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**NATIONAL STANDARD OF THE
PEOPLE'S REPUBLIC OF CHINA**

GB 14923-2022

Replacing GB 14923-2010

Laboratory animal - Genetic quality control

实验动物 遗传质量控制

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Foreword

This document is in accordance with the provisions of GB/T 1.1-2020 "Guidelines for Standardization Work Part

1. Structure and Drafting Rules for Standardization Documents" drafting. This document replaces GB 14923-2010 "Genetic Quality Control of Laboratory Animals and Mammalian Animals", and GB 14923-2010 In comparison, except for structural adjustments and editorial changes, the main technical changes are as follows:

a) Changed the definitions of the terms "outly related group" and "closed group" (see 3.12, 3.13,

2.12 of the.2010 edition);

b) Added the nomenclature for the preparation of genetically modified animals using technologies such as CRISPR/Cas9 (see 4.2.1.11);

c) Added microsatellite and SNP locus detection method (see 6.2.3). Please note that some contents of this document may refer to patents. The issuing agency of this document assumes no responsibility for identifying patents. This document is proposed and managed by the Ministry of Science and Technology of the People's Republic of China. The release status of previous versions of this document and the documents it replaces are as follows:

---First published as GB 14923-1994 in.1994, first revised in.2010;

--- This is the second revision. Laboratory Animal Genetic Quality Control

1 Scope

GB 14923 is the genetic counterpart of GB 14922: where that one keeps laboratory animals free of pathogens, this one keeps them genetically what they are said to be. It sets the classification of inbred, congenic, recombinant inbred, mutant, hybrid, closed colony and outbred stocks, the breeding systems that maintain each, the nomenclature, and the genetic monitoring - the marker sets, the sampling and frequency, and the criteria for judging whether a colony has drifted or been contaminated. Genetic identity is a precondition for reproducible experiments, which is why this is a mandatory standard.

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This document gives the genetic classification and nomenclature of experimental animals, breeding methods, and the genetic quality of animals in inbred lines, outbred groups, and hybrid groups. monitor. This document is applicable to the genetic quality control of experimental animals.

2 Normative references

This document has no normative references.

3 Terms and Definitions

The following terms and definitions apply to this document.

3.1 inbred strain inbredstrain In an animal population, more than 98.6% of the loci in any individual genome are homozygous strains.

Note. Classical inbred lines are bred by mating full-siblings for at least 20 consecutive generations. All individuals in the line can be traced back to the 20th generation or later Algebraic pair of common ancestors. After more than 20 consecutive generations, parent-child mating has the same effect as full-sibling mating. inbreeding coefficient

3.2 Substrain Substrain Branches within the inbred line.

Note. There are differences between animals of each branch due to genetic differentiation.

3.3 After crossing two inbred lines, the inbred line is bred through more than 20 consecutive generations of brother-sister mating.

3.4 After crossing two inbred lines, the progeny is backcrossed with one of the two parental inbred lines several times (usually 2 times), and then passed through the wrong special Inbred lines bred by continuous brother-sister mating (usually more than 14 generations) selected by special genes.

3.5 Except for the alleles of a specific locus, two inbred lines with the same genetic genes.

Note. It is generally formed by gene mutation or artificial mutagenesis (such as gene knockout) in inbred lines. Use inbreeding algebra to represent the algebra of mutation, such as F110 F23 means that the inbred line was inbred for 23 generations after the mutation appeared in the 110th generation.

3.6 congenicstrain Congener A specific marker is selected from the donor line, and an

inbred line formed by backcrossing is only in a small chromosome segment

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