



**Figure S3** Bayesian integration (BI) is biased when protein data are analyzed; maximum likelihood (ML) is unbiased. The proportion of 500 replicates from which each possible tree was recovered and mean posterior probability of each tree are plotted; bars indicate standard error. Sequence data of 5,000 and 50,000 amino acids were simulated on an unresolved star tree with two long (0.75 substitutions/site) and two short (0.05) terminal branches using the JTT model. Analyses were conducted using the true model.