CLAIMS

1. A nucleic acid comprising a modified sequence of the adenovirus E2a gene, which comprises a modification selected from the group:

i. deletions of sequence regions corresponding to 1696-2321 bp, 2400-2634 bp, 2839-3492 bp; or

ii. deletion of a sequence region corresponding to 1696-3492 bp; or

iii. deletion of a sequence region corresponding to 1696-2321 bp; or

iv. deletion of a sequence region corresponding to 2400-2634 bp; or

v. deletion of a sequence region corresponding to 2839-3492 bp; or

vi. deletions of sequence regions corresponding to 1696-2321 bp, 2400-2634 bp; or

vii. deletions of sequence regions corresponding to 1696-2321 bp, 2839-3492 bp; or

viii. deletions of sequence regions corresponding to 2400-2634 bp, 2839-3492 bp

in the sequence of SEQ ID NO:1 or in a sequence homologous to the sequence of SEQ ID NO:1 with a degree of identity of at least 63%, wherein the sequence homologous to the sequence of SEQ ID NO: 1 with a degree of identity of at least 63% is a sequence of the E2a gene of an adenovirus serotype other than the serotype with SEQ ID NO: 1, or a codon-optimized variant of the sequence of SEQ ID NO: 1.

2. The nucleic acid according to claim 1, comprising a modified sequence of the adenovirus E2a gene, which comprises deletions of sequence regions corresponding to the regions of 1696-2321 bp, 2400-2634 bp and 2839-3492 bp in the sequence of SEQ ID NO: 1 or in a sequence homologous to the sequence of SEQ ID NO: 1 with a degree of identity of at least 63%, and includes the sequence of SEQ ID NO: 2 or a sequence homologous to the sequence of SEQ ID NO: 2 with identity of at least 62%, respectively, wherein the sequence homologous to the sequence of SEQ ID NO: 2 with a degree of identity of at least 62% is a sequence of the E2a gene of an adenovirus serotype other than the serotype with SEQ ID NO: 2, or a codon-optimized variant of the sequence of SEQ ID NO: 2.

3. The nucleic acid according to claim 1, comprising a modified sequence of the adenovirus E2a gene, which comprises a deletion of a sequence region corresponding to the region of 1696-3492 bp in the sequence of SEQ ID NO: 1 or in a sequence homologous to the sequence of SEQ ID NO: 1 with a degree of identity of at least 63%, and includes the sequence of SEQ ID NO: 3 or a sequence homologous to the sequence of SEQ ID NO: 3 with identity of at least 61%, respectively, wherein the sequence homologous to the sequence of SEQ ID NO: 3 with a degree of identity of at least 61% is a sequence of the E2a gene of an adenovirus serotype other than the serotype with SEQ ID NO: 3, or a codon-optimized variant of the sequence of SEQ ID NO: 3.

4. The nucleic acid according to claim 1, comprising a modified sequence of the adenovirus E2a gene, which comprises a deletion of a sequence region corresponding to the region of 1696-2321 bp in the sequence of SEQ ID NO: 1 or in a sequence homologous to the sequence of SEQ ID NO: 1 with a degree of identity of at least 63%, and includes the sequence of SEQ ID NO: 4 or a sequence homologous to the sequence of SEQ ID NO: 4 with identity of at least 64%, respectively, wherein the sequence homologous to the sequence of SEQ ID NO: 4 with identity of at least 64% is a sequence of the E2a gene of an adenovirus

serotype other than the serotype with SEQ ID NO: 4, or a codon-optimized variant of the sequence of SEQ ID NO: 4.

5. The nucleic acid according to claim 1, comprising a modified sequence of the adenovirus E2a gene, which comprises a deletion of a sequence region corresponding to the region of 2400-2634 bp in the sequence of SEQ ID NO: 1 or in a sequence homologous to the sequence of SEQ ID NO: 1 with a degree of identity of at least 63%, and includes the sequence of SEQ ID NO: 5 or a sequence homologous to the sequence of SEQ ID NO: 5 with identity of at least 64%, respectively, wherein the sequence homologous to the sequence of SEQ ID NO: 5 with identity of at least 64% is a sequence of the E2a gene of an adenovirus serotype other than the serotype with SEQ ID NO: 5, or a codon-optimized variant of the sequence of SEQ ID NO: 5.

6. The nucleic acid according to claim 1, comprising a modified sequence of the adenovirus E2a gene, which comprises a deletion of a sequence region corresponding to the region of 2839-3492 bp in the sequence of SEQ ID NO: 1 or in a sequence homologous to the sequence of SEQ ID NO: 1 with a degree of identity of at least 63%, and includes the sequence of SEQ ID NO: 6 or a sequence homologous to the sequence of SEQ ID NO: 6 with identity of at least 61%, respectively, wherein the sequence homologous to the sequence of SEQ ID NO: 6 with identity of at least 61% is a sequence of the E2a gene of an adenovirus serotype other than the serotype with SEQ ID NO: 6, or a codon-optimized variant of the sequence of SEQ ID NO: 6.

7. The nucleic acid according to claim 1, comprising a modified sequence of the adenovirus E2a gene, which comprises deletions of sequence regions corresponding to the regions of 1696-2321 bp and 2400-2634 bp in the sequence of SEQ ID NO: 1 or in a sequence homologous to the sequence of SEQ ID NO: 1 with a degree of identity of at least 63%, and includes the sequence of SEQ ID NO: 7 or a sequence homologous to the sequence of SEQ ID NO: 7 with identity of at least 63%, respectively, wherein the sequence homologous to the sequence of SEQ ID NO: 7 with identity of at least 63% is a sequence of the E2a gene of an adenovirus serotype other than the serotype with SEQ ID NO: 7, or a codon-optimized variant of the sequence of SEQ ID NO: 7.

8. The nucleic acid according to claim 1, comprising a modified sequence of the adenovirus E2a gene, which comprises deletions of sequence regions corresponding to the regions of 1696-2321 bp and 2839-3492 bp in the sequence of SEQ ID NO: 1 or in a sequence homologous to the sequence of SEQ ID NO: 1 with a degree of identity of at least 63%, and includes the sequence of SEQ ID NO: 8 or a sequence homologous to the sequence of SEQ ID NO: 8 with identity of at least 62%, respectively, wherein the sequence homologous to the sequence of SEQ ID NO: 8 with identity of at least 62% is a sequence of the E2a gene of an adenovirus serotype other than the serotype with SEQ ID NO: 8, or a codon-optimized variant of the sequence of SEQ ID NO: 8.

9. The nucleic acid according to claim 1, comprising a modified sequence of the adenovirus E2a gene, which comprises deletions of sequence regions corresponding to the regions of 2400-2634 bp and 2839-3492 bp in the sequence of SEQ ID NO: 1 or in a sequence homologous to the sequence of SEQ ID NO: 1 with a degree of identity of at least 63%, and includes the sequence of SEQ ID NO: 9 or a sequence

homologous to the sequence of SEQ ID NO: 9 with identity of at least 61%, respectively, wherein the sequence homologous to the sequence of SEQ ID NO: 9 with identity of at least 61% is a respective sequence of the E2a gene of an adenovirus serotype other than the serotype with SEQ ID NO: 9, or a codon-optimized variant of the sequence of SEQ ID NO: 9.

10. A nucleic acid comprising a modified sequence of the adenovirus E2a gene, which comprises a sequence selected from the group:

i. the sequence of SEQ ID NO: 2 or a sequence homologous to the sequence of SEQ ID NO: 2 with identity of at least 62%; or

ii. the sequence of SEQ ID NO: 3 or a sequence homologous to the sequence of SEQ ID NO: 3 with identity of at least 61%; or

iii. the sequence of SEQ ID NO: 4 or a sequence homologous to the sequence of SEQ ID NO: 4 with identity of at least 64%; or

iv. the sequence of SEQ ID NO: 5 or a sequence homologous to the sequence of SEQ ID NO: 5 with identity of at least 64%; or

v. the sequence of SEQ ID NO: 6 or a sequence homologous to the sequence of SEQ ID NO: 6 with identity of at least 61%; or

vi. the sequence of SEQ ID NO: 7 or a sequence homologous to the sequence of SEQ ID NO: 7 with identity of at least 63%; or

vii. the sequence of SEQ ID NO: 8 or a sequence homologous to the sequence of SEQ ID NO: 8 with identity of at least 62%; or

viii. the sequence of SEQ ID NO: 9 or a sequence homologous to the sequence of SEQ ID NO: 9 with identity of at least 61%.

11. The nucleic acid according to claim 10, wherein

i. the sequence homologous to the sequence of SEQ ID NO: 2 with identity of at least 62% is a respective sequence of the E2a gene of an adenovirus serotype other than the serotype with SEQ ID NO: 2, or a codon-optimized variant of the sequence of SEQ ID NO: 2; or

ii. the sequence homologous to the sequence of SEQ ID NO: 3 with identity of at least 61% is a respective sequence of the E2a gene of an adenovirus serotype other than the serotype with SEQ ID NO: 3, or a codon-optimized variant of the sequence of SEQ ID NO: 3; or

iii. the sequence homologous to the sequence of SEQ ID NO: 4 with identity of at least 64% is a respective sequence of the E2a gene of an adenovirus serotype other than the serotype with SEQ ID NO: 4, or a codon-optimized variant of the sequence of SEQ ID NO: 4; or

iv. the sequence homologous to the sequence of SEQ ID NO: 5 with identity of at least 64% is a respective sequence of the E2a gene of an adenovirus serotype other than the serotype with SEQ ID NO: 5, or a codon-optimized variant of the sequence of SEQ ID NO: 5; or

v. the sequence homologous to the sequence of SEQ ID NO: 6 with identity of at least 61% is a respective sequence of the E2a gene of an adenovirus serotype other than the serotype with SEQ ID NO: 6, or a codon-optimized variant of the sequence of SEQ ID NO: 6; or

vi. the sequence homologous to the sequence of SEQ ID NO: 7 with identity of at least 63% is a respective sequence of the E2a gene of an adenovirus serotype other than the serotype with SEQ ID NO: 7, or a codon-optimized variant of the sequence of SEQ ID NO: 7; or

vii. the sequence homologous to the sequence of SEQ ID NO: 8 with identity of at least 62% is a respective sequence of the E2a gene of an adenovirus serotype other than the serotype with SEQ ID NO: 8, or a codon-optimized variant of the sequence of SEQ ID NO: 8; or

viii. the sequence homologous to the sequence of SEQ ID NO: 9 with identity of at least 61% is a respective sequence of the E2a gene of an adenovirus serotype other than the serotype with SEQ ID NO: 9, or a codon-optimized variant of the sequence of SEQ ID NO: 9.

12. A helper plasmid for producing vectors based on adeno-associated viruses, comprising a nucleic acid comprising a modified sequence of the adenovirus E2a gene according to any one of claims 1-11.

13. The helper plasmid for producing vectors based on adeno-associated viruses according to claim 12, comprising a nucleic acid comprising a sequence of the adenovirus VA RNA gene and a nucleic acid comprising a sequence of the adenovirus E4 gene.

14. The helper plasmid for producing vectors based on adeno-associated viruses according to claim 13, wherein the sequence of the adenovirus VA RNA gene comprises SEQ ID NO: 28.

15. The helper plasmid for producing vectors based on adeno-associated viruses according to claim 13, wherein the sequence of the adenovirus E4 gene is a full-length naturally-occurring sequence of the E4 gene, sequence of E4 orf6/7, or sequence of E4 orf6, wherein the full-length naturally-occurring sequence of the adenovirus E4 gene comprises SEQ ID NO: 29; or

wherein the sequence of adenovirus E4 orf6/7 is a sequence encoding SEQ ID NO: 30; or

wherein the sequence of adenovirus E4 orf6 is a sequence encoding SEQ ID NO: 31.

16. Use of the nucleic acid comprising a modified sequence of the adenovirus E2a gene according to any one of claims 1-11 or the helper plasmid according to any one of claims 12-15 for producing vectors based on adeno-associated viruses.