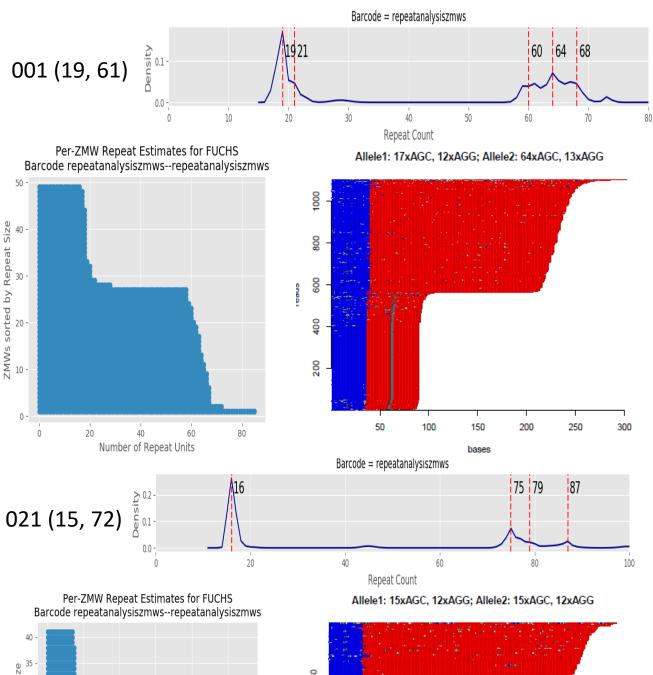
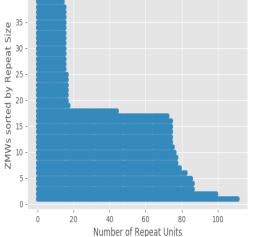
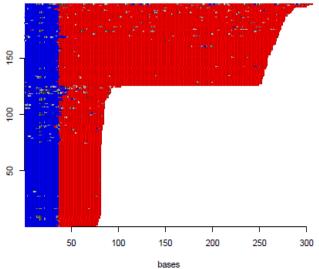
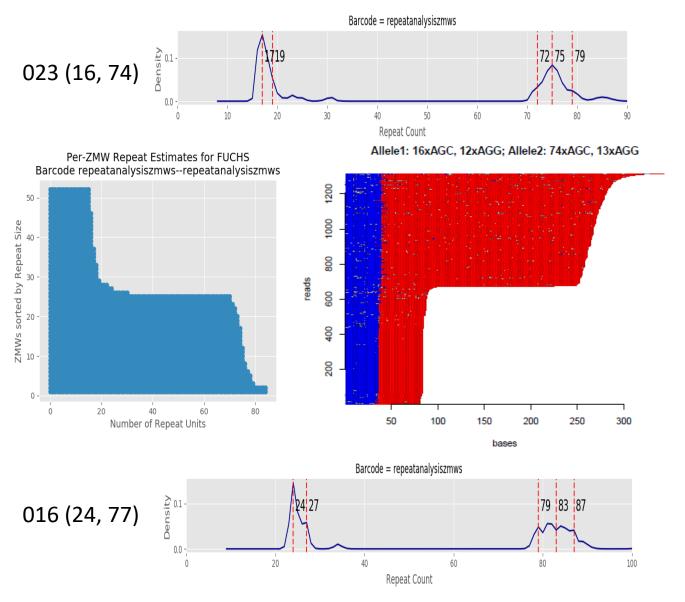
Supplementary Figure 2



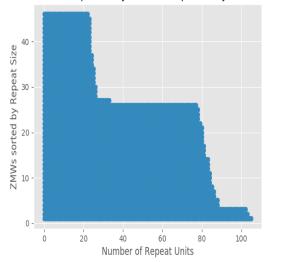
reads



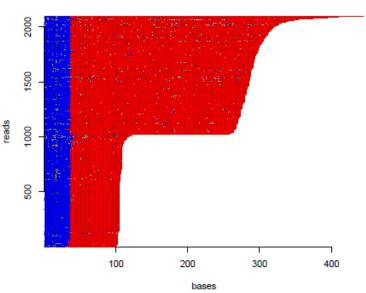


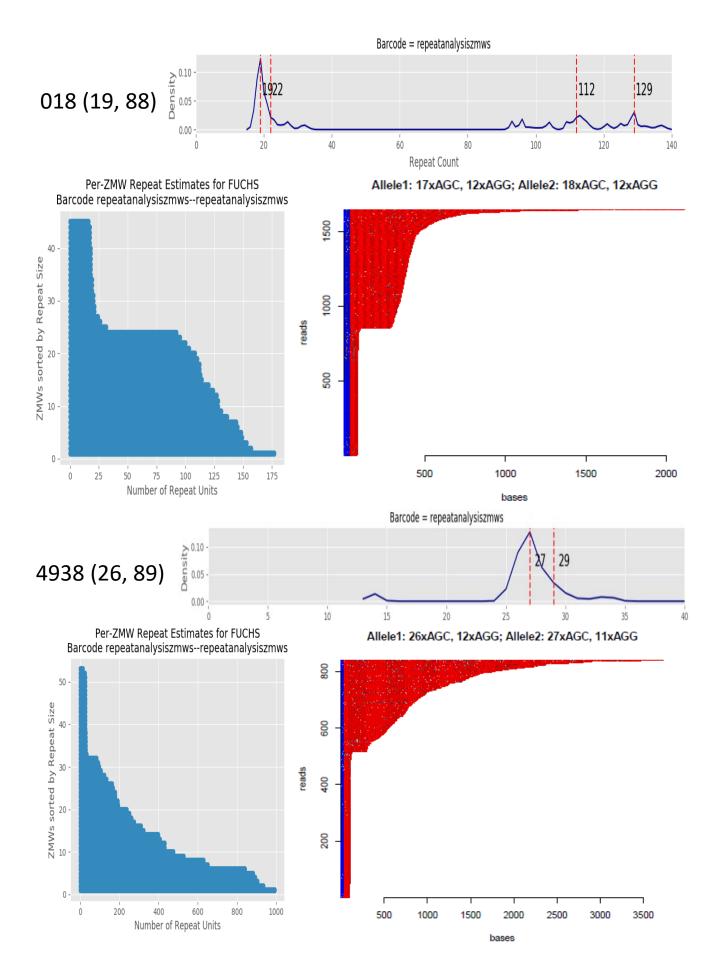


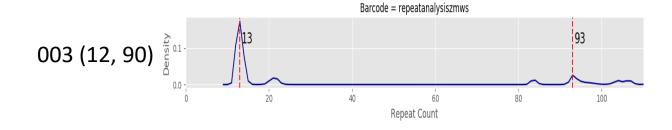
Per-ZMW Repeat Estimates for FUCHS Barcode repeatanalysiszmws--repeatanalysiszmws

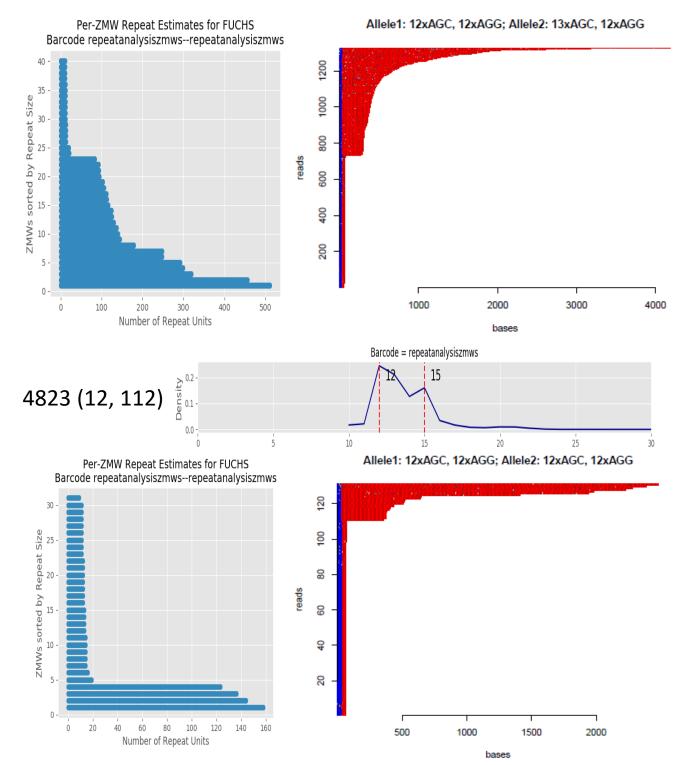


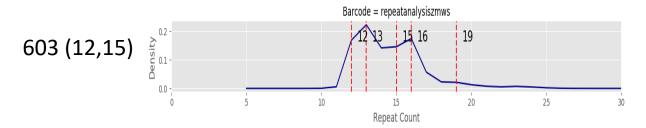
Allele1: 23xAGC, 12xAGG; Allele2: 85xAGC, 12xAGG



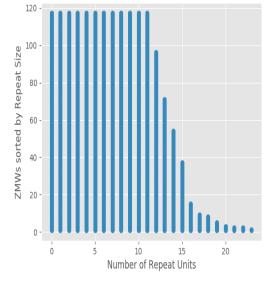




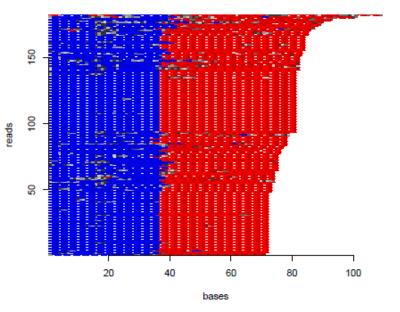


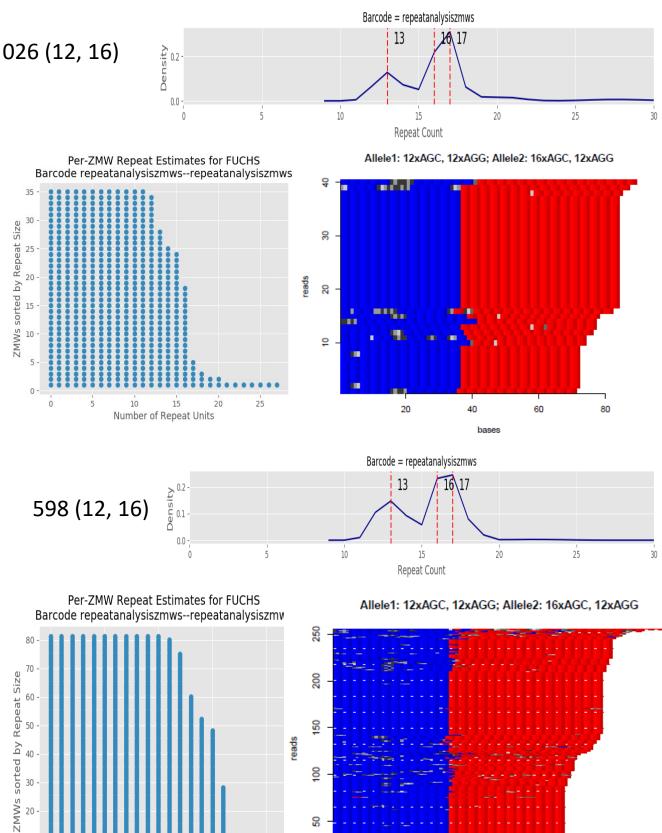


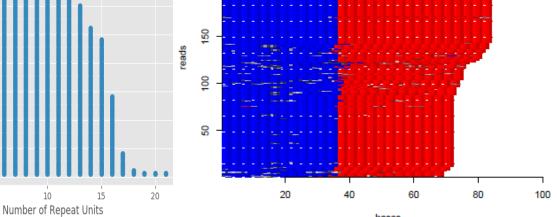
Per-ZMW Repeat Estimates for FUCHS Barcode repeatanalysiszmws-repeatanalysiszmws



Allele1: 12xAGC, 12xAGG; Allele2: 15xAGC, 12xAGG







bases

Supplementary Fig. 2. Assessment of repeat length by long-read SMRT sequencing for additional samples. The repeat count histograms, ZMW vs repeat length plots and HTT repeat analysis plots are provided for each sample in this study as described in the legend to Fig. 1. In each case, the STR results for that sample are given in parentheses immediately after the sample name.