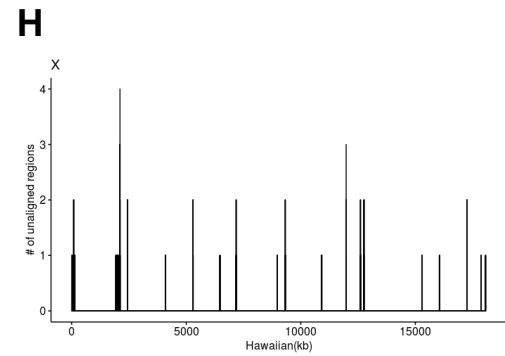
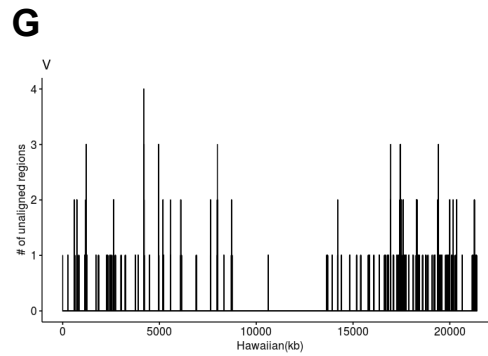
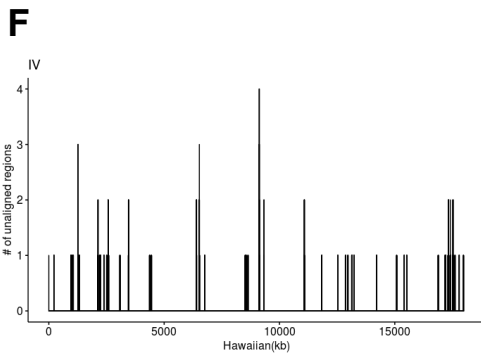
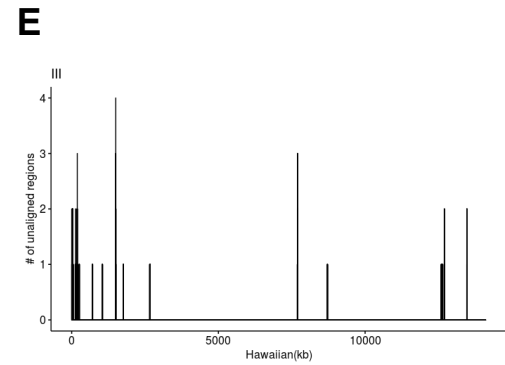
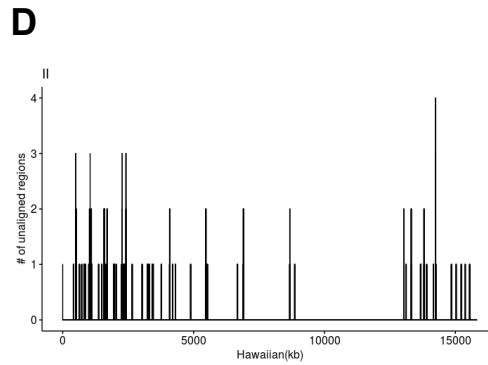
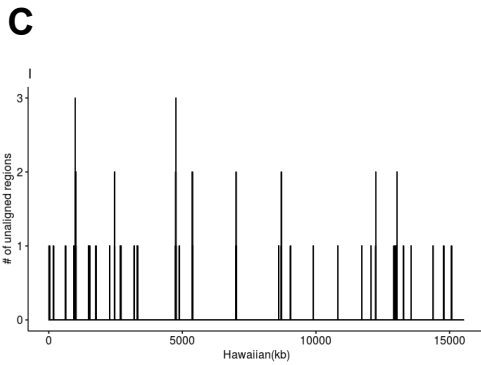


**B**

Variant type	Total base pairs
Insertion (Ins)	508,763
Deletion (Del)	58,165
<b>Ins-Del</b>	<b>450,598</b>
Tandem_expansion (Texp)	557,898
Tandem_contraction (Tcont)	47,733
<b>Texp-Tcont</b>	<b>510,165</b>
Repeat_expansion (Rexp)	999,426
Repeat_contraction (Rcont)	319,997
<b>Rexp-Rcont</b>	<b>679,429</b>
Unaligned base (Kim et al., 2019)	<b>4,019,041</b>
Unaligned base (Thompson et al., 2015)	<b>607,896</b>
<b>Total change</b>	<b>5,051,337</b>



**I**

Method	Subset	Subset	Intersection	Intersection
Offset	`+/- 0.5kb	`+/- 1kb	`+/- 0.5kb	`+/- 1kb
I	82.38%	84.63%	89.55%	90.16%
II	85.19%	87.59%	92.22%	92.41%
III	81.36%	85.04%	89.50%	90.81%
IV	82.55%	85.10%	90.59%	90.78%
V	85.77%	87.85%	91.16%	91.71%

**Supplemental Figure S6.** Direct comparison of the Kim genome and the Thompson genome. (A) SVs in the Kim genome with the Thompson genome as a reference. (B) Length of SVs in the Kim genome. (C-H) Distribution of unaligned bases. (I) Comparing SVs found in the Thompson genome and the Kim genome. ‘Subset’ case means an SV from one genome are completely included within an SV of the other genome, and the ‘intersection’ case means that the two SVs partially overlap each other.