

GENOMSYS MPEG-G CODEC SUITE



The **GENOMSYS MPEG-G CODEC SUITE** is a collection of CE-marked software tools to process genomic data compliant with the ISO/IEC 23092 genomic data standard (MPEG-G). The tools enable organizations to implement the standard and leverage its benefits by providing efficient encoding, transport, and decoding of genome sequencing data.

HIGH COMPRESSION

The MPEG-G standard offers substantial compression benefits, reducing genomic datasets' size by up to 70% compared to legacy formats.

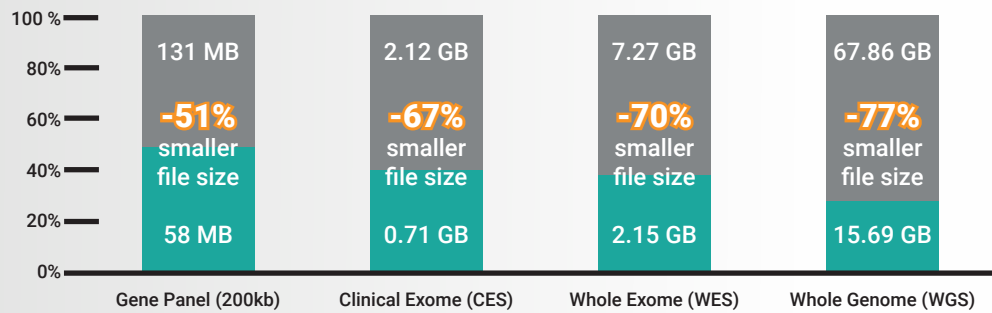


Figure 1 - Comparison of file sizes from Gene Panel to Whole-Genome datasets in the FASTQ format (dark grey) and the MPEG-G format (green).

RAPID SELECTIVE ACCESS¹

The standard's Selective Access enables direct access without the need of initially sorting and indexing the file, thus saving up to 99% of processing time.

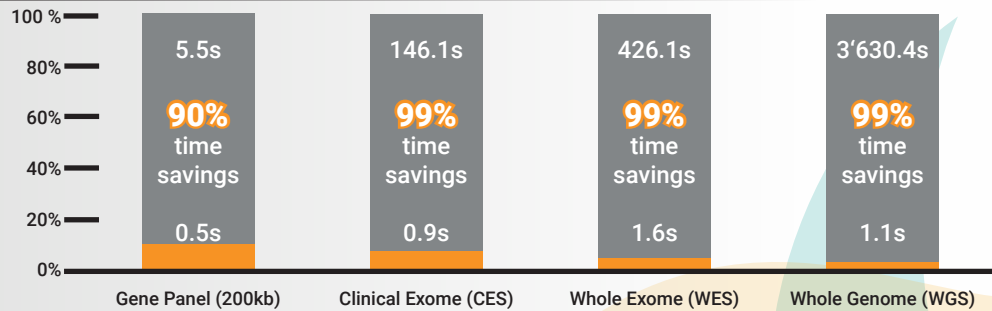
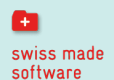


Figure 2 - Comparison of processing time for a dataset in the BAM format (light grey) and the MPEG-G format (orange) accessing multiple regions of the *CFTR* gene.

WIDE INTEROPERABILITY

The conformity with an open ISO standard enables everyone to develop interoperable solutions able to manipulate genome sequencing data encoded in a unified format for genome assemblies, raw and aligned sequencing data, and associated metadata. It is CE marked as in-Vitro Diagnostic Medical Device according to 98/79/CE directive and hence approved for clinical-grade diagnostic purposes.



BUILT-IN SECURITY

The new genomic standard addresses the need for a high level of genomic data privacy. The built-in data protection mechanisms support consistent traceability and precise access control, as well as role segregation. These features enable solutions providers to increase the data privacy of patients' genetic information.

CONTACT Us!

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

¹ The BAM file was processed with the program samtools 1.11 using the command 'samtools view -@ 4' for multiple regions of the *CFTR* gene.