Supporting Information S1. The benchmark dataset $\mathbb{S}$ constructed for identifying piRNA sequences and their functions. It is formed by three subsets: (1) $\mathbb{S}_{\text{inst}}^{+}$ contains 709 piRNA samples having the function of instructing target mRNA deadenylation; (2) $\mathbb{S}_{\text{non-inst}}^{+}$ contains 709 piRNA samples without the function of instructing target mRNA deadenylation; (3) $\mathbb{S}^{-}$ contains 1,418 non-piRNA samples. See Eq.1 and the relevant text for further explanation.

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(1) List of 709 samples in $\mathbb{S}_{\text{inst}}^{+}$

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(2) List of 709 samples in $\mathbb{S}^{+}_{\text{non-inst}}$

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(3) List of 1,418 samples in $\mathbb{S}^-$

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