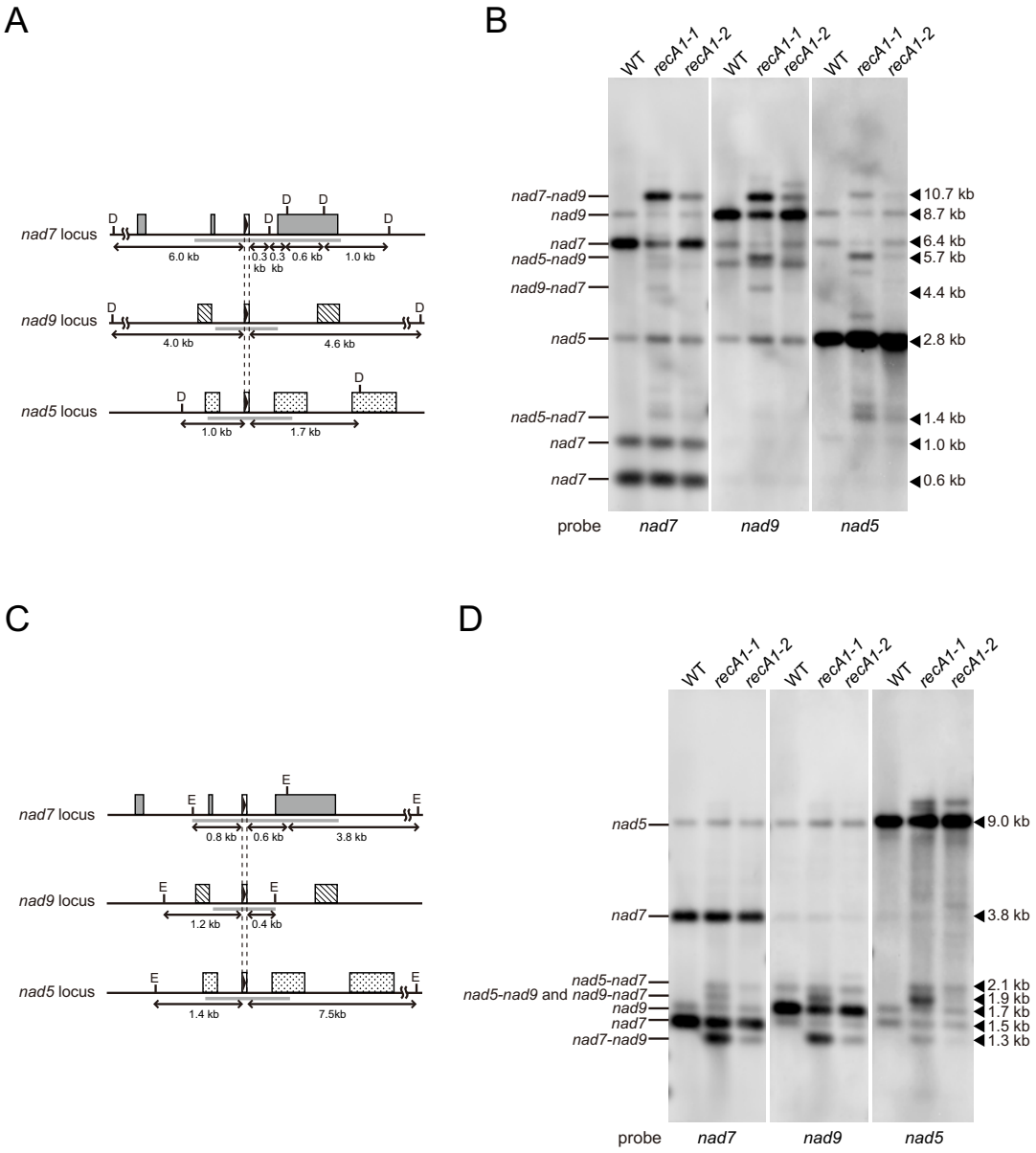
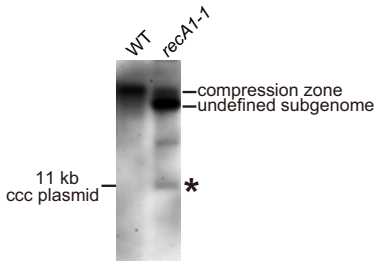


Supplemental Figure 1. Multiple Rearrangements of *RECA1* disruptant mtDNA.

(A) and **(C)** Schematic representation of the structures of the three copies of repeats located at the *nad7*, *nad9* and *nad5* loci and the flanking region. The repeats (78-84 bp, 96-100% identity) are indicated by the triangles in the boxes. The probes used in **(B)** and **(D)** are indicated by bold gray line. The *Dra*I- and the *Eco*RI recognition sites are indicated by D and E, respectively.

(B) and **(D)** Analysis of the mtDNA configuration at the *nad7*, *nad9* and *nad5* loci. Hybridizations using the probes indicated below the blots were performed with total genomic DNA of the WT background and of two *RECA1* null disruptants (*recA1-1* and *recA1-2*) digested with *Dra*I **(B)** or *Eco*RI **(D)**. The presumed structures and the lengths of the major bands are indicated on the left and right, respectively.



Supplemental Figure 2. Repeat-mediated Deletion of *RECA1* Disruptant mtDNA. Hybridization using the probe designed to detect the genomic region between *nad9* and *nad7* (see Figure 5C) was performed with total genomic DNA of the WT background and the *RECA1* null disruptant (*recA1-1*) extracted by the alkaline lysis method. The asterisk indicates subgenomic molecules that comigrated with an 11 kb covalently closed circular plasmid.