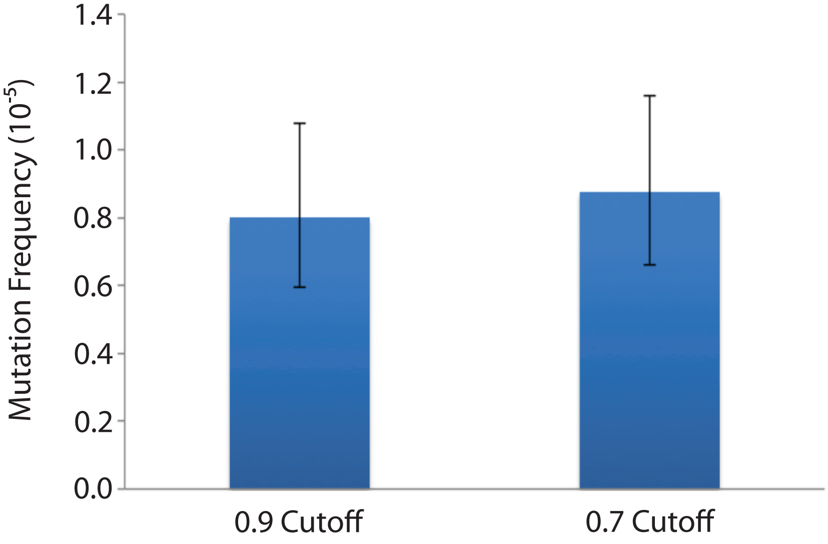

**Using a lower consensus cutoff does not affect mutation frequency.**
The plot shows the comparison of two different consensus cutoff values (0.9 vs 0.7) used to process the same sample of mtDNA. The original Duplex Sequencing paper (Schmitt *et al.* 2012)[19] used a consensus cutoff of 0.9 (i.e. 90% of bases a position have to agree in order for a consensus to be called). Reducing this cutoff to 0.7 does not result in a significant change in the mutation frequency. Error bars represent the 95% confidence interval (Wilson Score interval).

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