



BSI Standards Publication

Genomics informatics — Quality control metrics for DNA sequencing

National foreword

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*Informatique génomique — Mesures de contrôle de la qualité pour le
séquençage de l'ADN*



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Foreword

ISO (the International Organization for Standardization) is a worldwide federation of national standards bodies (ISO member bodies). The work of preparing International Standards is normally carried out through ISO technical committees. Each member body interested in a subject for which a technical committee has been established has the right to be represented on that committee. International organizations, governmental and non-governmental, in liaison with ISO, also take part in the work. ISO collaborates closely with the International Electrotechnical Commission (IEC) on all matters of electrotechnical standardization.

The procedures used to develop this document and those intended for its further maintenance are described in the ISO/IEC Directives, Part 1. In particular, the different approval criteria needed for the different types of ISO documents should be noted. This document was drafted in accordance with the editorial rules of the ISO/IEC Directives, Part 2 (see www.iso.org/directives).

Attention is drawn to the possibility that some of the elements of this document may be the subject of patent rights. ISO shall not be held responsible for identifying any or all such patent rights. Details of any patent rights identified during the development of the document will be in the Introduction and/or on the ISO list of patent declarations received (see www.iso.org/patents).

Any trade name used in this document is information given for the convenience of users and does not constitute an endorsement.

For an explanation of the voluntary nature of standards, the meaning of ISO specific terms and expressions related to conformity assessment, as well as information about ISO's adherence to the World Trade Organization (WTO) principles in the Technical Barriers to Trade (TBT), see www.iso.org/iso/foreword.html.

This document was prepared by Technical Committee ISO/TC 215, *Health informatics*, Subcommittee SC 1, *Genomics informatics*.

Any feedback or questions on this document should be directed to the user's national standards body. A complete listing of these bodies can be found at www.iso.org/members.html.

Introduction

The rapid progress in Next Generation Sequencing (NGS) technology has drastically reduced the cost and time for genomic analysis. A number of research institutions, corporations, and government agencies are competitively collecting a large volume of genomic data through multi-national, multi-institutional projects such as “DiscovEHR”^[9], “gnomAD”^[10] and “UK Biobank”^[11]. The demand for sharing of “high quality” genomic data is growing because large-scale reference data is required for reliable detection of mutation for both industrial and clinical applications.

However, the quality of available genomic data is less than desirable. To establish consistent quality control metrics, details of each stage of NGS process need to be recorded, shared and standardized (processes and data elements collected and coded for each stage and sub-stage). These processes include sample preparation, library preparation, sequencing, and data processing, among others, as shown in [Figure 1](#).

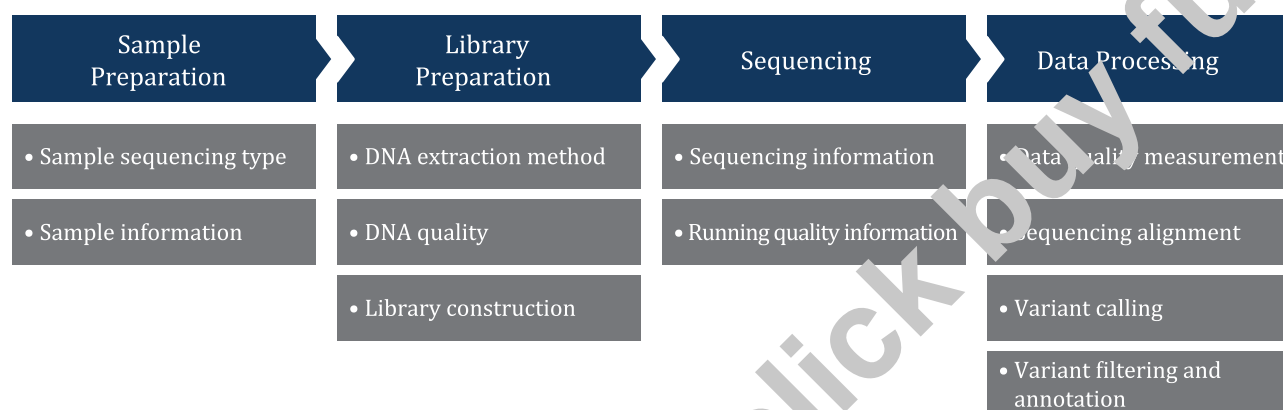


Figure 1 — NGS process

Genomics informatic — Quality control metrics for DNA sequencing

1 Scope

This document identifies quality metrics for the detection of DNA variants using next generation sequencing (NGS) technology. It also defines the data types, relationships, optionality, cardinalities and terminology bindings of the data.

This document provides a basis for sharing and for the application of “high quality” genomic data and contributes to the realization of the precision medicine and the development of relevant industries.

This document is intended to serve as a catalogue of sequencing data elements used to address quality metrics for various clinical, industrial and commercial applications. The exchange of these data allows researchers, commercial entities, and regulatory bodies to assess for the purpose of selective utilization of the data by setting application-specific quality criteria

This document is not intended for

- sequencing methods other than NGS, such as the Sanger sequencing,
- targets other than genome, such as transcriptome or proteome, or
- specimens of species other than humans.

2 Normative references

There are no normative references in this document.

3 Terms and definitions

For the purposes of this document the following terms and definitions apply.

ISO and IEC maintain terminological databases for use in standardization at the following addresses:

- ISO Online browsing platform: available at <https://www.iso.org/obp>
- IEC Electropedia: available at <http://www.electropedia.org/>

3.1

copy number variation

CNV

variation (3.18) in the number of copies of one or more sections of the *DNA* (3.3)

[SOURCE: ISO/TS 20428:2017, 3.7]

3.2

deletion

contiguous removal of one or more bases from a genomic sequence

[SOURCE: ISO/IEC 23092-2:2019, 3.4]