



**Figure S3** Comparison of the allele-frequency estimates on human chromosome 6 by different methods. The allele frequencies estimated using the method by Kim *et al.* (2011) (ANGSD) and the A) Samtools or B) GATK genotype likelihood model is compared to those estimated using the proposed method. The points and bars represent the mean and standard deviation of the ANGSD allele-frequency estimates in each bin of the allele-frequency estimates of size 0.05 by the proposed method.