Claims

1. A deaminase-recruiting RNA (dRNA) of 60-200 nucleotides, wherein:

a) the dRNA comprises a complementary RNA sequence capable of hybridizing to a target RNA;

b) the dRNA is capable of recruiting a deaminase or a construct comprising a deaminase or a construct comprising a catalytic domain of a deaminase to deaminate a target adenosine in the target RNA; and

c) the dRNA comprises one or more chemical modifications,

wherein the target adenosine is in a three-base motif selected from the group consisting of UAG, UAC, UAA, UAU, CAG, CAC, CAA, CAU, AAG, AAC, AAA, AAU, GAG, GAC, GAA and GAU in the target RNA;

wherein the complementary RNA sequence comprises a cytidine, adenosine or uridine directly opposite to a target adenosine in the target RNA;

wherein the cytidine, adenosine or uridine directly opposite to the target adenosine locates at least 7 nucleotides away from the 3' end of the complementary RNA sequence of the dRNA, and at least 25 nucleotides away from the 5' end of the complementary RNA sequence of the dRNA; and

wherein the length of the 5' sequence within the complementary RNA sequence flanking the cytidine, adenosine or uridine directly opposite to the target adenosine is longer than the 3' sequence within the complementary RNA sequence.

2. The dRNA of claim 1, wherein the dRNA is longer than any of 60nt, 65nt, 70nt, 80nt, 90nt, 100nt, or 110nt.

3. The dRNA of claim 1 or 2, comprising one or more mismatches, wobbles and/or bulges with the complementary target RNA region.

4. The dRNA of any one of claims 1-3, comprising a cytidine directly opposite to the target adenosine in the target RNA, and/or wherein the complementary RNA sequence comprises one or more guanosines each opposite to a non-target adenosine in the target RNA.

5. The dRNA of any one of claims 1-4, wherein the complementary sequence comprises two or more consecutive mismatch nucleotides opposite to a non-target adenosine in the target RNA.

6. The dRNA of any one of claims 1-5, wherein the three-base motif is UAG, and wherein the dRNA comprises an adenosine directly opposite to the uridine in the three-base motif, a cytidine directly opposite to the target adenosine, and a cytidine, guanosine or uridine directly opposite the guanosine in the three-base motif.

7. The dRNA of claim 6, wherein the dRNA comprises a 5'-CCA-3' directly opposite to the three-base motif of UAG.

8. The dRNA of any one of claims 1-7, wherein the chemical modification comprises methylation and/or phosphorothioation.

9. The dRNA of claim 8, wherein the chemical modification comprises a 2'-O-methylation and/or internucleotide phosphorothioate linkage.

10. The dRNA of claim 8, wherein the chemical modification comprises a 2'-O-methylationin the first and last 1-5, 2-5, 3-5, 4-5 nucleotides and/or phosphorothioations in the first and last 1-5, 2-5, 3-5, 4-5 internucleotide linkages.

11. The dRNA of claim 8, wherein the chemical modification comprises a 2'-O-methylation and/or a 3'-phosphorothioation in the nucleotide opposite to the target adenosine and/or its 5' and/or 3' most adjacent nucleotides.

12. The dRNA of claim 8, wherein the chemical modification is selected from a group consisting of:

1) 2’-O-methylations in the first and last 3 nucleotides and/or phosphorothiations in the first and last 3 internucleotide linkages;

2) i) 2’-O-methylations in the first and last 3 nucleotides and/or phosphorothiations in the first and last 3 internucleotide linkages, and ii) 2’-O-methylations in a single, multiple, or all uridines;

3) i) 2’-O-methylations in the first and last 3 nucleotides, ii) phosphorothiations in the first and last 3 internucleotide linkages, iii) 2’-O-methylations in a single, multiple, or all uridines, and iv) a modification in the nucleotide opposite to the target adenosine, and/or the 5’ and/or 3’ most adjacent nucleotides of the nucleotide opposite to the target adenosine;

4) i) 2’-O-methylations in the first and last 3 nucleotides, ii) phosphorothiations in the first and last 3 internucleotide linkages, iii) 2’-O-methylations in a single, multiple, or all uridines, and iv) 2’-O-methylation in the nucleotide most adjacent to the 3’ terminus and/or 5’ terminus of the nucleotide opposite to the target adenosine;

5) i) 2’-O-methylations in the first and last 3 nucleotides, ii) phosphorothiations in the first and last 3 internucleotide linkages, iii) 2’-O-methylations in a single, multiple, or all uridines, and iv) phosphorothioatie linkage in the nucleotide opposite to the target adenosine and/or in the 5’ and/or 3’ most adjacent nucleotides of the nucleotide opposite to the target adenosine; and

6) 2’-O-methylations in the first and last 1-5 nucleotides and/or phosphorothiations in the first and last 1-5 internucleotide linkages.

13. The dRNA of claim 12, wherein the modification in the nucleotide opposite to the target adenosine, and/or one or two nucleotides most adjacent to the nucleotide opposite to the target adenosine is 2’-O-methylation and/or phosphorothioatie linkage.

14. The dRNA of any one of claims 1-13, which does not comprise an ADAR-recruiting domain capable of forming an intramolecular stem loop structure for binding an ADAR enzyme.

15. A construct comprising or encoding a dRNA of any one of claims 1-14.

16. An *in vitro* method for editing a target RNA in a host cell, comprising introducing a dRNA of any one of claims 1-14 into the host cell, or introducing a plurality of the dRNAs each targeting a different target RNA into the host cell.

17. The method of claim 16, further comprises introducing an exogenous ADAR to the host cell.

18. A construction, composition, cell, library or kit comprising the dRNAs of any one of claims 1-14.

19. Use of the dRNA of any one of claims 1-14 in the preparation of a medicament for editing a target RNA in a host cell, wherein the dRNA is to be introduced into the host cell; or a plurality of the dRNAs are to be introduced into the host cell each targeting a different target RNA into the host cell.

20. Use of the dRNA of any one of claims 1-14 in the preparation of a medicament for use in treating or preventing a disease or condition in an individual, wherein the disease or condition is a hereditary genetic disease or is associated with one or more acquired genetic mutations.