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

GB/T 47347-2026

**Information technology - Biometrics - Annotation format for
genotyping data based on high-throughput sequencing**

信息技术 生物特征识别 高通量测序基因分型数据注释格式

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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 and is under the jurisdiction of the National Information Technology Standardization Technical Committee (SAC/TC28). This document was drafted by: Shanxi Medical University, Jiangsu Saixi Technology Development Co., Ltd., China Electronics Technology Standardization Institute, and Guangdong Province. Zhongyi Forensic Science Center, Shenzhen BGI Forensic Technology Co., Ltd., Forensic Science Research Institute, Shenzhen BGI Genomics Co., Ltd. Shenzhen Zhongyi Zhiyuan Technology Group Co., Ltd., Xi'an Jiaotong University, Shanghai International Human Phenome Institute, Shandong First Medical University Shenyang Medical College, Yantai University, Guangdong Mingzhi Medical Laboratory Co., Ltd., and the Research Center for Procuratorial Technology and Information of the Supreme People's Procuratorate. Harbin Institute of Technology, Guangdong Provincial Public Security Department, South China Hospital Affiliated to Shenzhen University, Meiyitian Biopharmaceutical (Wuhan) Co., Ltd., Wuhu Municipal Public Security Bureau Bureau, Guangzhou Jinmanli Pharmaceutical Technology Co., Ltd., Nordas (Hangzhou) Technology Co., Ltd., Shenzhen Sailu Medical Technology Co., Ltd., Yiyuan Longevity Shenzhen BGI Genomics Technology Co., Ltd., Shenzhen BGI Life Science Research Institute, The Chinese University of Hong Kong (Shenzhen), Shenzhen BGI Genomics Technology Co., Ltd. company. The main drafters of this document are. Yan Jiangwei, Liu Qianying, Gao Shengjie, Li Zeqin, Liu Xiling, Wang Wenfeng, Yang Luyu, and Halimuret Simayijiang. Su Liwei, Zhong Chen, Lai Jianghua, Lai Yue, Geng Li, Zhao Kai, Fang Chen, Guo Yunfeng, Ding Guohui, Liu Bo, Mu Haofang, Guo Fei, Ren Fu, Wang Xumin, Tang Honghao Ye Changqin, Jiang Huayan, Wu Song, Lei Qifang, Shen Hexiao, Hao Ting, Zhou Mi, Meng Xianfa, Zhu Yongsheng, Zhao Luyang, Hu Chenglin, Zhang Kun, Fan Haoliang, Liu Jinding Hao Bo, Jia Juan, Liu Xiaonan, Zhang Jun, Yang Fenglong,

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Information technology biometric identification High-throughput sequencing genotyping
data annotation format

1 Scope

GB/T 47347-2026 is the Chinese national standard covering how genotyping results from high-throughput sequencing are annotated and exchanged - the variants, their positions and the reference they are called against, in a format that stays interpretable when the data outlives the software that produced it. First edition, in force since 1 October 2026. It was issued on 31 March 2026 and takes effect on 1 October 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 2026 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 annotation format requirements for human genotyping data generated by high-throughput sequencing. This document applies to the storage, exchange, and comparison of human genotyping data generated by high-throughput sequencing.

2 Normative references

This document has no normative references.

3 Terms and Definitions

The following terms and definitions apply to this document.

3.1 high-throughput sequencing A technology that enables parallel sequencing of a large number of nucleic acid molecules in one go.

Note. Typically, a single sequencing reaction can produce at least 100Mb of sequencing data. [Source: GB/T 33767.14-2023, 3.1, with modifications]

3.2 A digital nucleotide sequence database assembled from the genome sequences of multiple human individuals.

Note. Human reference genome sequences are commonly used as benchmark genome reference sequences. The most commonly used version of the human reference genome sequence is GRCh38. Save in FASTA format.

3.3 Short tandem repeat (STR) The tandem repeat sequences on chromosomes, with repeat units ranging from 2bp to 6bp, exhibit high individual variability. [Source: GB/T 33767.14-2023, 3.14]

3.4 Deoxyribonucleic acid sequence polymorphism caused by changes in a single

nucleotide. [Source: GB/T 33767.14-2023, 3.15]

3.5 Insertion deletion; InDel Sexual genetic markers.

3.6 Mitochondrial DNA (MtDNA) Genetic material in mitochondria.

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