**WHAT IS CLAIMED IS:**

1. A composition comprising a trans-splicing nucleic acid, comprising: (a) one or more replacement domains that encode a therapeutic sequence; (b) one or more intronic domains that promote RNA splicing of the one or more replacement domains, wherein the one or more intronic domains each comprises a trans-splicing enhancer sequence; and (c) one or more antisense domains that bind to a target RNA molecule.

2. The composition of claim 1, wherein the trans-splicing enhancer sequence consists of a chain of RNA nucleobases comprising at least one RNA motif having the formula $X_1X_2X_3X_4X_5X_6$, wherein: $X_1$ is selected from the group consisting of adenine (A), uracil (U) and guanine (G); $X_2$ is selected from the group consisting of adenine (A), uracil (U) and guanine (G); $X_3$ is selected from the group consisting of adenine (A), uracil (U) and guanine (G); $X_4$ is selected from the group consisting of adenine (A), uracil (U), cytosine (C) and guanine (G); $X_5$ is selected from the group consisting of adenine (A), cytosine (C), uracil (U) and guanine (G); and $X_6$ is selected from the group consisting of adenine (A), uracil (U) and guanine (G).

3. The composition of claim 1, wherein the trans-splicing enhancer sequence consists of a chain of RNA nucleobases comprising at least one RNA motif having the formula $X_1X_2X_3X_4X_5X_6$, wherein: $X_1$ is selected from the group consisting of adenine (A), uracil (U) and guanine (G); $X_2$ is selected from the group consisting of adenine (A), uracil (U) and guanine (G); $X_3$ is selected from the group consisting of adenine (A), uracil (U) and guanine (G); $X_4$ is selected from the group consisting of adenine (A), uracil (U) and guanine (G); $X_5$ is selected from the group consisting of adenine (A), uracil (U) and guanine (G); and $X_6$ is selected from the group consisting of uracil (U) and guanine (G).

4. The composition of claim 1, wherein the trans-splicing enhancer sequence consists of a chain of RNA nucleobases comprising at least one RNA motif having the formula $X_1X_2X_3X_4X_5X_6$, wherein: $X_1$ is selected from the group consisting of adenine (A), uracil (U) and guanine (G); $X_2$ is selected from the group consisting of uracil (U) and guanine (G); $X_3$ is selected from the group consisting of adenine (A), uracil (U) and guanine (G); $X_4$ is

selected from the group consisting of uracil (U) and guanine (G); $X_5$ is selected from the group consisting of uracil (U) and guanine (G); and $X_6$ is selected from the group consisting of uracil (U) and guanine (G).

5. The composition of any one of claims 1-4, wherein the trans-splicing enhancer sequence is adjacent to RNA motifs that further increase trans-splicing efficiency.

6. The composition of any one of claims 1-5, wherein the trans-splicing enhancer sequence is less than 300 bases from a 3' splice site of the trans-splicing nucleic acid.

7. The composition of any one of claims 1-6, wherein the trans-splicing enhancer sequence is less than 300 bases from a 5' splice site of the trans-splicing nucleic acid.

8. The composition of any one of claims 1-7, wherein each of the one or more intronic domains comprises 2 or more trans-splicing enhancer sequences.

9. The composition of any one of claims 1-8, wherein the trans-splicing nucleic acid further comprises a 3' untranslated region that increases trans-splicing efficiency.

10. The composition of any one of claims 1-9, wherein the trans-splicing nucleic acid further comprises a 5' untranslated region that increases trans-splicing efficiency.

11. The composition of any one of claims 1-10, wherein the one or more replacement domains each comprises a gene expression-enhancing element.

12. The composition of claim 11, wherein the gene expression-enhancing element comprises a sequence derived or isolated from the group consisting of: Woodchuck Hepatitis Vims (WHV) Posttranscriptional Regulatory Element (WPRE), triplex from MALAT1, the PRE of Hepatitis B vims (HPRE), and an iron response.

13. The composition of any one of claims 1-12, further comprising an RNA-binding protein that strengthens the interaction between the trans-splicing nucleic acid and the target RNA molecule and increases trans-splicing efficiency.

14. The composition of any one of claims 1-13, wherein the trans-splicing nucleic acid is RNA, DNA, a DNA/RNA hybrid, a nucleic acid analog, a chemically-modified nucleic acid, or a chimera composed of two or more nucleic acids or nucleic acid analogs.

15. The composition of any one of claims 1-14, wherein the trans-splicing nucleic acid further comprises a heterologous promoter.

16. A vector comprising or encoding the composition of any one of claims 1-15.

17. The vector of claim 16, wherein the vector is selected from the group consisting of: adeno-associated virus, retrovirus, lentivirus, adenovirus, nanoparticle, micelle, liposome, lipoplex, polymersome, polyplex, and dendrimer.

18. A cell comprising the vector of claim 16 or claim 17.

19. Use of the composition of any one of claims 1-15 or the vector of claim 16 or claim 17 in the manufacture of a medicament for treating a disease in a subject in need thereof.

20. Use of the composition of any one of claims 1-15 or the vector of claim 16 or claim 17 in the manufacture of a medicament for correcting a genetic defect in a subject in need thereof.