

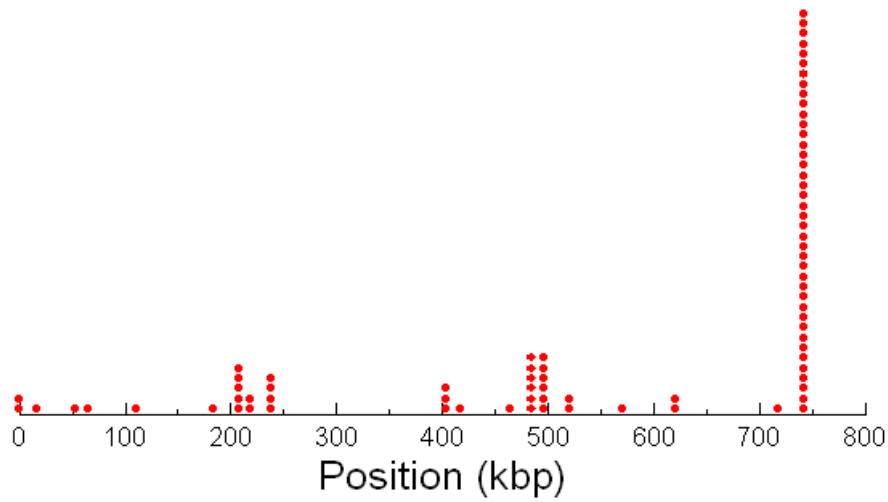
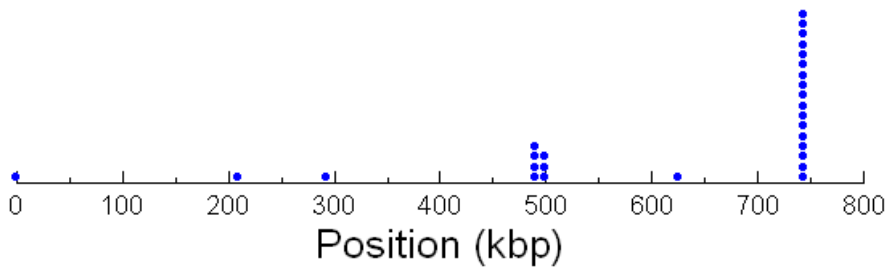
A**B**

Figure S1 Assembly errors in contig JSAE01000257 (MHAP assembly). Assembly errors were identified by comparison with Illumina short reads using two methods. (A) Unmatched *k*-mers (YGS program; see Material and Methods). (B) Runs of zero Illumina coverage (*bwa* alignment). The *Mst77Y* region, which spans from 85kb to 181kb, has very few errors: the two methods detected only one error (an unmatched *k*-mer caused by a C/T substitution at position 110,630), whereas detailed inspection with the *IGV* browser revealed a T insertion at 85,619 (in a run of five T). The two errors are in intergenic regions; note that both could actually be residual polymorphisms or new mutations in the sequenced strain. Contig size is 747 kb.