

Supplemental Figure 1 Distribution of BAC clone insert lengths. Paired BAC end sequences aligned within the same genomic sequencing scaffold, providing an estimate of their physical size. Apparent insert lengths ranged from 1 kb to 107 kb, distributed bimodally, with 79% of the clones having mean length of 70 ± 10 kb and 21% of clones having a shorter mean length of 17 ± 10 kb (parameters estimated by Maximum Likelihood of a mixture of two Normal distributions, predicted distribution shown by dotted line). This length distribution allows reliable estimates of physical gap sizes to be calculated adjacent scaffold spanned by BAC clones.

