Claims

1. A recombinant HSV virus, which does not express a functional ICP0 protein and ICP34.5 protein; but is capable of expressing a functional UL43 protein, a functional UL41 protein (i.e., a vhs protein), a functional UL48 protein (i.e., a VMW65 protein), or any combination thereof;

preferably, the recombinant HSV virus is a recombinant HSV-1 virus, a recombinant HSV-2 virus, or an HSV-1/HSV-2 chimeric virus;

preferably, the recombinant HSV virus is derived from a HSV-1 strain KOS.

2. The recombinant HSV virus according to Claim 1, wherein the genome of the recombinant HSV virus comprises the following modifications:

two copies of the ICP0 gene each independently comprises a loss-of-function mutation (e.g., addition, deletion, and/or substitution of one or more bases) or is deleted or substituted with an exogenous nucleotide sequence (e.g., a nucleotide sequence encoding a foreign protein); and

two copies of the ICP34.5 gene each independently comprises a loss-of-function mutation (e.g., addition, deletion, and/or substitution of one or more bases) or is deleted or substituted with an exogenous nucleotide sequence (e.g., a nucleotide sequence encoding a foreign protein);

for example, in the genome of the recombinant HSV virus,

(a1) one copy of the ICP0 gene comprises a loss-of-function mutation (e.g., addition, deletion, and/or substitution of one or more bases), and the other copy of the ICP0 gene comprises a loss-of-function mutation (e.g., addition, deletion, and/or substitution of one or more bases) or is deleted or substituted with an exogenous nucleotide sequence (e.g., a nucleotide sequence encoding a foreign protein); or

(b1) one copy of the ICP0 gene is deleted, and the other copy of the ICP0 gene comprises a loss-of-function mutation (e.g., addition, deletion, and/or substitution of one or more bases) or is deleted or substituted with an exogenous nucleotide sequence (e.g., a nucleotide sequence encoding a foreign protein); or

(c1) one copy of the ICP0 gene is substituted with an exogenous nucleotide sequence (e.g., a nucleotide sequence encoding a foreign protein), and the other copy of the ICP0 gene comprises a loss-of-function mutation (e.g., addition, deletion and/or substitution of one or more bases) or is deleted or substituted with an exogenous nucleotide sequence (e.g., a nucleotide sequence encoding a foreign protein); and

(a2) one copy of the ICP34.5 gene comprises a loss-of-function mutation (e.g., addition, deletion, and/or substitution of one or more bases), and the other copy of the ICP34.5 gene comprises a loss-of-function mutation (e.g., addition, deletion and/or substitution of one or more bases) or is deleted or substituted with an exogenous nucleotide sequence (e.g., a nucleotide sequence encoding a foreign protein); or

(b2) one copy of the ICP34.5 gene is deleted, and the other copy of the ICP34.5 gene comprises a loss-of-function mutation (e.g., addition, deletion, and/or substitution of one or more bases) or is deleted or substituted with an exogenous nucleotide sequence (e.g., a nucleotide sequence encoding a foreign protein); or

(c2) one copy of the ICP34.5 gene is substituted with an exogenous nucleotide sequence (e.g., a nucleotide sequence encoding a foreign protein), and the other copy of the ICP34.5 gene comprises a loss-of-function mutation (e.g., addition, deletion and/or substitution of one or more bases) or is deleted or substituted with an exogenous nucleotide sequence (e.g., a nucleotide sequence encoding a foreign protein);

preferably, the two copies of the ICP0 gene comprise the same loss-of-function mutation or different loss-of-function mutations; or are all deleted; or are substituted with the same exogenous nucleotide sequence or different exogenous nucleotide sequences;

preferably, the two copies of the ICP34.5 gene comprise the same loss-of-function mutation or different loss-of-function mutations; or are all deleted; or are substituted with the same exogenous nucleotide sequence or different exogenous nucleotide sequences;

preferably, in the genome of the recombinant HSV virus,

(1) the two copies of the ICP0 genes each independently comprises a loss-of-function mutation (e.g., addition, deletion, and/or substitution of one or more bases), and, the two copies of the ICP34.5 gene each independently comprises a loss-of-function mutation (e.g., addition, deletion, and/or substitution of one or more bases); or

(2) the two copies of the ICP0 gene each independently comprises a loss-of-function mutation (e.g., addition, deletion, and/or substitution of one or more bases), and, the two copies of the ICP34.5 gene are deleted; or

(3) the two copies of the ICP0 gene each independently comprises a loss-of-function mutation (e.g., addition, deletion, and/or substitution of one or more bases), and, the two copies of the ICP34.5 gene each is independently substituted with an exogenous nucleotide sequence (e.g., a nucleotide sequence encoding a foreign protein); or

(4) the two copies of the ICP0 gene are deleted; and, the two copies of the ICP34.5 gene each independently comprises a loss-of-function mutation (e.g., addition, deletion, and/or substitution of one or more bases) ); or

(5) the two copies of the ICP0 gene are deleted; and, the two copies of the ICP34.5 gene are deleted; or

(6) the two copies of the ICP0 gene are deleted; and, the two copies of the ICP34.5 gene each is independently substituted with an exogenous nucleotide sequence (e.g, a nucleotide sequence encoding a foreign protein) ); or

(7) the two copies of the ICP0 gene each is independently substituted with an exogenous nucleotide sequence (e.g., a nucleotide sequence encoding a foreign protein), and, the two copies of the ICP34.5 gene each independently comprises a loss-of-function mutation (e.g., addition, deletion, and/or substitution of one or more bases); or

(8) the two copies of the ICP0 gene each is independently substituted with an exogenous nucleotide sequence (e.g., a nucleotide sequence encoding a foreign protein), and, the two copies of the ICP34.5 gene are deleted; or

(9) the two copies of the ICP0 gene each is independently substituted with an exogenous nucleotide sequence (e.g., a nucleotide sequence encoding a foreign protein), and, the two copies of the ICP34.5 gene each is independently substituted with an exogenous nucleotide sequence (e.g., a nucleotide sequence encoding a foreign protein);

preferably, in the genome of the recombinant HSV virus,

(1) the first copy of the ICP0 gene comprises a first loss-of-function mutation, the second copy of the ICP0 gene comprises a second loss-of-function mutation; and, the first copy of the ICP34.5 gene comprises a third loss-of-function mutation, the second copy of the ICP34.5 gene comprises a fourth loss-of-function mutation; or

(2) the first copy of the ICP0 gene comprises a first loss-of-function mutation, the second copy of the ICP0 gene comprises a second loss-of-function mutation; and, the two copies of the ICP34.5 gene are deleted; or

(3) the first copy of the ICP0 gene comprises a first loss-of-function mutation, the second copy of the ICP0 gene comprises a second loss-of-function mutation; and, the first copy of the ICP34.5 gene is substituted with a third exogenous nucleotide sequence, the second copy of the ICP34.5 gene is substituted with a fourth exogenous nucleotide sequence; or

(4) the two copies of the ICP0 gene are deleted; and, the first copy of the ICP34.5 gene comprises a third loss-of-function mutation, and the second copy of the ICP34.5 gene comprises a fourth loss-of-function mutation; or

(5) the two copies of the ICP0 gene are deleted; and, the two copies of the ICP34.5

gene are deleted; for example, the genome of the recombinant HSV virus has deletion of a base sequence of nt510 to nt5439 and a base sequence of nt120802 to nt125731 of the wild-type HSV-1 virus genome; or

(6) the two copies of the ICP0 gene are deleted; and, the first copy of the ICP34.5 gene is substituted with a third exogenous nucleotide sequence, and the second copy of the ICP34.5 gene is substituted with a fourth exogenous nucleotide sequence; or

(7) the first copy of the ICP0 gene is substituted with a first exogenous nucleotide sequence, the second copy of the ICP0 gene is substituted with a second exogenous nucleotide sequence; and, the first copy of the ICP34.5 gene comprises a third loss-of-function mutation, the second copy of the ICP34.5 gene comprises a fourth loss-of-function mutation; or

(8) the first copy of the ICP0 gene is substituted with a first exogenous nucleotide sequence, and the second copy of the ICP0 gene is substituted with a second exogenous nucleotide sequence; and, the two copies of ICP34. 5 genes are deleted; or

(9) the first copy of the ICP0 gene is substituted with a first exogenous nucleotide sequence, the second copy of the ICP0 gene is substituted with a second exogenous nucleotide sequence; and, the first copy of the ICP34.5 gene is substituted with a third exogenous nucleotide sequence, and the second copy of the ICP34.5 gene is substituted with a fourth exogenous nucleotide sequence.

3. The recombinant HSV virus according to Claim 2, wherein

the first loss-of-function mutation, the second loss-of-function mutation, the third loss-of-function mutation, and the fourth loss-of-function mutation each is independently selected from the group consisting of: missense mutation, nonsense mutation, frameshift mutation, base deletion, base substitution, base addition, and any combination thereof (e.g., deletion or substitution or addition of a gene fragment); and/or,

the first exogenous nucleotide sequence, the second exogenous nucleotide sequence, the third exogenous nucleotide sequence, and the fourth exogenous nucleotide sequence each independently encodes a foreign protein selected from the group consisting of: fluorescent protein, immunomodulatory polypeptide, cytokine, chemokine, antibody, and cytotoxic peptide;

preferably, the fluorescent protein is selected from the group consisting of green fluorescent protein (e.g., a green fluorescent protein having an amino acid sequence set forth in SEQ ID NO: 7), red fluorescent protein, blue fluorescent protein, yellow fluorescent protein, and any combination thereof;

preferably, the immunomodulatory polypeptide is selected from the group consisting of CD40L, OX40L, inducible costimulatory molecule (ICOS), FTL3L, LIGHT, CD137L, CD70, 4-1BB, GITR, CD28, and any combination thereof;

preferably, the cytokine is selected from the group consisting of interleukin (e.g., IL-2, IL-12, and IL-15), interferon (e.g., IFNα, IFNβ, IFNγ), tumor necrosis factor (e.g., TNFα), colony stimulating factor (e.g., GM-CSF), and any combination thereof;

preferably, the chemokine is selected from the group consisting of CCL2, RANTES, CCL7, CCL9, CCL10, CCL12, CCL15, CCL19, CCL21, CCL20, XCL-1, and any combination thereof;

preferably, the cytotoxic peptide is selected from the group consisting of thymidine kinase TK (TK/GCV), TRAIL, FasL, and any combination thereof;

preferably, the antibody is selected from the group consisting of anti-PD-1 antibody, anti-PD-L1 antibody, anti-TIGIT antibody, anti-BTLA antibody, anti-CTLA-4 antibody, anti-Tim-3 antibody, anti-Lag-3 antibody, anti-CD137 antibody, anti-OX40 antibody, anti-GITR antibody, anti-CD73 antibody, anti-KIR antibody, anti-ICOS antibody, anti-CSF1R antibody, anti-EGFR antibody, anti-VEGFR antibody, anti-HER2 antibody,

anti-PDGFR antibody, and any combination thereof.

4. The recombinant HSV virus according to any one of Claims 1 to 3, wherein the genome of the recombinant HSV virus comprises a UL43 gene capable of expressing a functional UL43 protein, and a UL41 gene (i.e., a vhs gene) capable of expressing a functional UL41 protein, and/or, a UL48 gene (i.e., a VMW65 gene) capable of expressing a functional UL48 protein;

preferably, the recombinant HSV virus further has one or more of the following characteristics selected from the group consisting of:

(1) one or more non-essential genes are deleted or mutated (e.g., comprising a loss-of-function mutation, or being substituted with an exogenous nucleotide sequence); preferably, the non-essential gene is selected from the group consisting of UL3 gene, UL4 gene, UL14 gene, UL16 gene, UL21 gene, UL24 gene, UL31 gene, UL32 gene, US3 gene, UL51 gene, UL55 gene, UL56 gene, US2 gene, US12 gene (i.e., ICP47 gene), LAT gene, nucleotide fragment corresponding to nt5853-nt7485 of JQ673480.1, and any combination thereof; preferably, one or more of the UL55 gene, the US2 gene, the LAT gene, and the nucleotide fragment corresponding to nt5853-nt7485 of JQ673480.1 are deleted or mutated (e.g., comprise a loss-of-function mutation, or are substituted with an exogenous nucleotide sequence);

(2) an essential gene of the recombinant HSV virus is not deleted, and does not contain a loss-of-function mutation; preferably, a native promoter of one or more essential genes (e.g., ICP27 gene, ICP4 gene, VP5 gene, gL gene, gH gene, gD gene, gK gene, gB gene, gN gene, UL5 gene, UL6 gene, UL8 gene, UL9 gene, UL12 gene, UL25 gene, UL26 gene, UL28 gene, UL29 gene, UL30 gene, UL33 gene, UL36 gene, UL38 gene, UL42 gene, UL48 gene and/or UL52 gene) is substituted with a tumor-specific promoter, such as a promoter of hTERT; and

(3) except for the two copies of the ICP0 gene and the two copies of the ICP34.5 gene, the genome of the recombinant HSV virus comprises all other genes of the wild-type HSV virus, and none of the other genes comprises a loss-of-function mutation; preferably, the genome of the recombinant HSV virus further comprises a modification in which a native promoter of one or more HSV genes is substituted with a tumor-specific promoter, such as a promoter of hTERT; preferably, the HSV gene is selected from VP5 gene, ICP27 gene and ICP4 gene;

preferably, the genome of the recombinant HSV virus further comprises one or more modifications selected from the group consisting of:

(1) substitution of a native promoter of the VP5 gene with a tumor-specific promoter, such as a promoter of hTERT;

(2) substitution of a native promoter of the ICP27 gene with a tumor-specific promoter, such as a promoter of hTERT;

(3) substitution of a native promoter of the ICP4 gene with a tumor-specific promoter, such as a hTERT promoter; and

(4) deletion or mutation of one or more of the UL55 gene, the US2 gene, the LAT gene, and the nucleotide fragment corresponding to nt5853-nt7485 of JQ673480.1 (e.g., comprising a loss-of-function mutation, or being substituted with an exogenous nucleotide sequence);

preferably, the hTERT promoter has the sequence set forth in SEQ ID NO: 5.

5. The recombinant HSV virus according to any one of Claims 1 to 4, wherein the recombinant HSV virus further comprises a fifth exogenous nucleotide sequence;

preferably, the fifth exogenous nucleotide sequence encodes a foreign protein selected from the group consisting of fluorescent protein, immunomodulatory polypeptide, cytokine,

chemokine, antibody, and cytotoxic peptide.

6. A viral vector, comprising the genome of the recombinant HSV virus according to any one of Claims 1-5 or consisting of the genome of the recombinant HSV virus according to any one of Claims 1-5.

7. A viral vector, comprising or consisting of a mutated HSV genome; wherein the mutated HSV genome does not express a functional ICP0 protein and a functional ICP34.5 protein, but is capable of expressing a functional UL43 protein, a functional UL41 protein (i.e., a vhs protein), a functional UL48 protein (i.e., a VMW65 protein), or any combination thereof;

preferably, the mutated HSV genome is derived from a genome of an HSV-1 virus, an HSV-2 virus, or an HSV-1/HSV-2 chimeric virus;

preferably, the mutated HSV genome is derived from a genome of an HSV-1 strain KOS;

preferably, the mutated HSV genome is derived from a genome as set forth in GenBank: JQ673480.1.

8. The viral vector according to Claim 7, wherein the mutated HSV genome comprises the following modifications:

two copies of the ICP0 gene each independently comprises a loss-of-function mutation (e.g., addition, deletion, and/or substitution of one or more bases) or is deleted or substituted with an exogenous nucleotide sequence (e.g., a nucleotide sequence encoding a foreign protein); and

two copies of the ICP34.5 gene each independently comprises a loss-of-function mutation (e.g., addition, deletion, and/or substitution of one or more bases) or is deleted or substituted with an exogenous nucleotide sequence (e.g., a nucleotide sequence encoding a foreign protein);

for example, in the mutated HSV genome,

(a1) one copy of the ICP0 gene comprises a loss-of-function mutation (e.g., addition, deletion, and/or substitution of one or more bases), and the other copy of the ICP0 gene comprises a loss-of-function mutation (e.g., addition, deletion, and/or substitution of one or more bases) or is deleted or substituted with an exogenous nucleotide sequence (e.g., a nucleotide sequence encoding a foreign protein); or

(b1) one copy of the ICP0 gene is deleted, and the other copy of the ICP0 gene comprises a loss-of-function mutation (e.g., addition, deletion, and/or substitution of one or more bases) or is deleted or substituted with an exogenous nucleotide sequence (e.g., a nucleotide sequence encoding a foreign protein); or

(c1) one copy of the ICP0 gene is substituted with an exogenous nucleotide sequence (e.g., a nucleotide sequence encoding a foreign protein), and the other copy of the ICP0 gene comprises a loss-of-function mutation (e.g., addition, deletion and/or substitution of one or more bases) or is deleted or substituted with an exogenous nucleotide sequence (e.g., a nucleotide sequence encoding a foreign protein); and

(a2) one copy of the ICP34.5 gene comprises a loss-of-function mutation (e.g., addition, deletion, and/or substitution of one or more bases), and the other copy of the ICP34.5 gene comprises a loss-of-function mutation (e.g., addition, deletion and/or substitution of one or more bases) or is deleted or substituted with an exogenous nucleotide sequence (e.g., a nucleotide sequence encoding a foreign protein); or

(b2) one copy of the ICP34.5 gene is deleted, and the other copy of the ICP34.5 gene comprises a loss-of-function mutation (e.g., addition, deletion, and/or substitution of one or more bases) or is deleted or substituted with an exogenous nucleotide sequence (e.g., a

nucleotide sequence encoding a foreign protein); or

(c2) one copy of the ICP34.5 gene is substituted with an exogenous nucleotide sequence (e.g., a nucleotide sequence encoding a foreign protein), and the other copy of the ICP34.5 gene comprises a loss-of-function mutation (e.g., addition, deletion and/or substitution of one or more bases) or is deleted or substituted with an exogenous nucleotide sequence (e.g., a nucleotide sequence encoding a foreign protein);

preferably, the two copies of the ICP0 gene comprise the same loss-of-function mutation or different loss-of-function mutations; or are all deleted; or are substituted with the same exogenous nucleotide sequence or different exogenous nucleotide sequences;

preferably, the two copies of the ICP34.5 gene comprise the same loss-of-function mutation or different loss-of-function mutations; or are all deleted; or are substituted with the same exogenous nucleotide sequence or different exogenous nucleotide sequences;

preferably, in the mutated HSV genome,

(1) the two copies of the ICP0 genes each independently comprises a loss-of-function mutation (e.g., addition, deletion, and/or substitution of one or more bases), and, the two copies of the ICP34.5 gene each independently comprises a loss-of-function mutation (e.g., addition, deletion, and/or substitution of one or more bases); or

(2) the two copies of the ICP0 gene each independently comprises a loss-of-function mutation (e.g., addition, deletion, and/or substitution of one or more bases), and, the two copies of the ICP34.5 gene are deleted; or

(3) the two copies of the ICP0 gene each independently comprises a loss-of-function mutation (e.g., addition, deletion, and/or substitution of one or more bases), and, the two copies of the ICP34.5 gene each is independently substituted with an exogenous nucleotide sequence (e.g., a nucleotide sequence encoding a foreign protein); or

(4) the two copies of the ICP0 gene are deleted; and, the two copies of the ICP34.5 gene each independently comprises a loss-of-function mutation (e.g., addition, deletion, and/or substitution of one or more bases) ); or

(5) the two copies of the ICP0 gene are deleted; and, the two copies of the ICP34.5 gene are deleted; or

(6) the two copies of the ICP0 gene are deleted; and, the two copies of the ICP34.5 gene each is independently substituted with an exogenous nucleotide sequence (e.g, a nucleotide sequence encoding a foreign protein) ); or

(7) the two copies of the ICP0 gene each is independently substituted with an exogenous nucleotide sequence (e.g., a nucleotide sequence encoding a foreign protein), and, the two copies of the ICP34.5 gene each independently comprises a loss-of-function mutation (e.g., addition, deletion, and/or substitution of one or more bases); or

(8) the two copies of the ICP0 gene each is independently substituted with an exogenous nucleotide sequence (e.g., a nucleotide sequence encoding a foreign protein), and, the two copies of the ICP34.5 gene are deleted; or

(9) the two copies of the ICP0 gene each is independently substituted with an exogenous nucleotide sequence (e.g., a nucleotide sequence encoding a foreign protein), and, the two copies of the ICP34.5 gene each is independently substituted with an exogenous nucleotide sequence (e.g., a nucleotide sequence encoding a foreign protein);

preferably, in the mutated HSV genome,

(1) the first copy of the ICP0 gene comprises a first loss-of-function mutation, the second copy of the ICP0 gene comprises a second loss-of-function mutation; and, the first copy of the ICP34.5 gene comprises a third loss-of-function mutation, the second copy of the ICP34.5 gene comprises a fourth loss-of-function mutation; or

(2) the first copy of the ICP0 gene comprises a first loss-of-function mutation, the second copy of the ICP0 gene comprises a second loss-of-function mutation; and, the two copies of the ICP34.5 gene are deleted; or

(3) the first copy of the ICP0 gene comprises a first loss-of-function mutation, the second copy of the ICP0 gene comprises a second loss-of-function mutation; and, the first copy of the ICP34.5 gene is substituted with a third exogenous nucleotide sequence, the second copy of the ICP34.5 gene is substituted with a fourth exogenous nucleotide sequence; or

(4) the two copies of the ICP0 gene are deleted; and, the first copy of the ICP34.5 gene comprises a third loss-of-function mutation, and the second copy of the ICP34.5 gene comprises a fourth loss-of-function mutation; or

(5) the two copies of the ICP0 gene are deleted; and, the two copies of the ICP34.5 gene are deleted; for example, the genome of the recombinant HSV virus has deletion of a base sequence of nt510 to nt5439 and a base sequence of nt120802 to nt125731 of the wild-type HSV-1 virus genome; or

(6) the two copies of the ICP0 gene are deleted; and, the first copy of the ICP34.5 gene is substituted with a third exogenous nucleotide sequence, and the second copy of the ICP34.5 gene is substituted with a fourth exogenous nucleotide sequence; or

(7) the first copy of the ICP0 gene is substituted with a first exogenous nucleotide sequence, the second copy of the ICP0 gene is substituted with a second exogenous nucleotide sequence; and, the first copy of the ICP34.5 gene comprises a third loss-of-function mutation, the second copy of the ICP34.5 gene comprises a fourth loss-of-function mutation; or

(8) the first copy of the ICP0 gene is substituted with a first exogenous nucleotide sequence, and the second copy of the ICP0 gene is substituted with a second exogenous nucleotide sequence; and, the two copies of ICP34. 5 genes are deleted; or

(9) the first copy of the ICP0 gene is substituted with a first exogenous nucleotide sequence, the second copy of the ICP0 gene is substituted with a second exogenous nucleotide sequence; and, the first copy of the ICP34.5 gene is substituted with a third exogenous nucleotide sequence, and the second copy of the ICP34.5 gene is substituted with a fourth exogenous nucleotide sequence.

9. The viral vector according to Claim 8, wherein

the first loss-of-function mutation, the second loss-of-function mutation, the third loss-of-function mutation, and the fourth loss-of-function mutation each is independently selected from missense mutation, nonsense mutation, frameshift mutation, base deletion, base substitution, base addition, and any combination thereof (e.g., deletion or substitution or addition of a gene fragment); and/or,

the first exogenous nucleotide sequence, the second exogenous nucleotide sequence, the third exogenous nucleotide sequence, and the fourth exogenous nucleotide sequence each independently encodes a foreign protein selected from the group consisting of: fluorescent protein, immunomodulatory polypeptide, cytokine, chemokine, antibody, and cytotoxic peptide;

preferably, the fluorescent protein is selected from the group consisting of green fluorescent protein (e.g., a green fluorescent protein having the amino acid sequence as set forth in SEQ ID NO: 7), red fluorescent protein, blue fluorescent protein, yellow fluorescent protein, and any combination thereof;

preferably, the immunomodulatory polypeptide is selected from the group consisting of CD40L, OX40L, inducible costimulatory molecule (ICOS), FTL3L, LIGHT, CD137L, CD70, 4-1BB, GITR, CD28, and any combination thereof;

preferably, the cytokine is selected from the group consisting of interleukin (e.g., IL-2, IL-12, and IL-15), interferon (e.g., IFNα, IFNβ, IFNγ), tumor necrosis factor (e.g., TNFα), colony stimulating factor (e.g., GM-CSF), and any combination thereof;

preferably, the chemokine is selected from the group consisting of CCL2, RANTES,

CCL7, CCL9, CCL10, CCL12, CCL15, CCL19, CCL21, CCL20, XCL-1, and any combination thereof;

preferably, the cytotoxic peptide is selected from the group consisting of thymidine kinase TK (TK/GCV), TRAIL, FasL, and any combination thereof;

preferably, the antibody is selected from the group consisting of anti-PD-1 antibody, anti-PD-L1 antibody, anti-TIGIT antibody, anti-BTLA antibody, anti-CTLA-4 antibody, anti-Tim-3 antibody, anti-Lag-3 antibody, anti-CD137 antibody, anti-OX40 antibody, anti-GITR antibody, anti-CD73 antibody, anti-KIR antibody, anti-ICOS antibody, anti-CSF1R antibody, anti-EGFR antibody, anti-VEGFR antibody, anti-HER2 antibody, anti-PDGFR antibody, and any combination thereof.

10. The viral vector according to any one of Claims 7-9, wherein the mutated HSV genome comprises a UL43 gene capable of expressing a functional UL43 protein, a UL41 gene capable of expressing a functional UL41 protein (i.e., a vhs gene), and/or a UL48 gene capable of expressing a functional UL48 protein (i.e., a VMW65 gene);

preferably, the mutated HSV genome further has one or more characteristics selected from the group consisting of:

(1) one or more non-essential genes are deleted or mutated (e.g., comprise a loss-of-function mutation, or are substituted with an exogenous nucleotide sequence); preferably, the non-essential gene is selected from UL3 gene, UL4 gene, UL14 gene, UL16 gene, UL21 gene, UL24 gene, UL31 gene, UL32 gene, US3 gene, UL51 gene, UL55 gene, UL56 gene, US2 gene, US12 gene (i.e., ICP47 gene), LAT gene, nucleotide fragment corresponding to nt5853-nt7485 of JQ673480.1, and any combination thereof; preferably, one or more of the UL55 gene, the US2 gene, the LAT gene, and the nucleotide fragment corresponding to nt5853-nt7485 of JQ673480.1 are deleted or mutated (e.g., comprise a loss-of-function mutation, or are substituted with an exogenous nucleotide sequence);

(2) an essential gene in the mutated HSV genome is not deleted and does not comprise a loss-of-function mutation; preferably, a native promoter of one or more essential genes (e.g., ICP27 gene, ICP4 gene, VP5 gene, gL gene, gH gene, gD gene, gK gene, gB gene, gN gene, UL5 gene, UL6 gene, UL8 gene, UL9 gene, UL12 gene, UL25 gene, UL26 gene, UL28 gene, UL29 gene, UL30 gene, UL33 gene, UL36 gene, UL38 gene, UL42 gene, UL48 gene and/or UL52 gene) is substituted with a tumor-specific promoter, such as a promoter of hTERT; and

(3) except for the two copies of the ICP0 gene and the two copies of the ICP34.5 gene, the mutated HSV genome comprises all other genes of the wild-type HSV virus, and none of the other genes comprises a loss-of-function mutation; preferably, the mutated HSV genome further comprises a modification in which a native promoter of one or more HSV genes is substituted with a tumor-specific promoter, such as a promoter of hTERT; preferably, the HSV gene is selected from VP5 gene, ICP27 gene and ICP4 gene;

preferably, the mutated HSV genome further comprises one or more modifications selected from the group consisting of:

(1) substitution of a native promoter of the VP5 gene with a tumor-specific promoter, such as a promoter of hTERT;

(2) substitution of a native promoter of the ICP27 gene with a tumor-specific promoter, such as a promoter of hTERT;

(3) substitution of a native promoter of the ICP4 gene with a tumor-specific promoter, such as a promoter of hTERT;

(4) deletion or mutation of one or more of the UL55 gene, the US2 gene, the LAT gene, and the nucleotide fragment corresponding to nt5853-nt7485 of JQ673480.1 (e.g., comprising a loss-of-function mutation, or being substituted with an exogenous nucleotide sequence);

preferably, the promoter of hTERT has a sequence as set forth in SEQ ID NO: 5.

11. The viral vector according to any one of Claims 7 to 10, wherein the mutated HSV genome further comprises a fifth exogenous nucleotide sequence;

preferably, the fifth exogenous nucleotide sequence encodes a foreign protein selected from the group consisting of fluorescent protein, immunomodulatory polypeptide, cytokine, chemokine, antibody, and cytotoxic peptide.

12. A host cell, which is infected with the recombinant HSV virus according to any one of Claims 1-5, or comprises a genome of the recombinant HSV virus according to any one of Claims 1-5, or is transfected with the viral vector according to any one of Claims 6-11;

preferably, the cell is a tumor cell selected from the group consisting of lung cancer cell, liver cancer cell, breast cancer cell, osteosarcoma cell, ovarian cancer cell, cervical cancer cell, prostate cancer cell, glioma cell, melanoma cell, colorectal cancer cell, and pancreatic cancer cell.

13. A method of obtaining the recombinant HSV virus according to any one of Claims 1 to 5, comprising:

(1) cultivating a host cell according to Claim 12;

(2) collecting and lysing the host cell after the host cell has undergone a lesion to obtain a lysate of the host cell;

(3) recovering the recombinant HSV virus from the lysate.

14. A pharmaceutical composition, which comprises the recombinant HSV virus according to any one of Claims 1 to 5, or a genome of the recombinant HSV virus according to any one of Claims 1 to 5, or the viral vector according to any one of Claims 6 to 11, and a pharmaceutically acceptable carrier or excipient.

15. The pharmaceutical composition of claim 14, wherein the pharmaceutical composition is for use in treating a tumor, for example, a lung cancer, a liver cancer, a breast cancer, an osteosarcoma, an ovarian cancer, a prostate cancer, a glioma, a melanoma, a colorectal cancer, and a pancreatic cancer; and/or

wherein the pharmaceutical composition is an injectable solution or a lyophilized powder; and/or

wherein the pharmaceutical composition comprises a therapeutically effective amount (e.g., an amount therapeutically effective for treating a tumor) of the recombinant

HSV virus or the genome of the recombinant HSV virus or the viral vector; and/or

wherein the pharmaceutical composition is present in an unit dose form; for example, 102-109 pfu of the recombinant HSV virus is contained in per unit dose of the pharmaceutical composition.

16. A use of the recombinant HSV virus according to any one of Claims 1 to 5 or the viral vector according to any one of Claims 6 to 11 in manufacture of a pharmaceutical composition for treating a tumor in a subject;

preferably, the tumor is selected from the group consisting of lung cancer, liver cancer, breast cancer, osteosarcoma, ovarian cancer, prostate cancer, glioma, melanoma, colorectal cancer, and pancreatic cancer;

preferably, the subject is a mammal, such as a human.