

Supplementary information

Genome annotation

Table S1: BUSCO scores for *C. magnifica*, *T. freemani* and *C. maculatus* genome annotations

BUSCO category	<i>C. magnifica</i>	<i>T. freemani</i>	<i>C. maculatus</i>
Complete BUSCOs	972 (96.0%)	978 (96.6%)	999 (98.7%)
Complete and single-copy BUSCOs	877 (86.6%)	896 (88.5%)	731 (72.2%)
Complete and duplicated BUSCOs	95 (9.4%)	82 (8.1%)	268 (26.5%)
Fragmented BUSCOs	9 (0.9%)	14 (1.4%)	6 (0.6%)
Missing BUSCOs	32 (3.1%)	21 (2.0%)	8 (0.7%)
Total BUSCO groups searched	1013	1013	1013

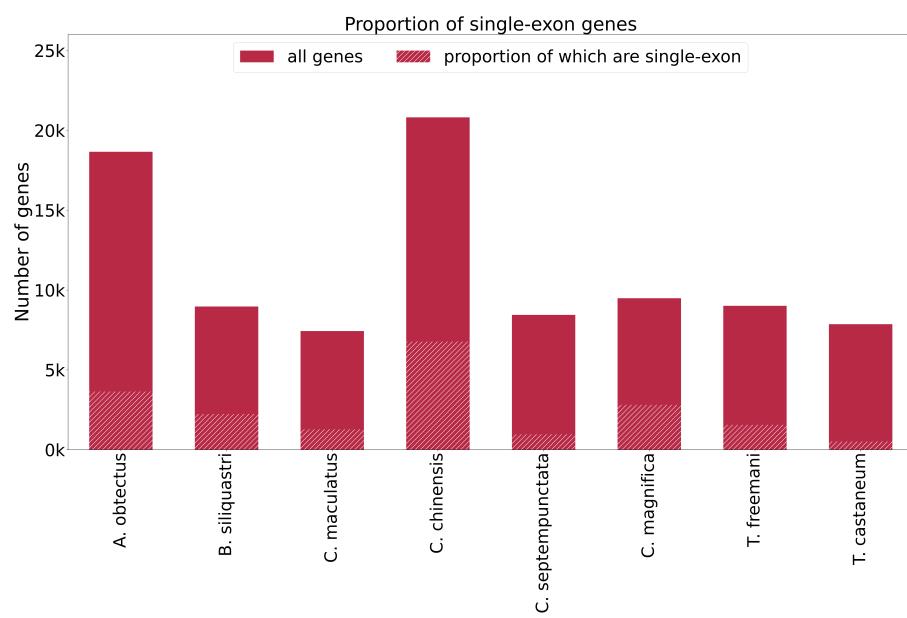


Figure S1: Number of genes with highlighted proportion of single exon genes in all species included.

Synteny

B. siliquastri vs. *A. obtectus*

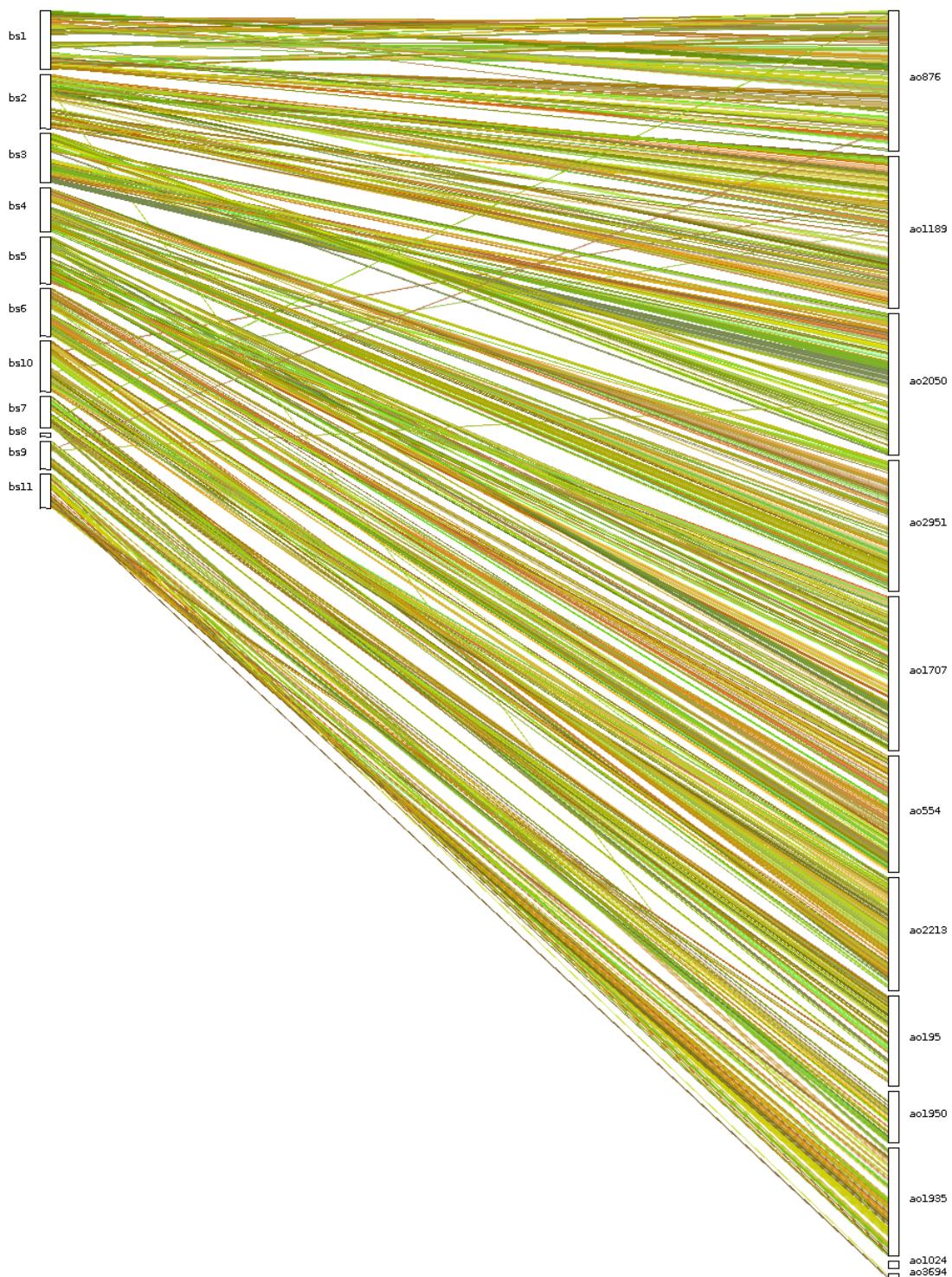


Figure S2: Synteny plot of *B. siliquastri* (left) and *A. obtectus* (right), the X-chromosomes are bs9 for *B. siliquastri* and ao1950 for *A. obtectus* (second from the bottom).

C. maculatus vs. *A. obtectus*

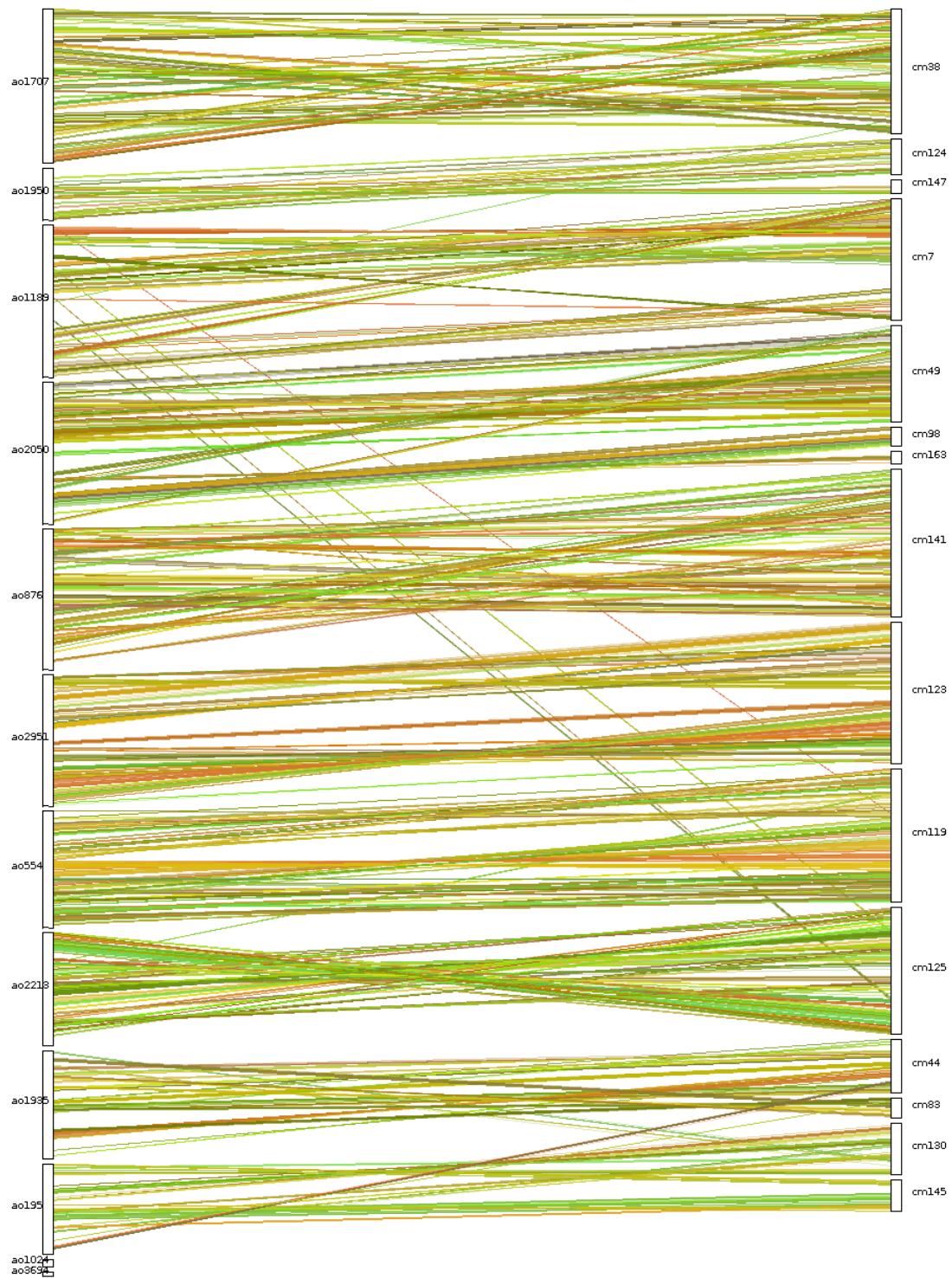


Figure S3: Synteny plot of *A. obtectus* (left) and *C. maculatus* (right), the X-chromosomes are cm124 for *C. maculatus* and ao1950 for *A. obtectus* (second from the top).

C. magnifica vs. *C. septempunctata*

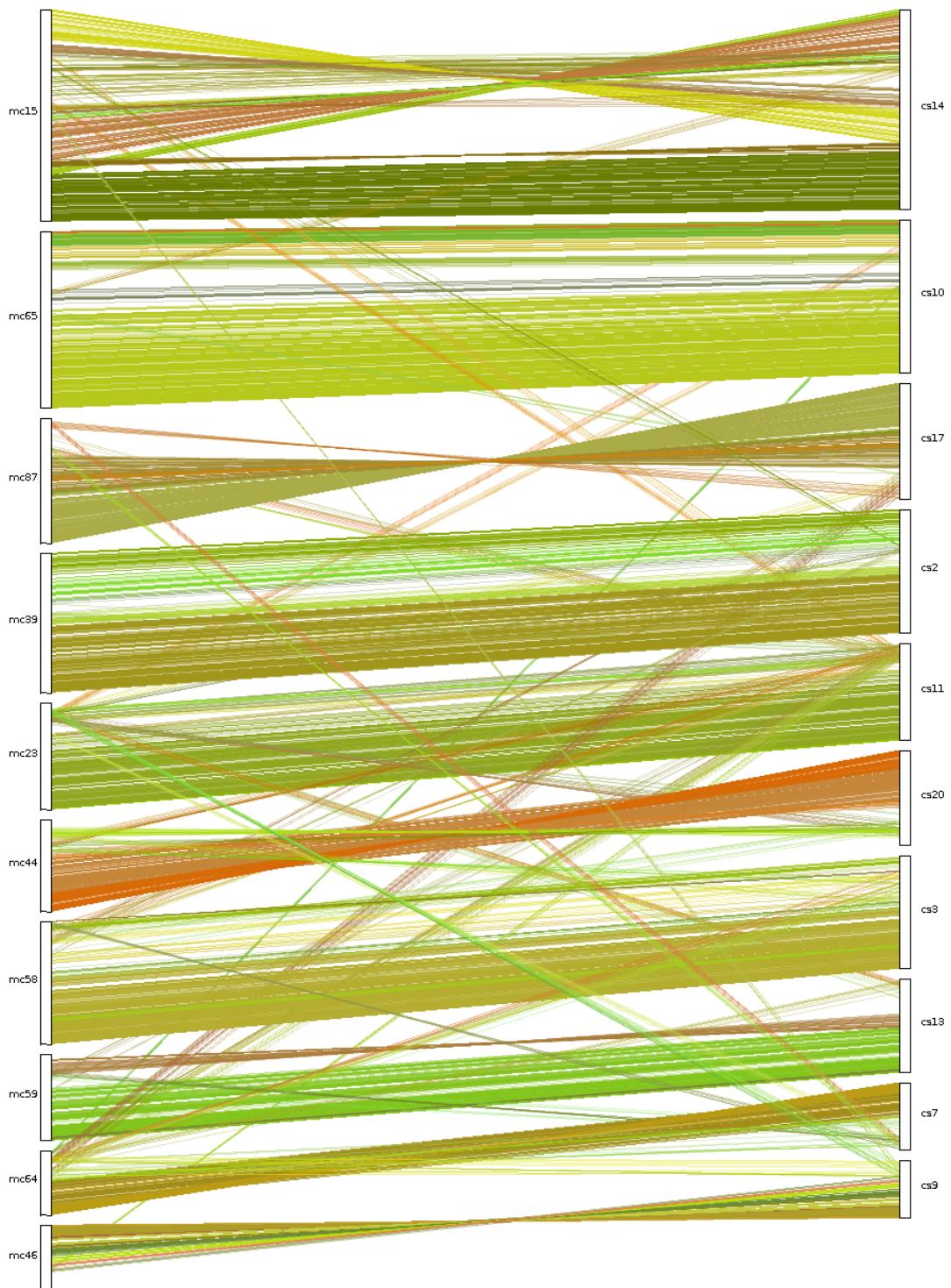


Figure S4: Synteny plot of *C. magnifica* (left) and *C. septempunctata* (right), the X-chromosomes are mc64 for *C. magnifica* and cs7 for *C. septempunctata* (second from the bottom).

T. castaneum vs. *T. freemani*

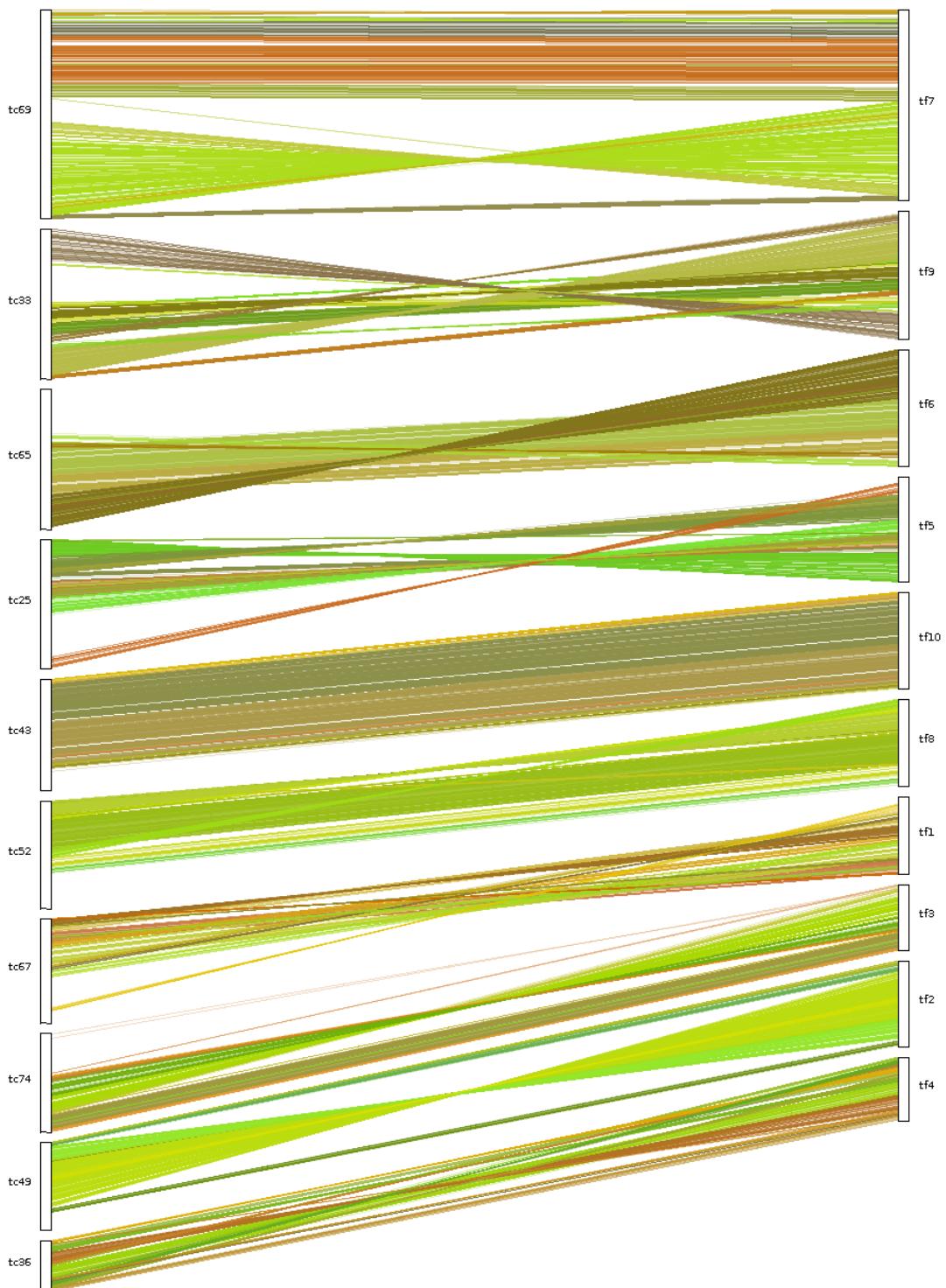


Figure S5: Synteny plot of *T. castaneum* (left) and *T. freemani* (right), the X-chromosomes are tc36 for *T. castaneum* and tf4 for *T. freemani* (first from the bottom).

B. siliquastrum vs. *T. castaneum*

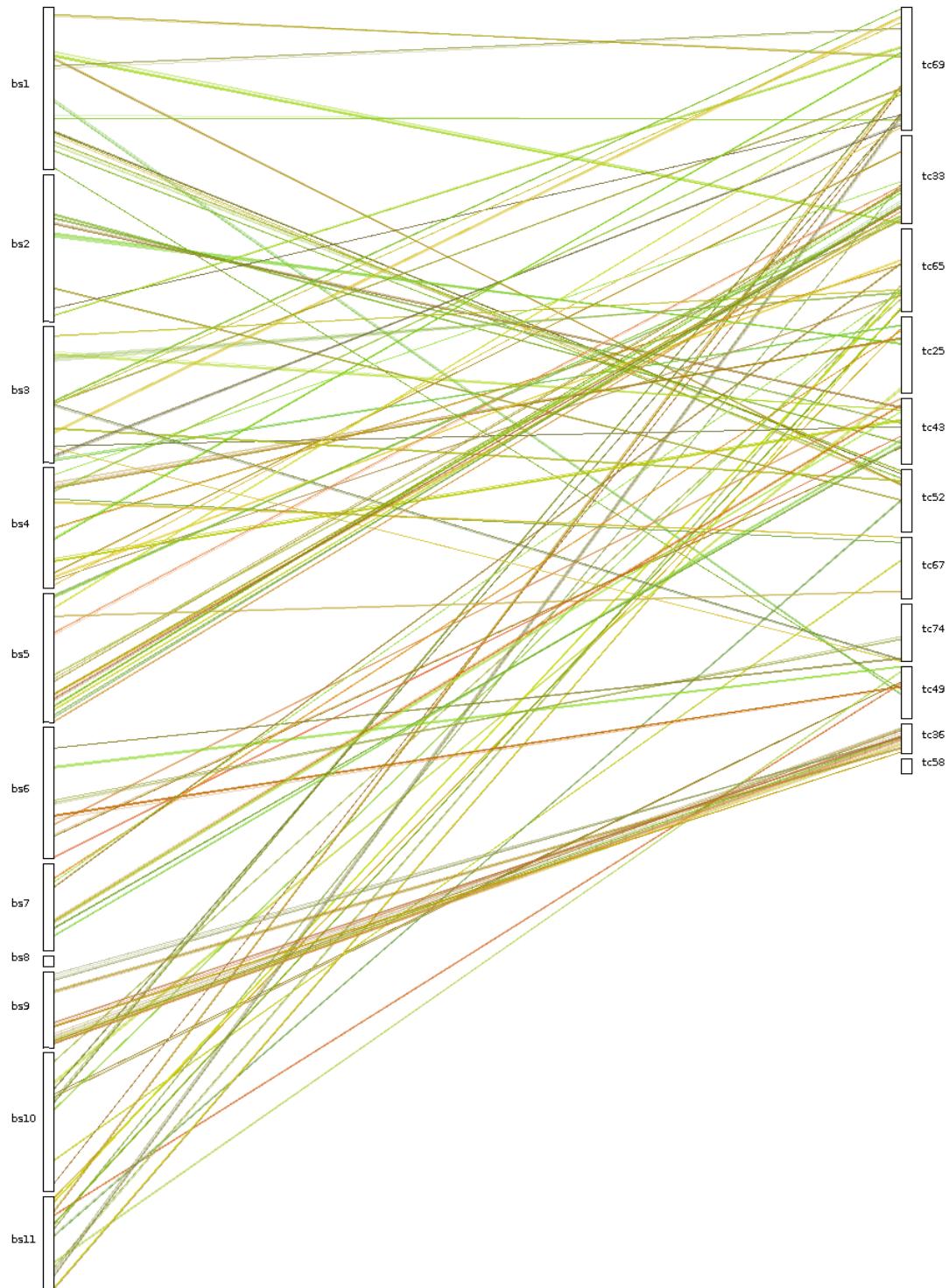


Figure S6: Synteny plot of *B. siliquastrum* (right) and *T. castaneum* (right), the X-chromosomes are bs9 for *B. siliquastrum* and tc36 for *T. castaneum* (third and second from the bottom).