

Potential Roles of the Sirtuins in Promoting Longevity for Larger *Argopecten*
Scallops

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Supplemental Information
Supplemental Figs. S1-S13

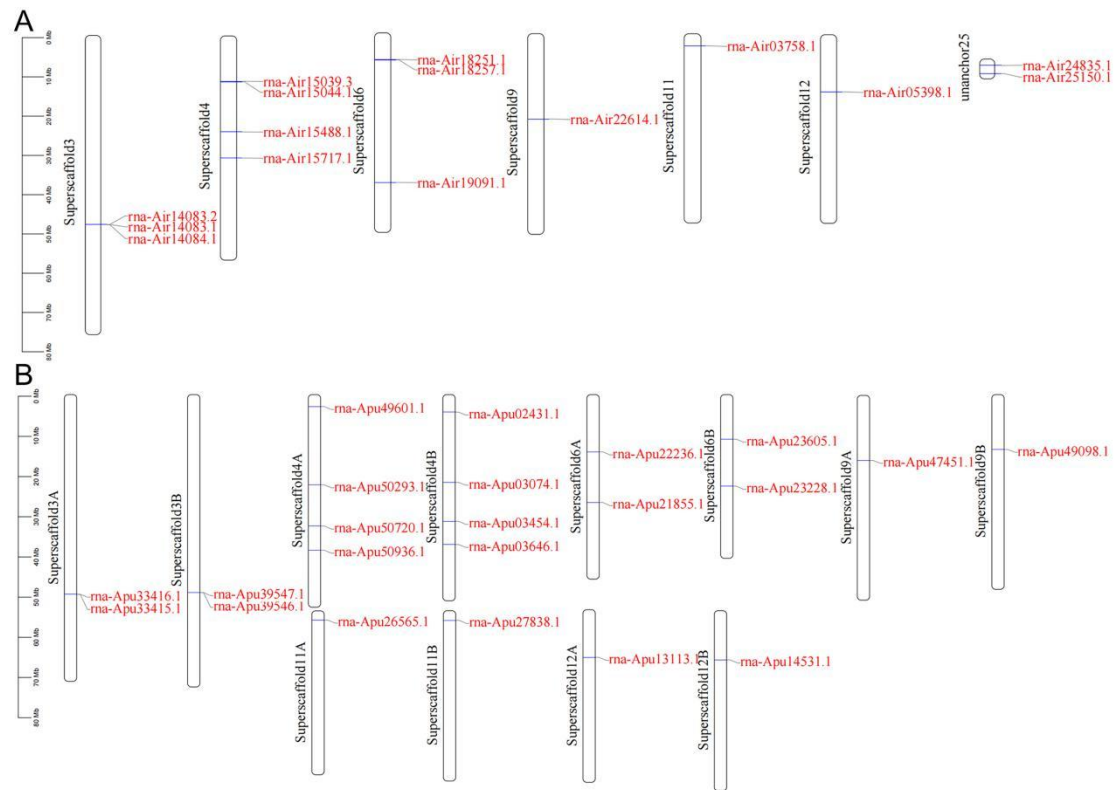


Fig. S1. Chromosome distribution of *SIRT* genes in the two scallop species. (A) the bay scallop; (B) the Peruvian scallop with two homologous chromosomes.

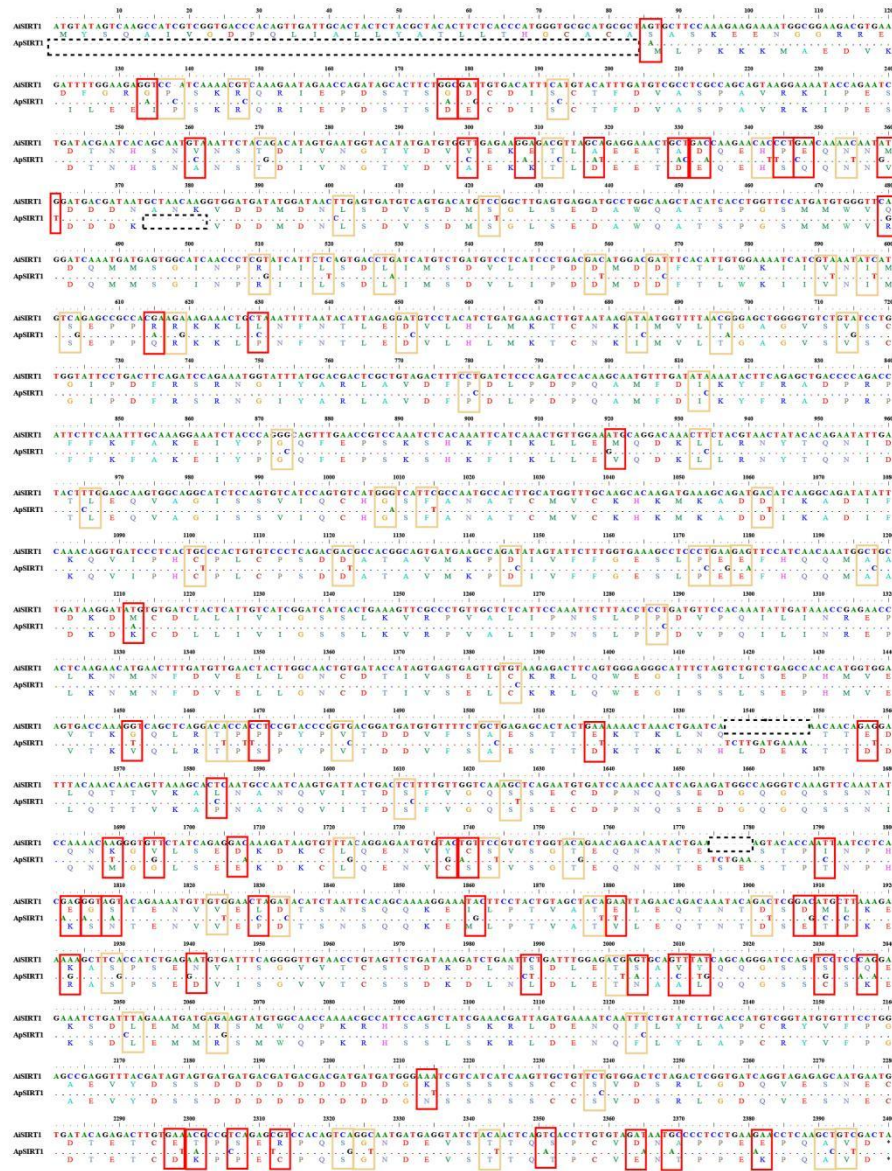


Fig. S2. Nucleotide and amino acid variations between *AiSIRT1* and *ApSIRT1*. The red box and orange box indicate the nonsynonymous and synonymous variations. The dash box indicates Indels.

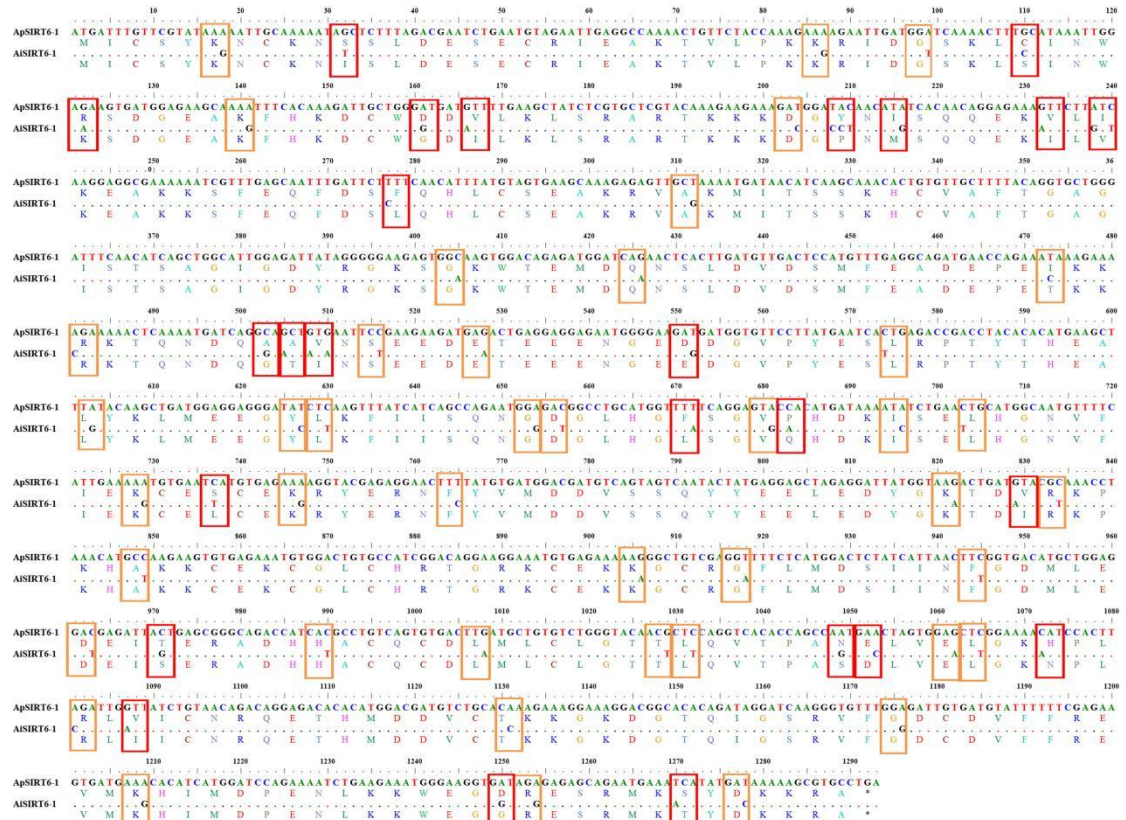


Fig. S3. Nucleotide and amino acid variations between *AiSIRT6-1* and *ApSIRT6-1*. The red box and orange box indicate the nonsynonymous and synonymous variations. The dash box indicates Indels.

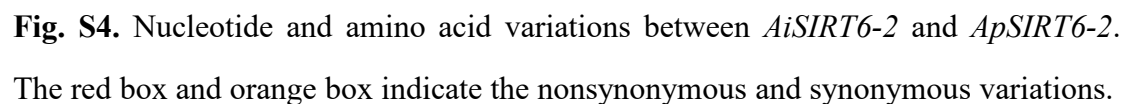
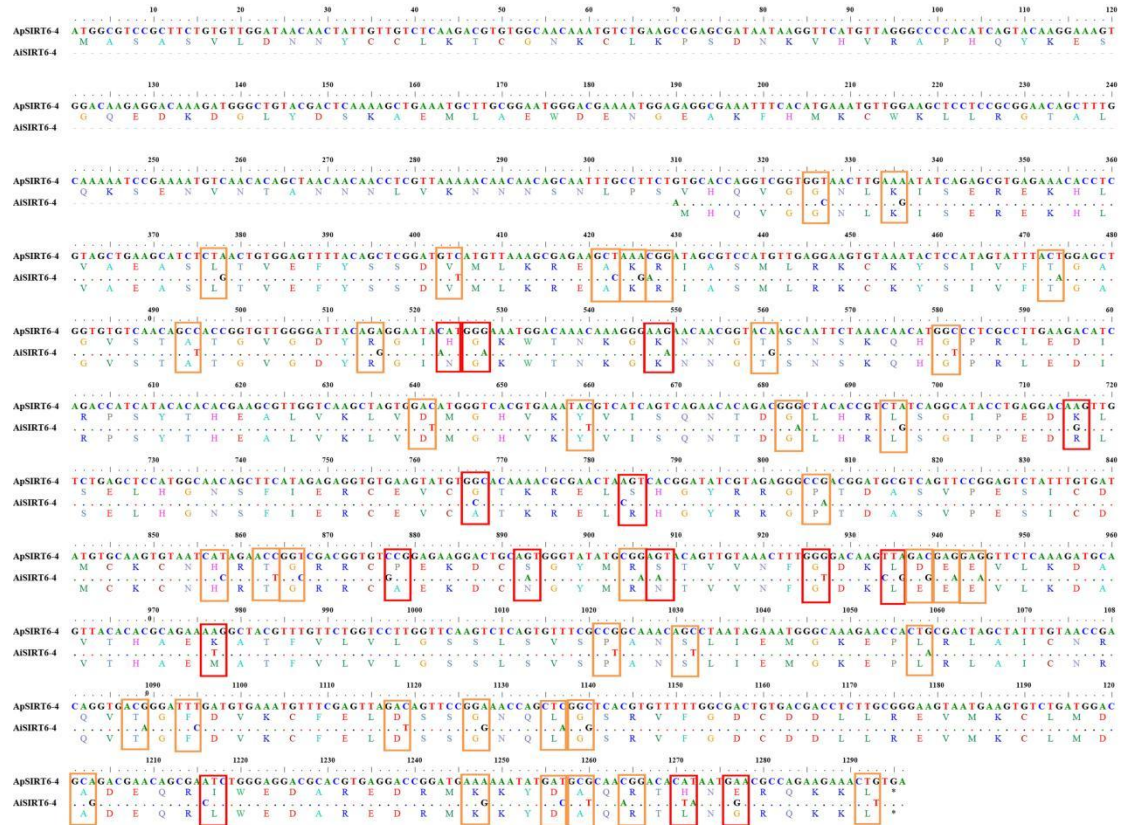


Fig. S5. Nucleotide and amino acid variations between *AiSIRT6-3* and *ApSIRT6-3*. The red box and orange box indicate the nonsynonymous and synonymous variations. The dash box indicates Indels.



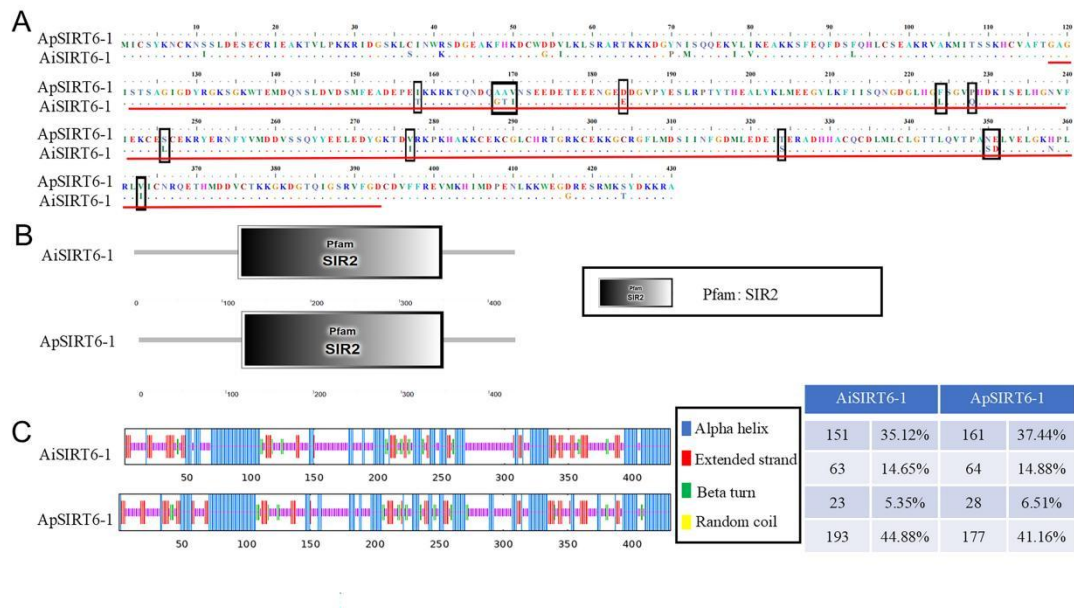


Fig. S7. The sequence alignments (A), the signal peptide (B), the structure domains (C) the secondary structure (D) of AiSIRT6-1 and ApSIRT6-1. The changes in the SIRT domain and amino acids changes are marked by red line and black box, respectively.

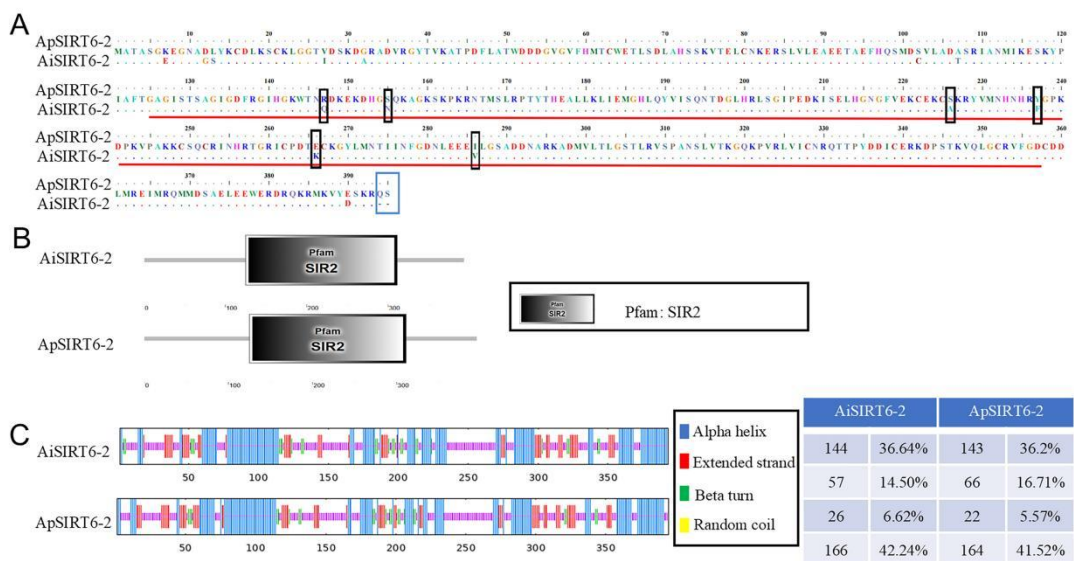


Fig. S8. The sequence alignments (A), the signal peptide (B), the structure domains (C) the secondary structure (D) of AiSIRT6-2 and ApSIRT6-2. The SIRT domain and the amino acids changes are marked by red line and black box, respectively. The blue box represents the InDels.

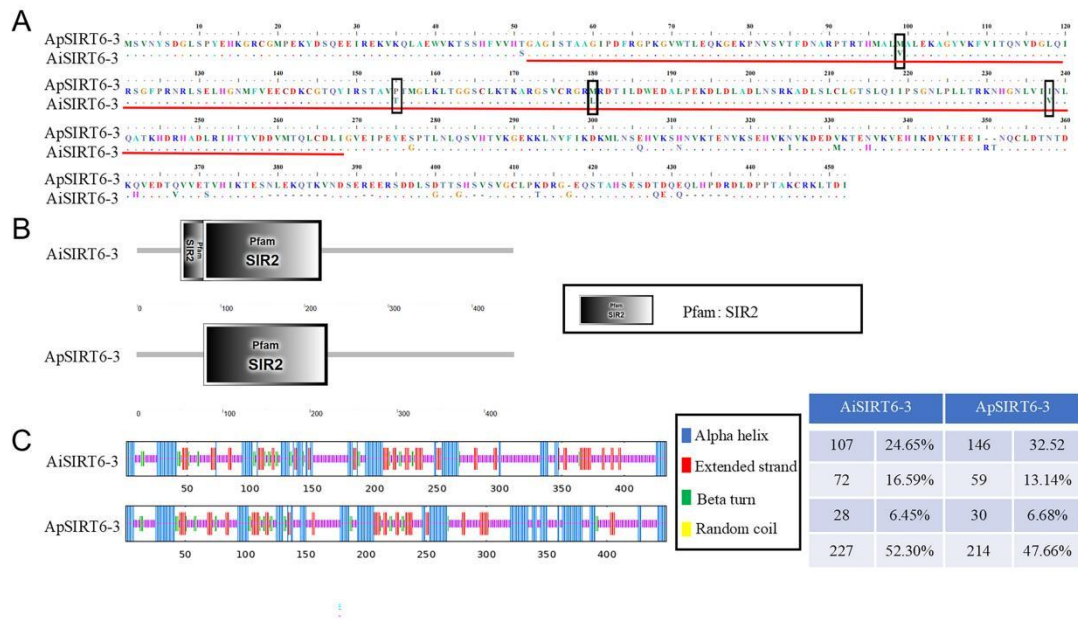


Fig. S9. The sequence alignments (A), the signal peptide (B), the structure domains (C) the secondary structure (D) of AiSIRT6-3 and ApSIRT6-3. The SIRT domain and the amino acids changes are marked by red line and black box, respectively.

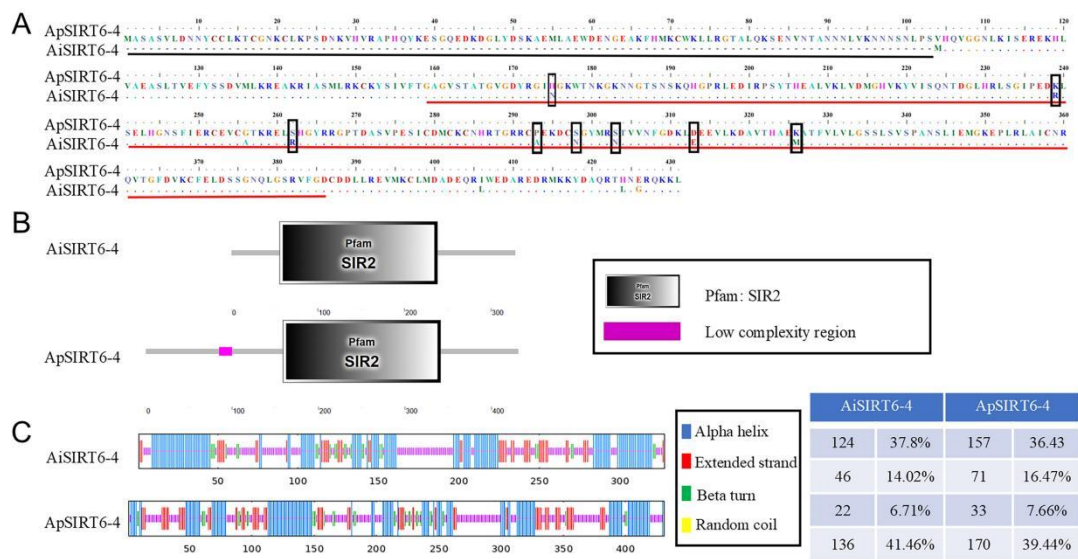


Fig. S10. The sequence alignments (A), the signal peptide (B), the structure domains (C) the secondary structure (D) of AiSIRT6-4 and ApSIRT6-4. The SIRT domain and the amino acids changes are marked by red line and black box, respectively. The black line represents the InDels.

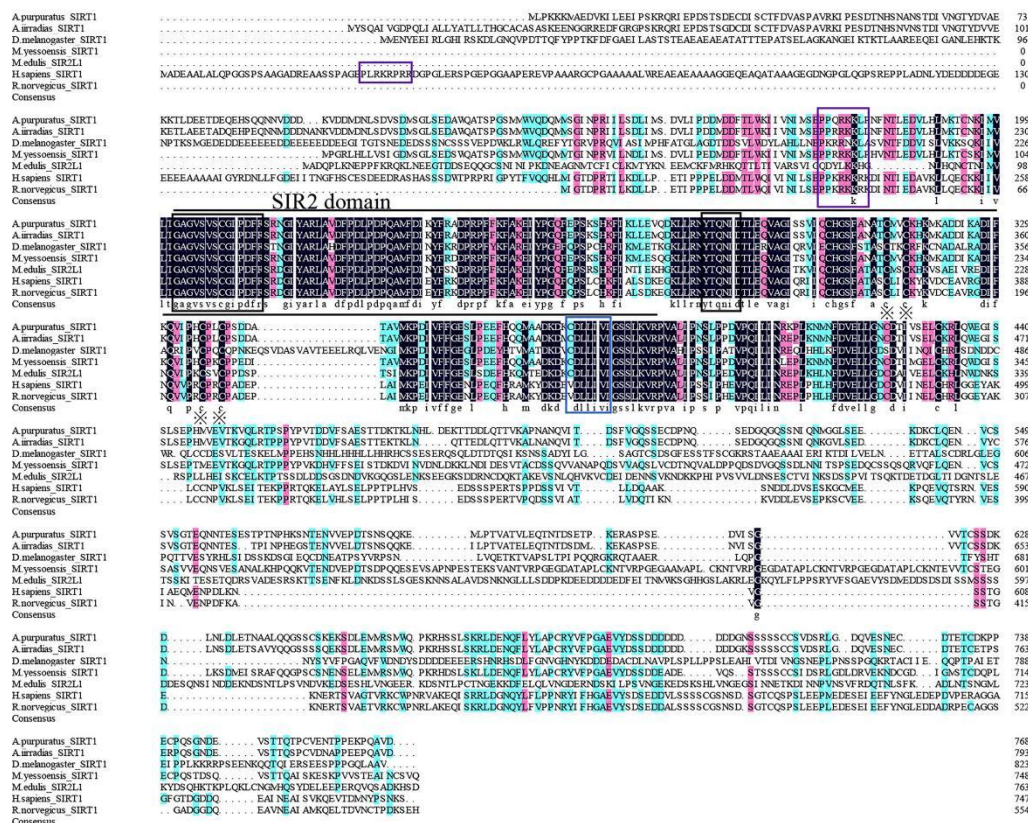




Fig. S12. Amino acid sequence alignment of SIRT6 proteins in two scallop species. The predicted SIR2 domain was lined in black. The Zn binding sites were indicated by the “※”. The blue box indicated the NLS. The black box was the necessary motif.

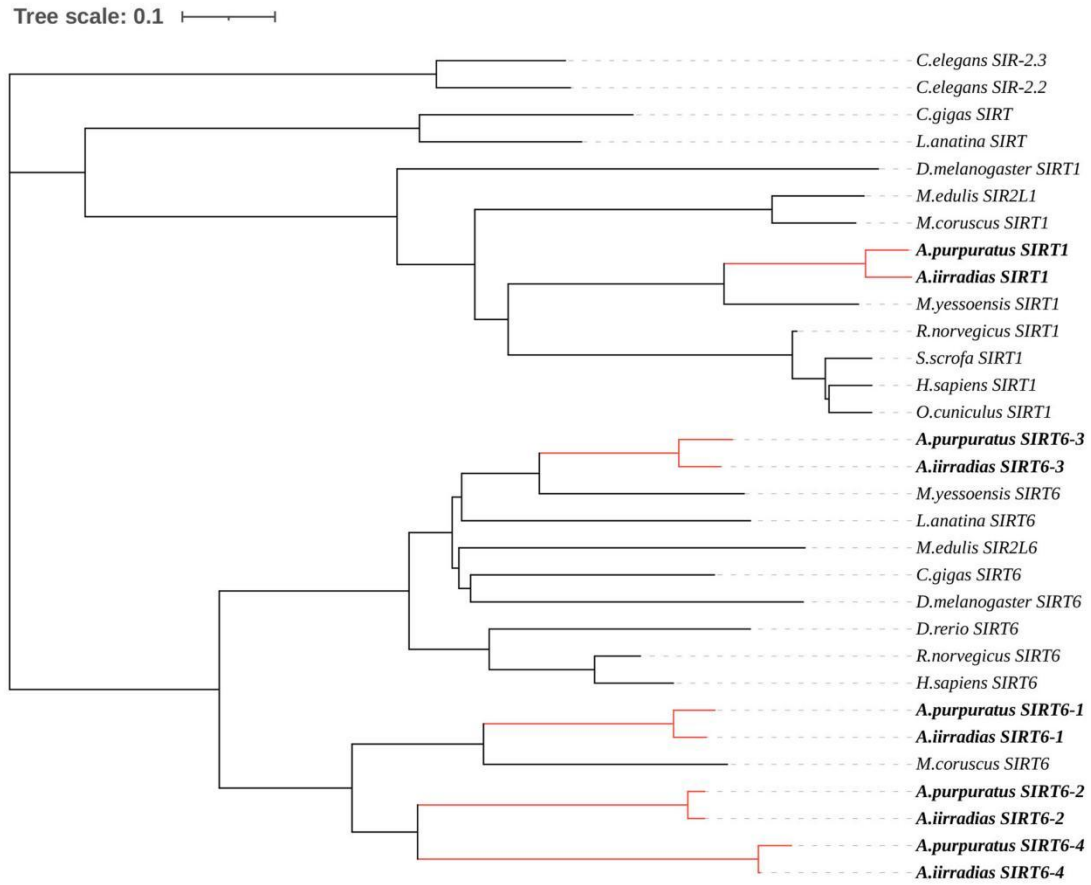


Fig. S13. The phylogenetic analysis for *SIRT1* and *SIRT6* in two scallop species.