Figure S1. (a) Histogram of SCONE score p-values in neutral (ancestral repeat) positions. All histograms are represented as line plots for the sake of presentation. (b) ROC curve discriminating between high-coverage ancestral repeat regions and low-coverage ancestral repeat regions, using SCONE rate scores (green) and SCONE p-values (red), demonstrating that p-value scores are unbiased with respect to coverage; high- and low-coverage AR regions are considered comparably conserved by this measure. (c) SCONE score mean p-value vs. mutation rate (substitutions per site between human and chimp in ancestral repeats) for each ENCODE region. Correlation (R^2) between mean p-value and mutation rate is 0.26.