

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 |

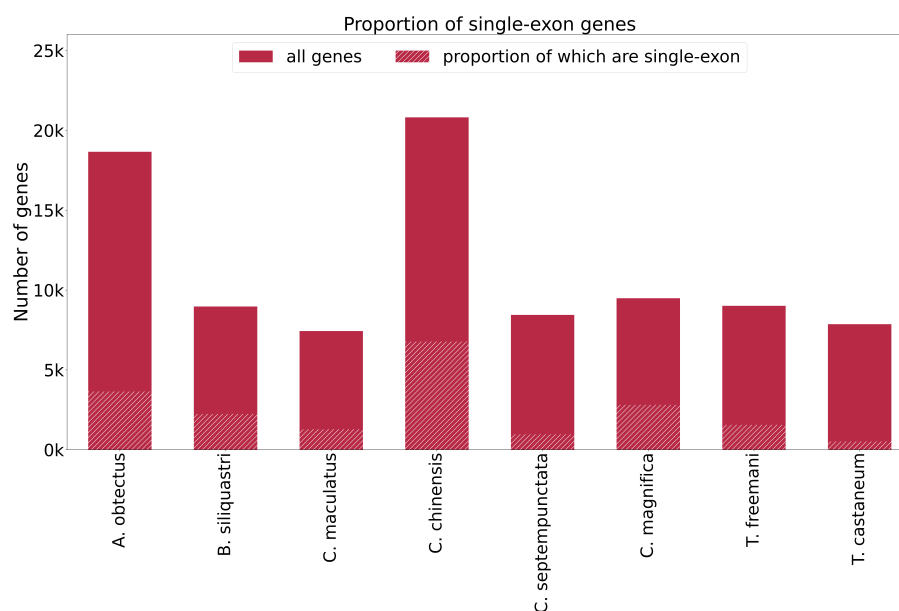


Figure S1: Number of genes with highlighted proportion of single exon genes in all species included.

Synteny

B. siliquastris vs. *A. obtectus*

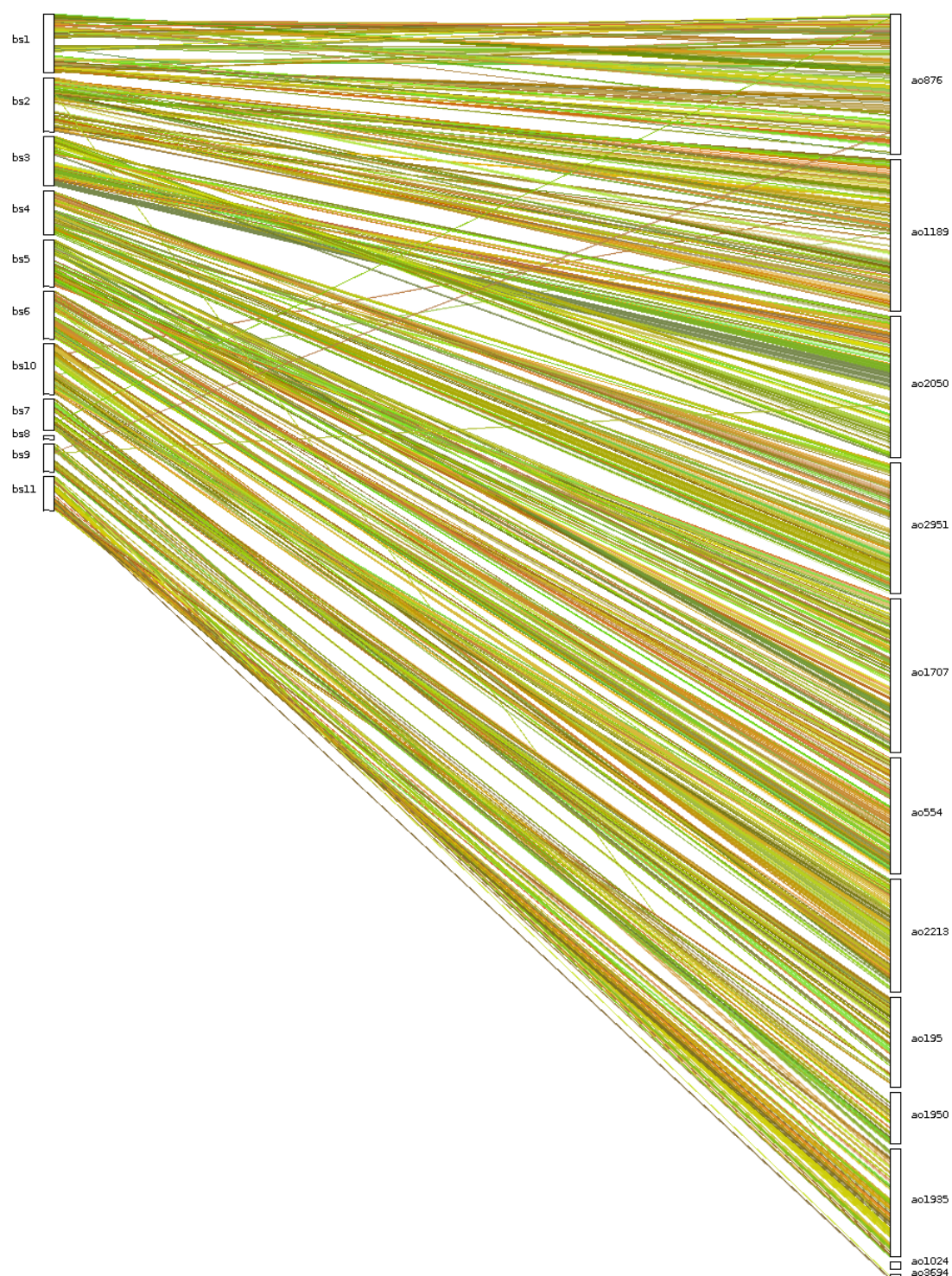


Figure S2: Synteny plot of *B. siliquastris* (left) and *A. obtectus* (right), the X-chromosomes are bs9 for *B. siliquastris* and ao1950 for *A. obtectus* (second from the bottom).

C. maculatus vs. *A. obtectus*

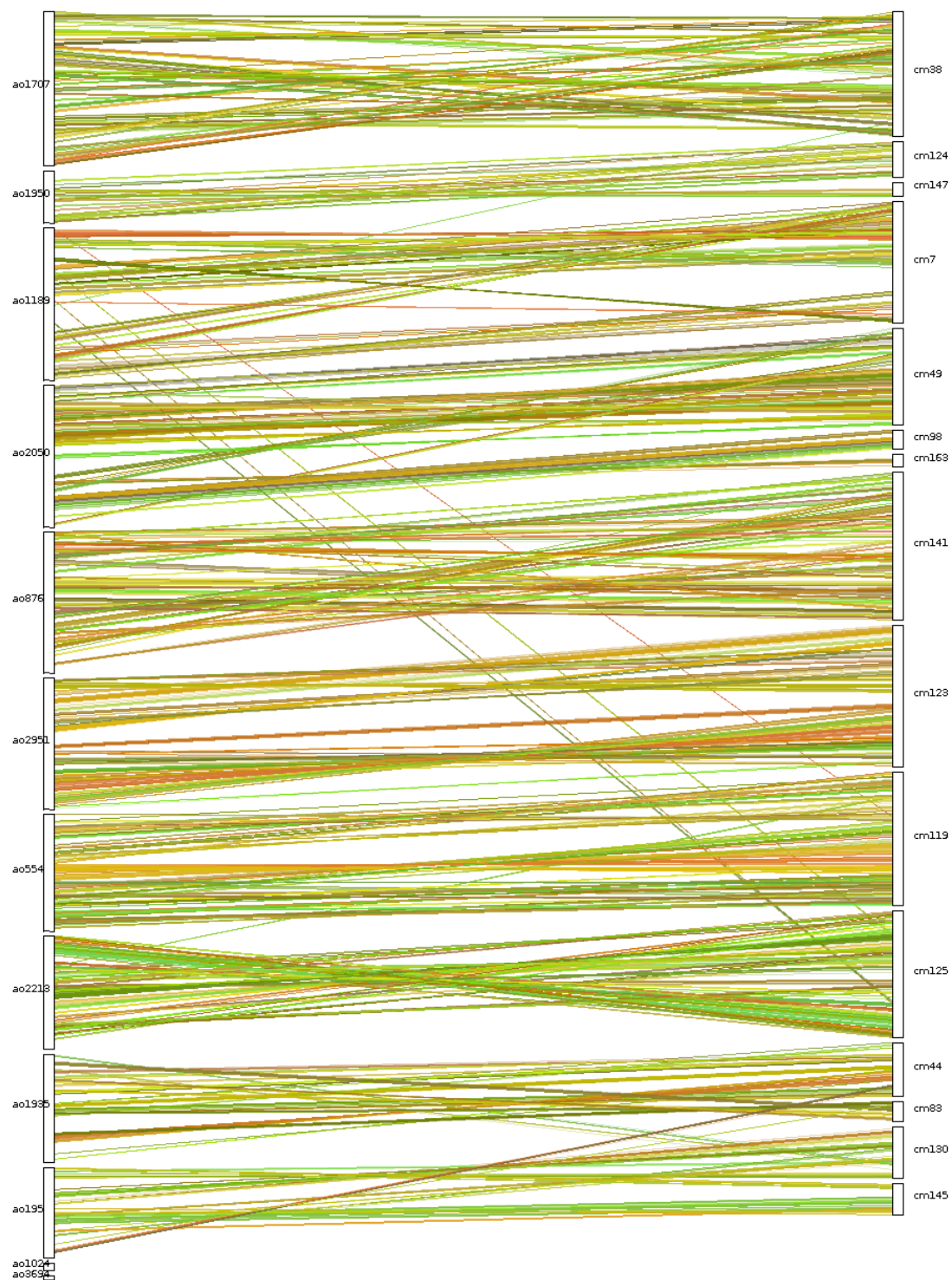


Figure S3: Synteny plot of *A. obtectus* (left) and *C. maculatus* (right), the X-chromosomes are cm124 for *C. maculatus* and ao1950 for *A. obtectus* (second from the top).

C. magnifica vs. *C. septeimpunctata*

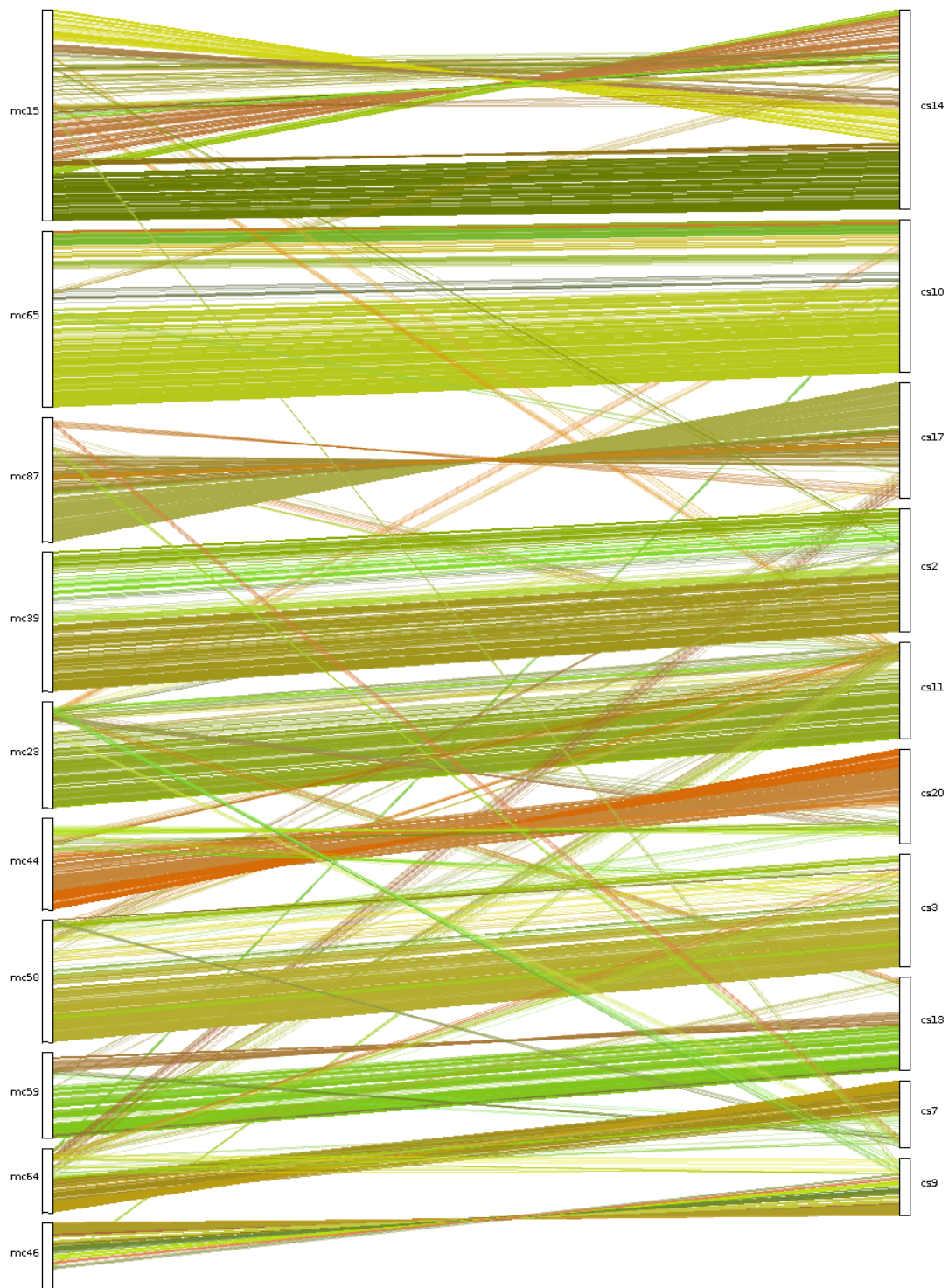


Figure S4: Synteny plot of *C. magnifica* (left) and *C. septeimpunctata* (right), the X-chromosomes are mc64 for *C. magnifica* and cs7 for *C. septeimpunctata* (second from the bottom).

T. castaneum vs. *T. freemani*

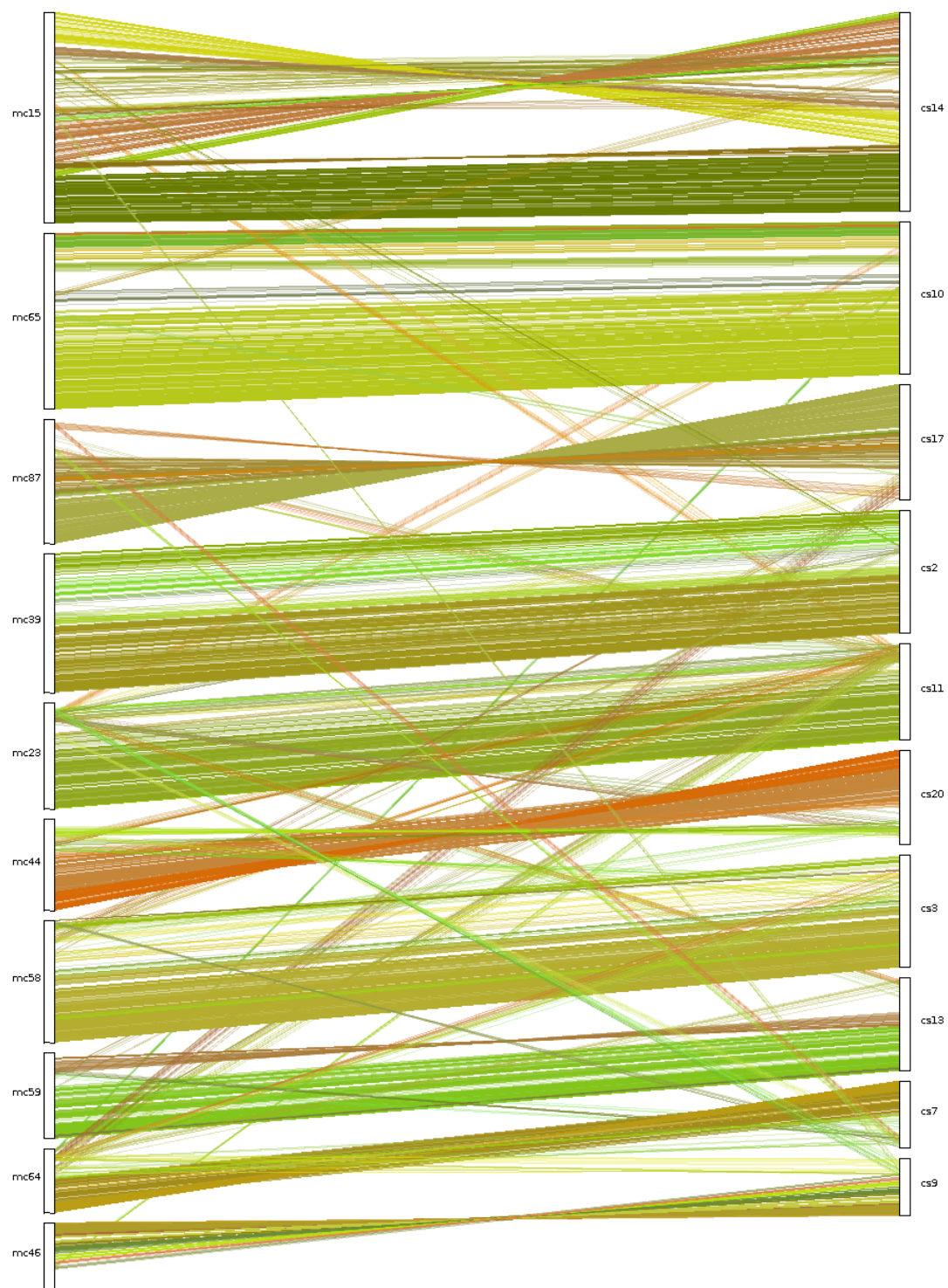


Figure S5: Synteny plot of *T. castaneum* (left) and *T. freemani* (right), the X-chromosomes are tc36 for *T. castaneum* and tf4 for *T. freemani* (first from the bottom).