Following similar steps to the above but truncating between 1 and 1500, we get,

Conditioning on does not have the same effect of removing the variable from the model. This means that when is geometric, the relative densities of between 2 and 1500 are independent of , but the density of at 1 relative to still depends on . We again index our random variable with , but this time, we also define as the probability of allele conversion at positions within tract . Then,

When estimating , the mean gene conversion tract length, we remove all observed tract lengths that are 1 bp long and use the distribution of truncated between 2 and 1500. Thus, when is geometric, we need not estimate for any tract for estimating . In the Supplementary Materials, we use to obtain the proportion of observed tract lengths that are 1 bp long under the model.