

Supporting Information S1. The benchmark dataset constructed for training and analyzing the model. It consists of (1) a positive subset and (2) a negative subset. The former contains 3,000 experiment-confirmed A-to-I editing RNA samples, and the latter contains 3,000 experiment-confirmed non-A-to-I editing RNA samples. Each of these samples is 51-bp long with the adenosine (A) at the center. None of the included samples has $\geq 60\%$ pairwise sequence identity to any other in a same subset. See the main text for further explanation.

(1) List of 3,000 A-to-I editing site samples

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