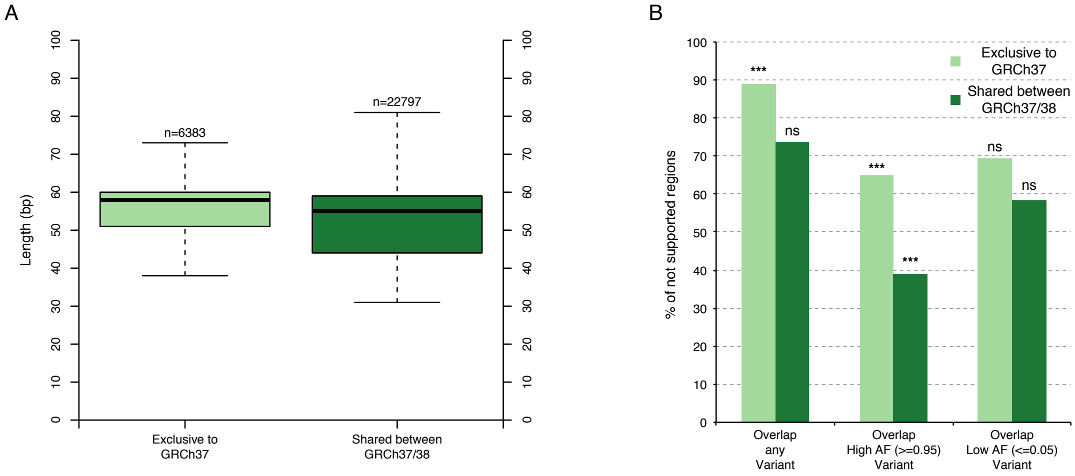

Supplemental Fig 2. Analysis of not supported regions in GRCh37. (A) Size distribution of regions covered by unsupported reference 31-mers (light green: exclusive to GRCh37, dark green: shared with GRCh38) (B) Bar plot showing the fraction of unsupported regions in the GRCh37 reference assembly containing high or low allele frequency variants. Significance testing was based on selecting 1,000 random regions from the genome.