



Figure S7 Test of SDpop's performance on the human exome-targeted sequencing data from the 1000 genome project, using 5 individuals per sex (top graphs) or 20 (bottom graphs). Smoothed gene-level posterior probabilities for autosomal (black), X-hemizygote (blue) and XY (red) segregation are shown; haploid and paralogous posterior probabilities are indicated in gray. The right panels show the results on the X chromosome: the extremities corresponding to the pseudo-autosomal regions are predicted to be autosomal by SDpop, while most XY gametologous genes are found close to the pseudo-autosomal region on the left arm, which represents the youngest stratum where Y copies have not yet been lost. The rest of the chromosome consists of X-hemizygous genes, that lack a Y copy.