



**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.