CLAIMS

1. A method for analyzing a higher-order structure of RNA comprising the steps of:

   (a) preparing one or a plurality of RNA probes, each comprising an RNA to be analyzed attached to a barcode sequence,

   (b) contacting the RNA probes and an RNA modification reagent,

   (c) detecting a position and a frequency of modified nucleotides in a sequence of the RNA probe obtained in step (b),

   wherein the RNA modification reagent selectively modifies a single chain region in the RNA probe, and each of the barcode sequences is a sequence that forms a structure comprising a plurality of base pairs; and

   wherein the RNA modification agent is a reagent that reacts with a ribose-2'-hydroxy group in the RNA, preferably comprising isatoic anhydride derivatives, such as 1-methyl-7-nitroisatoic anhydride (1M7), 1-methyl-6-nitroisatoic anhydride (1M6), NMIA (N-methylisatoic anhydride) or 2-methylnicotinic acid imidazolide (NAI); or a reagent that reacts with base portions of the RNA, preferably dimethyl sulfate (DMS) that forms adducts at N1 position of adenosine, N3 position of cytosine, and N3 position of uridine, and N1 position of guanosine.

2. The method of claim 1 wherein step (c) comprises:

   (c1) synthesizing complementary DNAs using a mixture of the RNA probes obtained in step (b) as a template by a reverse transcriptase,

   (c2) determining nucleotide sequences of the complementary DNAs and aligning the nucleotide sequences comprising the barcode sequence, and

   (c3) detecting a position and a frequency of mutations occurred in the aligned nucleotide sequences.

3. The method of claim 1 or 2, wherein the structure comprising a plurality of base pairs is a complementary double-stranded structure, a triple chain structure or a quadruple chain structure.

4. The method of claim 1 or 2, wherein the plurality of base pairs are present in a stem region of a stem-loop structure or a pseudo-knot structure.

5. The method of claim 1 or 2, wherein the structure comprising a plurality of base pairs is a stem-loop structure comprising one or more bulge and/or an internal loop in the stem region.

6. The method of any one of claims 1 to 5, wherein the structure comprising a plurality of base pairs is obtained from an RNA structure deposited in PDB (Protein Data Bank).

7. The method of any one of claims 1 to 6, wherein the RNA to be analyzed comprises at least one RNA structural motif.

8. An RNA probe when used in a method of any one of claims 1 to 7, wherein the RNA probe comprising an RNA to be analyzed attached to a barcode sequence that forms a structure comprising a plurality of base pairs.

9. The RNA probe of claim 8 when used in a method of any one of claims 1 to 7, wherein the structure comprising a plurality of base pairs is a complementary double-stranded structure, a triple chain structure or a quadruple chain structure.

10. The RNA probe of claim 8 when used in a method of any one of claims 1 to 7, wherein the plurality of base pairs are present in a stem region of a stem-loop structure or a pseudo-knot structure.

11. The RNA probe of claim 8 when used in a method of any one of claims 1 to 7, wherein the structure comprising a plurality of base pairs is a stem-loop structure comprising one or more bulge and/or an internal loop in the stem region.

12. The RNA probe of claim 8 when used in a method of any one of claims 1 to 7, wherein the structure comprising a plurality of base pairs is obtained from an RNA structure deposited in PDB (Protein Data Bank).

13. An RNA probe library comprising a plurality of RNA probes of any one of claims 8 to 12 when used in a method of any one of claims 1 to 7, wherein the RNA probe comprised in each of the compositions comprises an RNA to be analyzed that has a different sequence.

14. A group of RNA probe libraries comprising two or more replicates of the RNA probe libraries of claim 13 comprising a plurality of RNA probes of any one of claims 8 to 12 when used in a method of any one of claims 1 to 7, wherein all the replicated RNA probes further comprise second barcode sequences, and the second barcode sequences are identical within each of the RNA probe libraries, while distinguishable between other RNA probe libraries.