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**NATIONAL STANDARD OF THE
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GB/T 46205-2025

**Requirements for processing and analyzing of metagenomic
data**

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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 by the Ministry of Science and Technology of the People's Republic of China. This document is under the jurisdiction of the National Technical Committee on Standardization of Science and Technology Platforms (SAC/TC486). This document was drafted by: Institute of Microbiology, Chinese Academy of Sciences; National Institutes for Food and Drug Control, Chinese Center for Disease Control and Prevention. Infectious Disease Prevention and Control Institute, Beijing Hongcheng Innovation Technology Co., Ltd., Shenzhen BGI Life Science Research Institute, China National Research Institute of Food Fermentation Industries Limited Company, Hainan Provincial Center for Disease Control and Prevention, Beijing University of Aeronautics and Astronautics, Institute of Agricultural Genomics, Chinese Academy of Agricultural Sciences, Sichuan University Western Medicine Hospital, Guangzhou Weiyuan Medical Devices Co., Ltd., Beijing Berry Genomics Co., Ltd., Guangdong Meggene Technology Co., Ltd. Beijing Institute of Standardization. The main drafters of this document are. Wu Linhuan, Ma Juncai, Fan Guomei, Sun Qinglan, Zuo Liyuan, Sun Yan, Liu Donglai, Shen Shu, Cui Zhigang, and Zhou Haijian. Lu Xin, Du Xiaoli, Tian Chuan, Han Simiao, Li Xin, Xu Xun, Wang Ran, Sun Chuyang, Gan Xiaoting, Hua De, Cai Yinggui, Yu Xiaojie, He Zilong, Liu Yongxin, Yong Xin, Wang Xiaorui, Zhang Hongtao, Lu Hongfeng, Yan Xiaoqian, Shu Wensheng, Jin Tao, Wang Jia.

Metagenomics is the sum of genetic material extracted from all microorganisms in a specific environment; it includes the genetic makeup of all microorganisms in the

environment. Due to the widespread adoption of high-throughput sequencing technology, metagenomic sequencing technology has been widely applied in life sciences and clinical research, and has generated [data/information]. This resulted in a massive amount of metagenomic sequencing data. Standardization of sequencing data processing and workflows is crucial in metagenomic data analysis. Standardized data formats and metadata descriptions are essential for promoting data sharing, and standardized data analysis processes and methods are also crucial. The identification and qualitative analysis of species in complex ecological communities greatly affect the reliability of the analytical results. This document proposes metagenomics. Data processing and workflow guidelines and specific requirements help improve the accuracy, completeness, consistency, and reliability of data generated by metagenomic sequencing. Use of sex to promote the sharing and utilization of metagenomic data. Metagenomic data processing and handling requirements

1 Scope

GB/T 46205-2025 is the Chinese national standard covering the metagenomics pipeline - the quality control and host sequence removal, the assembly and binning, the taxonomic and functional annotation with the databases and versions recorded, and the reporting that makes a result reproducible by someone else. First edition, under the Ministry of Science and Technology. In force from 1 February 2026. Issued on 5 October 2025, it has been in force since 1 February 2026.

This document specifies the workflow for metagenomic data processing and manipulation, including metagenomic metadata description requirements, raw data processing, and manipulation procedures. Requirements for data storage and publishing. This document applies to the quality control of metagenomic data processing and analysis by scientific and technological resource platforms at all levels in the field of microbiology and metagenomic sequencing companies. Quantitative evaluation and assessment.

2 Normative references

This document has no normative references.

3 Terms and Definitions

The following terms and definitions apply to this document.

3.1 Metagenomics Describes the total genetic material of all microorganisms in a specific environment.

3.2 A method for sequencing the genomes of all microorganisms in a sample.

Note. Metagenomic sequencing can describe the species composition and function of an

entire community at the gene level.

3.3 marker gene sequencing To determine the microbial phylogeny of a sample, targeted genes (e.g., 16S rRNA used for bacterial and archaea identification) were used. A method for sequencing primers in specific regions of the internal transcribed spacer (ITS) region for fungal identification.

3.4 raw data Unprocessed data generated by sequencers through base identification.

3.5 Derived data Data formed after processing the original data, such as splicing and annotation.

3.6 metadata Data that defines and describes other data.

Note. In this document, this refers to the description of the characteristics of metagenomic sequencing data. [Source: GB/T 18391.1-2009, 3.2.16]

3.7 annotation Using bioinformatics methods and tools, we can identify genes, determine species, and predict the functions of all genes in the genome.