ICS 07.080
CCS A 40

NATIONAL STANDARD OF THE PEOPLE'S REPUBLIC OF CHINA

GB/T 46945-2025

Determination of single nucleotide polymorphisms - Matrix-assisted laser desorption/ionization time-of-flight mass spectrometry

单核苷酸多态性位点分析 基质辅助激光解吸电离飞行时间质谱法

Issued on: December 31, 2025 **Implemented on: July 1, 2026**

Issued by: State Administration for Market Regulation;
Standardization Administration of the PRC

Table of Contents

Foreword

This document complies with the provisions of GB/T 1.1-2020 "Standardization Work Guidelines Part

1.Structure and Drafting Rules of Standardization Documents". Drafting. Please note that some content in this document may involve patents. The issuing organization of this document assumes no responsibility for identifying patents. This document was proposed and is under the jurisdiction of the National Technical Committee on Standardization of Biochemical Testing (SAC/TC387). This document was drafted by: China Academy of Testing Technology, Rongzhi Biotechnology (Qingdao) Co., Ltd., Xihua University, and Shandong Yingsheng Biotechnology Co., Ltd. Technology Co., Ltd., Lanzhou Baiyuan Gene Technology Co., Ltd., Nuclear Industry 416 Hospital, Chengdu University of Traditional Chinese Medicine, Beijing Yixin Bochuang Biotechnology Co., Ltd. Limited Liability Company, Yantai Zhigong Biomedical Technology Co., Ltd., Sichuan Zhongce Standard Technology Co., Ltd., Guojian Pharmaceutical (Shenzhen) Group Co., Ltd. The company is Sichuan Zhenxing Testing Technology Co., Ltd. The main drafters of this document are. Zhou Lihua, Zou Yan, Li Chen, Zhang Yuanyuan, He Yang, Feng Zhen, Ma Qingwei, Shi Bo, Yi Yan, Jiang Zhanyue, and Dai Jihai. Shen Xiaoman, Zhang Chengwei, Liu Dongfang, Xie Kun, Wu Caijun, Zhao Yue, Zheng Xiaoling, Xin Qian, Shen Qingyu, Zhang Meng, Luo Tingting, Zhang Hui. Matrix-assisted single nucleotide polymorphism site analysis Laser desorption/ionization time-of-flight mass spectrometry

1 Scope

GB/T 46945-2025 is the Chinese national standard covering genotyping single base variants by MALDI-TOF - the mass of an extended primer tells you which base was there, which is fast and cheap for a few dozen known positions across many samples, the case sequencing serves badly. First edition. It was issued on 31 December 2025 and has been in force since 1 July 2026, as a first edition. The document is under the responsibility of the Standardization Administration of China. This page is published from the official record of the 2025 edition; the clause text of a standard this recent is not yet in circulation, and the figures, limits and tables it contains are those of the document itself, delivered in full with

the English translation.

This document describes an experimental method for analyzing single nucleotide polymorphism (SNP) sites using matrix-assisted laser desorption/ionization time-of-flight mass spectrometry. method. This document is applicable to the qualitative analysis of differences in SNPs between nucleic acid sequences.

2 Normative references

The contents of the following documents, through normative references within the text, constitute essential provisions of this document. Dated citations are not included. For references to documents, only the version corresponding to that date applies to this document; for undated references, the latest version (including all amendments) applies. This document.

GB/T 6682 Specifications and test methods for water used in analytical laboratories

GB/T 19495.2 Technical Requirements for Laboratories Testing Genetically Modified Products

GB/T 34796 Determination of Concentration and Purity of Nucleic Acids in Aqueous Solutions - Ultraviolet Spectrophotometry

3 Terms, Definitions and Abbreviations

3.1 Terms and Definitions The following terms and definitions apply to this document.

3.1.1 Changes in DNA sequence caused by variations in a single nucleotide at the genomic level result in chromosome differences between species, including humans. Somatic genome diversity.

Note. This variation is caused by a single base conversion (C<-->T, or G<-->A on its complementary strand) or transversion (C<-->A, G<-->T, C<-->G, A<-->T). It can be caused by the insertion or deletion of bases, or by the formation of bases (T).

3.1.2 ASE primers An oligonucleotide single strand is created by adding a base to an SNP site as a template, used to distinguish the base quality of the SNP site.

3.2 Abbreviations The following abbreviations apply to this document. ASE. Allele-specific extension