Figure S1: **Post-mortem damage pattern profiles of ancient samples**. Plotted is the frequency of reads showing T at all sites where the reference is C (top panels) and the frequency of reads showing A at all sites where the reference is G (bottom panels) as a function of the distance from the 5' and 3' end of the read, respectively, for each individual and read group. For single end sequencing runs, damage patterns are further shown individually for reads that are shorter (<cycles) or as long (=cycles) as the number of sequencing cycles used.
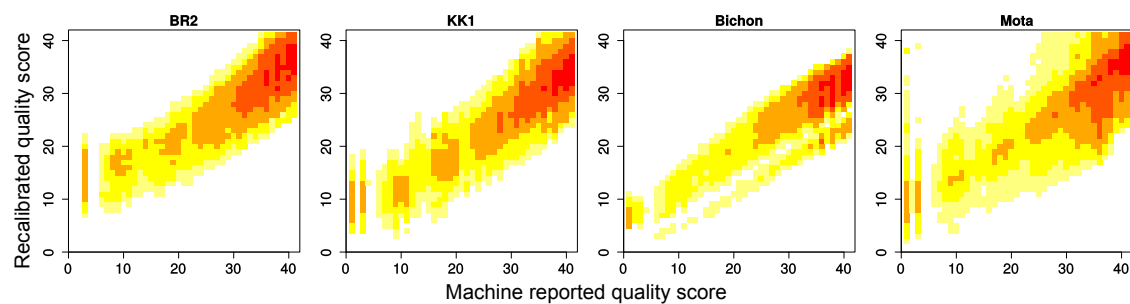
Figure S2: **Effect of Recalibration on Quality Scores.** Shown are the density distributions of the quality transformations as a result of the applied quality recalibration for each sample. It appears that the machine-reported qualities were overall too high, and in particular for the qualities > 30.