

“High evolutionary turnover of satellite families in *Caenorhabditis*”

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Supplementary Figures

Figure S1. Distribution of repeat sequences in each chromosome of *C. elegans*.

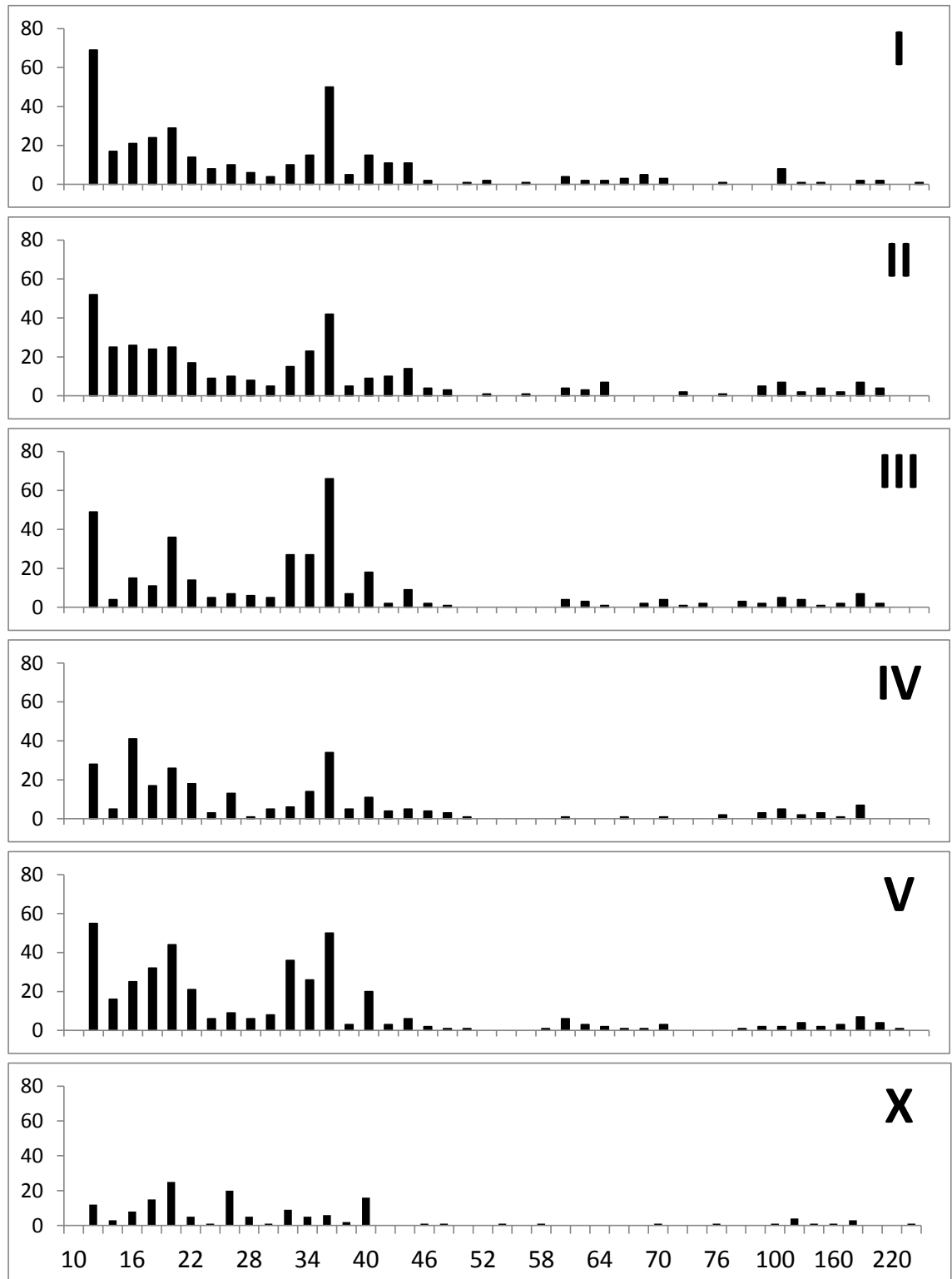
Figure S2. Size of satellites, as a function of their position in each chromosome.

Figure S3. Shared satellite families between pairs of *Caenorhabditis* species.

Figure S4. Distribution of the (ACTACAA)₂ sequence in chromosome I of *C. elegans* and *C. briggsae*.

Figure S5. Histogram of human satellites.

Figure S1. Distribution of repeat sequences in each chromosome of *C. elegans*. It is clear that all chromosomes have a similar distribution, with the exception of Chromosome X. Satellites longer than 80 bases have been merged into bins of 20 bases.



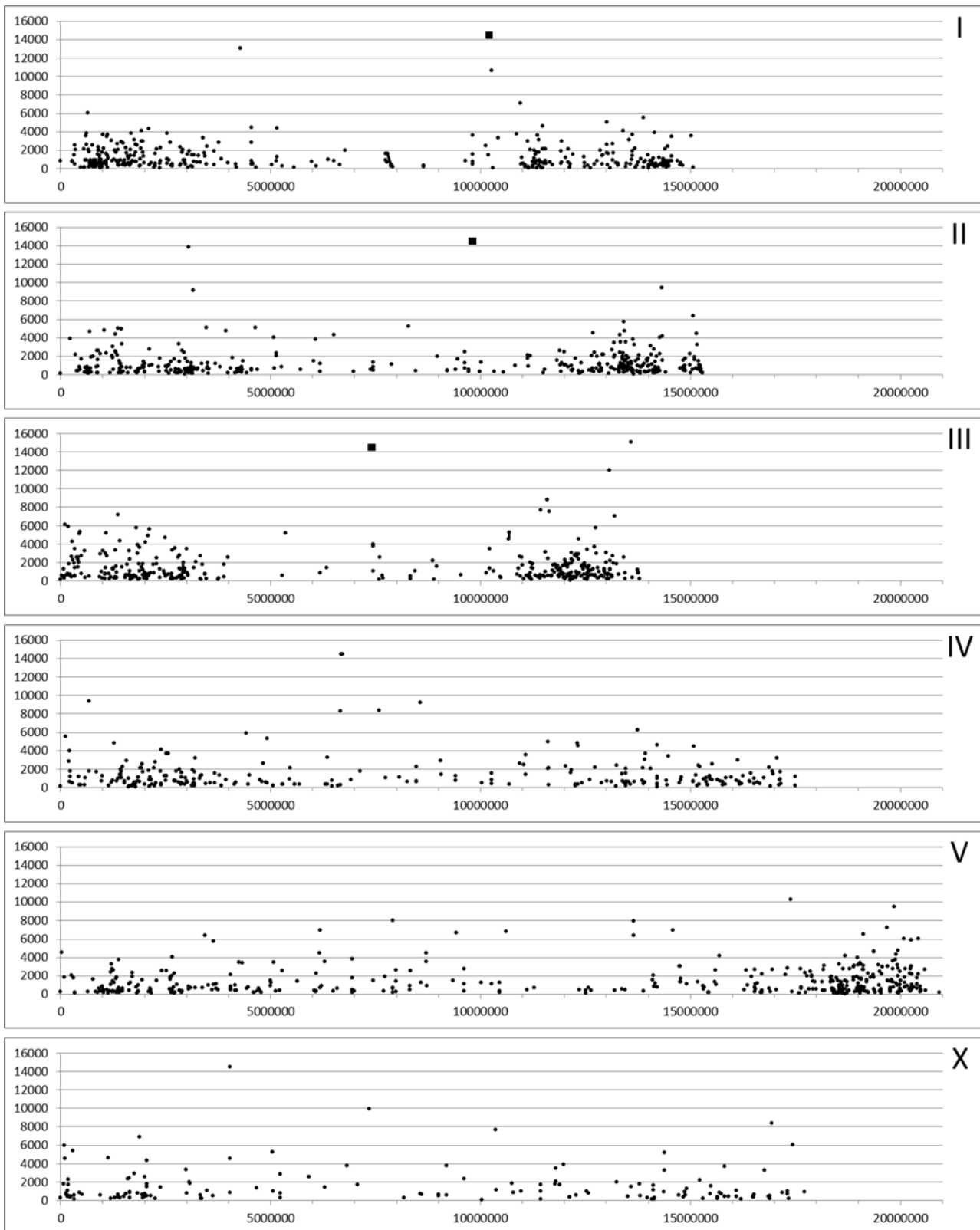


Figure S2. Size of satellites, as a function of their position in each chromosome. A few satellites are indicated by a square: they are longer than what is indicated in the figure. A more detailed presentation for chromosome I is given in Figure 2.

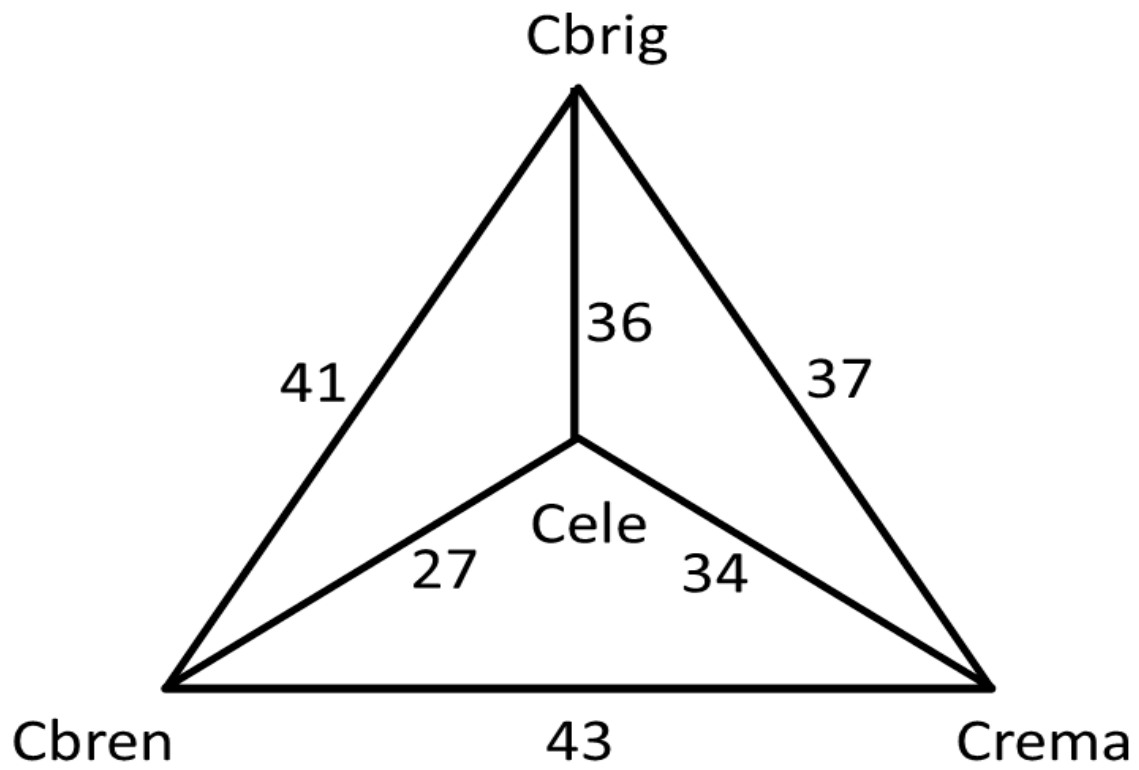


Figure S3. Shared satellite families between pairs of *Caenorhabditis* species.

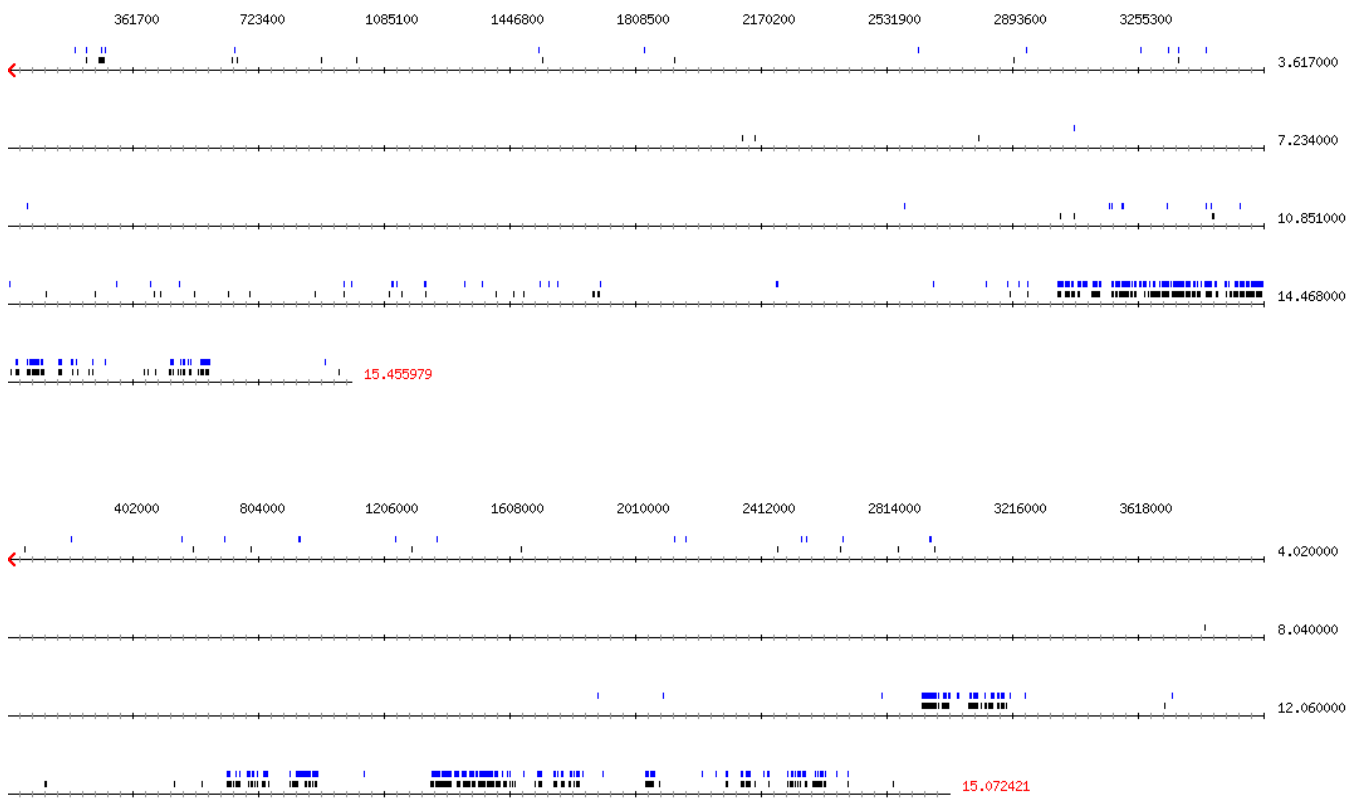


Figure S4. Distribution of the (ACTACAA)₂ sequence (black) and its reverse complement (blue) in chromosome I of *C. elegans* (lower frame) and *C. briggsae* (upper frame).

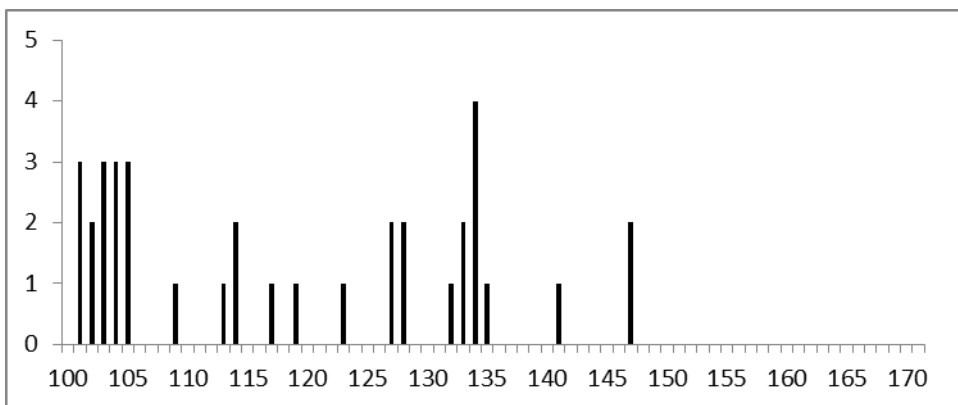
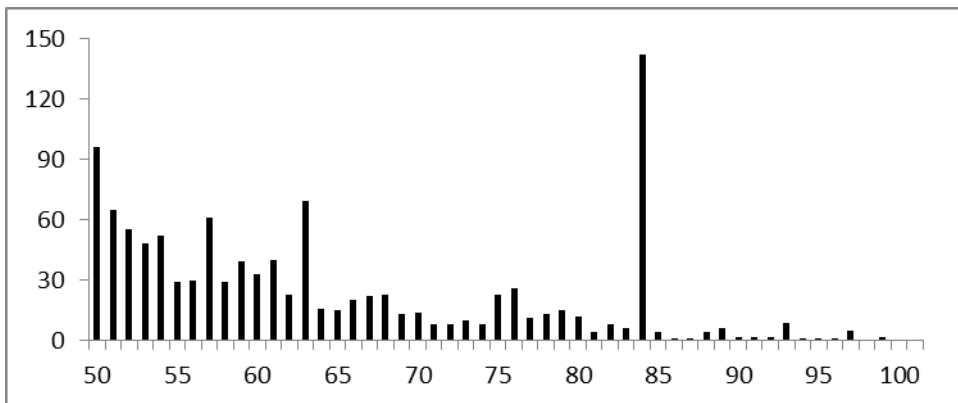
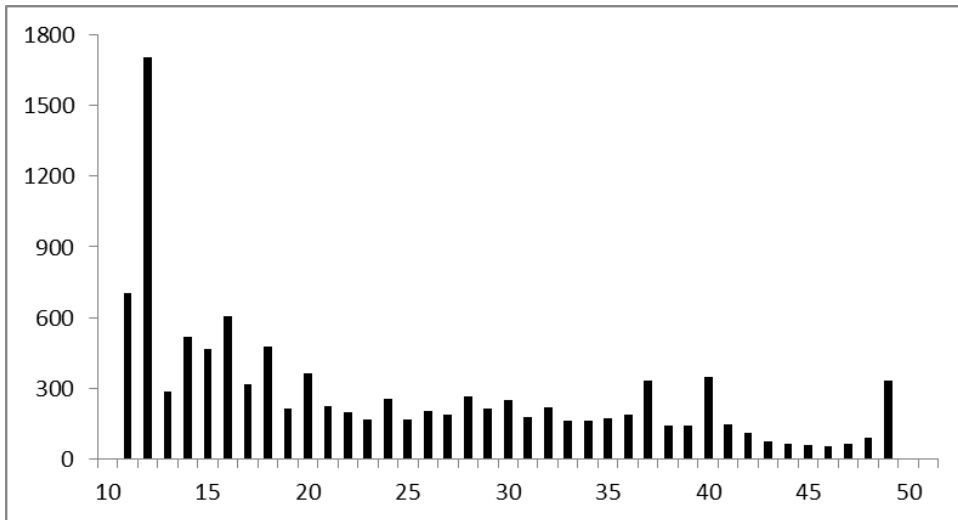


Figure S5. Histograms showing the number of human satellites as a function of the length of their repeats.