

Supplementary Figures

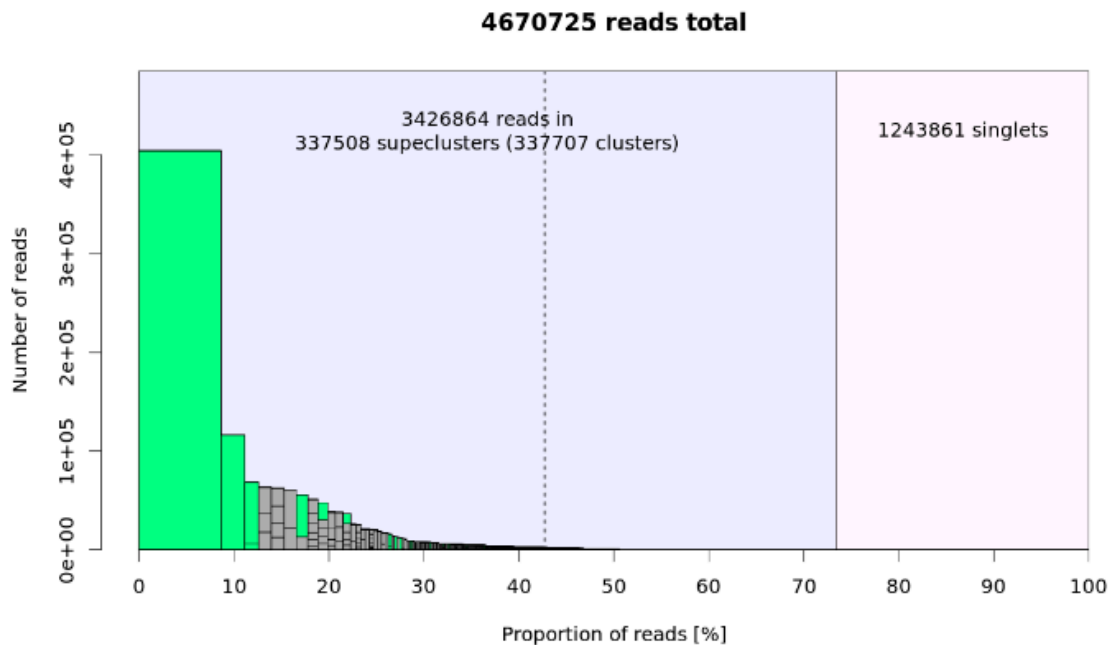


Figure S1. Graphical summary of the clustering results obtained with RepeatExplorer2, displaying the total number of reads used and the repetitive DNA clusters. The clusters representing more than 0.001% of the genome are located to the left of the dotted line. Bars represent superclusters, with their heights and widths corresponding to the numbers of reads in the superclusters (y-axis) and to their proportions in all analyzed reads (x-axis), respectively. Rectangles inside the supercluster bars represent individual clusters. Superclusters containing abundant satellites, as identified by RepeatExplorer, are highlighted in green.

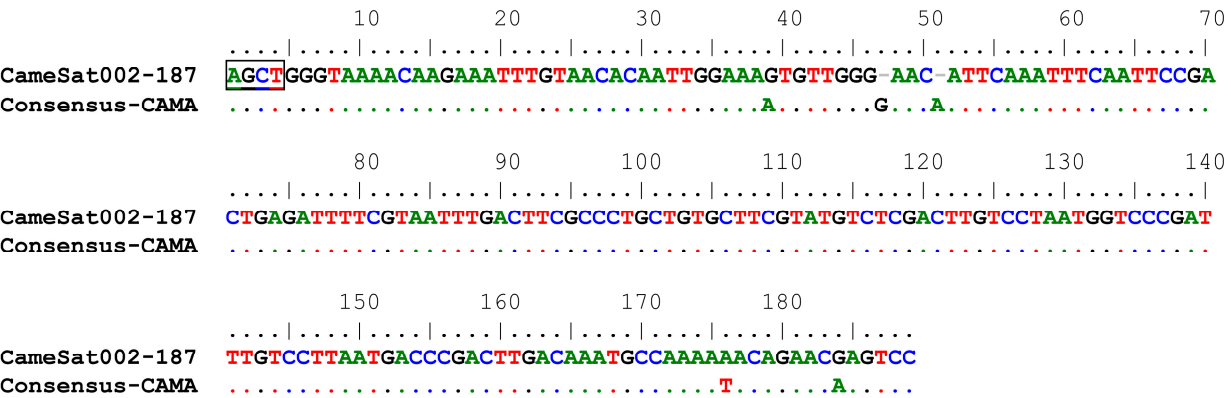


Figure S2. Alignment between the consensus sequence of the CameSat002-187 satDNA family and the consensus sequence of the CAMA satDNA family as described by Lorite *et al.* (2001). The alignment was performed by digesting the sequences with *A**lu*I restriction enzymes. In the presented sequence, the box denotes the specific target sequence for this enzyme (AGCT).

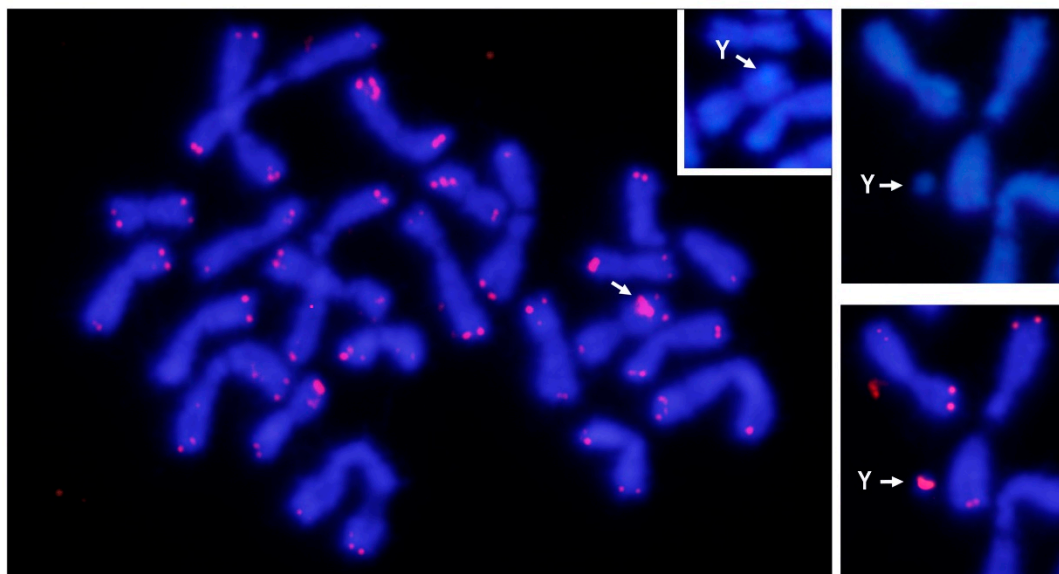


Figure S3. FISH with (TTAGG)<sub>n</sub> telomeric probe (red signals) on mitotic chromosomes (counterstained with DAPI in blue) of *Chrysolina americana*.

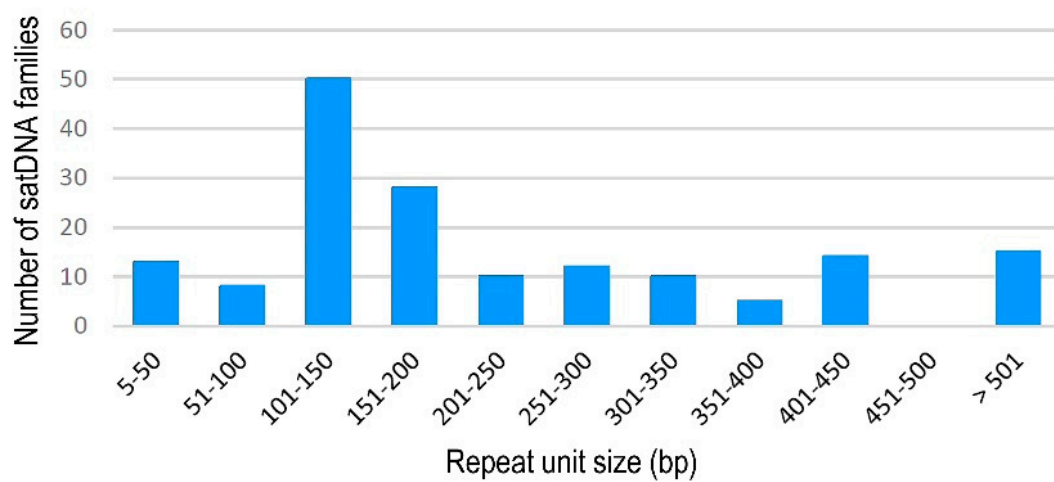
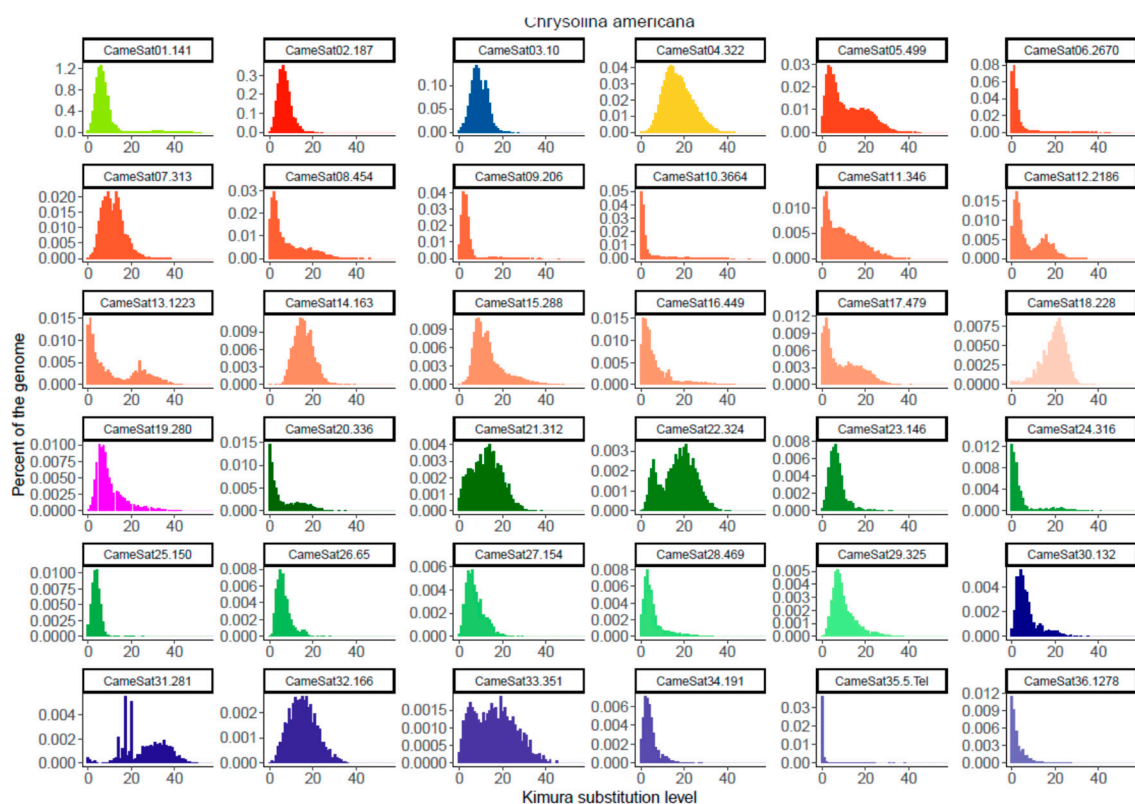
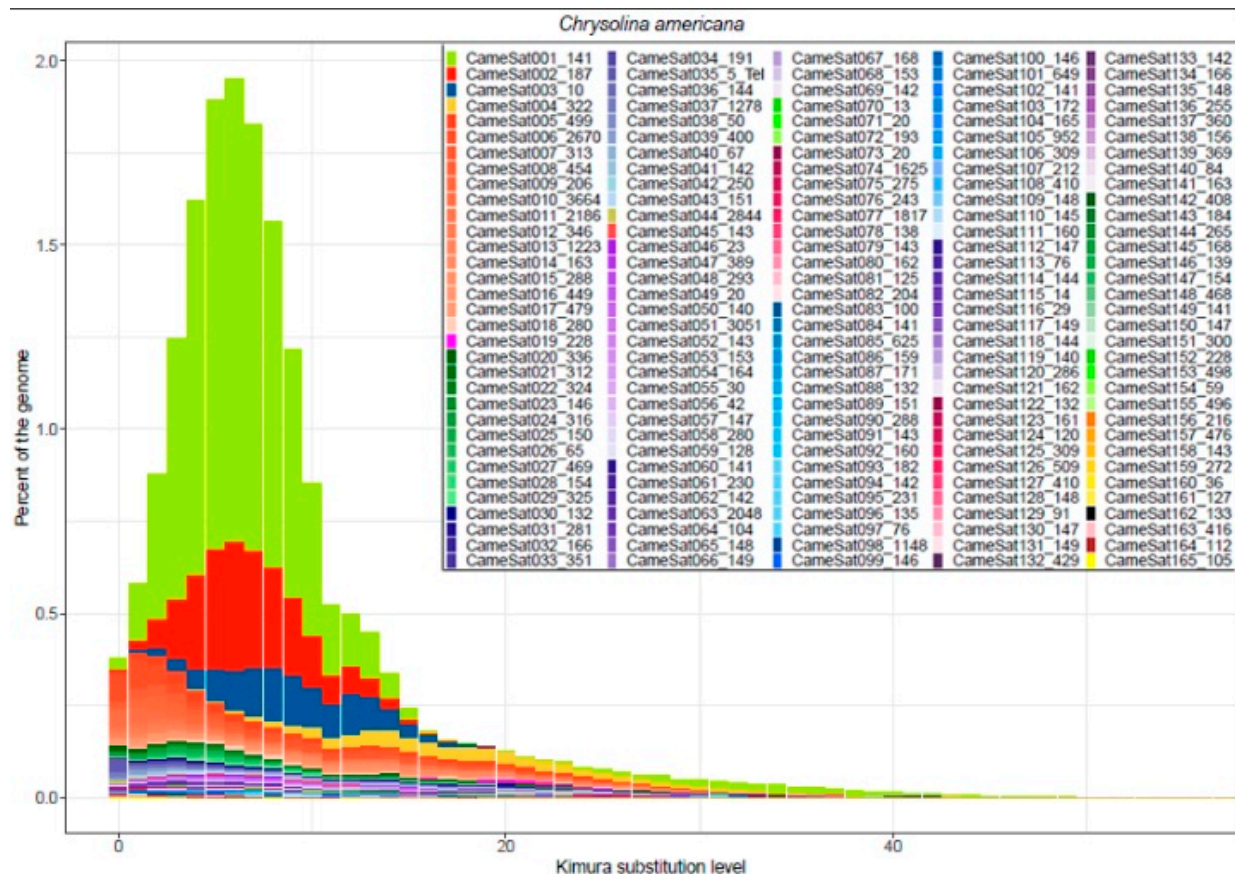


Figure S4. Distribution of satellite DNA families in *Chrysolina americana* based on the size of their repeat unit.



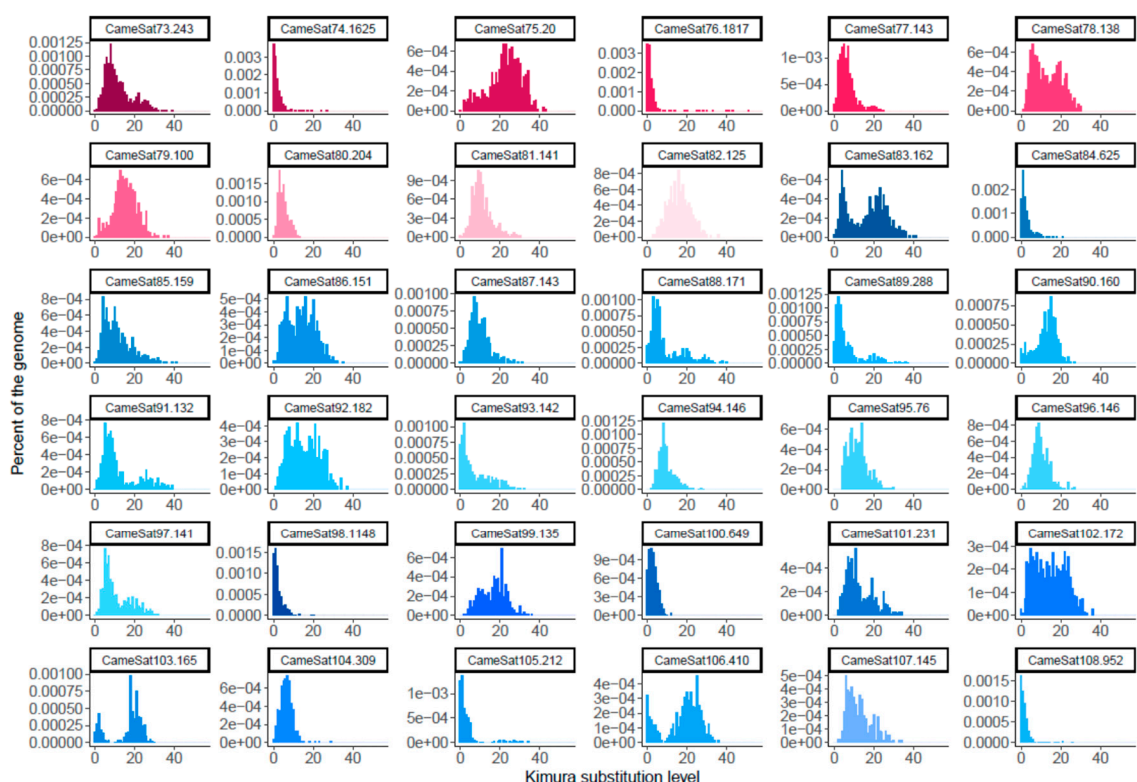
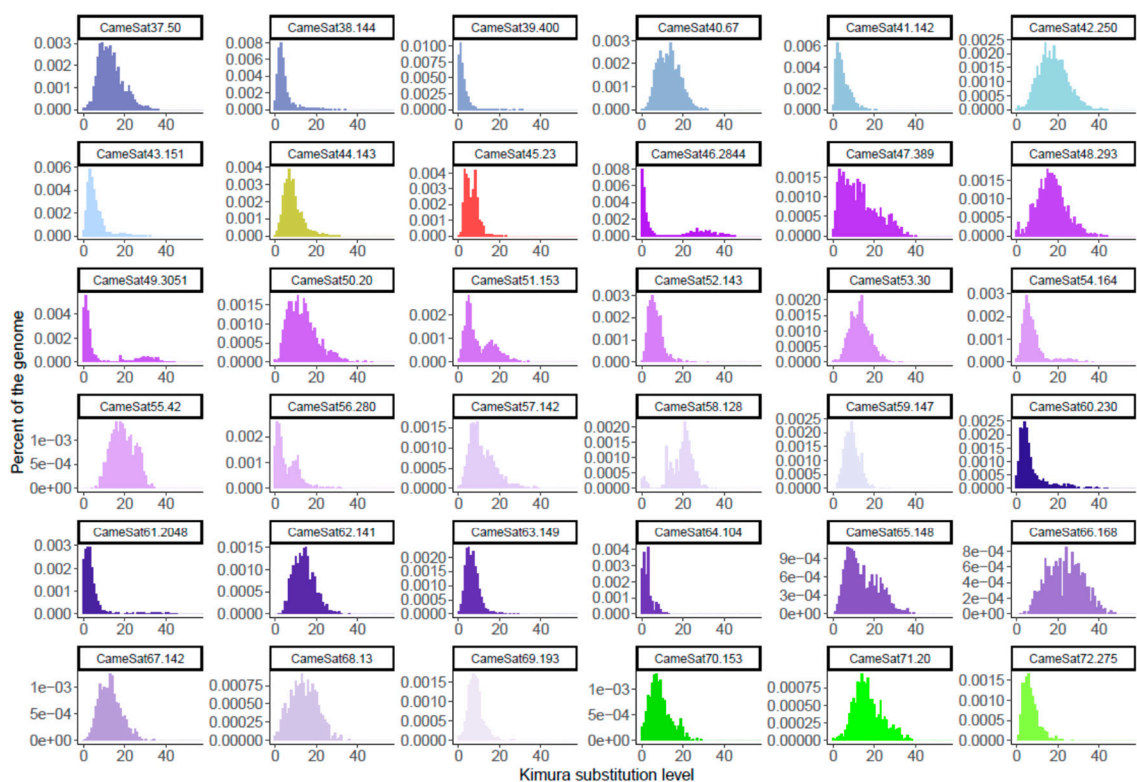
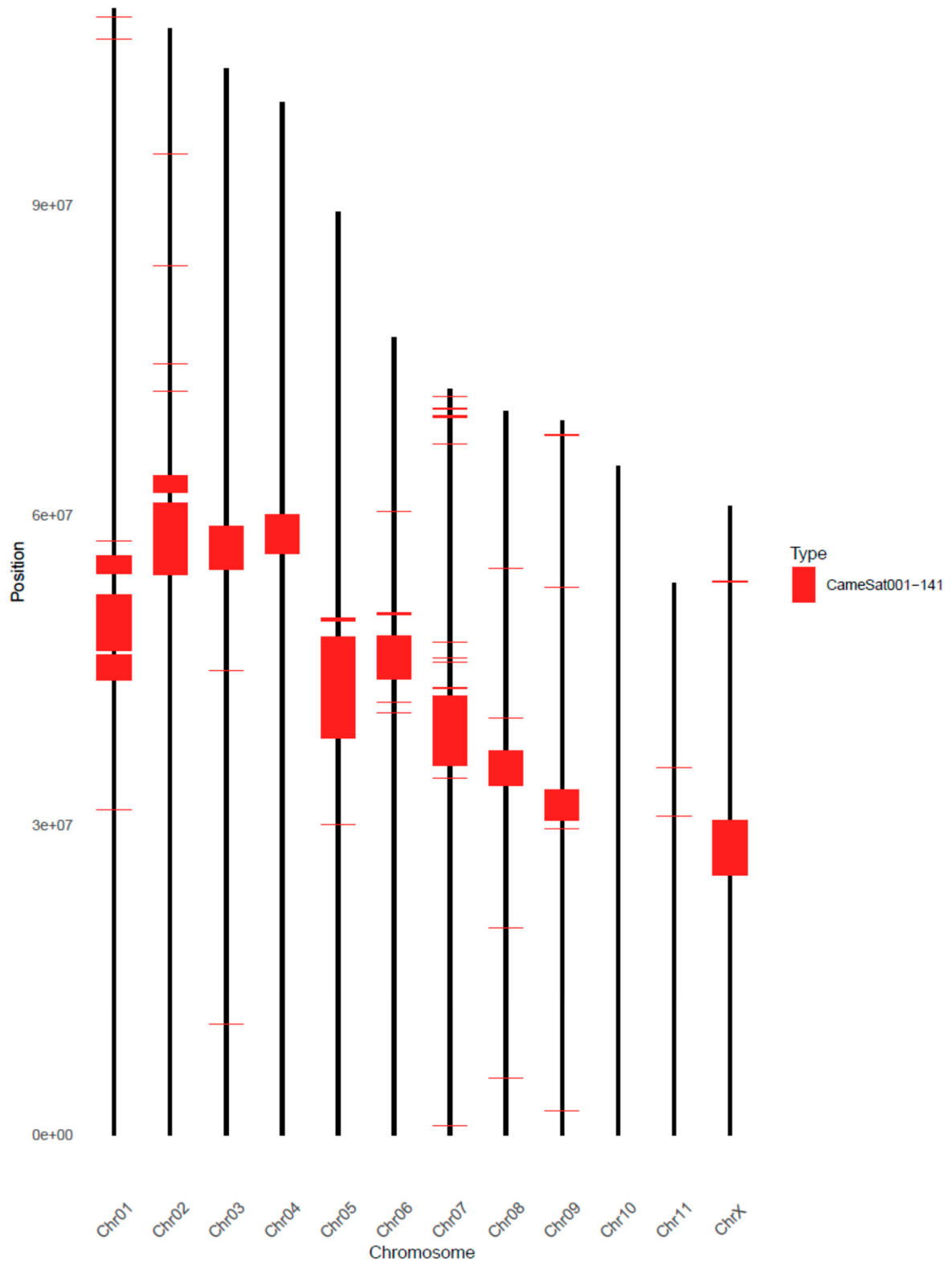




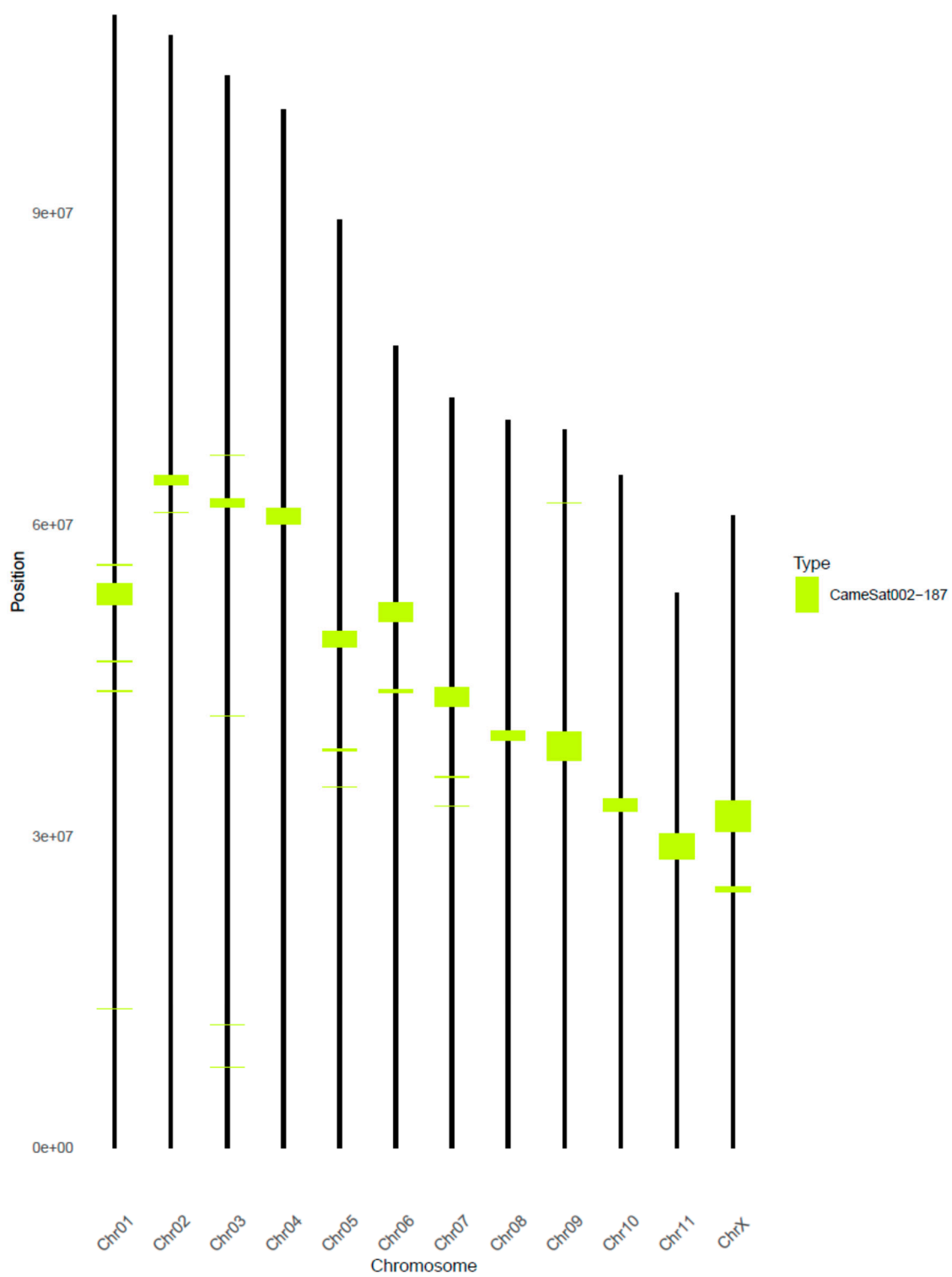


Figure S5. Satellite DNA landscapes for all satDNA families found in *Chrysolina americana*.

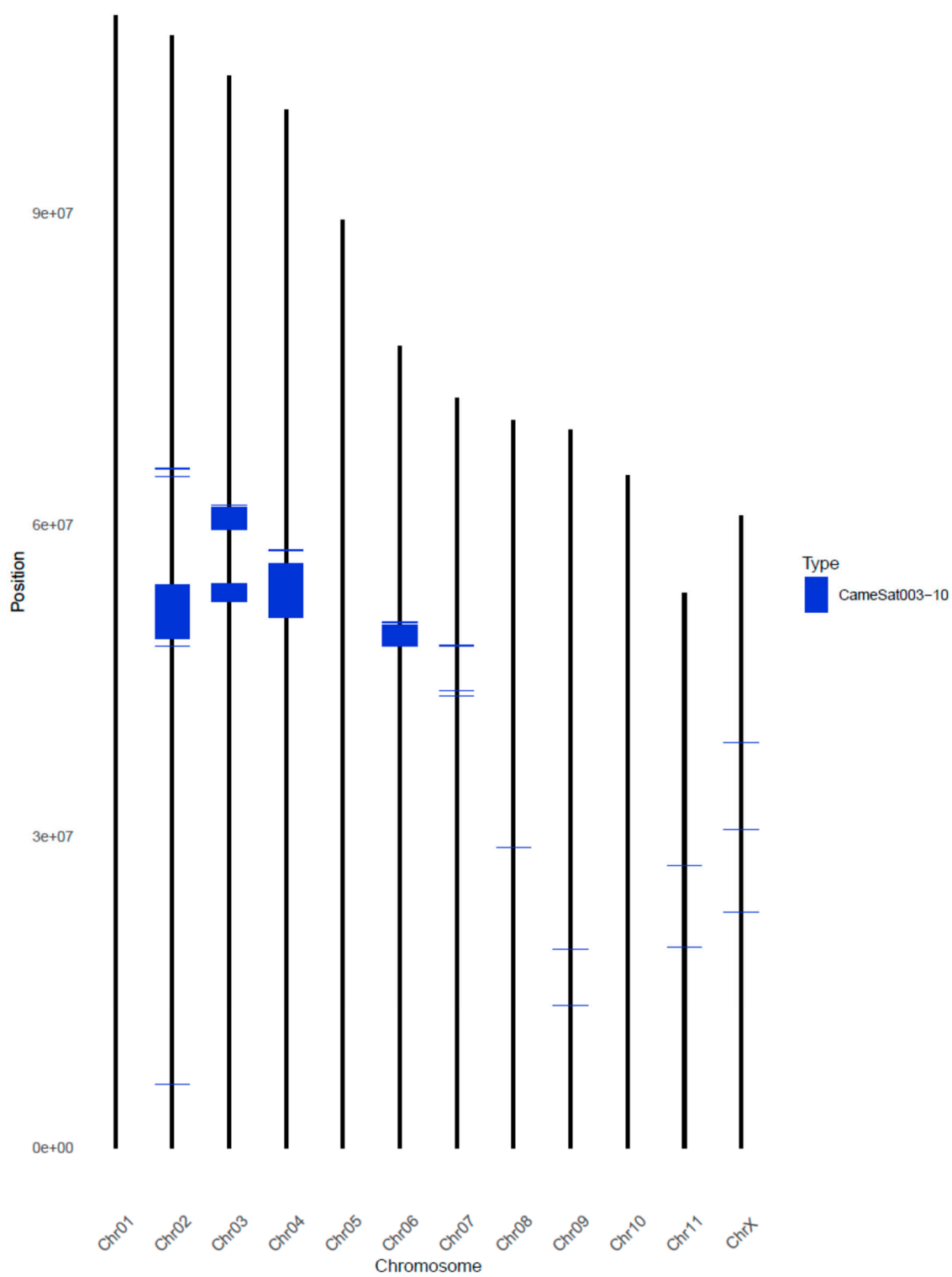
Annotation – Type: CameSat001–141



Annotation - Type: CameSat002-187

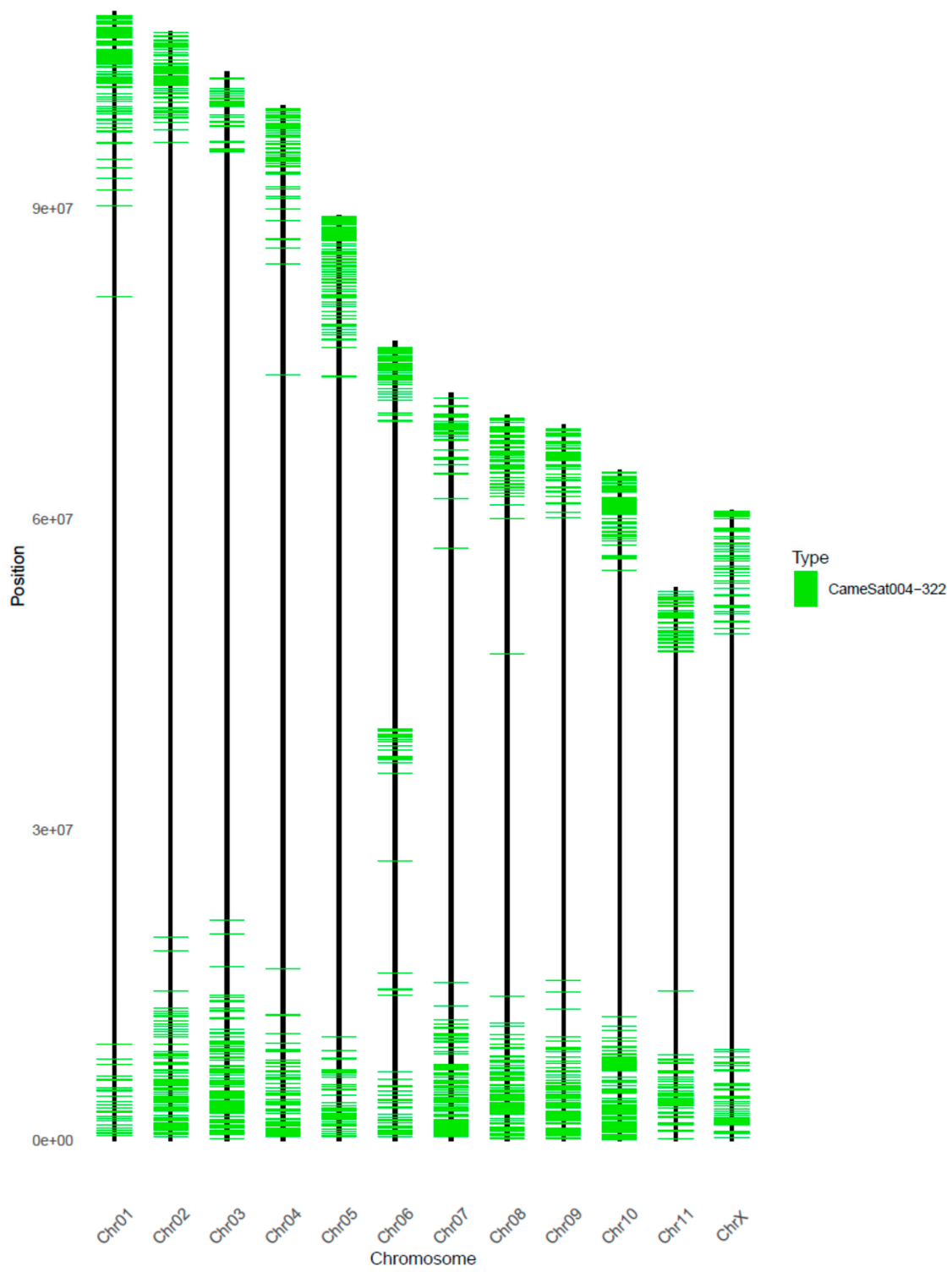


Annotation - Type: CameSat003-10





Annotation - Type: CameSat004-322



Annotation - Type: CameSat005-499

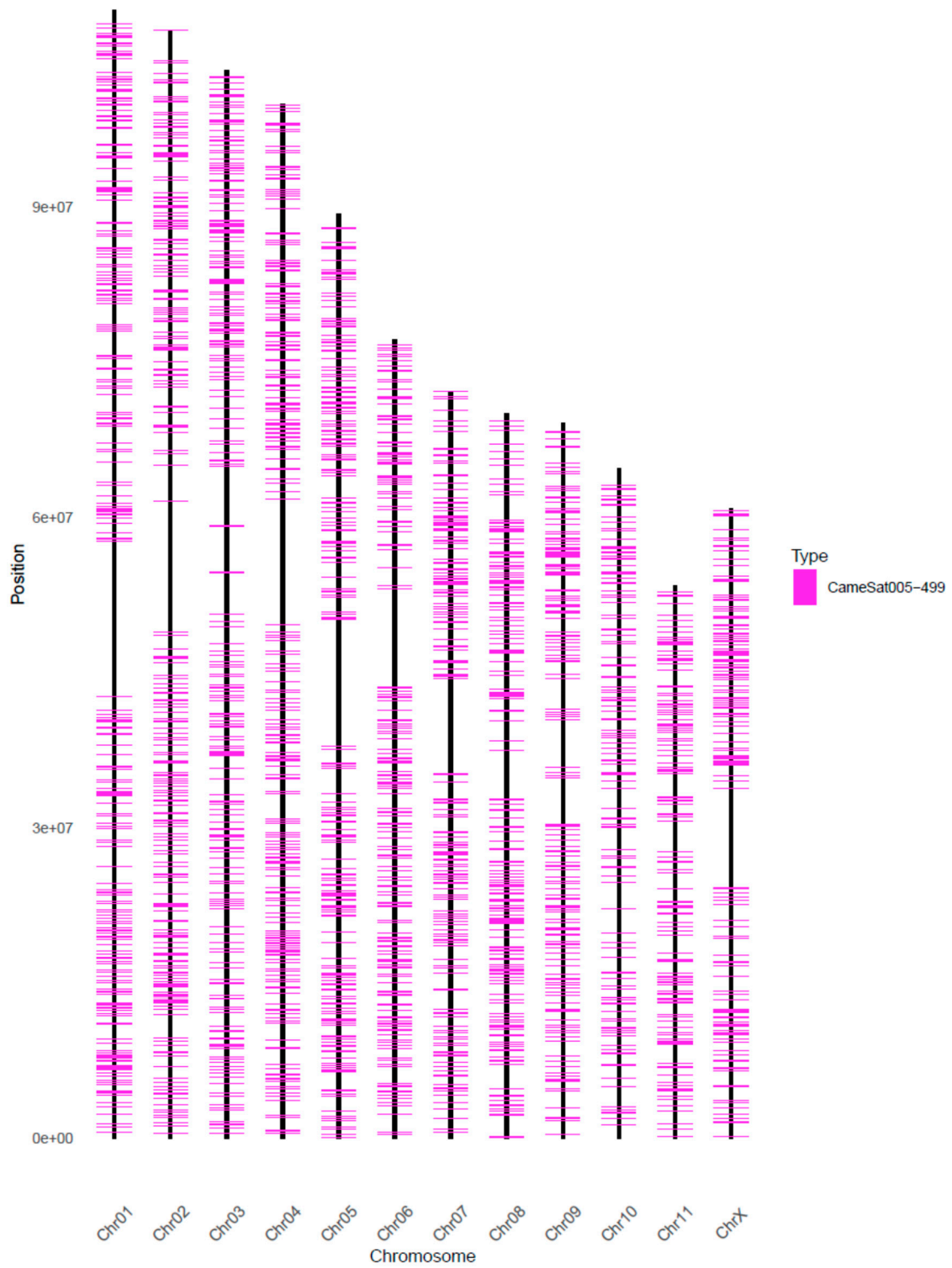


Figure S6. *Chrysolina americana* pseudo-chromosomes showing the distribution of the main satDNA families obtained through the CHRISMAPP approach.