

Supporting Information S1. The benchmark dataset \mathcal{S} taken from Chen et al. (*Analytical Biochemistry*, 2015, **5**: 26-33; *Data in Brief*, 2015, **5**: 376-378). It contains 2,614 RNA samples (51-bp long) with a consensus motif GAC at the center. Of the 2,614 samples, 1,307 can be methylated as confirmed by experiments, while the other 1,307 cannot. The former form the positive subset, and the latter the negative subset. See the main text for further explanation.

I. List of 1,307 RNA samples in the positive subset \mathcal{S}^+

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