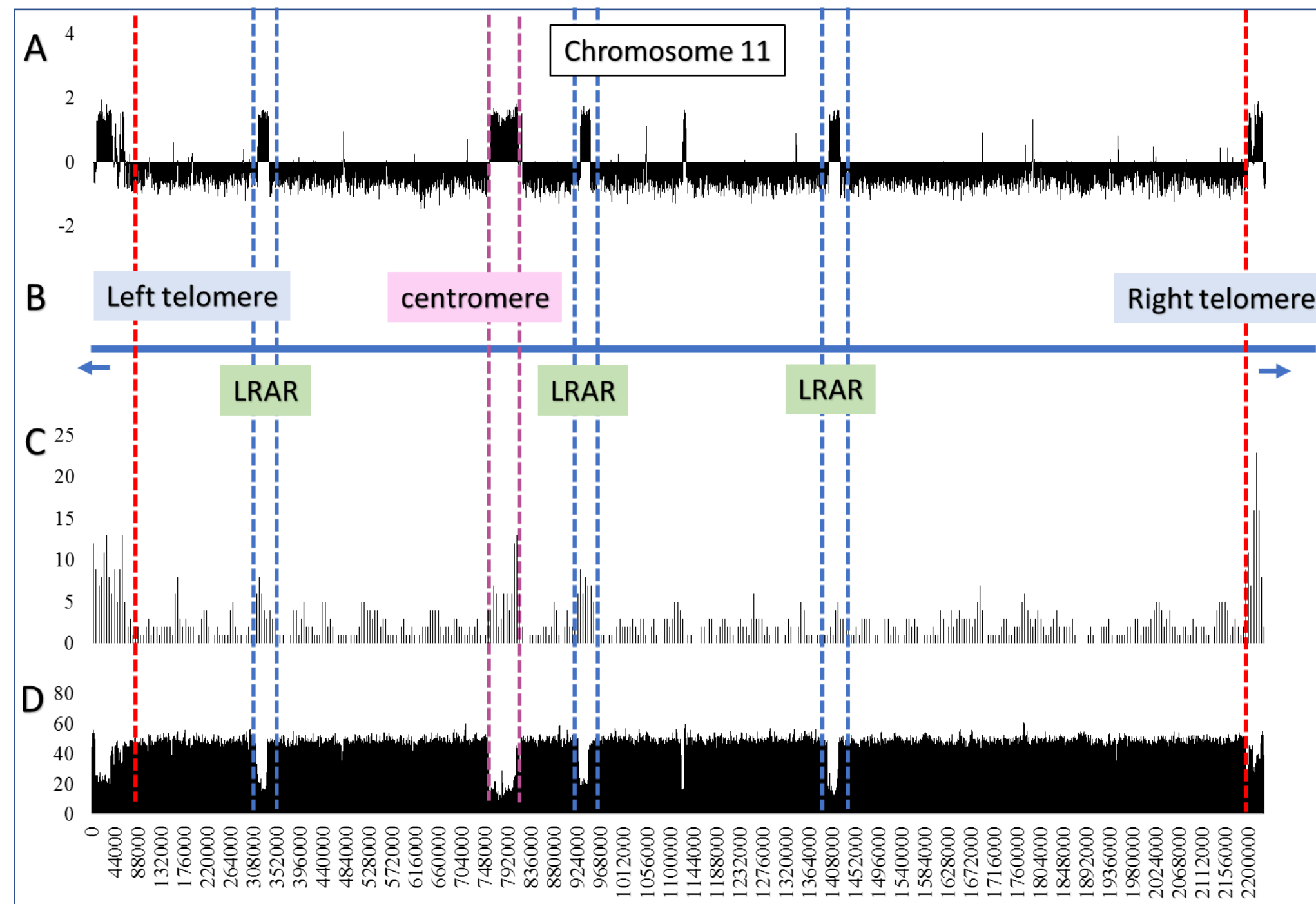
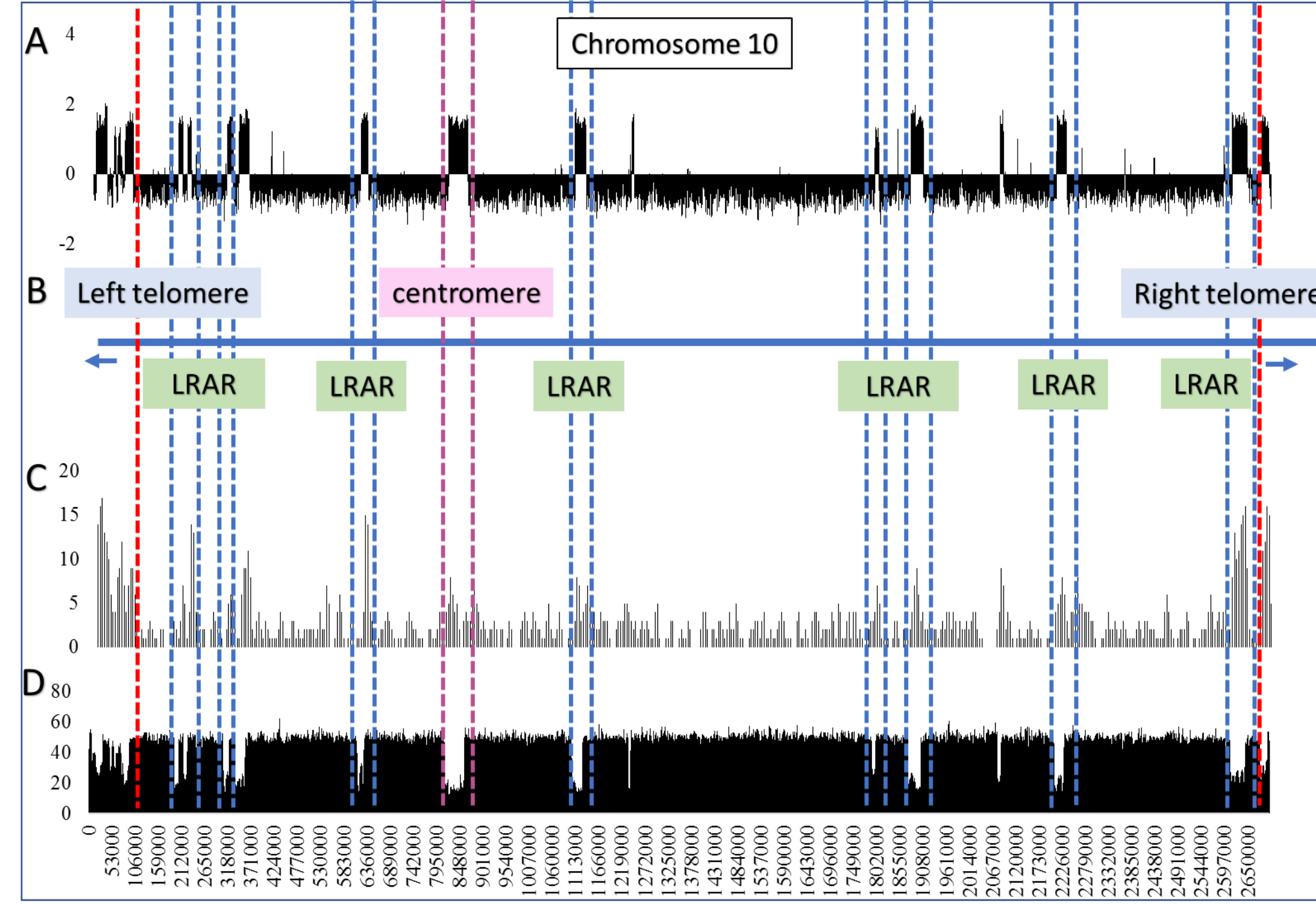
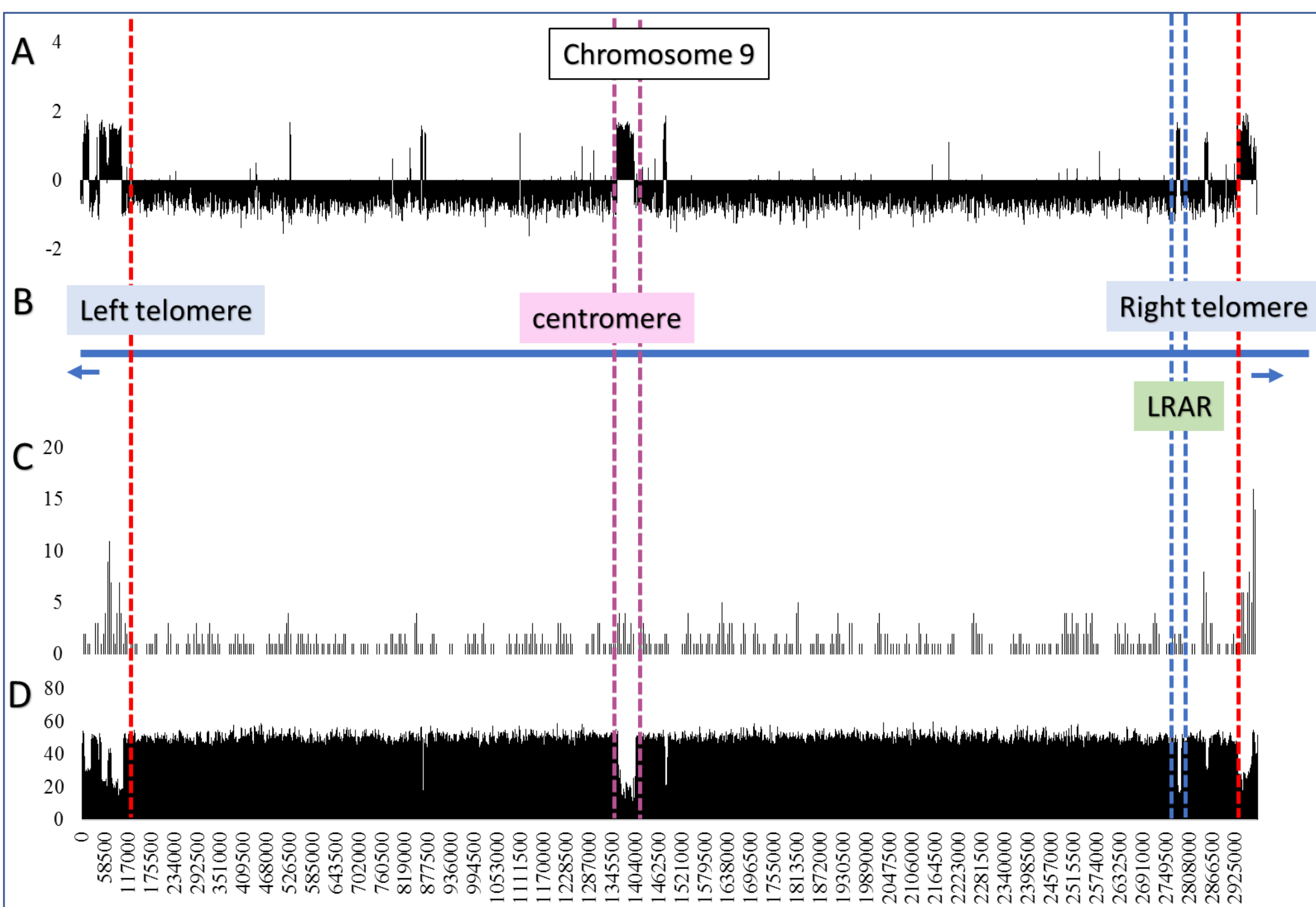
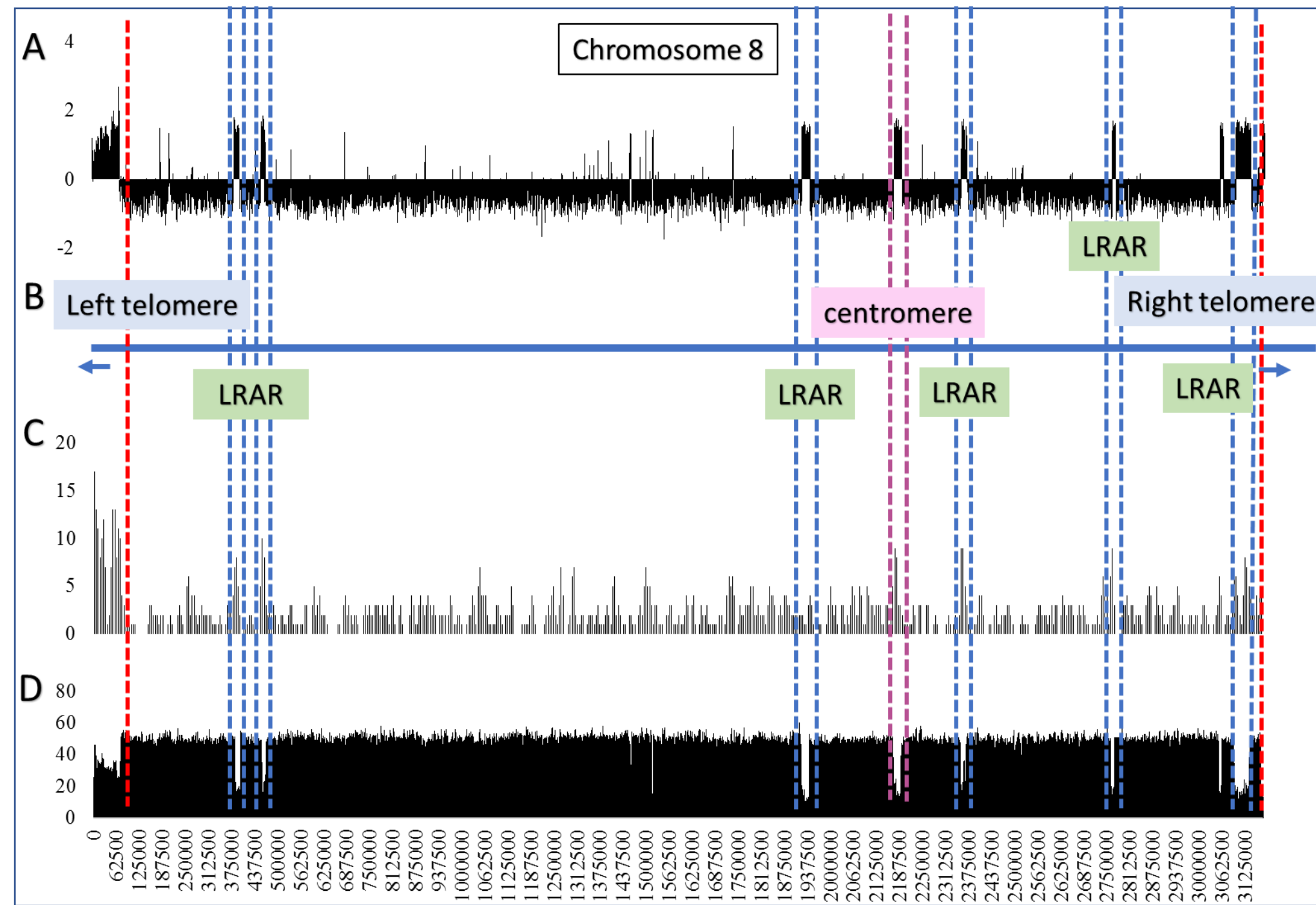
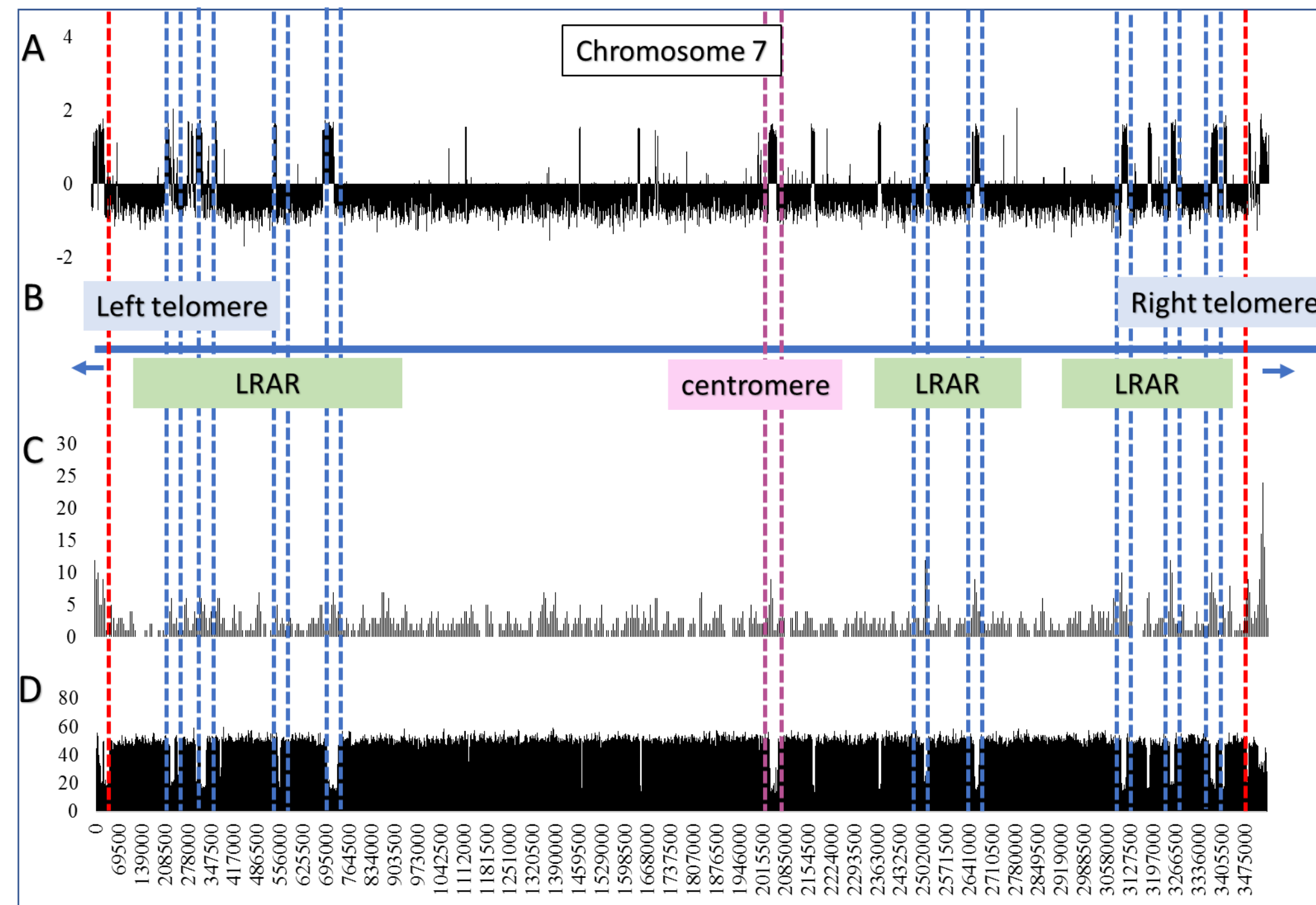
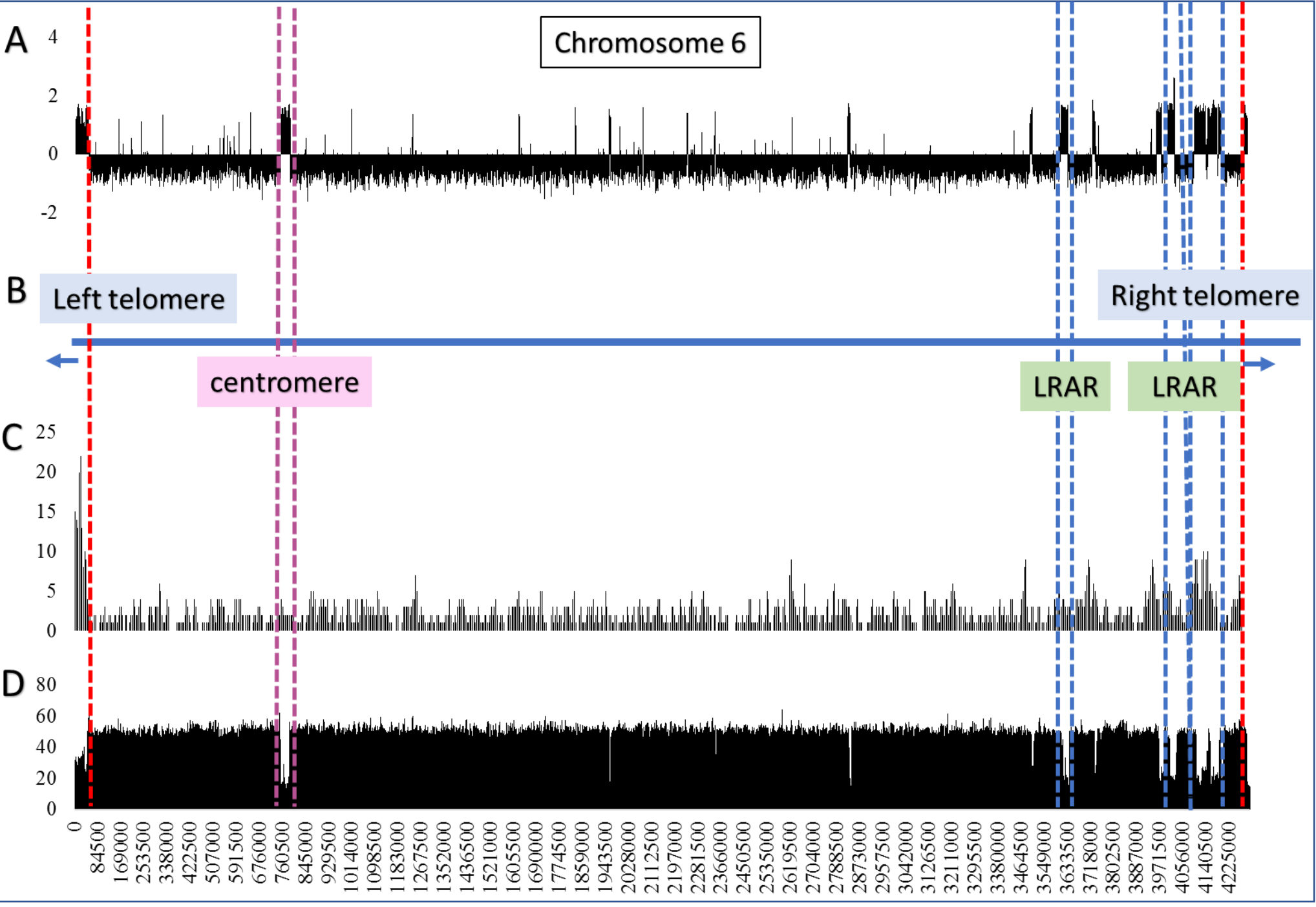
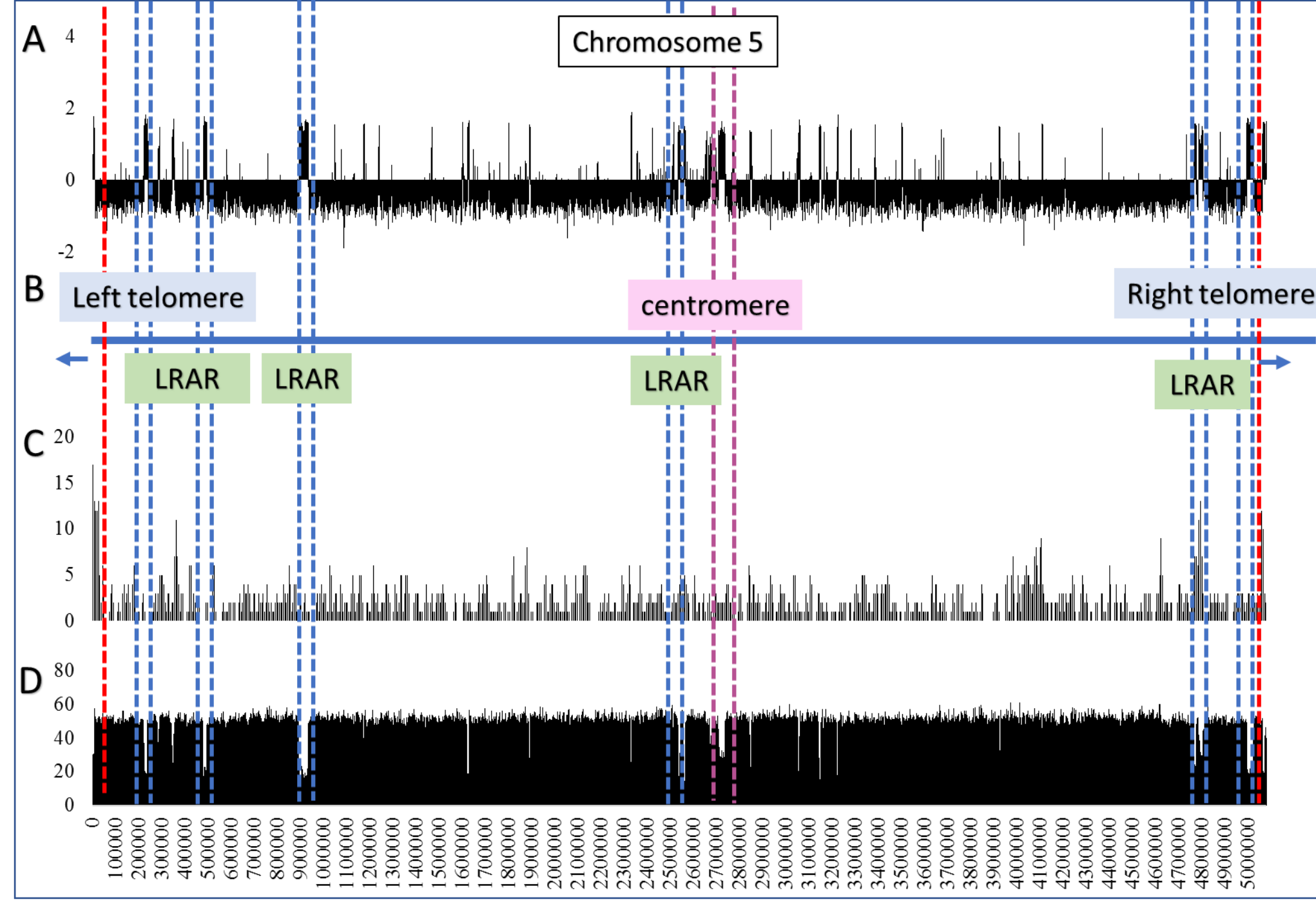
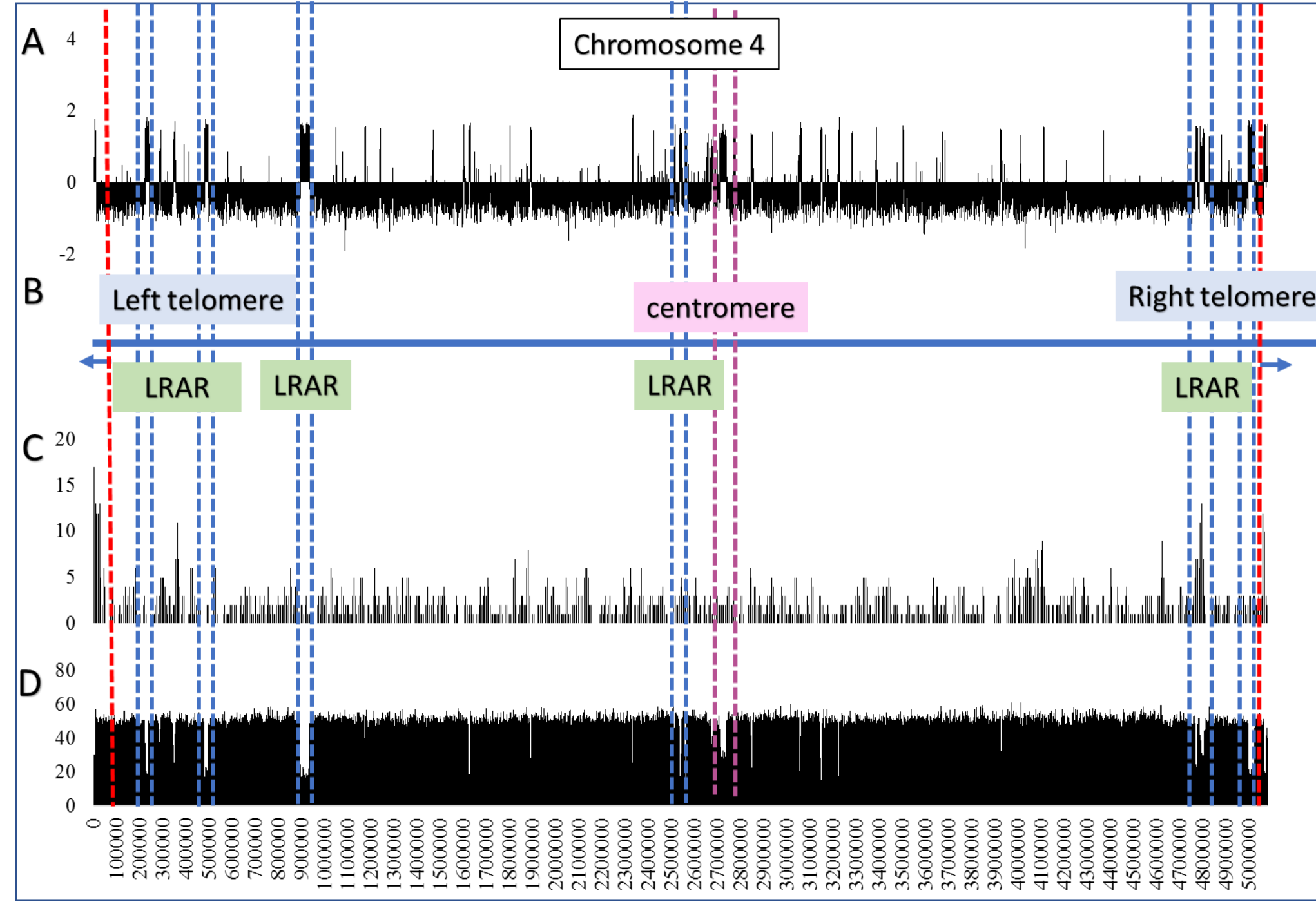
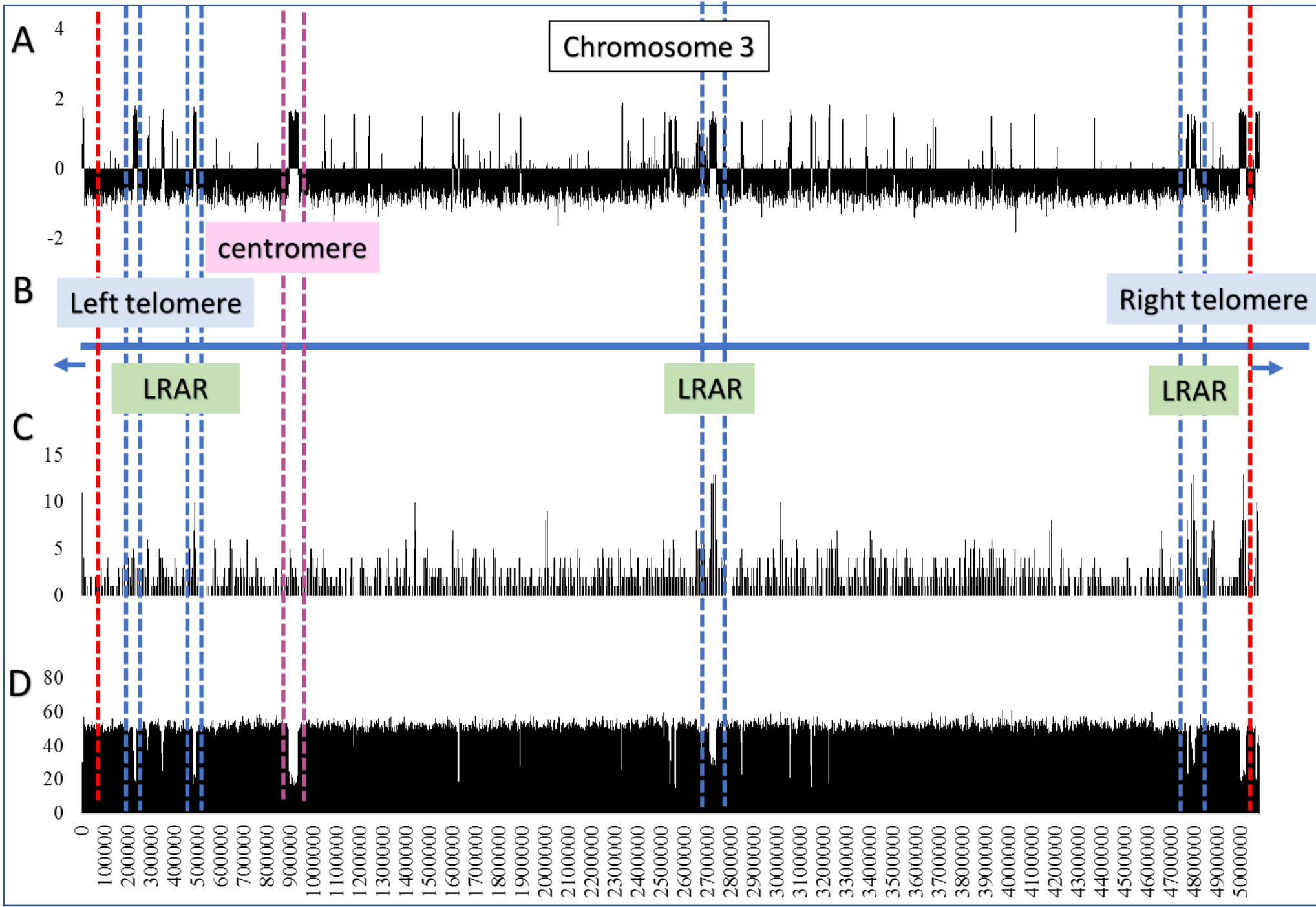
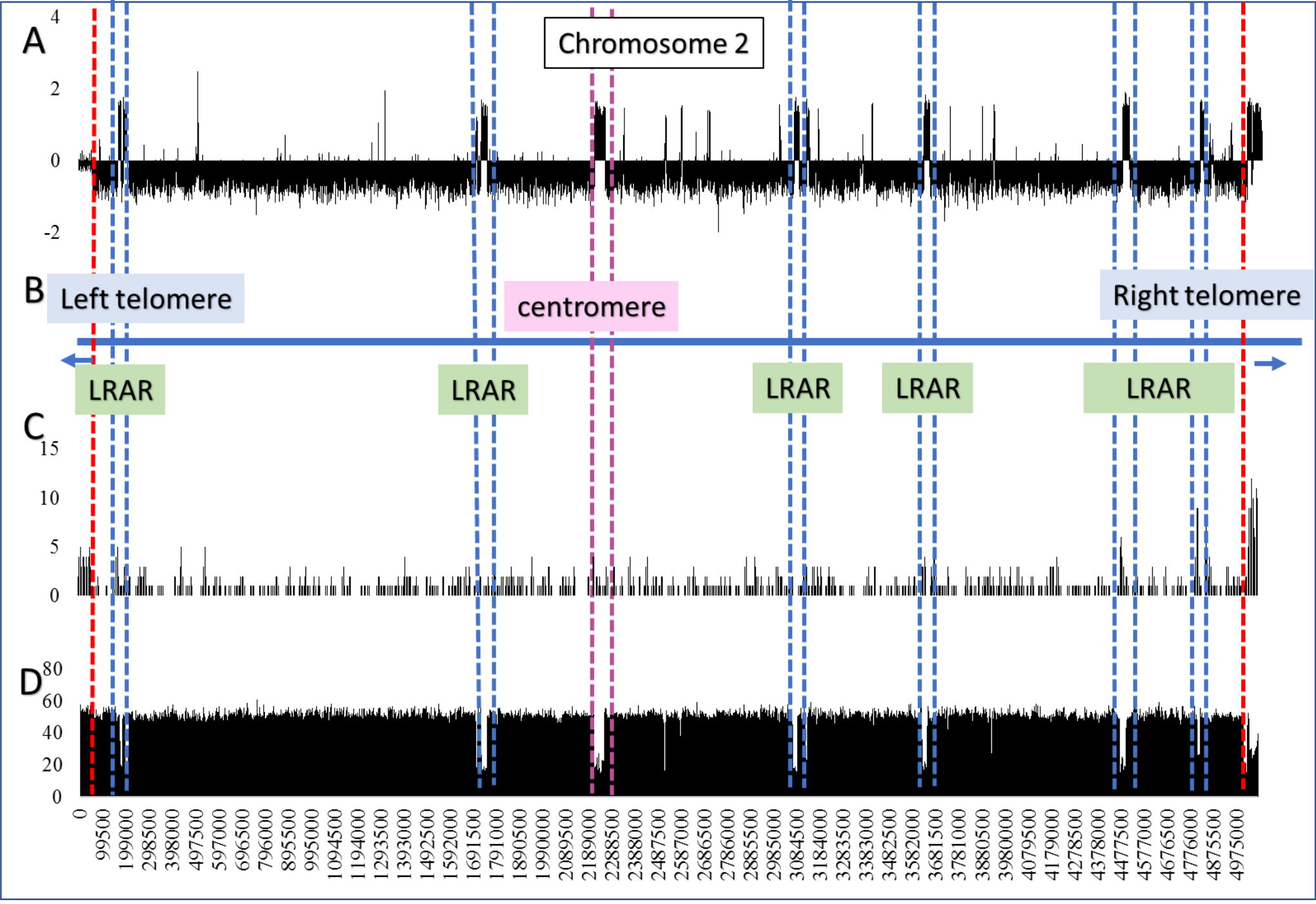
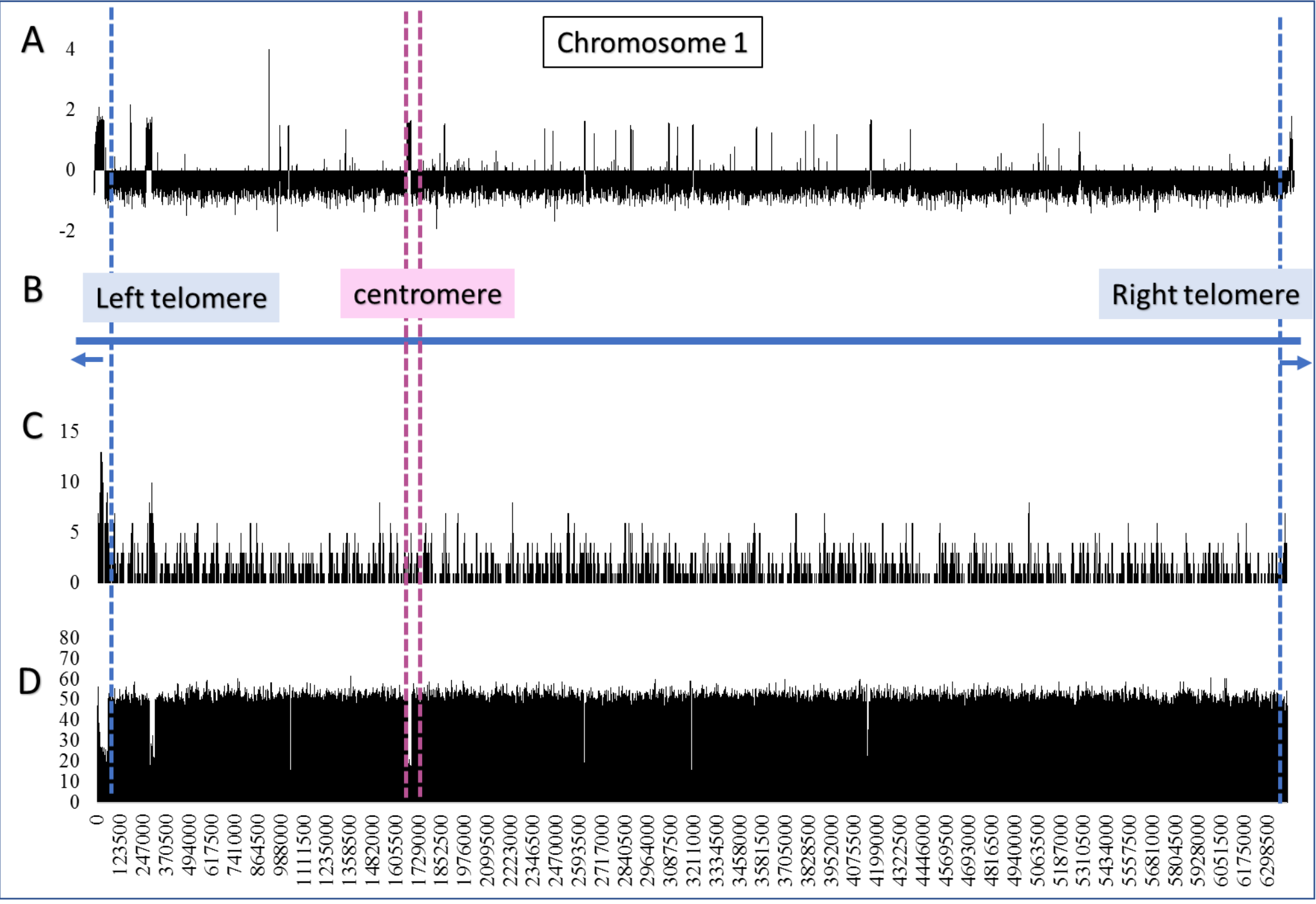
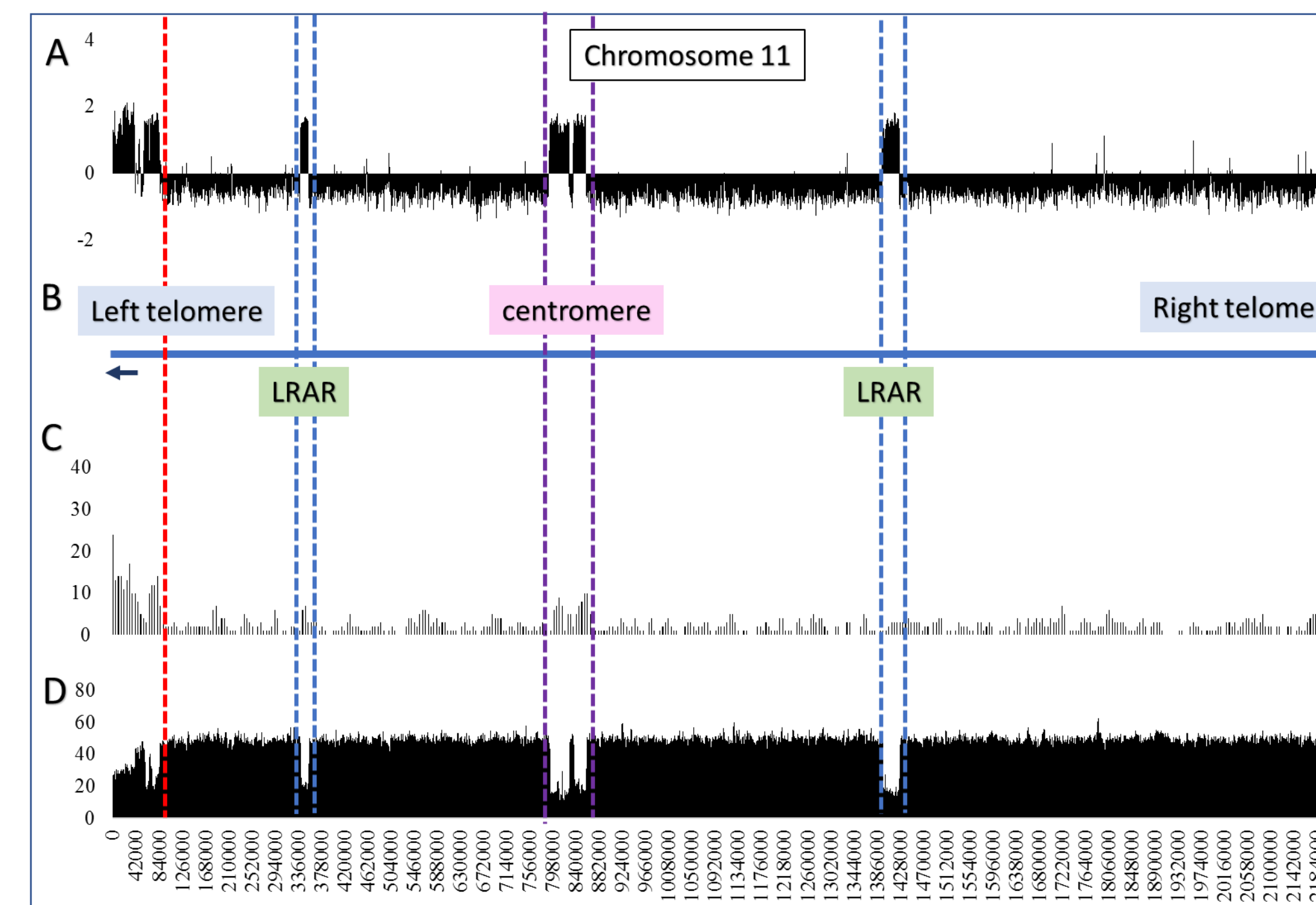
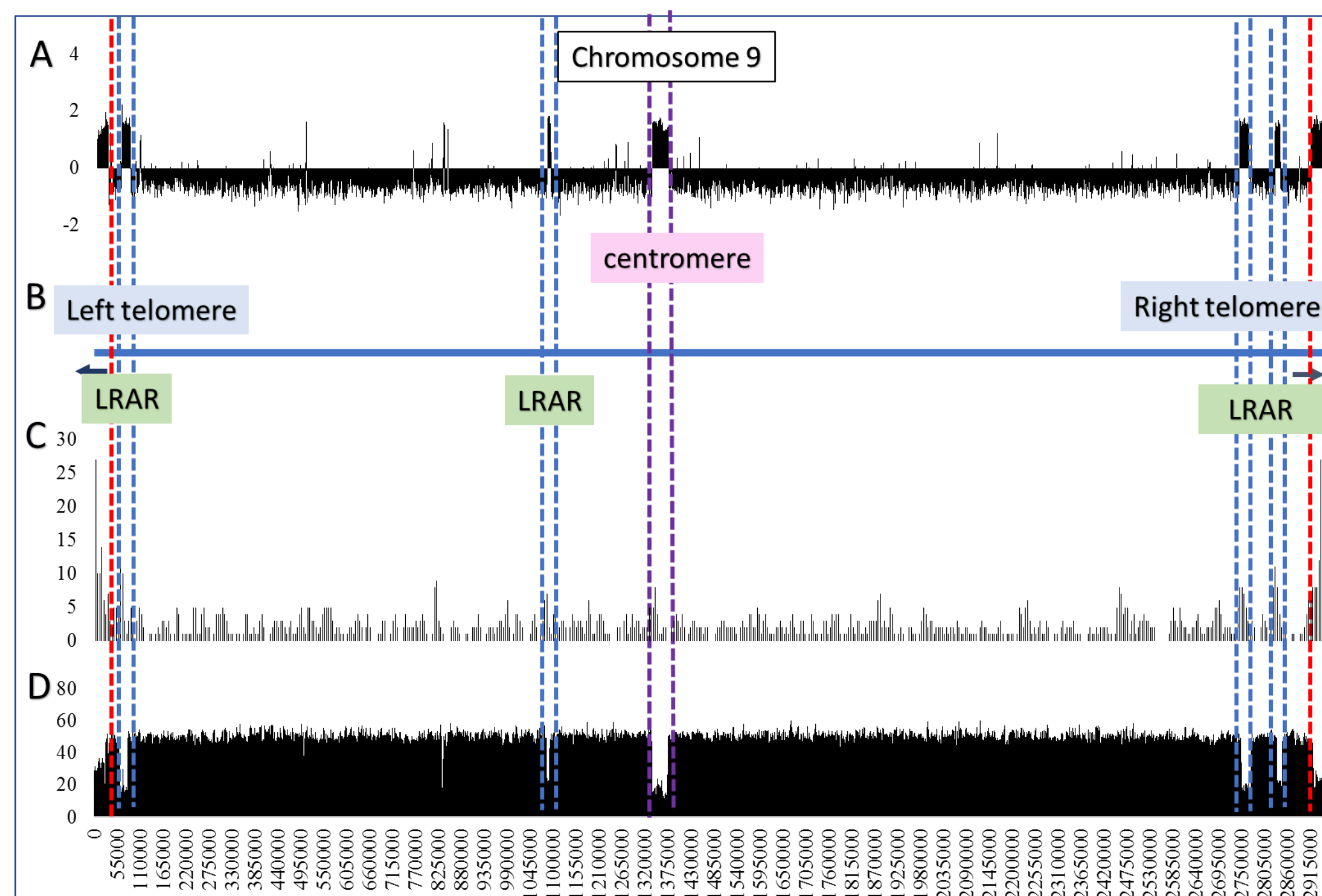
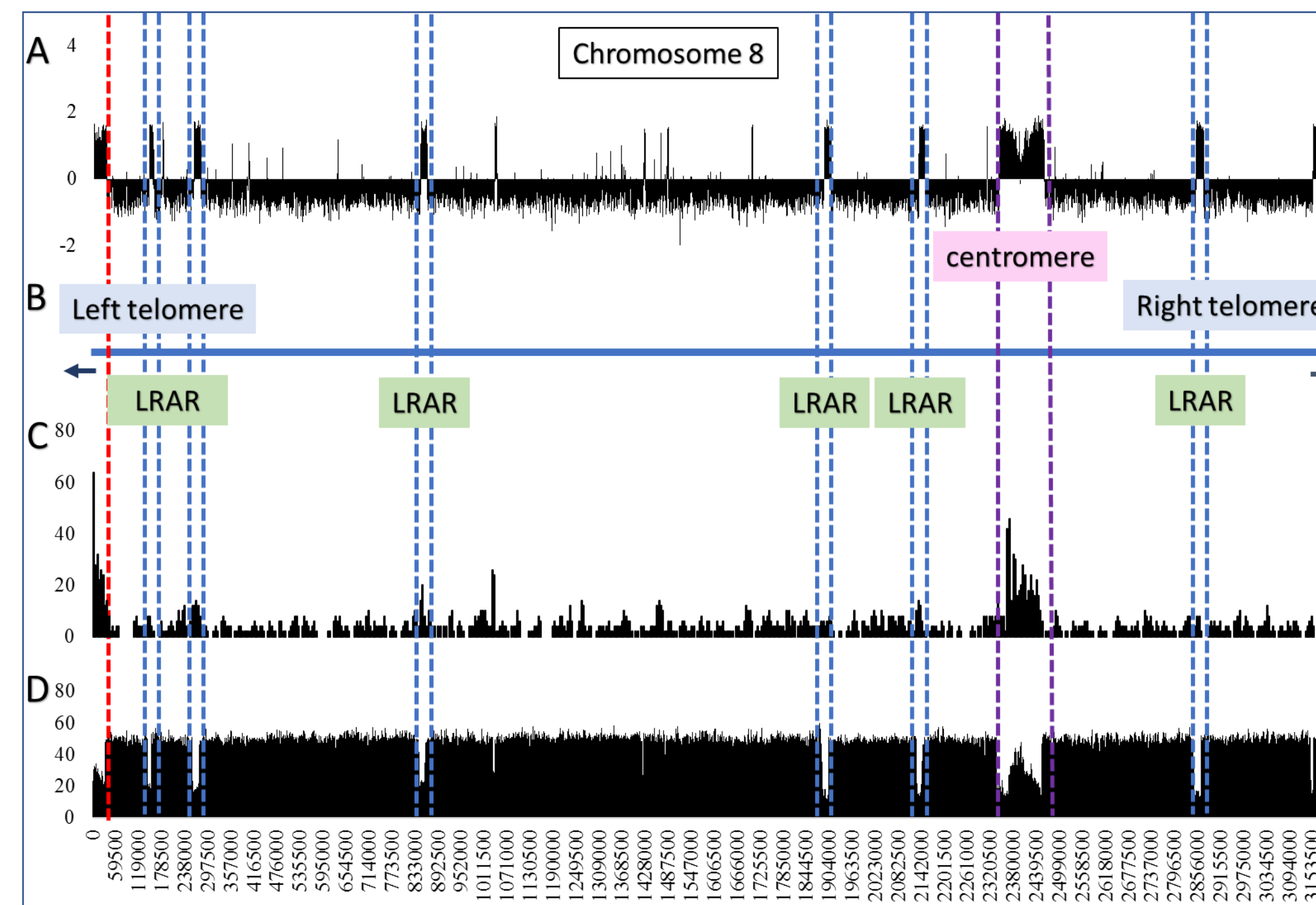
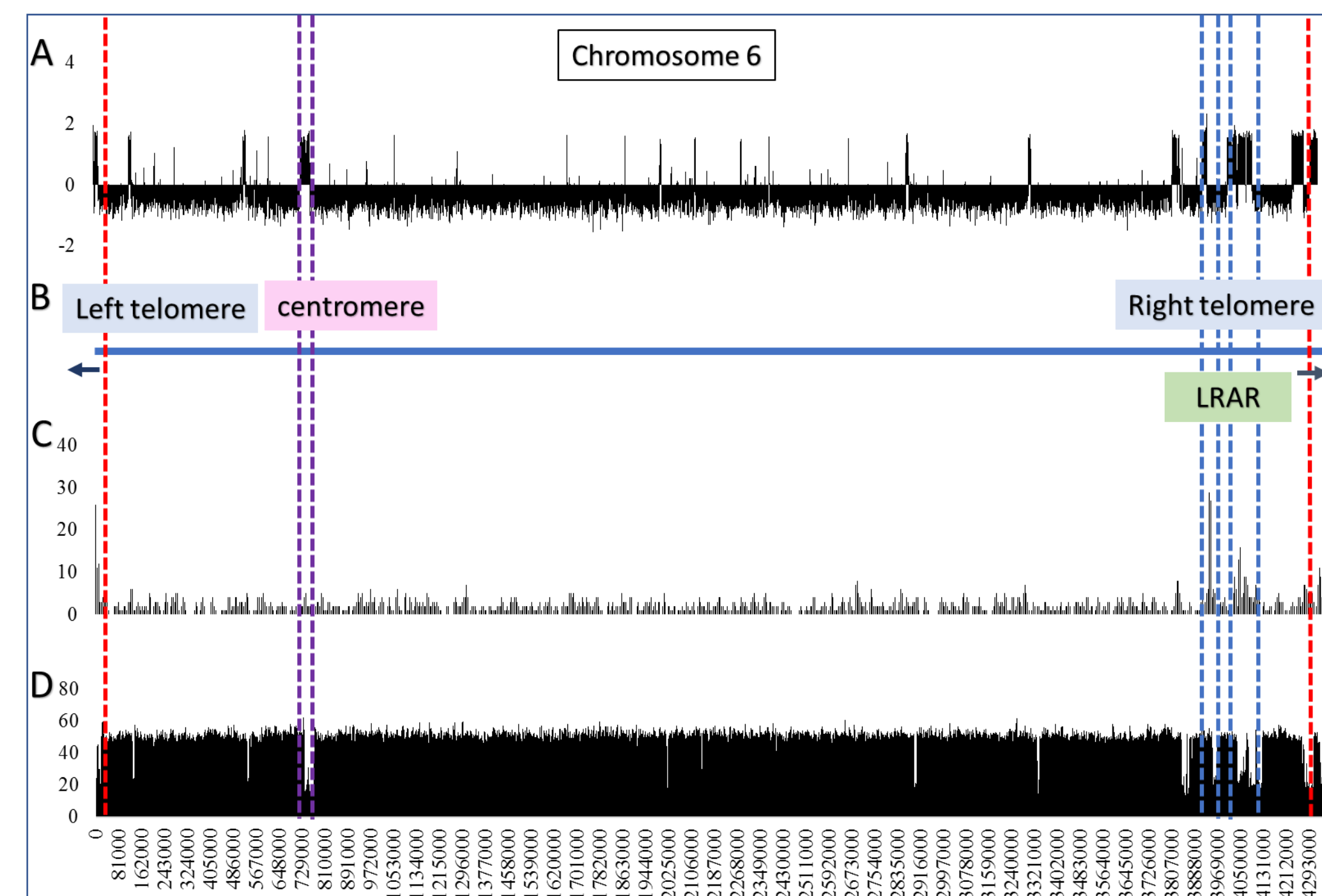
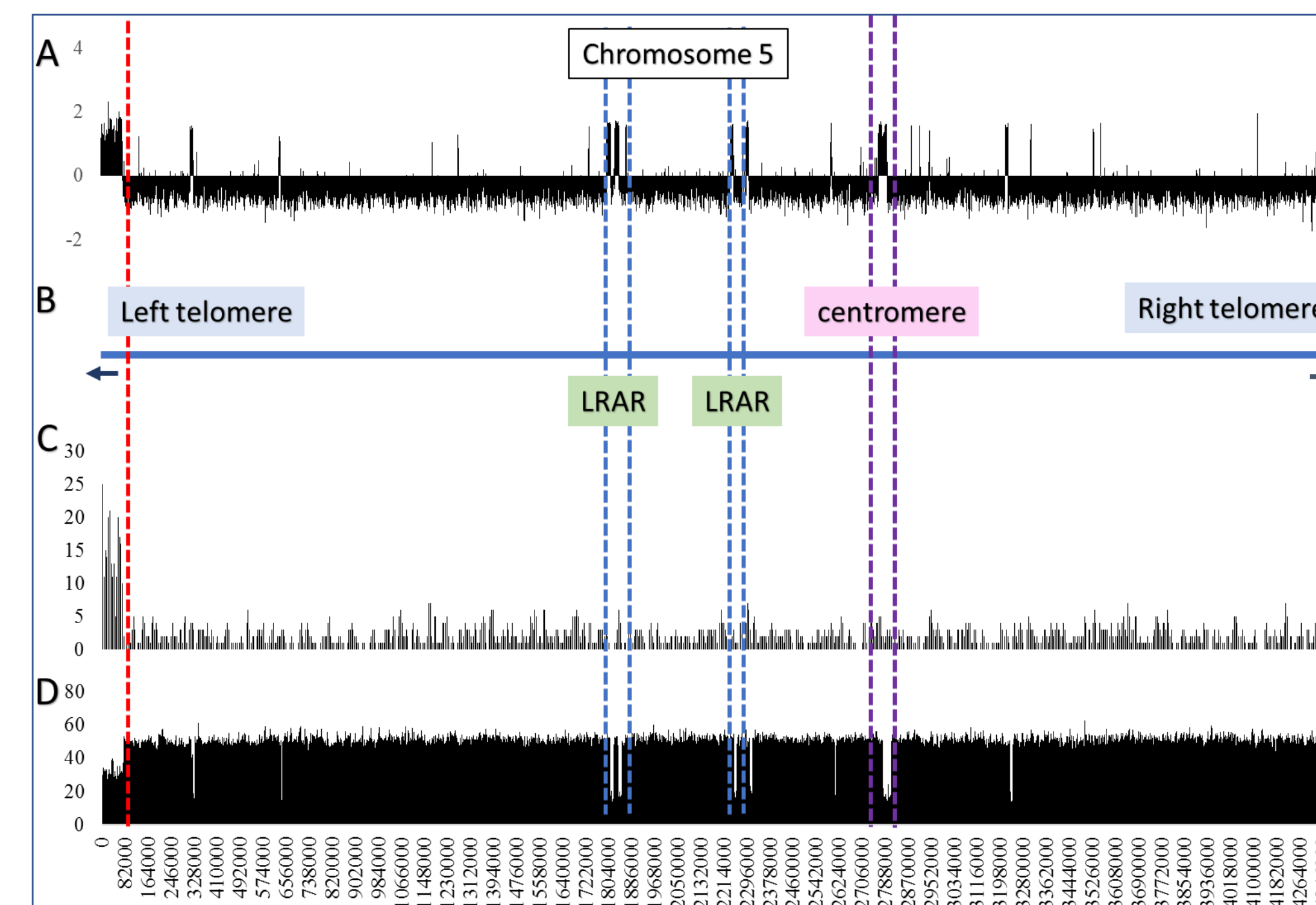
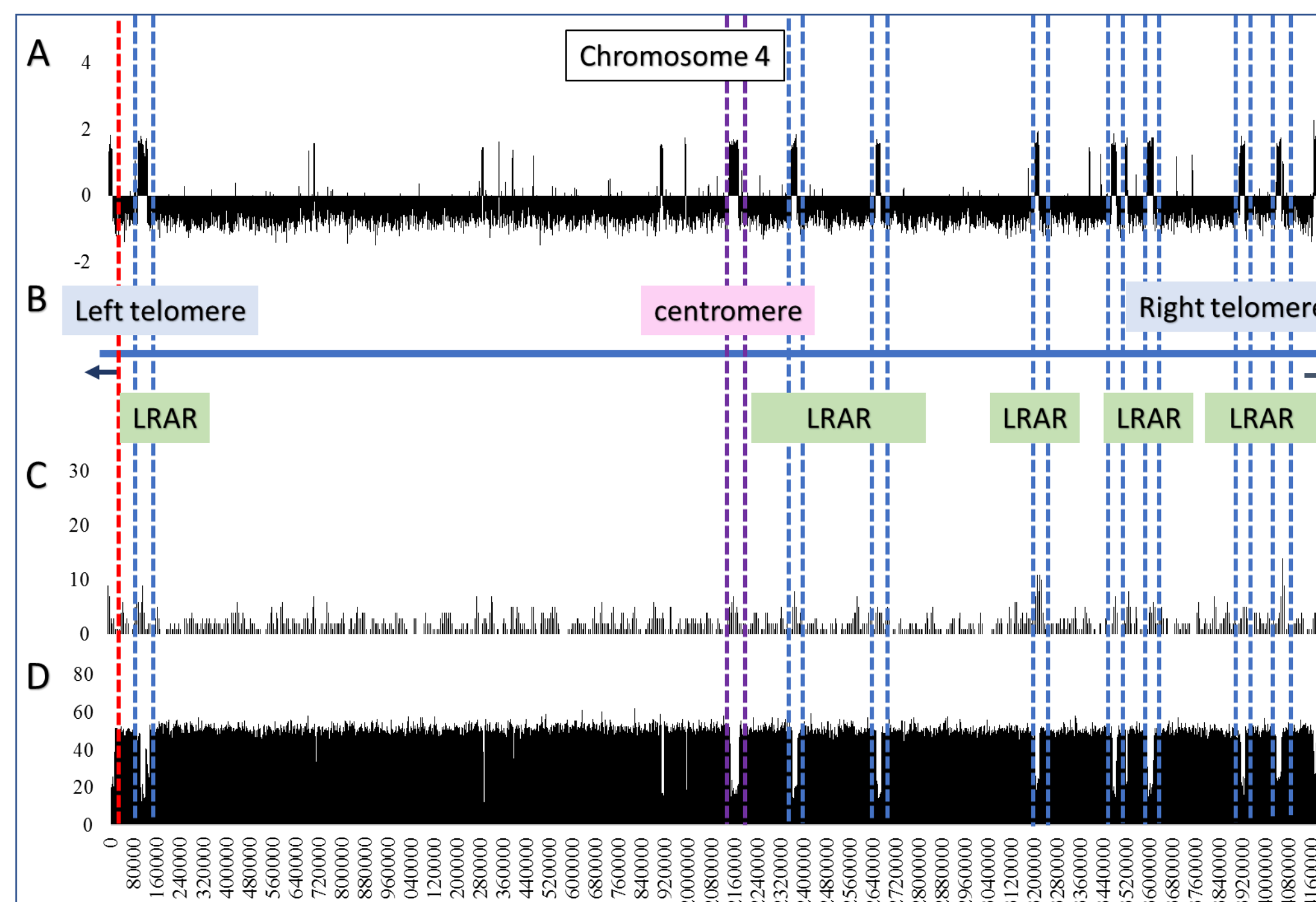
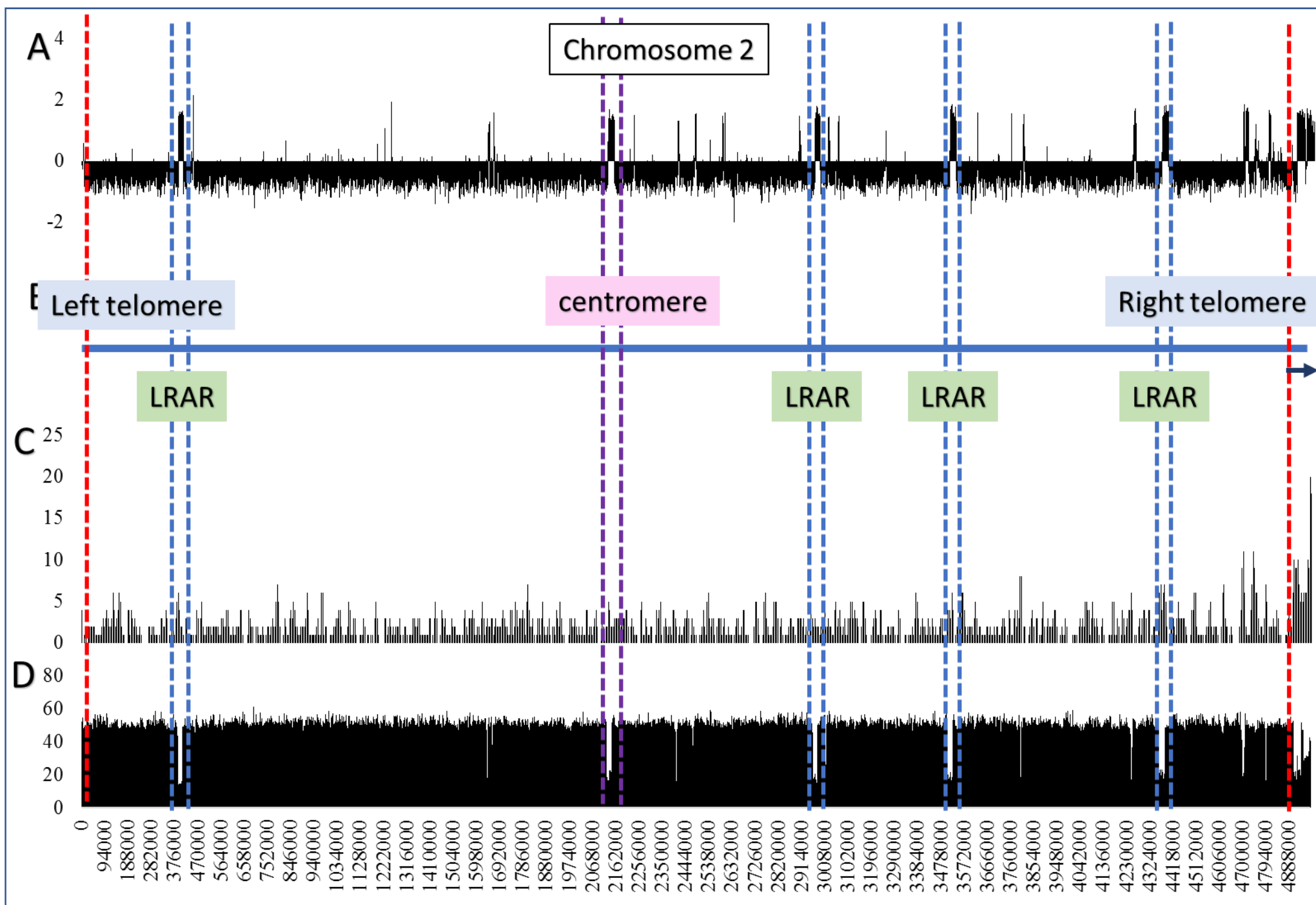


Figure S6: Graphical representation of the genetic features of the core 11 *Fusarium circinatum* chromosome assemblies for each isolate investigated in this study (Figures S6.1-S6.6 represent FSP34, UG27, CMWF567, FSOR, and FFRA, respectively). (A) The top panel depicts the changes in RIP composite index values. Values above 0 indicate RIP. (B) The second panel depicts the annotation across the length of the chromosome. The most extensively RIP affected regions are indicated. (C) The third panel illustrates the changes in the count of telomeric repeat sequences across the length of the chromosome. (D) The bottom panel depicts the GC content across the length of the chromosome. A full list of LRARs are listed in Table S14.

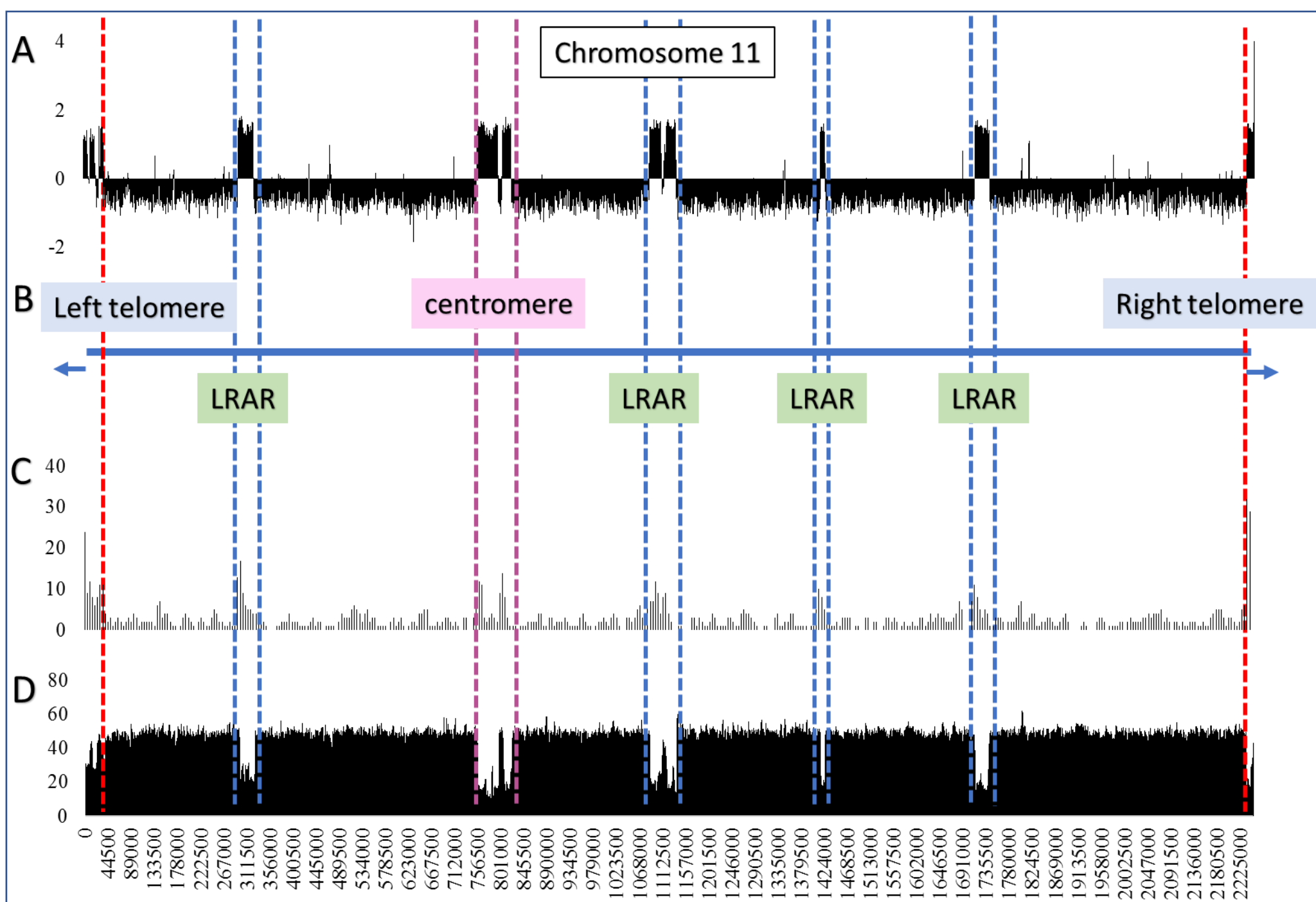
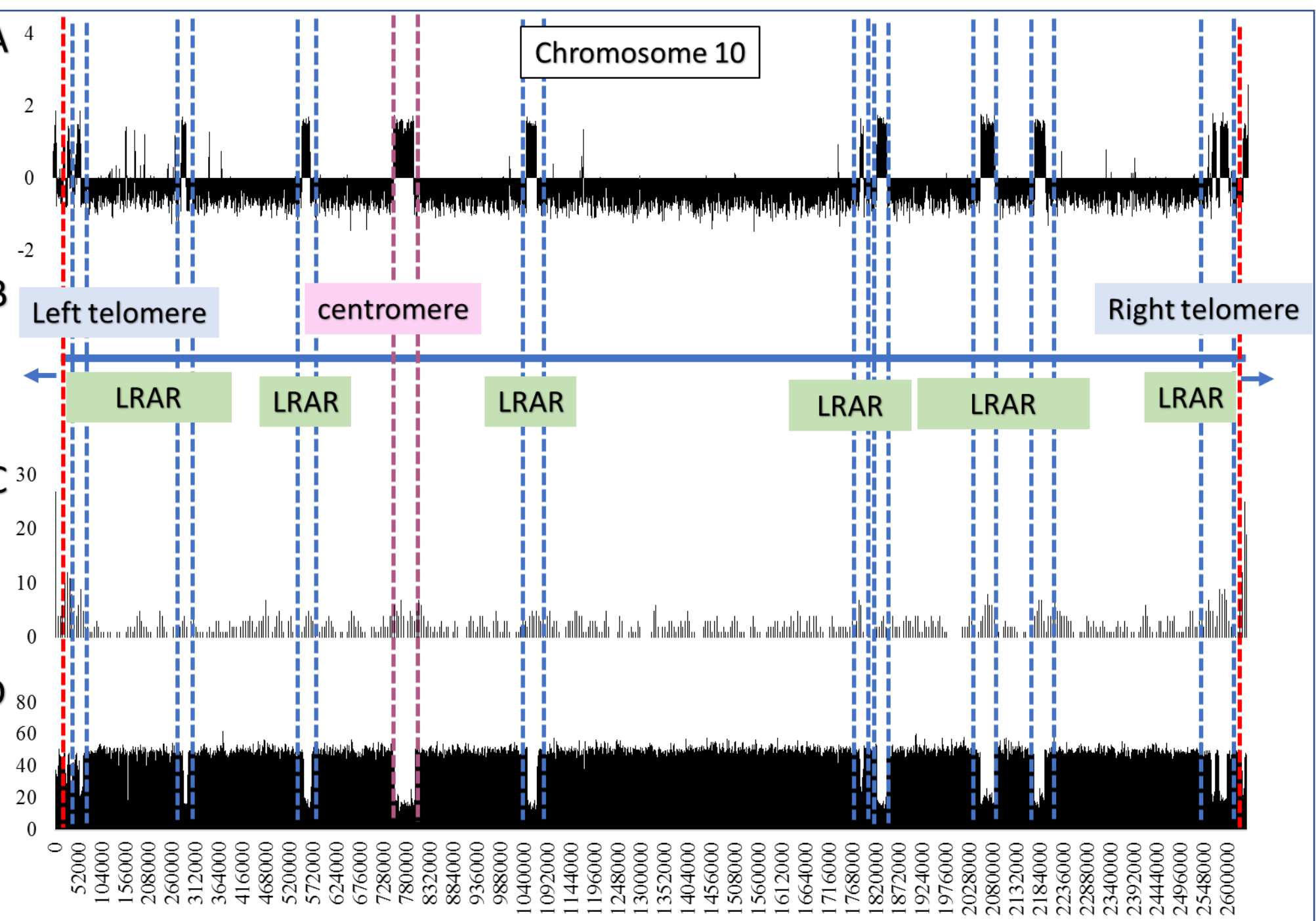
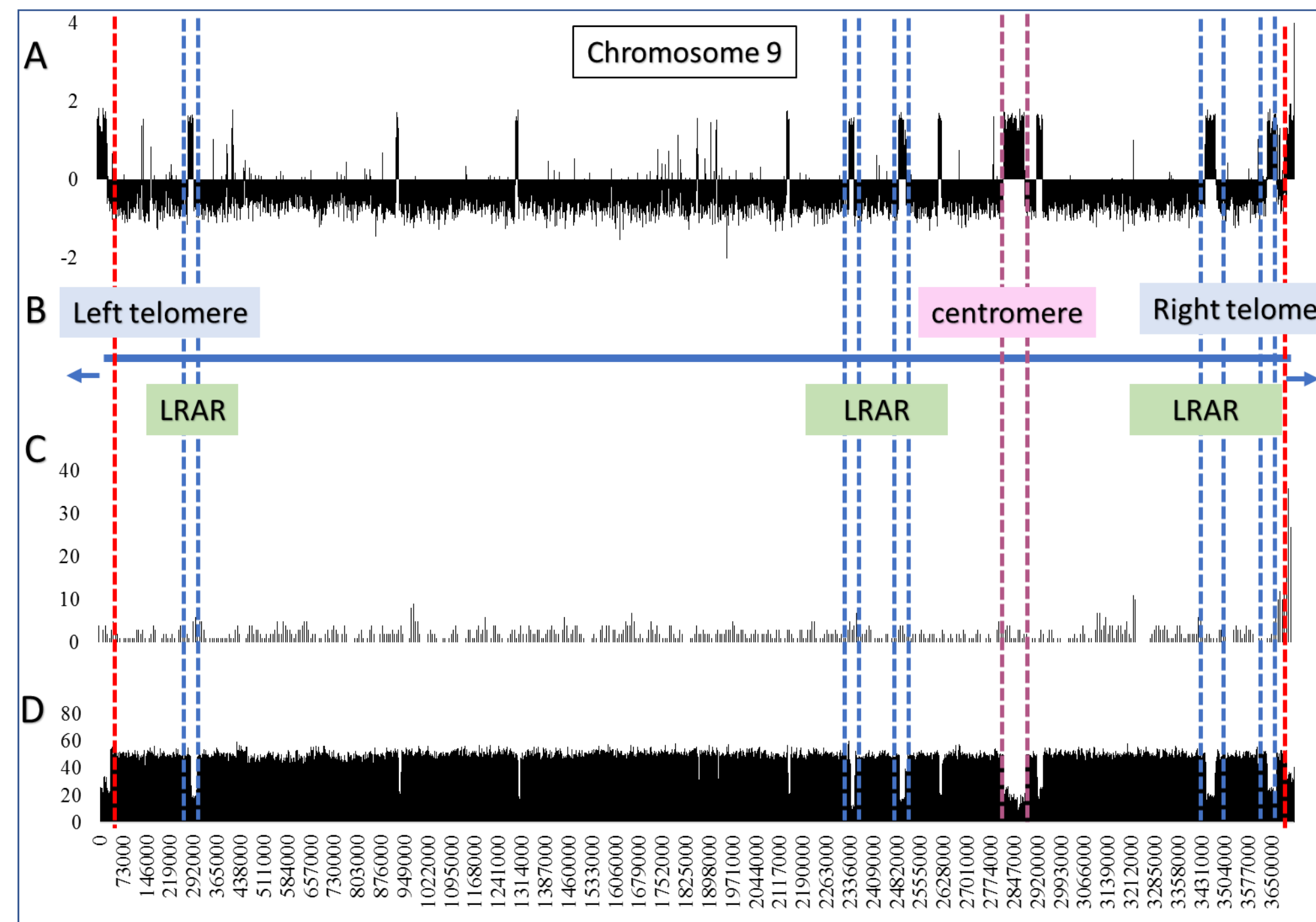
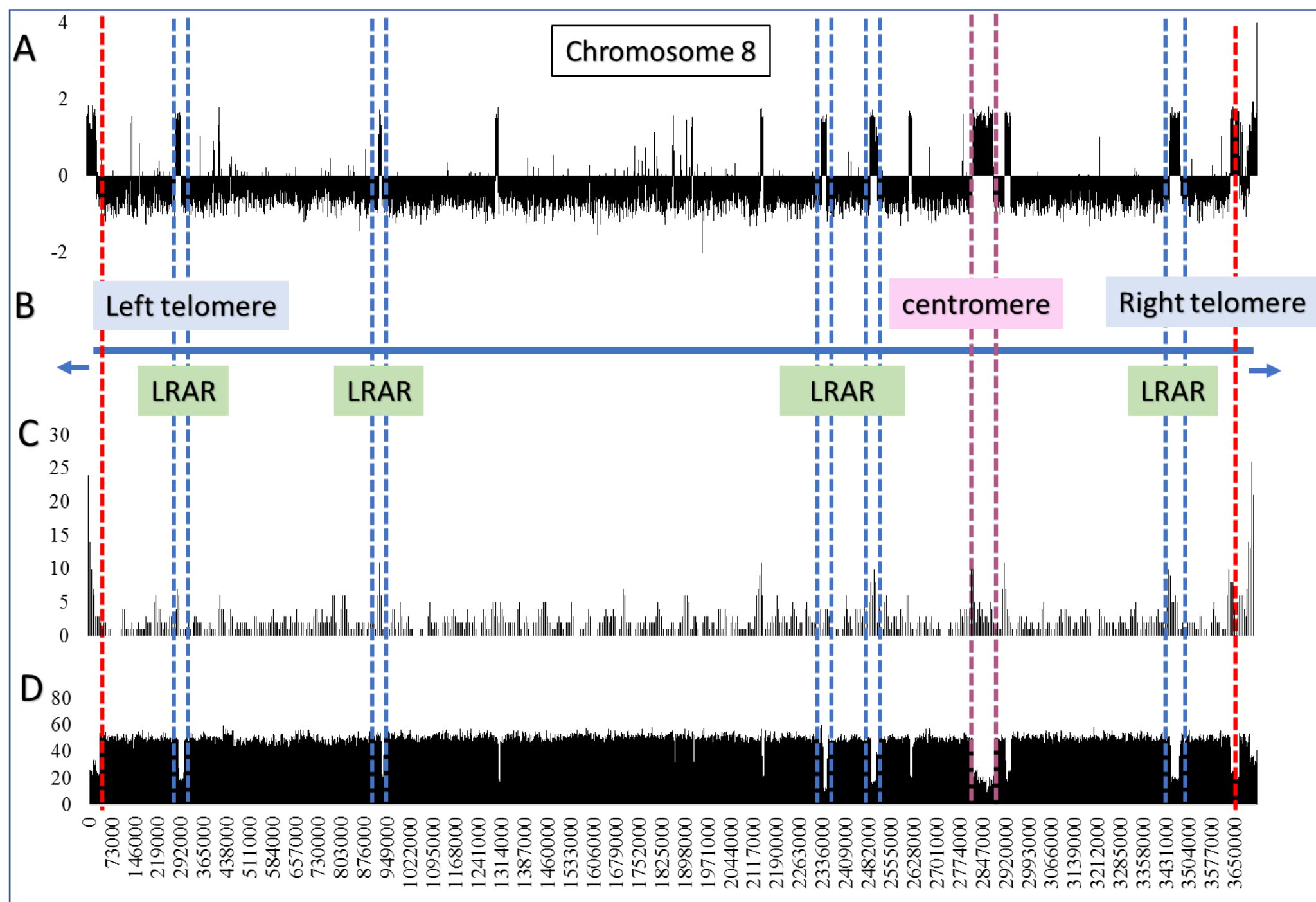
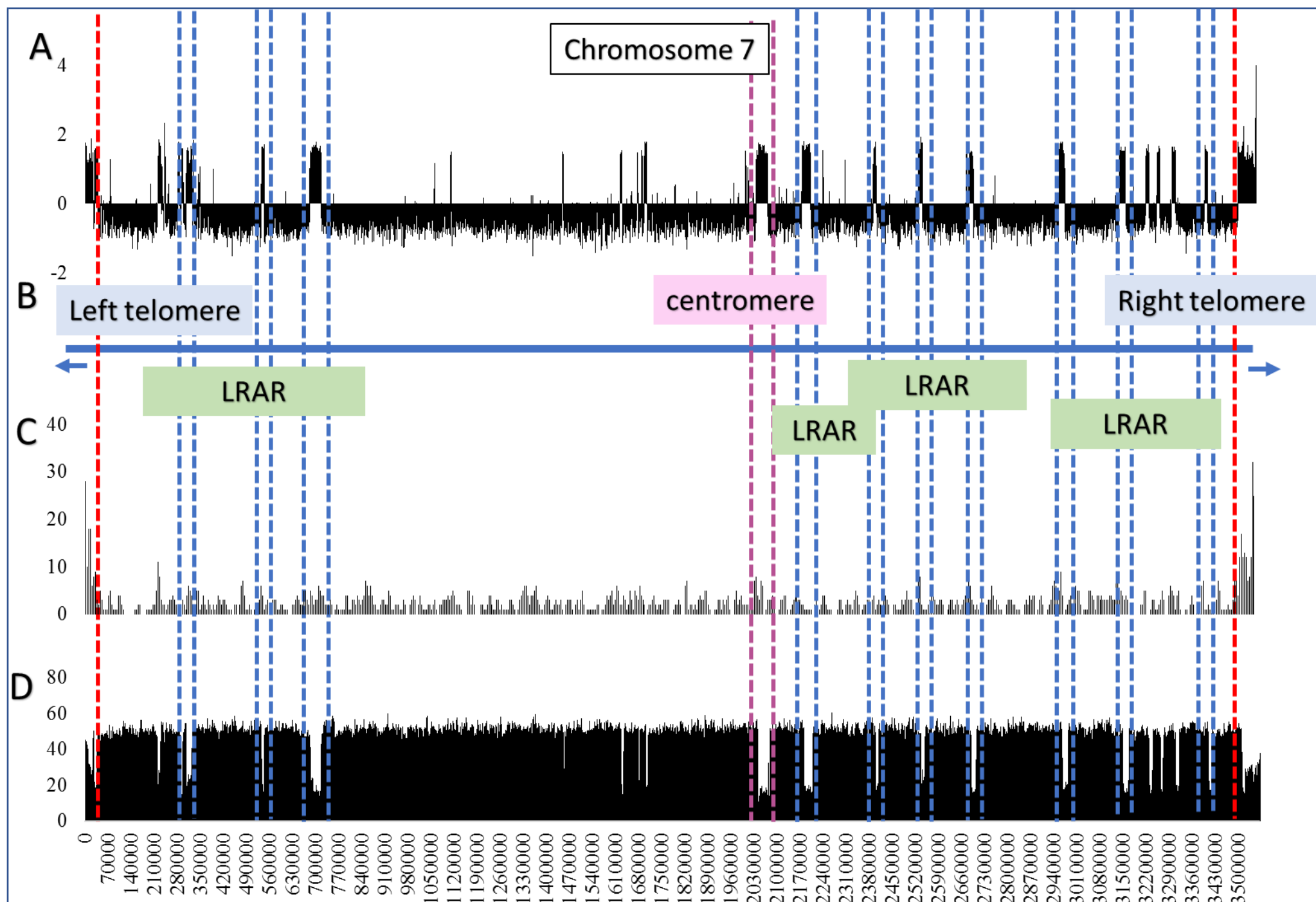
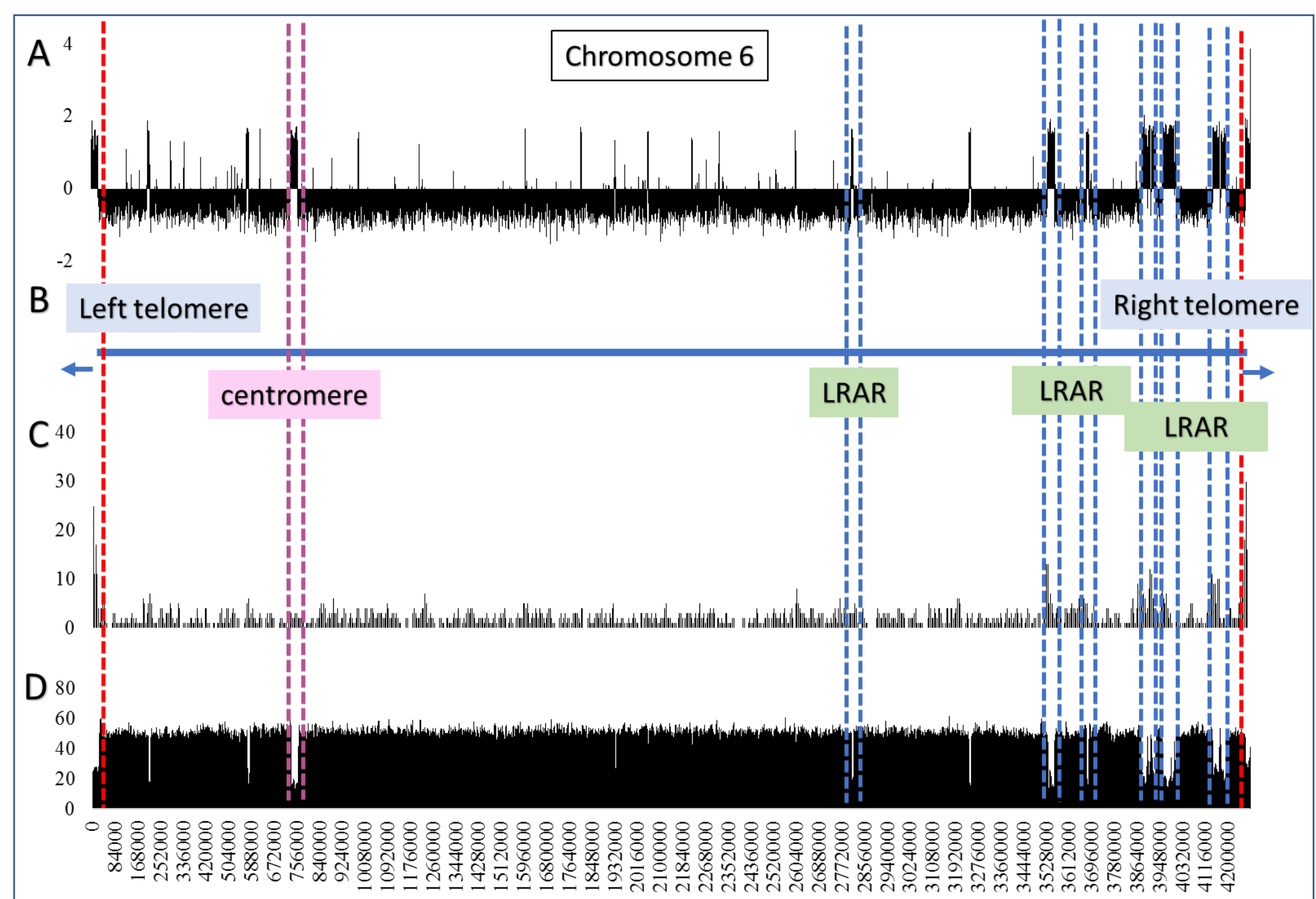
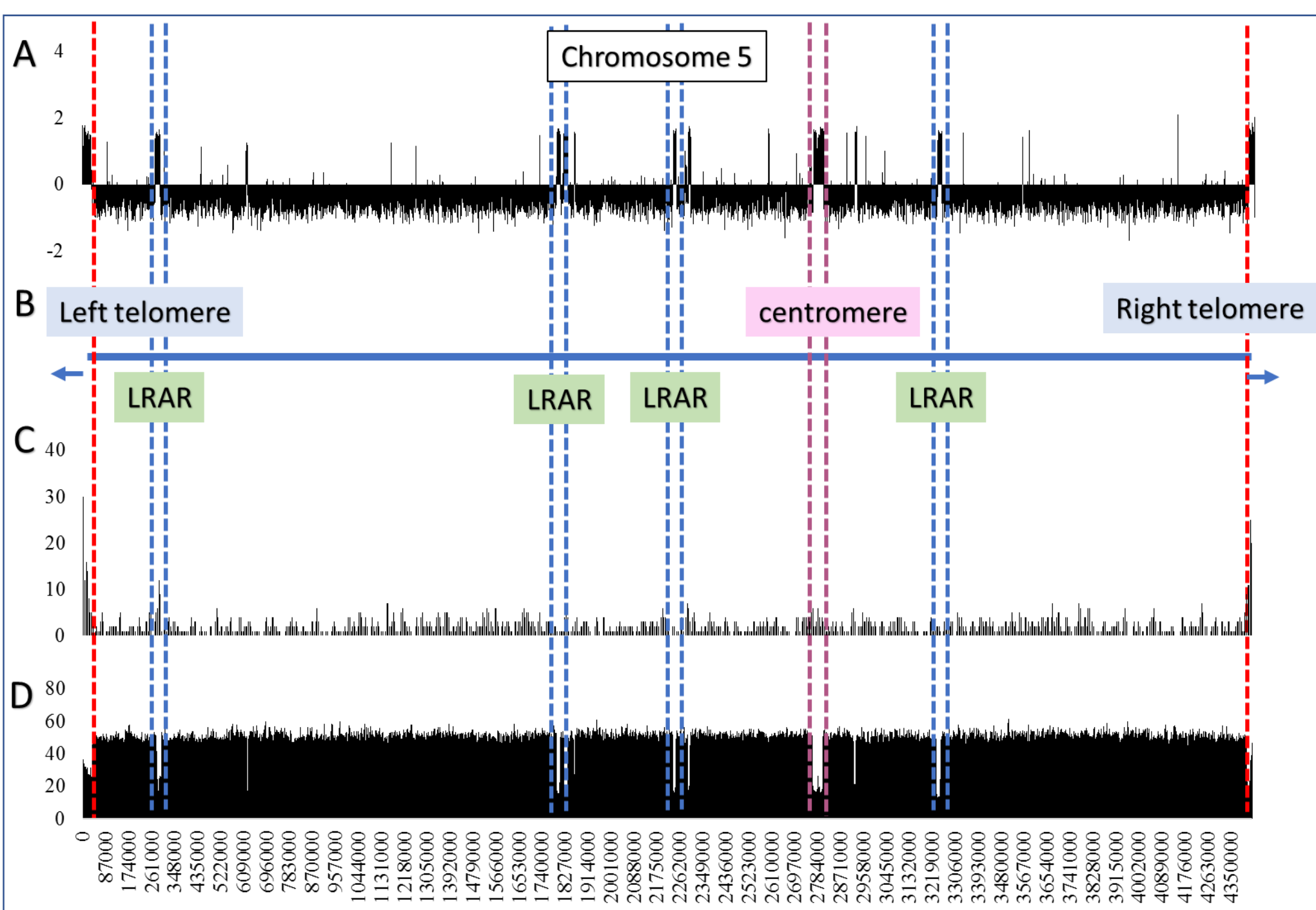
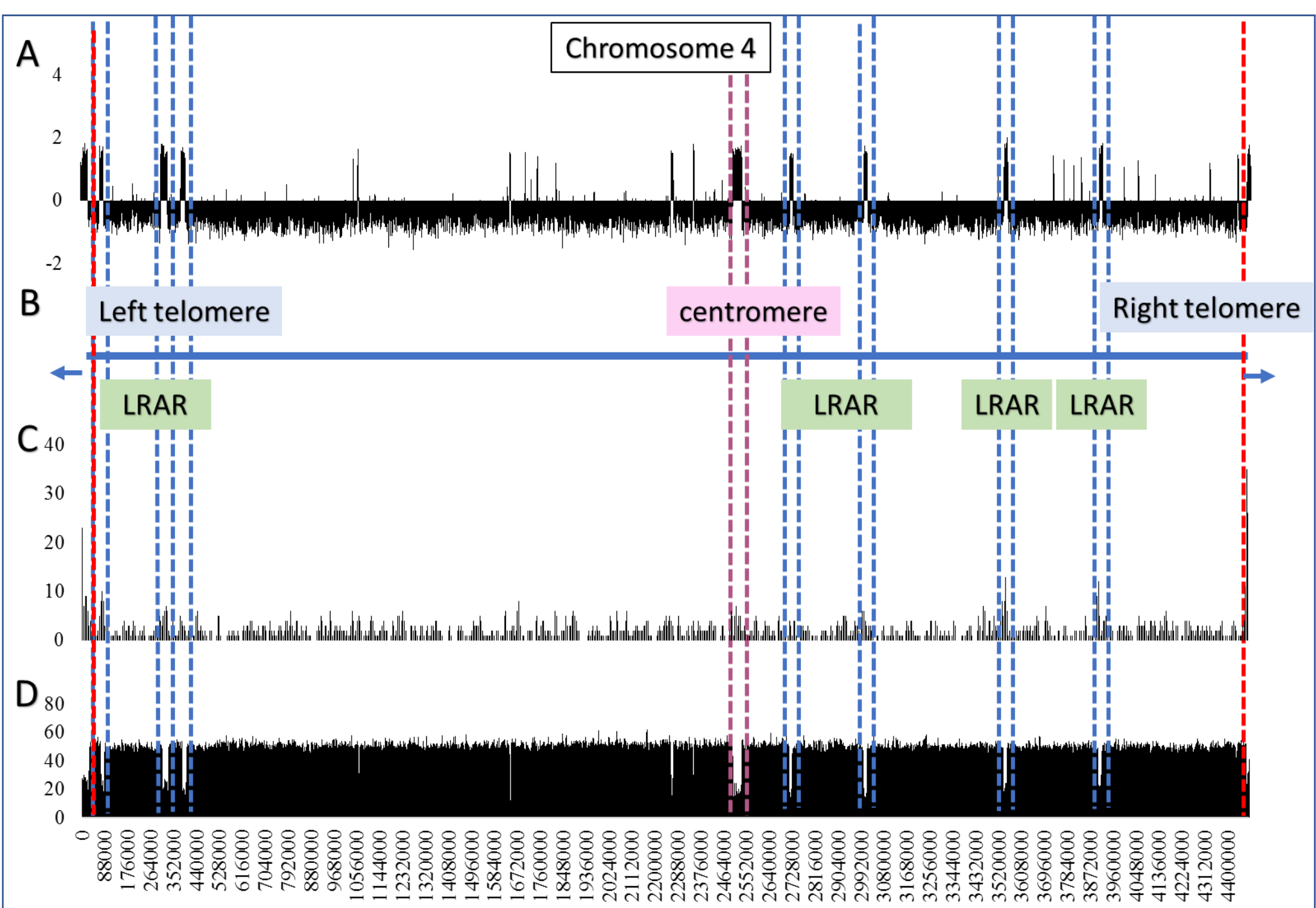
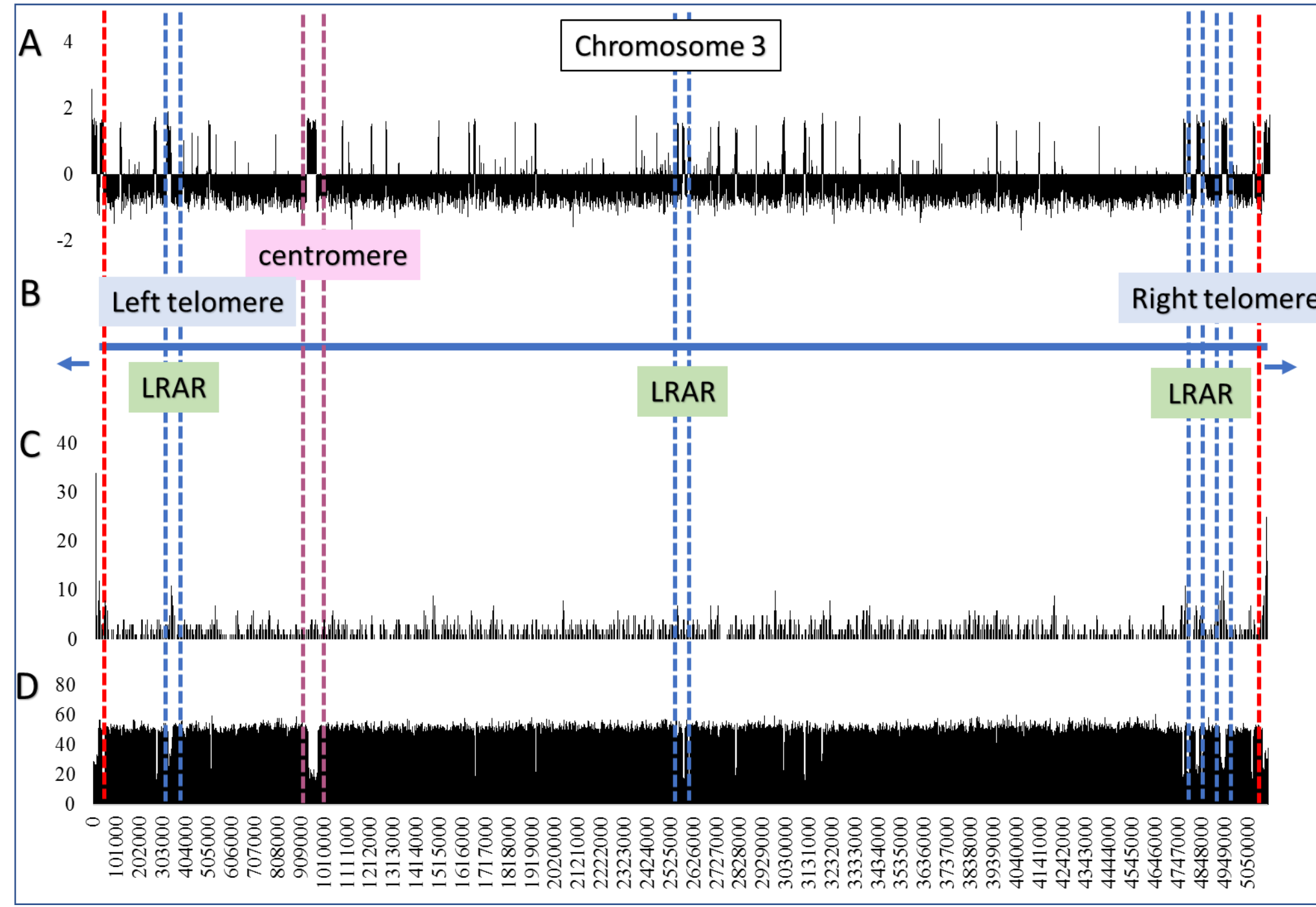
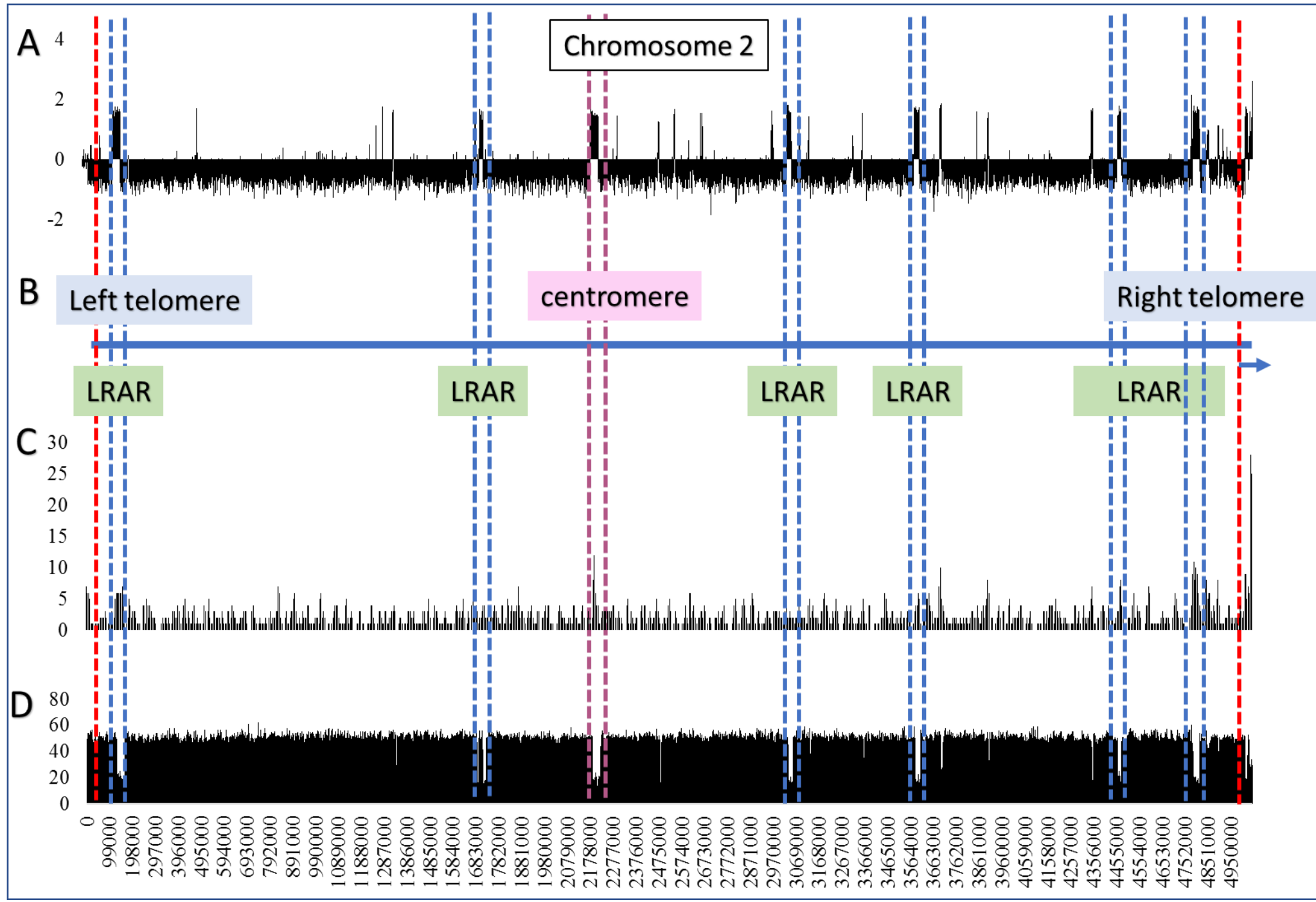
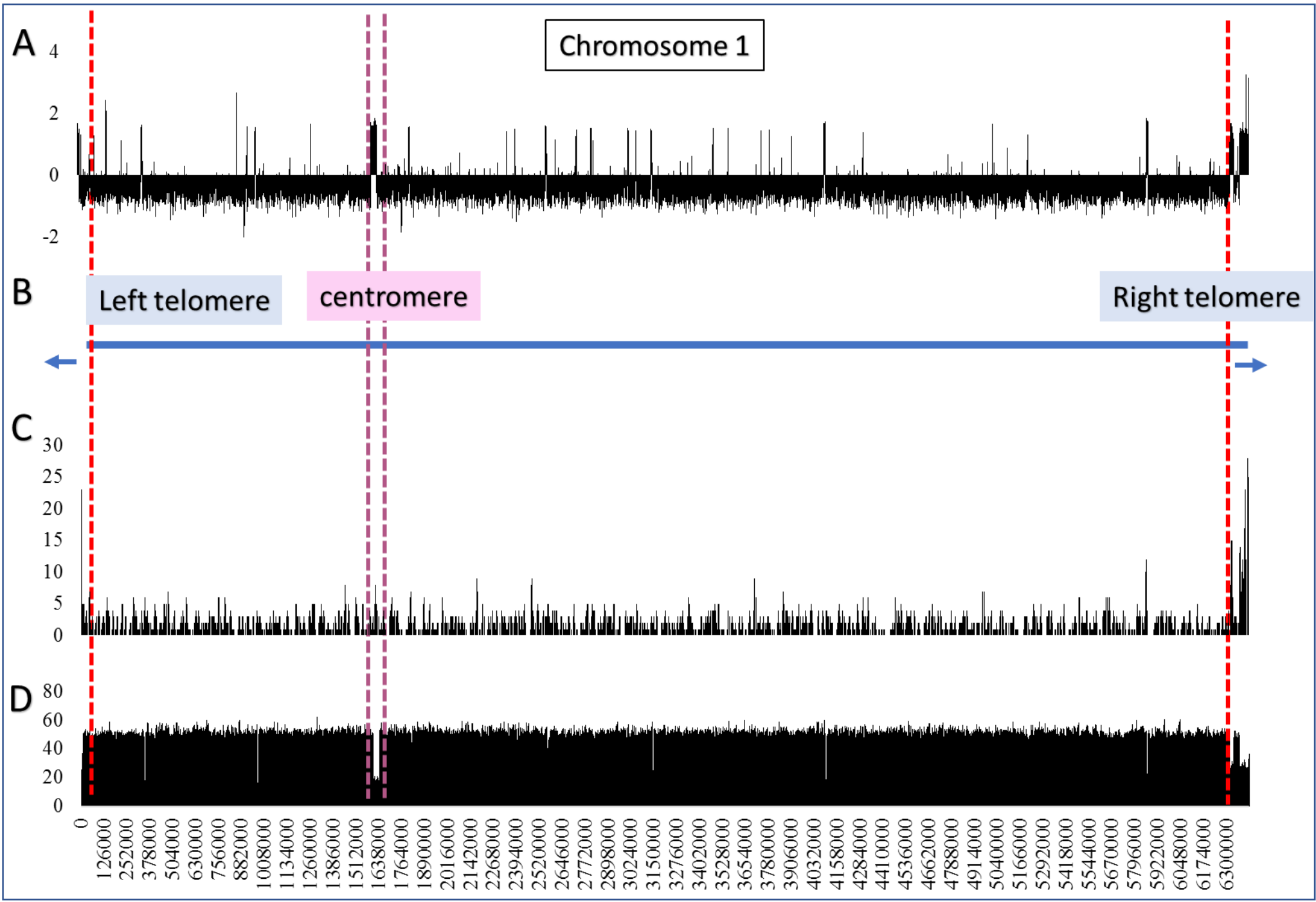
FSP34



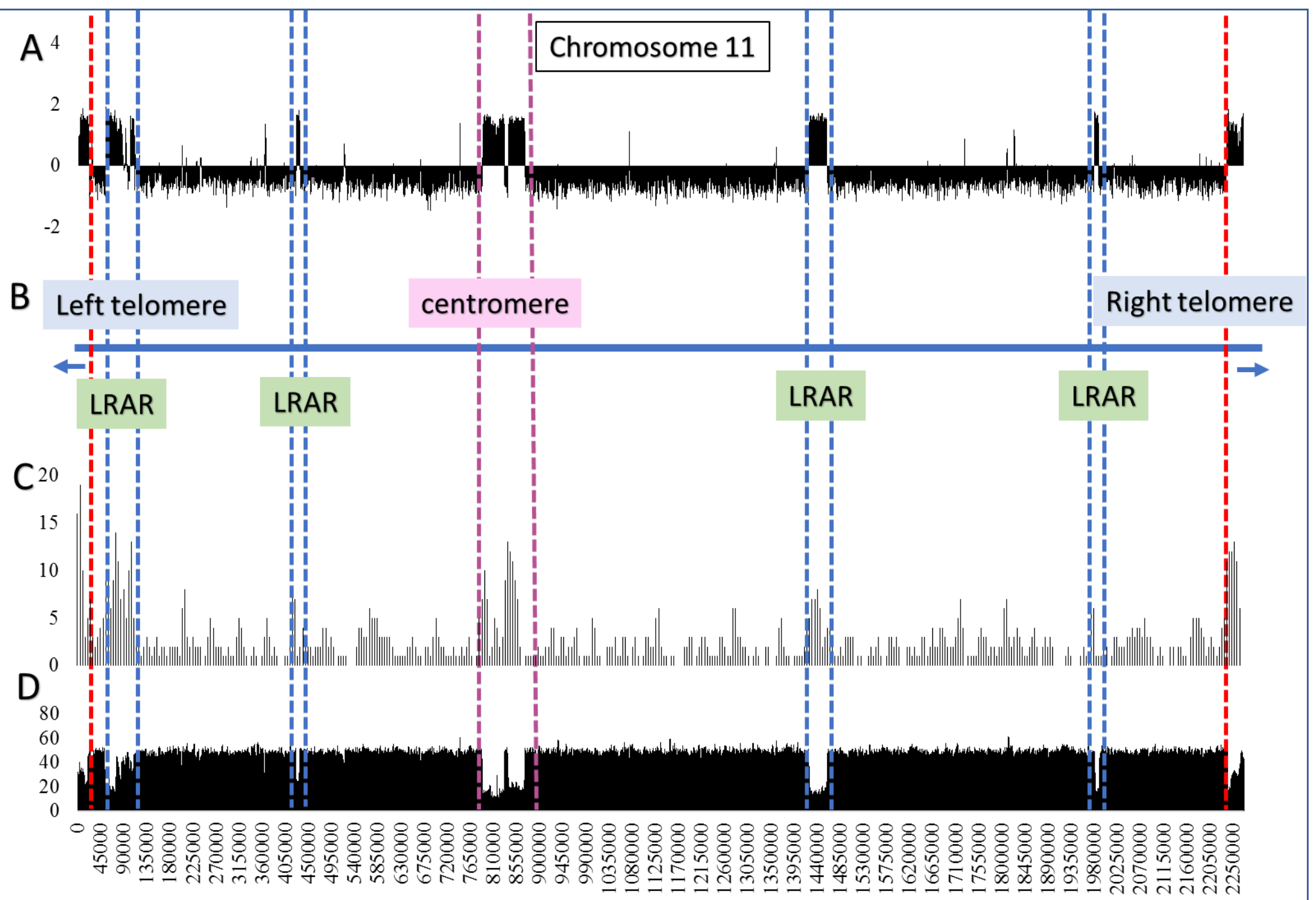
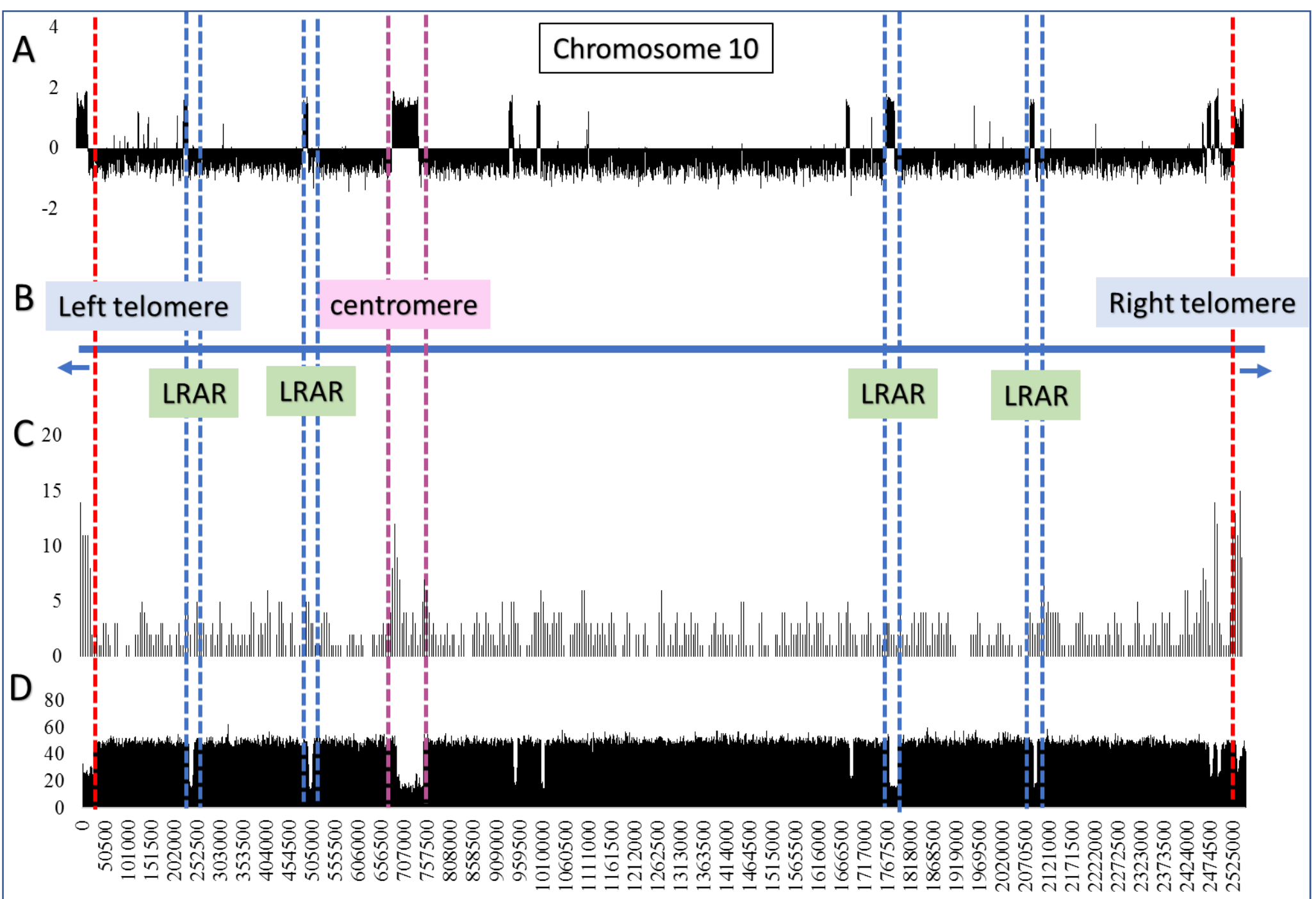
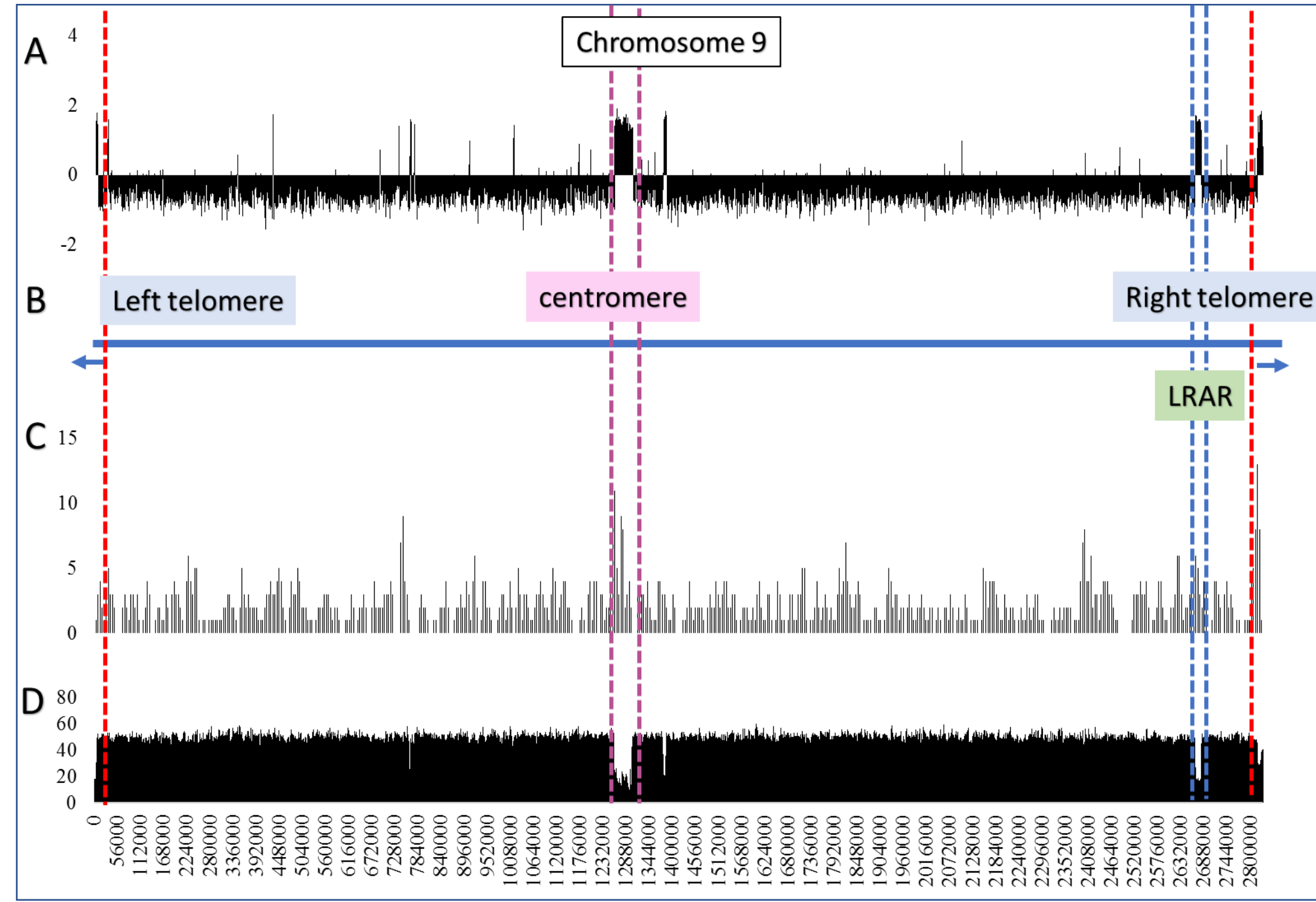
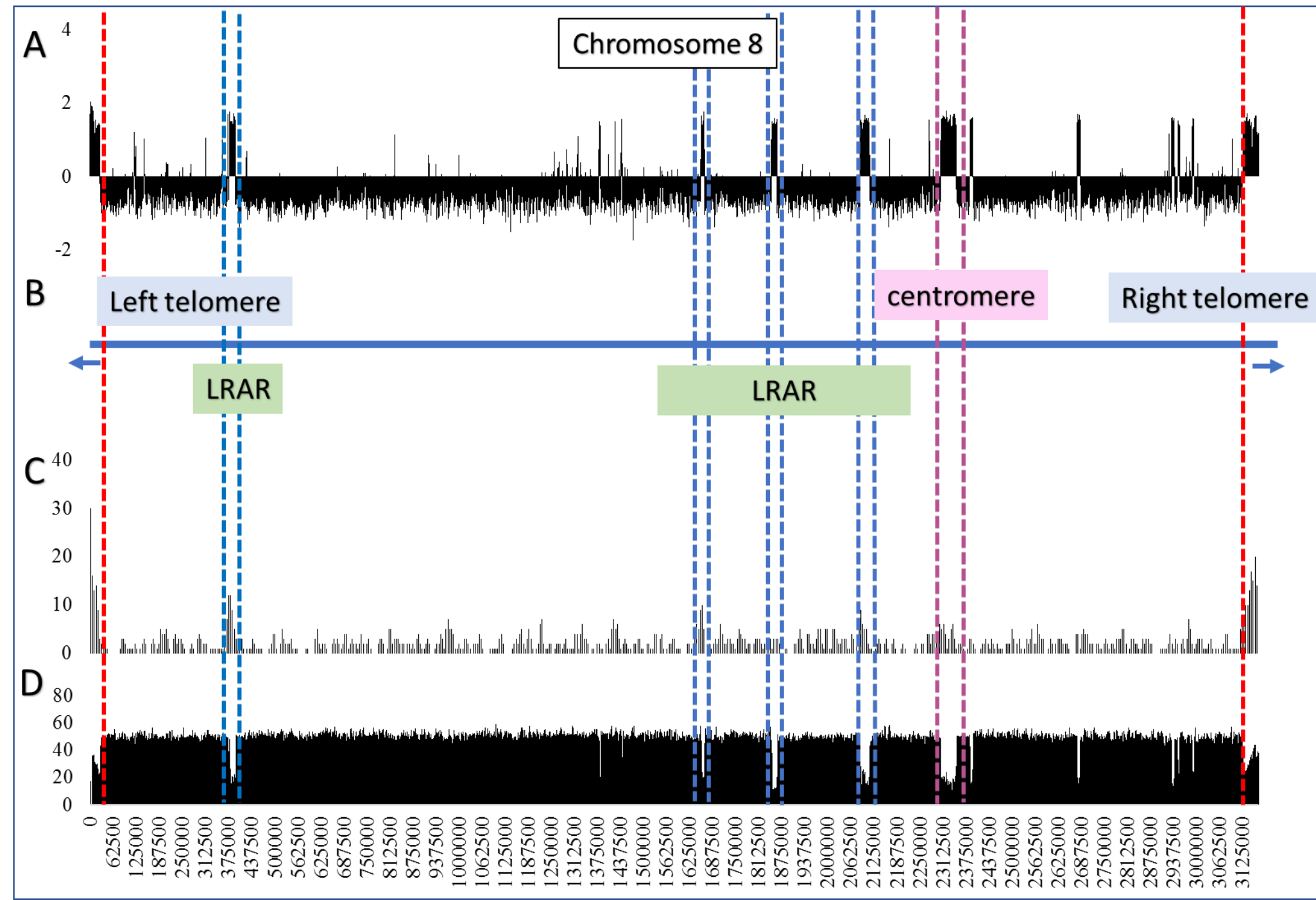
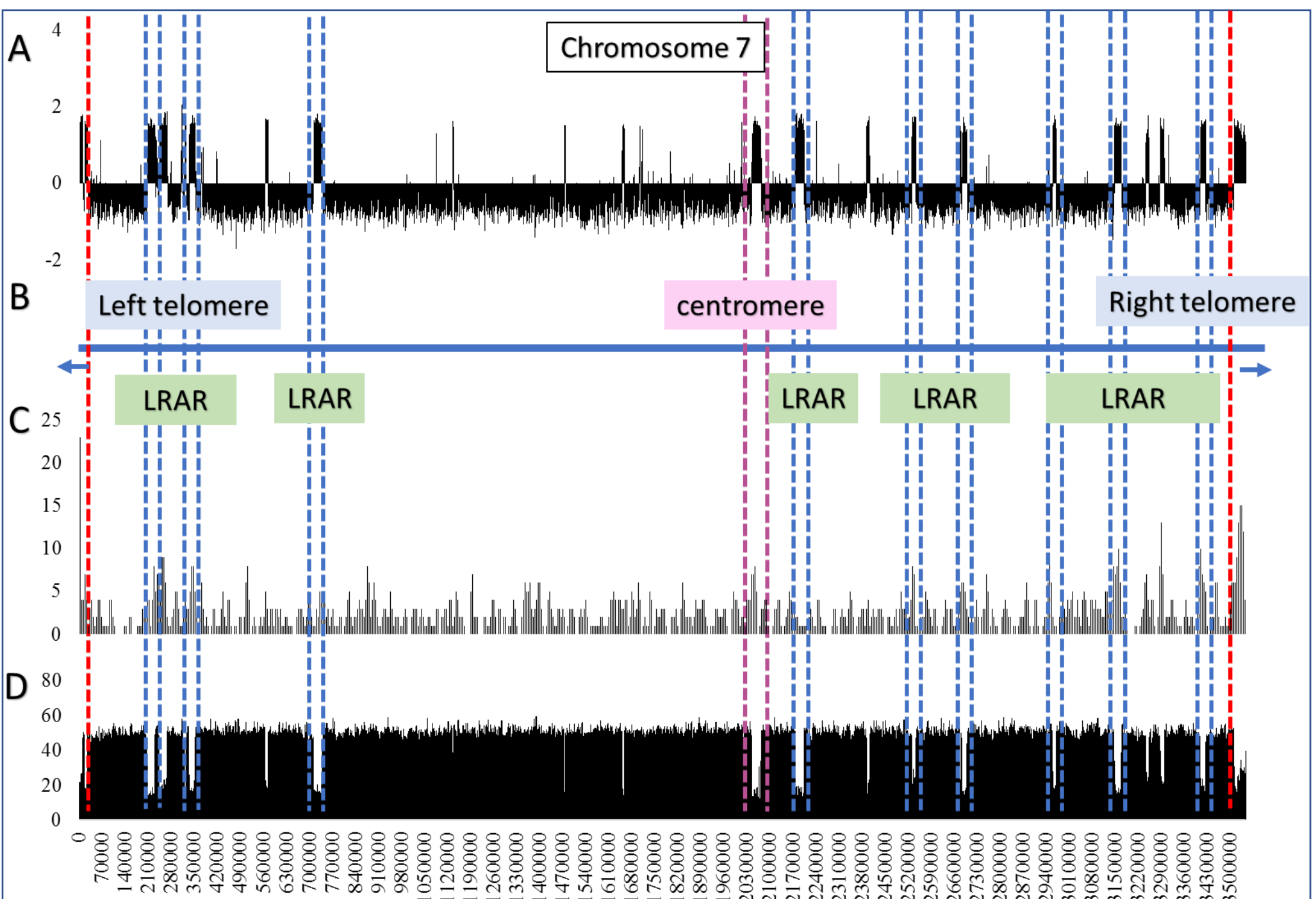
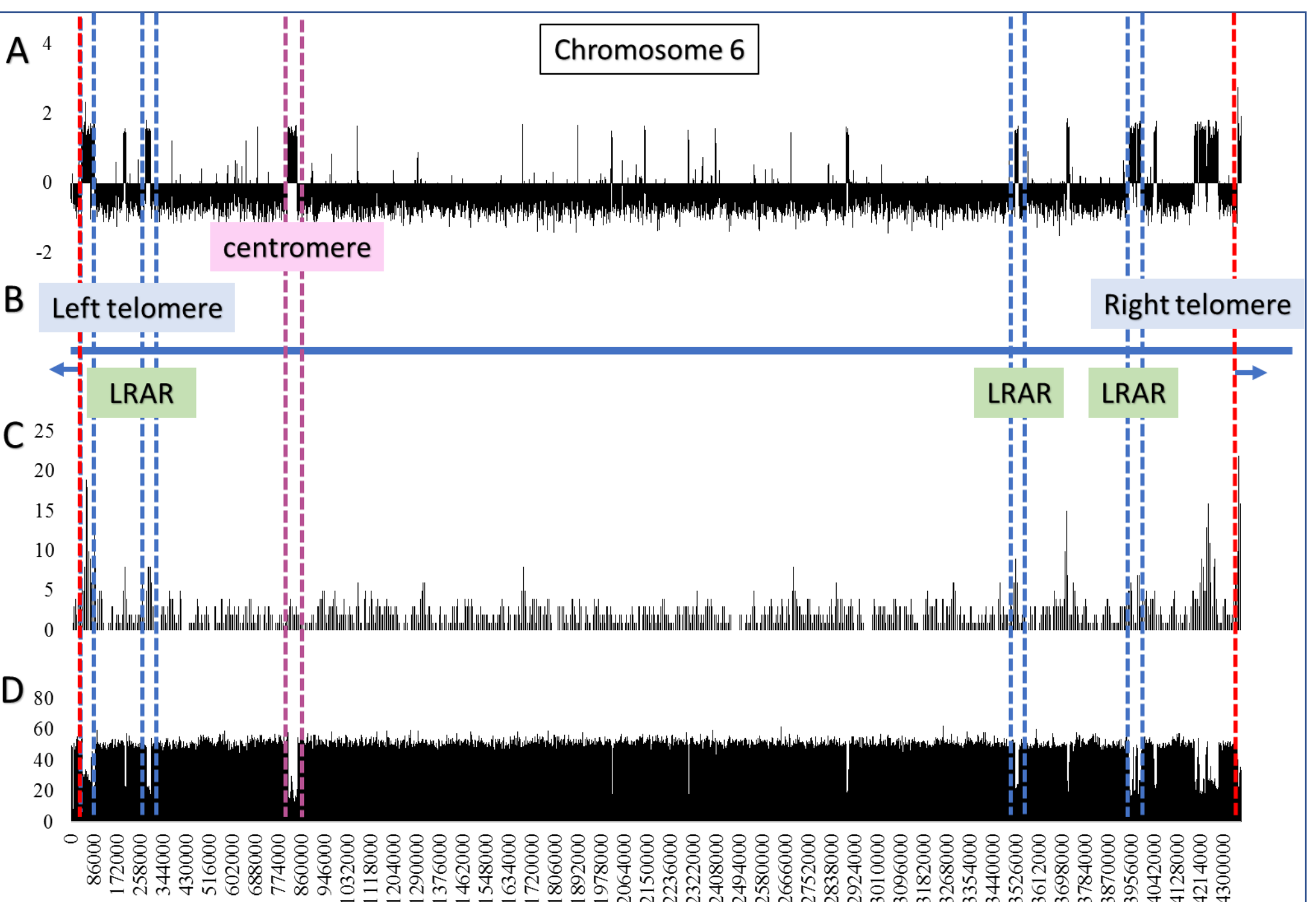
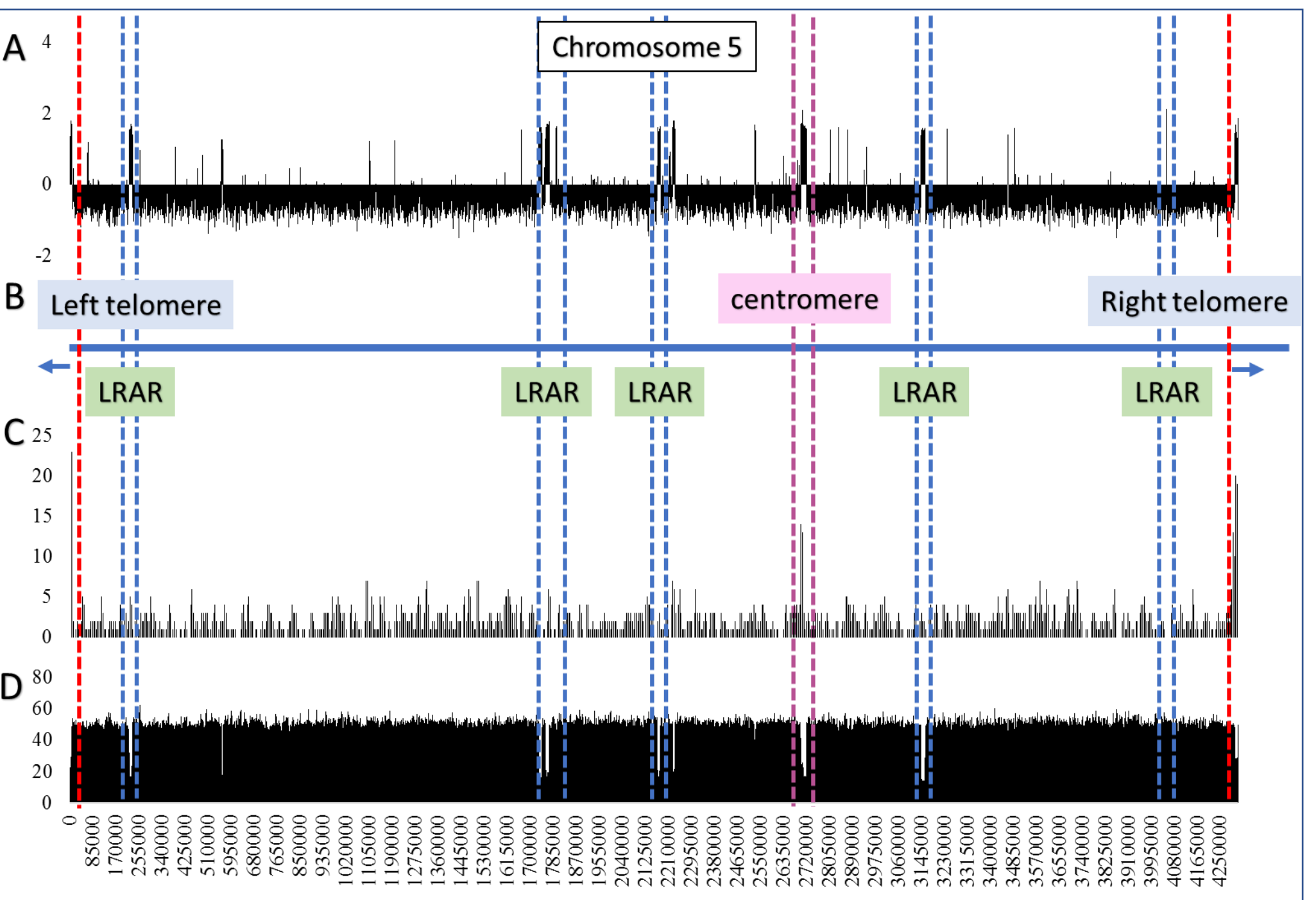
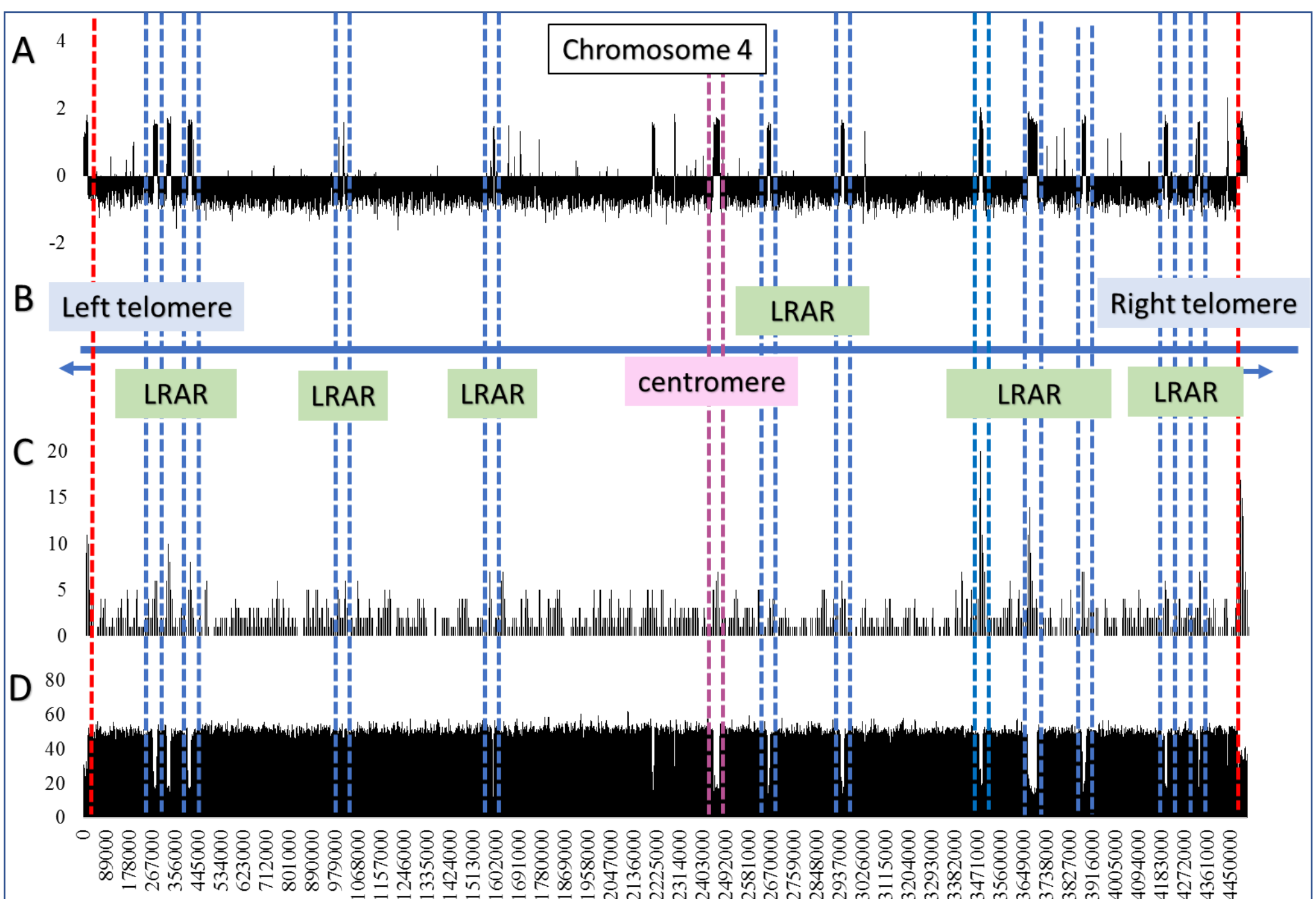
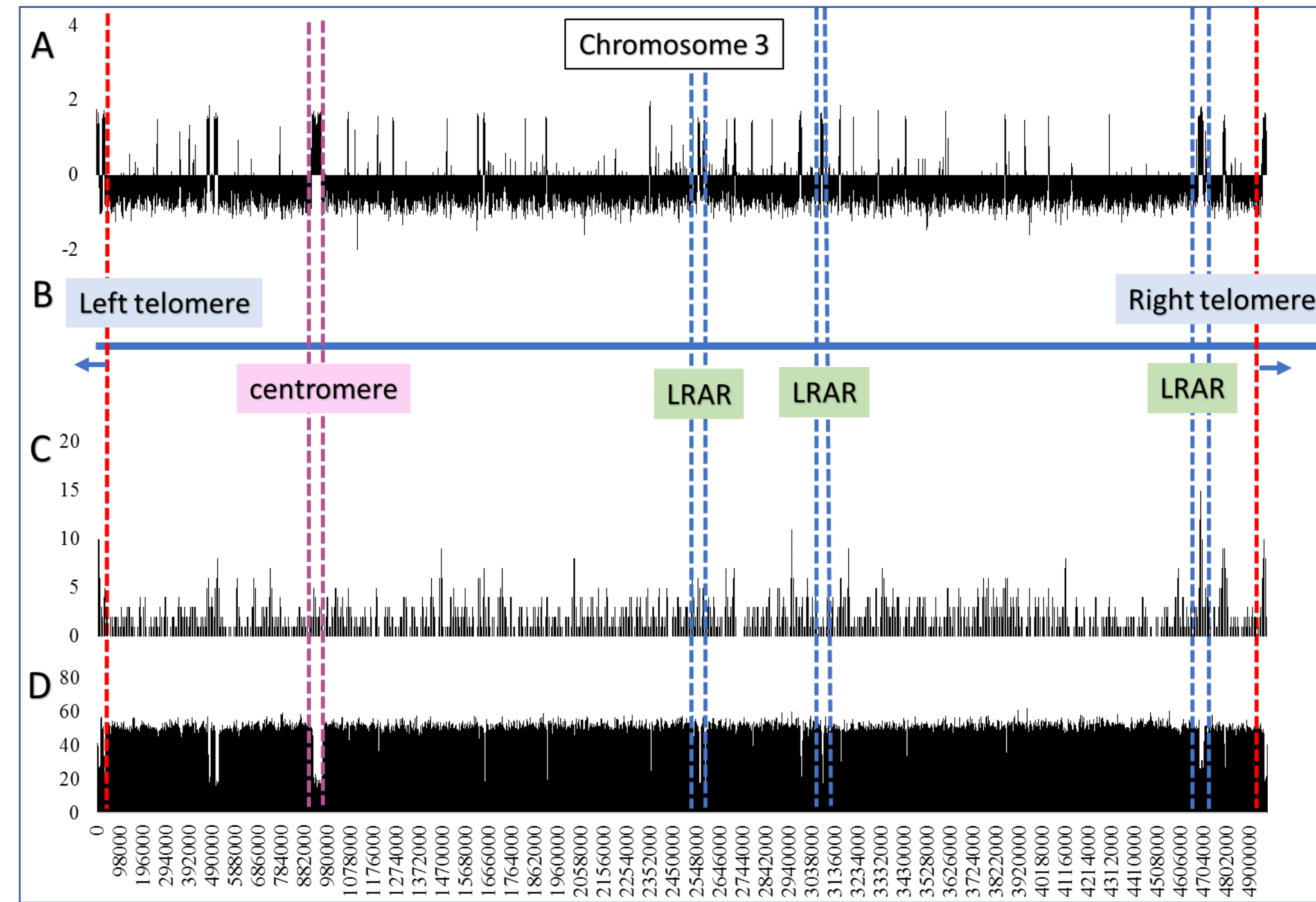
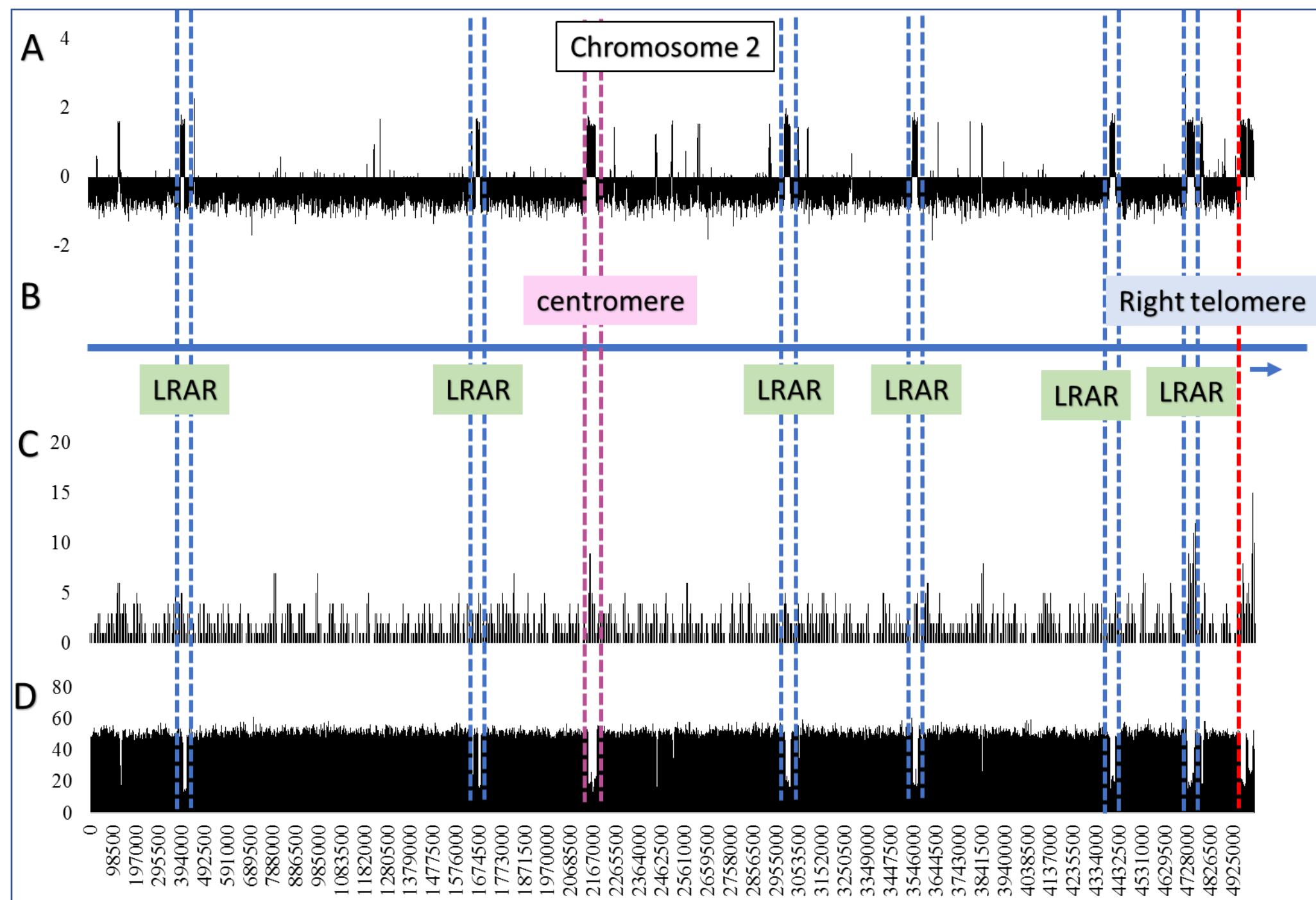
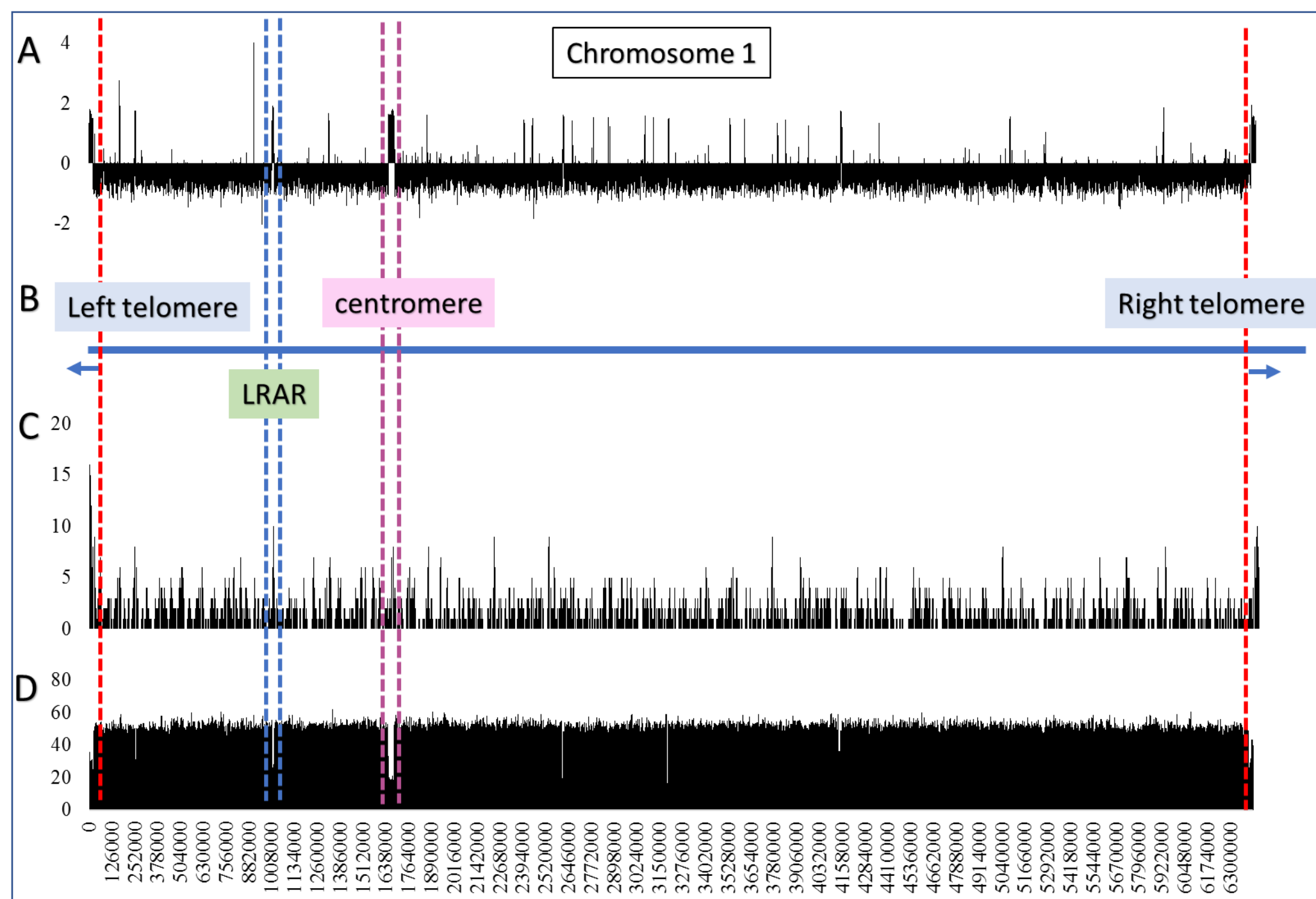
UG27



CMWF567



FSOR



FFRA

