



QIAGEN Digital Insights

QIAGEN CLC Product Profolio



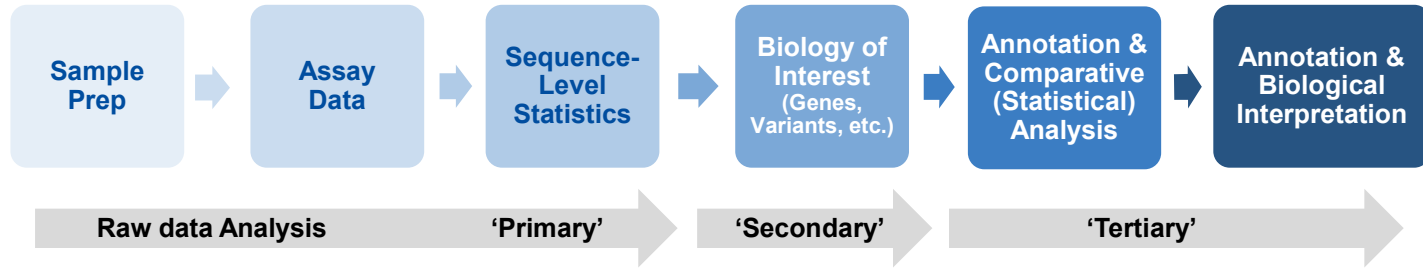
Amit Chaurasia, PhD

Associate Sales Development Manager

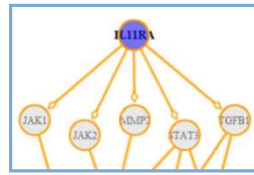
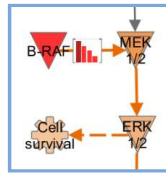
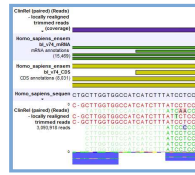
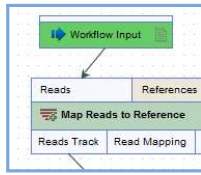
QIAGEN Digital Insights



QIAGEN Digital Insights solution

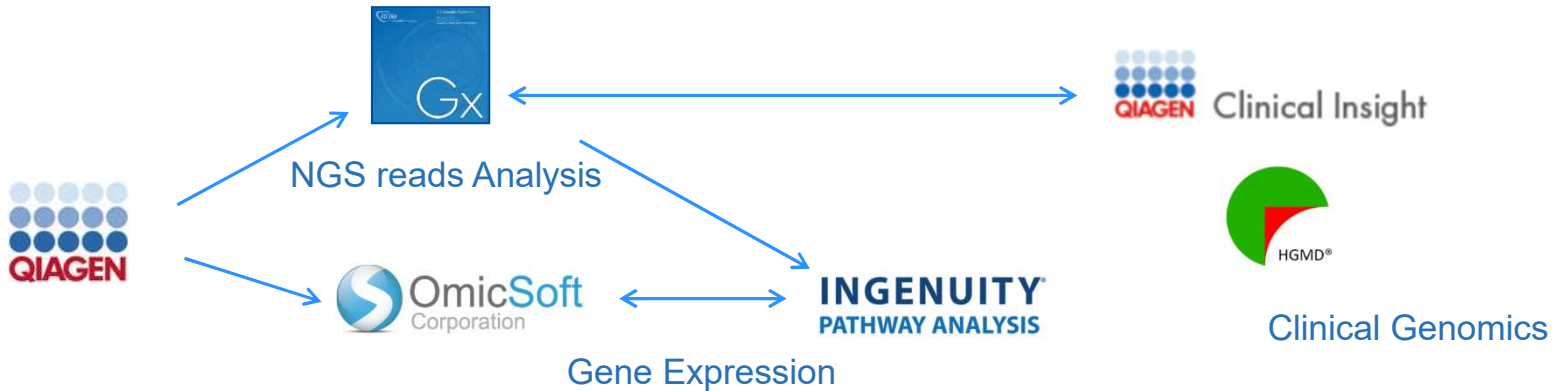


Sample



BRAF c.1798_1799del... p.V600K Likely Pathogenic	BRCA1 c.68_69delAG p.E23fs*17
MYBPC3 c.1624G>C p.E542Q Likely Pathogenic	PIK3CA c.3075C>T p.T1025T Benign

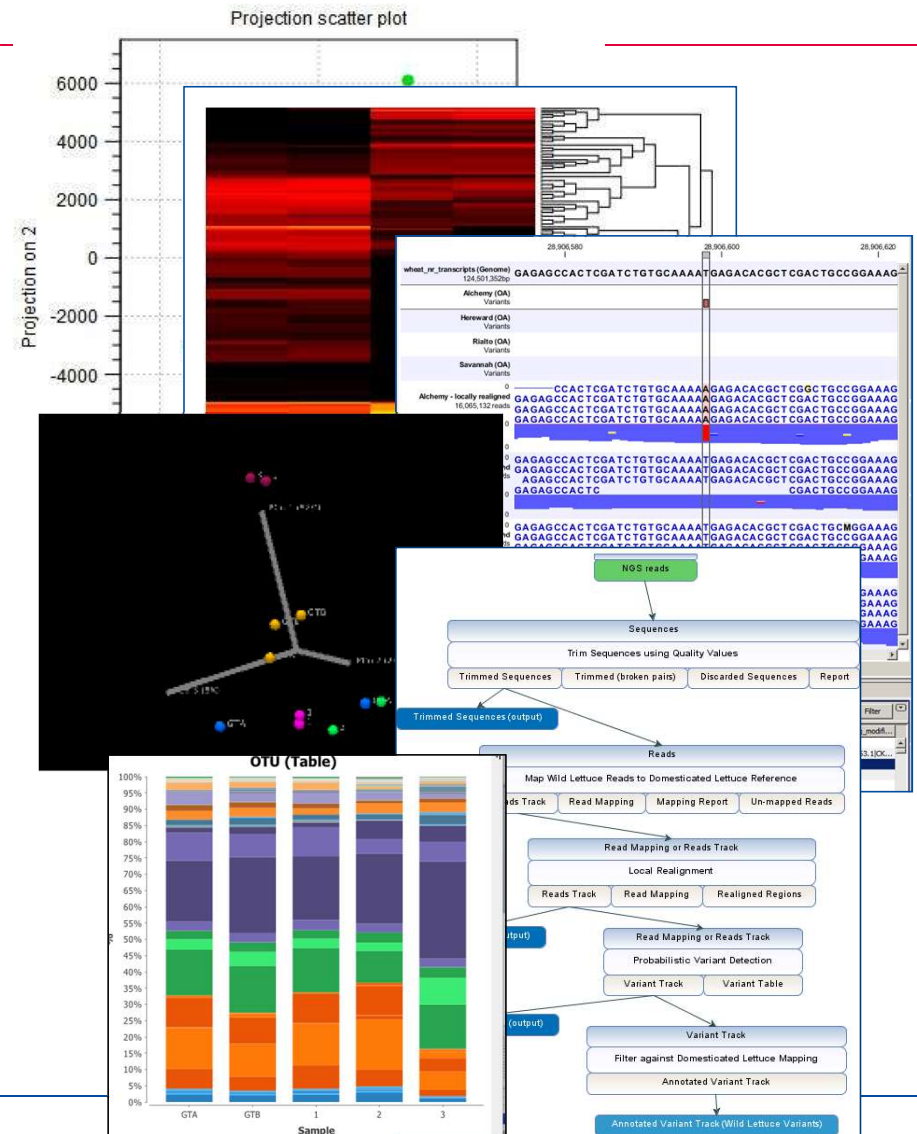
Insight





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



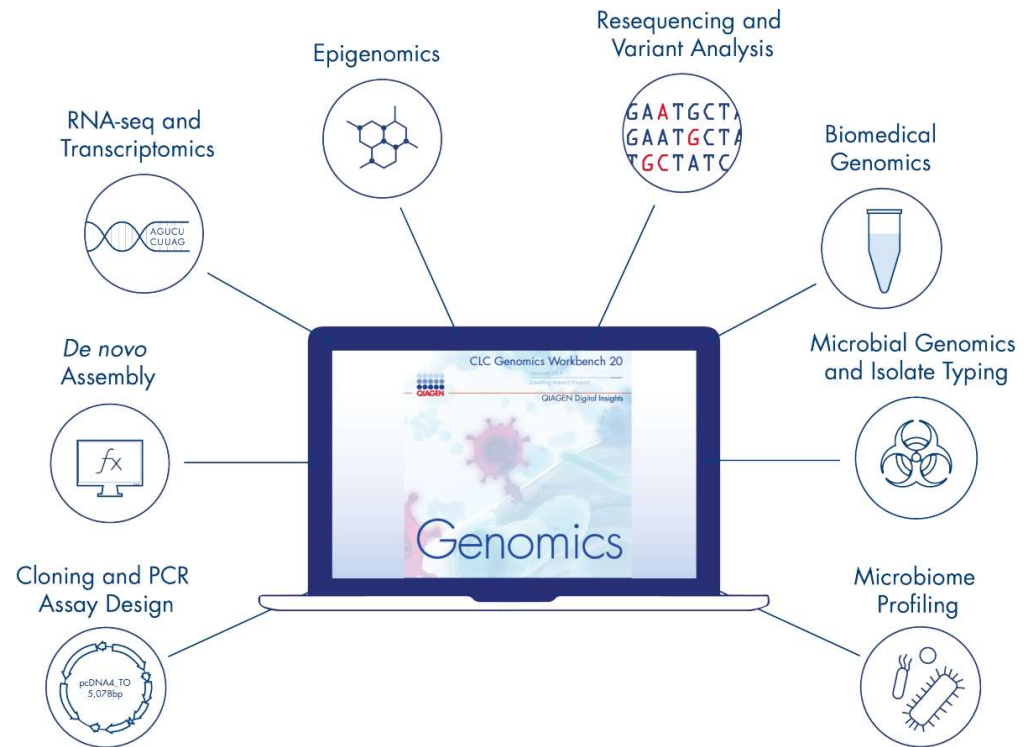
QIAGEN CLC Genomics Workbench

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



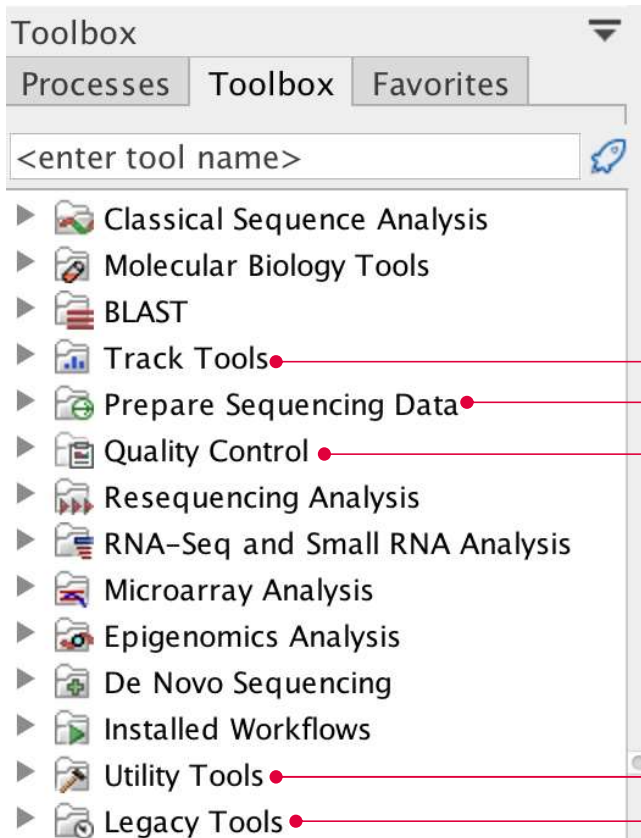
QIAGEN CLC Genomics Workbench features

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

Tools

- Genome Finishing Module
- GeneMark Gene Finding
- Microbial Genomics Module
- Long Read Support (beta)
- Blast2GO
- Classical Sequence Analysis
- Whole Genome Alignment (beta)
- Molecular Biology Tools
- BLAST
- Track Tools
- Prepare Sequencing Data
- Quality Control
- Resequencing Analysis
 - Trim Primers and their Dimers from Mapping
 - Map Reads to Reference
 - Prepare Guidance Variant Track
 - Local Realignment
 - Merge Read Mappings
 - Remove Duplicate Mapped Reads
 - Extract Consensus Sequence
 - Variant Detection
 - Basic Variant Detection
 - Fixed Ploidy Variant Detection
 - Low Frequency Variant Detection
 - InDels and Structural Variants
 - Advanced Structural Variant Detection (beta)
 - Identify Known Mutations from Mappings
 - Copy Number Variant Detection (CNVs)
- RNA-Seq and Small RNA Analysis
- Microarray Analysis
- Epigenomics Analysis
- De Novo Sequencing
 - De Novo Assembly
 - Map Reads to Contigs



One Click workflow on CLC Genomics Workbench

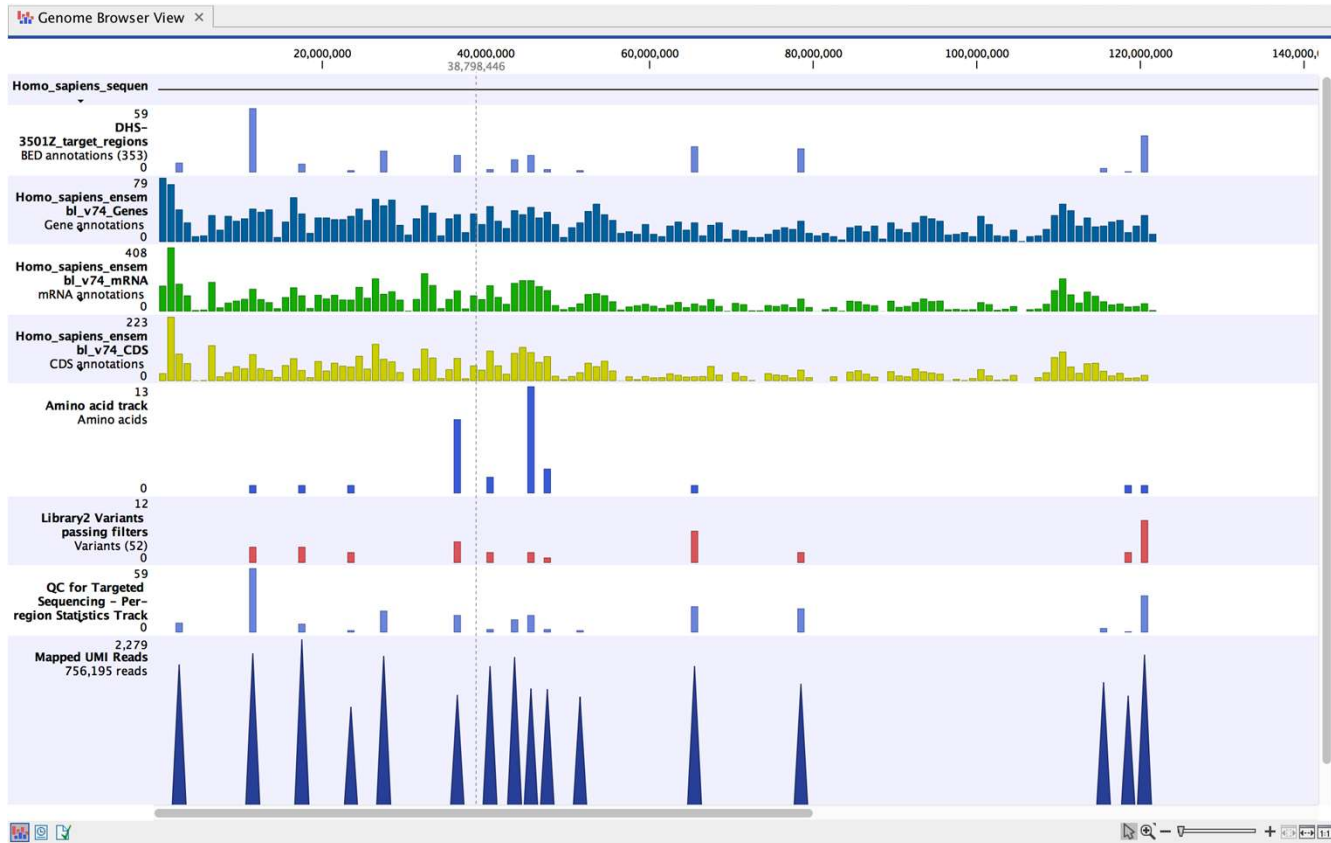
The screenshot displays the CLC Genomics Workbench 9.0.1 interface. The main window shows a genomic track with various annotations, including reads, gene models, and variant calls. A coverage distribution graph is overlaid on the track, showing the number of positions versus the number of reads. A dialog box titled "Build Functional Profile (Sun Apr 10 07:06:59 BST 2016)" is open, displaying the following information:

Build Functional Profile (Sun Apr 10 07:06:59 BST 2016)
Version: CLC Genomics Workbench 8.5
User: BonnerT
Parameters:
Reference = Not set
GO database = GO database - Tutorial subset
GO subset = Complete GO basic
Propagate GO mapping = Yes
profile = No
profile = Yes
lional profile = No

At the bottom of the interface, a table shows the results of a BLAST search:

Chromosome	Region	Type	Reference	Allele	Reference ...	Length	Zipity	Count	Coverage	Frequency	Probability	Forward re...	Reverse re...	Forward...
7	144045236	SNV	A	A	Yes	1	Heterozygous	242	328	87.80	1.00	1489	1114	0.46
11	115207144	SNV	C	G	No	1	Heterozygous	8690	2930	32.27	1.00	8688	8607	0.50
11	118799114	SNV	C	T	No	1	Heterozygous	4494	1494	33.24	1.00	4492	4492	1.00

Genome Browser Visualization





More Variant Annotations for DNA

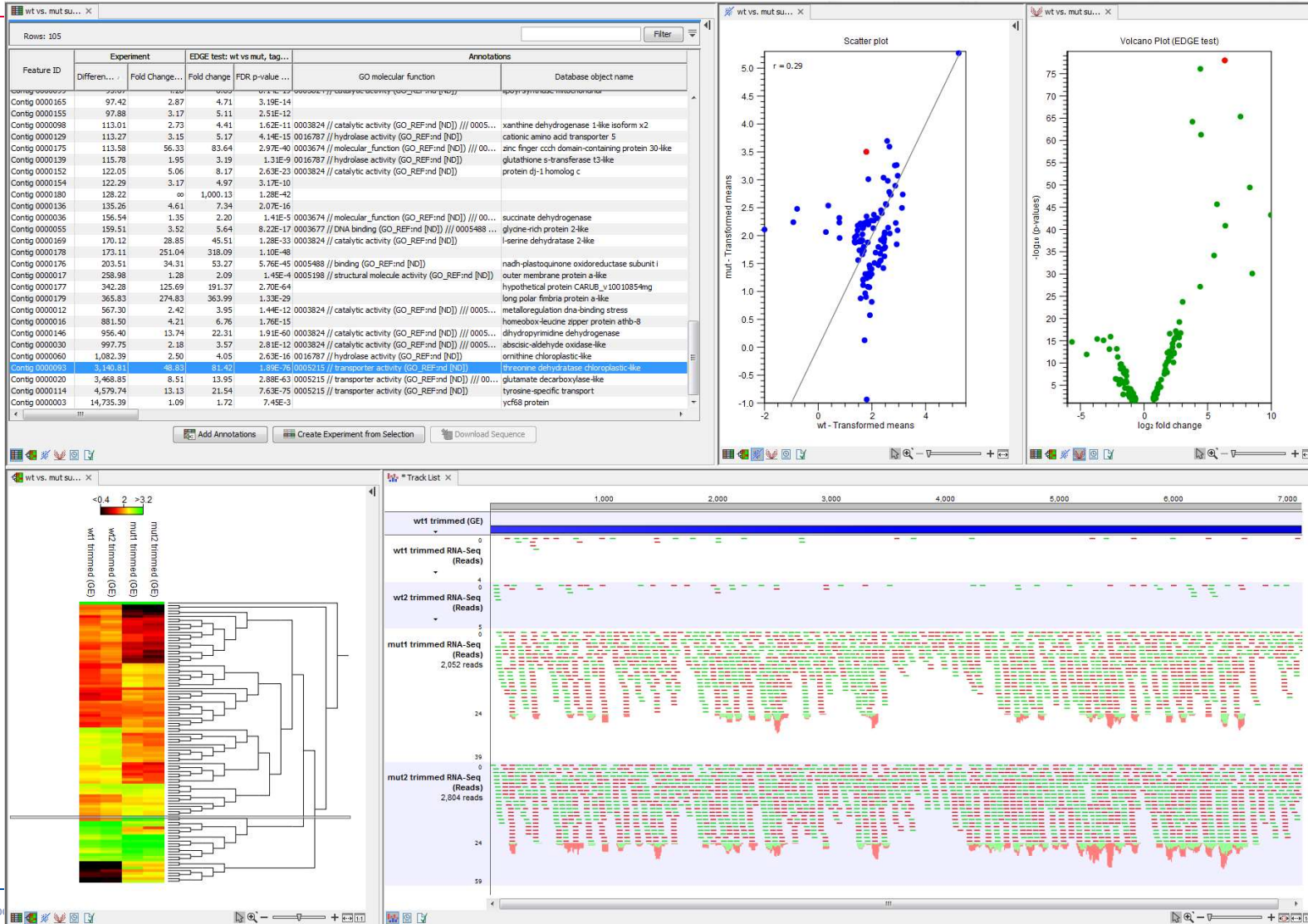
- Chromosome
- Region
- Type
- Reference
- Allele
- Reference allele
- Length
- Linkage
- Zygosity
- Count
- Coverage
- Frequency
- Probability
- Forward read count
- Reverse read count
- Forward/reverse balance
- Average quality
- Read count
- Read coverage
- # unique start positions
- # unique end positions
- BaseQRankSum
- Read position test probability
- Read direction test probability
- Homopolymer
- Homopolymer length
- QUAL
- Count (singleton UMI)
- Count (big UMI)

- Proportion (singleton UMIs)
- Homo_sapiens_ensembl_v74_Genes
- Gene Cards
- ENSEMBL
- Homo_sapiens_ensembl_v74_mRNA
- source (Homo_sapiens_ensembl_v74_mRNA)
- ENSEMBL (Homo_sapiens_ensembl_v74_mRNA)
- gene_name (Homo_sapiens_ensembl_v74_mRNA)
- gene_biotype (Homo_sapiens_ensembl_v74_mRNA)
- transcript_name (Homo_sapiens_ensembl_v74_mRNA)
- Coding region change
- Amino acid change
- Amino acid change in longest transcript
- Coding region change in longest transcript
- Other variants within codon
- Non-synonymous
- mRNA Accession
- Exon Number

These include:

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

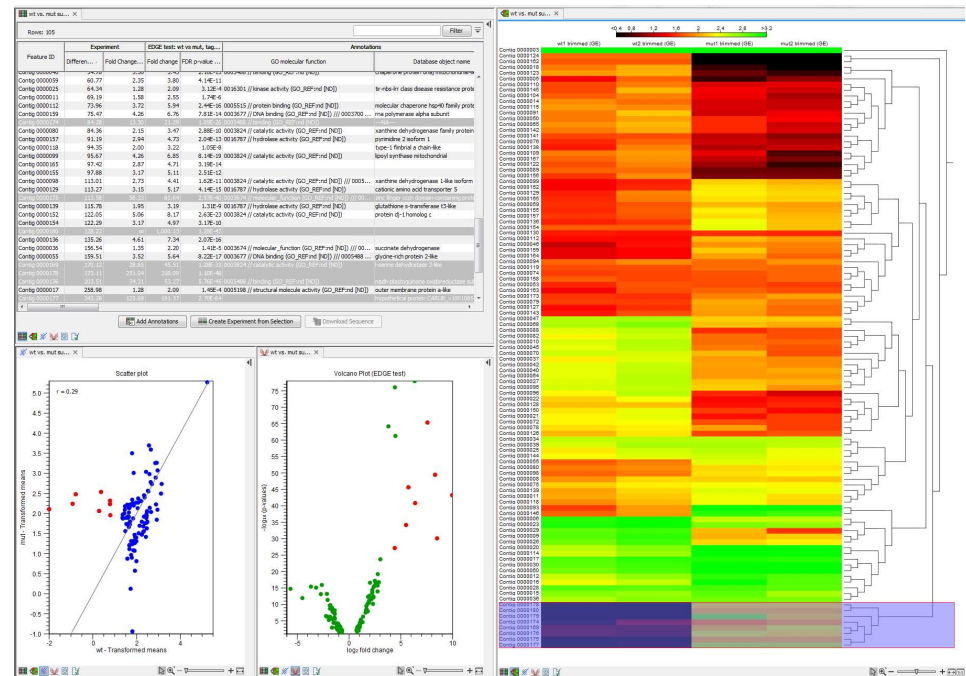
INTERACTIVE VISUALIZATION – NAVIGATE TO MAPPING



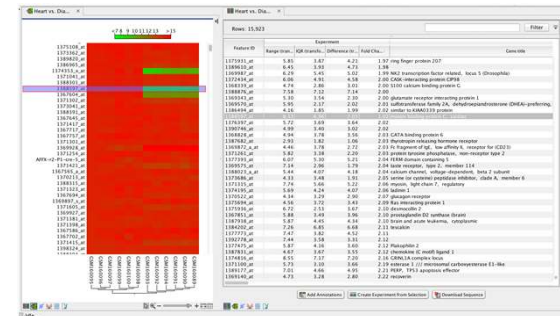
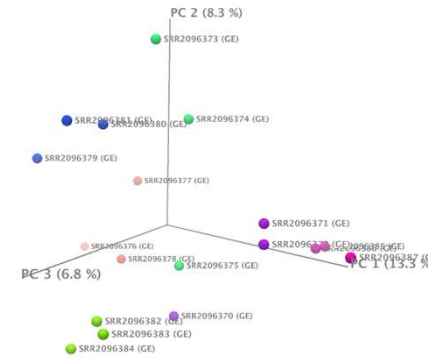
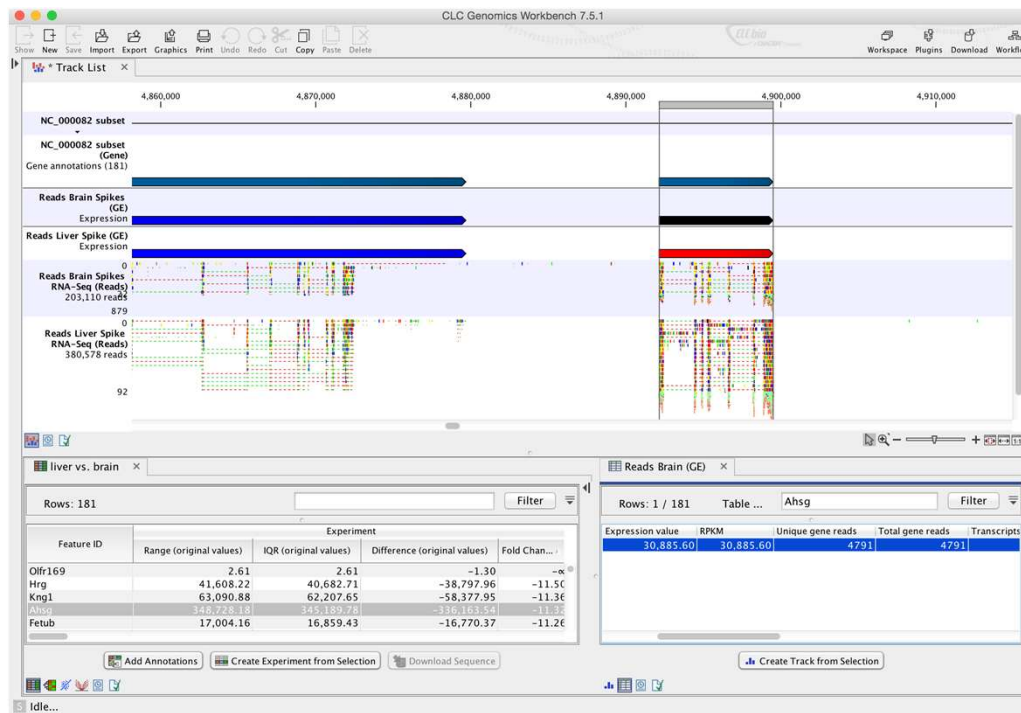
Transcriptomics Data analysis on CLC Genomics Workbench

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



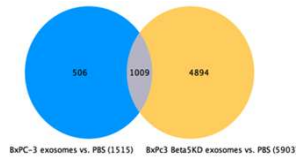
RNA-Seq, Microarrays, Statistical Expression Analysis



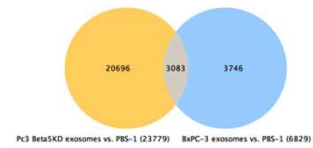
Analyze Expression Data and Upload Comparisons to IPA

- PCA for RNA-Seq
- Heat Map for RNA-Seq
- ExPC-3 exosomes vs. PBS
- ExPC3 Beta5KD exosomes vs. PBS
- Venn Diagram
- Analyze Expression Data and Upload Comparisons to IPA log
- ExPC3 Beta5KD exosomes vs. PBS-1
- ExPC-3 exosomes vs. PBS-1
- Heat Map for RNA-Seq-1
- Venn Diagram-1
- PCA for RNA-Seq-1
- Analyze Expression Data and Upload Comparisons to IPA log-1
- ExPC3 Beta5KD exosomes vs. ExPC-3 exosomes
- Heat Map for RNA-Seq-2
- Venn Diagram-2
- PCA for RNA-Seq-2
- Analyze Expression Data and Upload Comparisons to IPA log-2
- ExPC3 Beta5KD exosomes vs. ExPC-3 exosomes-1
- Venn Diagram-3
- PCA for RNA-Seq-3
- Heat Map for RNA-Seq-3
- Analyze Expression Data and Upload Comparisons to IPA log-3

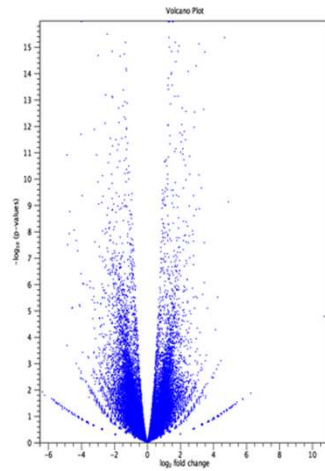
Venn Diagram (GE)



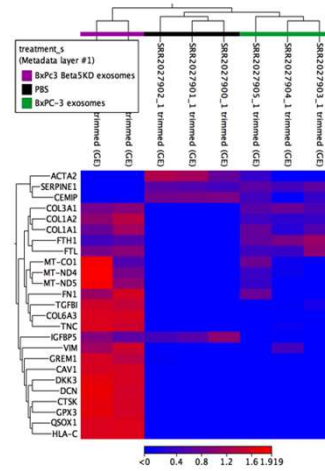
Venn Diagram (TE)



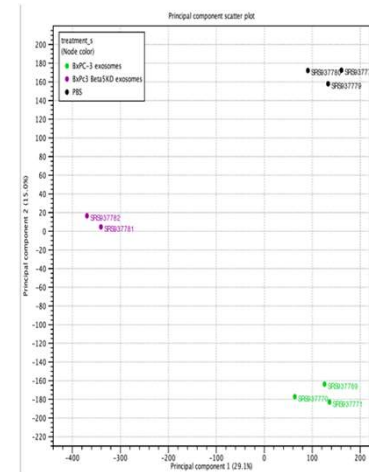
Volcano Plot



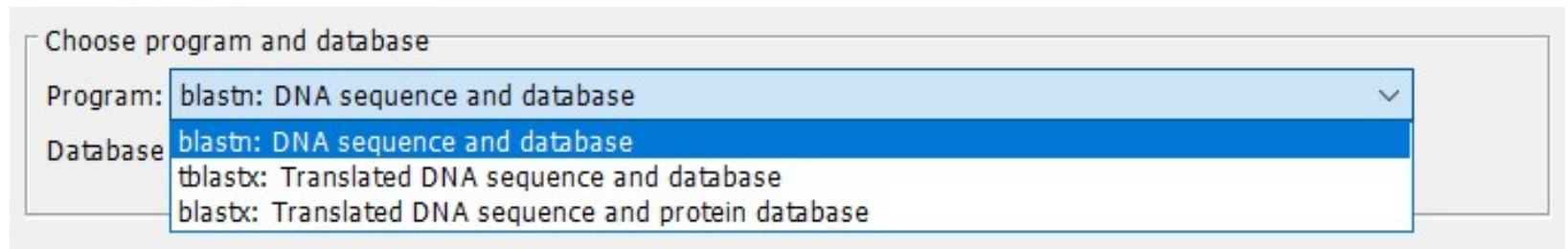
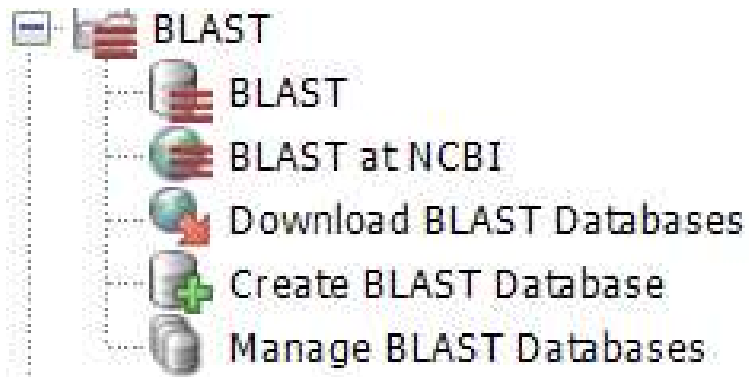
Heat Map



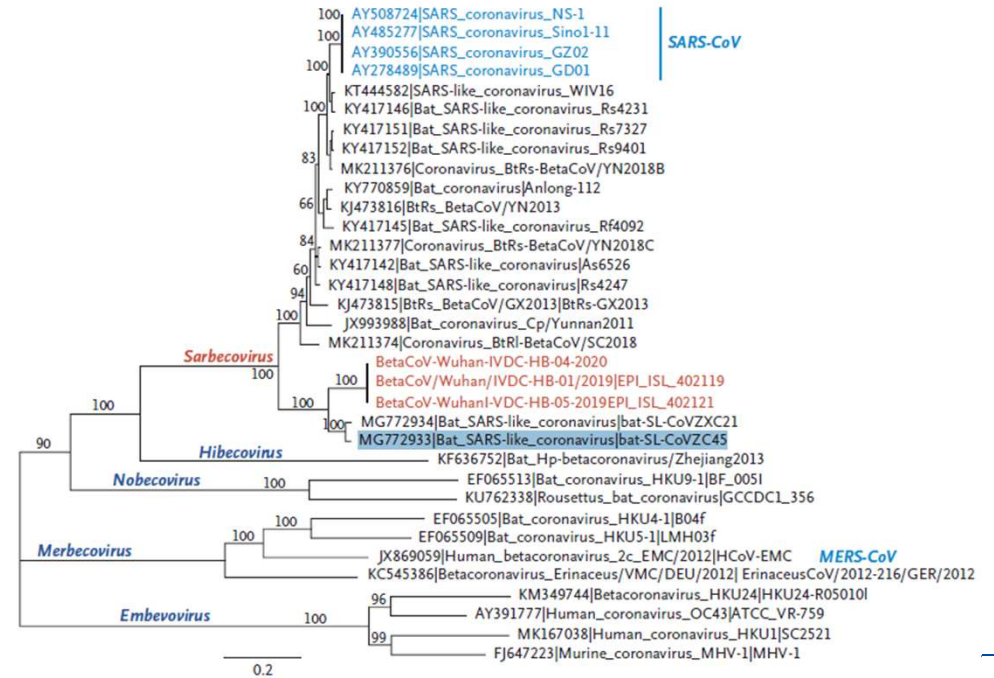
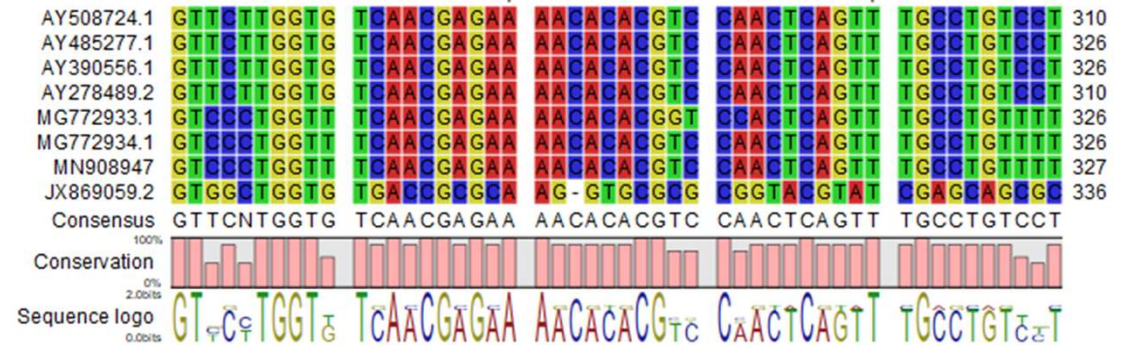
PCA plot



Genome annotation



Multi-sequence alignment



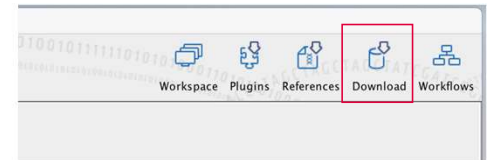
Software interface showing the 'Alignments and Trees' menu with options like 'Create Alignment...', 'Join Alignments...', 'Create Pairwise Comparison...', 'K-mer Based Tree Construction...', 'Create Tree...', 'Model Testing...', and 'Maximum Likelihood Phylogeny...'.

The reference data manager

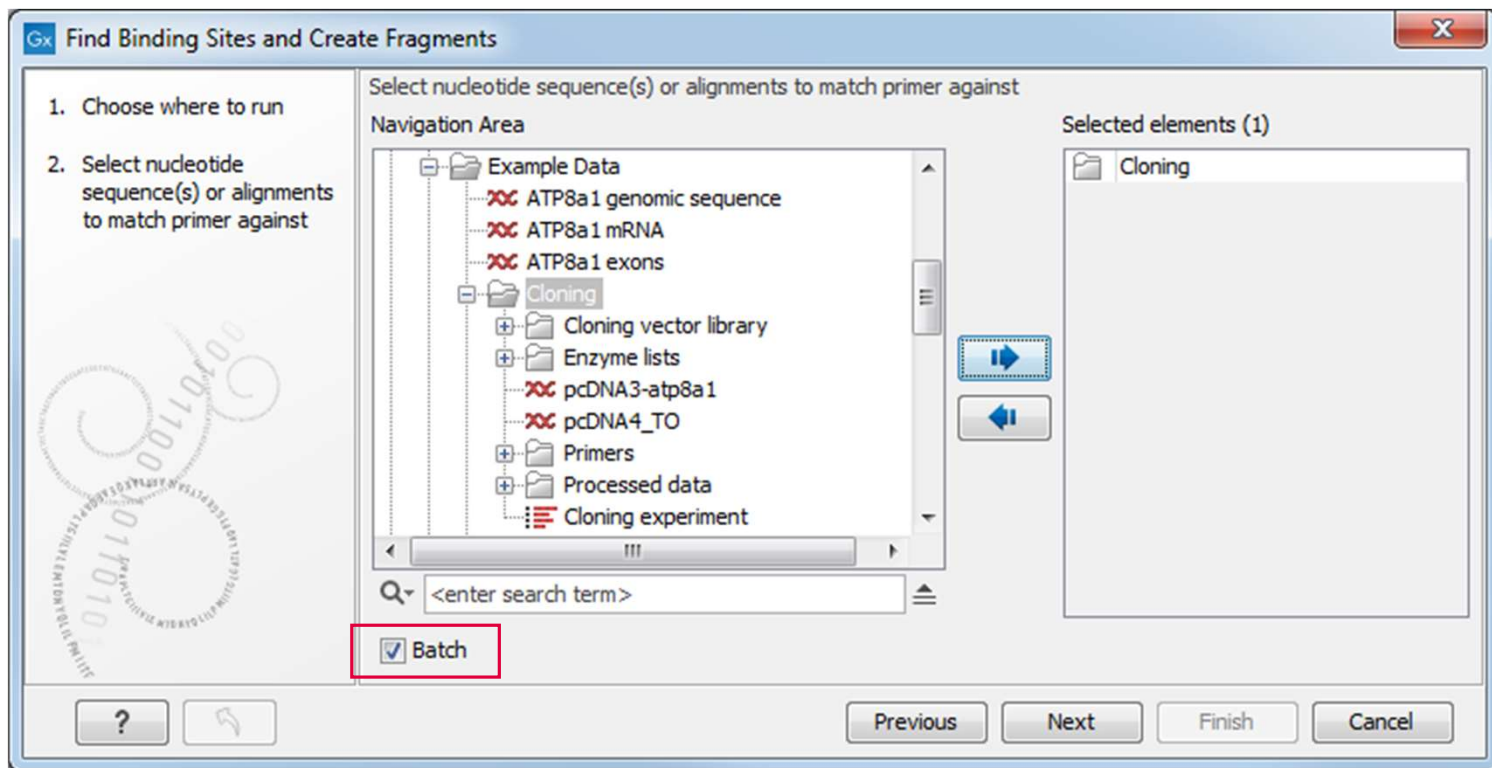
Convenient download of reference genomes and panel BED files

The screenshot displays the 'Manage Reference Data' application window. The interface is divided into several sections:

- Navigation Bar:** Includes icons for 'Download Genomes (Public Repositories)', 'QIAGEN Sets (Reference Data Library)', 'Custom Sets (Reference Data Sets)', and 'Imported Data (Imported Reference Data)'. A dropdown menu is set to 'Locally'. Storage information is shown: 'Free space in CLC_References location: 34.21 GB' and 'Free space in temporary folder location: 34.21 GB'.
- Species List (Left Panel):** A list of animal species under the heading 'Animal (mammals)'. Each entry includes a download icon and a description:
 - Bos taurus – Hereford: Select to download latest data for Bos taurus – Hereford
 - Canis lupus familiaris: Select to download latest data for Canis lupus familiaris
 - Equus caballus: Select to download latest data for Equus caballus
 - Homo sapiens – hg18: Select to download latest data for Homo sapiens – hg18
 - Homo sapiens – hg19: Select to download latest data for Homo sapiens – hg19
 - Homo sapiens – hg38: Select to download latest data for Homo sapiens – hg38
 - Mus musculus: Select to download latest data for Mus musculus
 - Rattus norvegicus: Select to download latest data for Rattus norvegicus
 - Sus scrofa: Select to download latest data for Sus scrofa
- Reference Data List (Right Panel):** A list of specific reference data items, each with a download icon:
 - Ensembl v74, dbSNP v138, ClinVar 20131203
 - QIAGEN GeneRead Panels hg19 (RefSeq GRCh37.p13, dbSNP v150, ClinVar 20171029)
 - QIaseq Small RNA (mirBase v22)
 - QIaseq RNAscan Panels hg38 (RefSeq GRCh38.p9)
 - QIaseq DNA Panels hg19 (Ensembl v74)
 - QIaseq RNA Panels hg38 (RefSeq GRCh38.p9)
 - QIaseq TMB Panels hg38 (RefSeq GRCh38.p12 (no alternative analysis set))
 - QIaseq UPX 3' Panels hg38 (RefSeq GRCh38.p12 (no alternative analysis set))
 - QIaseq Methyl Panels hg38 (RefSeq GRCh38.p12 (no alternative analysis set))
 - QIaseq Methyl Panels hg19 (Ensembl v74)
 - QIaseq RNA Fusion XP Panels hg38
- Bottom Bar:** Contains 'Help' and 'Close' buttons.



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.

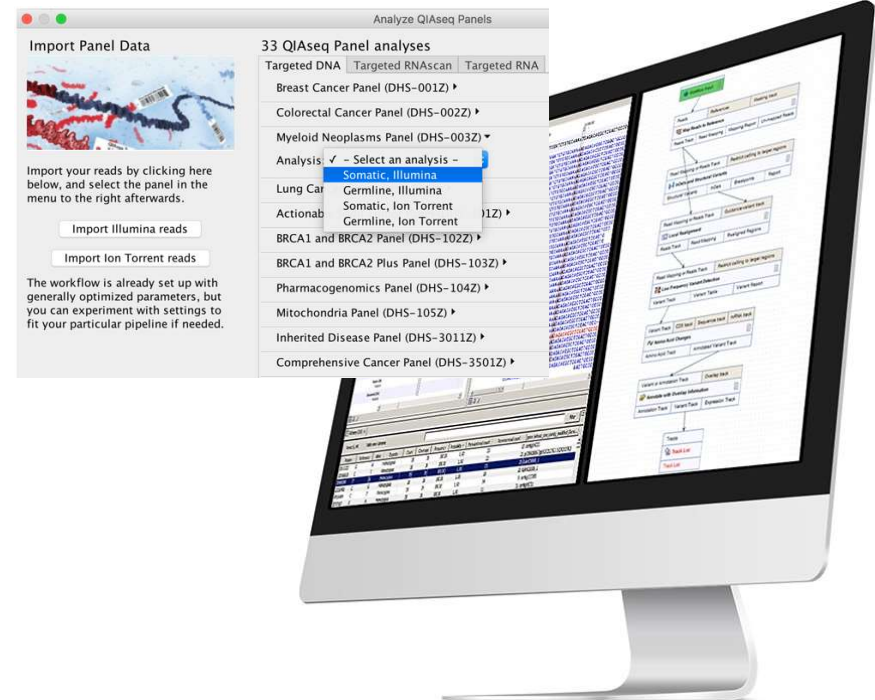
Source: Lab Director, Medium Enterprise Health Care Company

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*



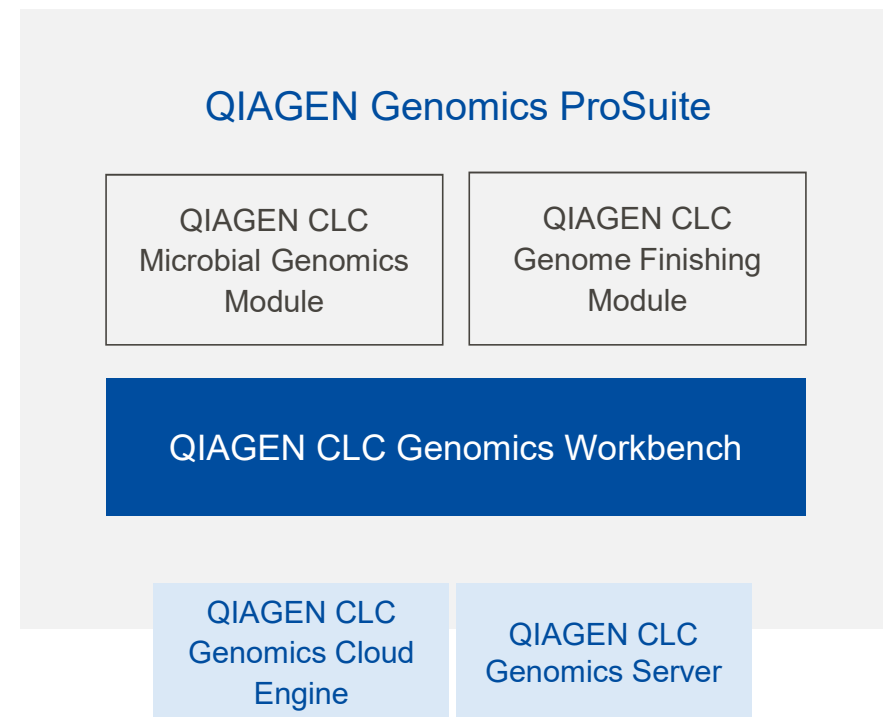
Key functionalities:

- 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

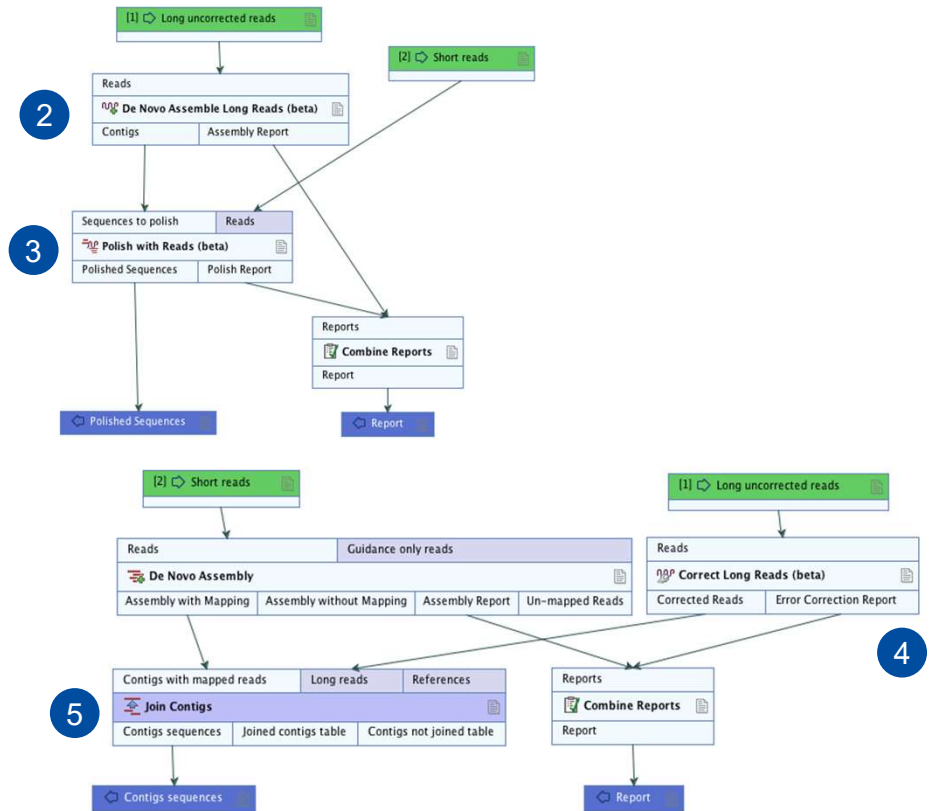
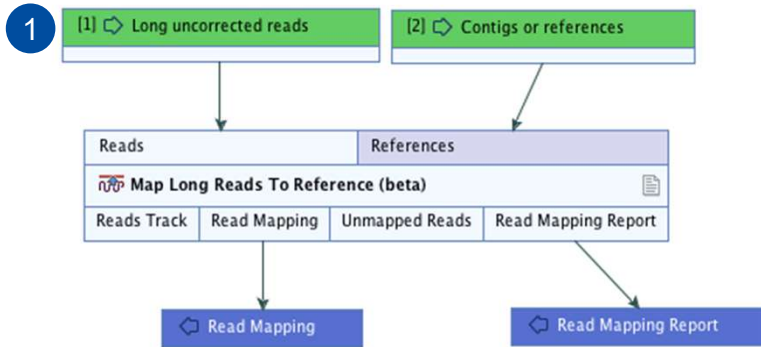


* Formerly "QIAGEN Microbial Genomics ProSuite"

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

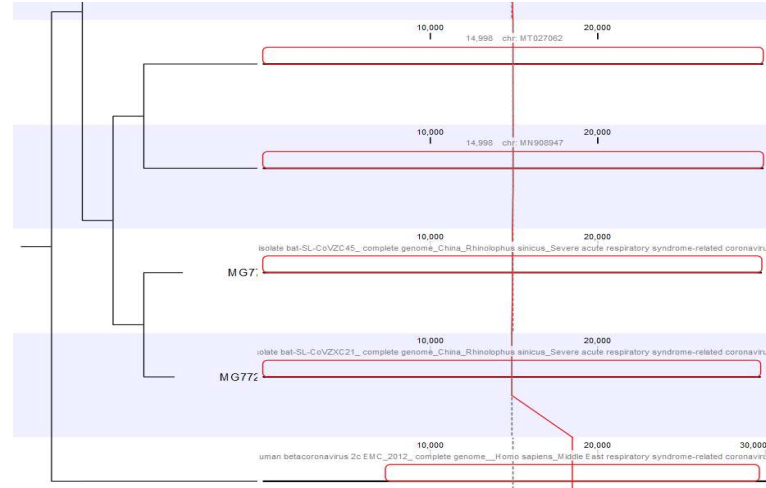
Support for PacBio data and Oxford Nanopore data

- 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

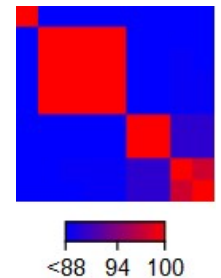


Whole Genome Alignment (beta) – free plug-in

- Whole Genome Alignment (beta)**
- Create Whole Genome Dot Plot (beta)
- Create Whole Genome Alignment (beta)
- Create Average Nucleotide Identity Comparison (beta)
- Create Tree from Comparison (beta)
- Create Heat Map from Comparison (beta)
- Extract Multiple Sequence Alignment (beta)



	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



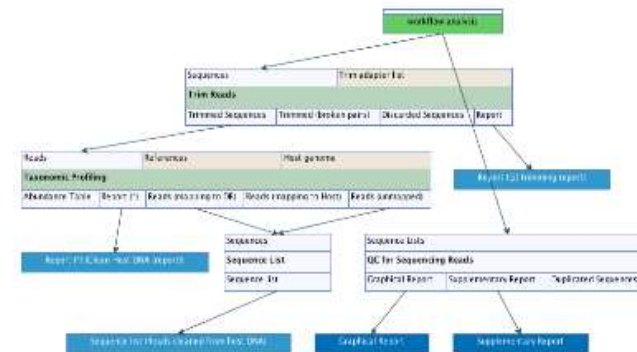
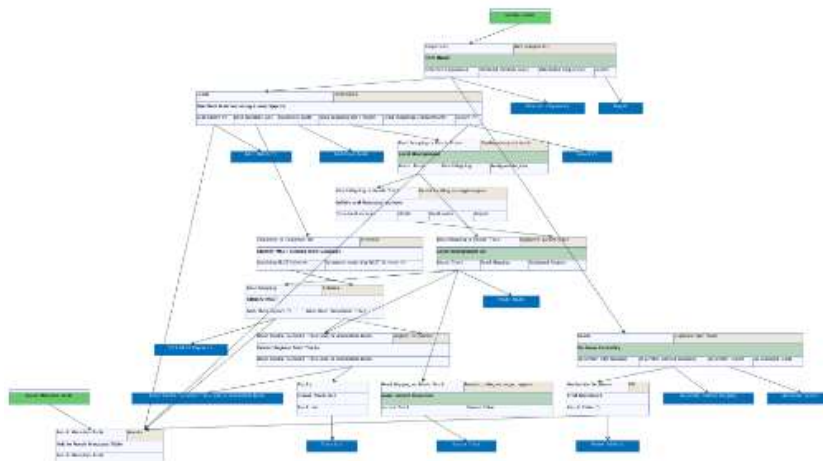
TechValidate
by Forrester

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

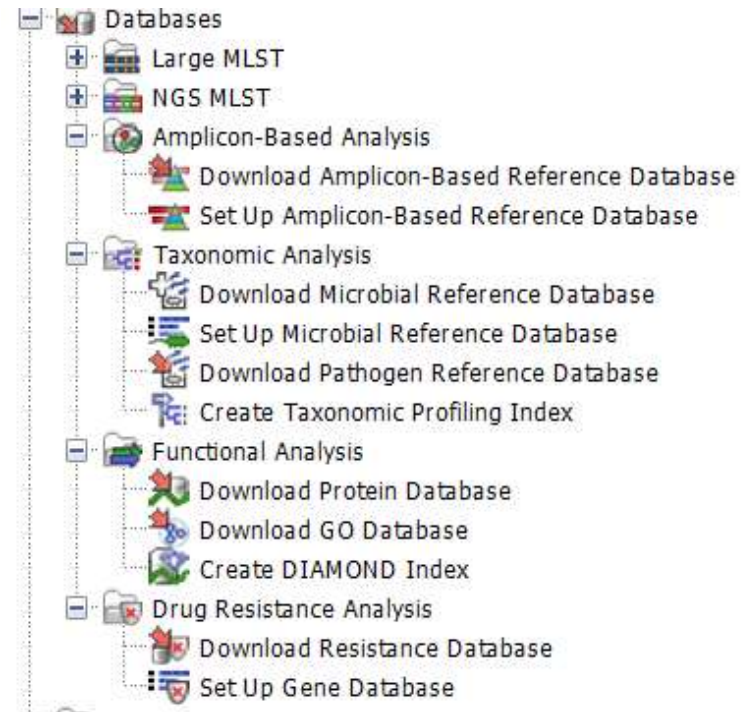
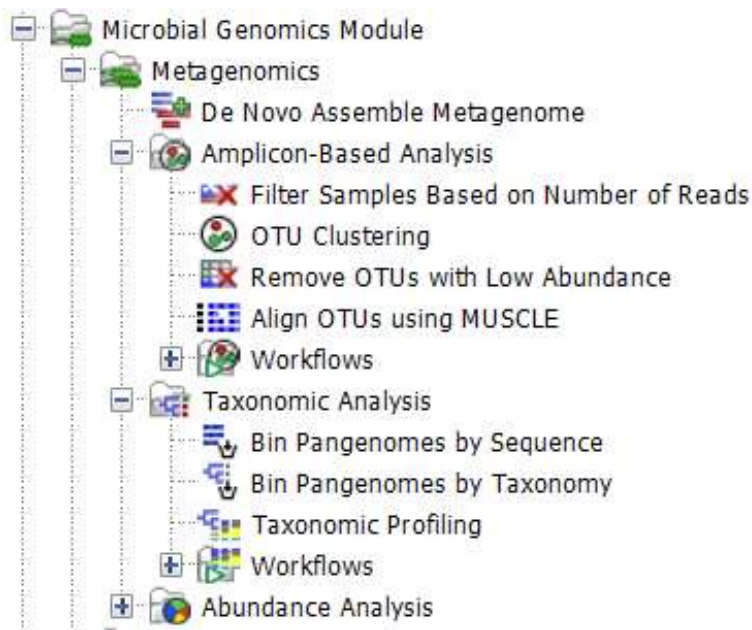


Workflows

- 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

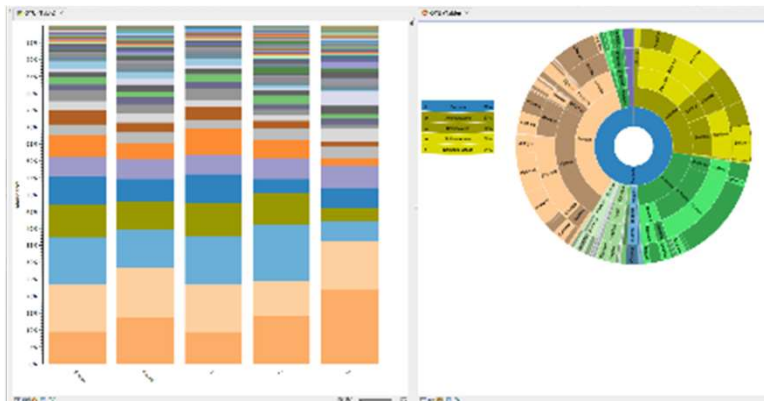


Build-in workflow + download / integrated database in QIAGEN CLC Microbial Genome Module

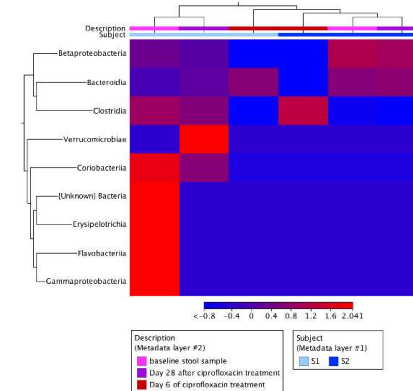


Amplicon-based profiling

- 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](#)



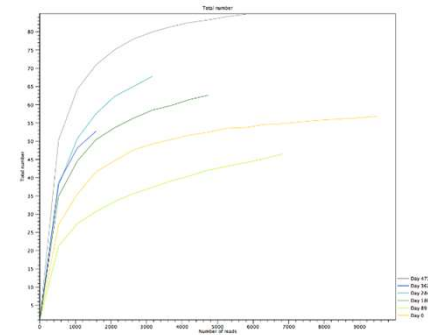
Webinar: [Microbiome profiling from day one](#)

Whole genome shotgun metagenomics

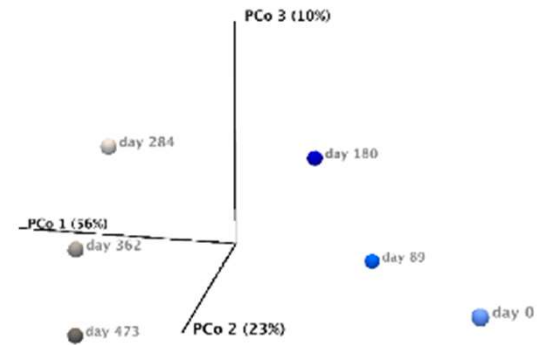
- Microbiome profiling based on shotgun data
- Direct access to microbial genome reference databases
 - Optimized to run on standard laptop
- Comparison of abundance across samples
- Estimation of diversity
- Functional annotation of metagenomes
 - Gene finding
 - Annotation with DIAMOND, BLAST and Pfam



Webinar: [Taxonomic profiling using shotgun metagenome data](#)

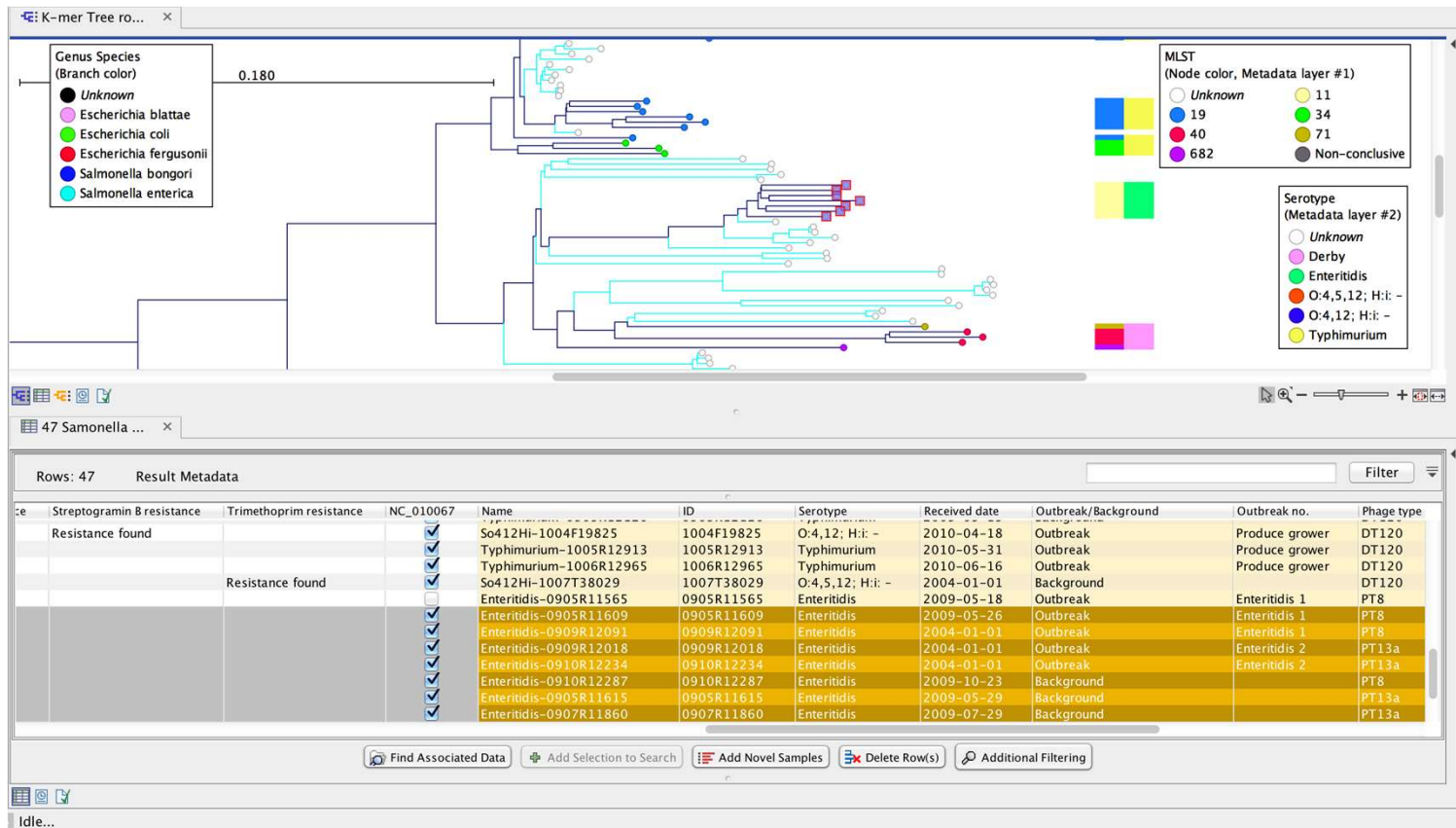


Visualization of alpha diversity






























Principal component analysis plot of beta diversity within a microbial community

Pathogen typing - primary output is an analysis dashboard

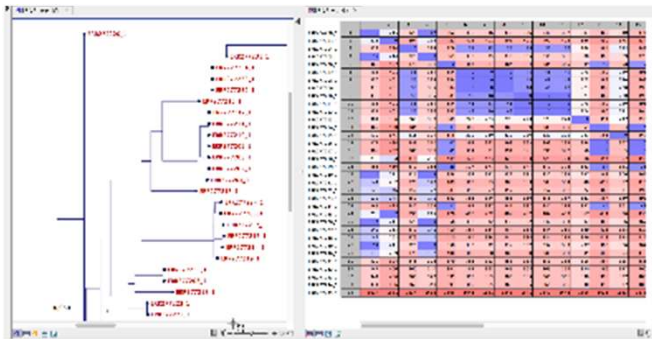


Toolbox

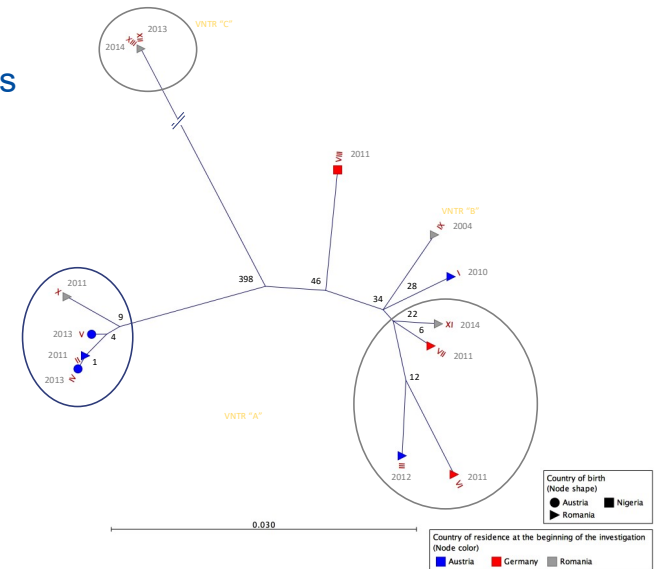
-  Launch Ctrl+Shift+T
-  Genome Finishing Module >
-  GeneMark Gene Finding >
-  Ready-to-Use Workflows >
-  **Microbial Genomics Module** >
 -  Metagenomics >
 -  **Typing and Epidemiology** >
 -  Find Best Matches using K-mer Spectra...
 -  Create K-mer Tree...
 -  **Create SNP Tree...**
 -  Extract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

Tracing pathogen outbreaks

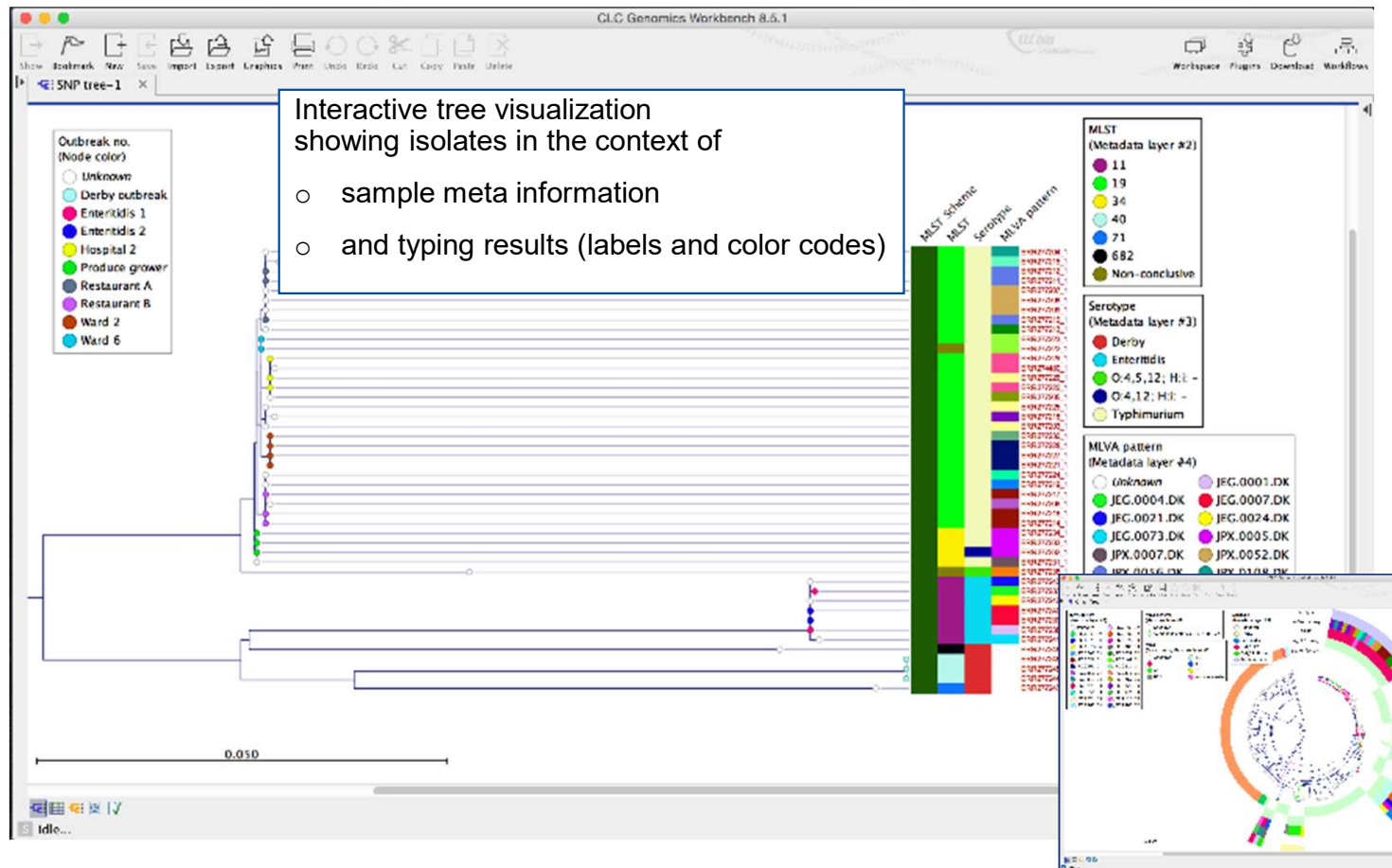
- Analyzing strain relatedness at maximum resolution
- Genome-wide comparison of single nucleotide polymorphisms
- Visualization of results
 - Dendrogram decorated with metadata
 - SNP matrix



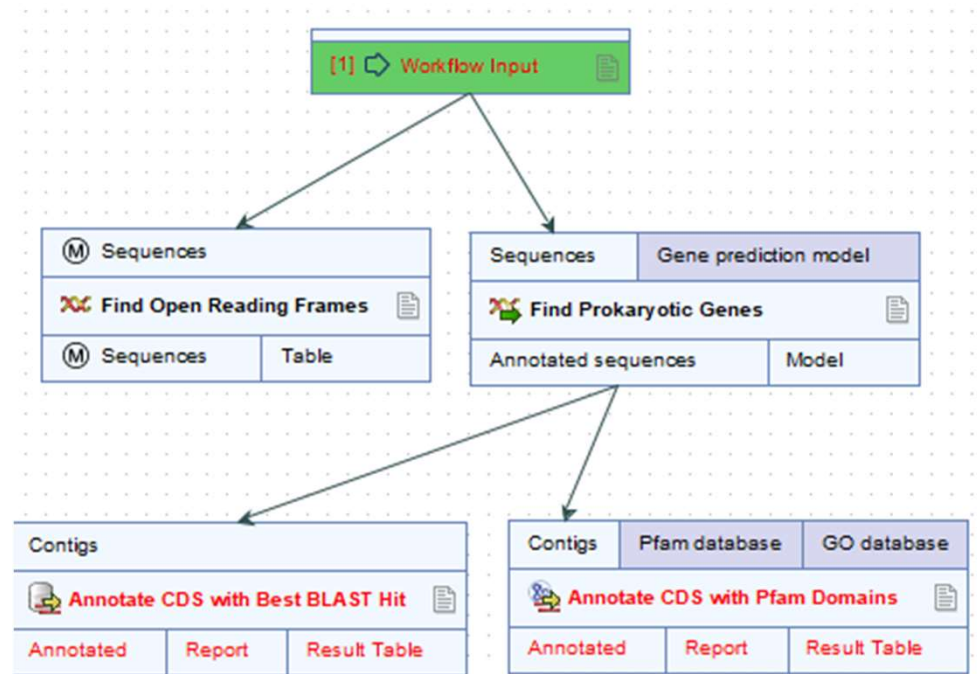
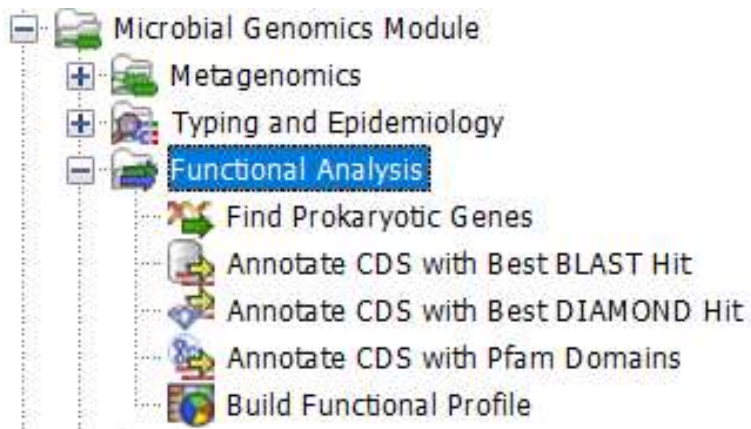
White paper: [High-resolution outbreak tracing and resistance detection using WGS in the case of a *Mycobacterium tuberculosis* outbreak](#)



Pathogen typing – outbreak analysis at highest resolution



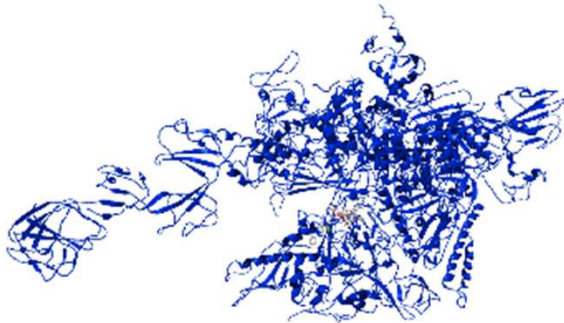
Advanced functions on QIAGEN CLC Microbial Genomics Module



*The workflow can be customized

Detection of antimicrobial resistance markers

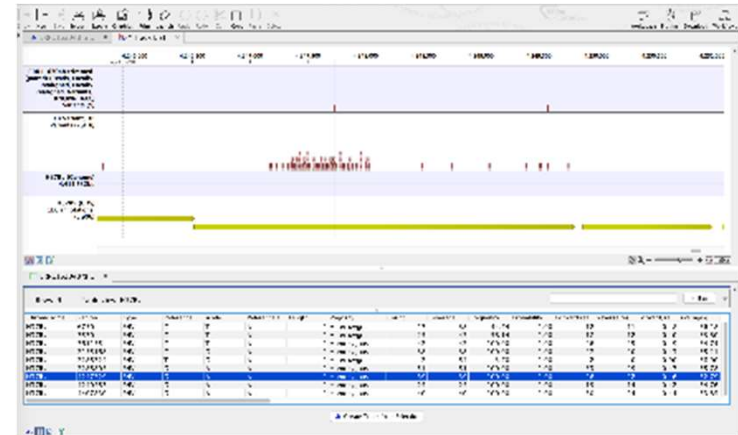
- AMR gene finding with ResFinder
- Calling AMR causing mutations with PointFinder
- Detect ARG-ANNOT resistance markers with ShortBRED
- Resolve plasmids from chromosomal regions



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



Poster: [Whole genome sequencing for antimicrobial resistance detection and surveillance](#)



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

Download Resistance Database

1. Choose where to run
2. **Database to download**
3. Terms of use
4. Result handling

Database to download

ShortBRED Marker Databases

- QMI-AR
- CARD
- ARG-ANNOT

Nucleotide Databases

- QMI-AR
- VFDB
- CARD
- ResFinder

Point Mutation Databases

- PointFinder

Integrated Databases

- ARES Database

× 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

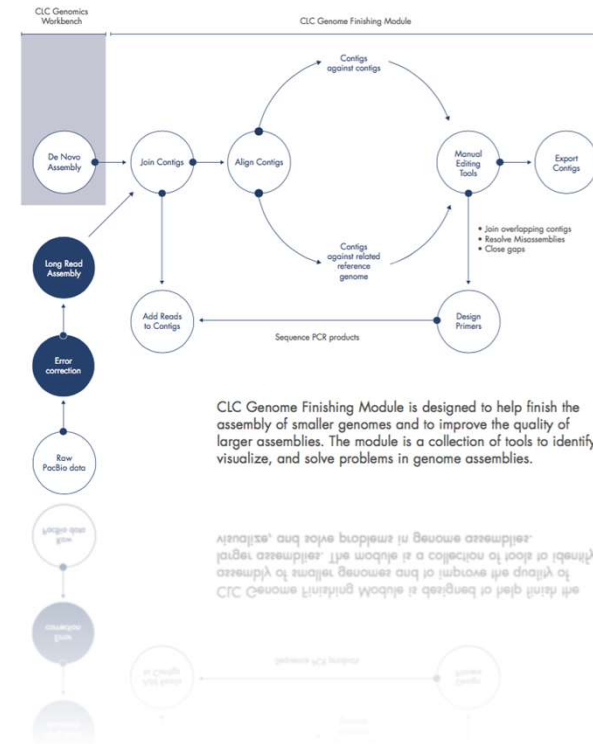
- to accelerate and simplify genome finishing, and
- to make this process accessible to life scientist without deep understanding of bioinformatics.

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.

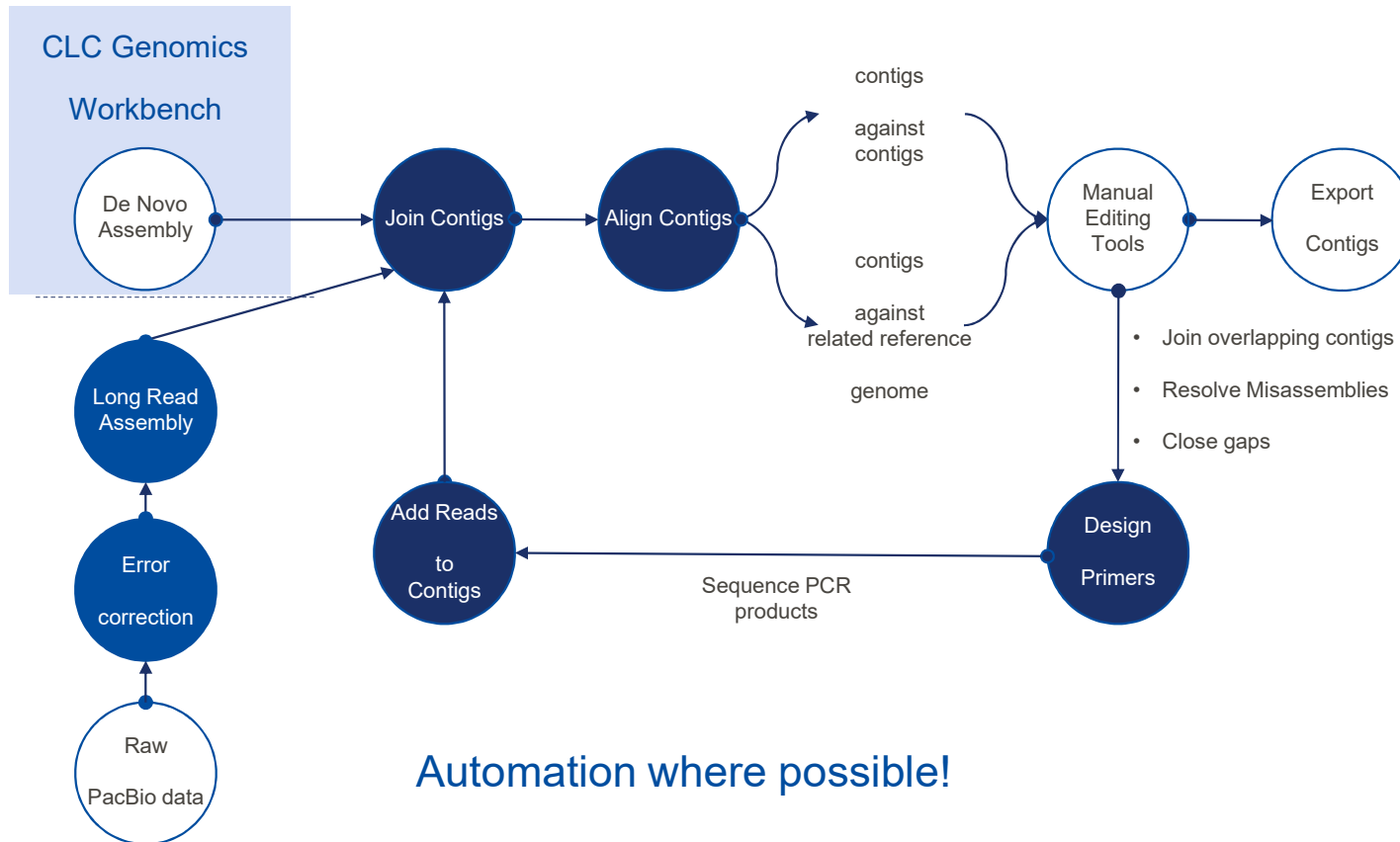
Technical Note

CLC Genome Finishing Module



CLC Genome Finishing Module is designed to help finish the assembly of smaller genomes and to improve the quality of larger assemblies. The module is a collection of tools to identify, visualize, and solve problems in genome assemblies.

De Novo Assembly and Genome Finishing



Automation where possible!



QIAGEN CLC Genomics
Server and QIAGEN
CLC Genomics Cloud
Engine v20

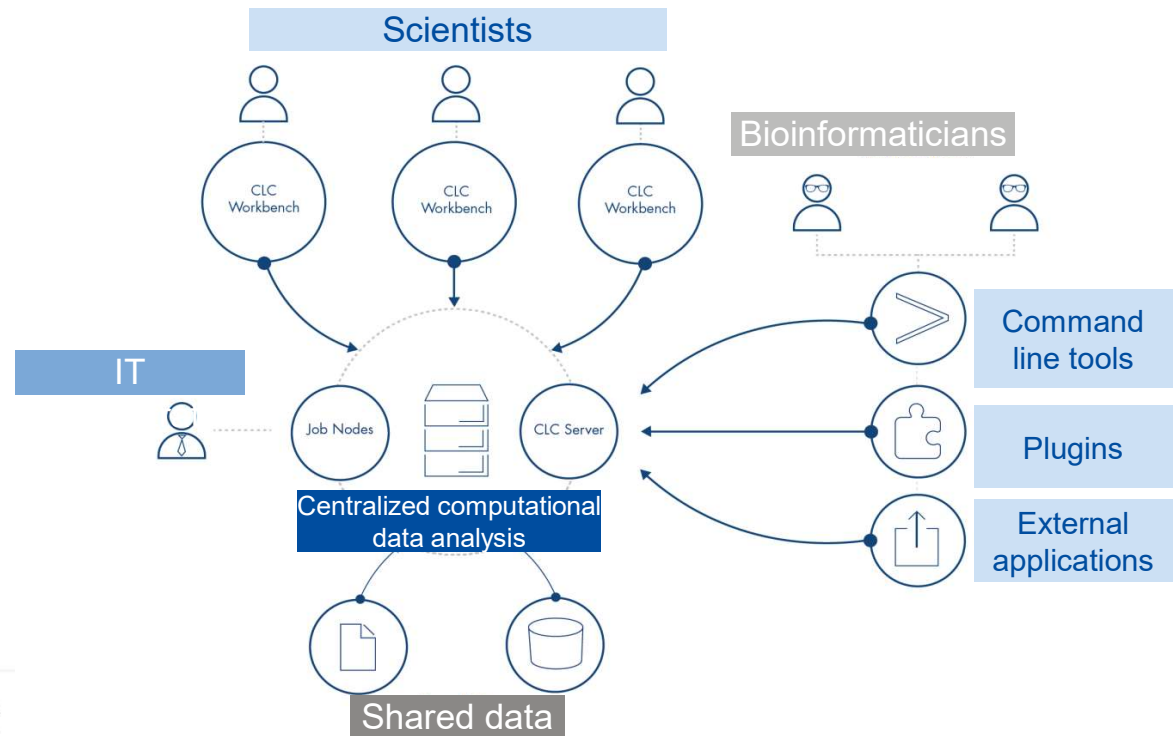
On-premise enterprise solution: QIAGEN CLC Genomics Server

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



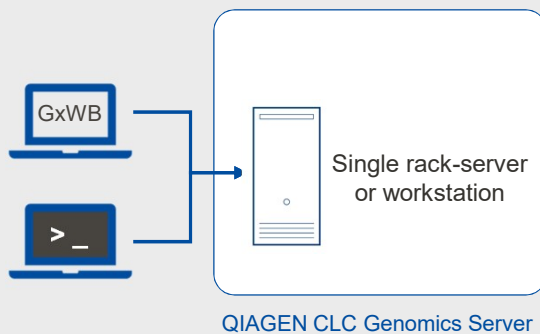
Source: Chief Scientist, Medium Enterprise Health Care Company

Validated | Published: Nov. 21, 2018 | TVID: E46-300-BA6



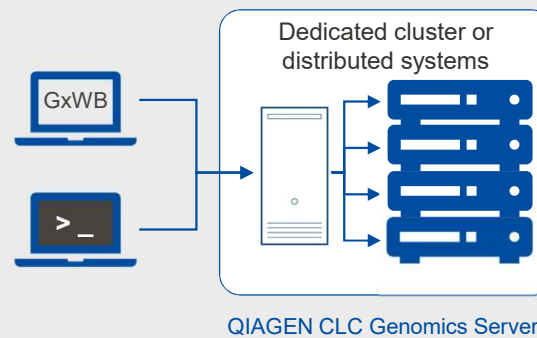
QIAGEN CLC Genomics Server – three deployment models

Single server



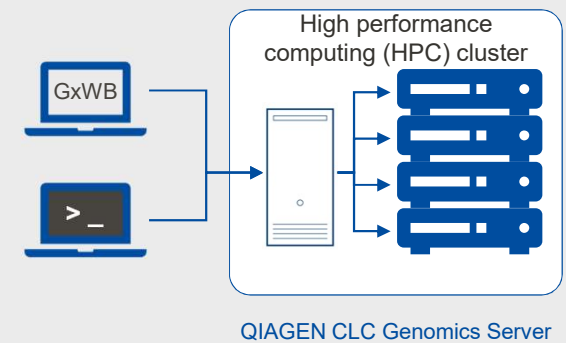
- Simple to set up in minutes
- Offloads workflows, ad hoc data analysis and storage to central hub
- Single rack server or workstation
- Same capabilities as cluster setup

Master server + Job nodes



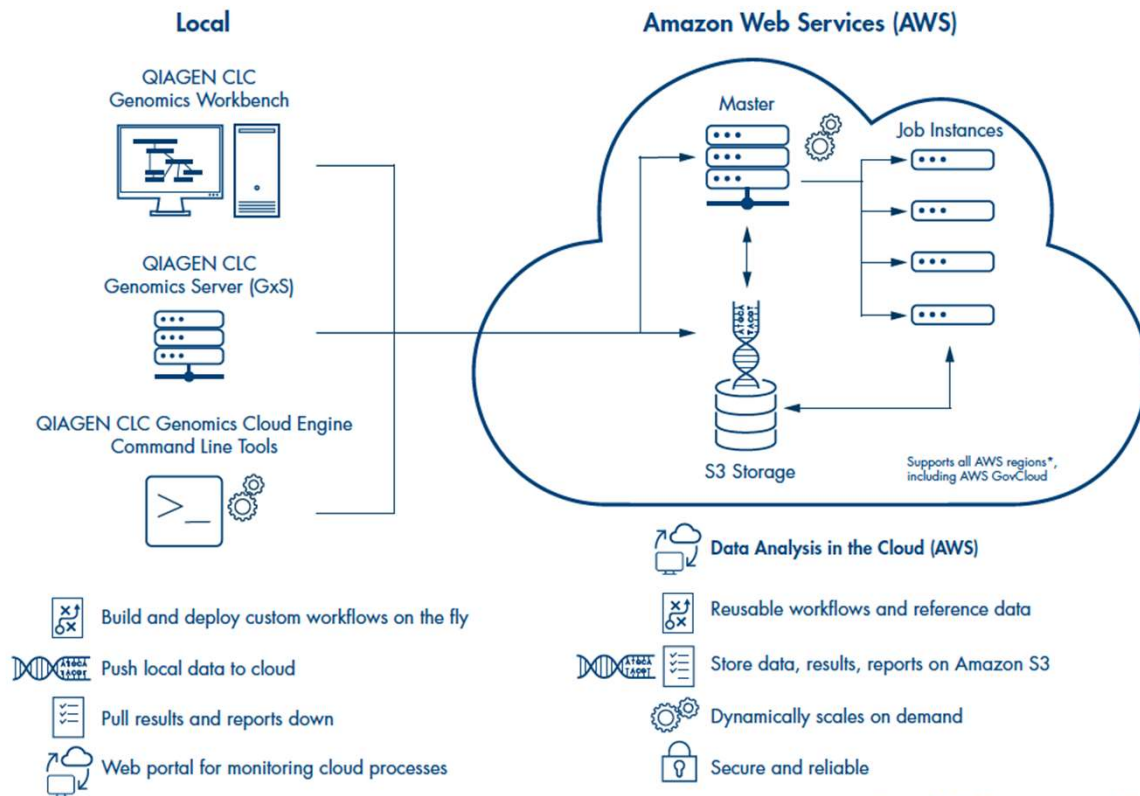
- Easy to install and manage
- Distributes workload across multiple dedicated job nodes
- Uses built in QIAGEN CLC queueing system
- Scalable to hundreds of nodes and users

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



* Support for AWS China regions coming in 2020

QIAGEN CLC Genomics Cloud Engine administration

Supported AWS regions

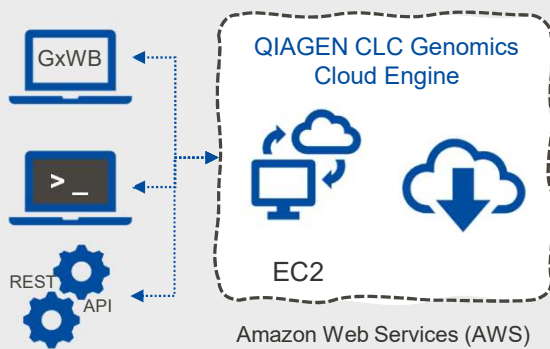
Region	Code
N. Virginia	us-east-1
Ohio	us-east-2
N. California	us-west-1
Oregon	us-west-2
Frankfurt	eu-central-1
Ireland	eu-west-1
Tokyo	ap-northeast-1
Seoul	ap-northeast-2
Sydney	ap-southeast-2
Mumbai	ap-south-1
GovCloud (US-East)	us-gov-east-1
GovCloud (US-West)	us-gov-west-1

Administration task

GCE Command Line Tools	<ul style="list-style-type: none"> • 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	<ul style="list-style-type: none"> • Change autoscaling behavior • Change or configure instance types used • Modifying OAuth configuration • Configure and enabling automatic platform updates
AWS DynamoDB Management Console	<ul style="list-style-type: none"> • Enter or exit from maintenance mode • Enable or configure signed URLs for files stored on S3
AWS CloudWatch	<ul style="list-style-type: none"> • Inspect license usage metrics and jobs • Monitor, inspect, and export the log files created • Changing Log Retention

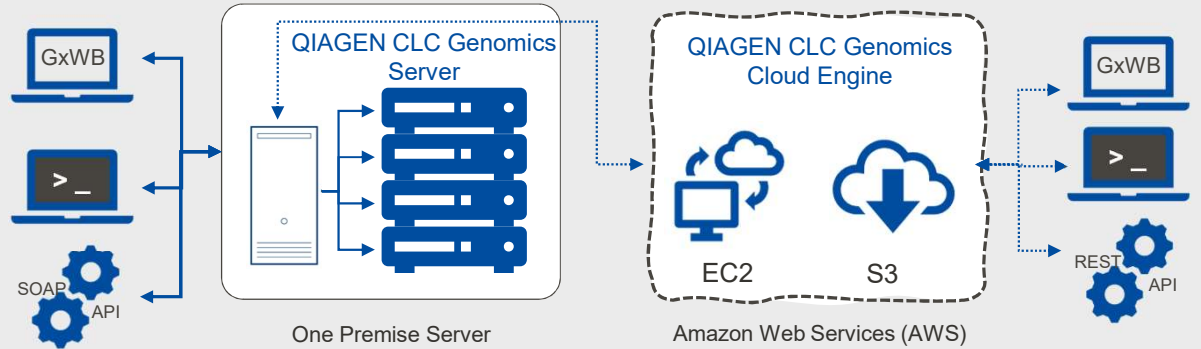
QIAGEN CLC Genomics Cloud Engine – two deployment models

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?

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