

# Mining for recurrent long-range interactions in RNA structures reveals embedded hierarchies in network families

## Supplementary Material

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### 1 Overview of the method

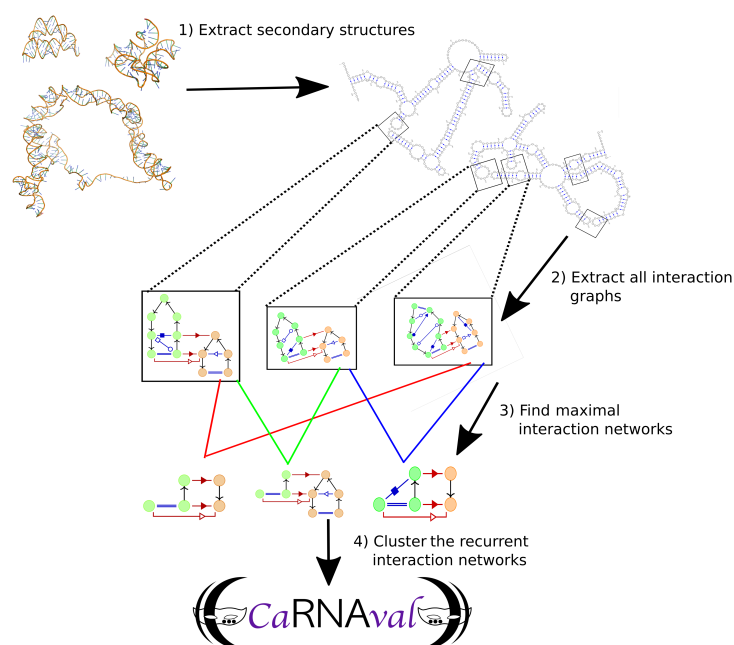


Figure S1: Overview of the method. **(1)** Extraction of the secondary structures from the crystallized tertiary structures. **(2)** All interaction graphs are extracted from the derived secondary structures. **(3)** The maximal interaction networks are extracted. **(4)** The recurrent interaction networks are clustered and gathered in a fully organized and searchable website.

## 2 A-minor Type I/II RIN RMSD

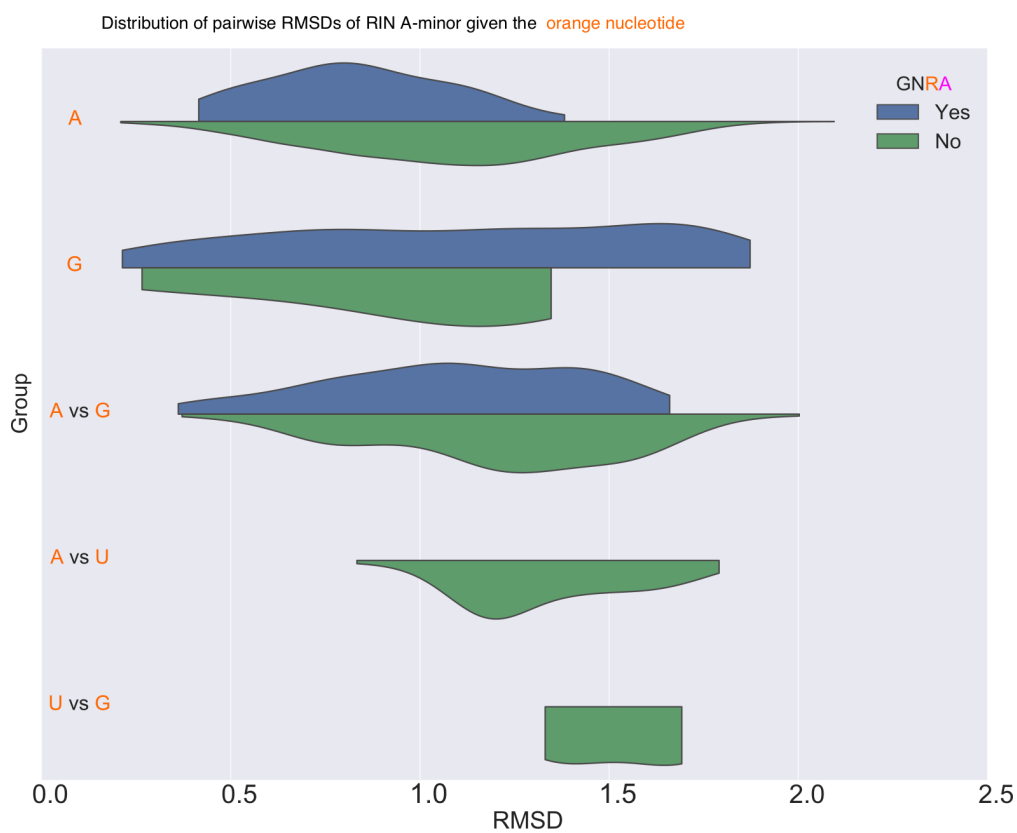


Figure S2: RMSD between the elements of the A-minor Type I/II RIN. Each plot is normalized to have an area of 1. The blue parts only consists of the elements that have a GNRA stem loop, the green part of all the others. The orange position is the nucleotide involved in a single cSS long-range interaction as shown in Fig. 6a.

### 3 Interaction Network

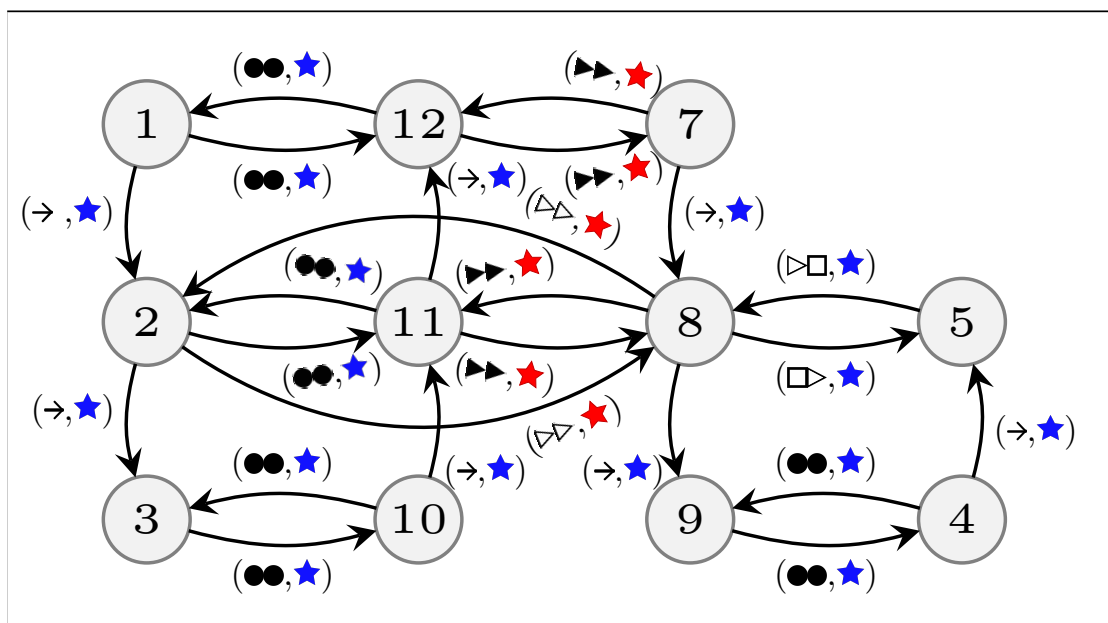


Figure S3: Figure2 bottom right in full page. The details of an interaction network.

## 4 The trans-Watson-Crick/Hoogsteen mesh

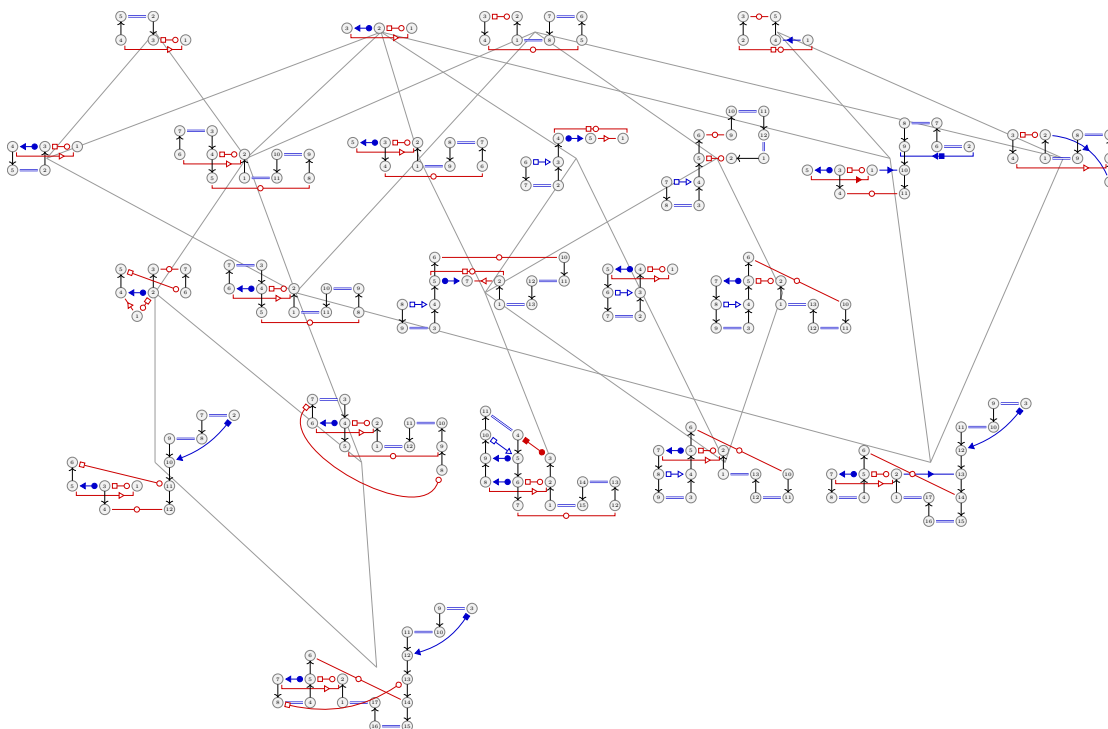


Figure S4: A major cluster of the *trans-Watson-Crick-Hoogsteen mesh* is based on a triple base pair between conserved residues in the core of tRNA structure.