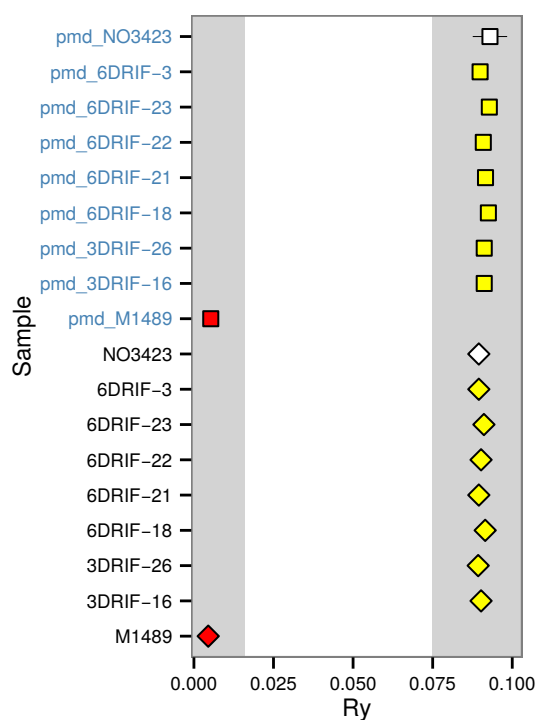**Supplementary Figure 6** - Comparison of aDNA misincorporation patterns at the 5′ end of sequencing reads (C to T) and 3' end (G to A) between the samples from Roman York, Iron Age and Anglo-Saxon.

Supplementary Figure 7 - Sex identification based on shotgun sequencing data and comparison of results using reads with evidence of deamination (PMD score 3, squares) and unfiltered reads (lozenges). Ry - Ratio of the number of reads aligned to the Y-chromosome divided by the sum of the number reads aligned to the Y- and X-chromosomes. Gray shaded areas represent threshold for acceptance of assignment, calibrated with modern and ancient genomes. Error bars correspond to 95% confidence intervals.