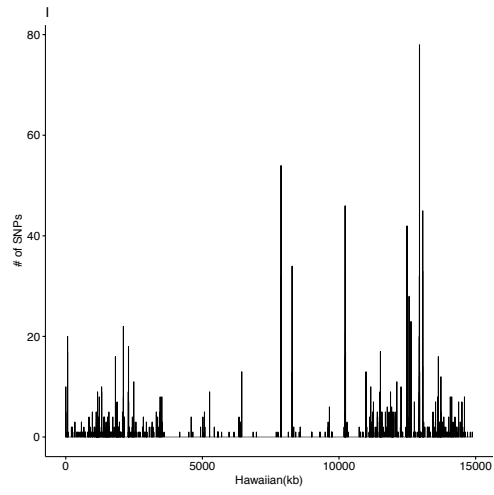
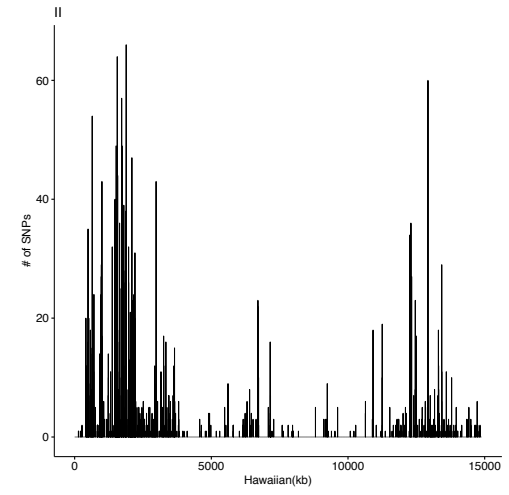
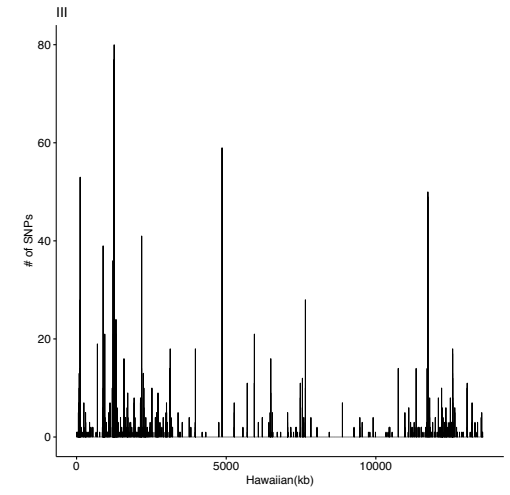
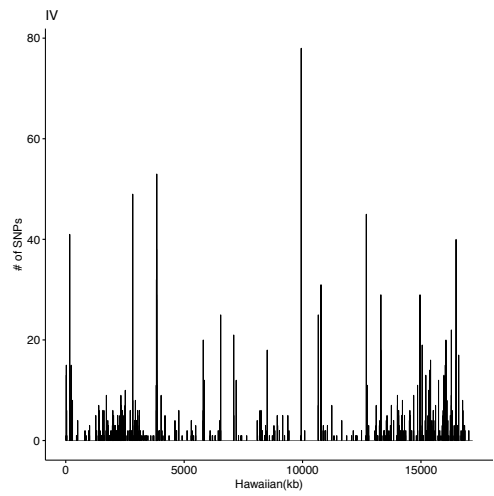
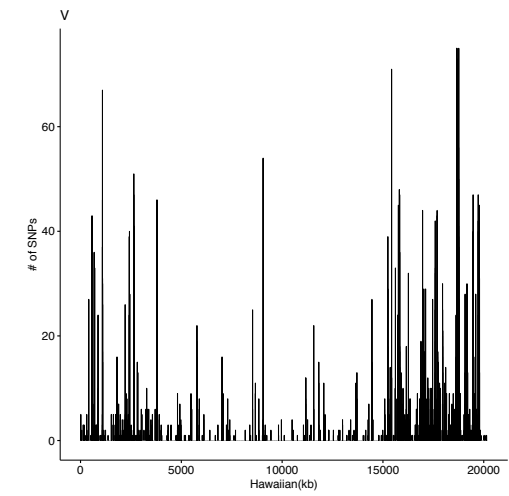
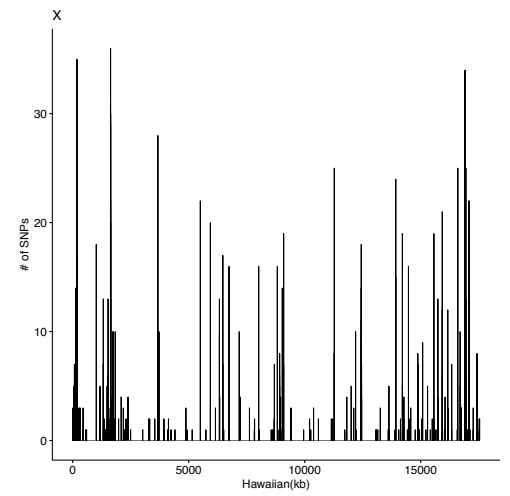
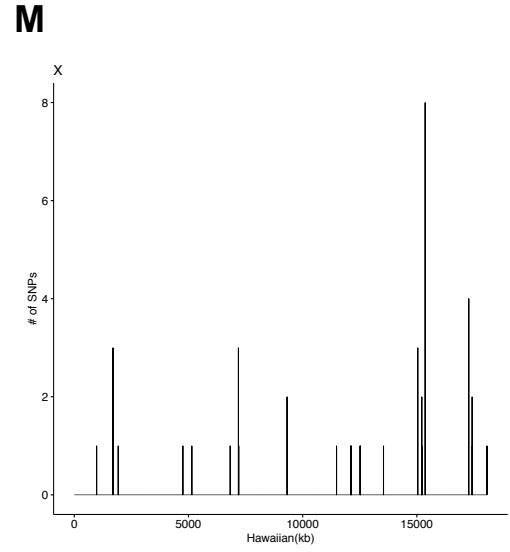
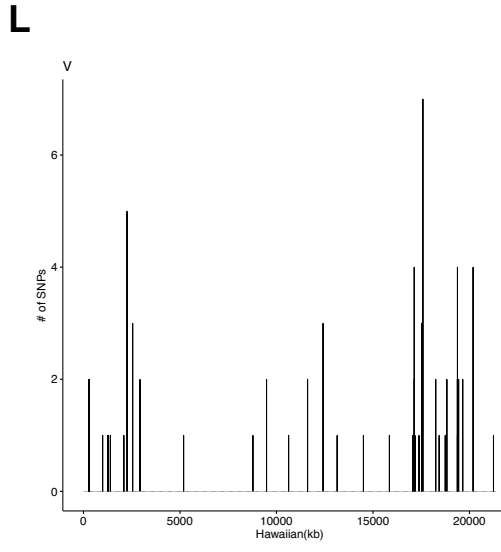
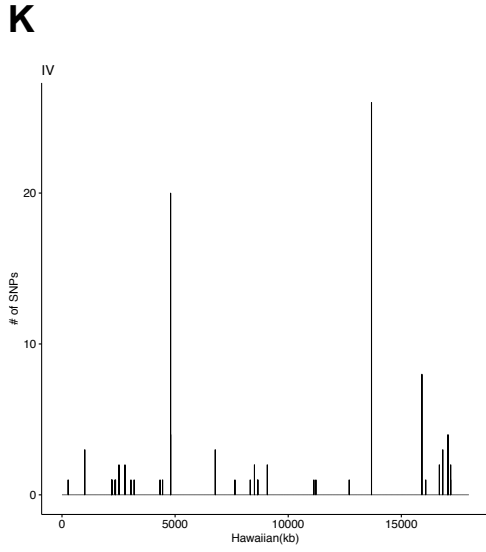
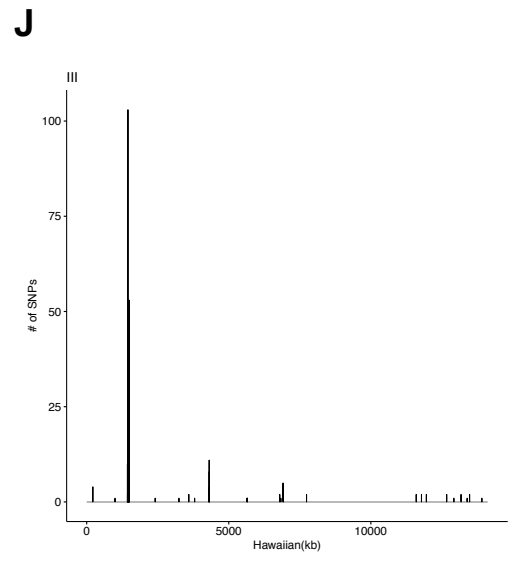
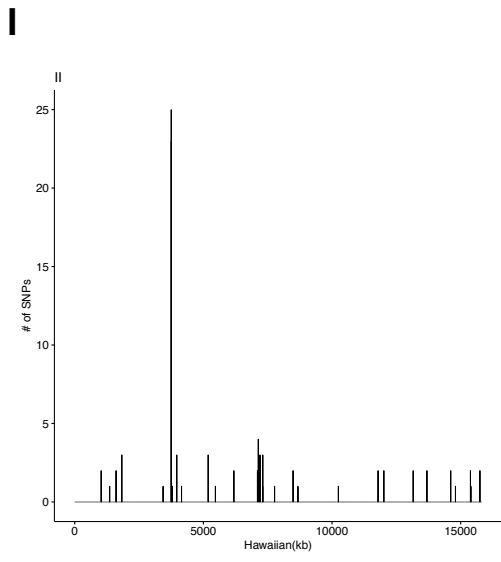
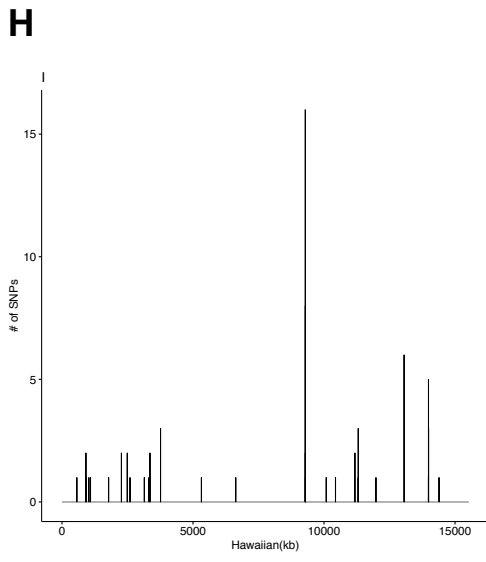


**A**

	Thompson genome	Kim genome
SNP	19827	987
Indel	8336	352

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



**Supplemental Figure S3.** Variant call by CB4856 HiSeq short read at both genomes. (A) Number of SNP and Indel in both genomes. (B-M) The chromosomal distributions of short read sequencing align against the Thompson genome (B-G), or the Kim genome (H-M).