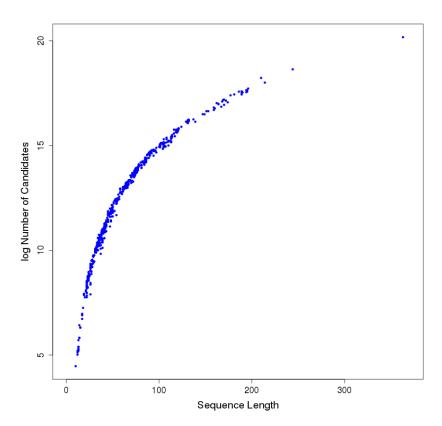
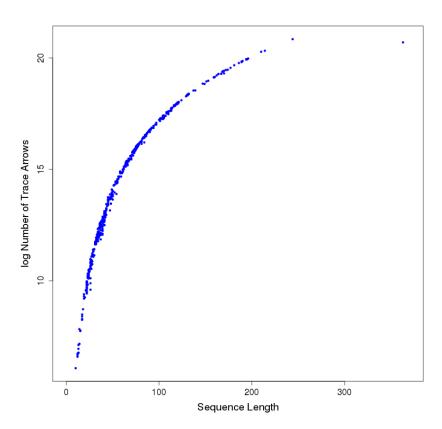
Supplementary Materials: Sparsification enables predicting kissing hairpin pseudoknot structures of long RNAs in practice

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(a) Log (total number of candidates used in Sparse CCJ) versus sequence length.



 $\mbox{(b)}\ \mathrm{Log}\ (\ \mathrm{maximum}\ \mathrm{number}\ \mathrm{of}\ \mathrm{trace}\ \mathrm{arrows}\ \mathrm{used}\ \mathrm{in}\ \mathrm{Sparse}\ \mathrm{CCJ})$ versus sequence length.

Figure 1 Total number of candidates and trace arrows used in SparseCCJ versus sequence length.