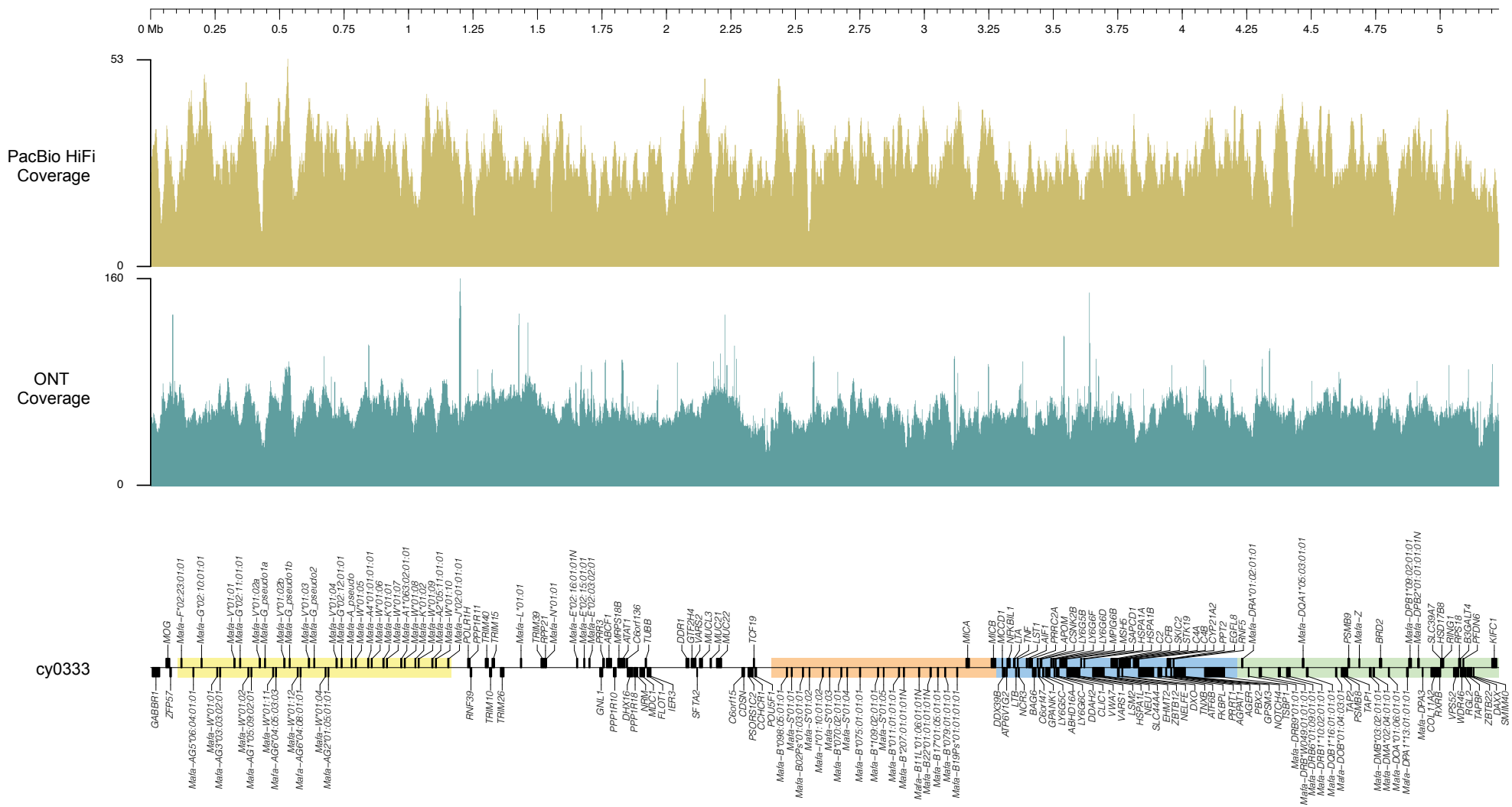

Supplemental Fig. S4. Oxford Nanopore and PacBio HiFi read coverage for cy0333 MHC assembly

Coverage was determined by mapping extracted FASTQ reads against the error-corrected, merged assembly using minimap2, and plots were generated using R. Length is depicted in Mb. Annotations for all protein-coding genes plus a subset of nonclassical MHC class I and class II pseudogenes are depicted on the bottom track. Coding regions are depicted by black boxes on top of or below the assembly. The class I A, class I B, class III, and class II regions are depicted by yellow, orange, blue, and green highlighting, respectively.