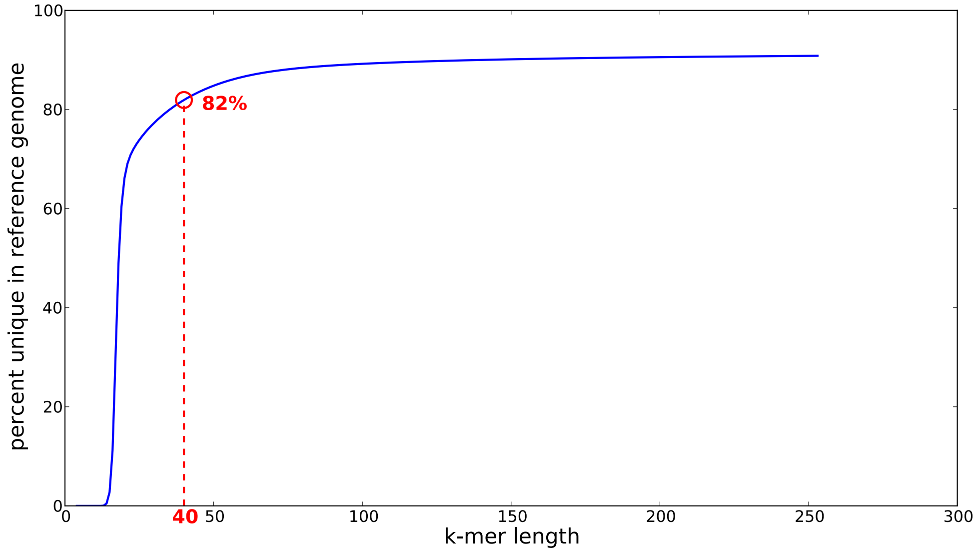

Supplemental Figure S1. Percent of genome unique as a function of k-mer length. A by-product of the suffix array used for mapping MUMs is the 'mappability' of each position in the genome. By using this data structure, we determine the proportion of the reference genome that is uniquely mappable for each k-mer length. For example, 82% of the reference genome is unique at a k-mer length of 40.