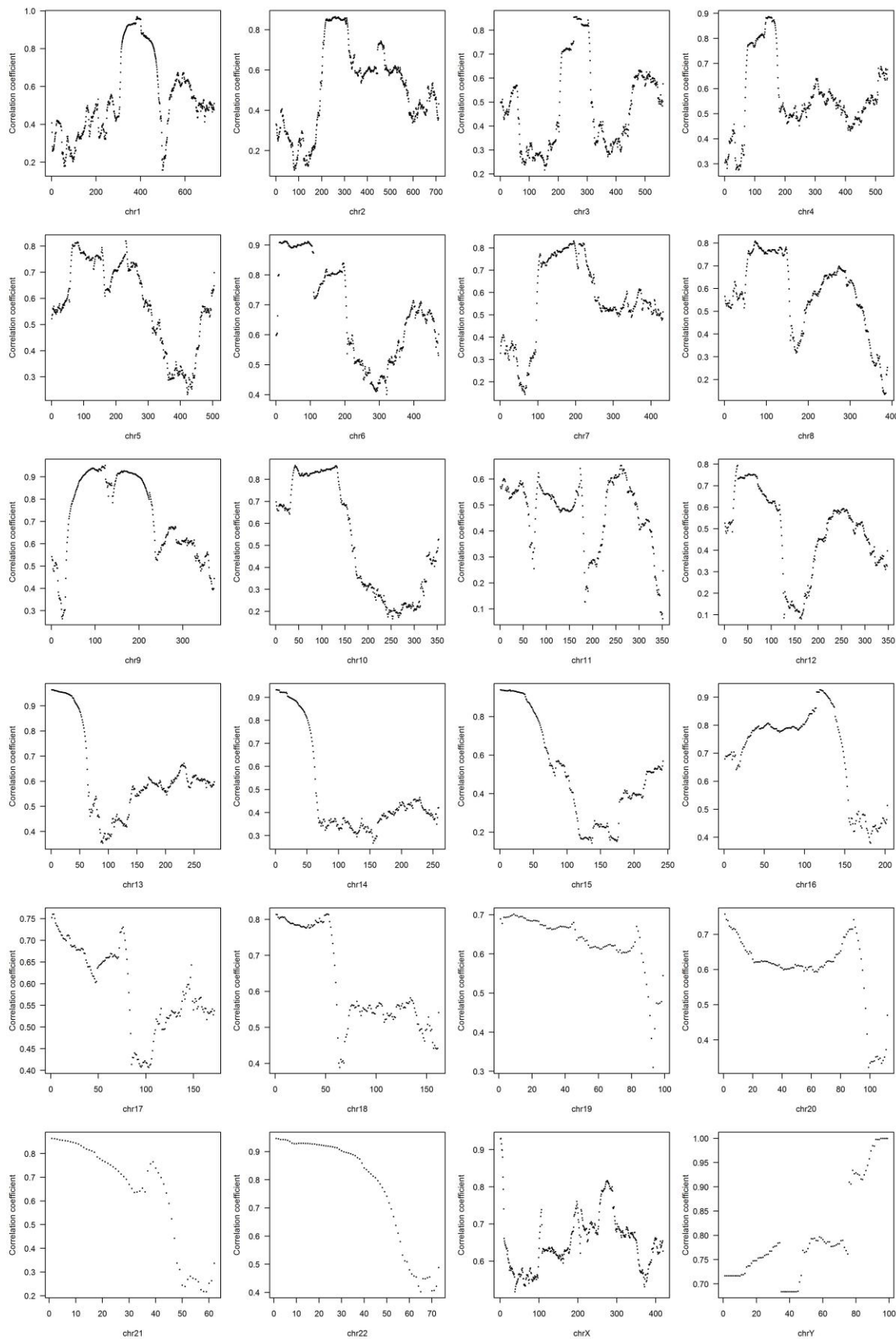
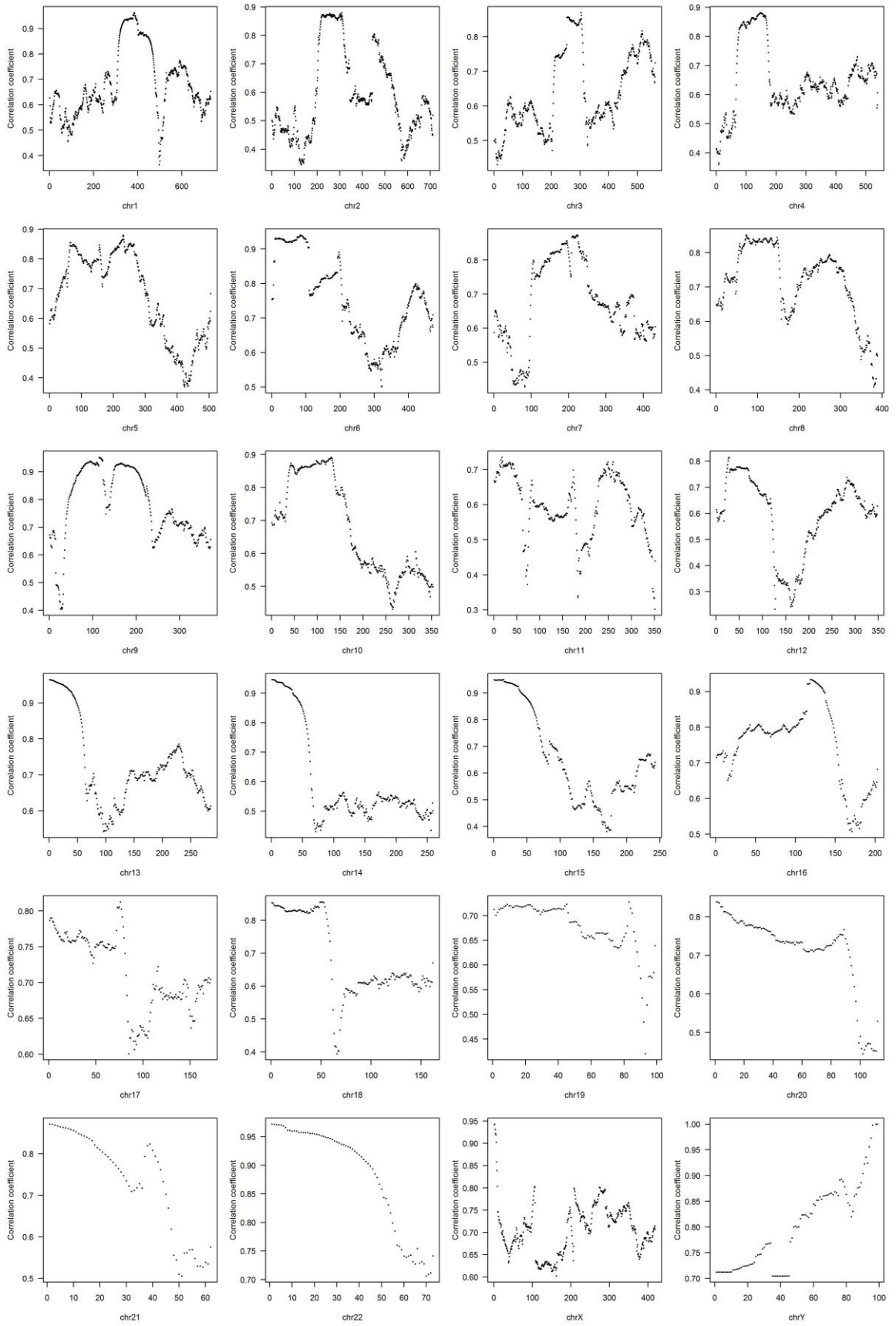


Figure S2. Genome-wide correlations between different types of variants. A) SNP~insertions, B) SNP~deletions, C) SNP~block substitutions, D) insertions~deletions, E) insertions~block substitutions, and F) deletions~block substitutions. The genomes were divided into consecutive 300-kb binned regions and counts of different types of variants were obtained for these binned regions. Pearson's correlation coefficient between two types of variants then was computed using variant counts from 100 consecutive binned regions through the *cor* function in R.

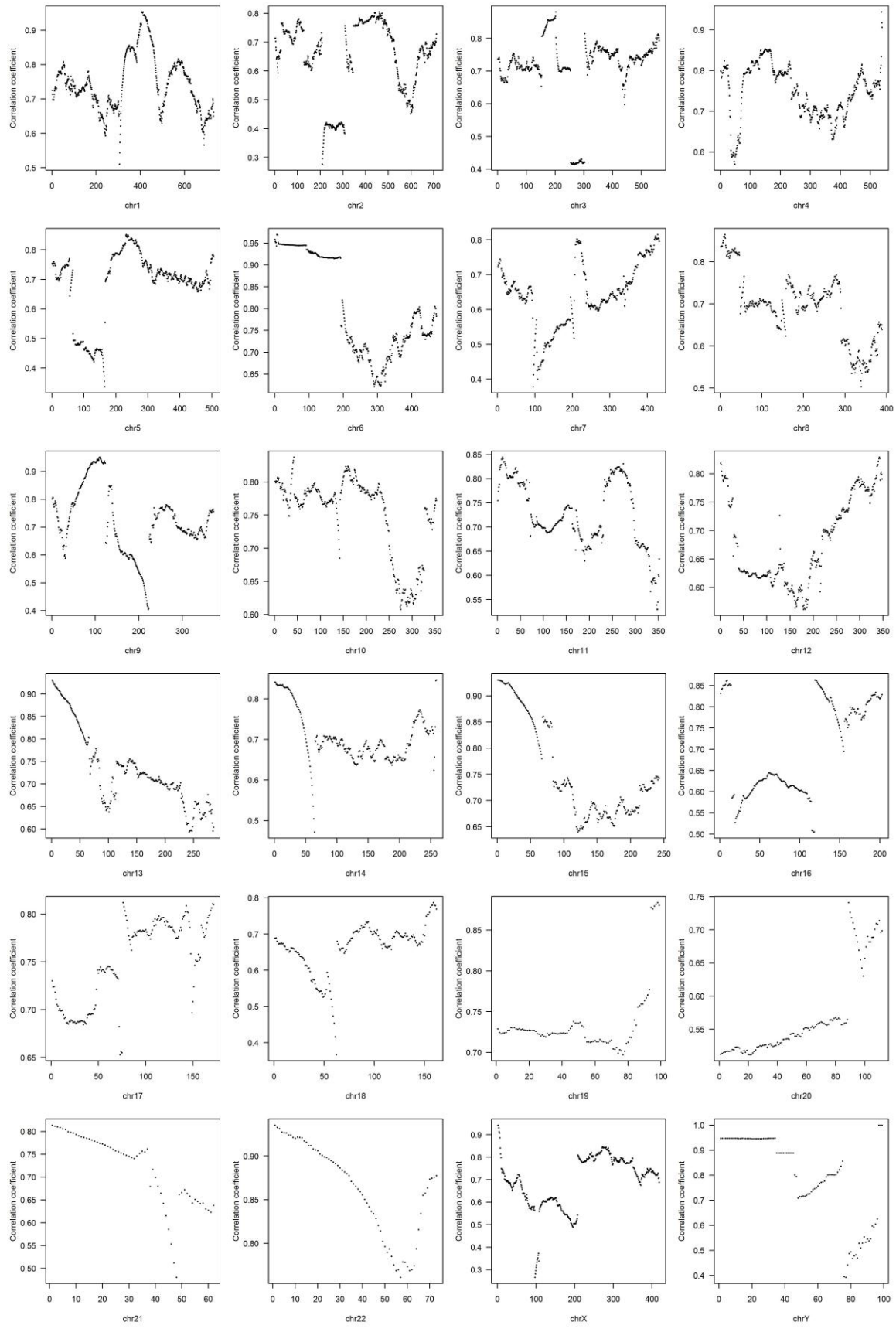
A.



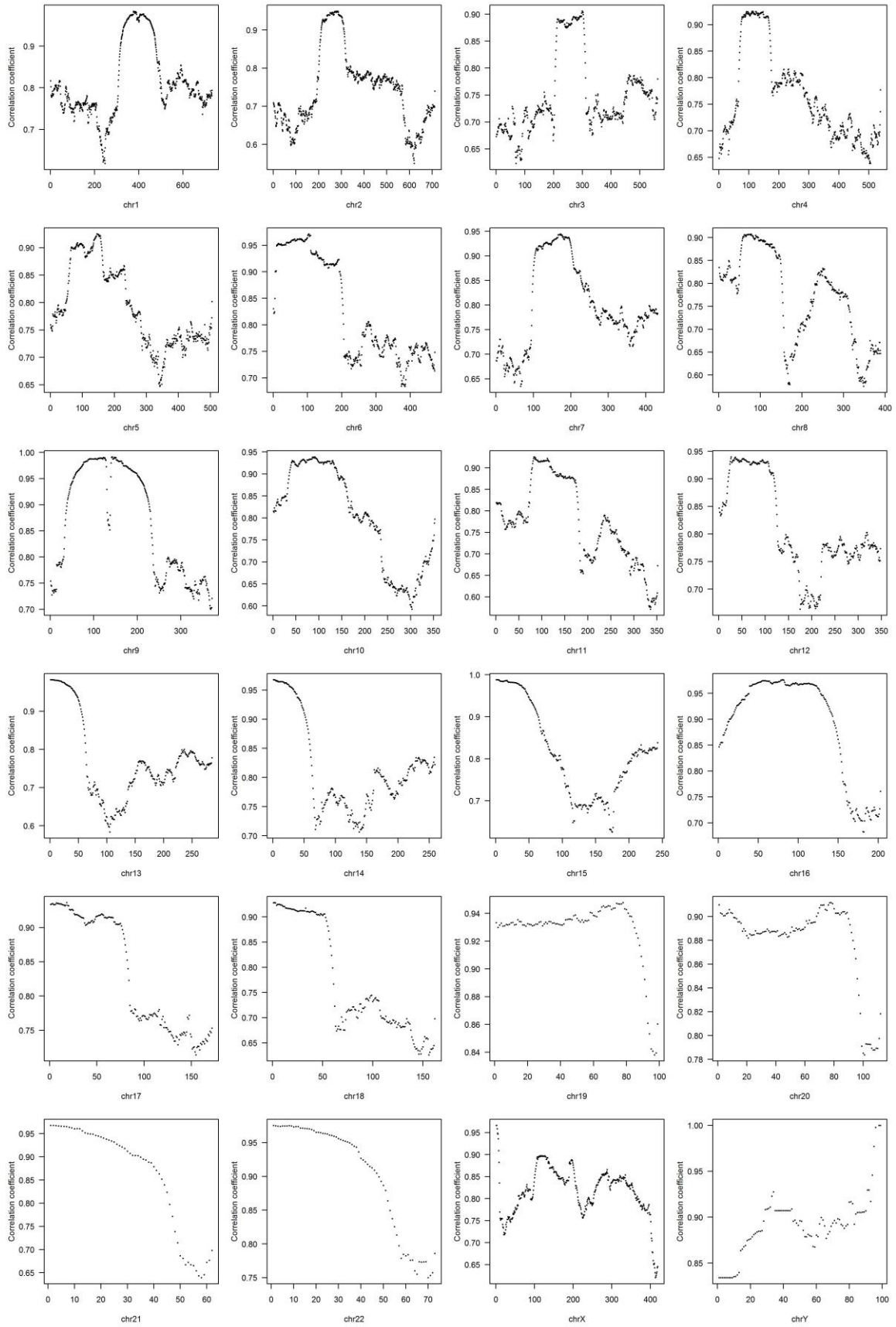
B.



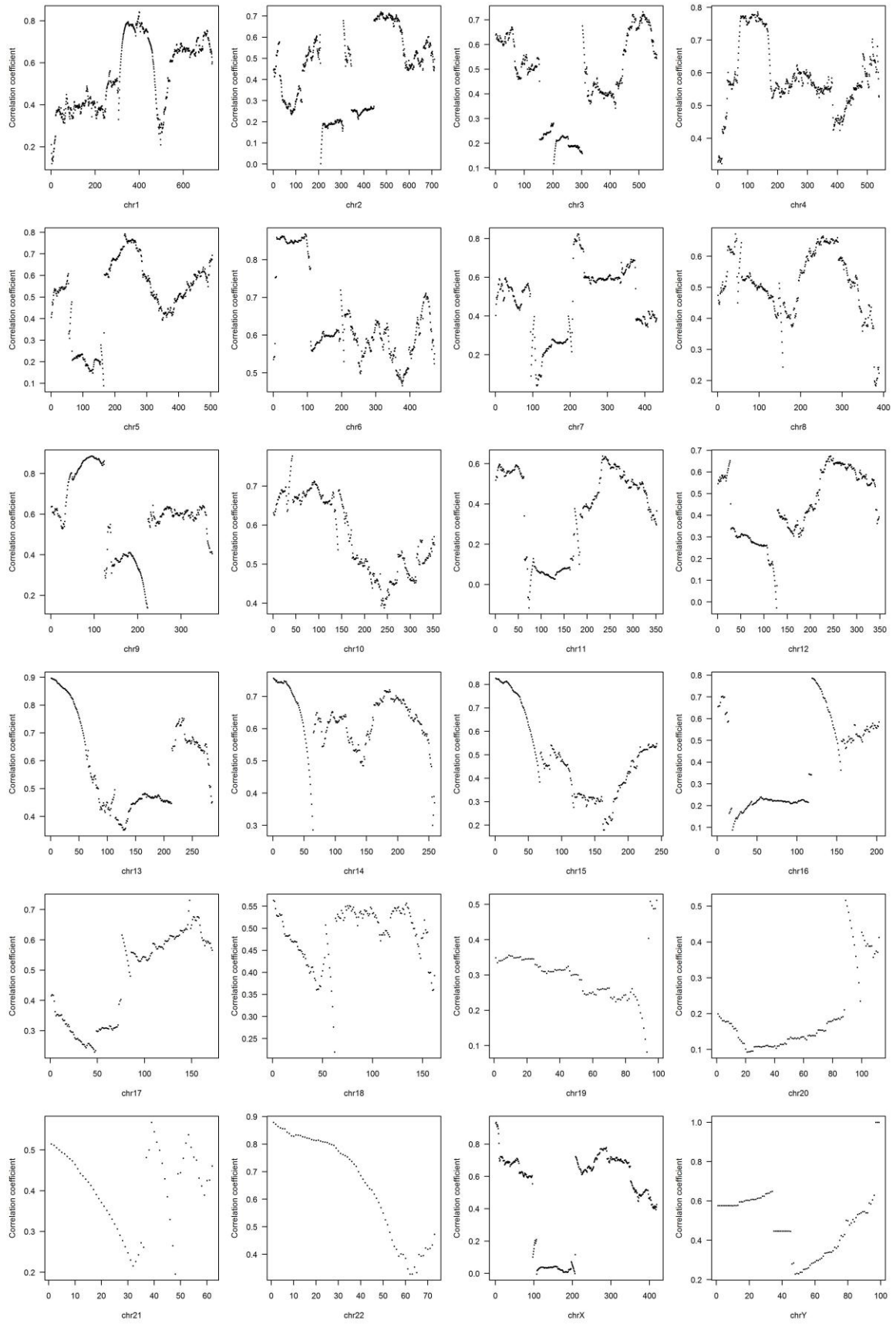
C.



D.



E.



F.

