



**Figure S2** Precision (positive predictive value, left) and power (true positive rate, right) of the detection of sex-linked contigs in simulated data, using a threshold for the posterior probability of 0.8. First three rows: XY gametologs, grouped by the proportion of simulated gametologs in the genome (0.1%, 1%, 5%). Bottom graphs: X-hemizygous genes, for which the simulated proportion in the genome was 5%. The color and line scales indicate the simulated time since recombination suppression  $t$ . Each point is the average of 100 simulations, with the bars representing the standard error. For all cases shown here, the simulated error rate was 0.001; for  $\epsilon = 0.0001$ , see Figure 2.