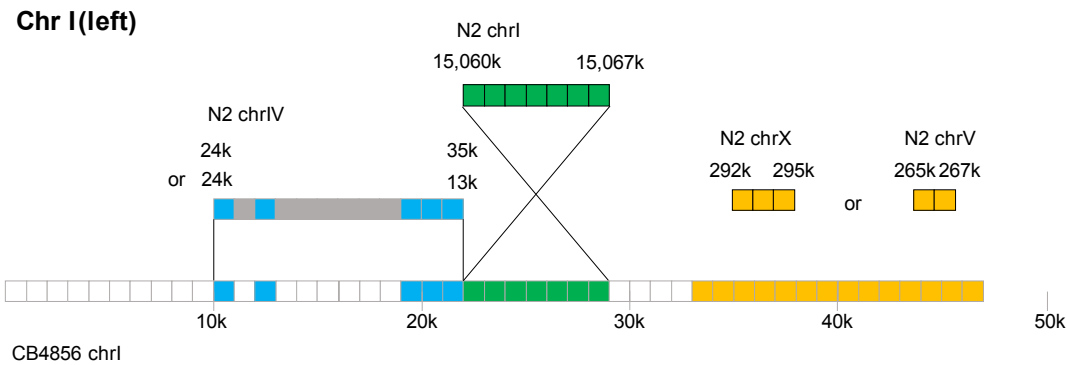
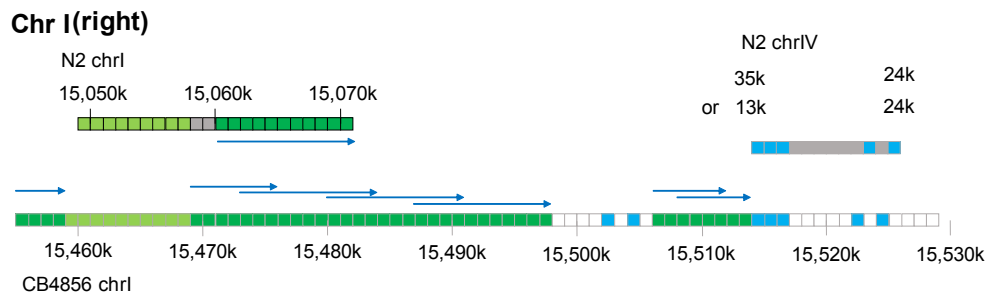
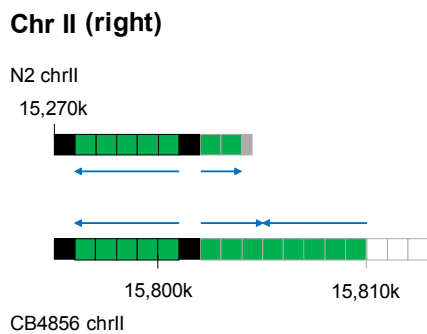
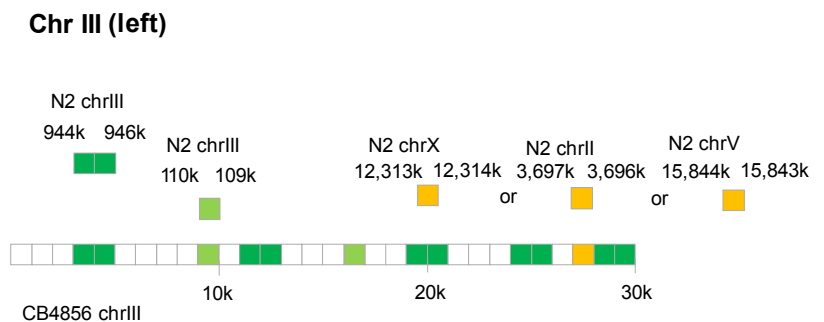
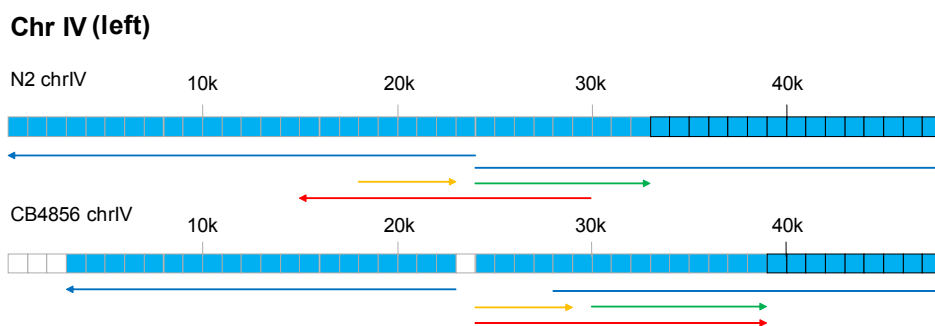
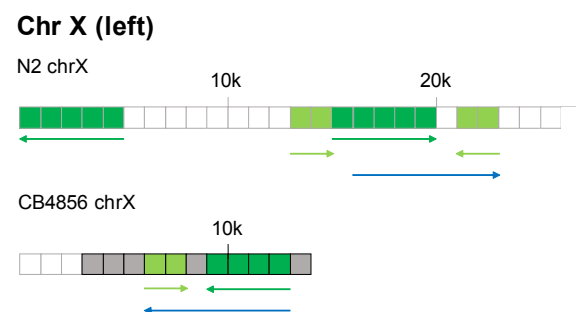


**A**

Location	N2	CB4856	Location	N2	CB4856
Chr IL	50,235	50,305	Chr IVL	5,937	4,396
Chr IR	64,274	24,112	Chr IVR	16,102	16,613
Chr IIL	3,823	3,803	Chr VL	3,356	3,354
Chr IIR	23,137	13,803	Chr VR	200,000	200,000
Chr IIIL	176,124	176,099	Chr XL	29,526	36,985
Chr IIIR	1,406	8,309	Chr XR	4,113	4,111

**B****C****D****E****F****G**

**Supplemental Figure S10. CB4856 subtelomeres.** (A) The number of unaligned bases of each subtelomere (200 kb) between N2 and CB4856 chromosomes obtained using nucmer. (B-G) Schematic representation of BLAST results of unaligned bases in each CB4856 subtelomere of Chr IL (B), Chr IR (C), Chr IIR (D), Chr IIIL (E), Chr IVL (F), and Chr XL (G) to the N2 genome. White blocks represent regions without any homology found using BLAST, and other colored blocks represent aligned regions with homology detected longer than 600 bp. Each block represents 1 kb of genome length and alignments with less than 600 bp in length are not included. Arrows indicate directions.