A
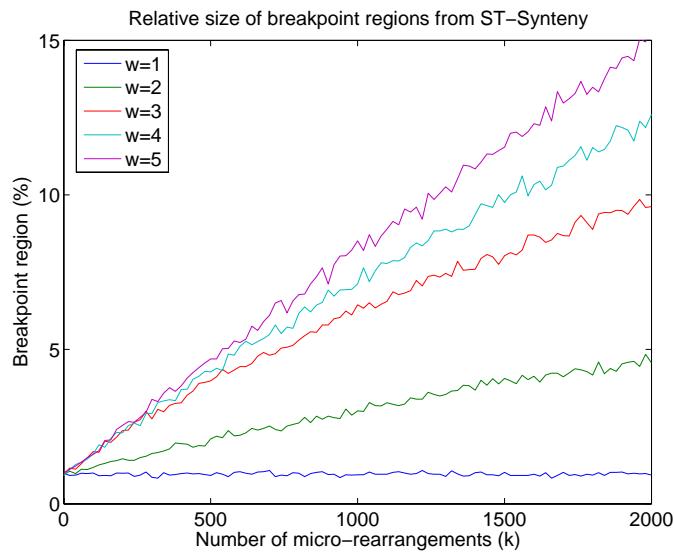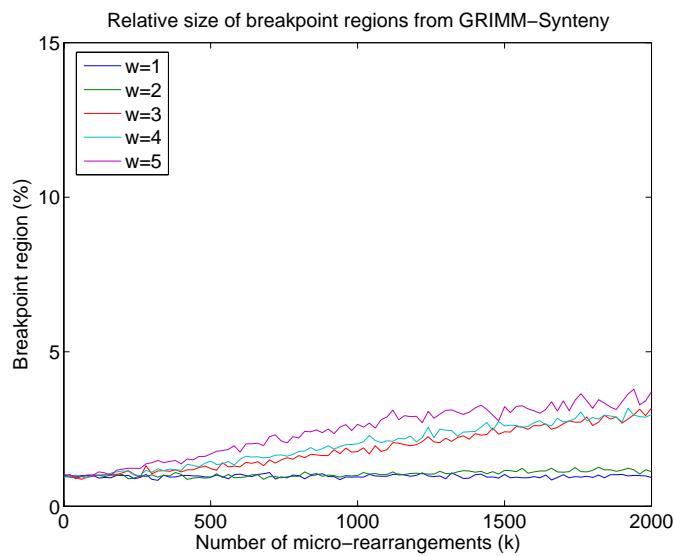

B

Figure S1. Breakpoint region size in simulations. Ratio of length of breakpoint region to length of genome in simulations as a function of number of micro-rearrangements k and micro-rearrangement size w, for (A) ST-Synteny, and (B) GRIMM-Synteny.