WHAT IS CLAIMED IS:

1. An engineered composition or system for ribonucleic acid (RNA) editing, comprising:

1) a modified adenosine deaminase protein or a catalytic domain thereof or a construct expressing the modified adenosine deaminase protein or the catalytic domain thereof, wherein the adenosine deaminase protein or the catalytic domain thereof has the activity of catalyzingcytidine deamination after being modified, and

2) an ADAR-recruiting RNA (arRNA) that recruits the modifiedadenosine deaminase protein or the catalytic domainthereof to a target RNA, or a construct comprisingthe arRNA or a coding sequence for the arRNA;

wherein the arRNAcomprisesa complementary RNA sequence that hybridizes to the target RNA, and the arRNA recruits the adenosine deaminase protein or the catalytic domain thereof to the target RNA, thereby deaminating a target cytidine in the target RNA,

particularly, the adenosine deaminase is modified by mutation in one or more sites to have the activity of deaminating cytidine which consequently converts to uridine

more particularly,the adenosine deaminase protein or the catalytic domain thereof is an ADAR2 protein or a homologous protein or catalytic domain thereof,

even more particularly, the mutation modification comprises: E488Q/V351G/S486A/T375S/S370C/P462A/N597I/L332I/I398V/K350I/M383L/D619G/S582T/V440I/S495N/K418E/S661T, wherein the numbering of the amino acid of the mutation modification is consistent with the numbering of the amino acid in NP_001103.1.

~~2. The engineered composition or system according to claim 1,wherein the adenosine deaminase is modified by mutation in one or more sites to have the activity of deaminating cytidine which consequently converts to uridine.~~

~~3. The engineered composition or system according to claim 2, wherein the adenosine deaminase protein or the catalytic domain thereof is an ADAR2 protein or a homologous protein or catalytic domain thereof.~~

~~4. The engineered composition or system according to claim 3, wherein the mutation~~

~~modification comprises: E488Q/V351G/S486A/T375S/S370C/P462A/N597I/L332I/I398V/K350I/M383L/D619G/S582T/V440I/S495N/K418E/S661T, wherein the numbering of the amino acid of the mutation modification is consistent with the numbering of the amino acid in NP_001103.1.~~

~~5~~2. The engineered composition or system according to ~~any one of~~ claim~~s~~ 1-~~4~~, wherein the arRNA hybridizes to the target RNA, and a targeting base in the arRNAopposite to the target cytidine is A, U, C, or G.

~~6. The engineered composition or system according to claim 5, wherein the targeting base is U or C.~~

~~7~~3. The engineered composition or system according to any one of claims 1-~~6~~2, wherein:

the arRNAcomprisesone or more mismatchesinone or more positions corresponding toupstream and/or downstream of thetarget base of the target RNA, particularly, the 3' mostadjacent base of the arRNA targeting base forms a mismatch with the target RNA, moreparticularly,the arRNA hybridizes to the target RNA, and the 3' mostadjacent base of the targeting base forms a G-G mismatch with the target RNA.

~~8. The engineered composition or system according to claim 7, whereinthe 3' mostadjacent base of the arRNA targeting base forms a mismatch with the target RNA.~~

~~9. The engineered composition or system according to claim 8, wherein the arRNA hybridizes to the target RNA, and the 3' mostadjacent base of the targeting base forms a G-G mismatch with the target RNA.~~

~~10~~4. The engineered composition or system according to any one of claims 1-~~9~~3, wherein the arRNA hybridizes to the target RNA, and the 5' mostadjacent base of the targeting base does not form a mismatch with the target RNA, particularly, the 5' mostadjacent base of the targeting base is U.

~~11. The engineered composition or system according to claim 10, wherein the 5’ mostadjacent base of the targeting base is U~~.

~~12. The engineered composition or system according to claim 9, wherein the arRNA hybridizes to the target RNA, and anorder of base preferencefrom high to low in the target RNA opposite to the 5' mostadjacent base of the targeting base of the arRNA is G or C, U or A.~~

~~13~~5. The engineered composition or system according to any one of claims 1-~~6~~4, wherein the arRNA hybridizes to the target RNA, a target base triplet formed by the target base and the 5' and 3' adjacent bases thereof forms a mismatch only at the target base, wherein the target base triplet is selected from: ACG, ACC, UCC, UCG, CCC, CCG, UCA, and UCU.

~~14~~6. The engineered composition or system according to any one of claims 1-~~13~~5, wherein the length of the arRNA is >50 nt,

particularly, the lengths from the targeting base to the 3’-terminal and 5’-terminal in the arRNA are equal,

more particularly, thelength from the targeting base to the 3’-terminal in the arRNAis 45-5nt,

even moreparticularly, the length from the targeting base to the 5’-terminal in the arRNAis 80-30nt.

~~15. The engineered composition or system according to any one of claims 1-14, whereinthe lengths from the targeting base to the 3’-terminal and 5’-terminal in the arRNA are equal.~~

~~16. The engineered composition or system according to any one of claims 1-14, wherein thelength from the targeting base to the 3’-terminal in the arRNAis 45-5nt, 40-5nt, 35-10nt, 25 nt-15nt, or24 nt-11nt.~~

~~17. The engineered composition or system according to any one of claims 1-14, wherein the length from the targeting base to the 5’-terminal in the arRNAis 80-30nt, 70-35nt, 60-40nt, 55nt-35nt, or55nt-45nt.~~

~~18~~7. The engineered composition or system according to any one of claims 1-~~17~~6, wherein the arRNA is chemically modified, particularly, the chemical modification comprises a 2'-O-methyl modification or an inter-nucleotide 3'-thio modification.

~~19. The engineered composition or system according to claim 18, wherein the chemical modification comprises a 2'-O-methyl modification or an inter-nucleotide 3'-thio modification.~~

~~20~~8. A method for deaminating a target cytosine in a target RNA in a cell, comprising introducing the followings 1) and 2) into the cell:

1) a modified adenosine deaminase protein or a catalytic domain thereof or a construct expressing the modified adenosine deaminase protein or the catalytic domain thereof, and

2) an arRNA that recruits the modifiedadenosine deaminase protein or the catalytic domainthereof to the target RNA or a construct comprisingthe arRNA or a coding sequence for the arRNA, wherein the adenosine deaminase protein or the catalytic domain thereof has the activity of catalyzingcytidine deamination after being modified, and the arRNAcomprisesa complementary RNA sequence that hybridizes to the target RNA, and the arRNA recruits the adenosine deaminase protein or the catalytic domain thereof to the target RNA, thereby deaminating a target cytidine in the target RNA.

~~21~~9. The method according to claim ~~20~~8, wherein the construct expressing the modified adenosine deaminase protein or the catalytic domain thereof and the construct comprising the coding sequence for the arRNA are the same construct, or the construct expressing the modified adenosine deaminase protein or the catalytic domain thereof and the construct comprisingthe coding sequence for the arRNAare separated constructs, and the separated constructs are introduced into the cell simultaneously or separately,

particularly, the adenosine deaminase is modified by mutation in one or more sites to have the activity of deaminating cytidine which subsequently converts to uridine

more particularly, the adenosine deaminase protein or the catalytic domain thereof is an ADAR2 protein or a homologous protein or catalytic domain thereof,

even more particularly, the mutation modification comprises: E488Q/V351G/S486A/T375S/S370C/P462A/N597I/L332I/I398V/K350I/M383L/D619G/S582T/V

440I/S495N/K418E/S661T, wherein the numbering of the amino acid of the mutation modification is consistent with the numbering of the amino acid in NP_001103.1.

~~22. The method according to claim 20 or 21, wherein the adenosine deaminase is modified by mutation in one or more sites to have the activity of deaminating cytidine which subsequently converts to uridine.~~

~~23. The method according to claim 22, wherein the adenosine deaminase protein or the catalytic domain thereof is an ADAR2 protein or a homologous protein or catalytic domain thereof.~~

~~24. The method according to claim 23, wherein the mutation modification comprises: E488Q/V351G/S486A/T375S/S370C/P462A/N597I/L332I/I398V/K350I/M383L/D619G/S582T/V440I/S495N/K418E/S661T, wherein the numbering of the amino acid of the mutation modification is consistent with the numbering of the amino acid in NP_001103.1.~~

~~25~~10. The method according to any one of claims ~~21-24~~8-9, wherein the arRNA hybridizes to the target RNA, and a targeting base in the arRNAopposite to the target cytidine is A, U, C, or G, particularly, the arRNA comprises one or more mismatches in one or more positions corresponding to upstream and/or downstream of the target base of the target RNA,

more particularly, the 3’ mostadjacent base of the arRNA targeting base forms a mismatch with the target RNA,

even more particularly, the arRNA hybridizes to the target RNA, and the 3’ mostadjacent base of the targeting base forms a G-G mismatch with the target RNA.

~~26. The method according to claim 25, wherein the targeting base is U or C.~~

~~27. The method according to any one of claims 21-26, wherein:~~

~~the arRNA comprises one or more mismatches in one or more positions corresponding to upstream and/or downstream of the target base of the target RNA.~~

~~28. The method according to claim 27, wherein the 3’ mostadjacent base of the arRNA~~

~~targeting base forms a mismatch with the target RNA.~~

~~29. The method according to claim 28, wherein the arRNA hybridizes to the target RNA, and the 3' mostadjacent base of the targeting base forms a G-G mismatch with the target RNA.~~

~~30~~11. The method according to any one of claims ~~21~~8-~~29~~10, wherein the arRNA hybridizes to the target RNA, and the 5' mostadjacent base of the targeting base does not form a mismatch with the target RNA,

particularly, the 5' mostadjacent base of the targeting base is U,

more particularly, the arRNA hybridizes to the target RNA, a target base triplet formed by the target base and the 5' and 3' adjacent bases thereof forms a mismatch only at the target base, wherein the target base triplet is selected from: ACG, ACC, UCC, UCG, CCC, CCG, UCA, and UCU.

~~31. The method according to claim 30, wherein the 5' mostadjacent base of the targeting base is U.~~

~~32. The methodaccording to claim 29, wherein the arRNA hybridizes to the target RNA, and anorder of base preferencefrom high to low in the target RNA opposite to the 5' mostadjacent base of the targeting base of the arRNA is G or C, U or A.~~

~~33. The methodaccording to any one of claims 21-26, wherein the arRNA hybridizes to the target RNA, a target base triplet formed by the target base and the 5' and 3' adjacent bases thereof forms a mismatch only at the target base, wherein the target base triplet is selected from: ACG, ACC, UCC, UCG, CCC, CCG, UCA, and UCU~~.

~~34~~12. The methodaccording to any one of claims ~~21~~8-11-~~33~~, wherein the length of the arRNA is >50 nt,

particularly, the lengths from the targeting base to the 3'-terminal and 5'-terminal in the arRNA are equal

more particularly, thelength from the targeting base to the 3'-terminal in the arRNAis 45-5nt

even more particularly, the length from the targeting base to the 5’-terminal in the arRNAis 80-30nt.

~~35. The methodaccording to any one of claims 21-34, whereinthe lengths from the targeting base to the 3’-terminal and 5’-terminal in the arRNA are equal.~~

~~36. The method according to any one of claims 21-34, wherein thelength from the targeting base to the 3’-terminal in the arRNAis 45-5nt, 40-5nt, 35-10nt, 25 nt-15nt, or24 nt-11nt.~~

~~37. The methodaccording to any one of claims 21-34, wherein the length from the targeting base to the 5’-terminal in the arRNAis 80-30nt, 70-35nt, 60-40nt, 55nt-35nt, or55nt -45nt.~~

~~38~~13. The methodaccording to any one of claims ~~21~~8-~~37~~12, wherein the arRNA is chemically modified, particularly,the chemical modification comprises a 2'-O-methyl modification or an inter-nucleotide 3'-thio modification.

~~39. The methodaccording to claim 38, wherein the chemical modification comprises a 2'-O-methyl modification or an inter-nucleotide 3'-thio modification.~~

~~40~~14. The method according to any one of claims ~~21~~8-~~39~~13, wherein the cell is a mammalian cell.

~~41. A method for treating a disease caused by a T-to-C mutation, comprising using the method according to any one of claims 21-39 to deaminate a target base C in a transcription-formed messenger RNAcomprising the T-to-Cmutation to correctthe mutation.~~

~~42~~15. A modified adenosine deaminase protein for use in treating a disease caused by a T-to-C mutation, wherein the adenosine deaminase protein is ADAR2comprisingthe following amino acid mutations corresponding toADAR2 withGenebank accession number NP_001103.1: E488Q/V351G/S486A/T375S/S370C/P462A/N597I/L332I/I398V/K350I/M383L/D619G/S582T/V440I/S495N/K418E/S661T, or an amino acid mutation in the corresponding position of a

homologous ADAR2 protein of the NP_001103.1, and the ADAR2 protein has the activity of catalyzingcytidinedeamination after being modified by the mutation, particularly, the modified adenosine deaminase catalyzes cytidinedeamination into uridine.

~~43. A use of the modified adenosine deaminase protein according to claim 42 for catalyzing cytidinedeamination into uridine.~~