

OMTN, Volume 7

## **Supplemental Information**

### **iRNA-PseColl: Identifying the Occurrence Sites of Different RNA Modifications by Incorporating Collective Effects of Nucleotides into PseKNC**

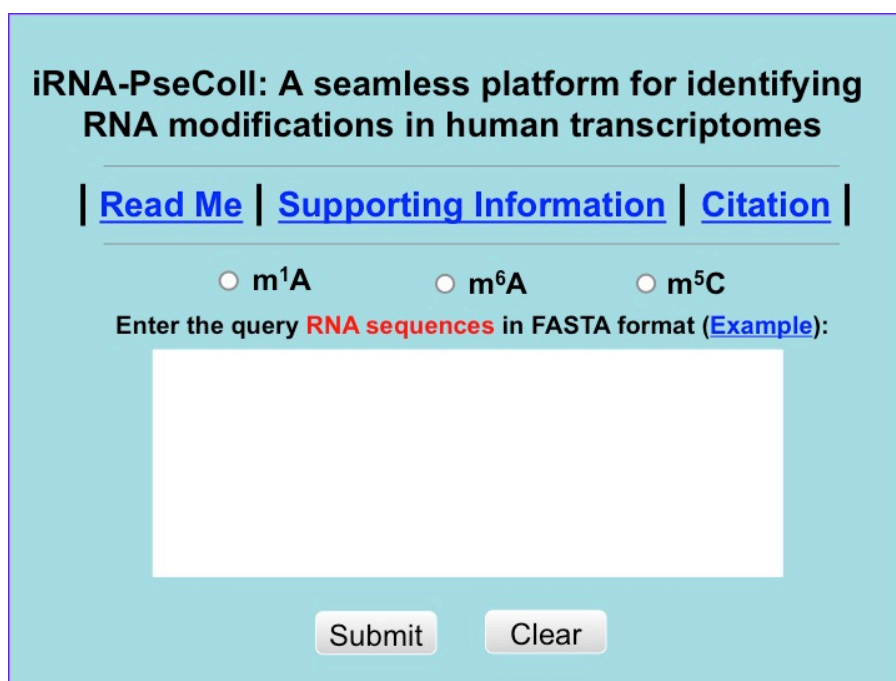
**Pengmian Feng, Hui Ding, Hui Yang, Wei Chen, Hao Lin, and Kuo-Chen Chou**

## Supporting Information S1. User Guide for the iRNA-PseColl predictor

To maximize users' convenience, a step-to-step guide of how to use the iRNA-PseColl predictor to identify the occurrence sites of the three different types of RNA modifications is given below.

**Step 1.** Open the iRNA-PseColl web-server at <http://lin.uestc.edu.cn/server/iRNA-PseColl> and you will see its top page on your computer screen, as shown in **Fig.S1**. Click on the [Read Me](#) button to see a brief introduction about the platform and the caveat when using it.

**Figure S1.** A semi-screenshot for the homepage of the proposed iRNA-PseColl predictor, which is freely accessible at <http://lin.uestc.edu.cn/server/iRNA-PseColl>.



**iRNA-PseColl: A seamless platform for identifying RNA modifications in human transcriptomes**

| [Read Me](#) | [Supporting Information](#) | [Citation](#) |

m<sup>1</sup>A       m<sup>6</sup>A       m<sup>5</sup>C

Enter the query **RNA sequences** in FASTA format ([Example](#)):

**Step 2.** Select which type of RNA modification you are concerned with. For example, if you are interested in the type of m<sup>1</sup>A, check the 1<sup>st</sup> button “m<sup>1</sup>A” on; if type of m<sup>6</sup>A, check the 2<sup>nd</sup> button “m<sup>6</sup>A” on; if type of m<sup>5</sup>C, check the 3<sup>rd</sup> button “m<sup>6</sup>C” on. Then, Either type or copy/paste the query RNA sequences into the input box at the center of **Fig.S1**. The input sequence should be in the FASTA format. For the examples of sequences in FASTA format, click the [Example](#) button right above the input box.

**Step 3.** Click on the [Submit](#) button to see the predicted outcome. For example, if you use the three query RNA sequences in the [Example](#) window as the input and select m<sup>1</sup>A type, after 15 seconds or so, you will see the following shown on the screen of your computer: (1) The 1<sup>st</sup> query sequence contains 14 A nucleotides, of which one is predicted to be for the m<sup>1</sup>A modification and it is at sequence position 21. (2) The 2<sup>nd</sup> query sequence contains 19 A nucleotides, of which none can be for

m<sup>1</sup>A modification. (3) The 3<sup>rd</sup> query sequence is only 25-nt long, too short for the current platform that requires a query RNA sequence with at least 41-nt long. However, if using the same first two query sequences but checking on the 3<sup>rd</sup> button “m<sup>6</sup>C”, you will see the following: (1) The 1<sup>st</sup> query sequence contains 2 C nucleotides, none of which can be for the m<sup>5</sup>C modification. (2) The 2<sup>nd</sup> query sequence contains 5 C nucleotides, of which none can be for m<sup>5</sup>C modification either. All these results are fully consistent with experimental observations.

**Step 4.** Click the [Supporting Information](#) button to download all the Supporting Informations mentioned in this paper.

**Step 5.** Click on the [Citation](#) button to find the relevant papers that document the detailed development and algorithm of the current platform.

**Supporting Information S2. The benchmark dataset  $\mathbb{S}_{\xi=20}(\text{m}^1\text{A})$  for m<sup>1</sup>A modification in RNA.** It contains 6,366 positive samples whose centers can be m<sup>1</sup>A modified as confirmed by experiments, and 6,366 negative samples whose centers cannot be m<sup>1</sup>A modified. All the sequences included are 41-nt long with the adenosine (A) located at the center.

**I. Positive subset  $\mathbb{S}_{\xi=20}^+(\text{m}^1\text{A})$**

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**Supporting Information S3. The benchmark dataset  $\mathbb{S}_{\xi=20}(\text{m}^6\text{A})$  for  $\text{m}^6\text{A}$  modification in RNA.** It contains 1,130 positive samples whose centers can be  $\text{m}^6\text{A}$  modified as confirmed by experiments, and 1,130 negative samples whose centers cannot be  $\text{m}^6\text{A}$  modified. All the sequences included are 41-nt long with the adenosine (A) located at the center.

**I. Positive subset  $\mathbb{S}_{\xi=20}^+(\text{m}^6\text{A})$**

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**Supporting Information S4. The benchmark dataset  $S_{\xi=20}(m^5C)$  for  $m^5C$  modification in RNA.** It contains 120 positive samples whose centers can be  $m^5C$  modified as confirmed by experiments, and 120 negative samples whose centers cannot be  $m^5C$  modified. All the sequences included are 41-nt long with the cytosine (C) located at the center.

**I. Positive subset  $S_{\xi=20}^+(m^5C)$**

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 >P5  
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**II. Negative subset  $\mathbb{S}_{\xi=20}^- (m^5C)$**

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