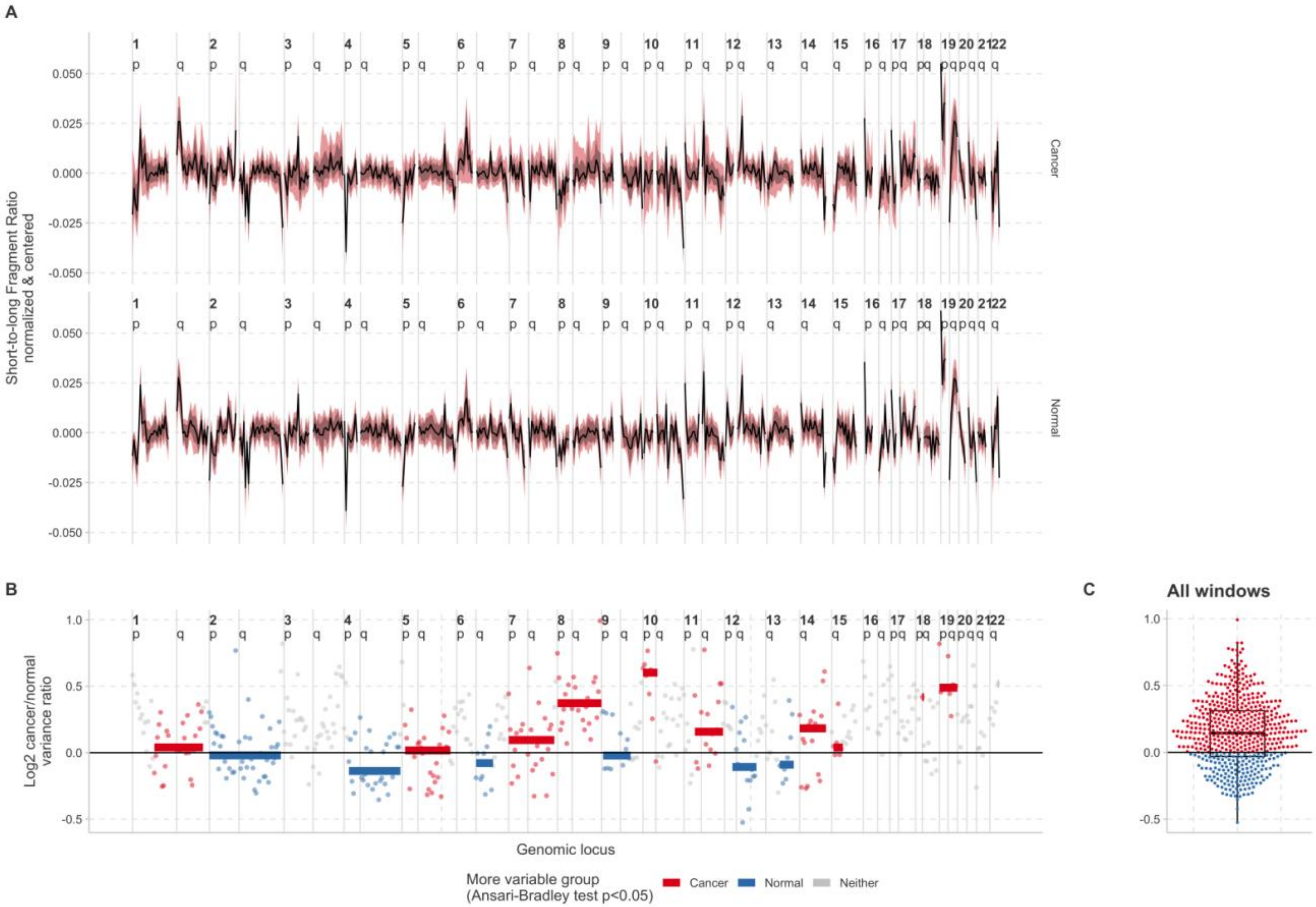
Supplementary Figure 5



Supplementary Figure 5. Cell-free DNA from cancer patients demonstrates greater fragment length variability. (A) Genome wide fragment lengths were computed and averaged within 5 megabase windows. Normalized short-to-long fragment ratios were calculated. Shaded confidence intervals represent 80% and 95% of the data. (B) The variance of mean fragment lengths across patients were compared and the log fold change between cancer and normal variances are shown for each window. Windows with significantly different variance between cancer and normal were identified using non-parametric Ansari-Bradley tests. Neighbouring windows were combined using Comb-p into regions. This revealed greater variability in cancer sample fragment lengths spanning 56.2% of the autosomal genome. (C) Beeswarm plot of fragment length variability. The median cancer window had 30.3% [range: -41.1, 228.] more fragment length variability in samples from cancer patients than normal controls.