Figure S15. Boxplot for the density of classification genes inside/outside SV/no-SV regions. A-B, Distribution of sex-biased gene density between *A. obtectus* and *C. chinensis* (A) or between *A. obtectus* and *C. maculatus* (B) along random regions. 'Reversible' represents the orthologous with different sex-biased expression patterns in different species. **C-D,** Sex-biased gene density between *A. obtectus* and *C. chinensis* (C) or between *A. obtectus* and *C. maculatus* (D) inside/outside random regions. **E-F,** Sex-biased gene density between *A. obtectus* and *C. chinensis* (E) or between *A. obtectus* and *C. maculatus* (F) inside/outside inversion regions. Genes are classified based on the sex bias of orthologous genes between *A. obtectus* and *C. chinensis*/*C. maculatus*. *P* values were derived from two-side Wilcoxon matched-pairs signed-rank tests.