

## **Description of Additional Supplementary Files**

### **Supplementary Data Legends:**

**Supplementary Data 1.** 548 positive selected genes (PSGs) identified in *T. rubra*. The “Symbol” column represents the gene IDs of *T. rubra*(P-value<0.05).

**Supplementary Data 2.** dN/dS value of the positive selected genes(PSGs) identified in *T. rubra*.

**Supplementary Data 3.** GO enrichment of positive selected genes(PSGs) in *T. rubra* (P value<0.05).

**Supplementary Data 4.** The RNA sequencing information of two tissues of four species.

**Supplementary Data 5.** The differentially expressed genes (DEGs) in the rhopalia of three Scyphozoans and the tentacle bulb of *T. rubra*.

**Supplementary Data 6.** Enrichment of gene ontology of downregulated DEGs in the tentacle bulb of *T. rubra* (P-value <0.05).

**Supplementary Data 7.** The differentially expressed genes (DEGs) of the sensory organs and control tissues in each species.

**Supplementary Data 8.** Enrichment of gene ontology of upregulated/downregulated DEGs of the sensory organs in each species (P-value <0.05).

**Supplementary Data 9.** KEGG enrichment of DEGs of the sensory organs and control tissues in four jellyfish species (P-value<0.05).

**Supplementary Data 10.** The list of expanded/contracted gene families in jellyfish species. (P-value<0.05).

**Supplementary Data 11.** GO enrichment of expanded/contracted gene families in *T. rubra* (P-value<0.05).

**Supplementary Data 12.** The list of of gene losses in *T. rubra* (Pvalue<0.05). The statistical tests were two-sided and the adjustments were made for multiple comparisons.

**Supplementary Data 13.** GO enrichment of lost gene families in *T. rubra* (P-value<0.05).

**Supplementary Data 14.** The relative expression of target genes in the si-OM and si-LRR groups.

**Supplementary Data 15.** Cell atlas marker of medusa. The “gene” column represents the gene IDs of *A. coerulea*.

**Supplementary Data 16.** The different expressed genes (DEGs) of hair cell between *T. rubra* and *A. coerulea*. The “gene” column represents the gene IDs of *A. coerulea*.

**Supplementary Data 17.** GO enrichment of hair cells in *T. rubra* and *A. coerulea* (P-value<0.05).

**Supplementary Data 18.** The different expressed genes (DEGs) of neural cell between *T. rubra* and *A. coerulea*. The “gene” column represents the gene IDs of *A. coerulea*.

**Supplementary Data 19.** GO enrichment of neural cell in *T. rubra* and *A. coerulea* (P-value<0.05).

**Supplementary Data 20.** The different expressed genes (DEGs) of triated muscle between *T. rubra* and *A. coerulea*. The “gene” column represents the gene IDs of *A. coerulea*.

**Supplementary Data 21.** GO enrichment of striated muscle in *T. rubra* and *A. coerulea* (P-value<0.05).

**Supplementary Data 22.** Cell atlas markers for different developmental stages of the *T. rubra*.

**Supplementary Data 23.** KEGG enrichment analysis of cyst and planula in *T. rubra*.

**Supplementary Data 24.** GO enrichment analysis of cyst and planula in *T. rubra* (P-value<0.05).

**Supplementary Data 25.** The different expressed genes (DEGs) of *T. rubra* across different life stages.

**Supplementary Data 26.** Homologous gene comparison between *T. rubra* and *A. coerulea*.

**Supplementary Software legends:**

**Supplementary Software 1.** Scripts for extracting protein sequences of one-to-one orthologues from each orthogroup.

**Supplementary Software 2.** Scripts for individual protein alignments.

**Supplementary Software 3.** Scripts for gene loss analyses.

**Supplementary Software 4.** Scripts for integrate the datasets corresponding to the medusa.