**Figure S5:** Re-running of Bayesian-approach STRUCTURE analysis on *P. knowlesi* of 512 human and 44 macaque infections using all microsatellite loci except for locus NC03\_2 and locus CD13\_61, which *FST* values > 0.3 between subpopulation clusters obtained from the initial STRUCTURE analysis results. (A) STRUCTURE analysis run with all loci except for locus NC03\_2 indicated two subpopulation clusters throughout the whole dataset the (*K* = 2, *∆K* = 142.50). (B) STRUCTURE analysis run with all loci except for locus CD13\_61 indicated two subpopulation clusters throughout the whole dataset the (*K* = 2, *∆K* = 23.17).

**A**



**B**

