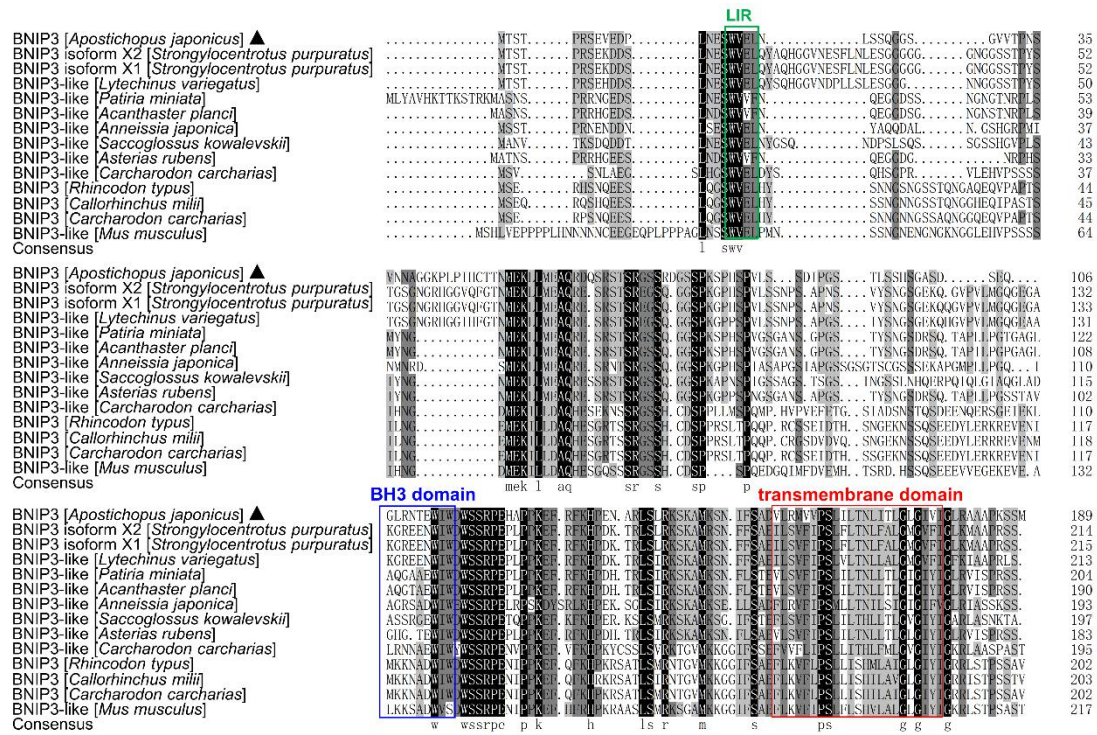
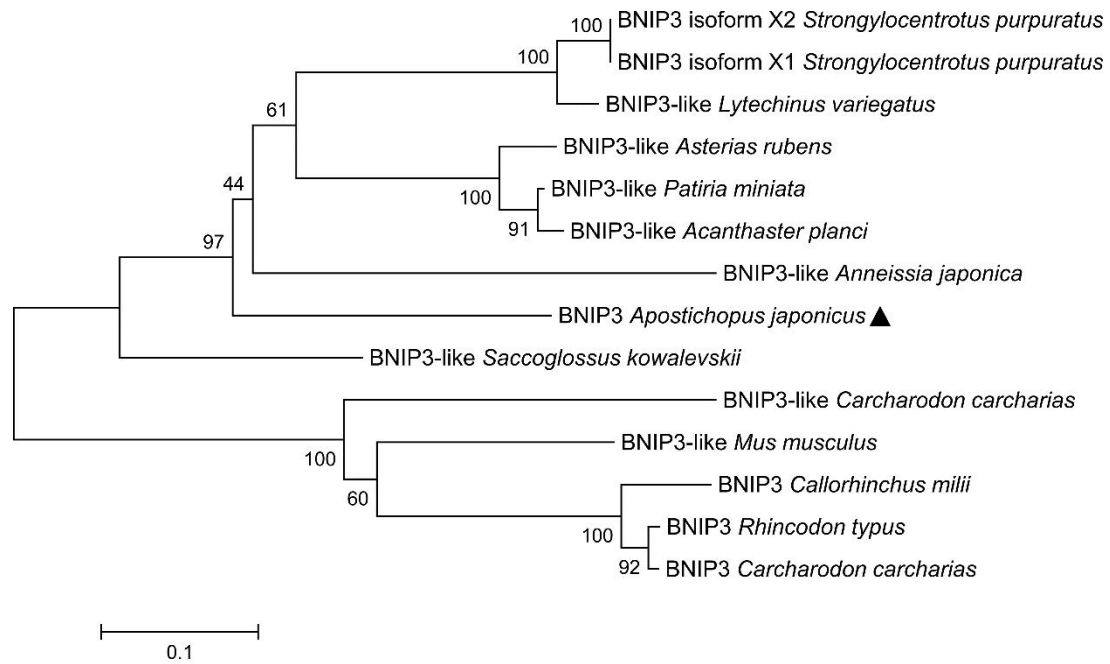


# Supplementary Materials



**Supplementary Figure S1. Multiple sequence alignment of AjBNIP3.** Multiple sequence alignment of deduced amino acid (aa) sequences of BNIP3 proteins from 14 vertebrate and invertebrate organisms. Numbers on right indicate aa positions. Identical or similar residues are indicated below alignment. AjBNIP3 contains a conserved LIR, BH3 domain, and transmembrane domain.



**Supplementary Figure S2. Phylogenetic tree analysis of AjBNIP3.** Phylogenetic tree was constructed according to alignment of aa sequences using neighbor-joining method in MEGA 5.1 with 1 000 bootstrap replications. Bootstrap values are indicated at tree nodes. BNIP3 proteins clustered into two major groups, namely, vertebrate BNIP3 and invertebrate BNIP3. GenBank accession numbers of each BNIP3 are listed on left side of species name. *A. japonicus*, *Strongylocentrotus purpuratus* (XP\_011683163.2 and XP\_792026.4), *Lytechinus variegatus* (XP\_041476352.1), *Patiria miniata* (XP\_038046383.1), *Acanthaster planci* (XP\_022080791.1), *Anneissia japonica* (XP\_033102733.1), *Saccoglossus kowalevskii* (XP\_002735536.1), *Asterias rubens* (XP\_033633280.1), *Carcharodon carcharias* (XP\_041042968.1 and XP\_041065695.1), *Rhincodon typus* (XP\_020389820.1), *Callorhinchus milii* (XP\_042192902.1), and *Mus musculus* (NP\_033891.1).