Figure S5  Sliding-window analyses of parameter estimates on human chromosome 6.  A) Sliding-window analysis of the disequilibrium coefficient estimates by the proposed method.  B) Sliding-window analysis of the per-site inbreeding coefficients estimated by the method by Vieira et al. (2013).  C) Sliding-window analysis of the error rate estimates by the proposed method.  A, B) Results are conditioned on significant polymorphism at the 5% level.  C) Results are based on all sites with sequence-read data.  $s = 100,000$ (bp) and $w = 150,000$ (bp) used for defining the step size and width of the windows, respectively.