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

GB/T 46935-2025

Single-cell sequencing - Dataset of single cell transcriptome

单细胞测序 单细胞转录组数据集

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Table of Contents

1.Scope	1
2 Normative References	1
3.Terms and Definitions	1
4.Symbols and Abbreviations	2
4.1 Symbol	2
4.2 Abbreviations	2
5.Data and Data File Requirements	3
5.1 Data File Composition	3
5.2 Data File Requirements	3
6.Data Metadirectory	5
6.1 Attribute	5
6.2 Common Attributes of Data Metadirectory	5
6.3 Data Metadirectory Specific Attributes	5
7 Data Archive Directory	6
7.1 Data Archiving Directory Structure	6
7.2 Single-cell data archiving catalog requirements	6
8 Data security management	7
8.1 Basic Requirements	7
8.2 Principles for Grading and Classifying Single-Cell Transcriptome Data	7
8.3 Hierarchical Classification Methods for Single-Cell Transcriptome Datasets	7
18 References	20

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: Shenzhen BGI Life Science Research Institute, Institute of Biology, China Academy of Testing Technology, and Hangzhou BGI Life Science Institute. Research Institute, Beijing Genomics Institute of the

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1 Scope

GB/T 46935-2025 is the Chinese national standard covering the dataset a single-cell RNA sequencing experiment produces - the cell and gene matrices, the quality metrics that say which cells and which reads to trust, the metadata describing the sample and the protocol, and the format in which all of it is deposited. 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 specifies the requirements for single-cell transcriptome data and data files, data metadata directory, data archive directory, and data security management. Require. This document applies to the storage, management, exchange, and sharing of single-cell transcriptome data in omics data.

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 43705 Guidelines for Classification and Grading of Scientific Data Security

GB/T 43708 General Requirements for Scientific Data Security

GB/T 43710 Requirements for Scientific Data Security Audit

3 Terms and Definitions

The following terms and definitions apply to this document.

3.1 FASTQ format FASTQ is a text-based database that stores biological sequences (usually nucleic acid sequences) and their sequencing quality information, with each sequence represented by four lines. The standard format of a column. [Source: GB/T 35890-2018, 3.9]

20 In the sequencing data, the accuracy of base identification with a quality value of 20 was 99%, or the error rate was 1%. [Source: GB/T 40226-2021, 3.5]

30 In the sequencing data, the accuracy of base identification with a quality value of 30 was 99.9%, or the error rate was 0.1%. [Source: GB/T 40226-2021, 3.6]

3.4 project Comprehensive research that is systematically planned, implemented, and managed to achieve specific scientific goals.

3.5 biological sample Biomaterials and their derivatives collected from organisms for scientific research.