CLAIMS

1. A method for stable integration of at least one exogenous sequence into genomic DNA of a Chinese hamster ovary (CHO) cell, the method comprises integrating the at least one exogenous sequence into a site within the genomic sequence NCBI Reference Sequence NW_003613934.1, Scaffold 979: 1,090,000 – 1,127,000.

2. The method of claim 1, wherein the at least one exogenous sequence encodes a protein or an RNA molecule.

3. The method of claim 2, wherein the protein is a therapeutic protein, a recombinant protein, or an industrial protein.

4. The method of claim 2, wherein the RNA molecule is a small interfering RNA (siRNA), a micro RNA (miRNA), a guide RNA (gRNA), or a precursor thereof.

5. The method of any one of claims 2 to 4, wherein the at least one exogenous sequence is operably linked to a promoter control sequence.

6. The method of claim 1, wherein the at least one exogenous sequence comprises at least one recognition sequence for a polynucleotide modification enzyme.

7. The method of claim 6, wherein the at least one recognition sequence comprises a nucleic acid sequence that does not exist endogenously in the genome of the mammalian cell.

8. The method of claim 6, wherein the polynucleotide modification enzyme is a site-specific recombinase or a targeting endonuclease.

9. The method of claim 8, wherein the site-specific recombinase is Bxb1 integrase, Cre recombinase, FLP recombinase, gamma delta resolvase, lambda integrase, phi C31 integrase, R4 integrase, Tn3 resolvase, or TP901-1 recombinase.

10. The method of claim 8, wherein the targeting endonuclease is a zinc finger nuclease (ZFN), a clustered regularly interspersed short palindromic repeats (CRISPR)/CRISPR-associated (Cas) (CRISPR/Cas) nuclease system, a CRISPR/Cas dual nickase system, a transcription activator-like effector nuclease (TALEN), a meganuclease, or a fusion protein comprising a programmable DNA-binding domain and a nuclease domain.

11. A method for preparing a Chinese hamster ovary (CHO) cell comprising an exogenous sequence integrated into genomic DNA, the method comprising:
    a) introducing into the cell (i) a targeting endonuclease or nucleic acid encoding a targeting endonuclease, which is targeted to a target site within the genomic sequence NCBI Reference Sequence NW_003613934.1, Scaffold 979: 1,090,000 – 1,127,000, and (ii) a donor polynucleotide comprising the exogenous sequence; and
    b) maintaining the cell under conditions such that the exogenous sequence is integrated into the target site of the genomic sequence.

12. The method of claim 11, wherein the exogenous sequence in the donor polynucleotide is flanked by sequences having at least 95% sequence identity to sequences flanking the target site in the genomic sequence, and wherein the sequences flanking the target site in the genomic sequence are 20-200bp in length.

13. The method of claim 12, wherein the exogenous sequence is integrated into the genome by a homology-directed process.

14. The method of claim 11, wherein the exogenous sequence in the donor polynucleotide is flanked by sequences recognized by the at least one targeting endonuclease.

15. The method of claim 14, wherein the exogenous sequence is integrated into the genome by a direct ligation process.

16. The method of any one of claims 11 to 15, wherein the targeting endonuclease is a zinc finger nuclease (ZFN), a clustered regularly interspersed short palindromic repeats (CRISPR)/CRISPR-associated (Cas) (CRISPR/Cas) nuclease system, a CRISPR/Cas dual nickase system, a transcription activator-like effector nuclease (TALEN), a meganuclease, or a fusion protein comprising a programmable DNA-binding domain and a nuclease domain.

17. The method of any one of claims 11 to 16, wherein the exogenous sequence encodes a protein or an RNA molecule.

18. The method of claim 17, wherein the protein is a therapeutic protein, a recombinant protein, or an industrial protein.

19. The method of claim 17, wherein the RNA molecule is a small interfering RNA (siRNA), a micro RNA (miRNA), a guide RNA (gRNA), or a precursor thereof.

20. The method of any one of claims 17 to 19, wherein the exogenous sequence is operably linked to a promoter control sequence.

21. The method of any one of claims 11 to 16, wherein the exogenous sequence comprises at least one recognition sequence for the targeting endonuclease.

22. The method of claim 21, wherein the at least one recognition sequence comprises a nucleic acid sequence that does not exist endogenously in the genome of the mammalian cell.

23. The method of claim 21, wherein the targeting endonuclease is a zinc finger nuclease (ZFN), a clustered regularly interspersed short palindromic repeats (CRISPR)/CRISPR-associated (Cas) (CRISPR/Cas) nuclease system, a CRISPR/Cas dual nickase system, a transcription activator-like effector nuclease (TALEN), a meganuclease, or a fusion protein comprising a programmable DNA-binding domain and a nuclease domain.