FIGURE S1.—Southern analysis of strain N4 for assessment of the copy number of Y-b. (A) Schematic genomic structures of several versions of the CBP gene. Asterisked double underline indicates the position of Southern probe for (B). (B) Southern analysis. Genomic DNA was fully digested with EcoRV. The amount of DNA was based on the absorbance at 260 nm. The lengths of the bands for Y-a, Y-b and +Y-a were predicted to be 8200, 5890, and 10320 bp, respectively. The band intensity of Y-b in the lane of 2 μg digested genomic DNA of strain N4 was comparable to that of Y-a in the lane of 6 μg digested genomic DNA of strain N4 and that of +Y-a in the lane of 6 μg digested genomic DNA of strain FL501 (+Y/Y), supporting our estimation that the copy number of Y-b in strain N4 is three and that of the others is one. (C) Ethidium bromide staining of digested genomic DNA as a loading control.
**FIGURE S2.**—Additional genotyping of CBP in multiple *B. mori* strains and *B. mandarina* individuals. (A) Schematic genomic structures of several versions of the CBP gene. Arrows indicate the location of PCR primers. (B) Genotyping of CBP in addition to fig. 3C. While amplification of approximately 80 bp nucleotide was expected from the UAS-CBP transgene in strain UAS-CBP by Primer-149 and -150, it would be difficult to distinguish it from primer dimmers. (C) Re-electrophoresis to show the presence of Y-a in *B. mandarina* no. 4.