

Supporting Information S1. The benchmark dataset for *H. sapiens*. It contains 3 subsets. The 1st one for analyzing m¹A modification, the 2nd one for m⁶A, and the 3rd one for A-to-I editing. Each subset contains a group of positive samples (with a red **A** at the sequence center) and an equal-size group of negative samples (with a blue **A** at the center). See the main text and Table for further explanation.

(1) The 1st subset contains 6,366 positive and 6,366 negative sequence samples for m¹A.

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(2) The 2nd subset contains 1,130 positive and 1,130 negative sequence samples for m⁶A.

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