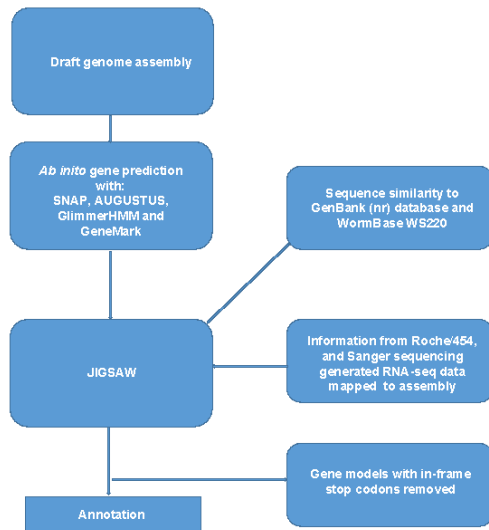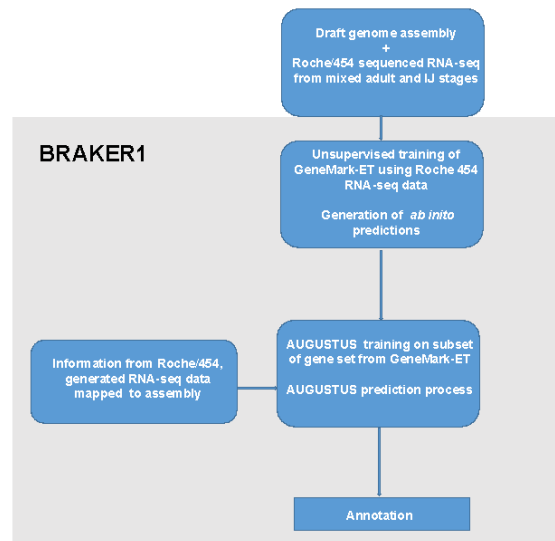# Supplementary File 9. BRAKER1 and JIGSAW annotation pipelines.

Published annotation method

Annotation method used here

Both methods used masking of the draft assembly before annotation, however the details of masking in the published methods are not explicit [13]. Of note, the published annotation method (left) made use of two transcriptome sets generated by different sequencing methods (Sanger sequencing and Roche 454 sequencing) from a mixture of adult and infective juvenile stages [13]. Only one of these publically available sets (the Roche 454 set) was selected for re-annotation with BRAKER1 as the coverage of those in the Sanger sequencing set was incompatible with the BRAKER1 pipeline (right).