

Supplementary Information

Figure S1. High performance liquid chromatography of STX in ACHK-T and ACHK-NT. **(A)** C1/C2 toxins; **(B)** GTX1/4 toxins. Y-axis: Fluorescence intensity (LU); X-axis: Retention time (min). Differences of chromatograms peak between ACHK-T and ACHK-NT were consistent with previous result [26].

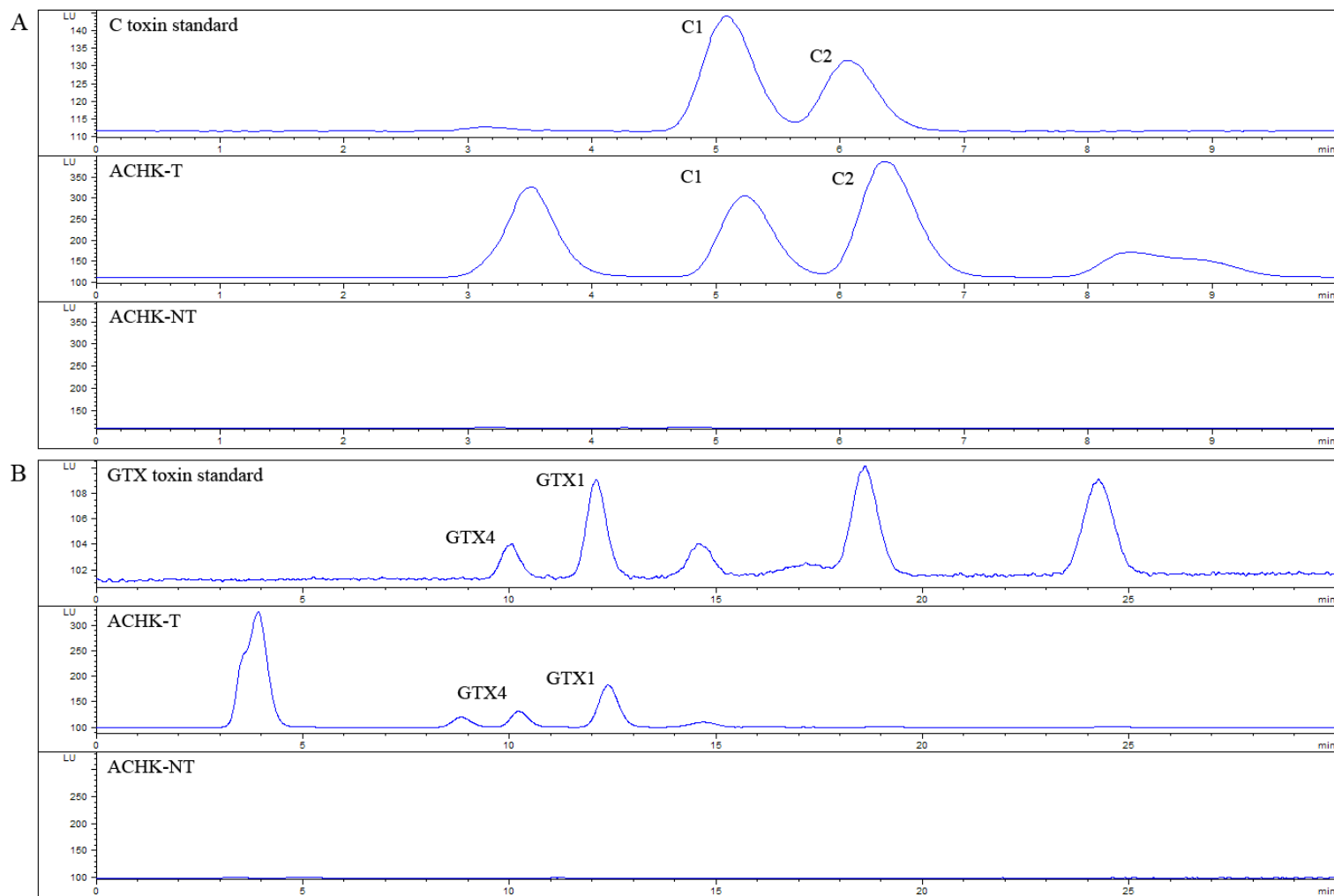


Figure S2. Cell cycle phase distribution of ACHK-T and ACHK-NT during the light period. Y-axis: Number of cells; X-axis: the relative amount of DNA. The results presented a similar phase distributions between the two strains.

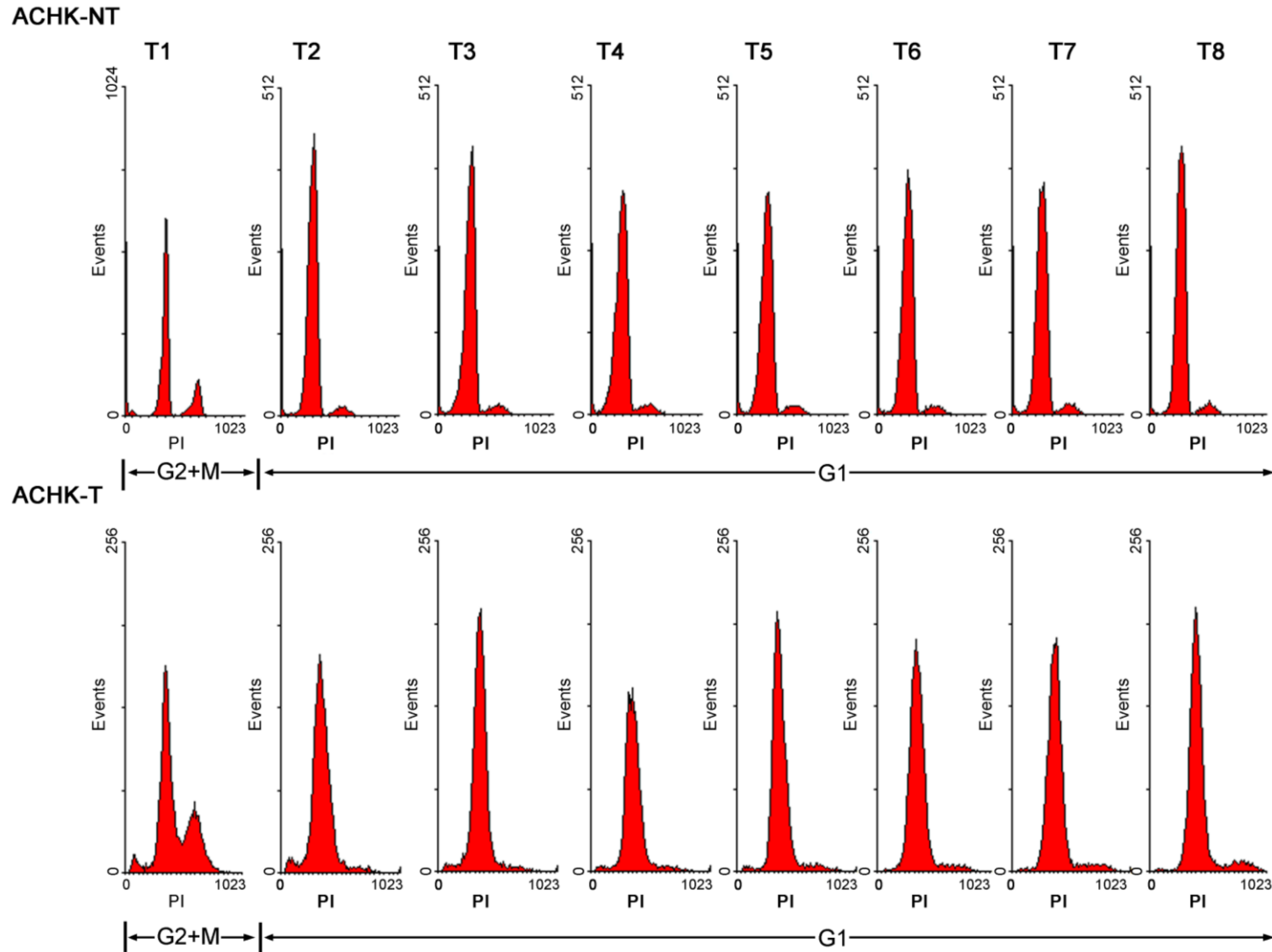


Figure S3. Uniform distribution of all reads from libraries of ACHK-NT and ACHK-T. Homogeneous distribution of reads which covered multiple locations in UTRs and coding regions of transcripts showed an evenly distributed coverage of reads to genes.

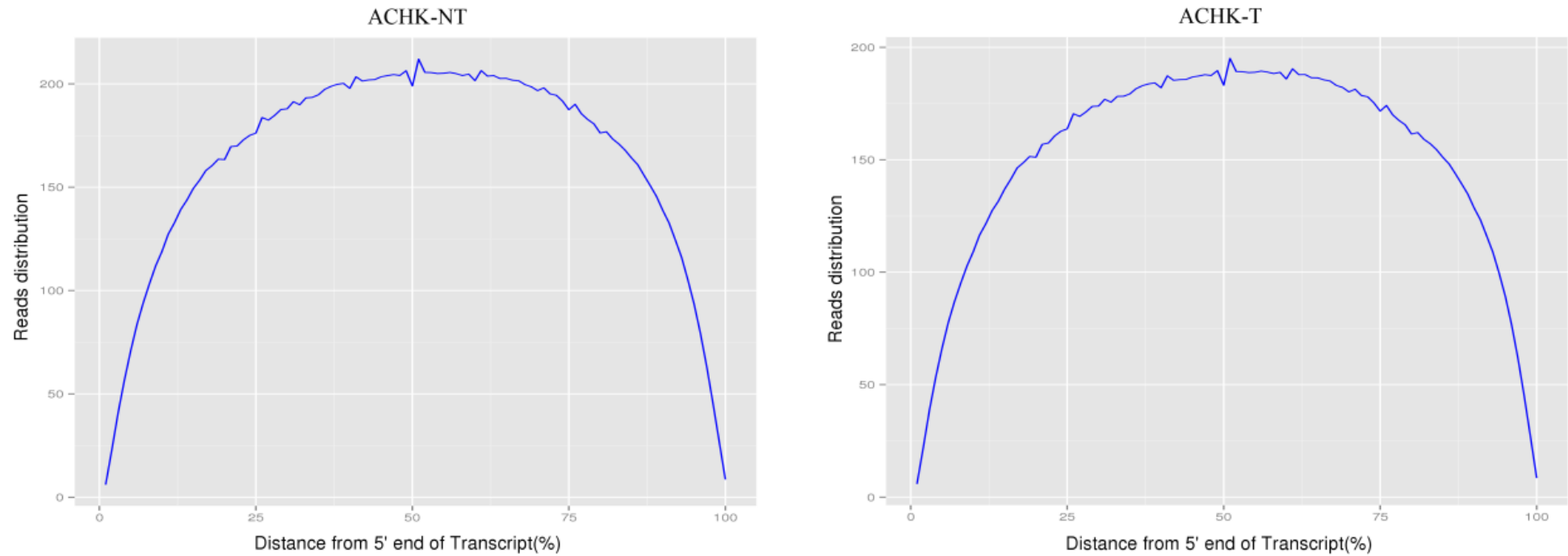


Figure S4. KOG classification of *A. catenella* unigenes. Letters represent the 26 classifications in KOG databases.

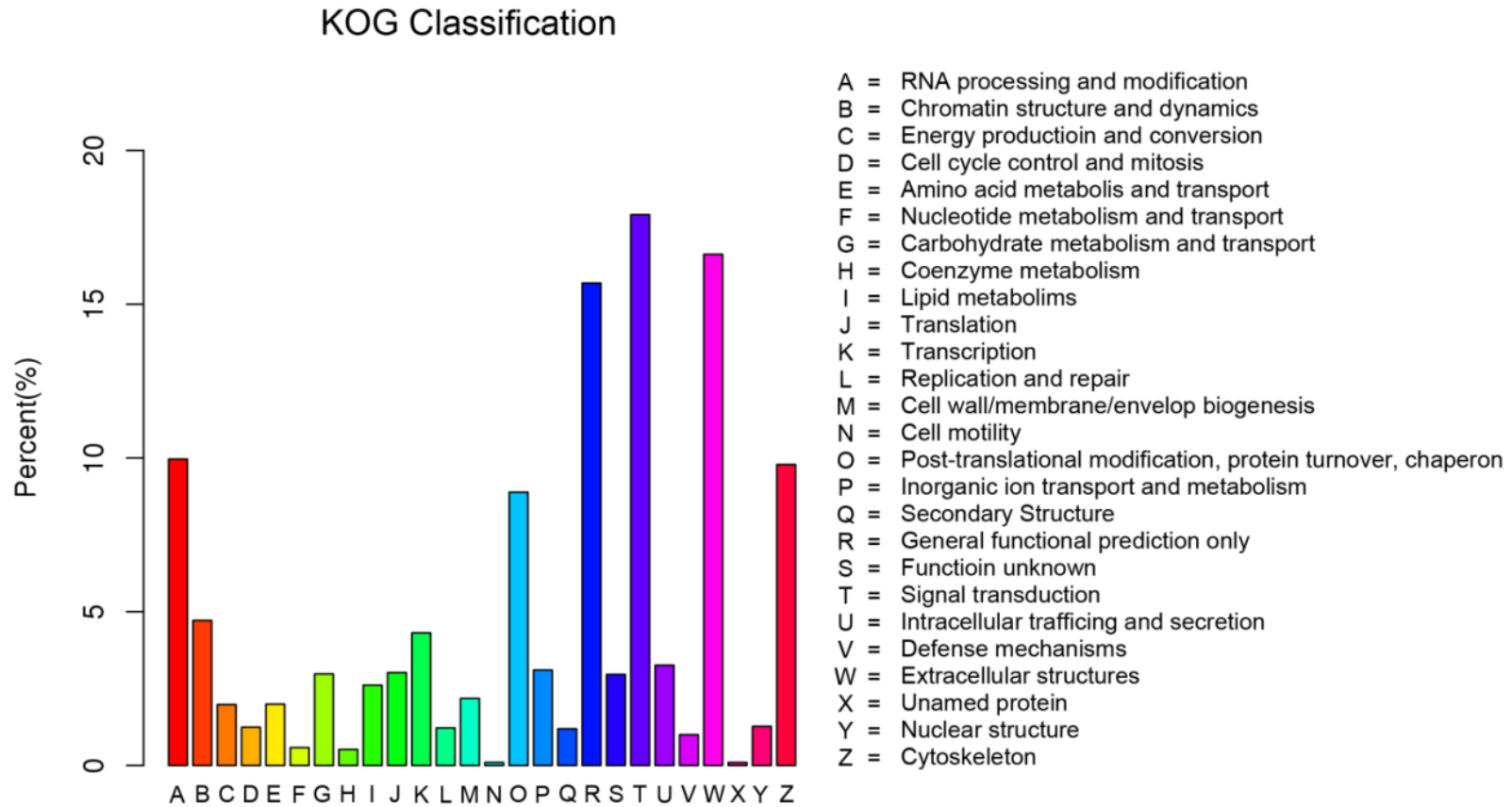


Figure S5. GO classification of *A. catenella* unigenes. Each annotated sequence was assigned to at least one GO term and classified into different groups within the three functional categories.

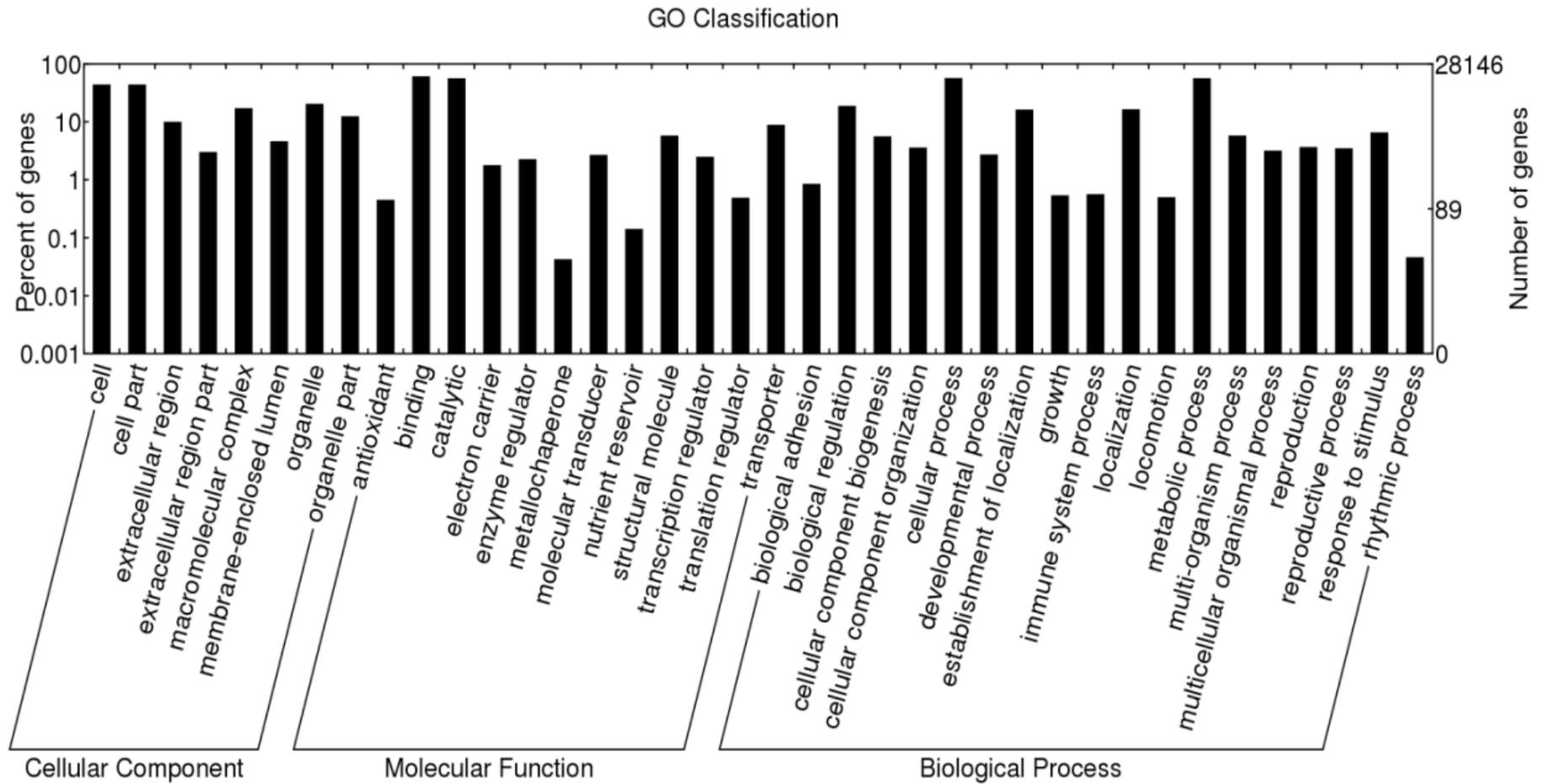


Figure S6. KEGG pathway annotation and KO annotation. (A) Top 10 represented KEGG pathway. Number of unigenes and EC numbers involved in each pathway is shown; (B) Top 10 KO terms with number of unigenes assigned to each term.

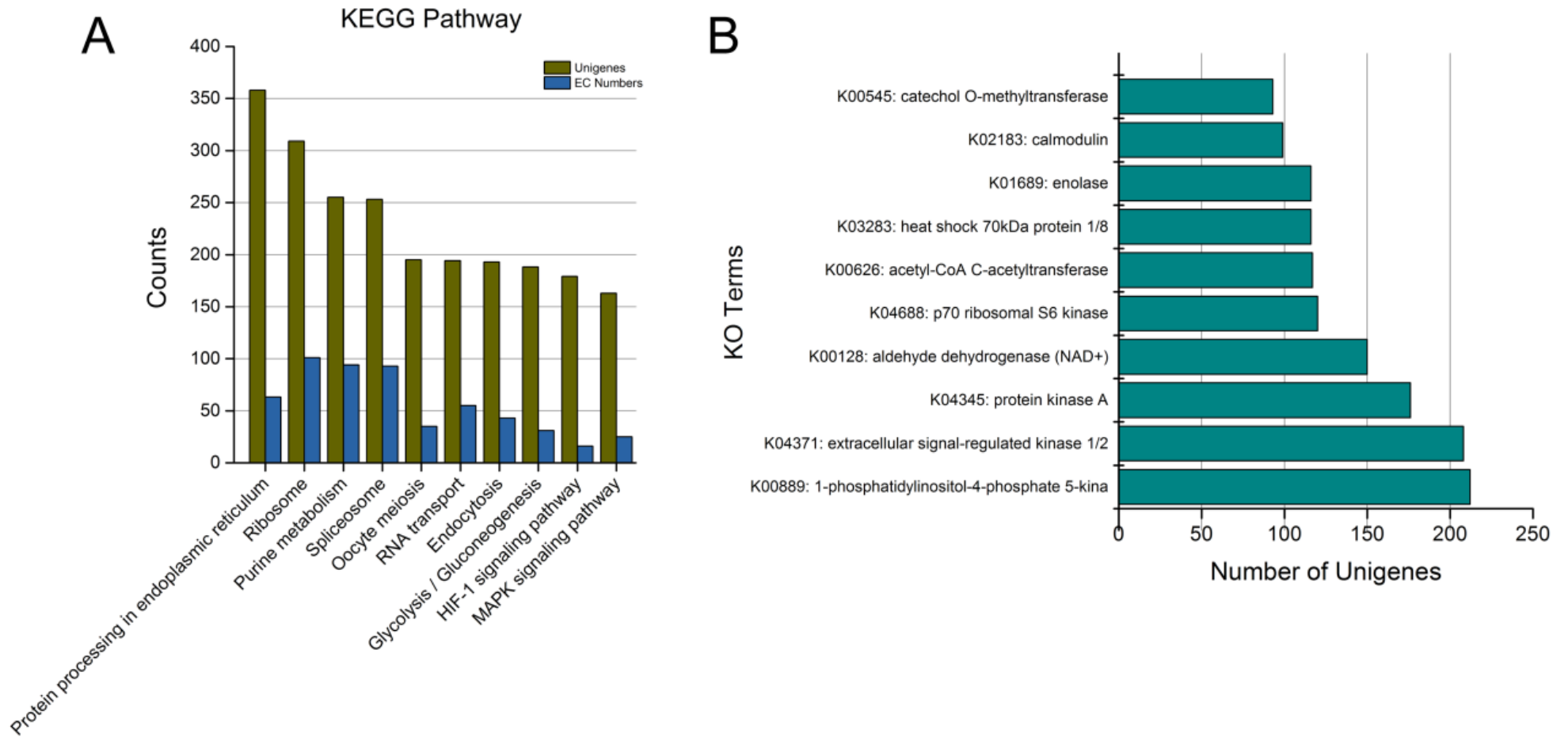


Figure S7. KEGG classifications of unigenes based on the secondary pathway hierarchy. Letters A to D represent the four primary hierarchies in KEGG database: **A:** Cellular Processes; **B:** Environmental Information Processing; **C:** Genetic Information Processing; **D:** Metabolism.

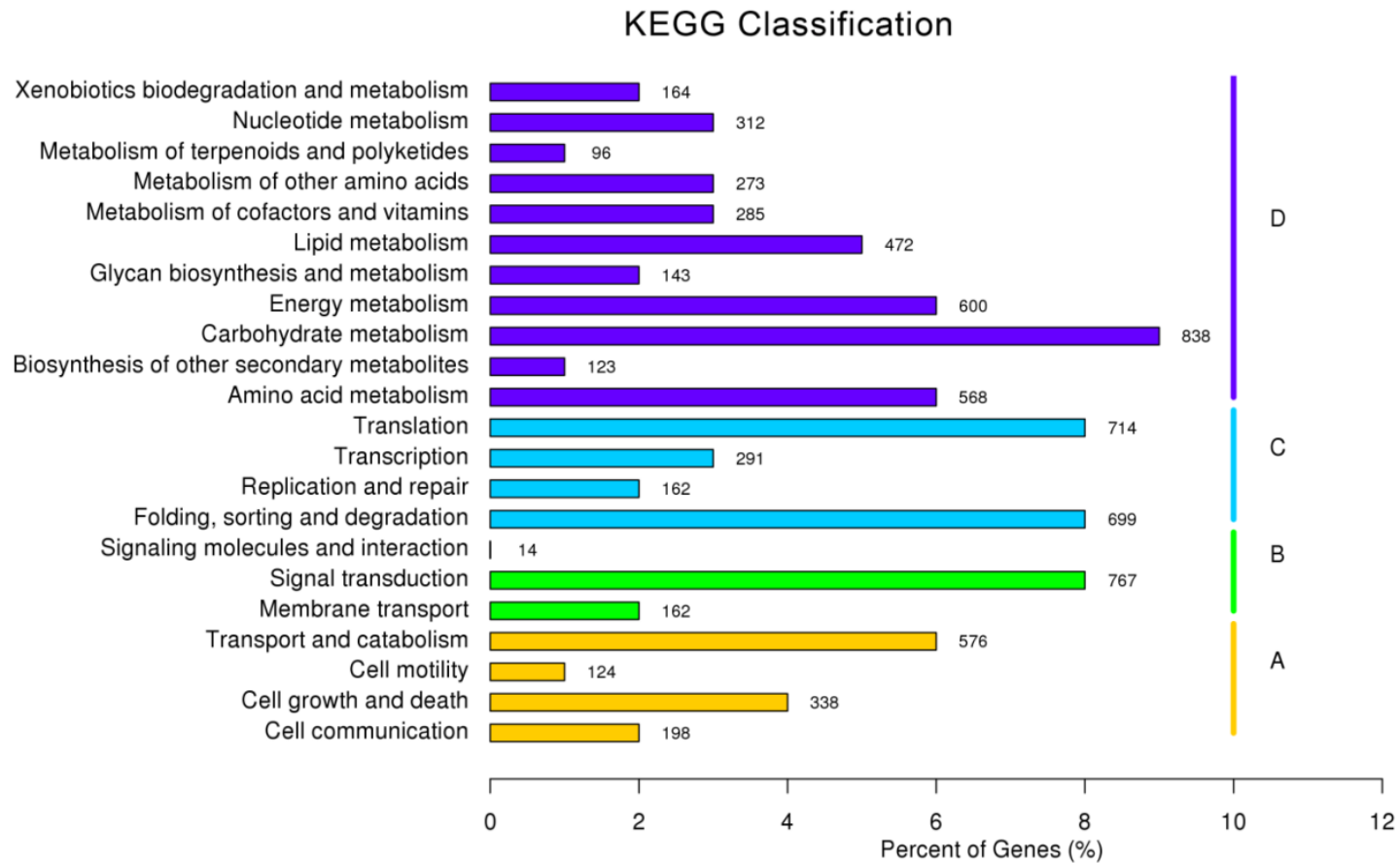


Figure S8. Protein families in *A. catenella* transcriptome. (A) Distribution of Pfam families versus unigenes; (B) Top 10 represented Pfam families.

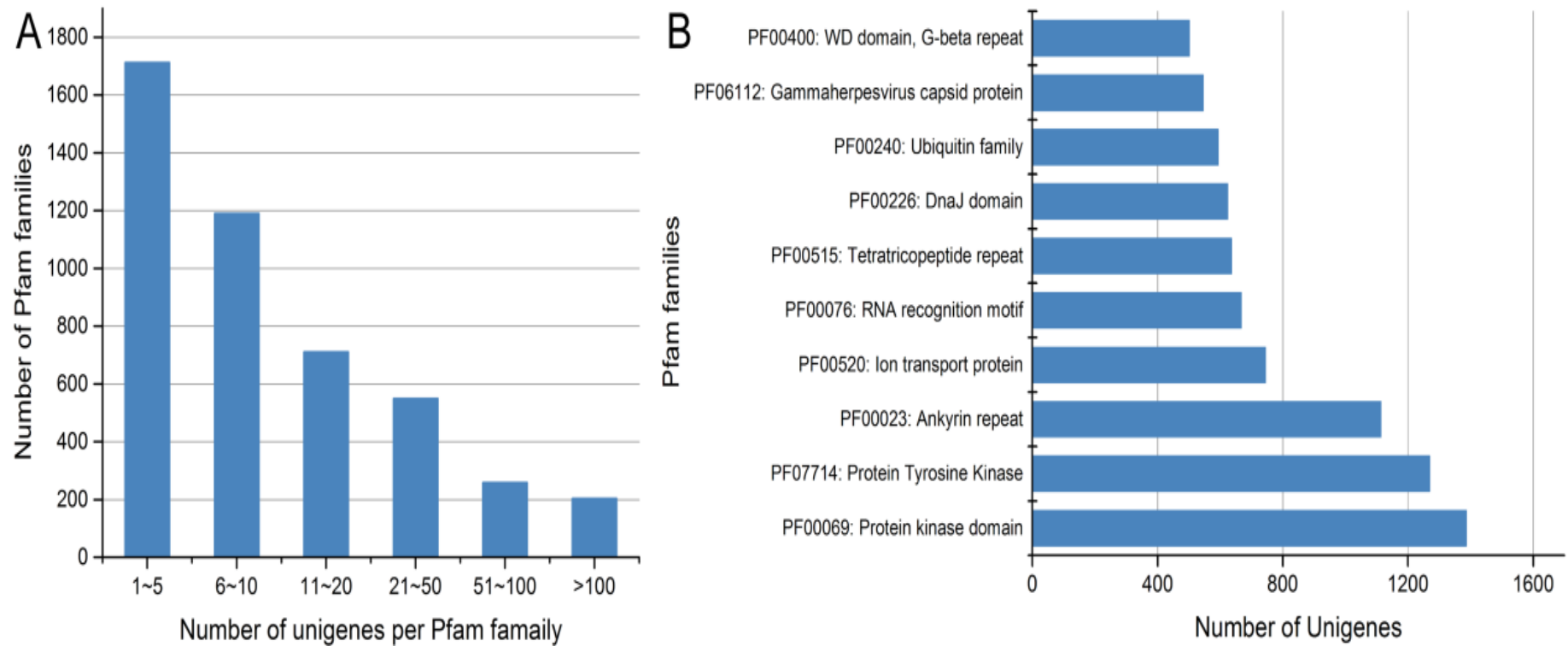


Figure S9. Cont.



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comp20666_r0 1597 GTTTCGCGGCAGTACATGGTCTCGC-CGGCGGCATTTACAATGGGAGCTGCCATGGCGGGCGTCCCTGGCTGGCGACTTCCGCGCCGTGGAGACGTATCCTGAGCA-CGGGAGATACAACCGAATGC

ss4shof 1727 TGAGCCAGCAGCTGGTCAAGAGGGCCCTTCAGGC-TGCCCTTGCAGAGGTTGCCGACCTCC-AGAGCCTCGTTCAATCGAAGAGCTGGCA-TGGCCCAAGCAGATGCAGGGAA-AGCCTGGAGGTTGCT
comp20666_r0 1721 TGAGCCAGCAGCTGGTCAAGAGGGCCCTTCAGGC-TGCCCTTGCAGAGGCC-CGCCAGCTCGTGAAGCCTCGTTGCT-TCGAAGAGCTGGCC-TGGCCCA-CGGGATGCAGGC-AGCCTGGAGGTTGCT

ss4shof 1861 CCGCAACAGACTGGAGCCCTCCCGCCACCACCAACCTTGTCTCCGACCTGGAGGGCAGGGTGGTTCGCGTGGCTTTACATGCCAACGGATCGAAGATCTTGCCTGCTGATCGGGTGCAGTTGATG
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ss4shof 2351 GTGGCCAGGGAGG- - - - - CGGGTGGGGCGCGCCCGCGAGGAGGGCGCGCGCGAGGACGAAGGTCCGCTCGGTTGCAGCTGGTGCAGGACCTGATGACGAGCATCGGGTACCGCCCGAAGC
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ss4shof 2580 GAGCCTGCACGACCTCCTGGAGCCCTGGAGCCAGGACCGGGCCCGCGGAGTCCGATGAGGACGAGGAGGATGTCGGGAGGAGGCGCAAGCGCAAGCGGCAAGCGCCCGGGCGGAGGCGAAAGCGCTGCGC
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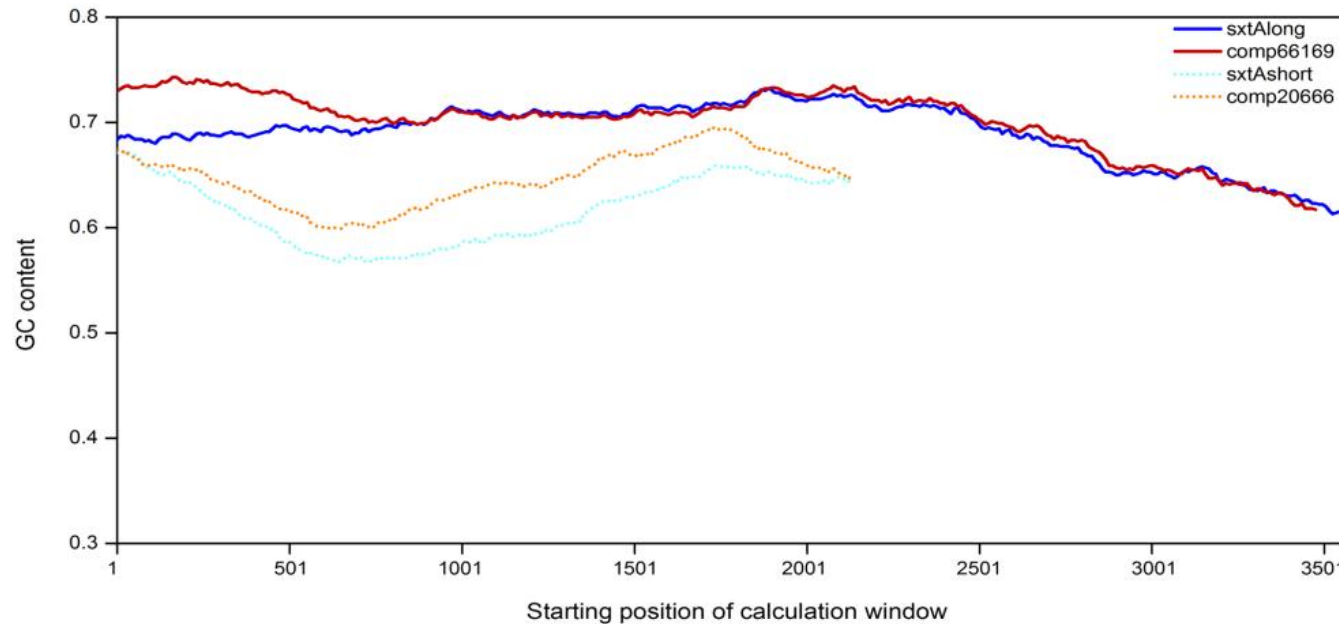
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Figure S9. Cont.

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S1. Sequences of *sxtA1* and *sxtA4* motifs in *A. catenella*

>ACHK-NT-sxtA1

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>ACHK-T-sxtA1

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GGATCTCGTGC GGCTCATTGACTCGGTCTTCGCGGGCGGGGACTTCGCGGCGCAGCCGGCGTTCGTCGTGGACACGGGGTGC GGCGACGG
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>ACHK-NT-sxtA4

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