We claim:

1. An isolated cell comprising an exogenous nucleic acid sequence integrated within a locus of the genome of the cell, wherein the locus comprises a nucleotide sequence that is:

(a) at least 90% identical to SEQ ID NO:1 or SEQ ID NO: 4, and

(b) capable of enhancing expression of a protein encoded by an exogenous nucleic acid sequence by at least 1.5-fold compared to expression typically observed by random integration into the genome.

2. The cell of claim 1, wherein the cell is a CHO cell.

3. The cell of claim 1 or 2, wherein the exogenous nucleic acid sequence comprises one or more recombination recognition sequences,

optionally wherein the exogenous nucleic acid sequence comprises at least two recombination recognition sequences and a selectable marker placed between the two recombination recognition sequences,

optionally wherein the one or more recombination recognition sequences are selected from the group consisting of a *Lox*P site, a *Lox511* site, a *Lox2272* site, a *Lox2372* site, a *Lox5171* site, a *Lox*m2 site, a *Lox*71 site, a *Lox*66 site, a *Lox*Fas site, and a frt site.

4. The cell of any one of claims 1 to 3, wherein the exogenous nucleic acid sequence comprises a first exogenous gene of interest (GOI) and a first exogenous promoter, wherein the first exogenous GOI is operably linked to the first exogenous promoter.

5. The cell of claim 4, wherein the exogenous nucleic acid sequence further comprises:

(a) a second exogenous GOI and a second exogenous promoter, wherein the second exogenous GOI is positioned 3' of the first GOI and is operably linked to the second exogenous promoter; and

(b) a first recombination recognition sequence 5' of the first exogenous GOI, a second recombination recognition sequence 3' of the first exogenous GOI; and a third recombinase recognition sequence 3' to the second exogenous GOI,

optionally wherein the first and second recombination recognition sequences are different, and are selected from the group consisting of a *Lox*P site, a *Lox511* site, a *Lox2272* site, a *Lox2372* site, a *Lox5171* site, a *Lox*m2 site, a *Lox*71 site, a *Lox*66 site, a *Lox*Fas site,

and a frt site.

6. The cell of claim 5, wherein the first exogenous GOI encodes a light chain of an antibody or fragment thereof, and the second exogenous GOI encodes a heavy chain of an antibody or fragment thereof.

7. The cell of claim 5 or claim 6, wherein the exogenous nucleic acid sequence further comprises a third exogenous GOI-,

optionally wherein the third exogenous GOI is positioned 3' of the second exogenous GOI,

optionally wherein the first, second and third GOI encode a polypeptide selected from the group consisting of (i) a first light chain of an antibody or antigen-binding fragment thereof, a second light chain of an antibody or antigen-binding fragment thereof, and a heavy chain of an antibody or antigen-binding fragment thereof, or (ii) a light chain of an antibody or antigen-binding fragment thereof, a first heavy chain of an antibody or antigen-binding fragment thereof, and a second heavy chain of an antibody or antigen-binding fragment thereof.

8. A method of modifying a CHO cell genome comprising introducing into a CHO cell an exogenous nucleic acid, wherein the exogenous nucleic acid integrates into a locus of the genome of the cell, the locus comprising a nucleotide sequence that is:

(a) at least 90% identical to SEQ ID NO:1 or SEQ ID NO:4, and

(b) capable of enhancing expression of a protein encoded by an exogenous nucleic acid sequence by at least 1.5-fold compared to expression typically observed by random integration into the genome.

9. The method of claim 8, wherein the exogenous nucleic acid comprises one or more recombination recognition sequences,

optionally wherein the exogenous nucleic acid comprises at least two recombination recognition sequences and a selectable marker placed between the two recombination recognition sequences,

optionally wherein the one or more recombination recognition sequences are selected from the group consisting of a *Lox*P site, a *Lox511* site, a *Lox2272* site, a *Lox2372* site, a *Lox5171* site, a *Lox*m2 site, a *Lox*71 site, a *Lox*66 site, a *Lox*Fas site, and a frt site.

10. The method of claim 9, wherein the exogenous nucleic acid comprises a first exogenous gene of interest (GOI),

optionally wherein the exogenous nucleic acid further comprises a second exogenous GOI and is placed 3' of the first exogenous GOI,

optionally wherein the first exogenous GOI encodes a light chain of an antibody or an antigen-binding fragment thereof, and the second exogenous GOI encodes a heavy chain of an antibody or an antigen-binding fragment thereof.

11. The method of any one of claims 8 to 10, wherein the exogenous nucleic acid is introduced using a vehicle comprising a vector, the vector comprising:

a) a 5' homology arm homologous to a sequence present in the nucleotide sequence of SEQ ID NO:1 or SEQ ID NO: 4,
b) the exogenous nucleic acid, and
c) a 3' homology arm homologous to a sequence present in the nucleotide sequence of SEQ ID NO:1 or SEQ ID NO: 4.

12. The method of claim 11, wherein the exogenous nucleic acid is introduced using a vehicle comprising at least an additional vector or an mRNA molecule,

optionally wherein the additional vector is selected from the group consisting of an adenovirus, a lentivirus, a retrovirus, an adeno-associated virus, an integrating phage vector, a non-viral vector, a transposon and/or transposase, an integrase substrate, and a plasmid, and/or the additional vector comprises a nucleic acid encoding a site-specific nuclease, the site-specific nuclease being optionally selected from the group consisting of a zinc finger nuclease (ZFN), a ZFN dimer, a transcription activator-like effector nuclease (TALEN), a TAL effector domain fusion protein, and an RNA-guided DNA endonuclease.

13. The method of any one of claims 8 to 12, wherein prior to introducing the exogenous nucleic acid, the CHO cell comprises one or more recombination recognition sequences integrated in said locus, and wherein the exogenous nucleic acid integrates into the one or more recombination recognition sequences in said locus,

optionally wherein prior to introducing the exogenous nucleic acid, the CHO cell comprises at least two recombination recognition sequences integrated in said locus, and a selectable marker placed between the two recombination recognition sequences, wherein optionally the at least two recombination recognition sequences are different, and are selected

from the group consisting of a *Lox*P site, a *Lox511* site, a *Lox2272* site, a *Lox2372* site, a *Lox5171* site, a *Lox*m2 site, a *Lox*71 site, a *Lox*66 site, a *Lox*Fas site, and a frt site.

14. The method of any one of claims 8 to 13, wherein the exogenous nucleic acid comprises a first exogenous gene of interest (GOI) operably linked to a first exogenous promoter, a first recombination recognition sequence placed at 5' of the first exogenous promoter, and a second recombination recognition sequence placed at 3' of the first exogenous GOI, and wherein the first and second recombination recognition sequences are identical, respectively, to the at least two recombination recognition sequences present in the locus of the genome prior to introducing the exogenous nucleic acid,

optionally wherein the first and second recombination recognition sequences are different, and are selected from the group consisting of a *Lox*P site, a *Lox511* site, a *Lox2272* site, a *Lox2372* site, a *Lox5171* site, a *Lox*m2 site, a *Lox*71 site, a *Lox*66 site, a *Lox*Fas site, and a frt site.

15. The method of claim 14, wherein the exogenous nucleic acid further comprises a second exogenous GOI operably linked to a second exogenous promoter, wherein the second exogenous GOI is placed 3’ of the first exogenous GOI and 5' of the second recombination recognition sequence,

optionally wherein the first exogenous GOI encodes a light chain of an antibody or an antigen-binding fragment thereof, and the second exogenous GOI encodes a heavy chain of an antibody or an antigen-binding fragment thereof.

16. A method of expressing a gene of interest (GOI) in a cell comprising:

a) providing a cell comprising an exogenous nucleic acid sequence integrated within a locus of the genome of the cell, wherein the exogenous nucleic acid sequence comprises a first exogenous (GOI) operably linked to a first promoter, wherein the locus comprises a nucleotide sequence that is: (i) at least 90% identical to SEQ ID NO:1 or SEQ ID NO: 4, and (ii) capable of enhancing expression of a protein encoded by an exogenous nucleic acid sequence by at least 1.5-fold compared to expression typically observed by random integration into the genome; and wherein the first exogenous GOI encodes a first protein of interest (POI); and

b) culturing the cell of (a) under conditions that allow expression of the first exogenous GOI; and
c) recovering the first POI.

17. The method of claim 16, wherein the cell is a CHO cell.

18. The method of claim 16 or 17, wherein the exogenous nucleic acid sequence further comprises a second exogenous GOI operably linked to a second promoter, and wherein the conditions allow expression of the first exogenous GOI and the second exogenous GOI,

optionally wherein the first exogenous GOI encodes a light chain of an antibody, and the second exogenous GOI encodes a heavy chain of an antibody.

19. A vehicle for modifying a CHO cell genome to (i) express a protein of interest or (ii) integrate a recognition sequence, comprising a vector that comprises:

a. a 5' homology arm homologous to a sequence present in the nucleotide sequence of SEQ ID NO:1 or SEQ ID NO: 4,
b. an exogenous nucleic acid sequence which (i) encodes the protein of interest or (ii) comprises the recognition sequence, respectively, and
c. a 3' homology arm homologous to a sequence present in the nucleotide sequence of SEQ ID NO:1 or SEQ ID NO: 4

20. The vehicle of claim 19, wherein the exogenous nucleic acid sequence comprises one or more recombination recognition sequences that flank a selectable marker, and/or comprises a first exogenous gene of interest (GOI),

optionally wherein the vehicle comprises at least an additional vector or an mRNA molecule, wherein the additional vector optionally comprises a nucleic acid encoding a site-specific nuclease for integrating the recognition sequence, and wherein the site-specific nuclease is optionally selected from the group consisting of a zinc finger nuclease (ZFN), a ZFN dimer, a transcription activator-like effector nuclease (TALEN), a TAL effector domain fusion protein, or an RNA-guided DNA endonuclease.