



Characterization of two DNA libraries prepared with and without uracil removal from a Neandertal DNA extract (panels on the right and left, respectively). A) Fragment length distributions of the amplified libraries obtained from chip electrophoresis using the Bioanalyzer 2100. B) Fragment size distributions obtained from sequencing (the fraction of mapped sequences is indicated by a dotted line). C) Frequency of C to T substitutions around 5' and 3' ends of Neandertal sequences. D) Average GC-content of Neandertal sequences as a function of fragment size.