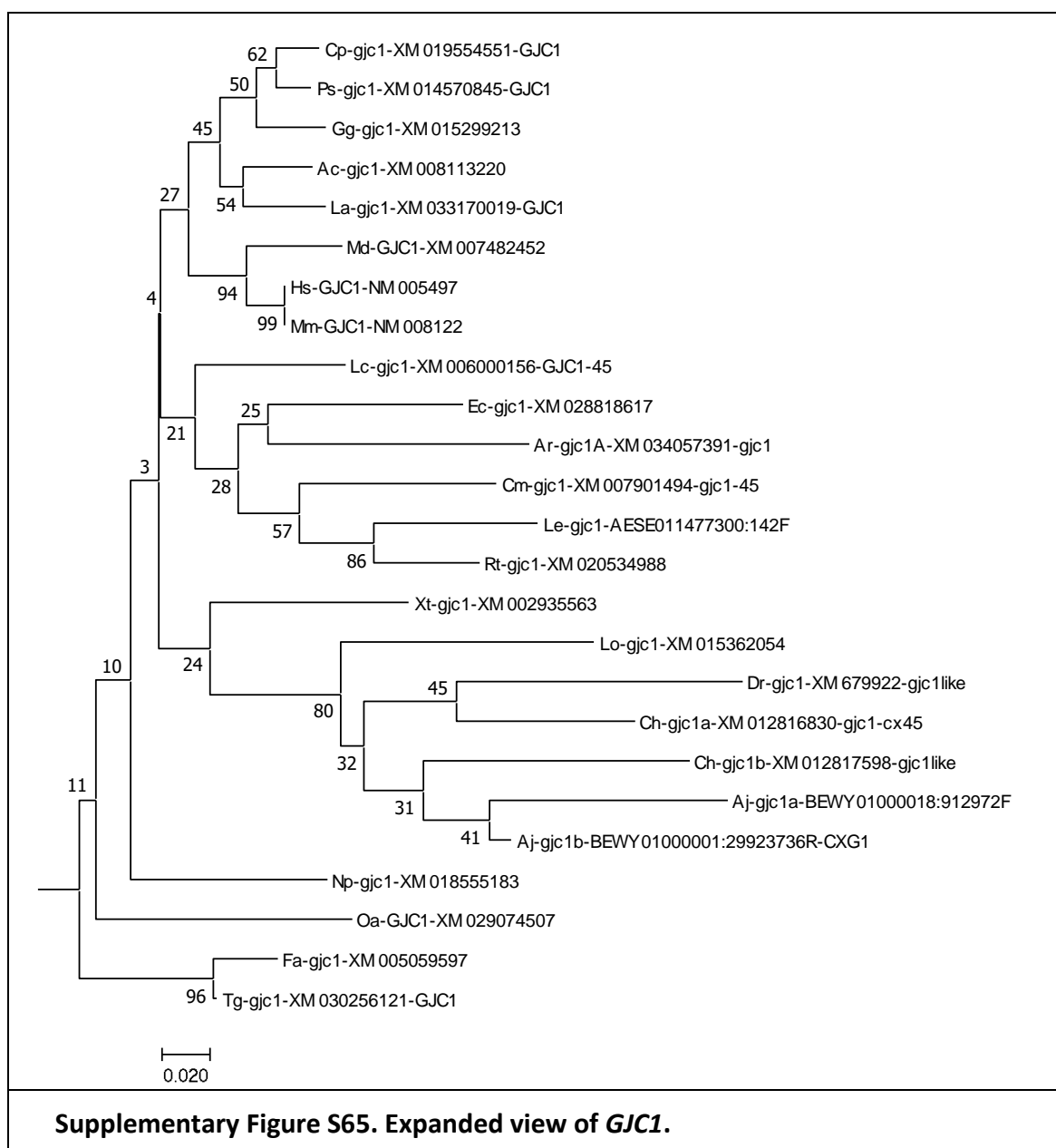
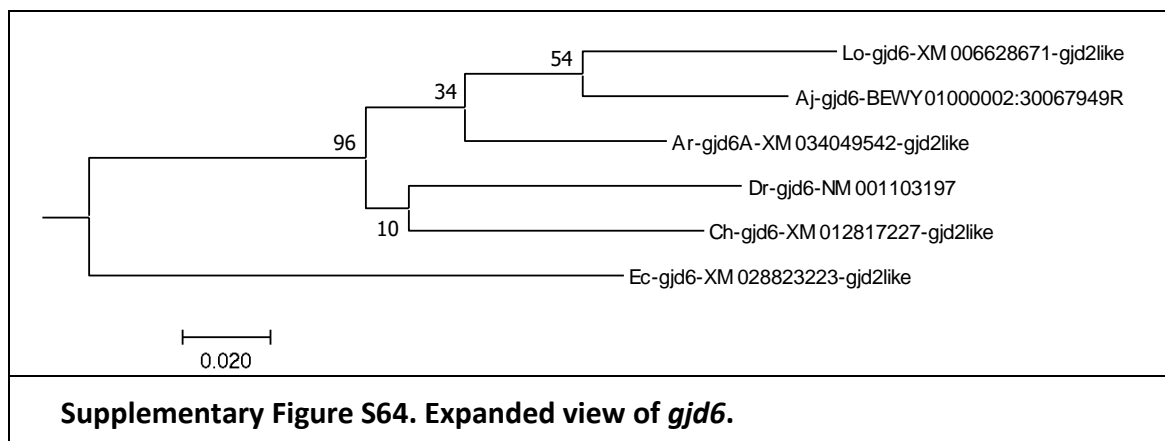


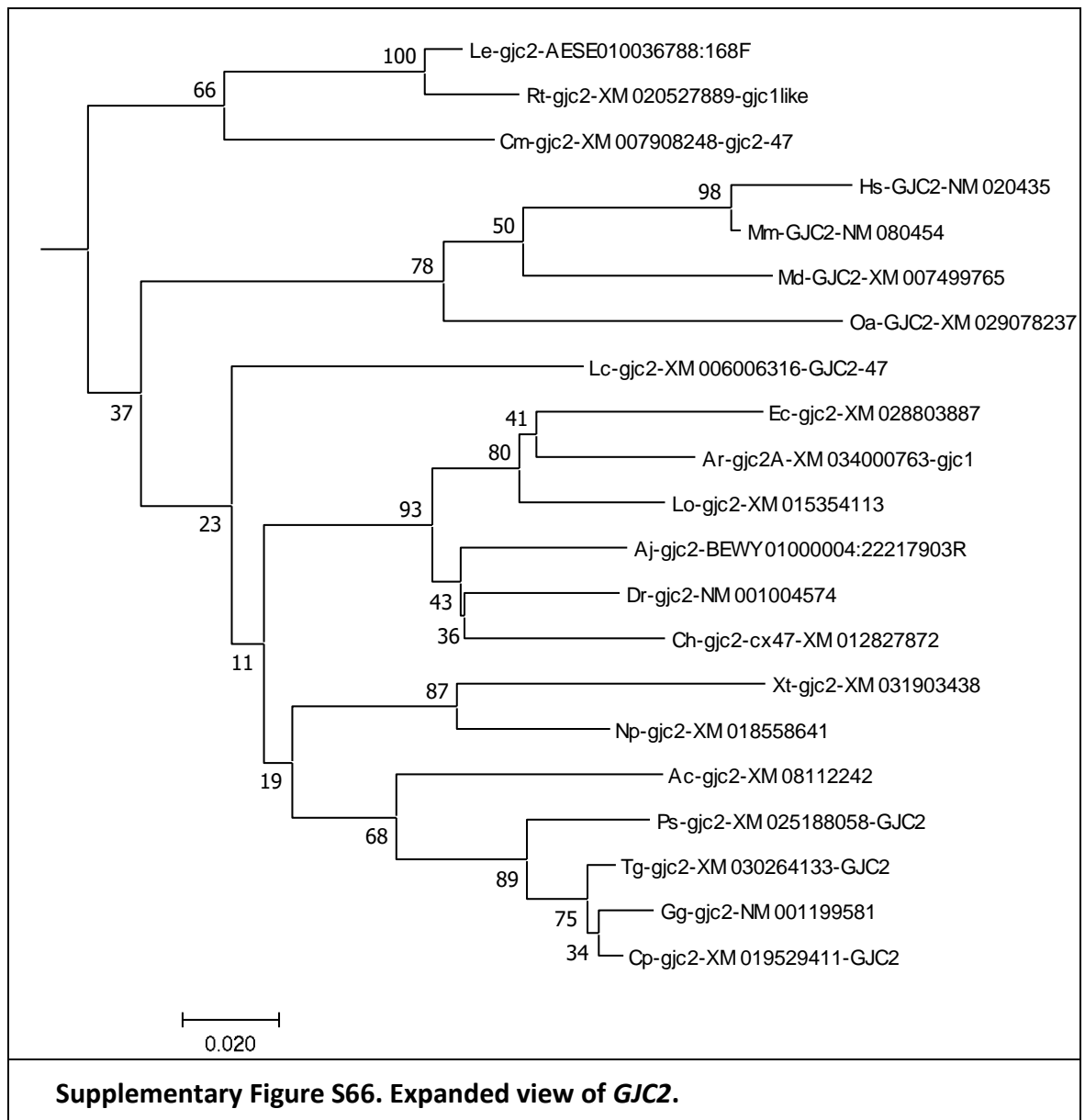
**Supplementary Figure S59. Expanded view of *gjb10*.**

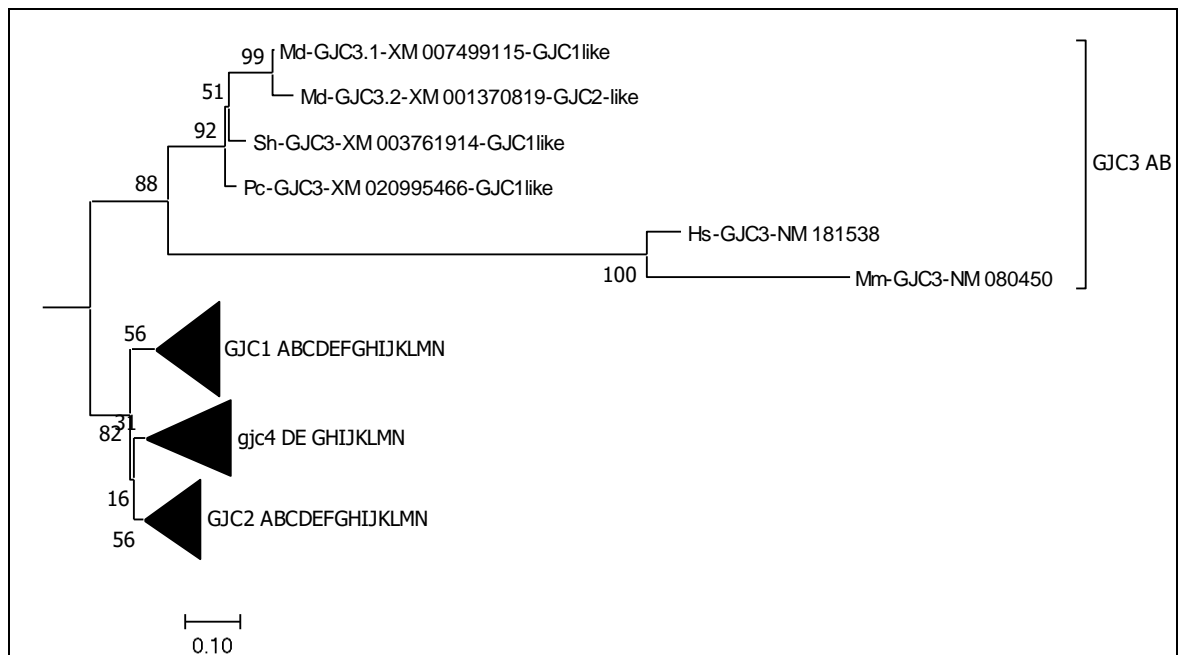




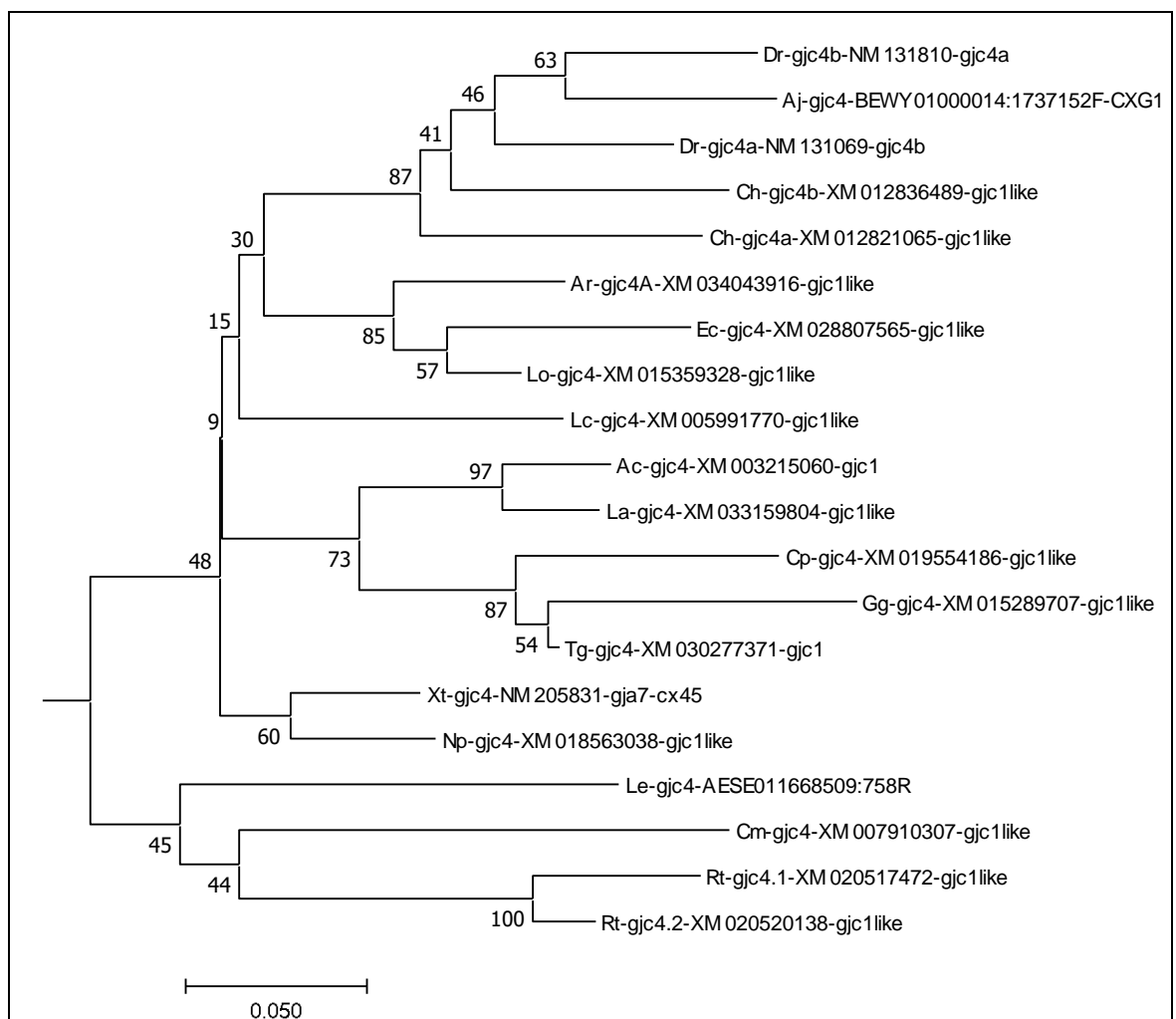




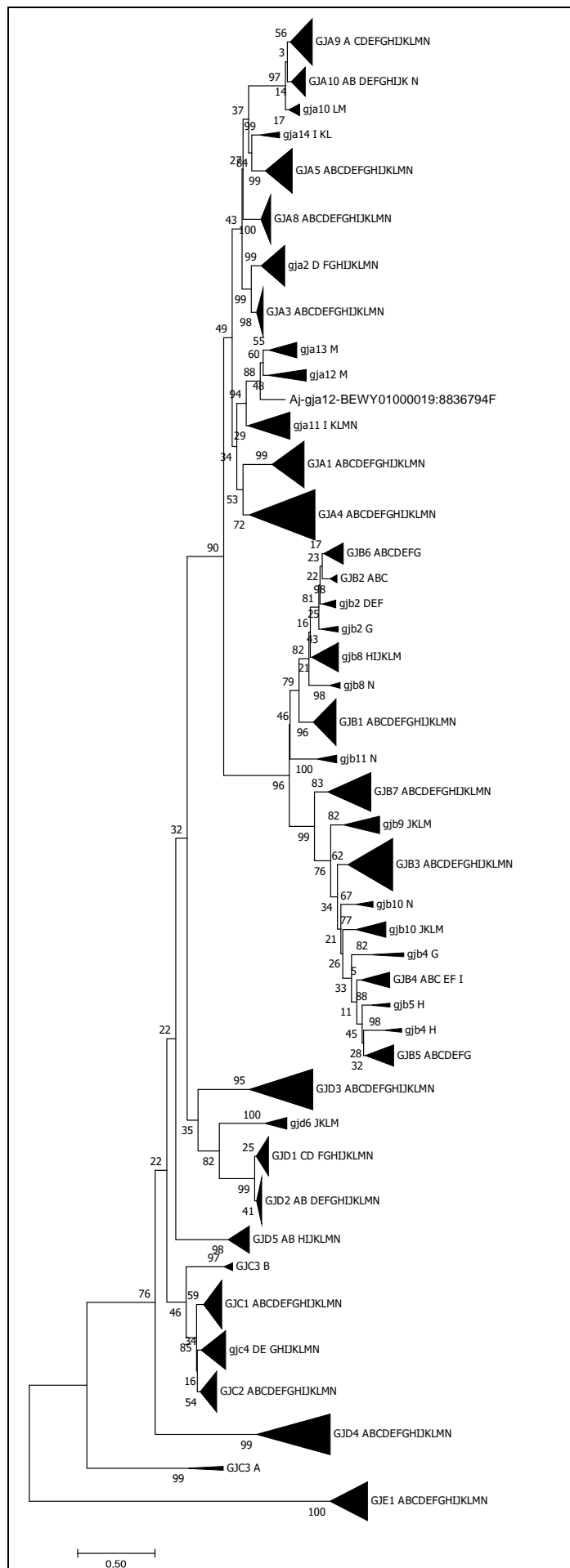




**Supplementary Figure S67. Expanded view of *GJC3*.**

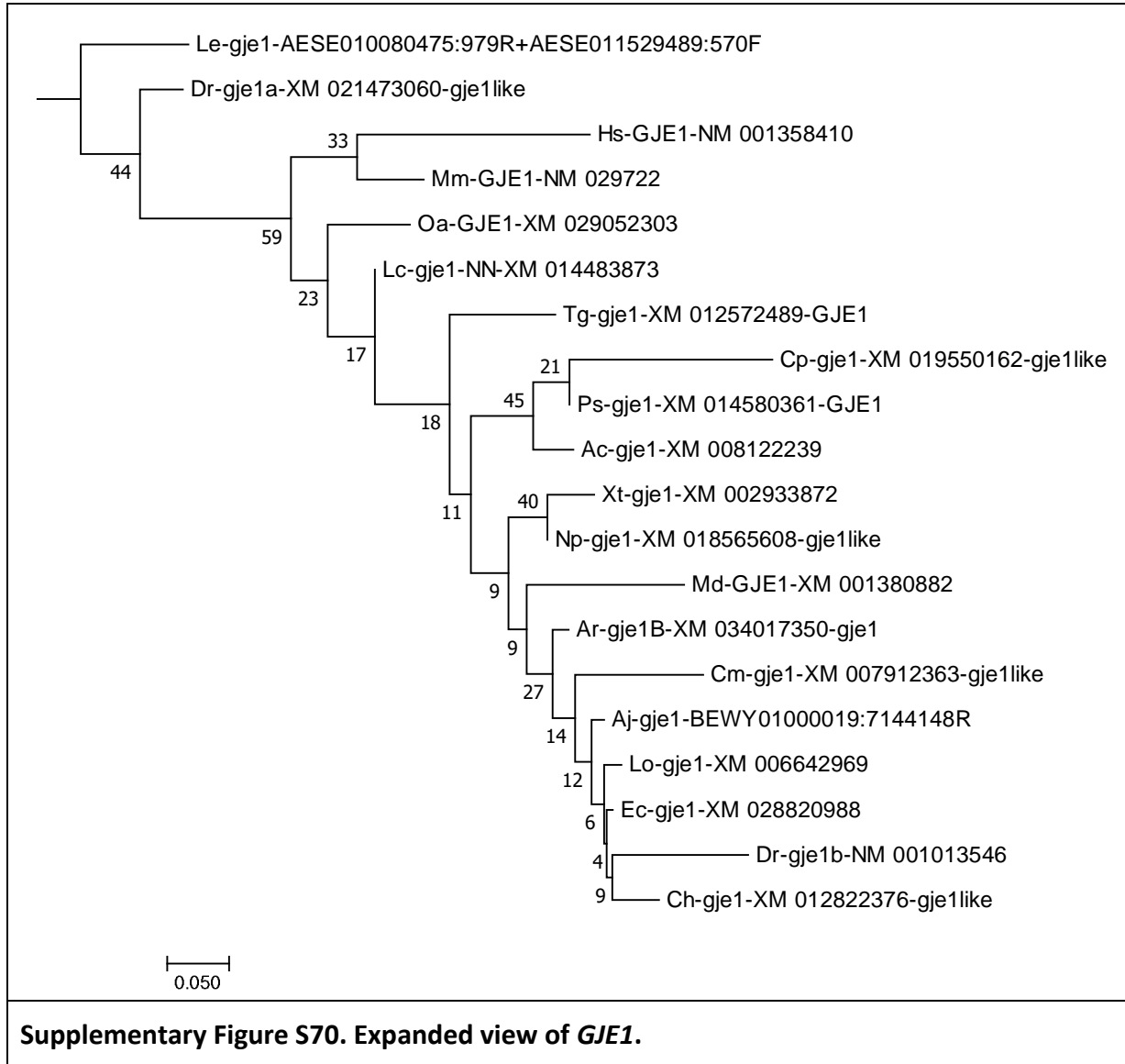


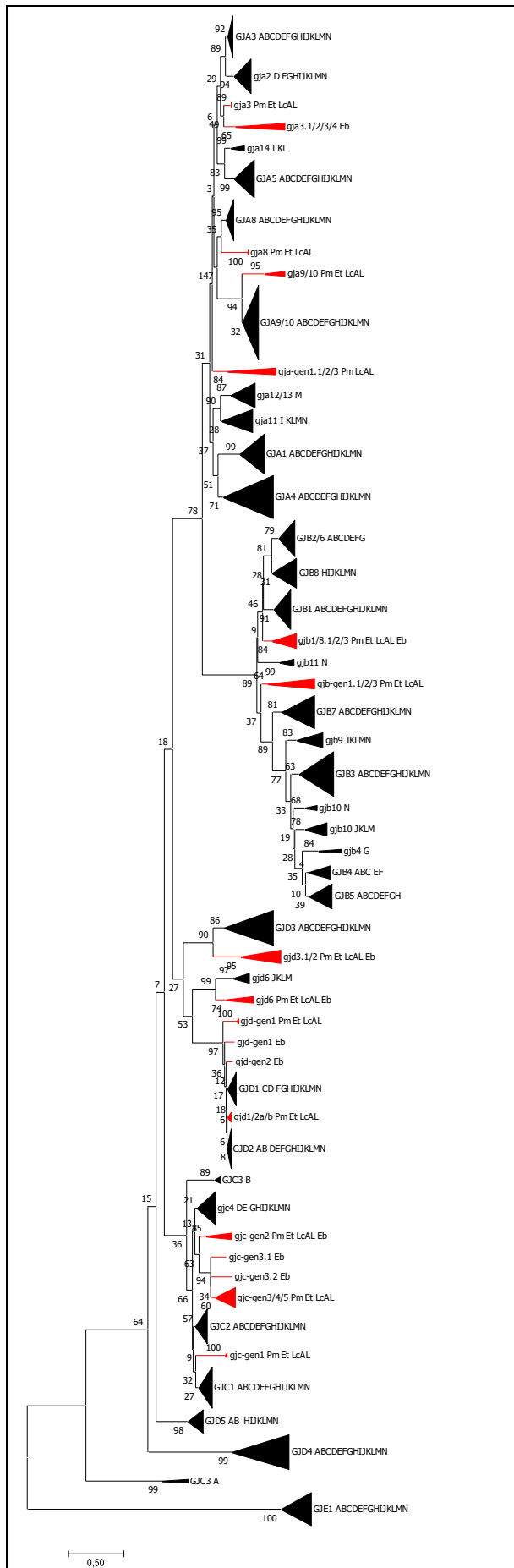
**Supplementary Figure S68. Expanded view of *gjc4*.**



**Supplementary Figure S69.**  
**Compressed phylogenetic tree including *GJE1* for all vertebrate groups except cyclostomes.** The orthologous gene groups are indicated by their Greek nomenclature, using upper case letters if mammalian sequences are included in the group, and lower case letters if mammalian sequences are not included in the group. The letters at each branch signify the vertebrate groups as follows: A, Placental mammals; B, Marsupials; C, Monotremata (platypus); D, Aves (birds); E, Crocodylians; F, Testudines (turtles); G, Squamata (lizards and snakes); H, Amphibia; I, Lobe-finned fish (*Latimeria*); J, Chondrostei - Polypteriformes (reedfish); K, Chondrostei - Acipenseriformes (sturgeons); L, Holostei (spotted gar); M, Teleostei; N, Chondrichthyes (cartilaginous fishes). A space is left in the sequence of the letters to make it more evident that one or more groups are lacking that particular gene. The tree was constructed on basis of the amino acid sequence (205 positions, 579 sequences) of the conserved domains by the Neighbor-Joining method using JTT substitution matrix and with rate variation among sites corresponding to a gamma shape parameter = 1. Five hundred bootstrap iterations were run.







### Supplementary Figure S71. Compressed phylogenetic tree (including *GJE1*) for all vertebrate groups including cyclostomes.

The orthologous gene groups are indicated by their Greek nomenclature, using upper case letters if mammalian sequences are included in the group, and lower case letters if mammalian sequences are not included in the group. The letters at each branch signify the vertebrate groups as follows: A, Placental mammals; B, Marsupials; C, Monotremata (platypus); D, Aves (birds); E, Crocodylians; F, Testudines (turtles); G, Squamata (lizards and snakes); H, Amphibia; I, Lobe-finned fish (*Latimeria*); J, Chondrostei - Polypteriformes (reedfish); K, Chondrostei - Acipenseriformes (sturgeons); L, Holostei (spotted gar); M, Teleostei; N, Chondrichthyes (cartilaginous fishes).

A space is left in the sequence of the letters to make it more evident that one or more groups are lacking that particular gene. The cyclostomal branches are indicated in red. The cyclostome sequences are indicated with their preliminary gene name (defined as described in the text) followed by the abbreviation describing the cyclostome species: Pm, *Petromyzon marinus* - sea lamprey; Et, *Entosphenus tridentatus*, Pacific lamprey; LcAL, *Lethenteron camtschaticum*, Arctic lamprey, Eb, *Eptatretus burgeri*, inshore hagfish.

The tree was constructed on basis of the amino acid sequence (205 positions, 655 sequences) of the conserved domains by the Neighbor-Joining method using JTT substitution matrix and with rate variation among sites corresponding to a gamma shape parameter = 0.8. Five hundred bootstrap iterations were run.