QIAGEN Digital Insights

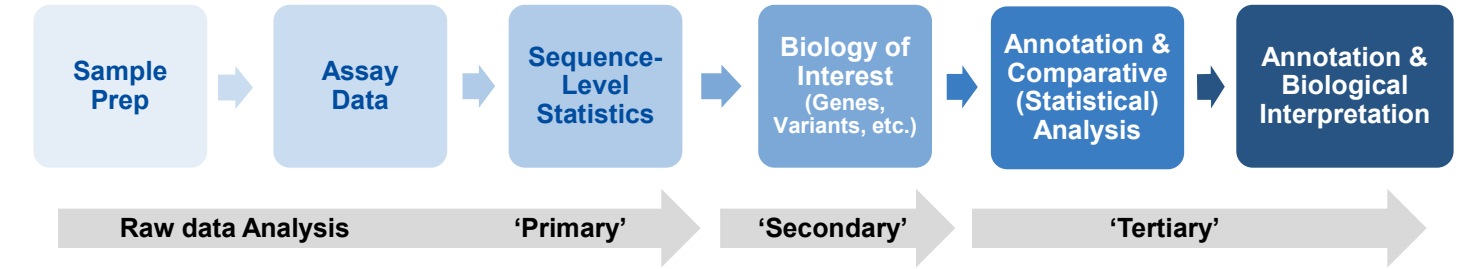
QIAGEN CLC Product Profolio

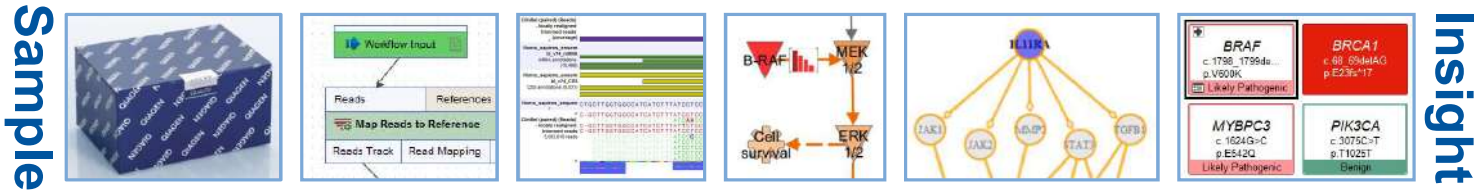
Amit Chaurasia, PhD

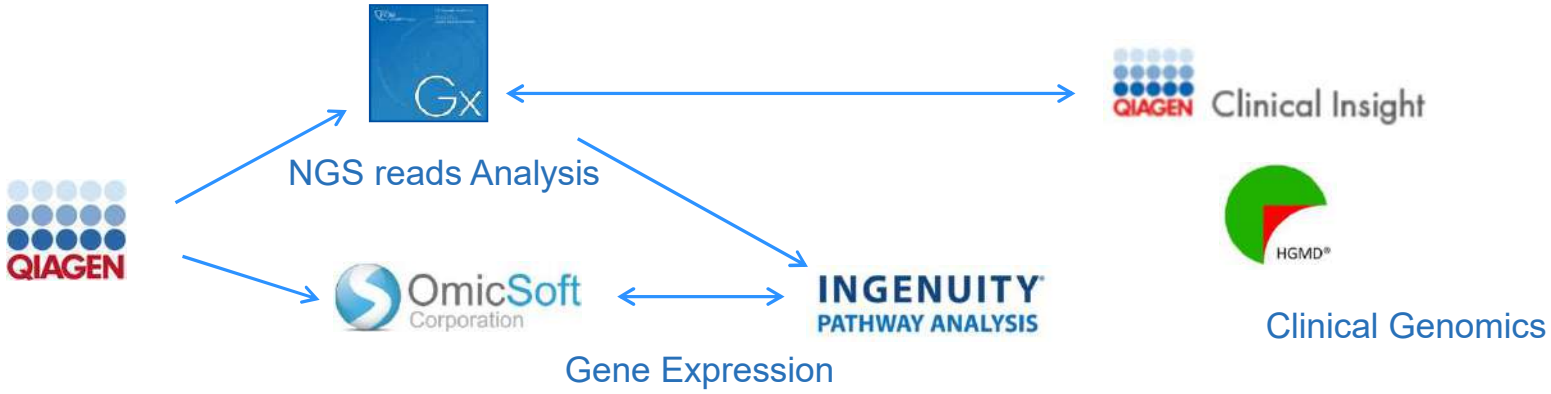
Associate Sales Development Manager

QIAGEN Digital Insights

QIAGEN Digital Insights solution

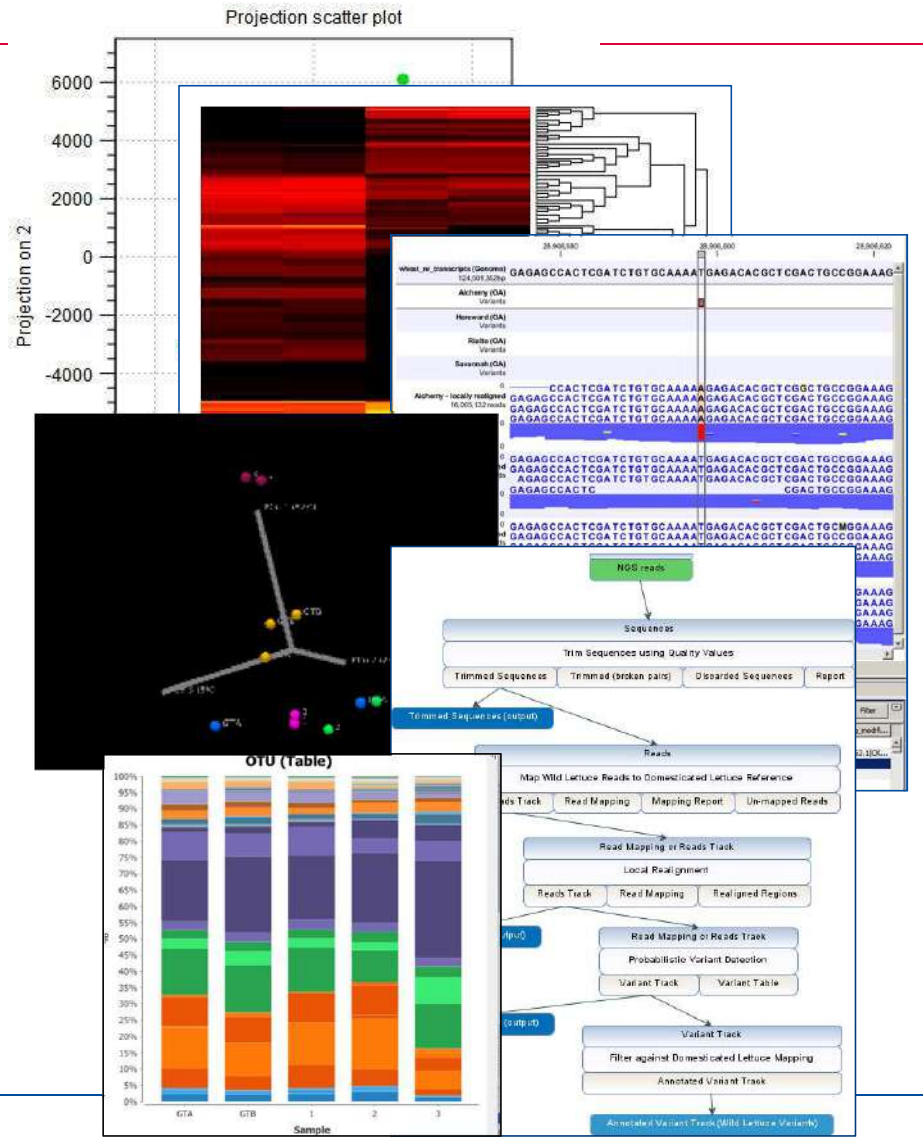






In QIAGEN CLC Genomics Workbench

1. QC and preprocess NGS data (RNA-Seq, miRNA, and genomic reads)
2. Perform RNA-Seq, Microarrays, Statistical Expression Analysis
3. Resequencing, Variant detection & analysis
4. De Novo genome assembly, genome finishing, BLAST
5. Epigenetics analysis (ChIP-Seq, Bisulfite Sequencing)
6. Facilitate analysis with interactive visualization
7. Construct automated workflows in user friendly interface



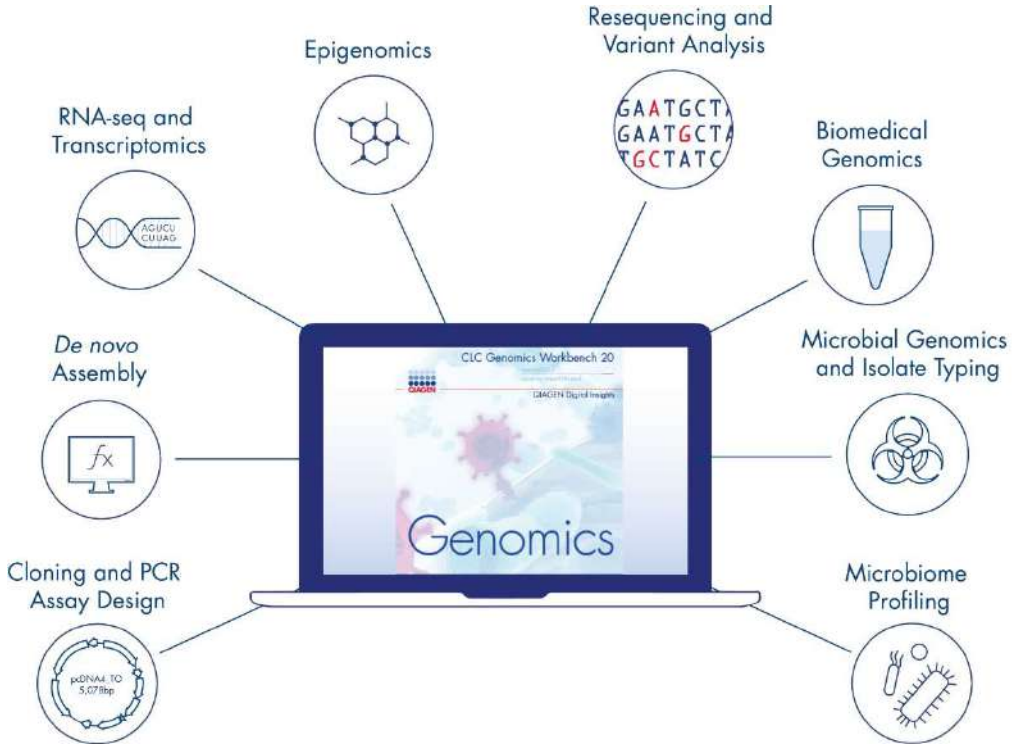
QIAGEN CLC Genomics Workbench

Any species, any platform, any workflow: The all-purpose power tool for NGS data analysis

- Analyze your data without waiting for bioinformatics experts
- High reproducibility
- End-to-end integration for all data types and workflows
- Highly visual

> The graphical interface and the inclusion of the most frequently used programs make the NGS analysis a one-stop shop without having to fiddle with file reformats, software updates, and pipeline incompatibilities.
>
> — Staff Scientist, Federal Government

Source: Staff Scientist, Federal Government
Validated | Published: Nov. 21, 2018 | TVID: D32-EA4-C5D

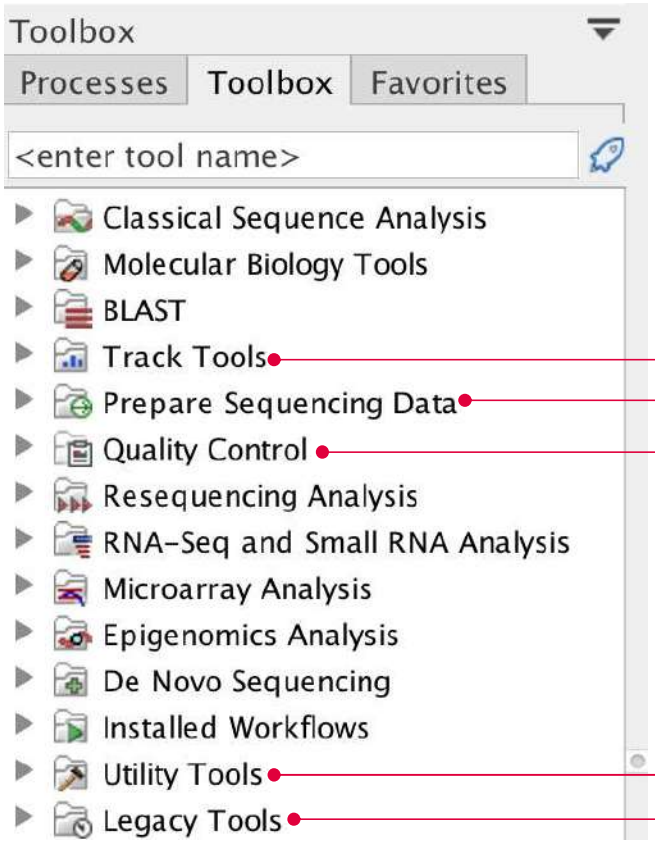


QIAGEN CLC Genomics Workbench features

Cross-platform desktop genomics application with a graphical user interface

- User-friendly interface
- Interactive visualization to facilitate analysis
- Ready-to-use and customizable workflows
  - For automated processing
  - For sharing with colleagues
- Modular design to add plugins
- Developed under quality guidelines set forth by ISO 9001:2015
  - TUV Rheinland-certified
- Works on Windows, Mac and Linux
- Works with reads from most platforms (Illumina, Ion Torrent, Oxford Nanopore, Pacific Bio)ences, BGI/MGI)
- Scalable to enterprise-wide deployment
- Fully documented and supported

Organization of the toolbox



For non-NGS data (e.g., multiple-sequence alignment, phylogenetics, cloning, Sanger etc.)

Tracks, Genome viewer

NGS QC, trim and demultiplex

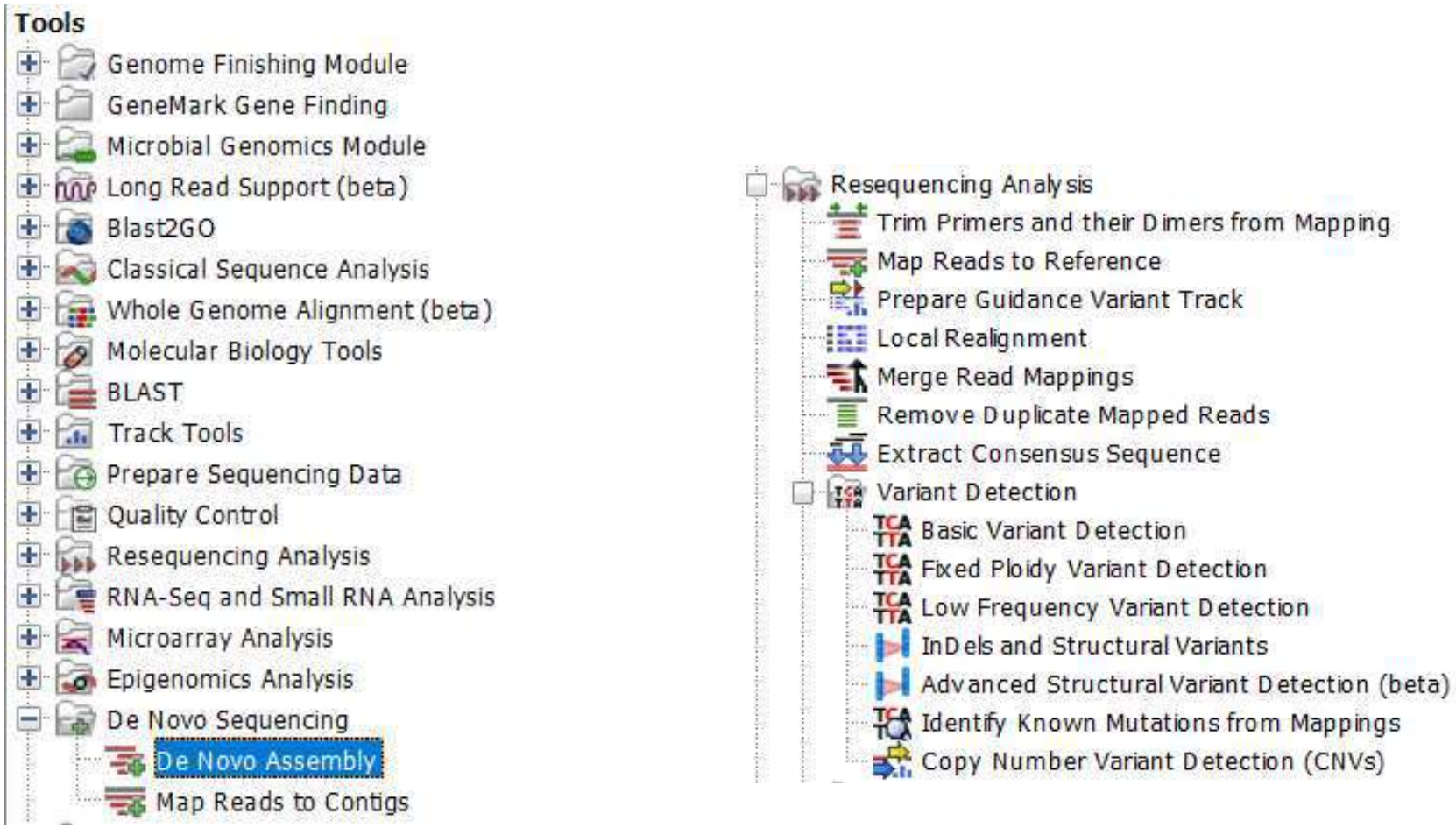
Mapping QC, combine reports

Application-specific tools

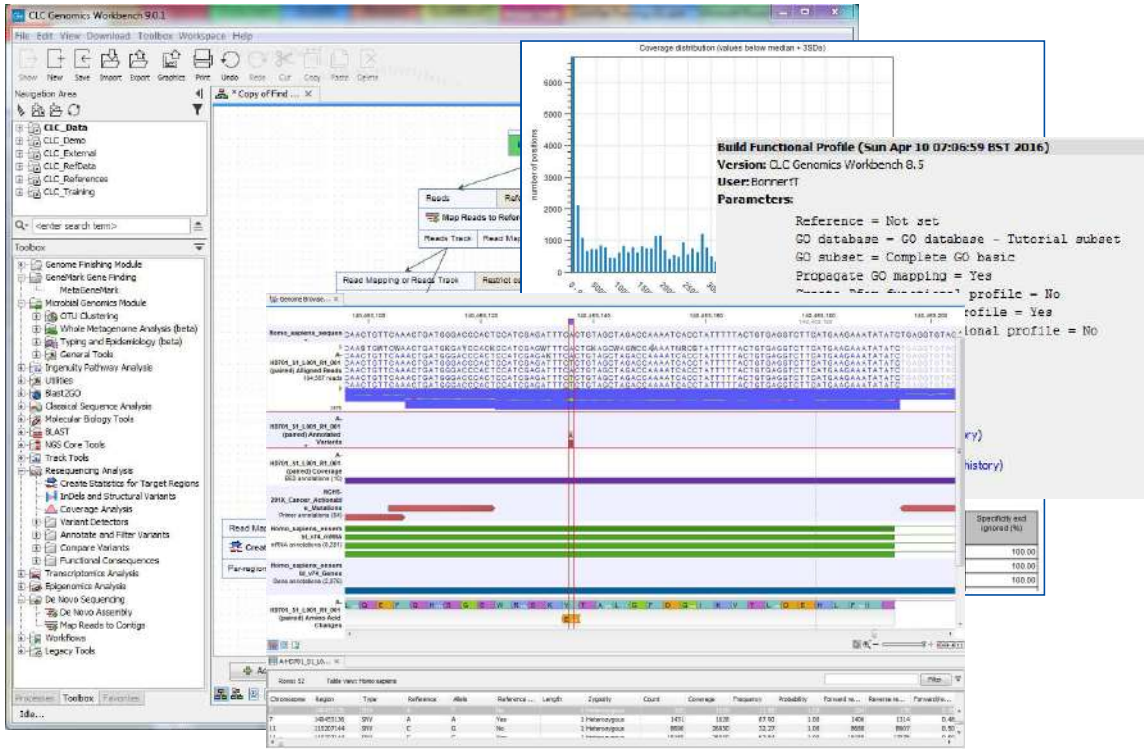
Renaming, sampling and extraction

Tools to-be-retired in the next version

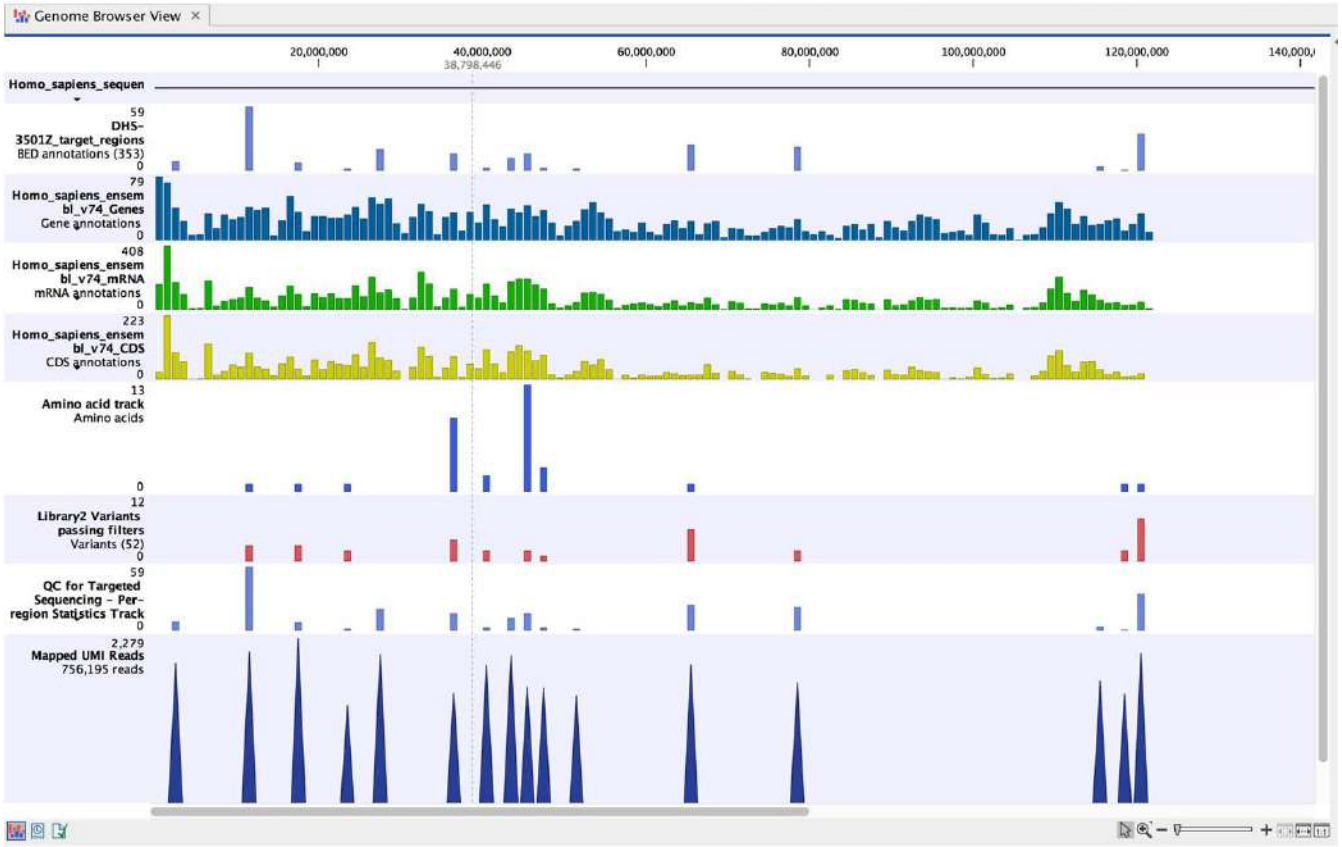
Build-in modules for reference mapping, variant calling and de novo assembly



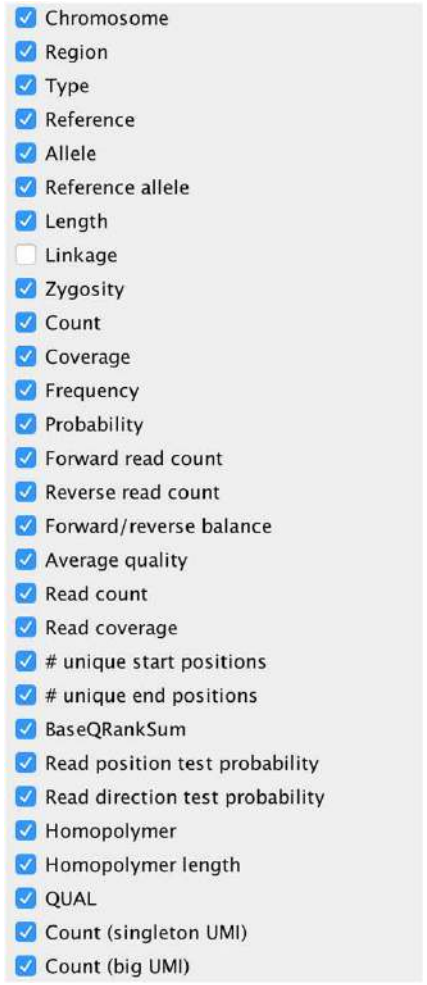
One Click workflow on CLC Genomics Workbench

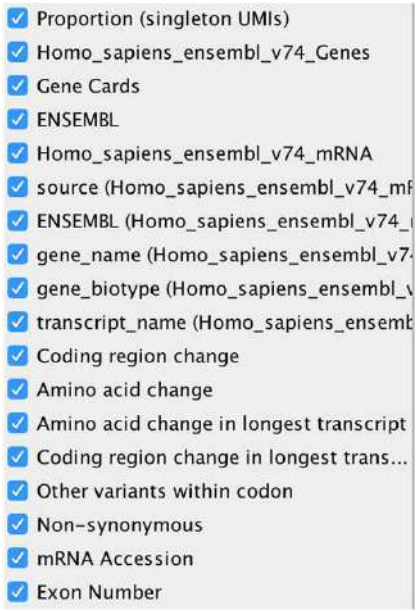


Genome Browser Visualization



More Variant Annotations for DNA

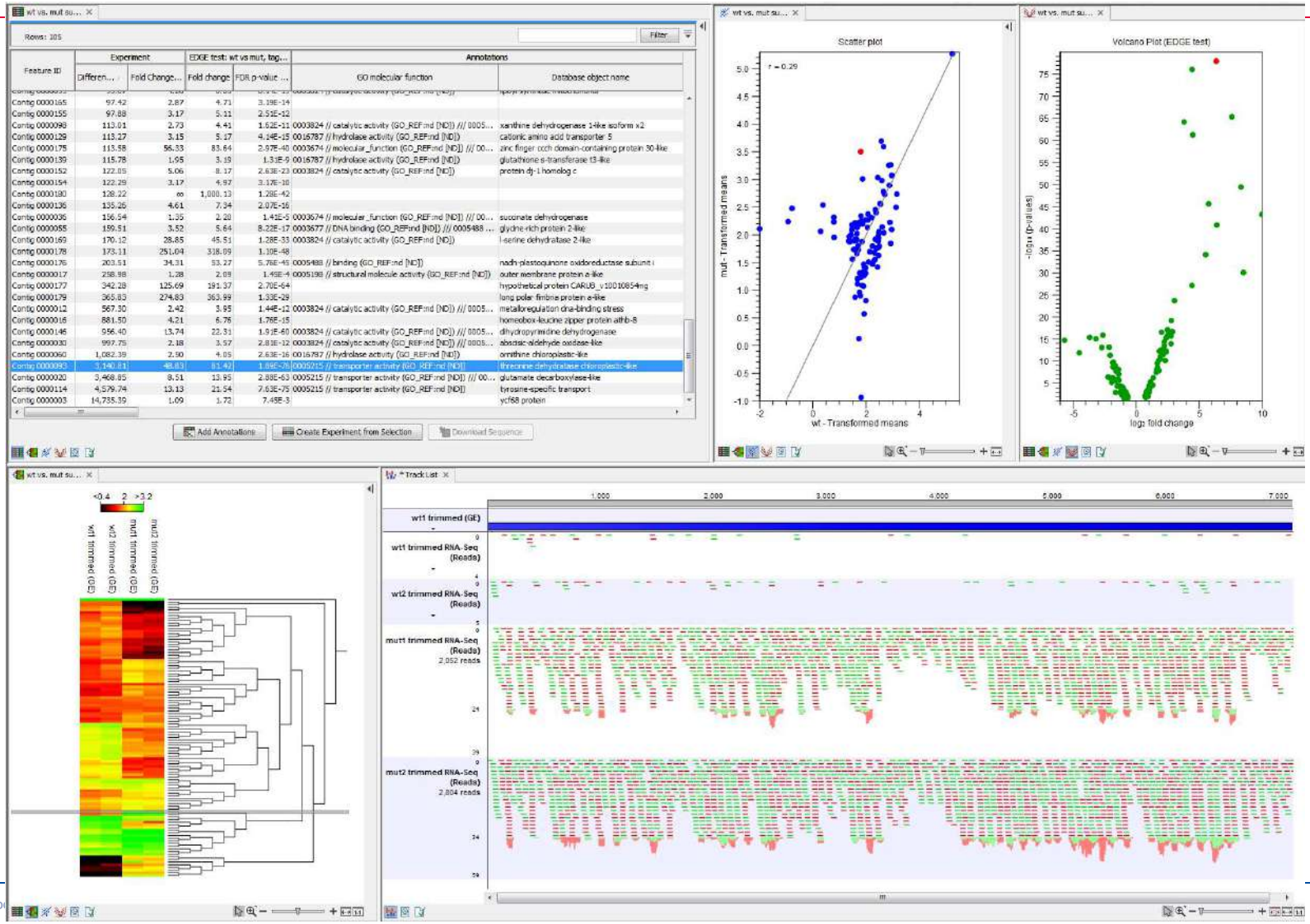




These include:

- Gene names.
- Transcript names
- Amino acid changes.
- non-synonymous.
- Exon number
- etc.

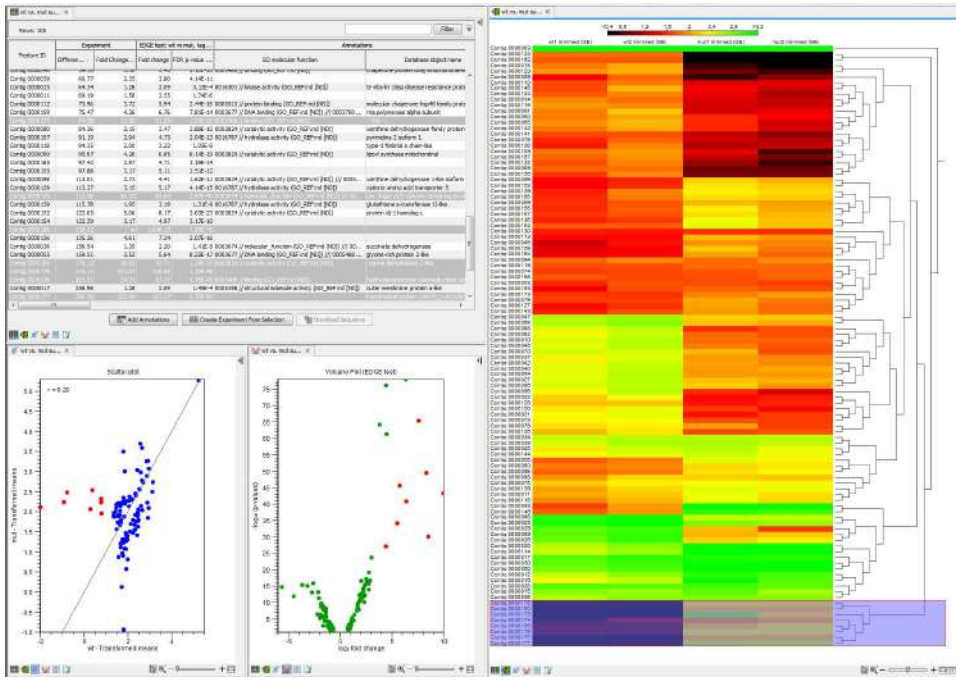
INTERACTIVE VISUALIZATION – NAVIGATE TO MAPPING



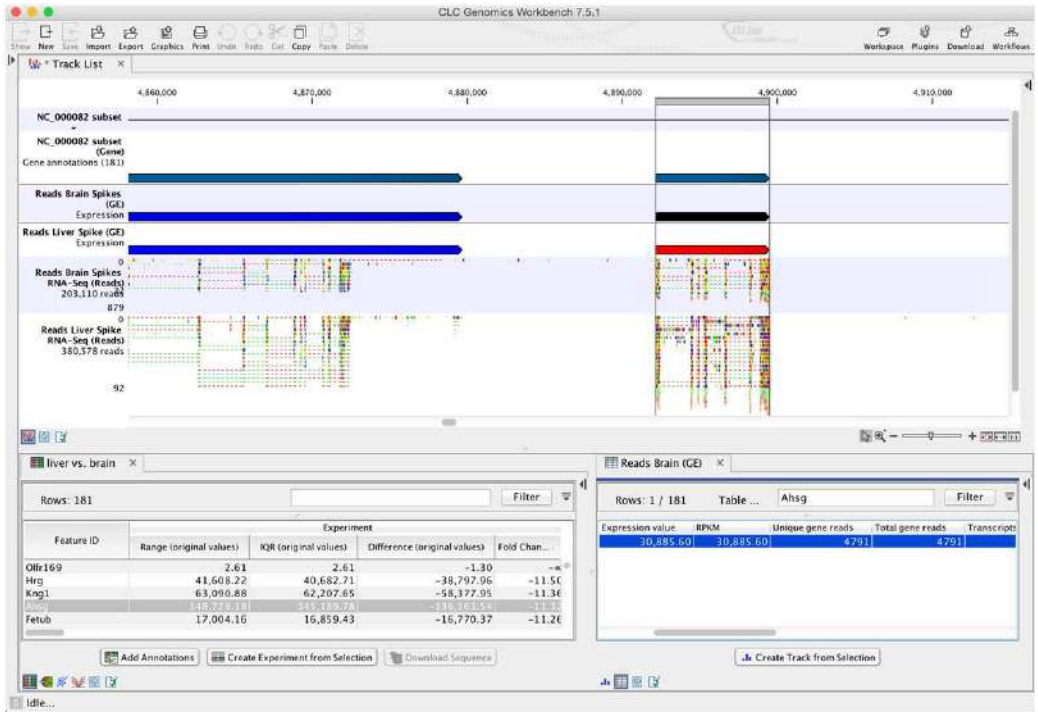
Transcriptomics Data analysis on CLC Genomics Workbench

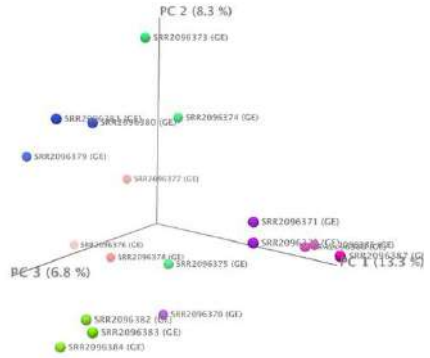
Key features

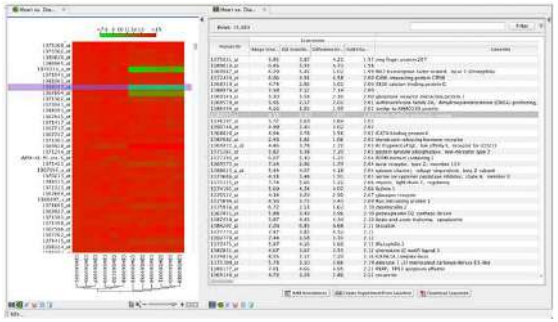
- Create UMI Reads for miRNA
- Quantify miRNA (seeds and mature)
- Annotate with RNA central Accession Numbers
- Create Combined miRNA Report
- Collect the reads that do not map to miRbase
- Visualize your data
- GO enrichment analysis
- Upload to Ingenuity IPA for biological interpretation



RNA-Seq, Microarrays, Statistical Expression Analysis

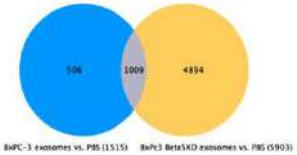




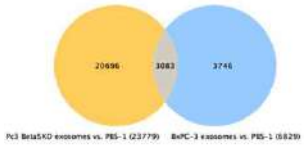


Analyze Expression Data and Upload Comparisons to IPA

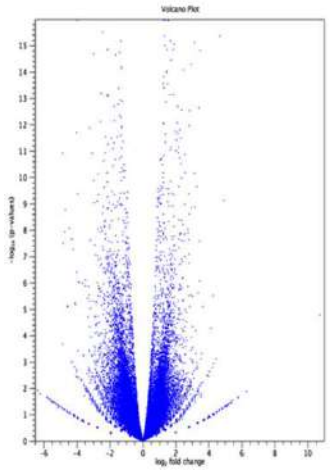
Venn Diagram (GE)



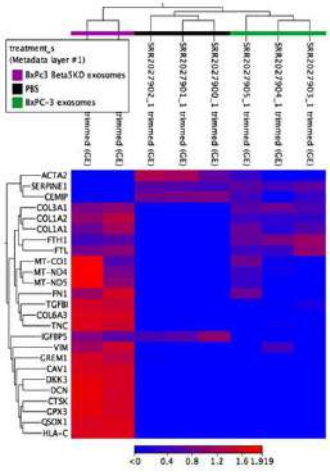
Venn Diagram (TE)



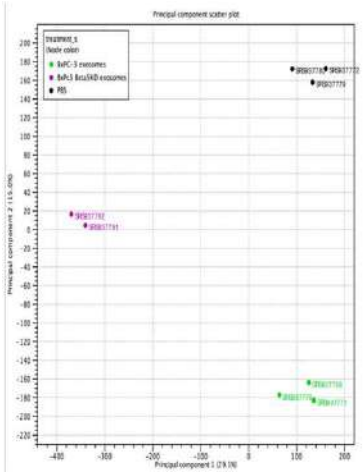
Volcano Plot



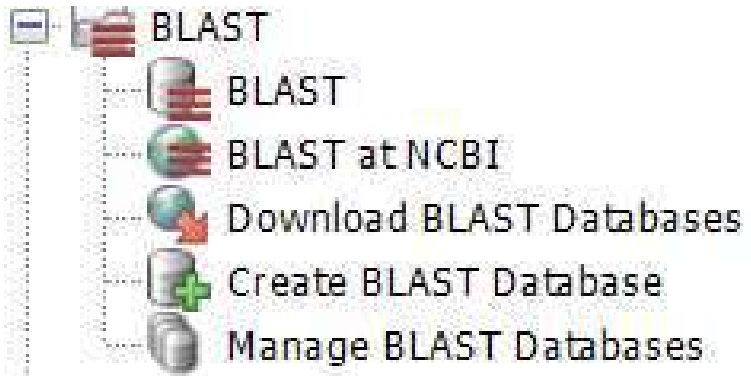
Heat Map

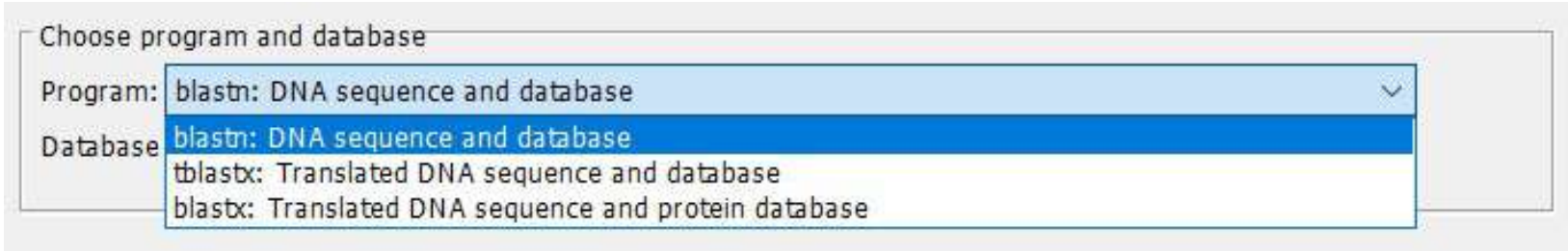


PCA plot

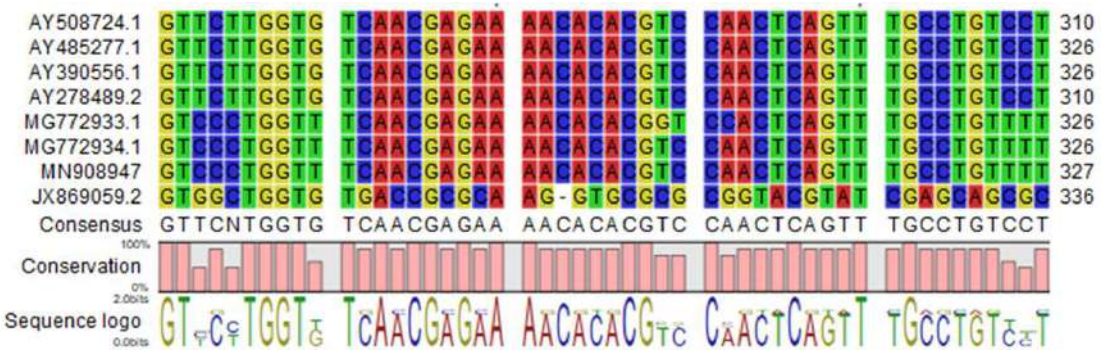


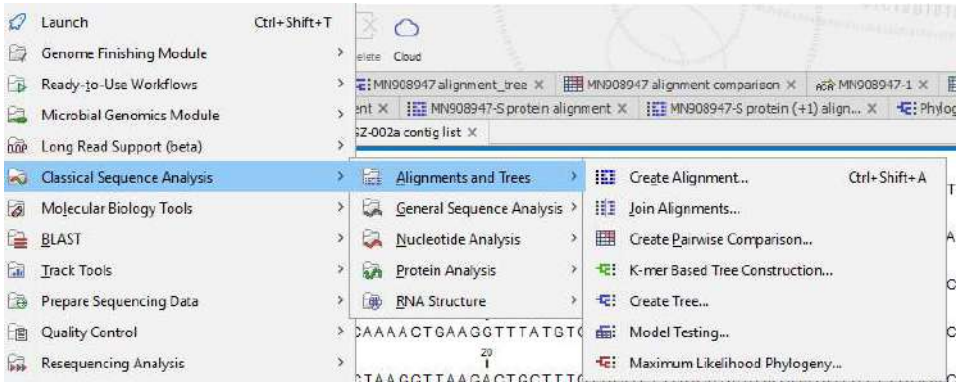
Genome annotation

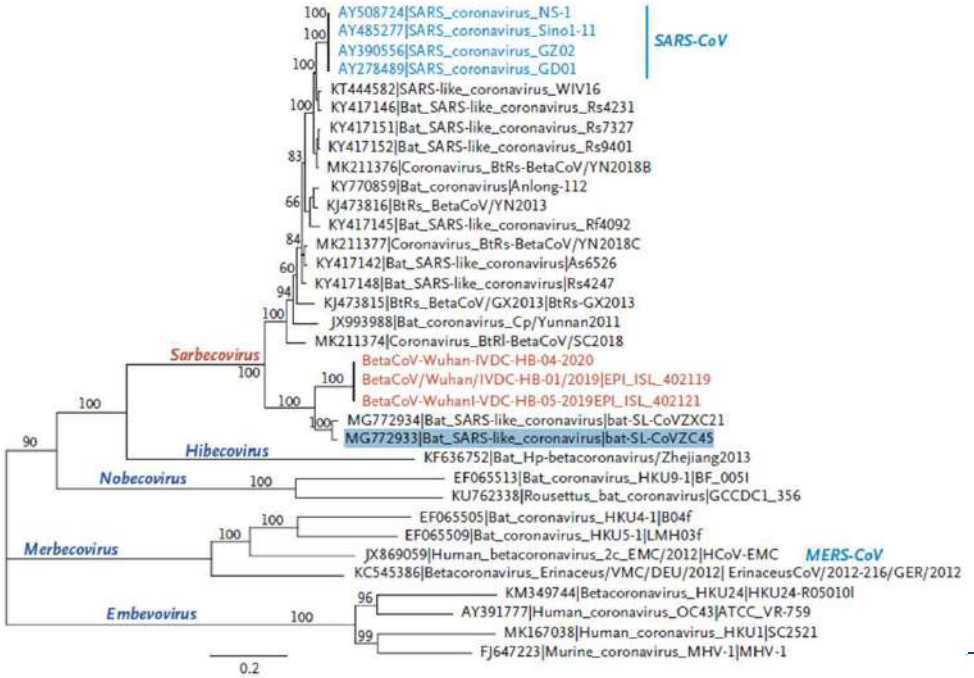




Multi-sequence alignment

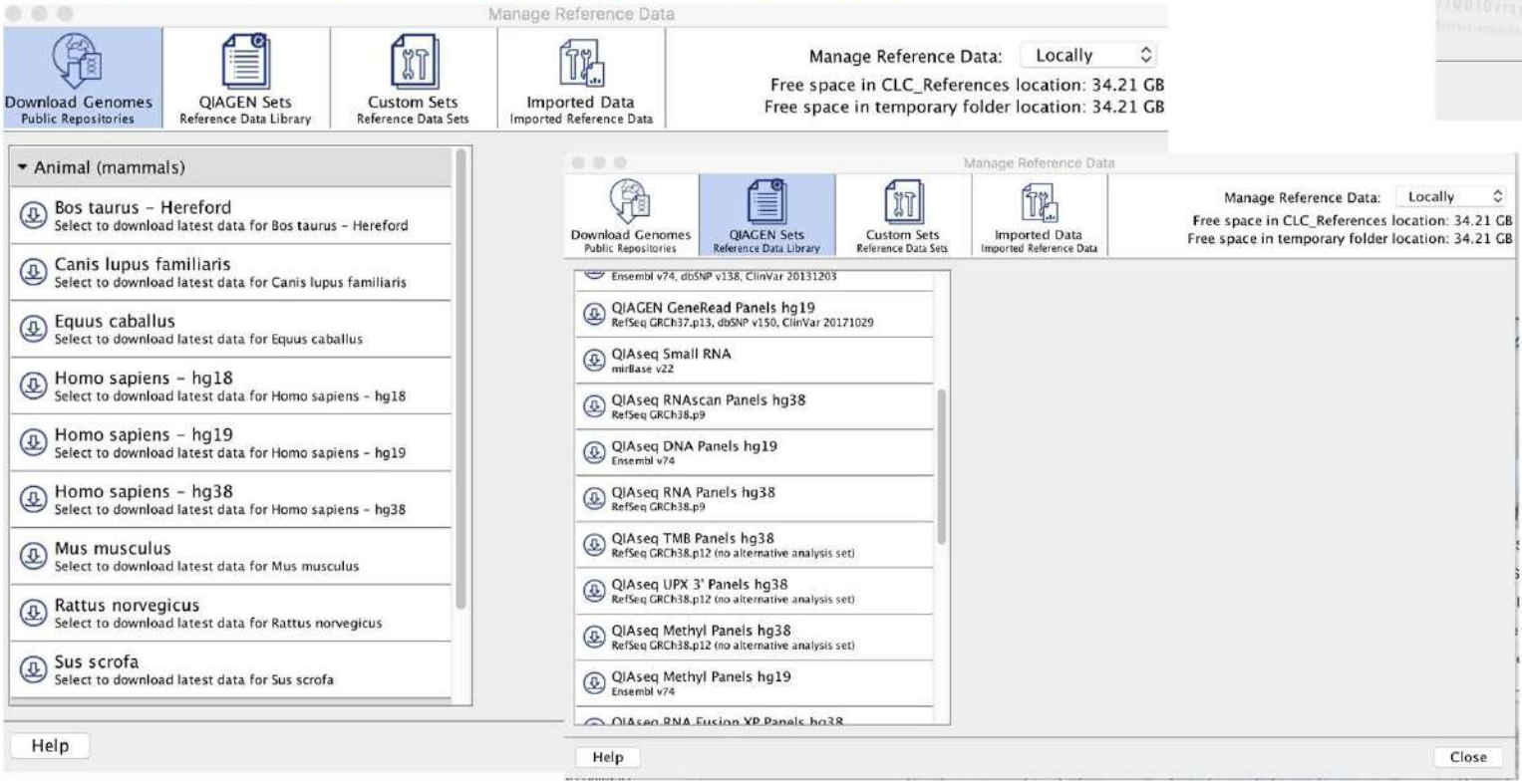


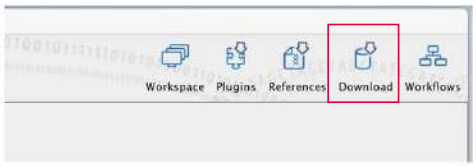




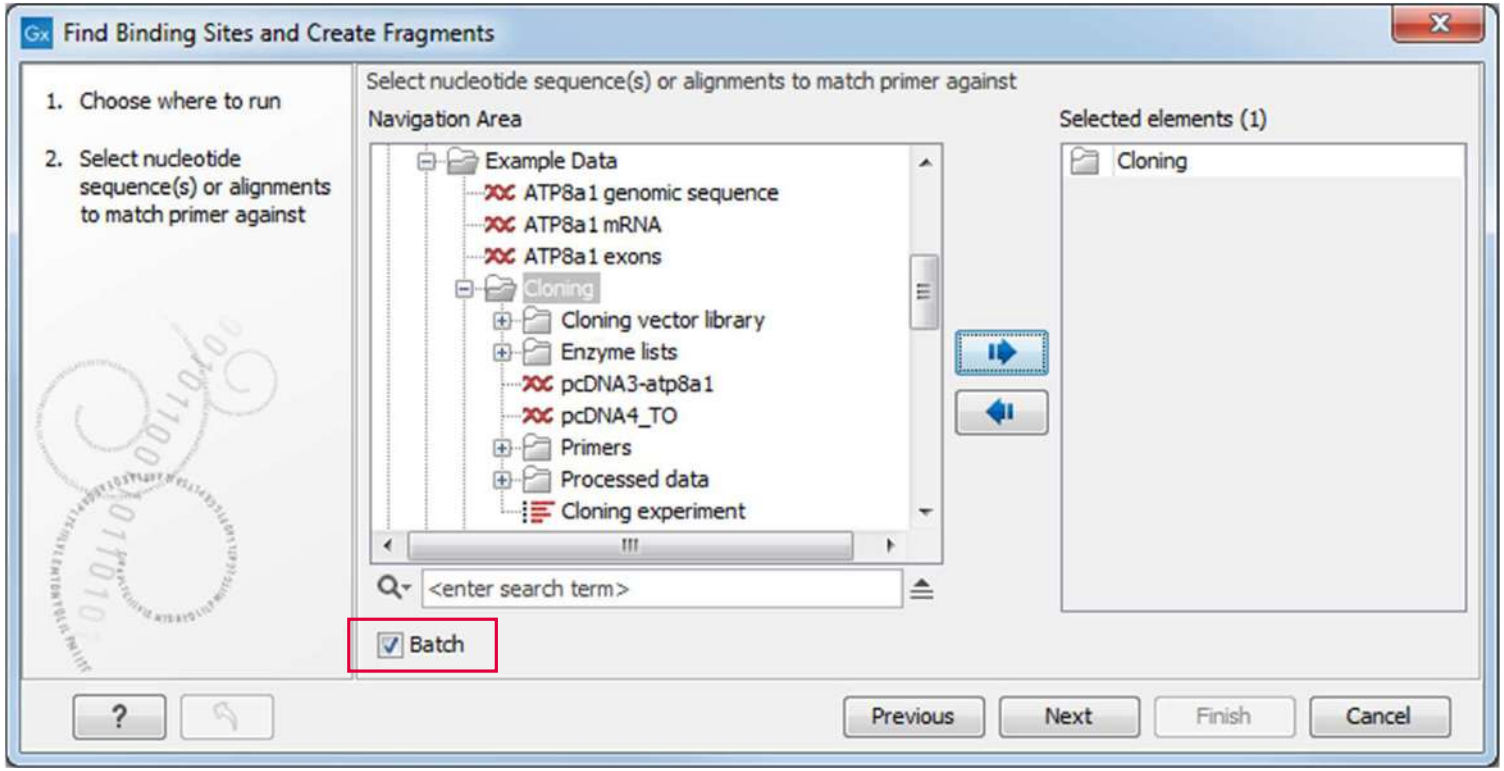
The reference data manager

Convenient download of reference genomes and panel BED files





Batching: Iterate tool or workflow execution over all input files



QIAGEN Biomedical Genomics Analysis Plugin

Biomedical genomics analysis and panel data analysis functionality is available through the QIAGEN CLC Genomics Workbench and the free plugin, Biomedical Genomics Analysis

- One-click workflows optimized for the sequencing platform and panel
- Reproducible results
- DNA methylation, RNA, MSI/TMB, point mutations, CNVs
- Highly visual

A Lab Director at a medium enterprise health care company would be very likely to recommend QIAGEN Bioinformatics for this reason:

> It is the best bioinformatics software in the market.

Source: Lab Director, Medium Enterprise Health Care Company

Validated Published: Sep. 13, 2019 TVID: 737-34B-6F4

TechValidate

Based on a response of 10 to the question "On a scale of 0-10, how likely would you be to recommend QIAGEN Bioinformatics?"

QIAGEN Biomedical Genomics Analysis Plugin supports QIAseq panels

QIAseq DNA Panels

- DHS-001Z Human Breast Cancer Panel
- DHS-002Z Human Colorectal Cancer Panel
- DHS-003Z Human Myeloid Neoplasms Panel
- DHS-005Z Human Lung Cancer Panel
- DHS-104Z Human Pharmacogenomics Panel
- DHS-3011Z Human Inherited Disease Panel
- DHS-3501Z Human Comprehensive Cancer Panel
- DHS-101Z Human Actionable Solid Tumor Panel
- DHS-102Z Human BRCA1 and BRCA2 Panel
- DHS-103Z Human BRCA1 and BRCA2 Plus Panel
- DHS-105Z Human Mitochondria Panel

QIAseq TMB/MSI Panels

- DHS-8800Z Human TMB and MSI Panel order online DHS-6600Z + MSI booster SDHS-10101-11981Z-48
- DHS-6600Z Human Tumor Mutational Burden Panel

QIAseq RNAscan Panels

- FHS-001Z Human Leukemia Panel
- FHS-002Z Human Solid Tumor Panel
- FHS-003Z Human Lung Cancer Panel
- FHS-004Z Human Oncology Panel

QIAseq Multimodal Panels

- UHS-003Z Human Sarcoma Panel
- UHS-005Z Human Lung Cancer Panel
- UHS-009Z Human Leukemia Panel

QIAseq 16S/ITS Panels

- 333812 QIAseq 16S/ITS Screening Panel (24)
- 333815 QIAseq 16S/ITS Screening Panel (96)
- 333842 QIAseq 16S/ITS Region Panel (24)
- 333845 QIAseq 16S/ITS Region Panel (96)
- 333832 QIAseq 16S/ITS Smart Control (10)

QIAseq RNA Panels

- RHS-001Z Human Angiogenesis and Endothelial Cell Biology
- RHS-002Z Human Apoptosis and Cell Death
- RHS-003Z Human Cancer Transcriptome
- RHS-004Z Human Extracellular Matrix and Cell Adhesion Molecules
- RHS-005Z Human Inflammation and Immunity Transcriptome
- RHS-006Z Human Molecular Toxicology Transcriptome
- RHS-007Z Human Signal Transduction PathwayFinder
- RHS-008Z Human Stem Cell and Differentiation Markers
- RHS-009Z Human Immuno-Oncology
- RMM-001Z Mouse Angiogenesis and Endothelial Cell Biology
- RMM-002Z Mouse Apoptosis and Cell Death
- RMM-003Z Mouse Cancer Transcriptome
- RMM-004Z Mouse Extracellular Matrix and Cell Adhesion Molecules
- RMM-005Z Mouse Inflammation and Immunity Transcriptome
- RMM-006Z Mouse Molecular Toxicology Transcriptome
- RMM-007Z Mouse Signal Transduction PathwayFinder
- RMM-008Z Mouse Stem Cell and Differentiation Markers
- RMM-009Z Mouse Immuno-Oncology

QIAseq UPX 3′ Transcriptome Kits

QIAseq UPX 3′ Targeted RNA Panels

Plugins and modules

Functionalities of the Workbench can be extended by installing plugins

Commercial modules	**Microbial Genomics Module** • Strain typing, epidemiology and antimicrobial resistance analysis • Metagenomics community profiling, assembly and functional analysis • Functional annotation tools • Pre-built or user-customized databases • Integrated support for QIAseq 16S/ITS panels	**Genome Finishing Module** • Automated and manual tools for genome finishing and polishing • Integrated support for PacBio + Illumina hybrid assembly and finishing
Free and third-party plugins	**Free plugins** Biomedical Genomics Analysis Long Read Support Whole genome alignment (beta) Ingenuity Pathway Analysis Ingenuity Variant Analysis	

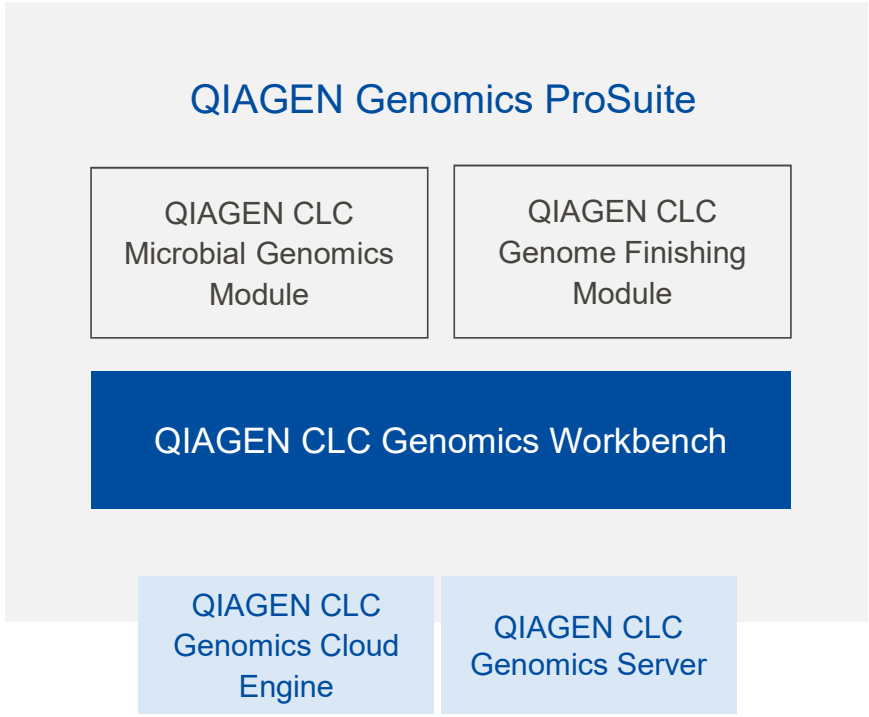
QIAGEN Genomics ProSuite*

Key functionalities:

- Genome assembly and annotation
- Strain typing and characterization
- Microbiome analyses

Key benefits:

- Only one solution needed
- Easy on-boarding
- Saves time
- Lower hardware requirements
- Greater biological insight

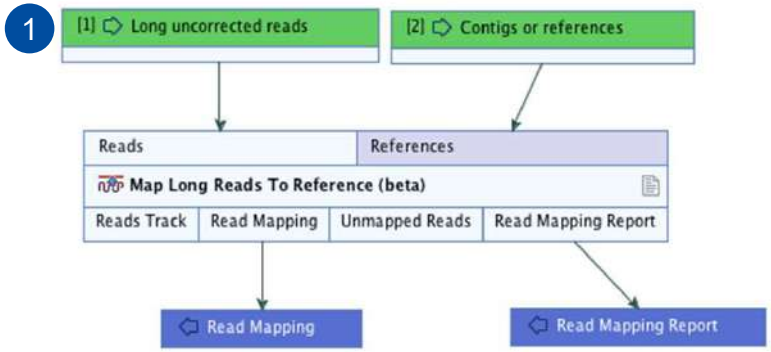


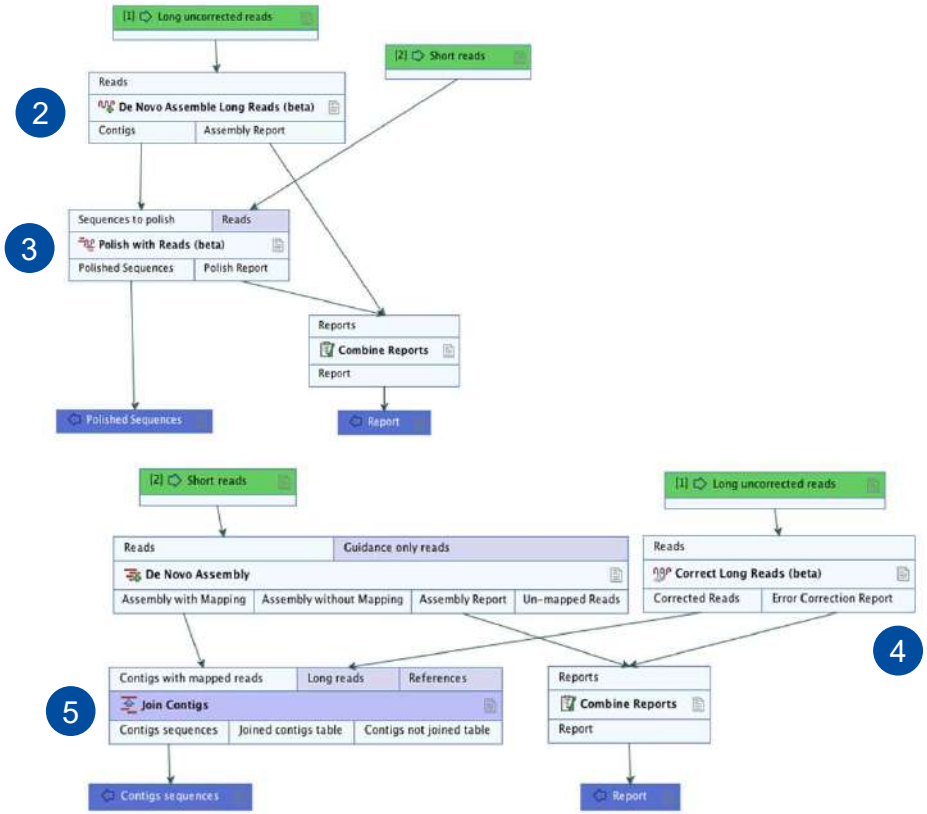
* Formerly “QIAGEN Microbial Genomics ProSuite”

Long Read Support plugin – available to all QIAGEN CLC Genomics Workbench users

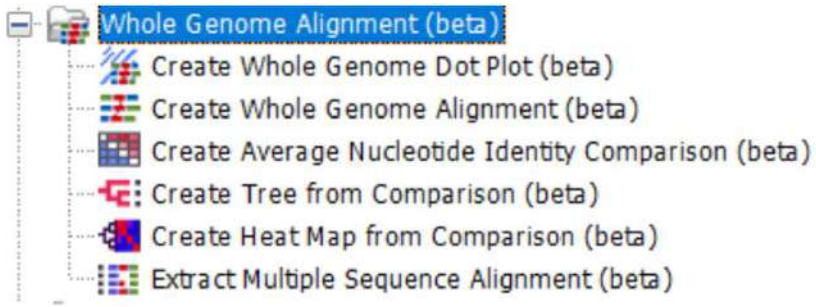
Support for PacBio data and Oxford Nanopore data

1. Long read mapping to reference
2. De novo assembly with long and short reads
3. Polishing with Illumina reads
4. Correct long reads
5. The use of long reads or contigs as scaffolds for Illumina assembly

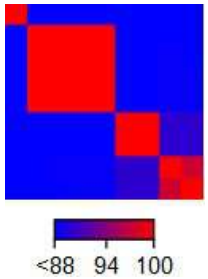




Whole Genome Alignment (beta) – free plug-in



	1	2	3	4	5	6	7	8	9
AY278489 _SARS coronavirus GD01_ complete genom		99.91	99.81	99.82	87.51	87.45	84.88	0.00	84.86
AY390556 _SARS coronavirus GZ02_ complete genome_Ch	99.95		99.85	99.84	87.63	87.14	84.97	0.00	84.96
AY485277 _SARS coronavirus Sino1-11_ complete genom	99.92	99.92		99.93	87.16	87.16	84.96	0.00	84.95
AY508724 _SARS coronavirus NS-1_ complete genom	99.94	99.90	99.96		87.59	87.53	84.91	0.00	84.90
MG772934 _Bat SARS-like coronavirus isolate bat-SL-CoVZXC21_ complete genome_China_Rhinolophus sin	54.76	54.77	58.16	54.70		97.43	89.33	0.00	89.32
MG772933 _Bat SARS-like coronavirus isolate bat-SL-CoVZC45_ complete genome_China_Rhinolophus sin	54.79	58.23	58.19	54.73	99.88		89.34	0.00	89.32
	54.88	54.89	54.85	54.82	92.82	92.93		0.00	99.99
JX869059 _Human betacoronavirus 2c EMC_2012_ complete genome__Homo sa	0.00	0.00	0.00	0.00	0.00	0.00	0.00		0.00
	54.89	54.91	54.85	54.81	92.79	92.91	99.96	0.00	



QIAGEN CLC Microbial Genomics Module

For microbiologists, public health laboratories, pharmaceutical, clinical and agricultural biology research

- Integrated, up-to-date microbial databases
- Operable without dedicated programmers or bioinformaticians
- Strain typing and epidemiology with MLST, AMR detection and outbreak tracing
- Microbiome analysis amplicon based (16S/ITS) and whole shotgun metagenomics

A Professor at an educational institution would be very likely to recommend QIAGEN Bioinformatics for this reason:

> CLC Genomics Workbench is easy to use and very powerful. The metagenomics plugin is fantastic!

Source: Professor, Educational Institution

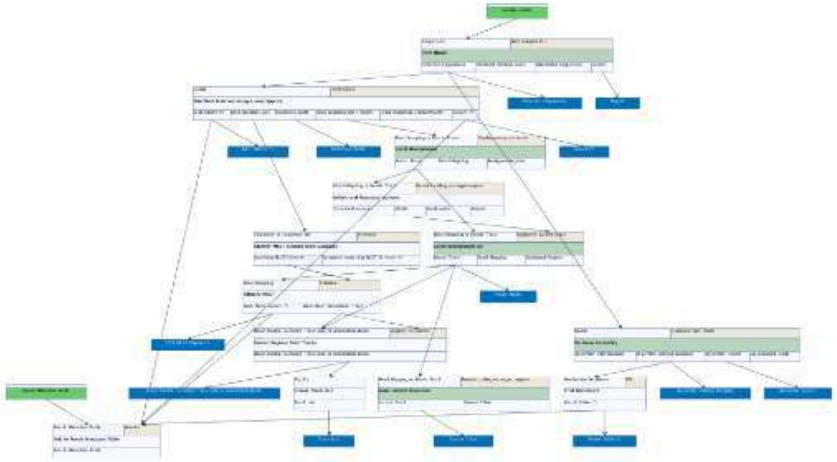
Validated Published: Sep. 18, 2019 TVID: 340-220-815

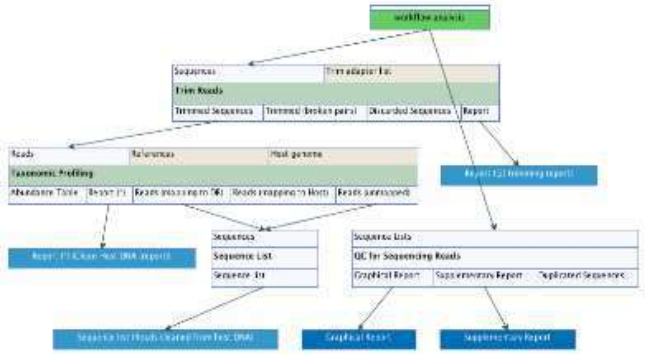
TechValidate

Based on a response of 10 to the question "On a scale of 0-10, how likely would you be to recommend QIAGEN Bioinformatics?"

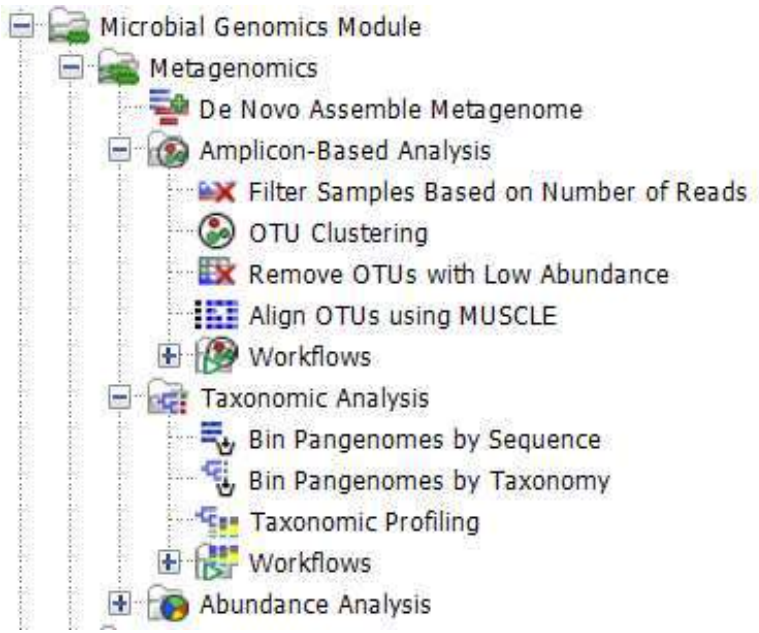
Workflows

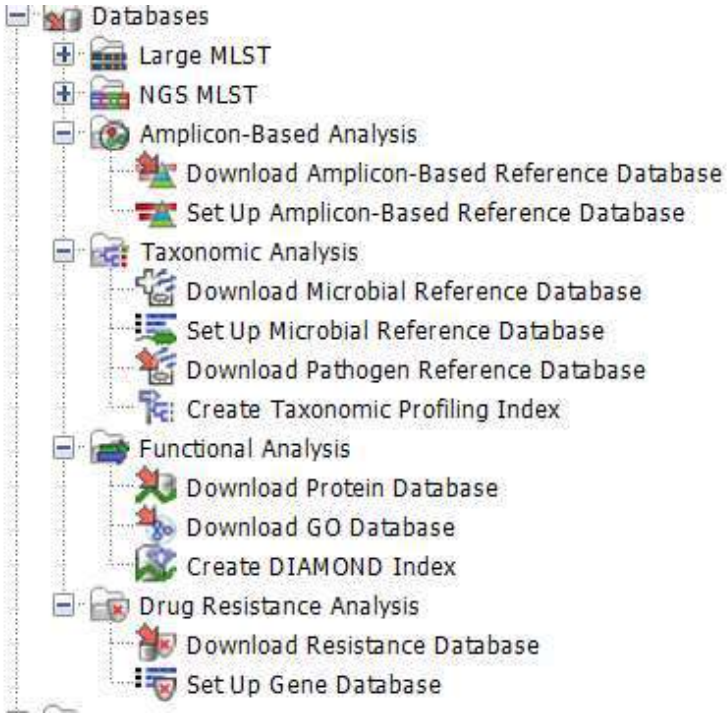
- Pre-configured workflows for commonly used functionalities
  - All parameters can be customized
  - Parameters can be locked to prevent editing
- Get you started easily
- Ensure consistency and reproducibility of analyses
- Allows for automatization





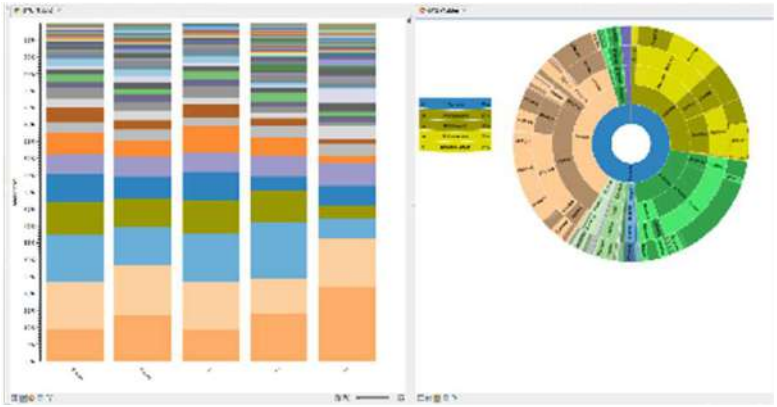
Build-in workflow + download / integrated database in QIAGEN CLC Microbial Genome Module



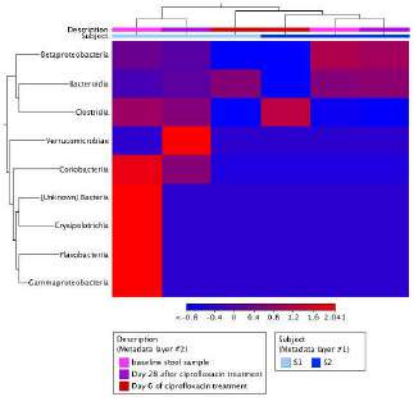


Amplicon-based profiling

- Microbiome profiling using marker genes, 16S rRNA and ITS
- Direct download of common databases: SILVA, Greengenes and UNITE
- Clustering sequences into OTUs
- Diversity estimates
- Comparison of abundances across samples



Bar chart and sunburst diagram of the relative abundance of a bacterial community



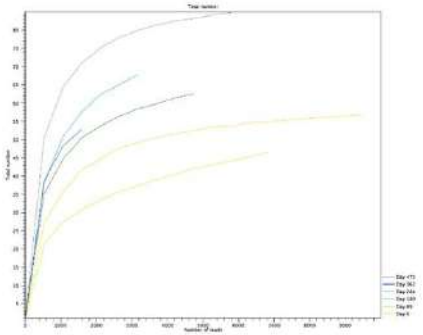
Heat map of the differential abundance across samples

White paper: Characterizing the microbiome through targeted sequencing of bacterial 16S rRNA and fungal ITS regions

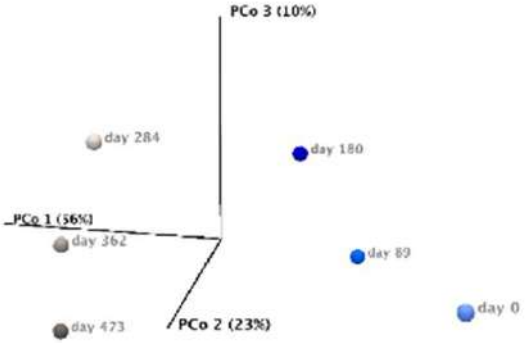
Webinar: Microbiome profiling from day one

Whole genome shotgun metagenomics

- Microbiome profiling based on shotgun data
- Direct access to microbial genome reference databases
  - Optimized to run on standard laptop
- Comparison of abundance across samples
- Estimation of diversity
- Functional annotation of metagenomes
  - Gene finding
  - Annotation with DIAMOND, BLAST and Pfam



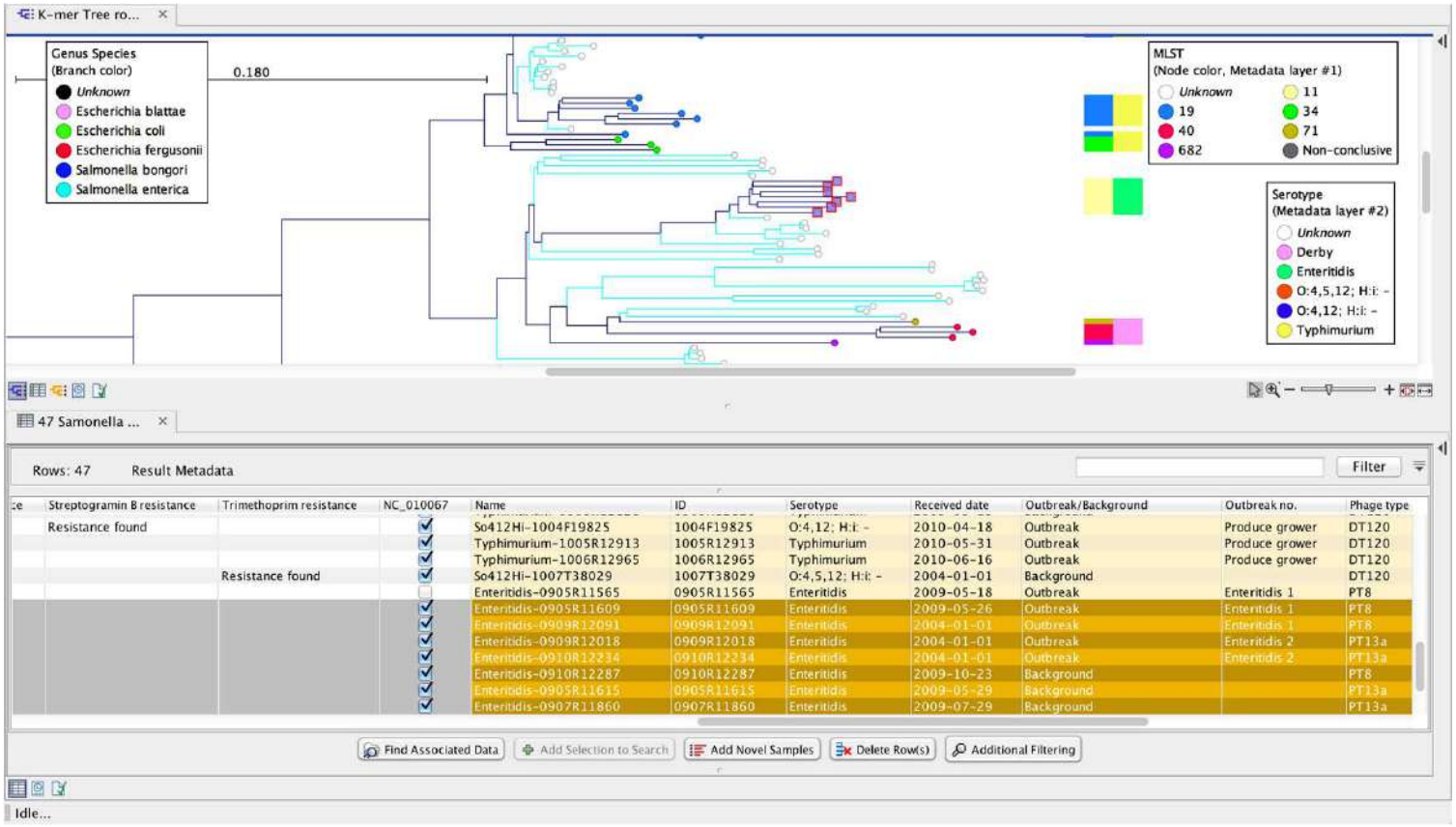
Visualization of alpha diversity

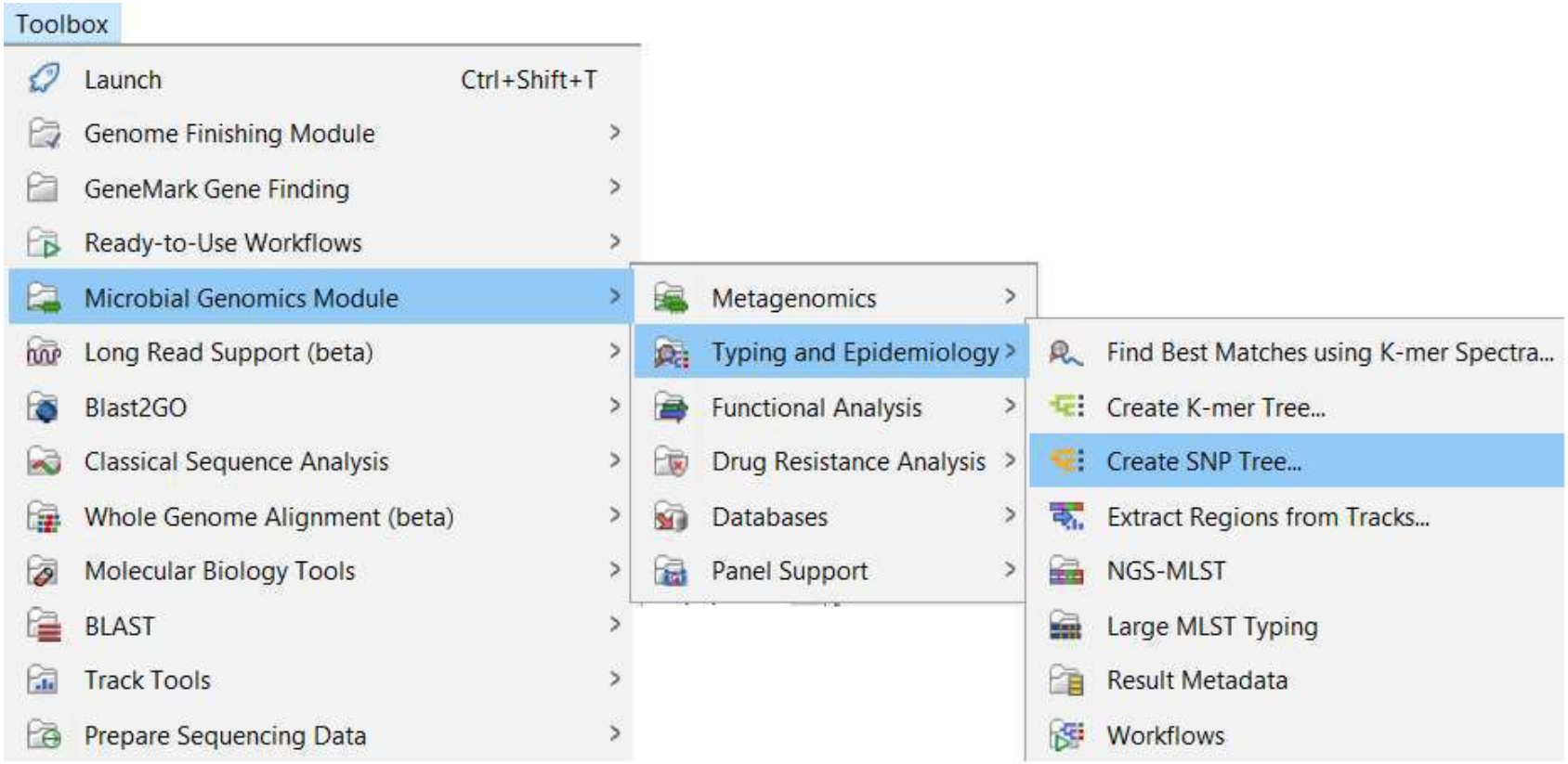


Principal component analysis plot of beta diversity within a microbial community

Webinar: Taxonomic profiling using shotgun metagenome data

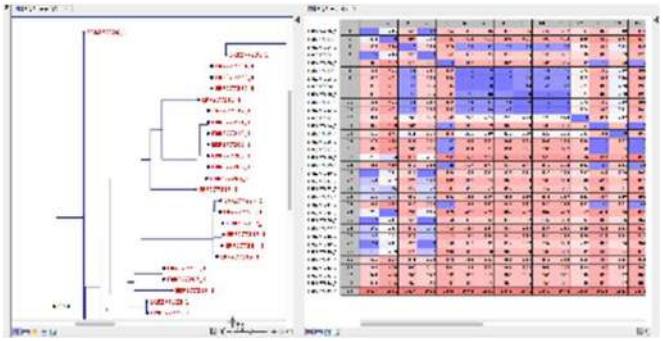
Pathogen typing - primary output is an analysis dashboard

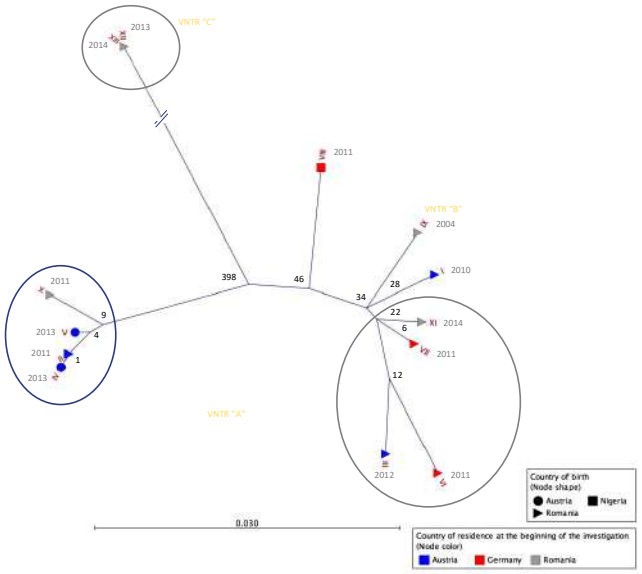



Toolbox
Launch Ctrl+Shift+T
Genome Finishing Module
GeneMark Gene Finding
Ready-to-Use Workflows
Microbial Genomics Module
Long Read Support (beta)
Blast2GO
Classical Sequence Analysis
Whole Genome Alignment (beta)
Molecular Biology Tools
BLAST
Track Tools
Prepare Sequencing Data
Metagenomics
Typing and Epidemiology
Functional Analysis
Drug Resistance Analysis
Databases
Panel Support
Find Best Matches using K-mer Spectra...
Create K-mer Tree...
Create SNP Tree...
Extract Regions from Tracks...
NGS-MLST
Large MLST Typing
Result Metadata
Workflows

Tracing pathogen outbreaks

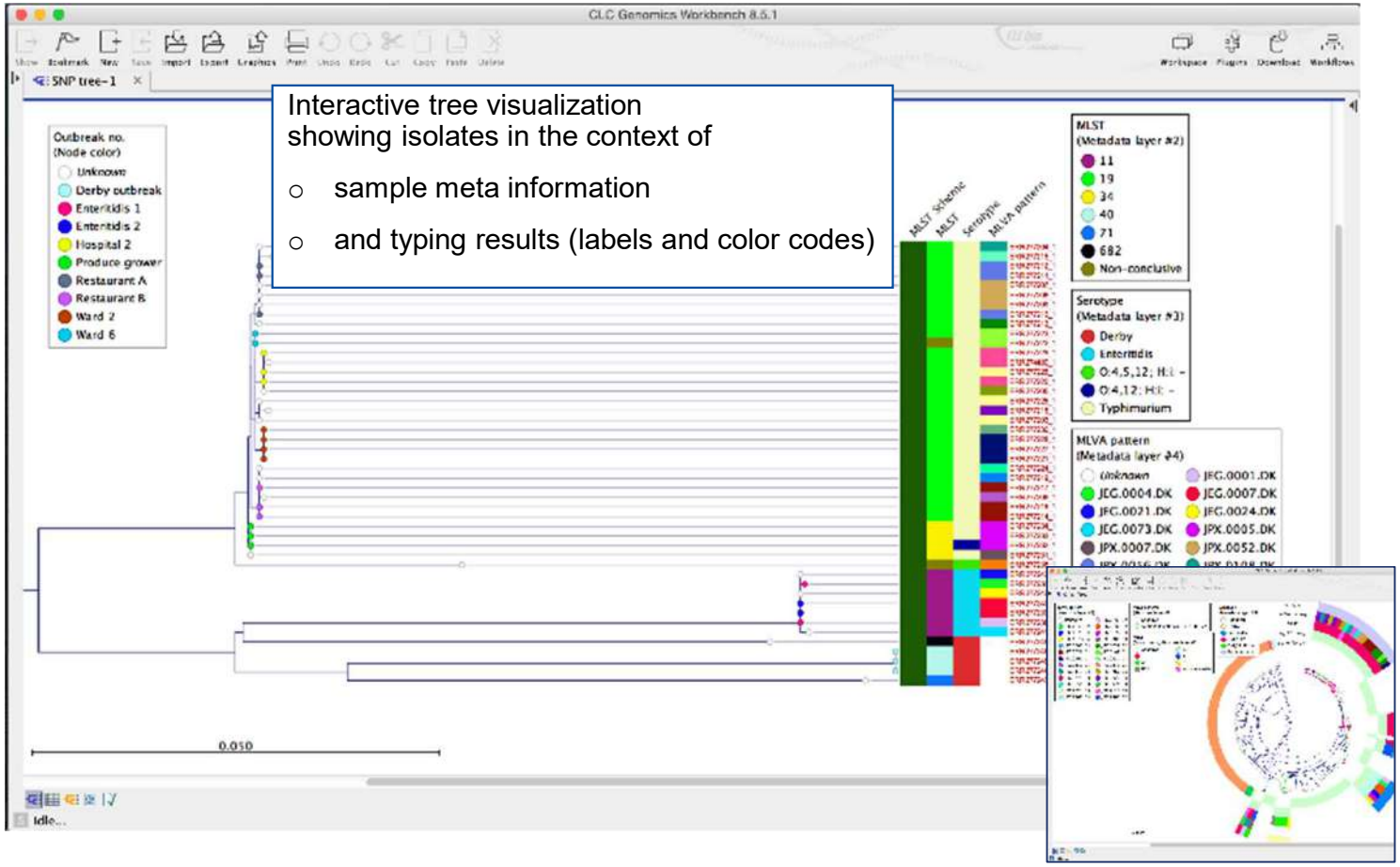
- Analyzing strain relatedness at maximum resolution
- Genome-wide comparison of single nucleotide polymorphisms
- Visualization of results
  - Dendrogram decorated with metadata
  - SNP matrix



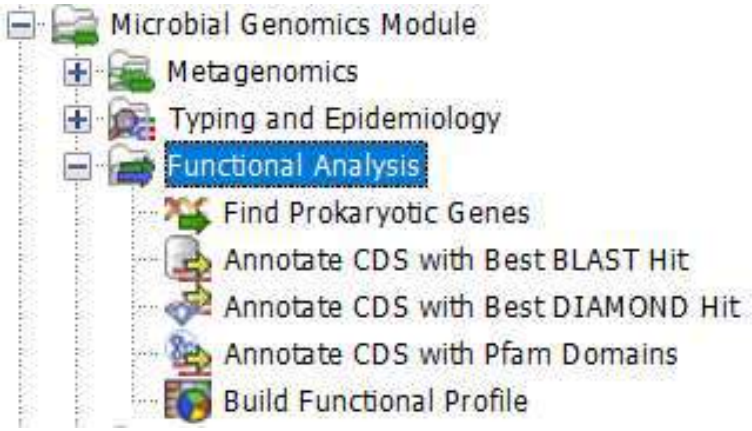


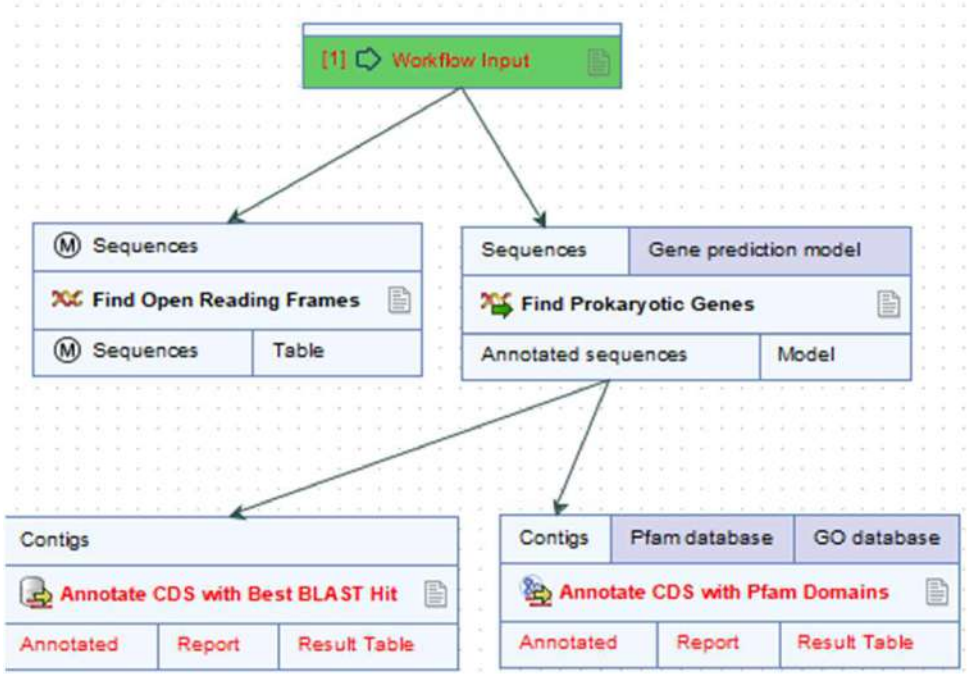
White paper: High-resolution outbreak tracing and resistance detection using WGS in the case of a *Mycobacterium tuberculosis* outbreak

Pathogen typing – outbreak analysis at highest resolution



Advanced functions on QIAGEN CLC Microbial Genomics Module

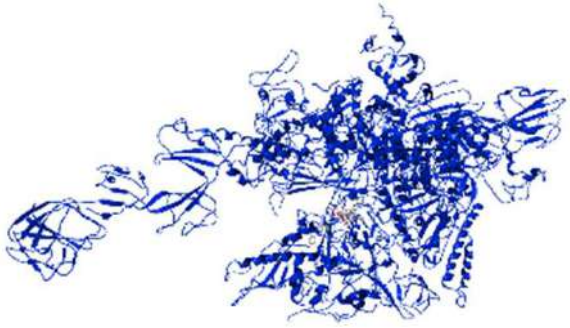




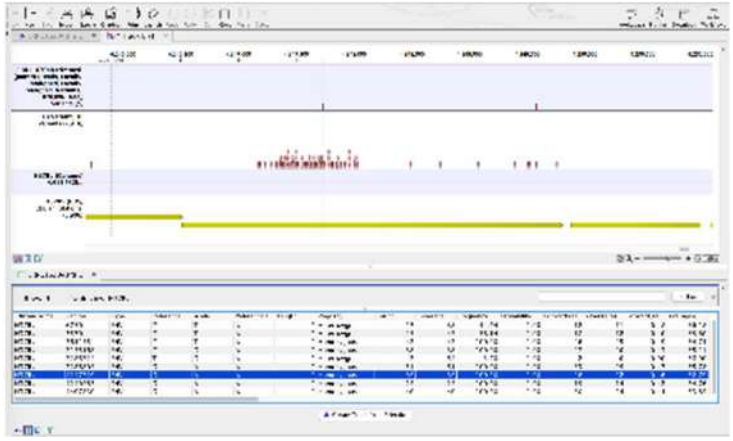
*The workflow can be customized

Detection of antimicrobial resistance markers

- AMR gene finding with ResFinder
- Calling AMR causing mutations with PointFinder
- Detect ARG-ANNOT resistance markers with ShortBRED
- Resolve plasmids from chromosomal regions



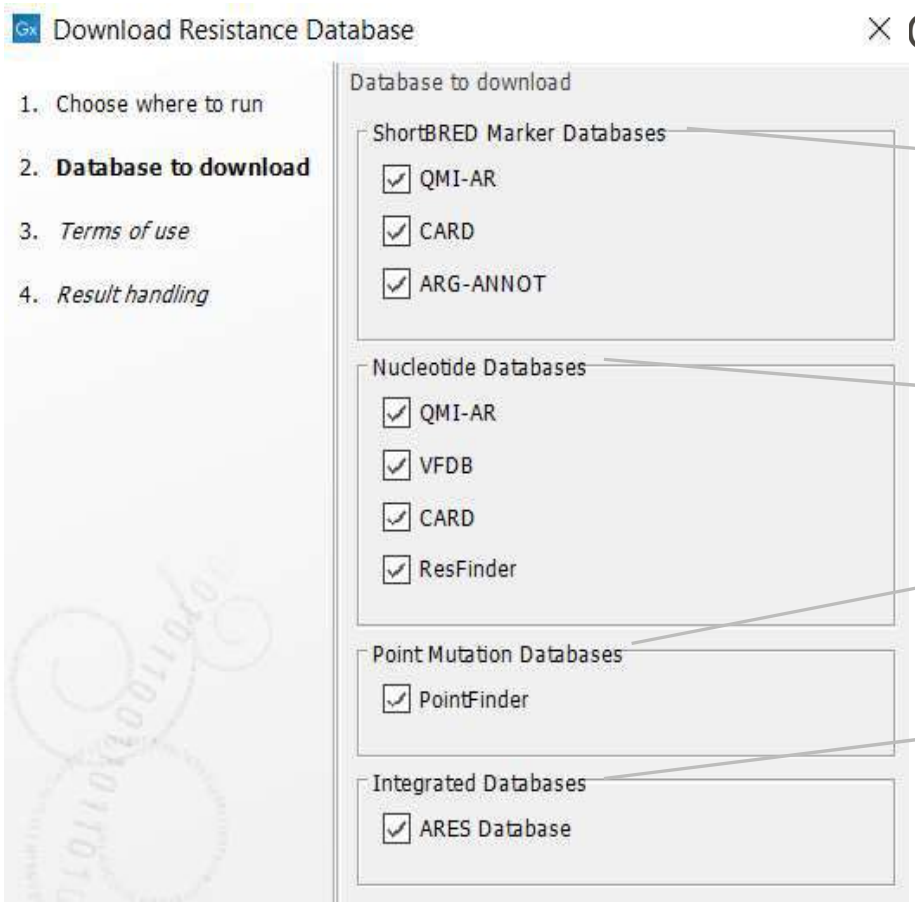
Antimicrobial resistance causing mutations can be visualized in the context of 3D protein models



Track list displaying detected variants in a TB isolate, the TB variant database and the reference genome annotations

Poster: Whole genome sequencing for antimicrobial resistance detection and surveillance

QIAGEN CLC Microbial Genome Module



- Find Resistance with ShortBRED tool.

  The databases are marker databases, containing peptide fragments that uniquely characterize sets of similar proteins, rather than a gene

- Find Resistance with Nucleotide DB tool. The databases contain full nucleotide gene sequences

- Find Resistance with PointFinder tool. The databases contain information about mutations in genes

- A Nucleotide Marker table for gene markers. From this view, it is possible to extract a sequence list which may be used with the Find Resistance with Nucleotide DB tool.
- A Protein Marker table for gene markers.
- A Point Mutation Marker table for Single Nucleotide Polymorphism (SNP) markers. From this view, it is possible to extract a sequence list which may be used with the Find Resistance with PointFinder tool.

CLC Genome Finishing Module

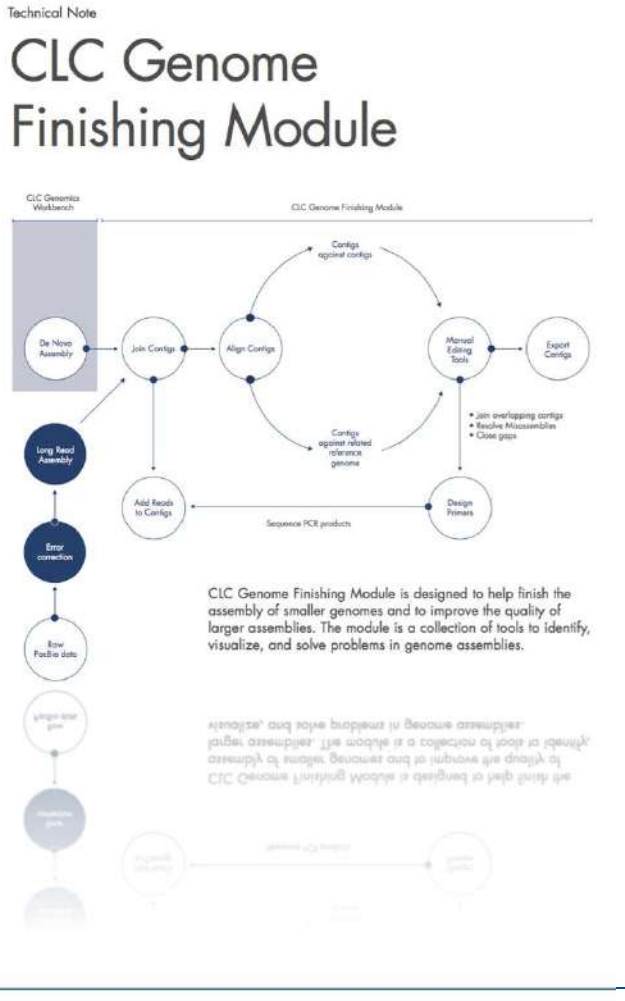
Our solution:

CLC Genome Finishing Module is an add-on to CLC Genomics Workbench, designed

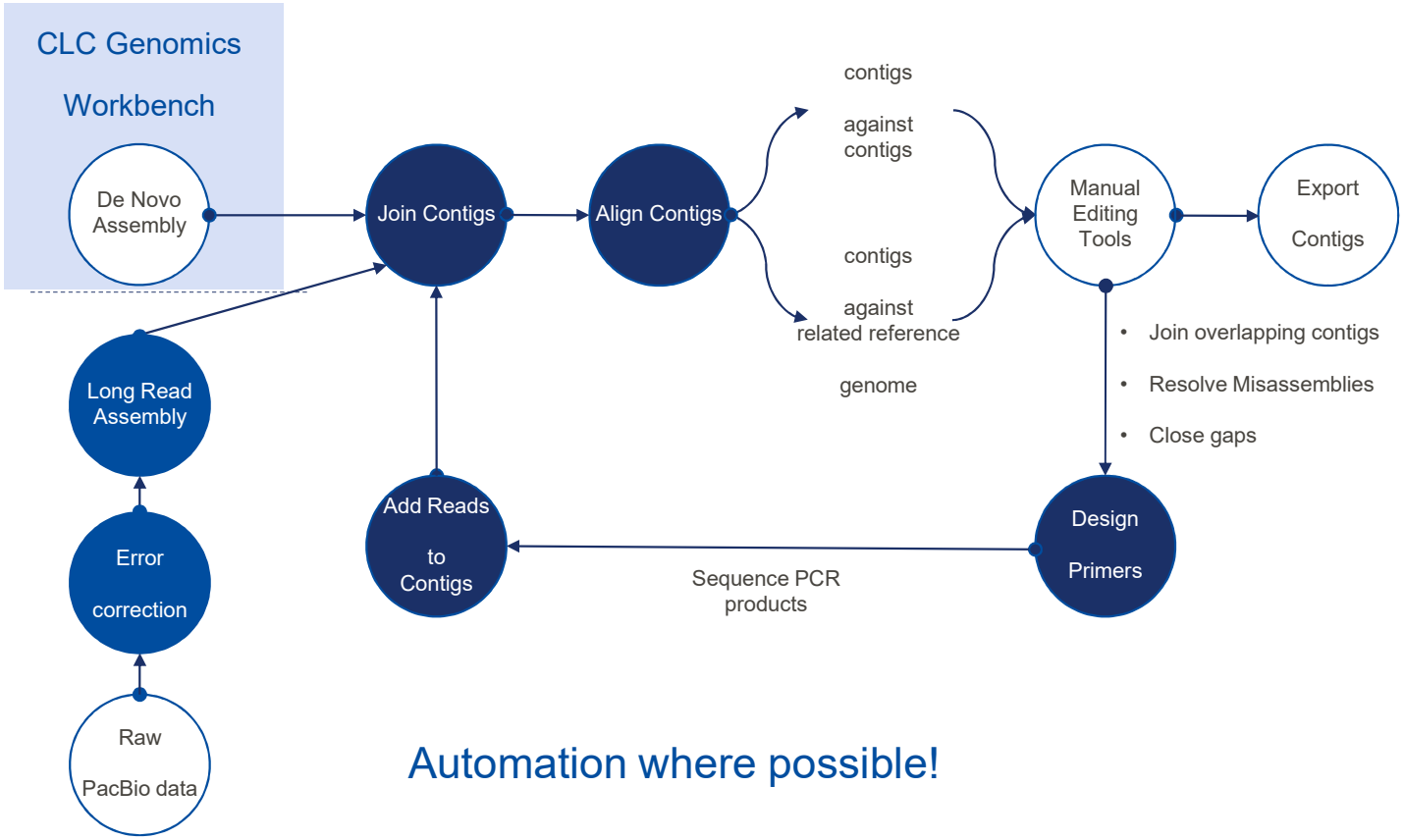
- to accelerate and simplify genome finishing, and
- to make this process accessible to life scientist without deep understanding of bioinformatics.

Supported genome finishing applications:

- Short read de novo assemblies
- Hybrid assemblies of short and long read data (e.g. Illumina, 454, and PacBio)
- Rapid error-correction and de novo assembly of PacBio data.



De Novo Assembly and Genome Finishing



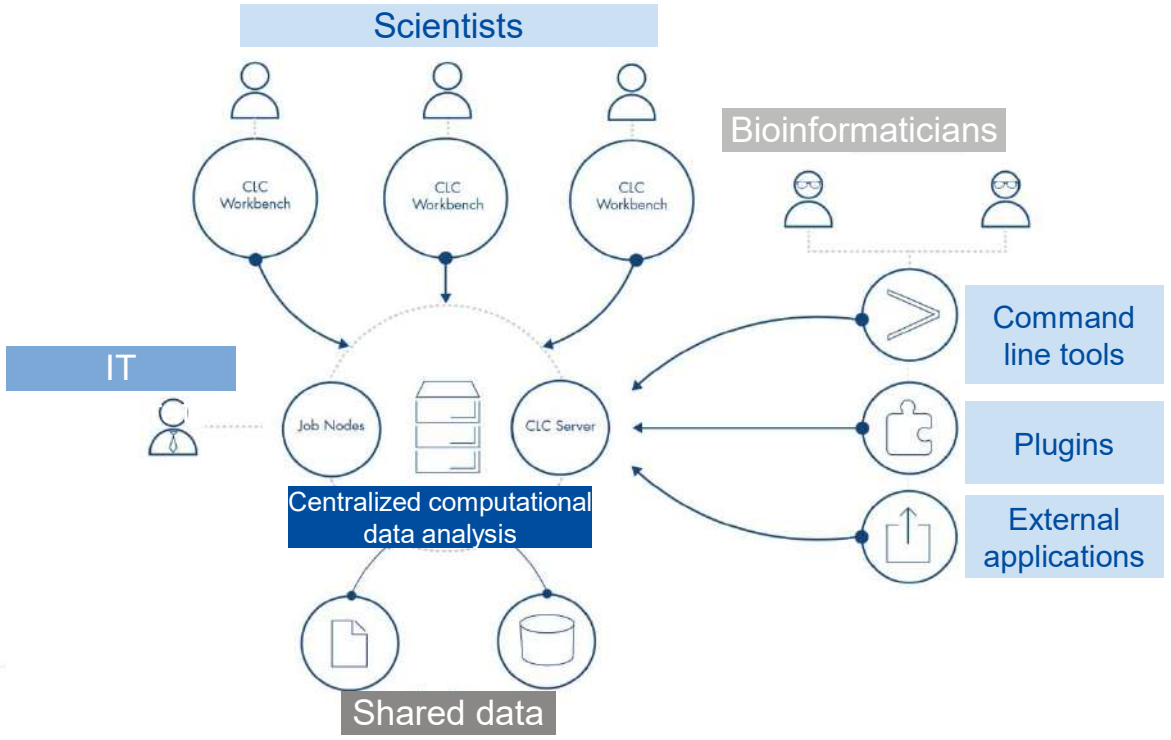
Automation where possible!

QIAGEN CLC Genomics Server and QIAGEN CLC Genomics Cloud Engine v20

On-premise enterprise solution: QIAGEN CLC Genomics Server

From single user to enterprise-friendly NGS analysis

- No waiting – accelerate turnaround time on data processing
- Eliminate costs for maintenance, bug fixing and upgrades
- Integrated access to in-house pipelines and external applications
- Workflow management and deployment

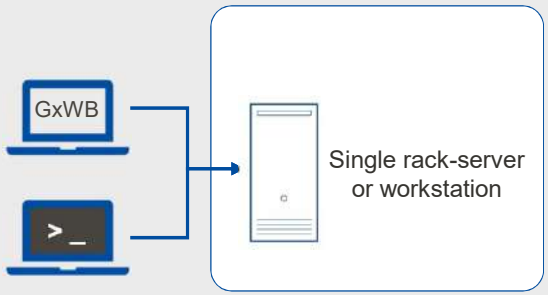


> "Has made us process a lot of data in a short time.
>
> — Chief Scientist, Medium Enterprise Health Care Company

Source: Chief Scientist, Medium Enterprise Health Care Company
Validated Published: Nov. 21, 2018 TVID: E46-3CC-8A6

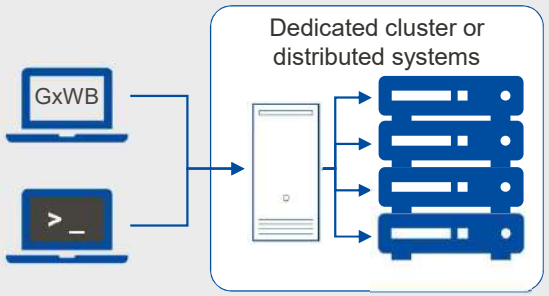
QIAGEN CLC Genomics Server – three deployment models

Single server



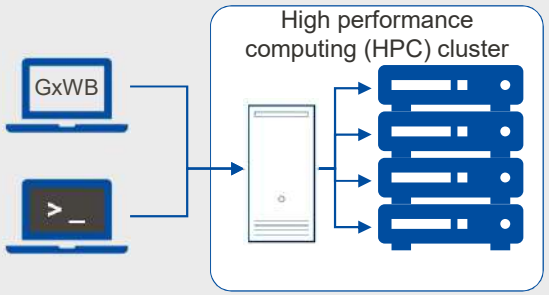
- Simple to set up in minutes
- Offloads workflows, ad hoc data analysis and storage to central hub
- Single rack server or workstation
- Same capabilities as cluster setup

Master server + Job nodes



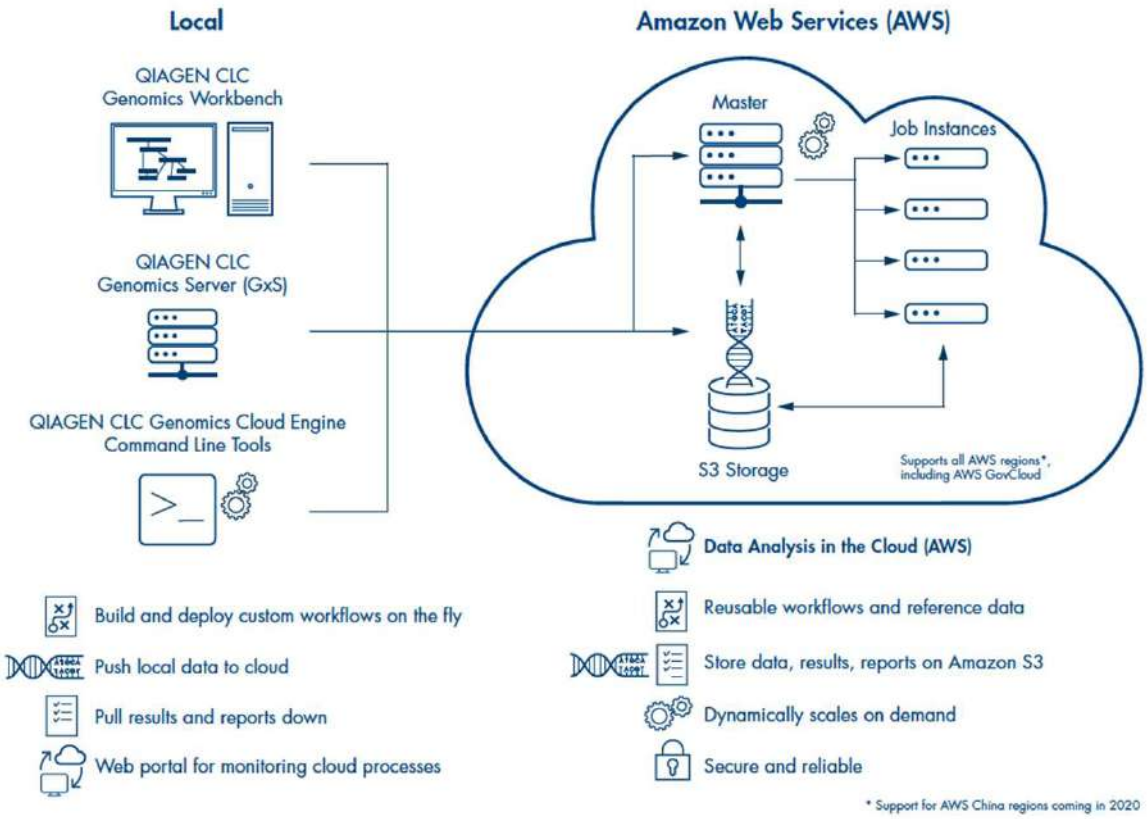
- Easy to install and manage
- Distributes workload across multiple dedicated job nodes
- Uses built in QIAGEN CLC queueing system
- Scalable to hundreds of nodes and users

Master server + GRID nodes



- Fully integrates into existing HPC clusters
- Supports DRMAA-compatible schedulers, i.e. UNIVA, SLURM, LFS, PBS
- Enterprise-level user management and scalability

Cloud-based enterprise solution: QIAGEN CLC Genomics Cloud Engine



- Avoid hardware purchasing and IT bureaucracy
- Scales immediately and on-demand
- Your compute & storage on Amazon AWS
- Access via CLC Genomics Workbench, Command Line Tools or REST API interface

amazon web services

QIAGEN CLC Genomics Cloud Engine administration

Supported AWS regions

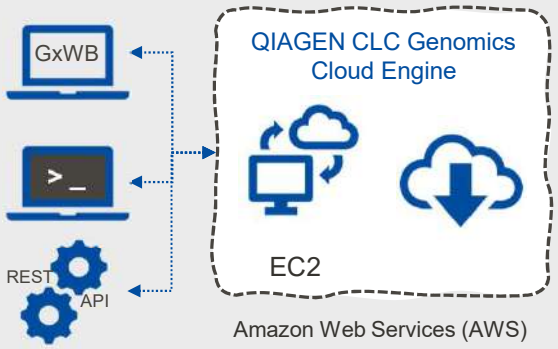
Region	Code
N. Virginia	us-east-1
Ohio	us-east-2
N. California	us-west-1
Oregon	us-west-2
Frankfurt	eu-central-1
Ireland	eu-west-1
Tokyo	ap-northeast-1
Seoul	ap-northeast-2
Sydney	ap-southeast-2
Mumbai	ap-south-1
GovCloud (US-East)	us-gov-east-1
GovCloud (US-West)	us-gov-west-1

Administration task

GCE Command Line Tools	• Changing running environment • Switch to another embedded version of the Genomics server • Updating or upgrading a GCE licenses • Adding and updating CLC Genomics Server Plugins
AWS Elastic Beanstalk Management Console	• Change autoscaling behavior • Change or configure instance types used • Modifying OAuth configuration • Configure and enabling automatic platform updates
AWS DynamoDB Management Console	• Enter or exit from maintenance mode • Enable or configure signed URLs for files stored on S3
AWS CloudWatch	• Inspect license usage metrics and jobs • Monitor, inspect, and export the log files created • Changing Log Retention

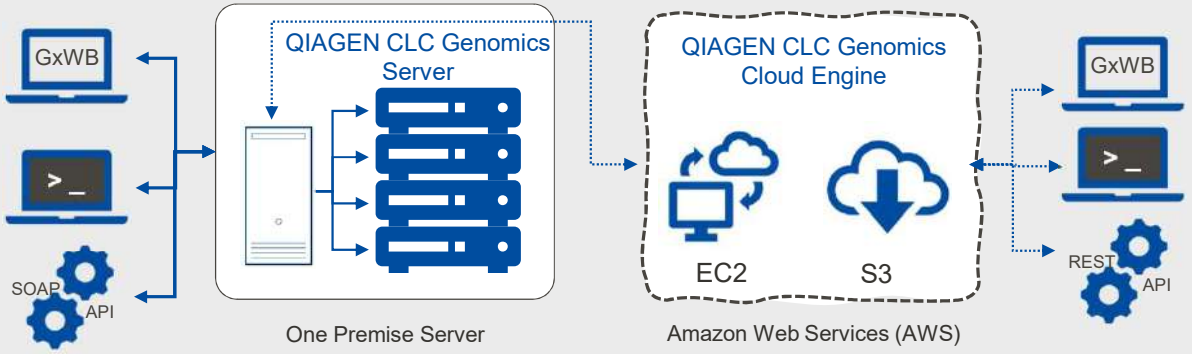
QIAGEN CLC Genomics Cloud Engine – two deployment models

Stand-alone cloud deployment



- Instantly run any QIAGEN CLC workflow in the cloud
- Installed, managed and runs on your Amazon AWS account
- Connect from QIAGEN CLC Workbench, command-line or REST interface

Hybrid server or cloud deployment



- Seamless extend existing QIAGEN CLC Genomics Server installations
- Provides virtual queues to offload workflows into the cloud
- Eliminates additional capital expenditures

- Multiple, secure access points via Workbench, Server, Command Line Tool or REST interface
- Web-based administration and job-monitoring tool
- QIAGEN Digital Insights expert installation and support

Educational Training License Program

Free QIAGEN CLC Genomics Workbench licenses for academic classroom settings

- Up to 30 licenses per academic course
- Available only to academic customers with active licenses for QIAGEN CLC Genomics Server or QIAGEN CLC Genomics Cloud Engine

Contact us for details: **bioinformaticssales@qiagen.com**

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Thank you for your attention. Questions?