

Supporting Information S2. The benchmark dataset for *M. musculus*. 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 1,064 positive and 1,064 negative sequence samples for m¹A.

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(2) The 2nd subset contains 725 positive and 725 negative sequence samples for m⁶A.

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(3) The 3rd subset contains 831 positive and 831 negative sequence samples for for A-to-I editing.

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