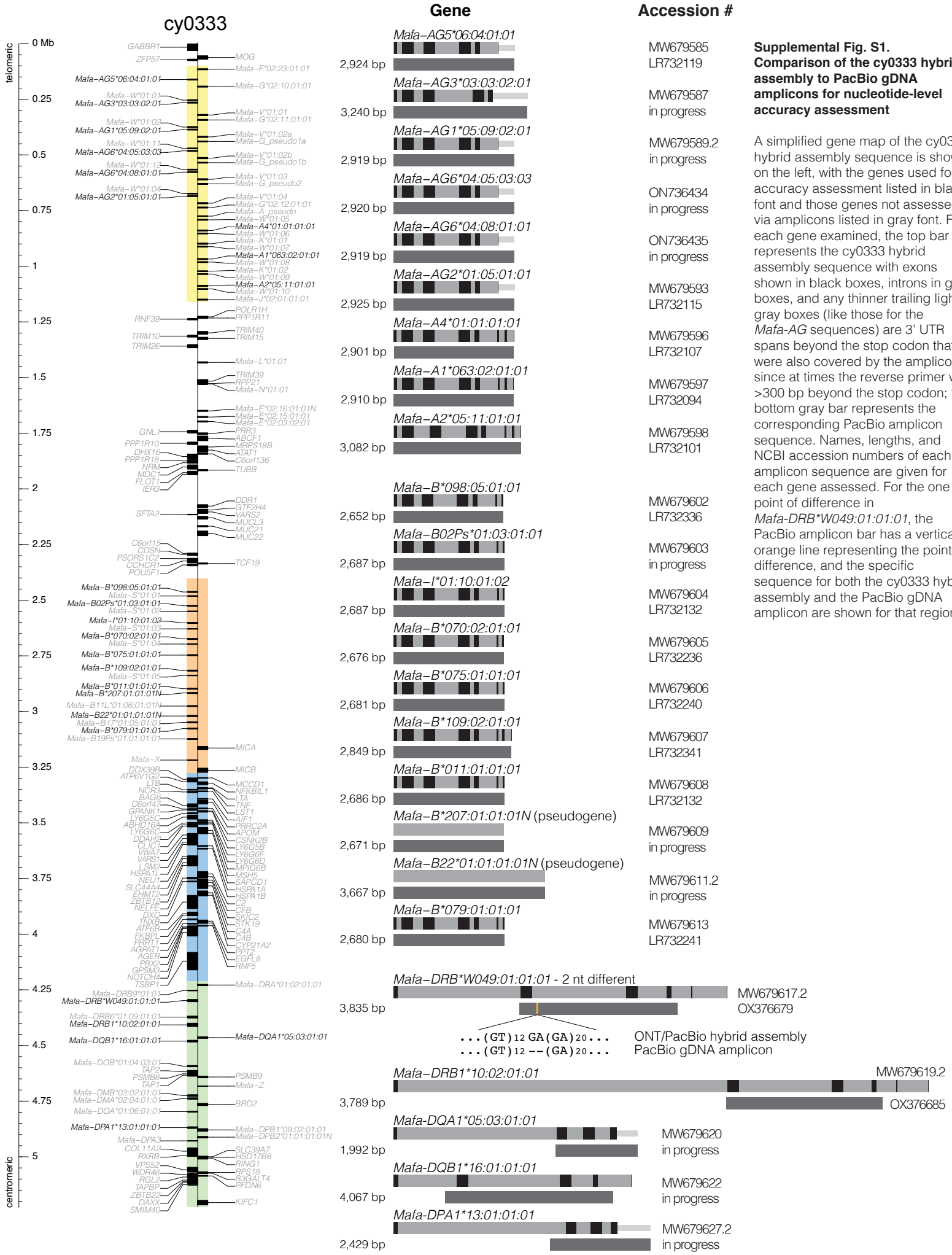

Supplemental Fig. S1. Comparison of the cy0333 hybrid assembly to PacBio gDNA amplicons for nucleotide-level accuracy assessment

A simplified gene map of the cy0333 hybrid assembly sequence is shown on the left, with the genes used for accuracy assessment listed in black font and those genes not assessed via amplicons listed in gray font. For each gene examined, the top bar represents the cy0333 hybrid assembly sequence with exons shown in black boxes, introns in gray boxes, and any thinner trailing light gray boxes (like those for the *Mafa-AG* sequences) are 3' UTR spans beyond the stop codon that were also covered by the amplicon since at times the reverse primer was >300 bp beyond the stop codon; the bottom gray bar represents the corresponding PacBio amplicon sequence. Names, lengths, and NCBI accession numbers of each amplicon sequence are given for each gene assessed. For the one point of difference in *Mafa-DRB*W049:01:01:01*, the PacBio amplicon bar has a vertical orange line representing the point of difference, and the specific sequence for both the cy0333 hybrid assembly and the PacBio gDNA amplicon are shown for that region.