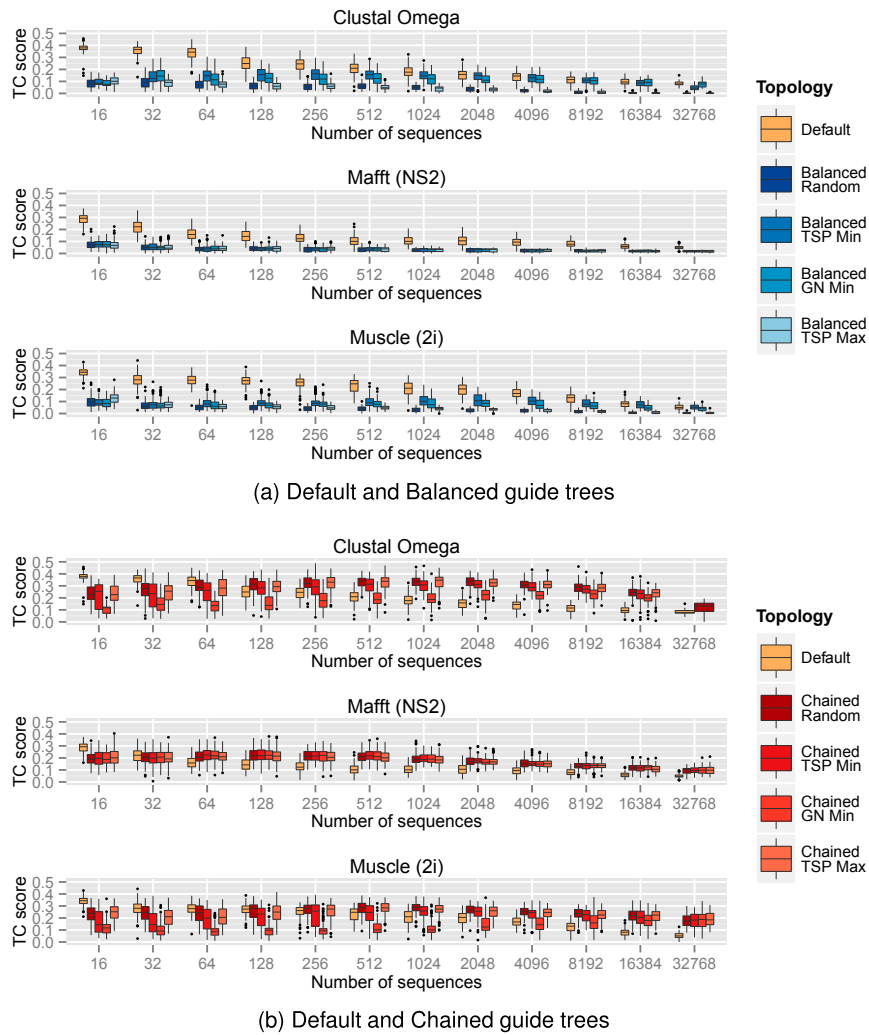


# Supporting Information

Boyce et al. 10.1073/pnas.1405628111

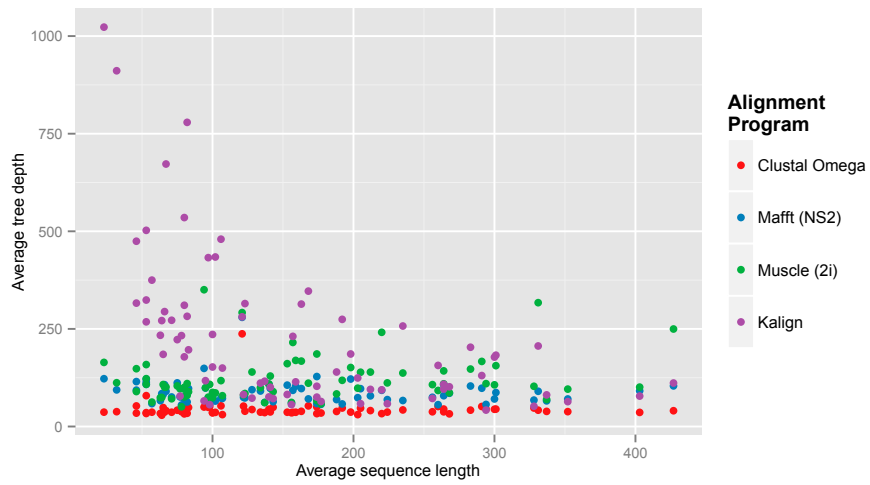


**Fig. S1.** Total Column (TC) scores for increasing numbers of short-chain dehydrogenases/reductases sequences for Clustal Omega, Mafft (FFT-NS-2 algorithm), and Muscle (two iterations) with (A) default and balanced and (B) default and chained guide trees. Four sets of balanced and chained guide trees were created for each dataset, with different sequence ordering: Random, Traveling Salesman Problem (TSP) Minimum, Greedy Neighbor Minimum, and TSP Maximum (100 samples per dataset, except 25 samples for the largest Clustal Omega datasets).









**Fig. S6.** Average default tree depths for Clustal Omega, Mafft (FFT-NS-2 algorithm), Muscle (two iterations), and Kalign 2 using 1,024 sequences from each HomFam family. Families with less than 1,024 sequences were excluded (10 samples per family).