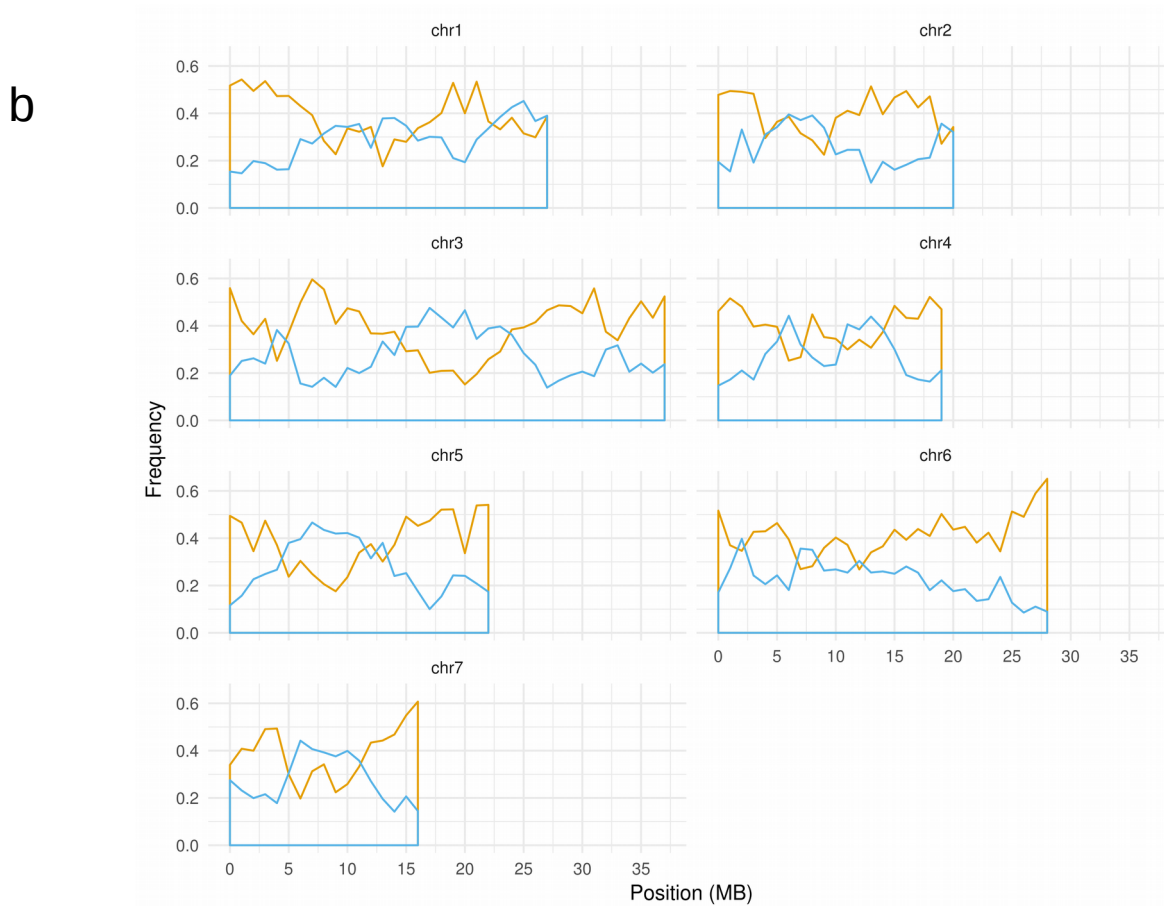
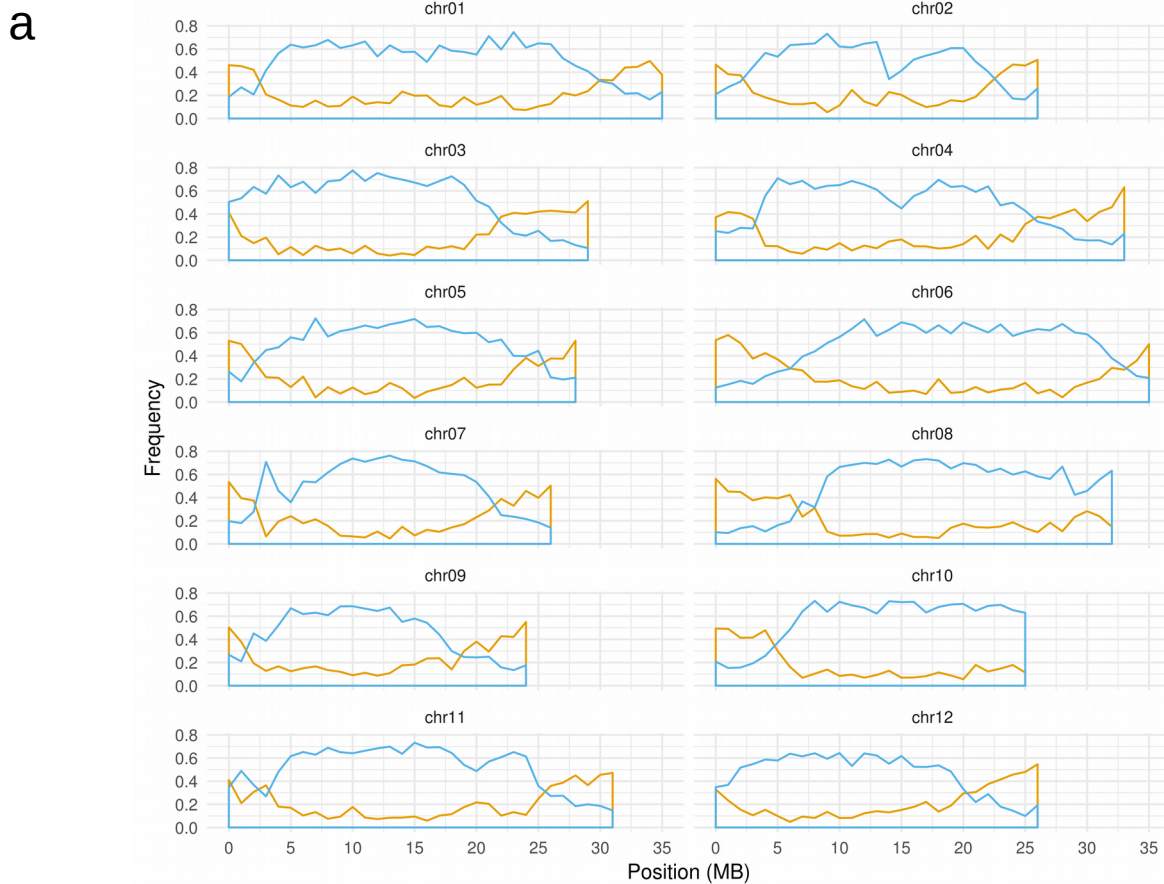
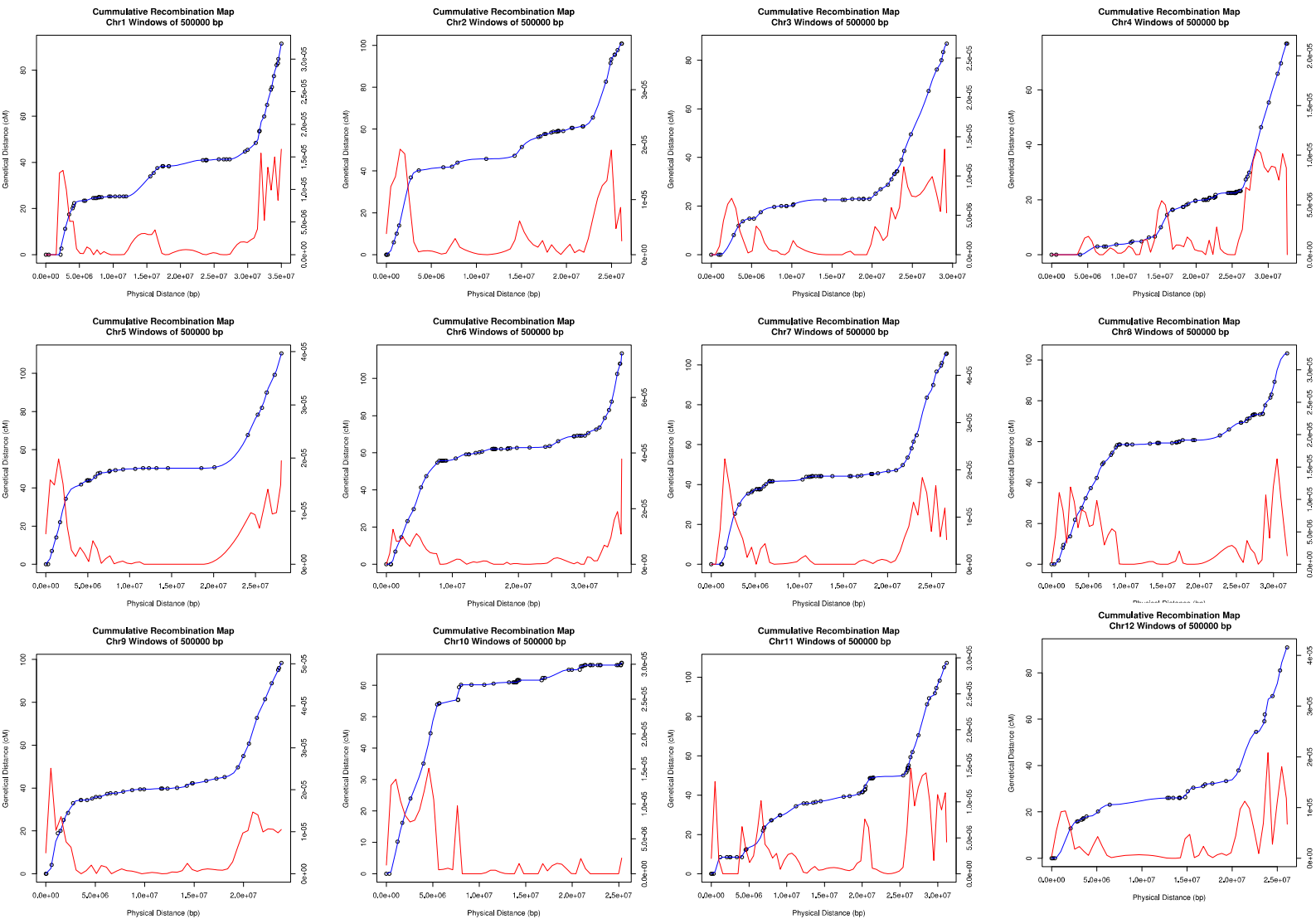


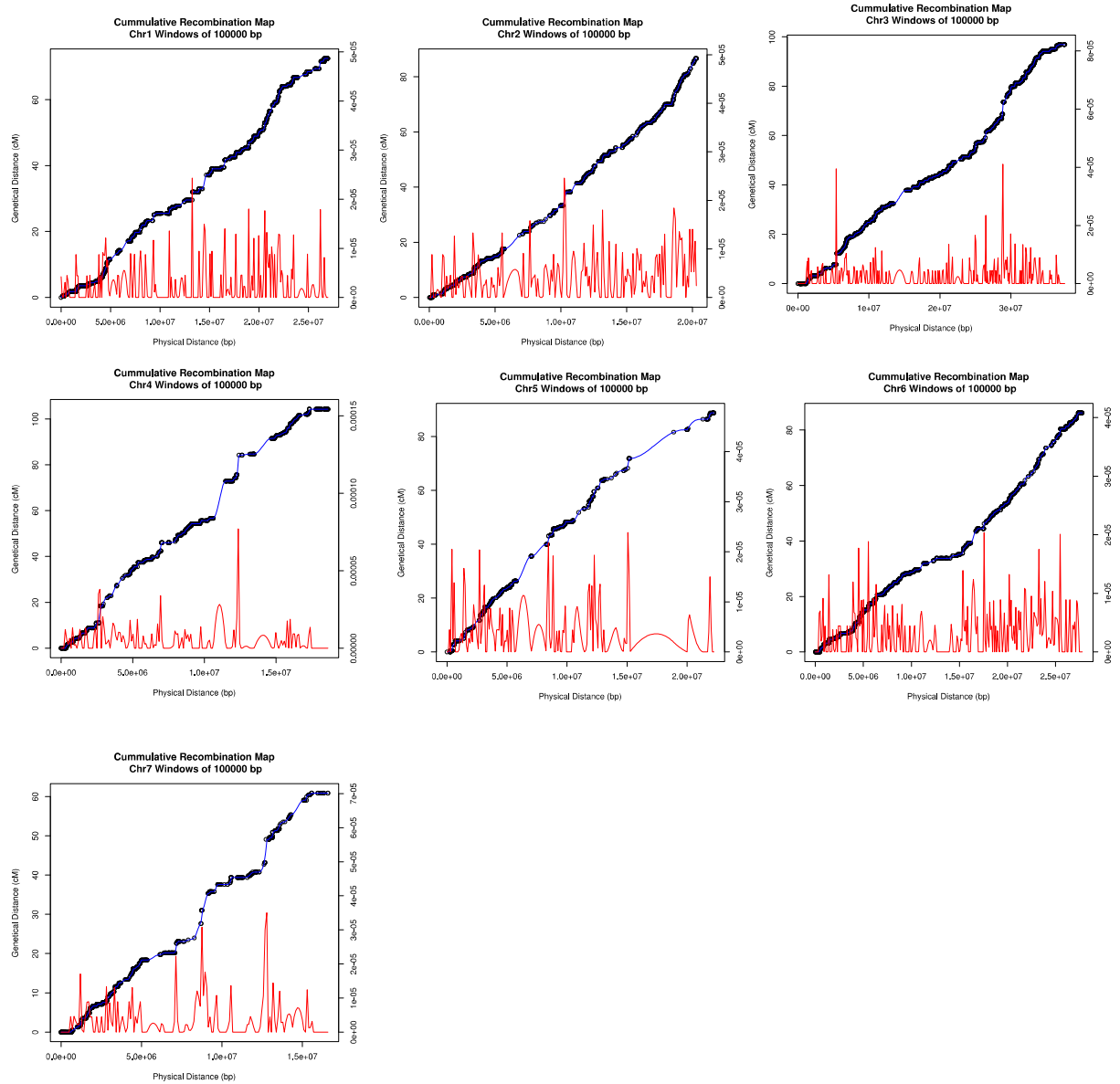
Supplementary Figure 1: Genome composition of melon (a, top) and cucumber (b, bottom) chromosomes. Fraction of gene (yellow) and TE (blue) nucleotides per 1MB window.



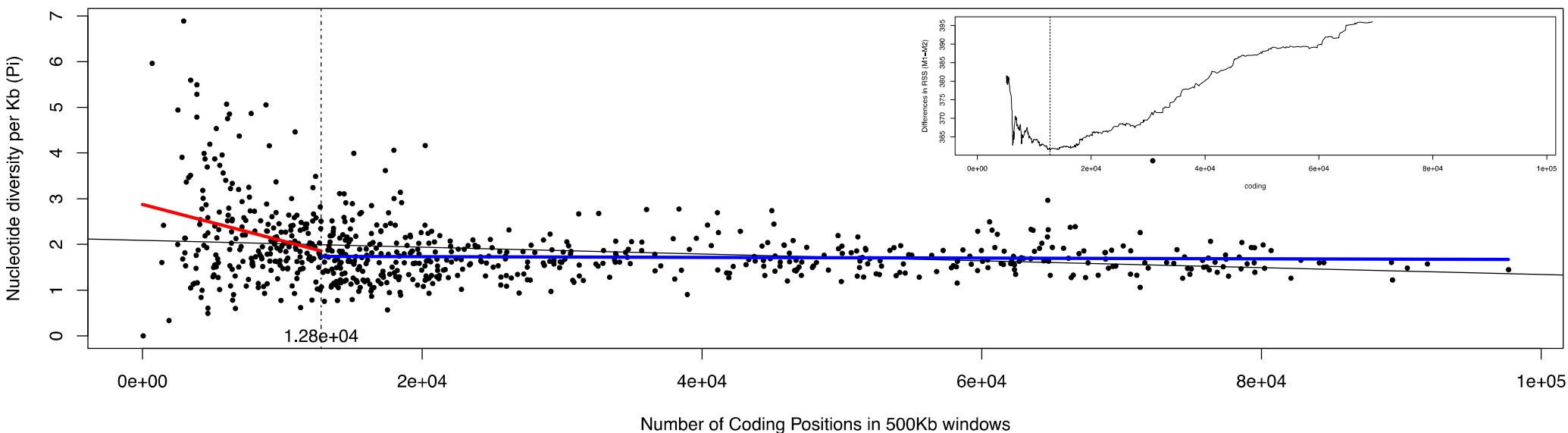
Supplementary Figure 2a: Distribution of recombination rate along 12 melon chromosomes in windows of 500 kb. Blue line indicates cumulative recombination rate.



Supplementary Figure 2b: Distribution of recombination rate along 7 cucumber chromosomes in windows of 100 kb. Blue line indicates cumulative recombination rate.



Supplementary Figure 3: The main plot is showing in x-axis the number of coding positions and in the y-axis the estimates of non-synonymous variability per position over 500Kb window sizes. The dashed line indicates the limit of coding density (from 0 to 1.25×10^4 , see Methods about the definition of the limit point) where this parameter is associated with the nonsynonymous variability (graphically represented by the straight red line), while beyond this limit there is no observed association (graphically represented by the straight blue line). The black line shows the linear correlation of the entire set of data. The above plot shows the sum of the RSS (Residual Sum of Squares) from the regression analysis when the data is separated in low and high. The minimum RSS indicates the better density to fit to this model (pointed out by a dashed line).



Supplementary Figure 4: Melon Gene Length (a) and Gene Exon Number (b) distribution in gene rich (blue) and gene poor (orange) regions. Mean values for each region cited in the main article are also depicted in dashed lines. For clarity reasons, gene length was limited to 10 kb and gene count to 20 exons. Density was adjusted by a factor of 4. The distributions from gene rich and gene poor regions were significantly different (Kolmorov-Smirnov test, P-value < 0.001) in both cases.

