What is claimed is:

1. A method for assaying a sample of viral particles comprising a single-stranded DNA genome for strand-specificity, comprising:

(a) synthesizing a synthetic DNA strand complementary to a native DNA strand of the sample of viral particles to yield a double-stranded DNA product, the synthetic DNA strand being synthesized by incorporating a modified base;

(b) purifying the synthesized double-stranded DNA product;

(c) sequencing the purified double-stranded DNA product on a sequencer, wherein the sequencer identifies the sequence of nucleotides in one sequenced strand of the double-stranded DNA product; and

(d) determining the specificity of the native DNA strand by identifying the specificity of the sequenced strand, and detecting whether the sequenced strand contains the modified base,

wherein the presence of the modified base indicates that the sequenced strand is the synthetic DNA strand of the double-stranded DNA product.

2. The method of claim 1, wherein the sample of viral particles comprises adeno-associated virus (AAV) particles.

3. The method of claim 2, wherein the AAV particles are of serotype AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAV9, AAV-DJ, AAV-DJ/8, AAV-Rh10, AAV-retro, AAV-PHP.B, AAV8-PHP.eB, or AAV-PHP.S.

4. The method of claim 1, wherein the modified base comprises 5-methylcytosine, 5-hydroxymethylcytosine, or N6-methyldeoxyadenosine.

5. The method of claim 4, wherein the modified base is 5-methylcytosine.

6. The method of claim 1, wherein the double-stranded DNA product is purified using magnetic beads.

7. The method of claim 1, wherein the sequencer is a nanopore sequencer.

8. The method of claim 7, wherein the nanopore sequencer allows entry of either the native DNA strand or the synthetic DNA strand of the purified double-stranded DNA product for sequencing.

9. The method of claim 7, wherein detection of the modified base distinguishes the synthetic DNA strand from the native DNA strand entering the nanopore sequencer.

10. The method of claim 1, wherein the native DNA strand or the synthetic DNA strand is sequenced using a long-read sequencing approach.

11. The method of claim 1, wherein the modified base of the synthetic DNA strand is detected by an alteration of a flow of current through a nanopore sequencer.

12. The method of claim 1, further comprising identifying a percentage of sense strand and anti-sense strand packaged in the sample of viral particles based on detection of the modified base of the synthetic DNA strand.

13. The method of claim 1, wherein the viral particles comprise an exogenous gene in the single-stranded DNA genome.

14. The method of claim 13, wherein the exogenous gene is a therapeutic gene.

15. The method of claim 1, further comprising determining a complete sequence of the sequenced strand.

16. The method of claim 15, further comprising identifying a complementary nucleotide sequence corresponding to the complete sequence, if the sequenced strand is the synthetic DNA strand of the double stranded DNA product.

17. The method of claim 1, wherein the sequencing identifies from about 100 to about 5000 nucleotides in the sequenced strand.

18. The method of claim 17, wherein the sequencing identifies from 100 to 1000 nucleotides in the sequenced strand.

19. The method of claim 18, wherein the sequencing identifies from 100 to 500 nucleotides in the sequenced strand.

20. The method of claim 1, wherein the sequencing is performed without fragmentation of the sequenced strand.

21. A method for distinguishing between a native DNA strand and a synthetic DNA strand in a sample of adeno-associated virus (AAV) particles comprising a single-stranded DNA genome, comprising:

(a) synthesizing the synthetic DNA strand complementary to the native DNA strand to yield a double-stranded DNA product, the synthetic DNA strand including a modified base which selectively labels the synthetic DNA strand;

(b) purifying the double-stranded DNA product;

(c) sequencing the purified double-stranded DNA product on a nanopore sequencer; and

(d) determining the specificity of the native DNA strand by identifying the specificity of the sequenced strand, and detecting whether the sequenced strand contains the modified base of the synthetic DNA strand during nanopore sequencing by detecting an alteration of a flow of current through the nanopore sequencer,

wherein the presence of the modified base indicates that the sequenced strand is the synthetic DNA strand of the double stranded DNA product.

22. The method of claim 21, wherein the modified base comprises 5-methylcytosine, 5-hydroxymethylcytosine, or N6-methyldeoxyadenosine.

23. The method of claim 22, wherein the modified base is 5-methylcytosine.

24. The method of claim 21, wherein the native DNA strand or the selectively labeled synthetic DNA strand is sequenced using a long-read sequencing approach.

25. The method of claim 21, wherein the double-stranded DNA product is purified using magnetic beads.

26. The method of claim 21, wherein the AAV particles are of serotype AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAV9, AAV-DJ, AAV-DJ/8, AAV-Rh10, AAV-retro, AAV-PHP.B, AAV8-PHP.eB, or AAV-PHP.S.