Figure S1: Examination of QQ-norm plot of residuals of input $d^{18}O$ relative to stack after Match alignment. Here we plot the residuals for 4 of the 35 sequences: DSDP 552, ODP 980, ODP 1089 and ODP 1146. If the points fall on or near a straight line, it implies a good fit of normal distribution.

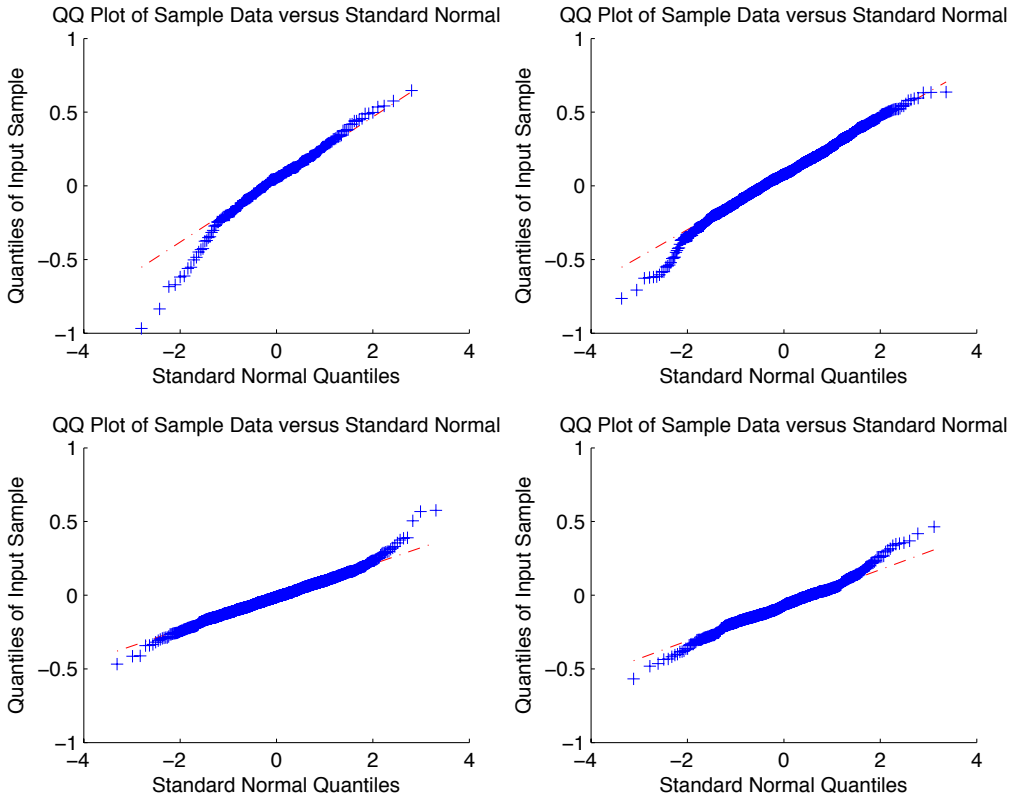

Figure S2: Example of Viterbi alignment falling outside of 95% confidence band from HMM-Match (DSDP Site 552)

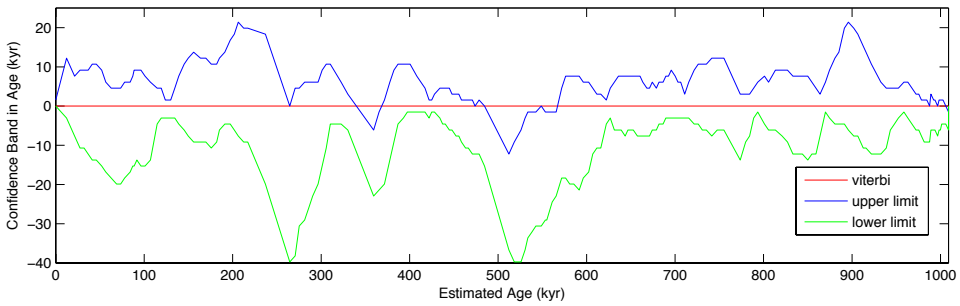

Figure S3: Example alignments, discretized by two different sub-interval sizes, illustrate how we select sub-interval size. Panel A shows an example in which the first two points in the input are only 1 unit apart; therefore, the algorithm is only able to generate ratios for expansion (1:1, 1:2, 1:3 and 1:4) and contraction is not possible. Panel B shows the same sequences using a finer sub-interval size (1/4 of sub-interval size in A) so that the first two points in the input are now 4 units apart. With a finer sub-interval size, the algorithm is able to generate 16 ratios from 4:1 to 1:4 covering both contraction and expansion. The figure also illustrates some of the possible alignment ratios between input points 2 and 3, which are approximately 1.5 units apart in A and 6 units apart in B.

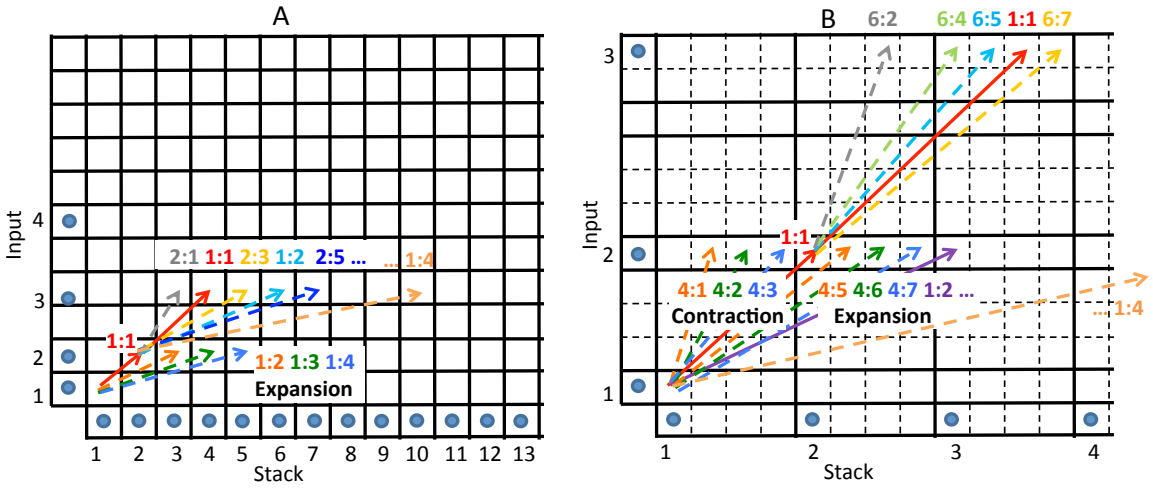

Figure S4. Radiocarbon-based estimates of sedimentation rate ratios versus time (kyr) from 37 cores with mean sedimentation rates of at least 8 cm/kyr. Sedimentation rate ratios are unitless and calculated by dividing each core's sedimentation rates by its mean sedimentation rate. Specifically, mean sedimentation rates are calculated using the first and last available ^{14}C dates. These are the data used to construct our model for sedimentation rate variability (Figure 2). References for ^{14}C data are provided in Table S1.

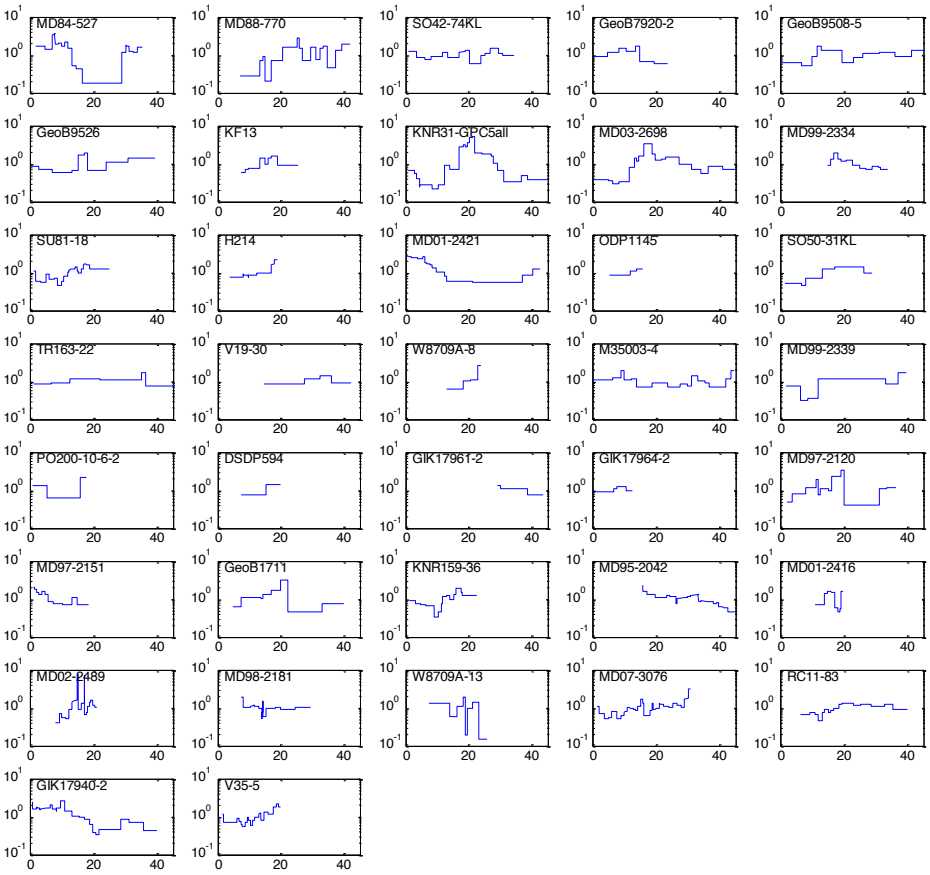

Figure S5: Scatter plot showing confidence band width vs. $d^{18}O$ changes measured by derivatives.

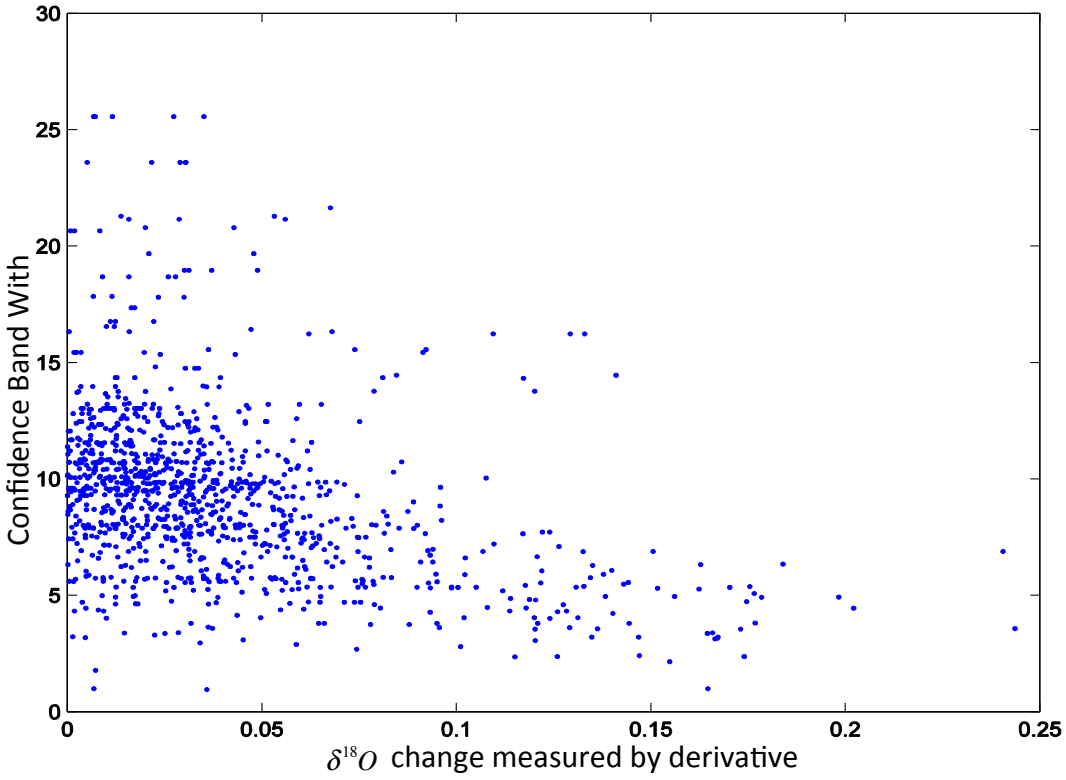

Figure S6: HMM model. B, M, E denote Begin, Matching and End states, and I^B, I^E, D^B, D^E denote the Insert and Delete states in the beginning and end of sequence correspondingly. δ 's are the transition probabilities between states. Part I is the processing of the beginning of the sequences; Part II is the main alignment illustrated in more detail in Figure 1, and Part III is the processing of the end of the sequences.

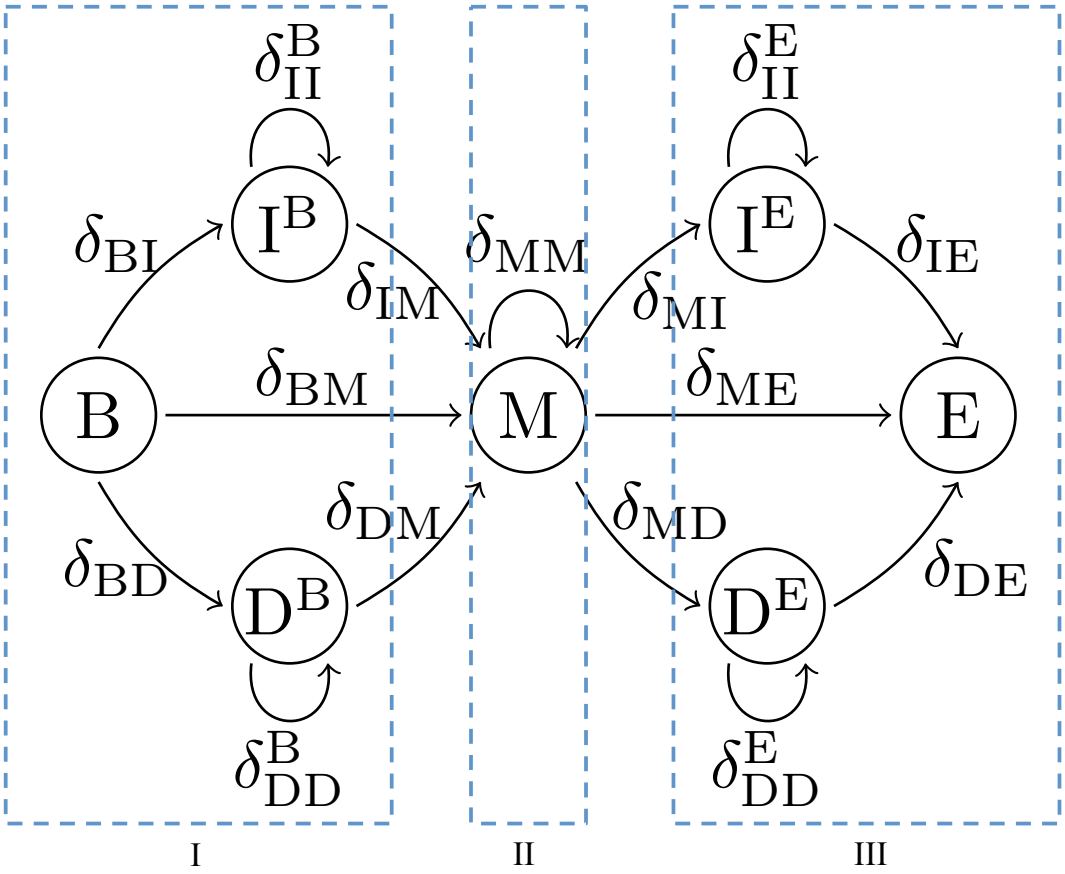

Figure S7: Histogram of sedimentation rate estimates generated for 37 radiocarbon-dated cores using Bchron software and corresponding mixture log-Gaussian fit as the red curve. These rates are partitioned into three groups: A-expression, B-1:1 and C-contraction. $f(r)$ is the density for rate r in the fitted Gaussian distribution; $\hat{f}(r \mid A)$ is the conditional probability of rate r given it is falling in group A, similar for $\hat{f}(r' \mid B)$. $P(r \to r')$ is the transition probability from r to r', which is composed of the transition probability from group A to group B and $\hat{f}(r' \mid B)$.