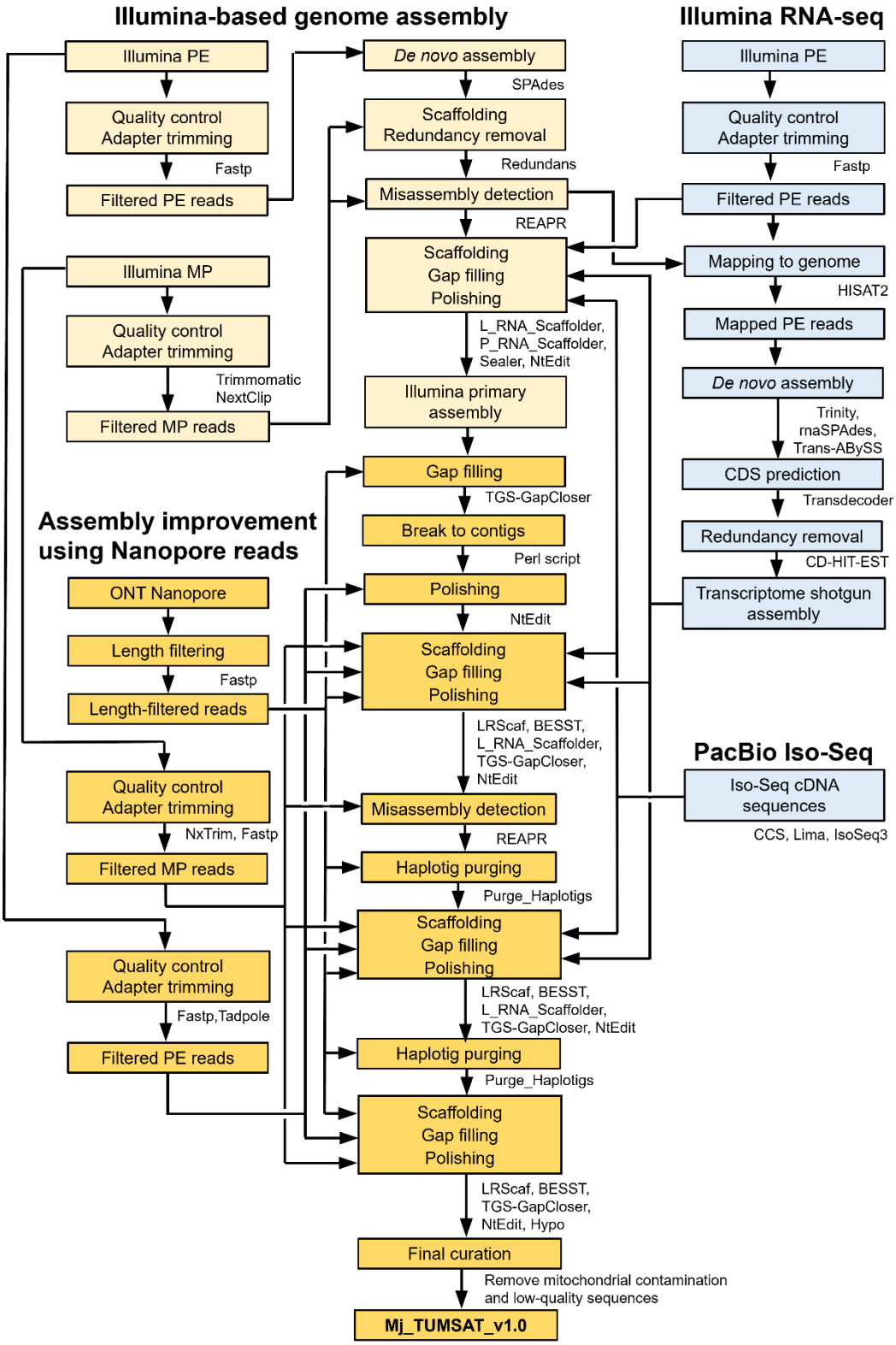
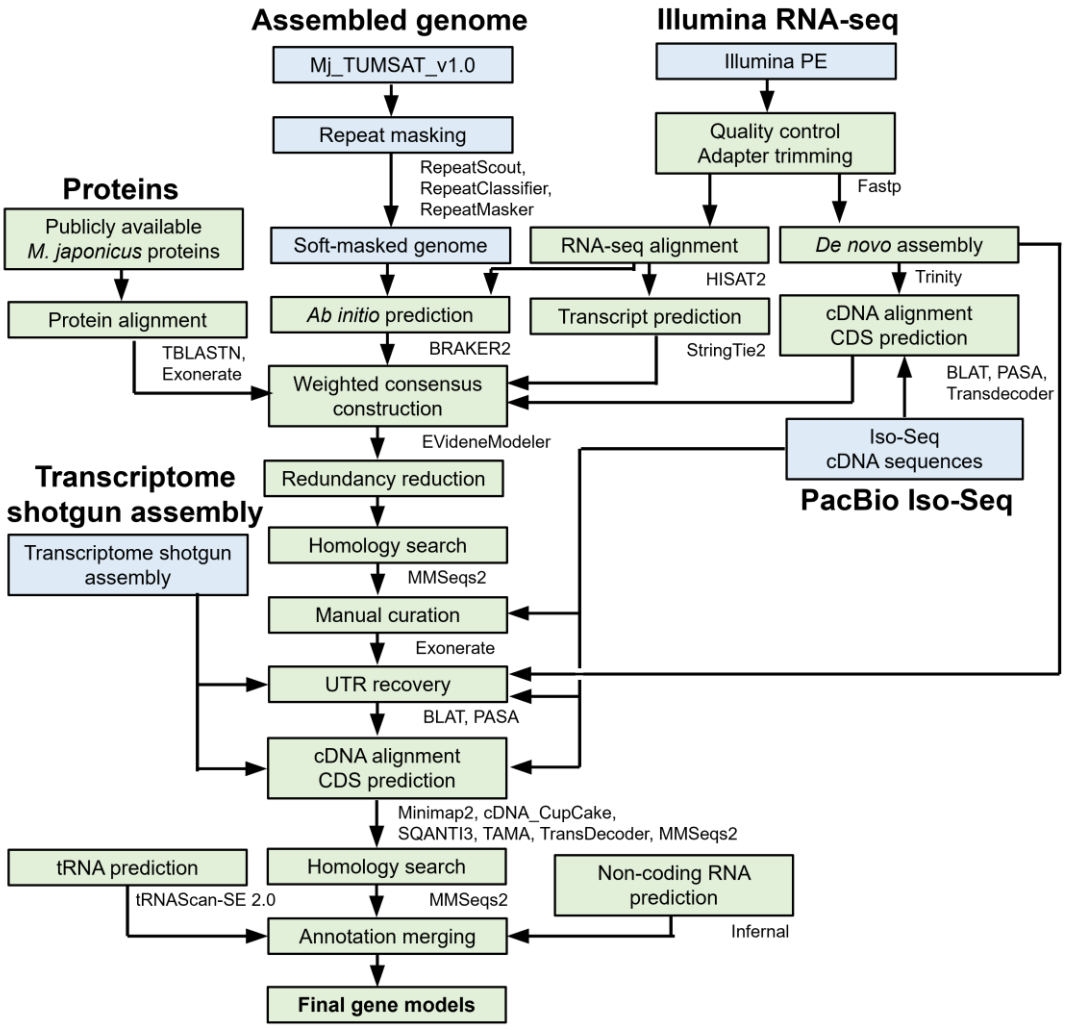
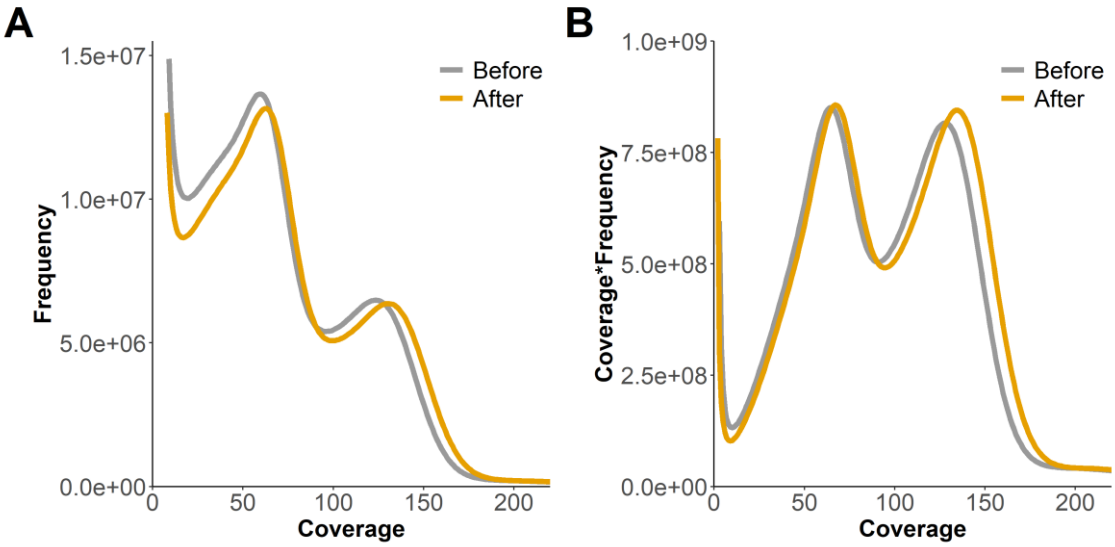


Supplementary Figure S1. ***M. japonicus*** **genome and transcriptome assembly workflow**



Supplementary Figure S2. *M. japonicus* genome annotation workflow



Supplementary Figure S3. 23-mer distributions of Illumina paired-end reads from the muscle library before and after error-correction by Tadpole

(A) Y-axis: Frequency; (B) Y-axis: Coverage*Frequency.