



GenomSys

# MPEG-G Codec Suite

The GenomSys MPEG-G Codec Suite is a collection of software tools to process genomic data compliant with ISO/IEC-23092 genomic data standard (MPEG-G). The tools enable organizations to implement the standard and leverage its benefits by encoding and decoding genomic data; they also include source code examples, a comprehensive user manual, and additional software to transcode from/to legacy formats and integrate functionalities into existing applications and pipelines. Our Codec Suite is CE Marked as in-Vitro Diagnostic Medical Device according to 98/79/CE directive and hence approved for clinical-grade diagnostic purposes.

High Compression

Rapid Selective Access

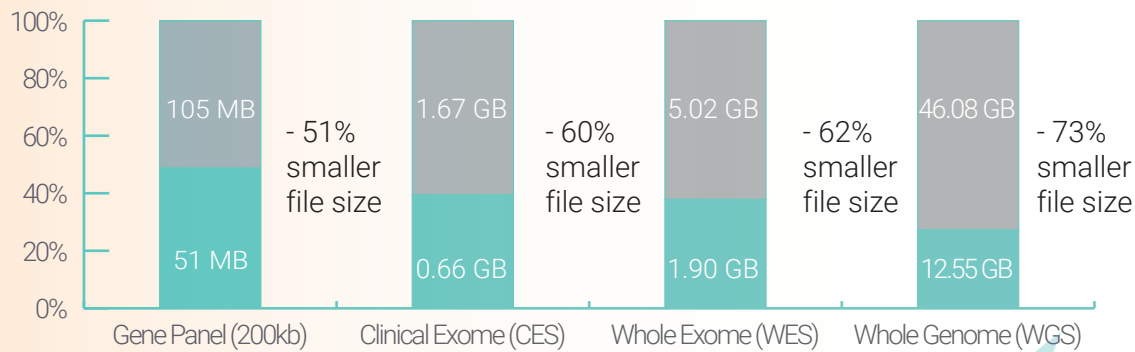
Wide Interoperability

Built-in Security

## High Compression<sup>1</sup>

This results in significant size benefits enabling cost savings for organizations handling large volumes of genomic data.

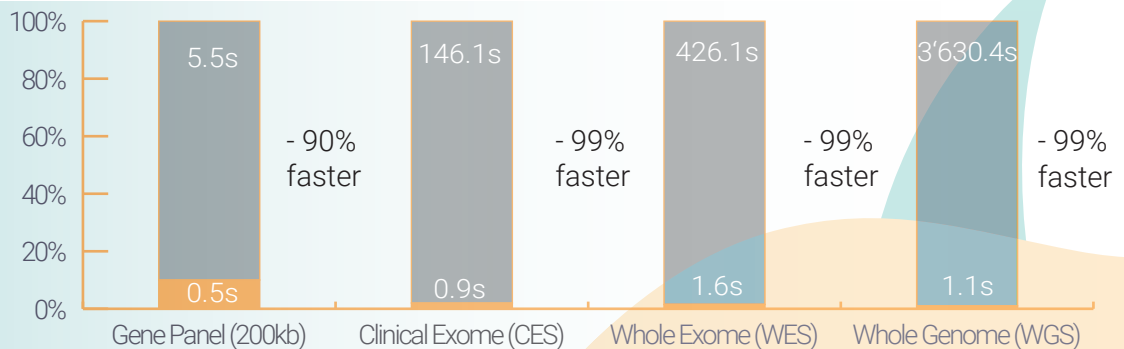
● BAM ● MPEG-G



## Rapid Selective Access<sup>12</sup>

Dramatically faster data access time reducing latency for geneticists running the analysis.

● BAM ● MPEG-G



## Wide Interoperability

Non-proprietary ISO-defined international standard enables everyone to write its own interoperable code in a single unified format for all genomic-connected file types, providing independence from any company's strategy or continuing support as well assuring the highest data integrity and interoperability.



## Built-in Security

Built-in security elements strengthen privacy protection of sensitive individual genomic data: possibility to encrypt natively within the file and grant different access permissions by intervals.

GCS - TPG - Rev.01

Should you be interested in learning more about GenomSys, please do not hesitate to reach out to us by phone **+41 21 691 10 00** or email **info@genomsys.com**.

<sup>1</sup> The comparison was made between BAM-formatted files and MPEG-G formatted files.  
<sup>2</sup> The BAM file was processed – sorting, indexing and accessing - with the program samtools 1.11 using the command 'samtools view -@ 4' for 27 regions of the *CFTR* gene. The graphic shows the initial processing (sorting, indexing, and accessing) time for BAM and MPEG-G. Follow-on accesses will be faster for BAM than portrayed but still slower for CES, WES and WGS files than with MPEG-G.