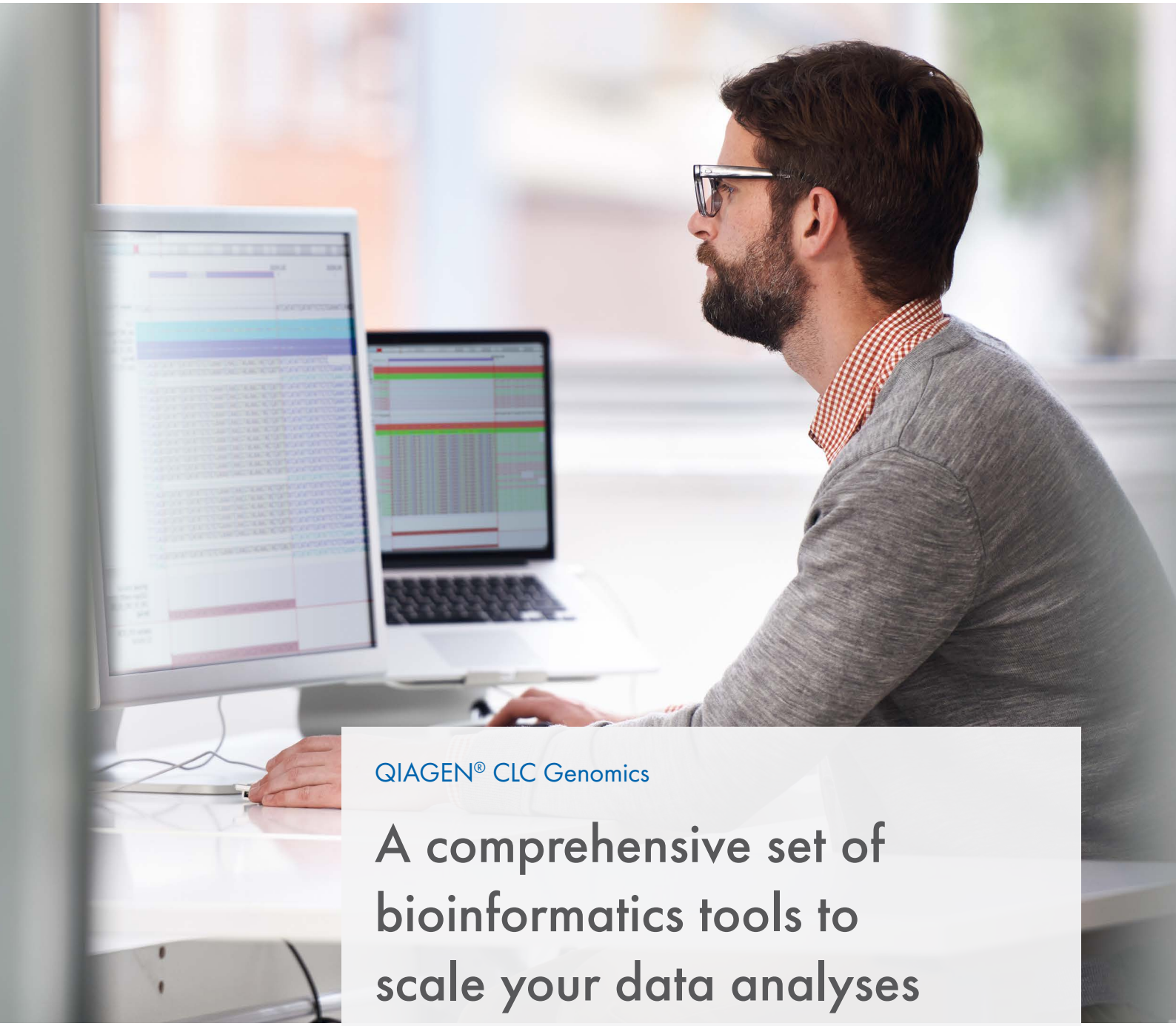
QIAGEN



QIAGEN® CLC Genomics

A comprehensive set of bioinformatics tools to scale your data analyses

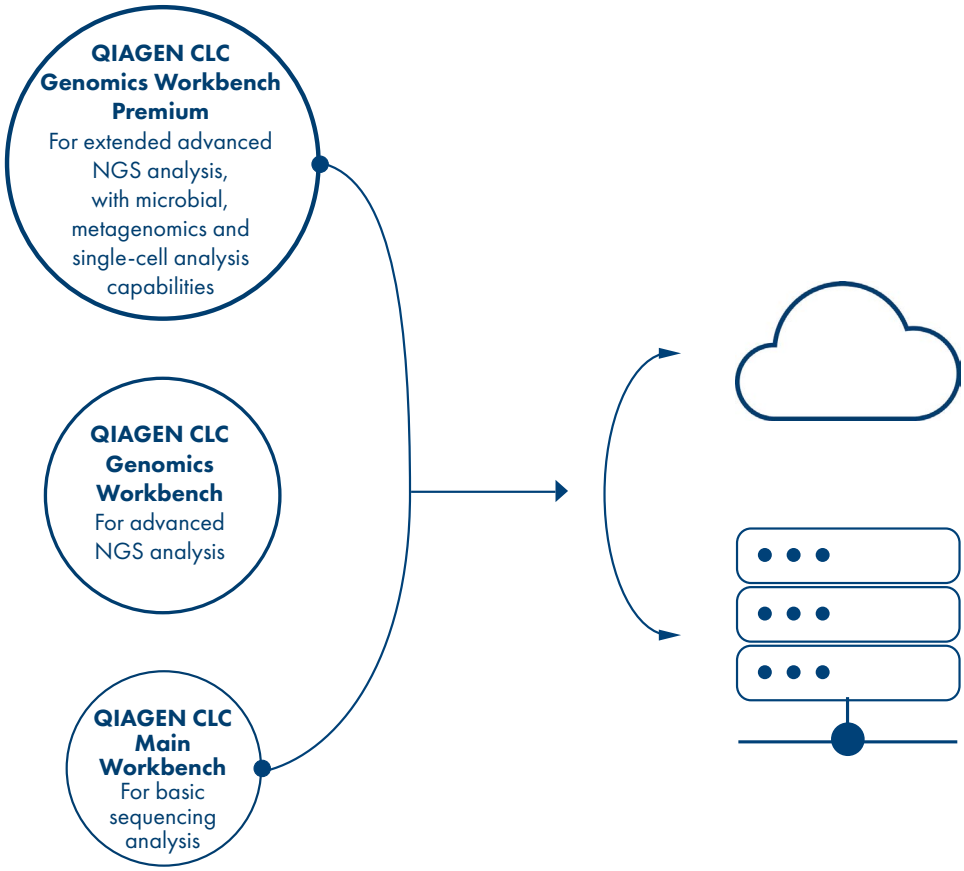
Flexible access from a laptop to a local server to the cloud

Sample to Insight

Scale your NGS research: A single platform for powerful sequencing and 'omics data analyses

The power of sequencing and 'omics data has led to incredible research advancements over the last decades. Yet this accelerated pace of biological data generation has brought with it several data analysis challenges for scientific researchers. There hasn't been any robust and scalable, yet easy-to-use platform that can handle all NGS data analysis use cases without requiring bioinformatics expertise and workflows, that offers both single-user and enterprise-wide solutions.

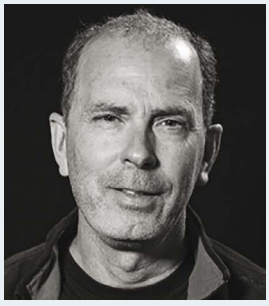
QIAGEN CLC Workbenches: Your access to scalable server and cloud solutions



QIAGEN CLC solutions for bioinformatics analyses: Get the features that meet your needs

QIAGEN CLC Genomics is a bioinformatics platform that reduces data analysis bottlenecks. The solutions are easy to use, even for non-bioinformaticians, and offer a range of tools and workflows in different packages. It is developed under ISO 9001 quality management certification standards, by scientists, for scientists.

QIAGEN CLC Genomics has three key offerings, with packages ranging from basic (QIAGEN CLC Main Workbench), advanced (QIAGEN CLC Genomics Workbench) and premium (QIAGEN CLC Genomics Workbench Premium), to meet your sequence and 'omics data analysis needs. With both single-user desktop and network options, as well as enterprise-wide server and cloud solutions, QIAGEN CLC offers flexibility at any scale.



"The top feature of QIAGEN CLC, which makes it so useful to us, is its utilizability. The thing that QIAGEN CLC does best of all is it makes access to the analysis easy."

Simon Andrews, Ph.D., Head of the Microbiology Research Group, University of Reading

QIAGEN CLC Genomics Workbench Premium:

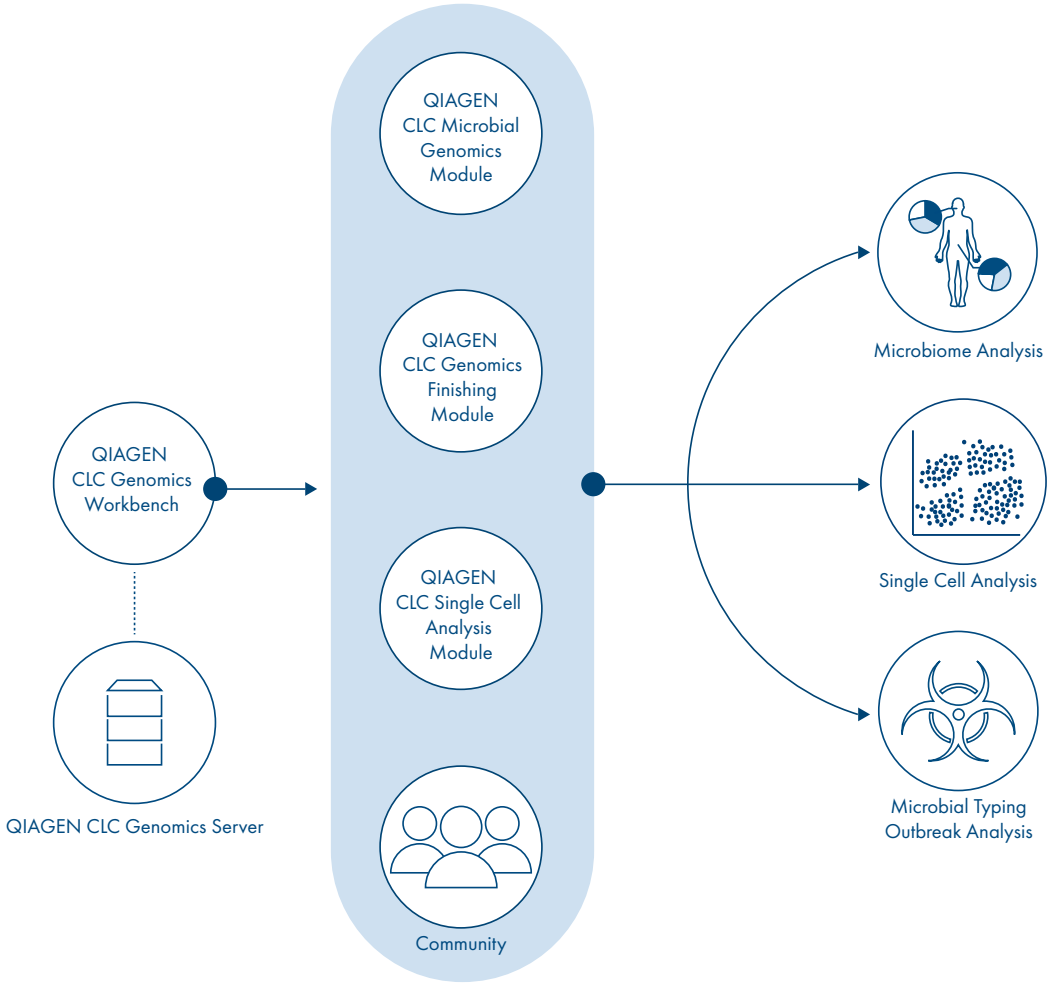
A comprehensive desktop bioinformatics software for ALL your genomics, transcriptomics and epigenomics analytic needs

QIAGEN CLC Genomics Workbench Premium is our comprehensive and full-featured solution that offers all the bioinformatics tools needed to power your research. Expand the functionality of QIAGEN CLC Genomics Workbench by adding features to support microbial and metagenomics (microbial typing, antimicrobial resistance and metagenomics characterization), single-cell analysis, genome finishing and NGS-based multilocus sequence typing (MLST). Readily integrated and streamlined NGS workflows combined with state-of-the art data interpretation and visualization enable you to shift your focus from data to discovery.

Microbial and metagenomics: The QIAGEN CLC Microbial Genomics Module provides tools and workflows for a broad range of bioinformatics needs for microbiome analysis, isolate characterization and multilocus sequence typing (MLST), functional metagenomics and antimicrobial resistance characterization. The module supports the analysis of bacterial, viral and eukaryotic (fungal) genomes and metagenomes.

Single-cell analysis: The QIAGEN CLC Single Cell Analysis module provides an analysis pipeline from raw Fastq through cell preparation steps to identification of clusters and automatic cell type prediction. The QIAGEN Cell Ontology is linked to the automatically predictable cell types and facilitates easy and intuitive manual curation of clusters. Expression plots can be generated for visualisation and differential expression analysis is easily executed from the UMAP or tSNE plot editor and resulting differential genes can be uploaded to QIAGEN Ingenuity® Pathway Analysis (IPA®).

Genome finishing: QIAGEN CLC Genome Finishing Module speeds-up and simplifies genome finishing, making this process accessible to life scientists without advanced bioinformatics skills. The module was designed for finishing smaller genomes, such as those of microbes or eukaryotic parasites. Automated tools for scaffolding or contig joining also improve results for larger genome assemblies.



Learn more about QIAGEN CLC Genomics Workbench Premium: Request a trial and browse tutorials, manuals and other resources at **digitalinsights.qiagen.com/GXWBP**

QIAGEN CLC Genomics Workbench: NGS data analysis for any species, any platform, any workflow

For advanced sequencing analysis, expand the functionality of QIAGEN CLC Main Workbench with the addition of a wide range of features for NGS and 'omics data analysis, including:

- De novo assembly of NGS reads
- Resequencing analysis and variant calling
- Support for reference genomes from any organism
- Long read analysis (PacBio®, Oxford Nanopore®)
- QIAseq® panel analysis workflows
- RNA-seq (including miRNA and lncRNA), ChIP-seq, DNA methylation
- Biomedical genomics analyses including WES, WGS, tumor-normal, trio and families of four workflows
- Biomedical genomics workflows for SARS-CoV-2 (QIAseq and Ion Ampliseq®) and TruSight Oncology 500 Illumina® DNA and RNA

Drive your discovery from raw sequencing files to publication-ready results with powerful analysis pipelines and interactive visualizations. Detect, compare and annotate variants or differentially expressed genes or transcripts, and effortlessly create QC reports across samples and tools.

Intuitive Interface
Interactive visualizations of your data, including a best-in-class genome browser

Platform Independent
Supports common sequencing platforms (Illumina, IonTorrent™, Oxford Nanopore, BGI, PacBio) and runs on most operating systems (Linux®, macOS®, Windows®)

Flexible Workflows
Build your own customized analysis workflows for a wide range of NGS data

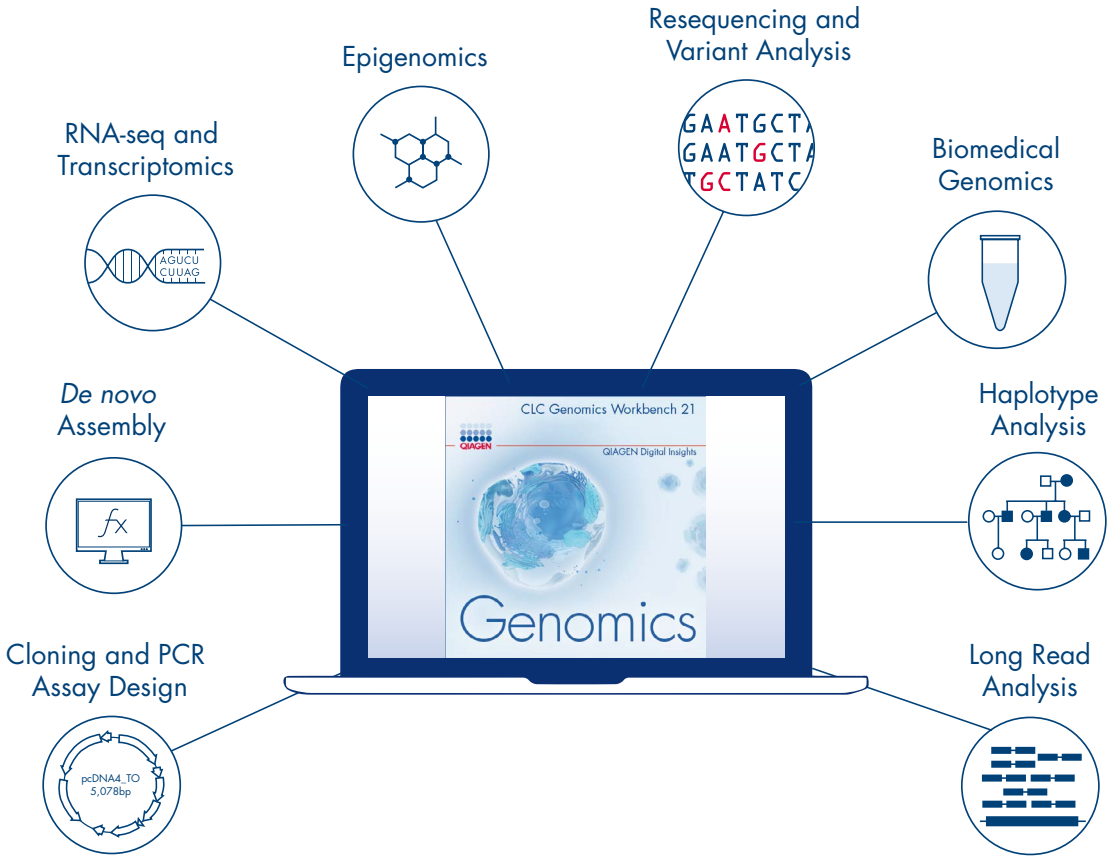
Share Results
Share and visualize results with the free Viewing Mode

Enterprise Ready
High-throughput analysis and automation via the QIAGEN CLC Genomics Server and the QIAGEN CLC Genomics Cloud Engine

Plugins and Modules
Expand functionality with prebuilt workflows and expert tools in plugins and modules

NGS data analysis simplified in one toolkit

QIAGEN CLC Genomics Workbench includes tools for whole genome and transcriptome de novo assembly, gene expression analysis, targeted resequencing, variant calling, ChIP-seq and DNA methylation. Easily import a wide range of NGS data file formats, whether raw data directly from your sequencer, results from a sequencing vendor or analysis output from an existing bioinformatics pipeline. Seamlessly integrate with other pipelines by exporting results in VCF, GFF, PDF, Excel, JSON and many other formats. Annotation with conservation scores and filtering steps on dbSNP and ClinVar are included.



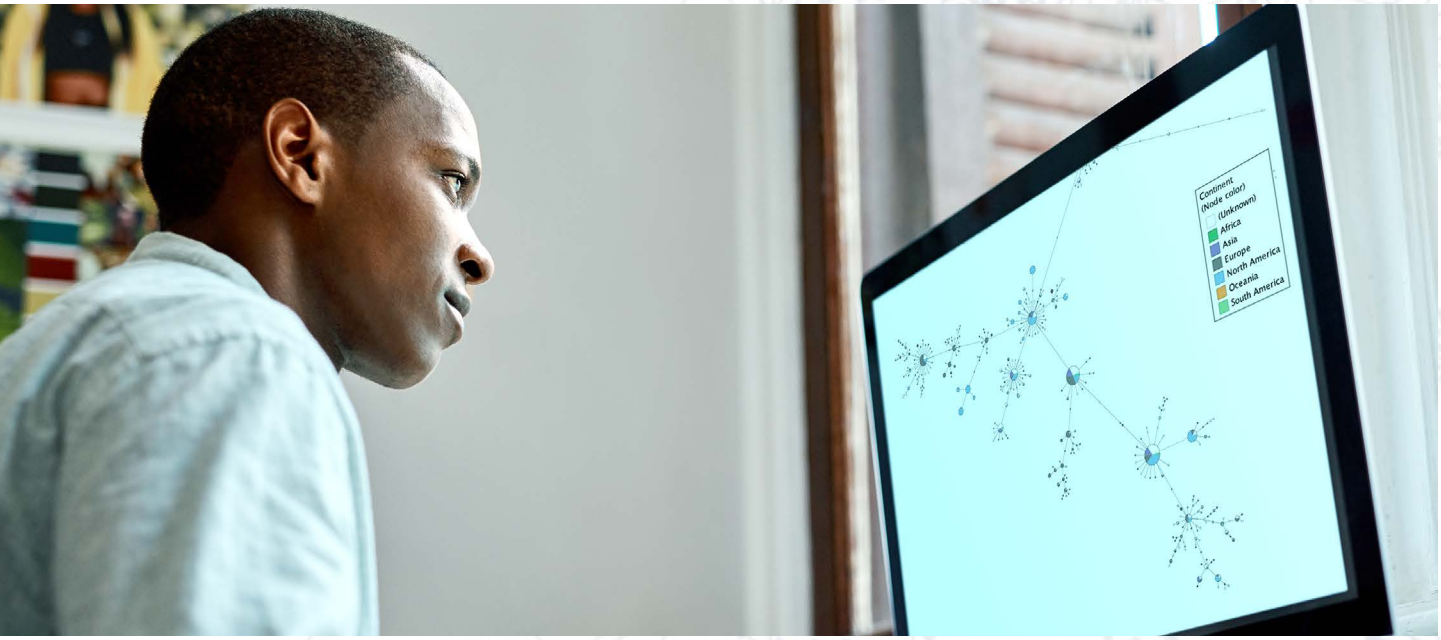
Learn more about QIAGEN CLC Genomics Workbench: Request a trial and browse tutorials, manuals and other resources at **digitalinsights.qiagen.com/GXWB**

QIAGEN CLC plugins: These feature-rich extensions are seamlessly integrated and provide advanced tools and workflows to meet your specific analysis needs.

Empower your biomedical analyses by installing the **Biomedical Genomics Analysis plugin**, which provides prebuilt workflows for human, mouse and rat genomics, including QIAseq UMI-based NGS library preparation kits and panels. Content includes hereditary disease workflows, oncology somatic mutation detection workflows for cancer FFPE or liquid biopsy (single sample or matched tumor-normal) samples, sensitive detection of SNPs, MNVs, tandem repeats, structural variants, fusion genes, CNVs, LoH and tumor purity estimation.

The **Long Read Analysis plugin**, available from February 2021, enables the analysis of erroneous long read data sets typically produced by PacBio or Oxford Nanopore sequencing technologies. Specific application areas enabled by this plugin are the analysis of long read RNA-seq data, assembly of long reads, hybrid assembly long read and short read data, as well as read mapping and variant calling.

The **Haplotype Caller plugin** is based on a variant representation that allows direct import, export and validation of variants and supports phasing information. The underlying genome model delivers variant locus, allele variants, haplotype alleles and haplotypes. Genotype and zygosity annotations are also supported.



Explore the full list of available QIAGEN CLC plugins at
digitalinsights.qiagen.com/products-overview/plugins/

QIAGEN CLC Main Workbench: The user-friendly solution for basic sequencing analysis

QIAGEN CLC Main Workbench is used by tens of thousands of researchers in academia as well as in industry for DNA, RNA and protein sequence data analysis. Its wide variety of features are presented through an intuitive graphical user interface, which requires no programming skills. QIAGEN CLC Main Workbench is available on Windows, macOS and Linux platforms.

QIAGEN CLC Main Workbench has many functionalities, including Sanger sequence analysis, gene expression analysis, primer design, molecular cloning, multiple sequence alignment, phylogenetic analyses and sequence data management. Its full compatibility with all types of CLC workbenches provides a collaborative platform supporting research within and across organizations.

Get equipped with the essentials via easy access to multiple integrated research tools and an intuitive user interface. Full documentation and best-in-class tutorials mean your research work will be easy to carry out.

The features include:

- Editor for graphically and algorithmically advanced primer design
- Multiple sequence alignment tools
- Whole genome alignment tools (recently updated in October 2020)
- Phylogenetic analysis tools
- Sanger sequencing analysis (workflow enabled with version 21)
- Molecular cloning
- Sanger-based multilocus sequence typing (MLST)
- RNA structure prediction and editing
- Gene expression analysis
- Integrated 3D protein molecule view
- Sharing of data among researchers
- All edits and data processing are logged for audit trailing
- Import sequences and databases in VectorNTI® and other formats

Learn more about QIAGEN CLC Main Workbench: Request a trial and browse tutorials, manuals and other resources at **digitalinsights.qiagen.com/MWB**

QIAGEN CLC Enterprise Solutions: For organization-wide and command line access

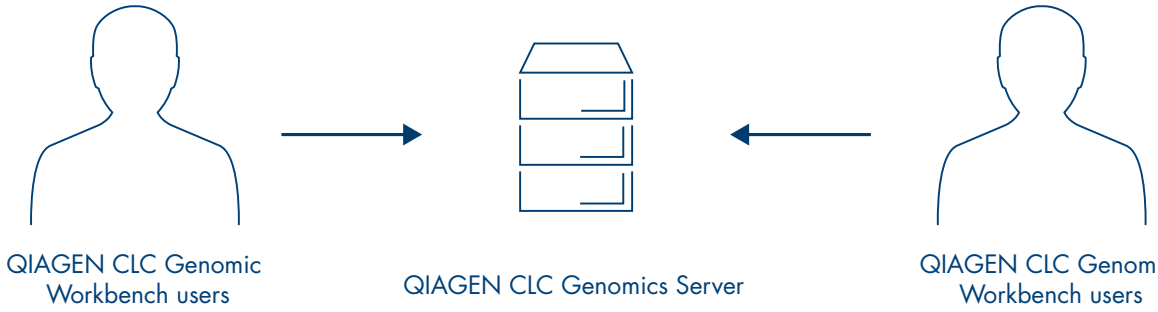
Scale your NGS: From single-user to enterprise-friendly data analysis, our NGS enterprise solutions are scalable and support multiple users in an intuitive way to speed up analyses.

Our QIAGEN CLC enterprise solutions include:

- QIAGEN CLC Genomics Server
- QIAGEN CLC Genomics Cloud Engine

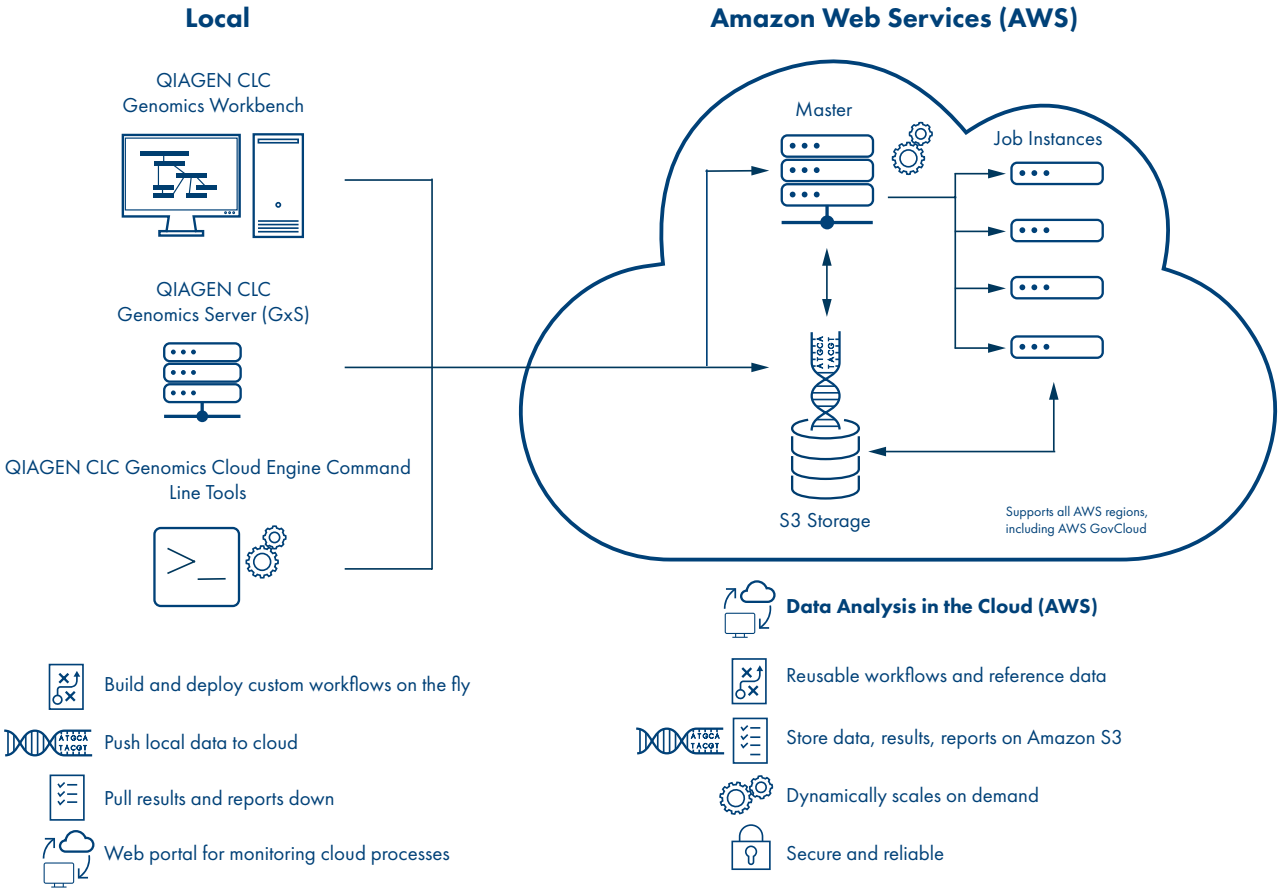
QIAGEN CLC Genomics Server provides a solution for building and managing a modern and efficient enterprise-wide bioinformatics analysis platform for commercial, academic or government organizations of any size. The QIAGEN CLC Genomics Server enables a fully integrated and scalable bioinformatics environment that can be used directly from QIAGEN CLC Main Workbench, Genomics Workbench, Genomics Workbench Premium or from QIAGEN CLC Command Line Interface, and supports all the tools from these Workbenches. Whether running a Windows, Linux or macOS operating system, QIAGEN CLC Genomics Server is a solution you can easily integrate into any existing IT environment. It also enables the use of third-party or open-source tools through the External Applications feature, providing any bioinformatics solution available to QIAGEN CLC Genomics Workbench users.

In addition, QIAGEN CLC Genomics Server delivers a central data storage and workflow execution platform, which includes a flexible queuing system that scales to handle large-scale analysis requirements by multiple users. It runs all the tools and analyses available within QIAGEN CLC Genomics Workbench in the fields of genomics, transcriptomics and epigenomics.



Learn more at **digitalinsights.qiagen.com/GxS**

QIAGEN CLC Genomics Cloud Engine is our scalable solution that makes bioinformatics analysis accessible to anyone involved in the processing of NGS data, whether you use advanced command line-driven scripting or need quick access to the cloud directly from QIAGEN CLC Genomics Workbench. QIAGEN CLC Genomics Cloud Engine offers the full range of QIAGEN CLC tools and enables you to affordably analyze your NGS data on the cloud with the nearly unlimited power of Amazon® Web Services (AWS).



Learn more at **digitalinsights.qiagen.com/GCE**

Get the right bioinformatics analysis tool for your research needs. Contact us to find the right solution for your research needs. **bioinformaticssales@qiagen.com**

Learn more and request a consultation at **digitalinsights.qiagen.com/CLC**

QIAGEN CLC Genomics products are intended for molecular biology applications. These products are not intended for the diagnosis, prevention or treatment of a disease.

For up-to-date licensing information and product-specific disclaimers, see the respective QIAGEN CLC Genomics product site. Further information can be requested from **ts-bioinformatics@qiagen.com** or by contacting your local account manager

Ordering **www.qiagen.com/shop/analytics-software** | Technical Support **digitalinsights.qiagen.com/support**

Website **digitalinsights.qiagen.com**