



**Figure S3** Population genetic inferences of SDpop at higher error rates than Figure 3; here,  $\epsilon = 0.001$ . The values of nucleotide diversity and divergence calculated directly from the simulation results are compared to the values inferred from SDpop's output. Comparisons are based on SDpop's assignment of the genes (i.e. all genes with a posterior probability  $> 0.8$  were used). Top: gametolog divergence ( $D_{XY}$ ); middle: X nucleotide diversity ( $d_X$ ); bottom: Y nucleotide diversity ( $d_Y$ ). Facets are separated according to the number of individuals per sex used ( $n$ ). Color indicates the time since recombination suppression  $t$ , and symbols indicate the simulated proportion of gametologs %XY. The black points indicate the theoretical values ( $D_{XY}$ : one for each  $t$ ;  $d_X$  and  $d_Y$ : one value for all runs).