Simulation details. We ran 4 simulations for MEDS. We used equal nucleotide substitution rates ($\theta_{ij} = 1$), and equal target nucleotide frequency parameters ($\pi_{ij} = 0.25$). The t parameter (as in e^{Qt}) for every branch was set to 0.05. We also needed to choose the synonymous rate α, the background non-synonymous rate β^B, and the foreground non-synonymous rate β^F. We let each of these be either 0.2 or 1, simulating sites with all possible combinations of these parameters. For example, if $\alpha = 0.2$, $\beta^B = 0.2$ but $\beta^F = 1$, we would have neutral selection on the background and diversifying selection on the foreground. ω_T assumed one of 5 values (2, 5, 10, 100, 1000), also described in the main text. An example of a balanced phylogenies used, along with the location of the foreground branches, is shown in Figure S3.