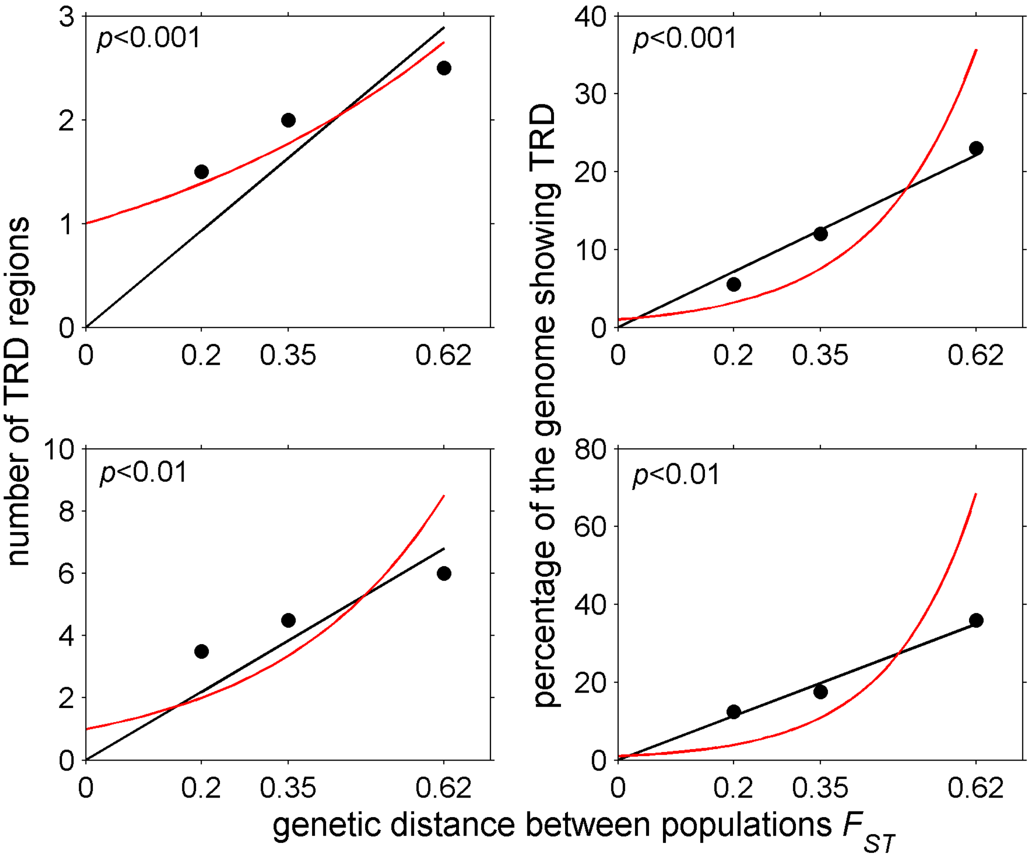

Figure S11 Analysis of "snowballing" of TRD. Fit of linear (black lines) and exponential (red lines) functions to the increase of the number of TRD regions (left panels) and percentage of the genome showing TRD (right panels) with genetic distance between hybridized populations (F_{ST}). Upper panels show results when a significance threshold of $p<0.001$ is used, lower panels show results for a threshold of $p<0.01$