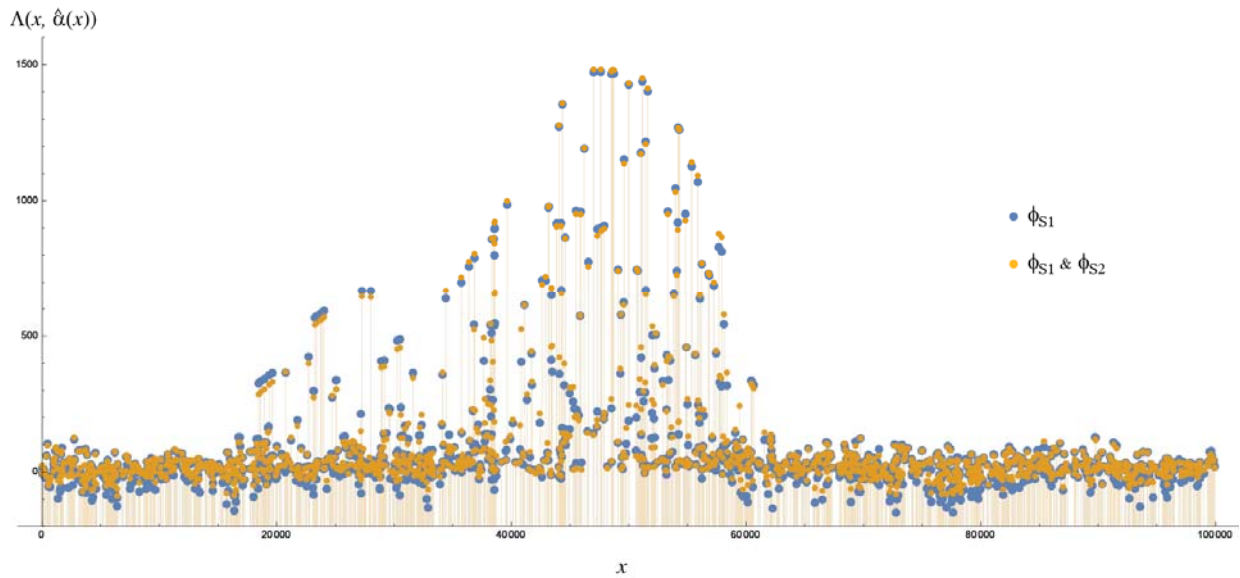**Figure S2**

Figure S2 legend: Composite likelihood ratio calculated for a simulated data set of 20 DNA sequences of 100kb long ($R = 4,000$). Advantageous mutation with $\alpha = 4,000$ is located in the middle (50kb). Blue dots are CLR calculated using ϕ_{S1}, approximation suggested by Nielsen et al. (2005), and yellow dots are CLR calculated using ϕ_{S1} for $r/s < 0.03$ but ϕ_{S2}, approximation based on Etheridge et al. (2006), for $r/s \geq 0.03$.

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