Supporting Information

Appendix **A The overall flow of miRNA library construction and Solexa high-throughput sequencing.** Fractions (18～30 nt) of total RNA were excised and purified with 15% PAGE. Then, 3' and 5' adaptors were ligated using T4 RNA ligase enzyme. The adaptor-ligated small RNAs were subjected to reverse transcription and the cDNA was further amplified. The PCR products were purified and used for sequencing analysis on a Solexa Genome Analyzer

Appendix **B The flow of bioinformatics analysis for Solexa high-throughput sequencing data.** The clean reads were processed for computational analysis after removing the low quality reads and adaptor sequences. The expression and distribution profiles of clean reads were analyzed by mapping to the Ovis aries genome. Afterwards, the standard bioinformatics analysis was used to annotate the clean tags into different categories and take those without annotation to any category to predict the novel miRNA

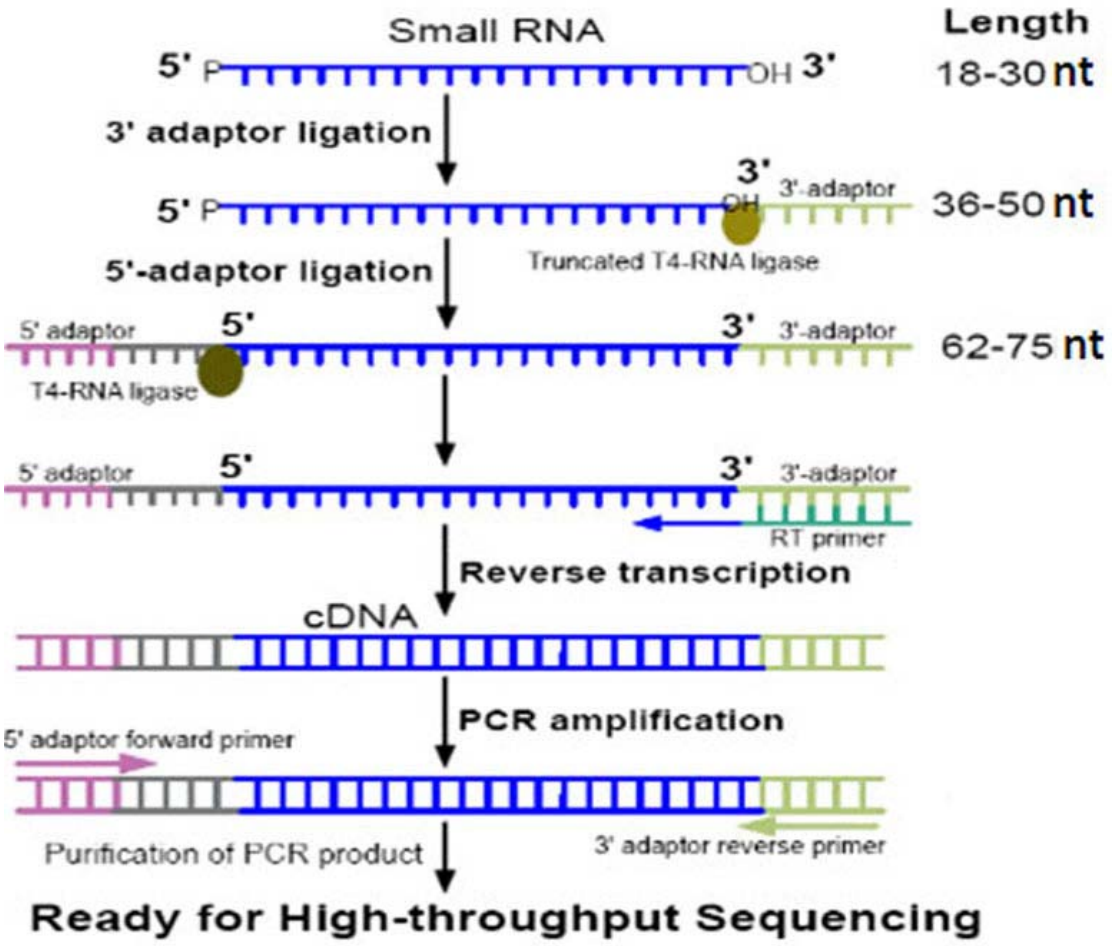
Appendix **C miRNA expression profiles in ovary and testis.**

Appendix **D Characteristics of novel miRNA candidates.**

Appendix **E Target genes for the differentially expressed potential miRNAs in ovary and testis predicted using MIREAPv0.2.** From left to right for each miRNA: miRNA name, miRNA length, target name, target length, match position, MFE, P-value, prediction value.

Appendix **F KEGG Pathway annotations for the predicted target genes.**

Appendix **G GO annotations for the predicted target genes.**



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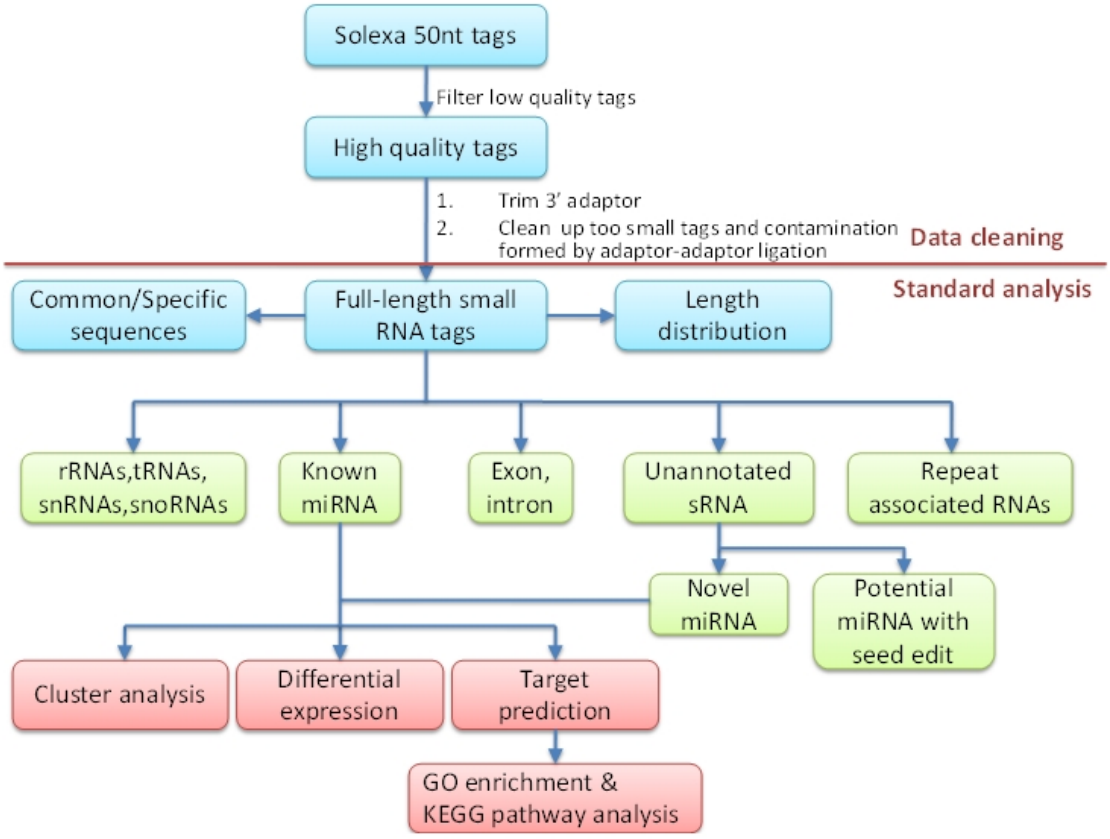

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