WHAT IS CLAIMED IS:

1. A search method for finding a target region on a genome for inserting a target gene, the search method comprising:

the following (1),

wherein the search method finds a TAD as the target region,

(1) calculating, for each TAD included in the genome, a TAD score indicating transcriptional activity, and selecting a TAD based on the TAD score.

2. The search method according to claim 1, further comprising:

the following (2);

(2) for at least one known safe harbor in the genome, identifying a TAD score-SH that is the TAD score of a TAD to which the safe harbor belongs,

determining a threshold value based on at least one TAD score-SH, and

selecting a TAD based on the threshold value and the TAD score.

3. A search method for finding a target region on a genome for inserting a target gene, the search method comprising:

the following (a) to (d),

wherein the search method finds, as the target region, a region identified by a boundary pair P described below,

(a) providing cells having a genome F in which an exogenous gene is integrated and expressing the exogenous gene,

(b) obtaining the genome F from the cells, analyzing the genome F, and identifying a region F that is a region including the exogenous gene and a boundary F that is a boundary between the region F and the genome,

(c) calculating, for each TAD included in the genome, a TAD score indicating transcriptional activity, identifying, for each boundary F, a TAD score-F that is the TAD score of a TAD to which the boundary F belongs, and selecting the boundary F based on the TAD score-F, and

(d) finding, from among the selected boundaries F, a boundary pair P sandwiching the region F.

4. The search method according to claim 3, further comprising:

the following (p),

wherein the (c) is performed for the boundary F selected in the following (p),

(p) measuring a methylation rate of the exogenous gene present in the region F and selecting a boundary F of the region F for which the methylation rate is low.

5. The search method according to claim 3 or 4, further comprising:

the following (q),

wherein the (d) is performed for the boundary F selected in (c) and the following (q),

(q) for at least one known safe harbor in the genome, identifying a TAD score-SH that is the TAD score of a TAD to which the safe harbor belongs,

determining a threshold value based on at least one TAD score-SH, and

selecting the boundary F based on the threshold value and the TAD score-F.

6. The search method according to any one of claims 3 to 5, further comprising:

the following (r),

(r) selecting, in the genome F, a boundary pair P in which the region F between the boundary pair P is not a region formed by chromosomal translocation.

7. The search method according to any one of claims 1 to 6,

wherein the TAD score is a value obtained by multiplying a density of genes present in the TAD by an average expression level.

8. The search method according to any one of claims 1 to 7,

wherein the genome is a genome of a mammalian cell.

9. The search method according to any one of claims 1 to 7,

wherein the genome is a genome of a CHO cell.

10. A method for producing a cell, the method comprising:

finding the TAD by the search method according to claim 1 or claim 2; and

inserting a target gene into an inside of the TAD in a genome having the TAD.

11. A method for producing a cell, the method comprising:

finding a region identified by the boundary pair P by the search method according to any one of claims 3 to 9; and

inserting a target gene into a region within ±10 kbp before and after the region in a genome having the region.

12. The method for producing a cell according to claim 10 or 11,

wherein the target gene is a gene encoding at least one selected from the group consisting of an enzyme, an antibody, an interleukin, a cytokine, a chemokine, a hormone, a growth factor, a transcription factor, a receptor, a transcription-regulatory nucleic acid, a non-coding RNA, a viral preparation, a vaccine, a therapeutic protein, subunits thereof, and fragments thereof.

13. A method for selecting a cell, which is a method for selecting a cell expressing a target gene, the method comprising:

the following (11),

(11) calculating, for each TAD included in a genome of a cell, a TAD score indicating transcriptional activity; selecting a TAD based on the TAD score; and selecting a cell in which the target gene is present in the selected TAD.

14. The method for selecting a cell according to claim 13, the method further comprising:

the following (12),

(12) for at least one known safe harbor in the genome, identifying a TAD score-SH that is the TAD score of a TAD to which the safe harbor belongs,

determining a threshold based on at least one TAD score-SH; selecting a TAD based on the threshold and the TAD score, and

selecting a cell in which the target gene is present in the selected TAD.

15. The method for selecting a cell according to claim 13 or 14, the method further comprising:

the following (13),

(13) measuring a methylation rate of the target gene present in the selected TAD, and selecting a cell having a low methylation rate.

16. The method for selecting a cell according to any one of claims 13-15,

wherein the TAD score is a value obtained by multiplying a density of genes present in the TAD by an average expression level.

17. The method for selecting a cell according to any one of claims 13 to 16,

wherein the cell is a mammalian cell.

18. The method for selecting a cell according to any one of claims 13 to 16,

wherein the cell is a CHO cell.

19. The method for selecting a cell according to any one of claims 13 to 18,

wherein the target gene is a gene encoding at least one selected from the group consisting of an enzyme, an antibody, an interleukin, a cytokine, a chemokine, a hormone, a growth factor, a transcription factor, a receptor, a transcription-regulatory nucleic acid, a non-coding RNA, a viral preparation, a vaccine, a therapeutic protein, subunits thereof, and fragments thereof.

20. A cell derived from a Chinese hamster,

wherein a target gene is inserted into at least one region selected from 40 regions shown in Table 1 below

[Table 1]

ID	RefSeq ID	start	end
ID001	NC_048599.1	14,718,000	14,719,000
ID002	NC_048596.1	51,129,000	51,130,000
ID003	NW_023276806.1	59,884,000	59,885,000
ID004	NC_048595.1	36,214,000	36,215,000
ID005	NC_048600.1	114,071,000	114,072,000
ID006	NC_048600.1	91,446,000	91,447,000
ID007	NW_023276806.1	130,298,000	130,299,000
ID008	NC_048595.1	399,476,000	399,478,000
ID009	NC_048600.1	44,678,000	44,679,000
ID010	NC_048597.1	133,640,000	133,641,000
ID011	NC_048596.1	49,747,000	49,748,000
ID012	NW_023276806.1	64,039,000	64,040,000
ID013	NC_048599.1	24,283,000	24,284,000
ID014	NC_048597.1	103,921,000	103,922,000
ID015	NW_023276807.1	98,900,000	98,901,000
ID016	NC_048596.1	52,669,000	52,670,000

ID017	NC_048595.1	4,234,000	4,235,000
ID018	NC_048600.1	128,311,000	128,312,000
ID019	NC_048598.1	101,190,000	101,191,000
ID020	NC_048596.1	74,294,000	74,296,000
ID021	NC_048597.1	135,053,000	135,054,000
ID022	NW_023276806.1	231,799,000	231,800,000
ID023	NC_048598.1	124,775,000	124,776,000
ID024	NW_023276806.1	99,361,000	99,364,000
ID025	NW_023276806.1	65,423,000	65,424,000
ID026	NW_023276806.1	65,250,000	65,251,000
ID027	NC_048600.1	128,983,000	128,984,000
ID028	NC_048595.1	376,666,000	376,667,000
ID029	NC_048595.1	17,007,000	17,010,000
ID030	NC_048596.1	53,710,000	53,712,000
ID031	NC_048597.1	102,218,000	102,219,000
ID032	NC_048595.1	402,863,000	402,867,000
ID033	NC_048596.1	160,455,000	160,457,000
ID034	NW_023276806.1	113,498,000	113,499,000
ID035	NC_048600.1	83,874,000	83,875,000
ID036	NC_048598.1	97,009,000	97,010,000
ID037	NC_048600.1	43,400,000	43,401,000
ID038	NC_048599.1	11,603,000	11,606,000
ID039	NC_048596.1	182,191,000	182,192,000
ID040	NC_048597.1	6,894,000	6,898,000

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21. The cell according to claim 20,

wherein the cell derived from a Chinese hamster is a CHO cell.

22. The cell according to claim 20 or 21,

wherein the target gene is a gene encoding at least one selected from the group consisting of an enzyme, an antibody, an interleukin, a cytokine, a chemokine, a hormone, a growth factor, a transcription factor, a receptor, a transcription-regulatory nucleic acid, a non-coding RNA, a viral preparation, a vaccine, a therapeutic protein, subunits thereof, and fragments thereof.

23. A method for producing a cell product, comprising:

culturing a cell produced by the method for producing a cell according to any one of claims 10 to 12 to express the target gene.

24. A method for producing a cell product, comprising:

culturing a cell selected by the cell selection method according to any one of claims 13 to 19 to express the target gene.

25. A method for producing a cell product, comprising:

culturing the cell according to any one of claims 20 to 22 to express the target gene.