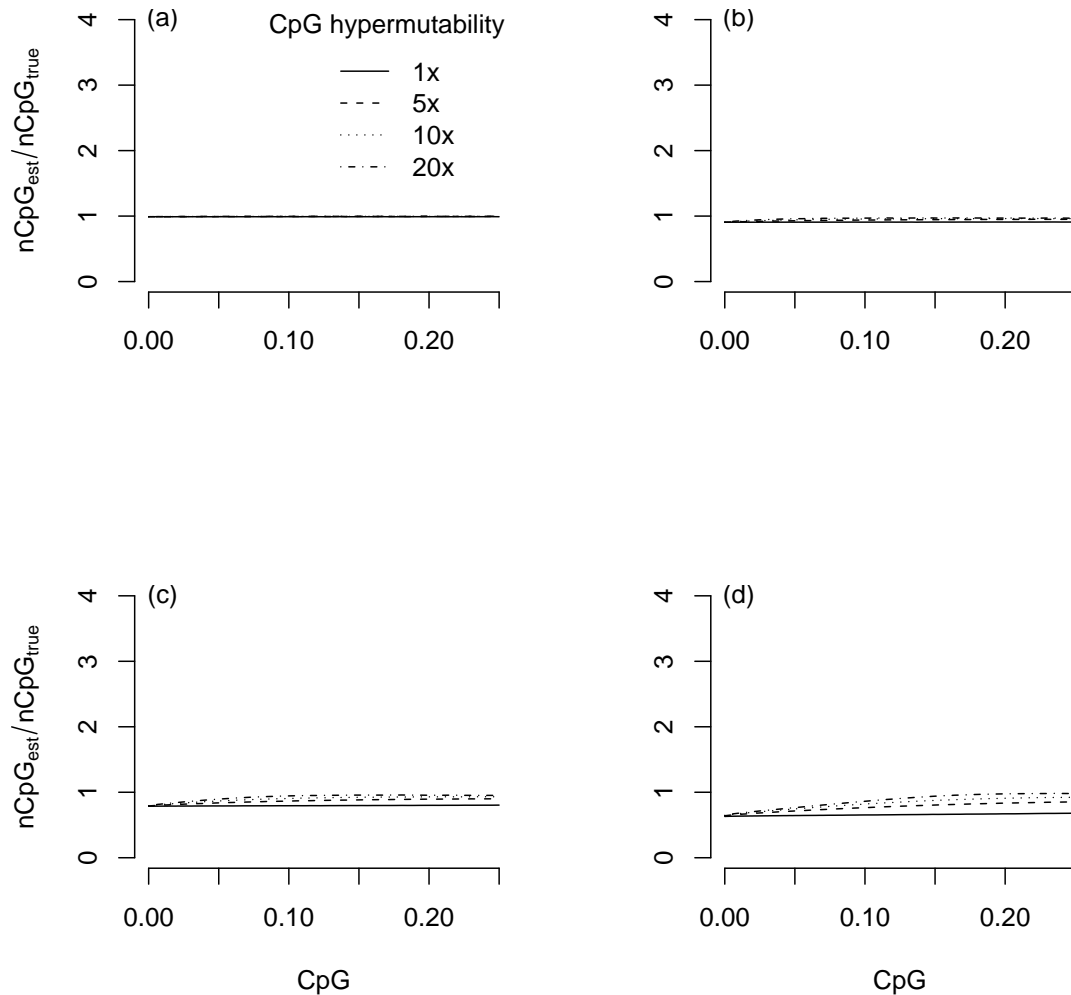# Supplementary Figures

Figure 1: Ratio of estimated $(nCpGp_{est})$ to true $(nCpGp_{true})$ non CpG-prone differences across a variety of ancestral CpG frequencies, in phylogenies derived from "artificial ancestral" sequences. Results are from trees of total length 0.01, 0.05, 0.1 and 0.5 (a,b,c and d respectively). Separate lines show results for different levels of hypermutability (no hypermutability, 5-fold, 10-fold and 20-fold hypermutability). Each line represents 101 data points, each of which represents 10 simulated replicates of a 1Mb sequence.
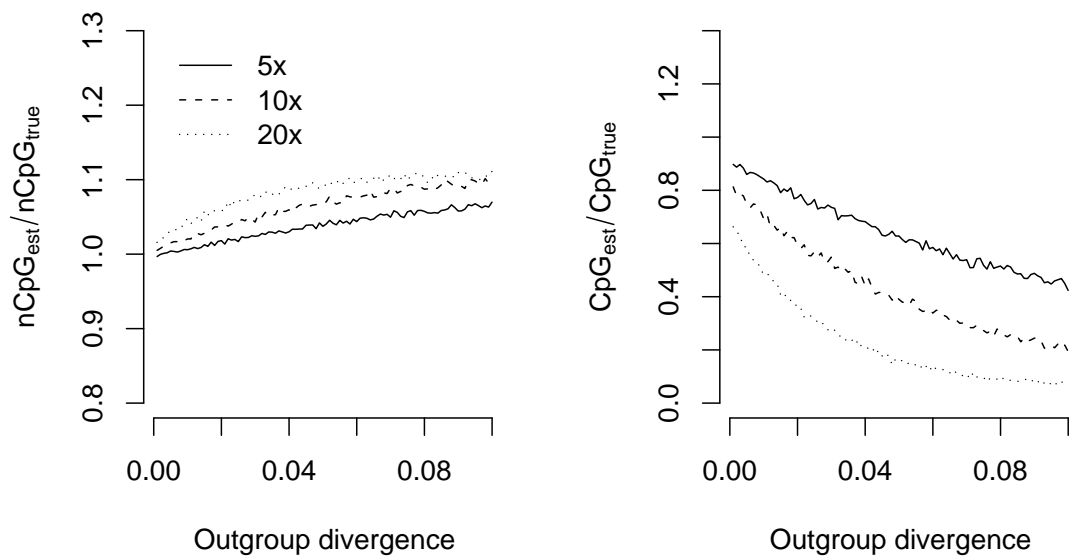
Figure 2: Ratio of estimated to true CpG differences and estimated to true non-CpG differences as a function of increasing outgroup sequence divergence for three-branch phylogenies derived from randomly generated sequences evolved to be at mutational equilibrium. Estimated numbers of CpG and non-CpG changes are corrected for multiple hits using the Jukes-Cantor model. Results are shown for three different levels of hypermutability: 5-fold,10-fold and 20-fold hypermutability. Each line represents 50 data points, each of which was estimated from the evolution of a single, randomly-generated 1Mb sequence.