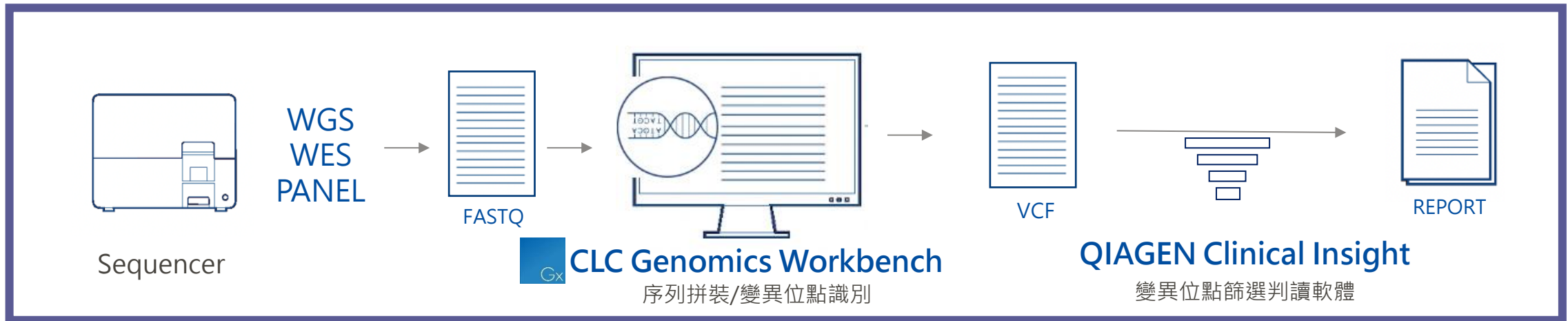


# QIAGEN變異位點全方面資訊解決方案介紹

2021.05.06

Clair Tsai 蔡宜庭 業務副理  
Willis Cheng 鄭耀璋 專案主任

# After sequencing, What's Next?



WES全外顯子約有  
60,000,000bp

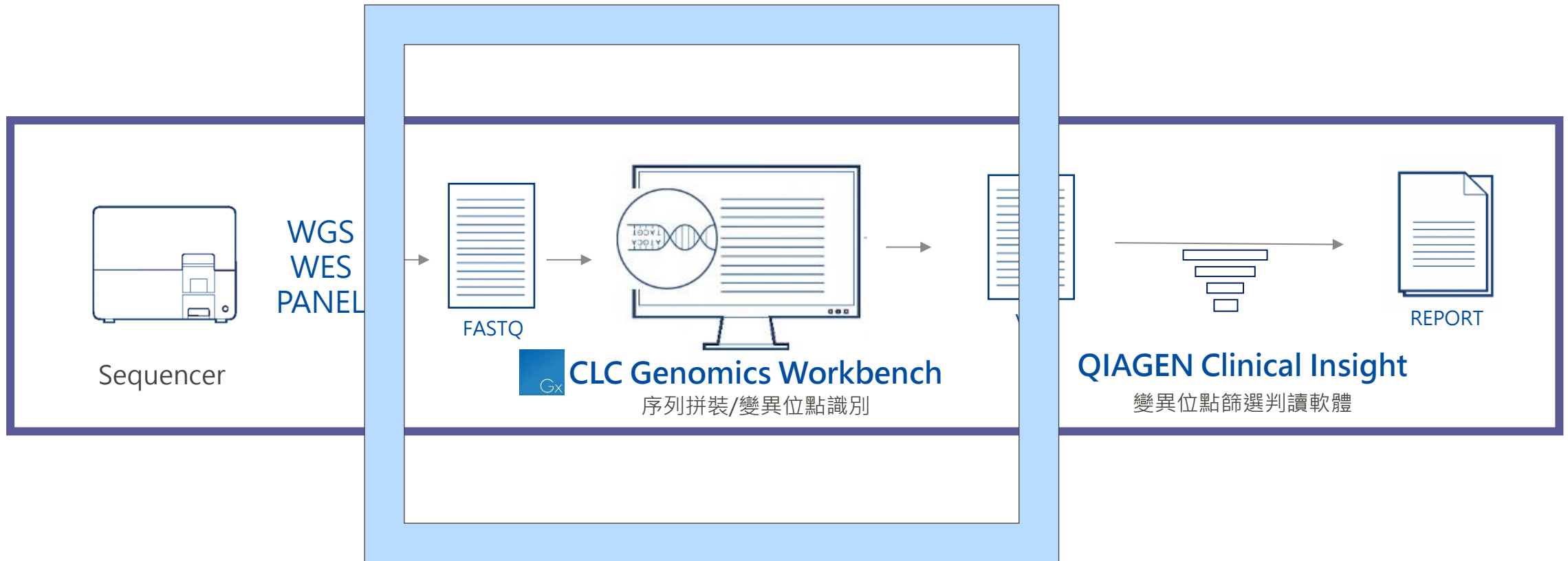
\*WGS有30億個鹼基對

與人體參考基因組比對  
約有30,000個變異位點

如何找到關鍵制病位點?

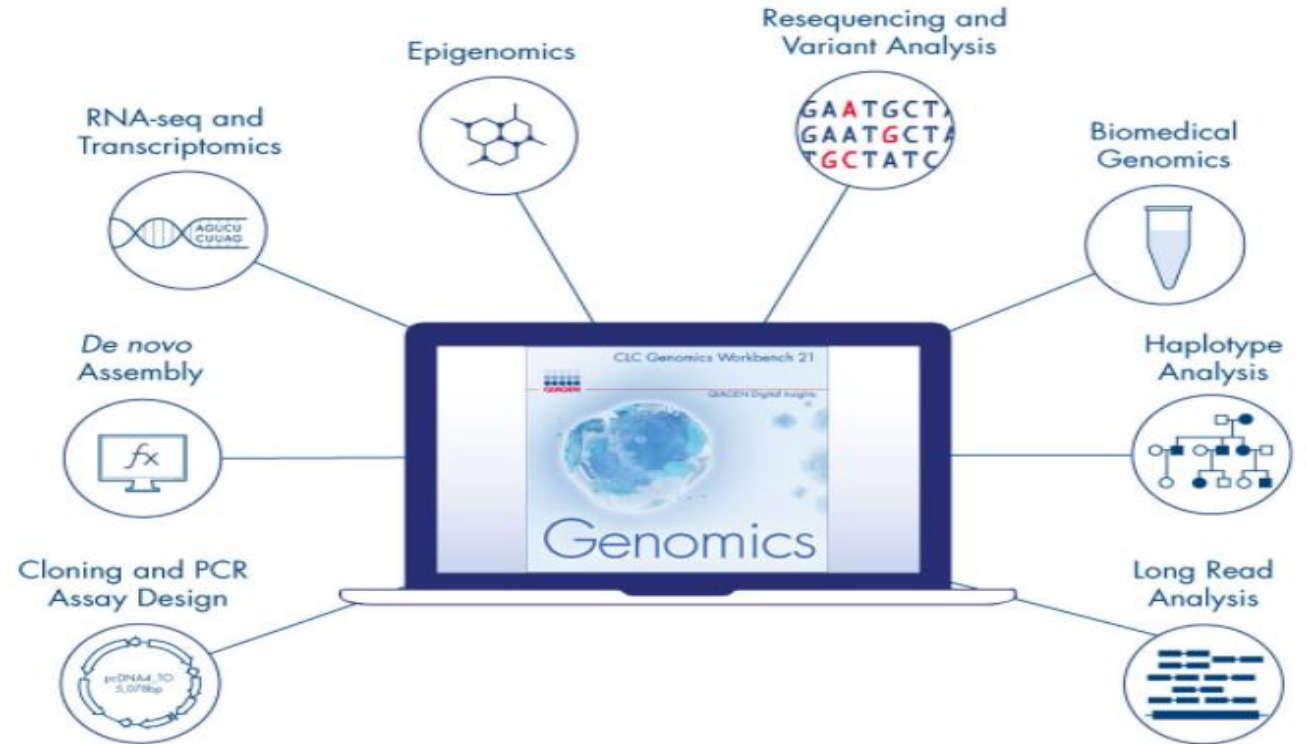
1. 常見位點篩選
2. 位點信心程度篩選
3. 資料庫評斷位點制病性
4. 位點與疾病的相關程度
5. 位點用藥資訊
6. 制病位點報告生成

# CLC Genomics Workbench









# QIAGEN CLC Genomics Workbench

- Cross-platform desktop genomics application
  - **User-friendly GUI interface**
    - Works on Windows, Mac and Linux
  - **Data Localization**
  - **Interactive visualization**
  - **Workflows**
    - For automated processing
    - For sharing with colleagues
  - **Modular design to add plugins**
  - **Compatible with most platforms**
    - **Illumina**, Ion Torrent, Oxford Nanopore, PacBio, **BGI/MGI**
  - **Fully documented** and supported
  - Developed under quality guidelines set forth by ISO 9001:2015
    - TUV Rheinland-certified

















# In CLC Workbenches you can..

## Ready-to-Use Workflows

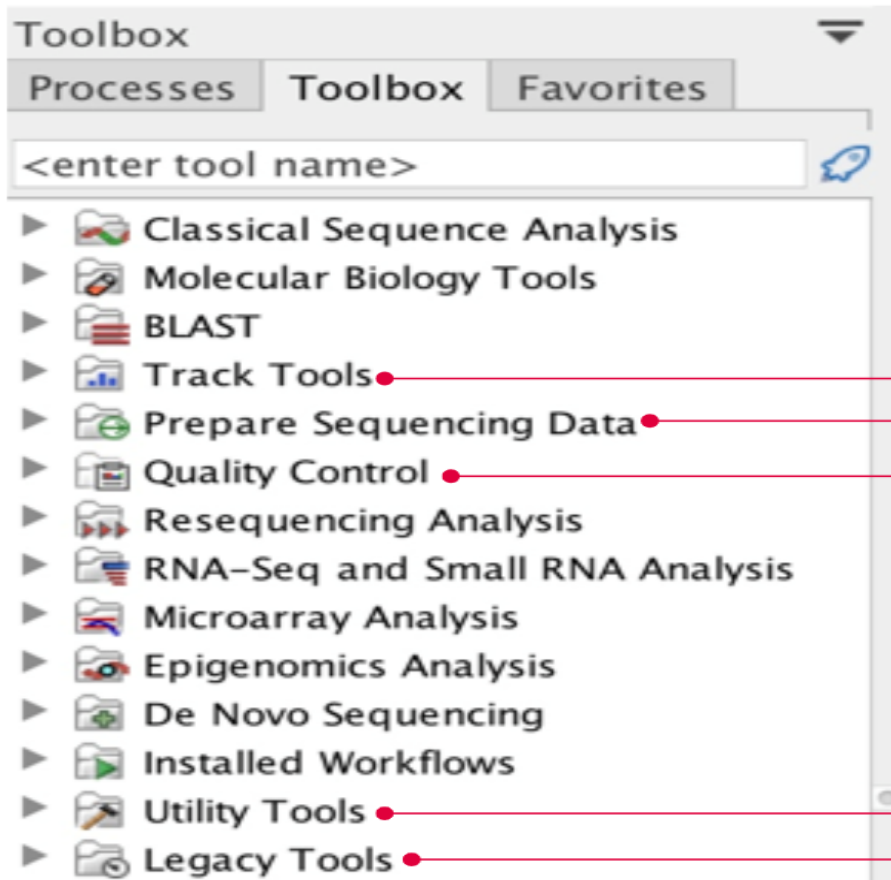
- +  Preparing Raw Data
- +  QIAseq Panel Analysis
- +  Whole Genome Sequencing
- +  Whole Exome Sequencing
- +  Targeted Amplicon Sequencing
- +  Whole Transcriptome Sequencing
- +  Small RNA Sequencing

## Tools

- +  Genome Finishing Module
- +  Microbial Genomics Module
- +  Long Read Support (beta)
- +  Classical Sequence Analysis
- +  Molecular Biology Tools
- +  BLAST
- +  Track Tools
- +  Prepare Sequencing Data
- +  Quality Control
- +  Resequencing Analysis
- +  RNA-Seq and Small RNA Analysis
- +  Microarray Analysis
- +  Epigenomics Analysis
- +  De Novo Sequencing
- +  Installed Workflows
- +  Utility Tools
- +  QIAseq Panel Expert Tools
- +  Legacy Tools

CLC Genomics Workbench	QC & Reads Processing	<input type="radio"/>
	Resequencing (whole genome, exome, targeted)	<input type="radio"/>
	Transcriptomics (RNA-Seq)	<input type="radio"/>
	Single Cell RNA-Seq Analysis	<input type="radio"/>
	De novo assembly	<input type="radio"/>
	Epigenomics	<input type="radio"/>
	Long Reads Supports (Oxford Nanopore & Pacbio)	<input type="radio"/>
	QIAseq Panel Analysis – TMB & MSI & TSO500	<input type="radio"/>
	Workflow (Pipeline)	<input type="radio"/>
	Microarray Analysis	<input type="radio"/>
	Phylogeny Tools	<input type="radio"/>
	Blast, Sanger Sequencing, Cloning, Primer Design, ...	<input type="radio"/>
Extended Modules	Microbiome Analysis (Microbial Genomics Module)	<input type="radio"/>
	Contigs Assembly (Genome Finishing Module)	<input type="radio"/>

# Organization of 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

# Plugins

## Premium 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

### Single Cell Analysis Module

- RNA-seq, t-SNE, UMAP, clustering, cell type annotation (automatic and manual)

## Free plugins

### Free plugins

- Biomedical Genomics Analysis
  - Long Read Support
  - Whole Genome Alignment
  - Ingenuity Pathway Analysis
  - Ingenuity Variant Analysis
- } Requires subscription

# Publication Roundup: QIAGEN CLC Genomics Workbench

Recently, there have been many noteworthy papers citing QIAGEN CLC Genomics Workbench, a comprehensive, easy-to-use toolbox that ensures continuity in your NGS workflow. Here, we round up just a few of them to offer a sense of the diversity of the research for which QIAGEN CLC Genomics Workbench makes a difference. Below are some examples of how researchers from all over the world use this solution as a tool for metagenomic analysis to characterize dengue viruses and pathogens, create *de novo* assemblies or investigate ocular diseases.

## Genomic characterization of SARS-CoV-2 identified in a reemerging COVID-19 outbreak in Beijing's Xinfadi market in 2020

First author: Yong Zhang

Should we be looking for new mutations in SARS-CoV-2 that Center for Disease Control and Prevention perform genomic reemerging outbreak in China. Discover how they use QIAGEN source of the virus in this second outbreak in Beijing's Xinfadi

## Genetic tracing of HCoV-19 for the re-emerging ou

☰
Google 學術搜尋

🔍

📁 文章

不限時間

2021 以後

2020 以後

2017 以後

自訂範圍...

---

按照關聯性排序

按日期排序

---

不限語言

搜尋所有中文網頁

搜尋繁體中文網頁

---

包含專利

只包含書目/引用資料

---

✉ 建立快訊

約有 15,300 項結果 (0.05 秒)

**Analysis of RNA sequencing data using CLC Genomics Workbench**

CH Liu, [YP Di](#) - Molecular Toxicology Protocols, 2020 - Springer

RNA sequencing (RNA-seq) is a recently developed approach to perform transcriptome profiling using next-generation sequencing (NGS) technologies. Studies have shown that RNA-seq provides accurate measurement of transcript levels as well as their isoforms, which ...

☆ 07 被引用 6 次 相關文章 全部共 6 個版本

**Identification and Characterization of LEA Genes in Ash Tree (Fraxinus excelsior) Genome**

AU BAYARSLAN - Kastamonu Üniversitesi Orman Fakültesi Dergisi, 2019 - dergipark.org.tr

... from LEAP database and ash protein sequence from Ash Tree Genome database were analyzed to identify ash LEA proteins in CLC Genomics Workbench 11 ... Genome-wide identification and comparative expression analysis of LEA genes in watermelon and melon genomes ...

☆ 07 相關文章 全部共 4 個版本

**[HTML] Genomic features of a highly virulent, ceftiofur-resistant, CTX-M-8-producing Escherichia coli ST224 causing fatal infection in a domestic cat**

MM Silva, FP Sellera, MR Fernandes, Q Moura... - Journal of global ..., 2018 - Elsevier

... A genomic library was prepared using a Nextera XT DNA Library Preparation Kit ... were trimmed and de novo assembled using CLC Genomics Workbench 10 (CLC Bio, Aarhus ... contigs were submitted to automatic annotation by the NCBI Prokaryotic Genome Annotation Pipeline ...

☆ 07 被引用 8 次 相關文章 全部共 4 個版本

[https://qiagen.pathfactory.com/gwb-trial/publication-roundup/?cmpid=CM\\_QDI\\_DISC\\_CLC-Webpage\\_0221\\_PF\\_website\\_GWB](https://qiagen.pathfactory.com/gwb-trial/publication-roundup/?cmpid=CM_QDI_DISC_CLC-Webpage_0221_PF_website_GWB)



# Document & Tutorial on Website



## Bisulfite sequencing

Find methylated cytosines and identify regions with high methylation levels in your sequencing reads.

Available as a [PDF tutorial](#)

QIAGEN CLC Genomics Workbench

## ChIP sequencing

This tutorial takes you through a complete ChIP sequencing workflow using CLC Genomics Workbench.

Available as a [PDF tutorial](#)

QIAGEN CLC Genomics Workbench

## Resequencing analysis using tracks

Find and annotate cancer specific variants by comparing normal and cancer tissue reads and by filtering for variants leading to amino acid changes.

Available as a [PDF tutorial](#)

QIAGEN CLC Genomics Workbench

## Reference genome and annotation tracks

Learn how to create a reference genome and manage track lists to visualize your data and associated annotations.

Available as a [PDF tutorial](#)

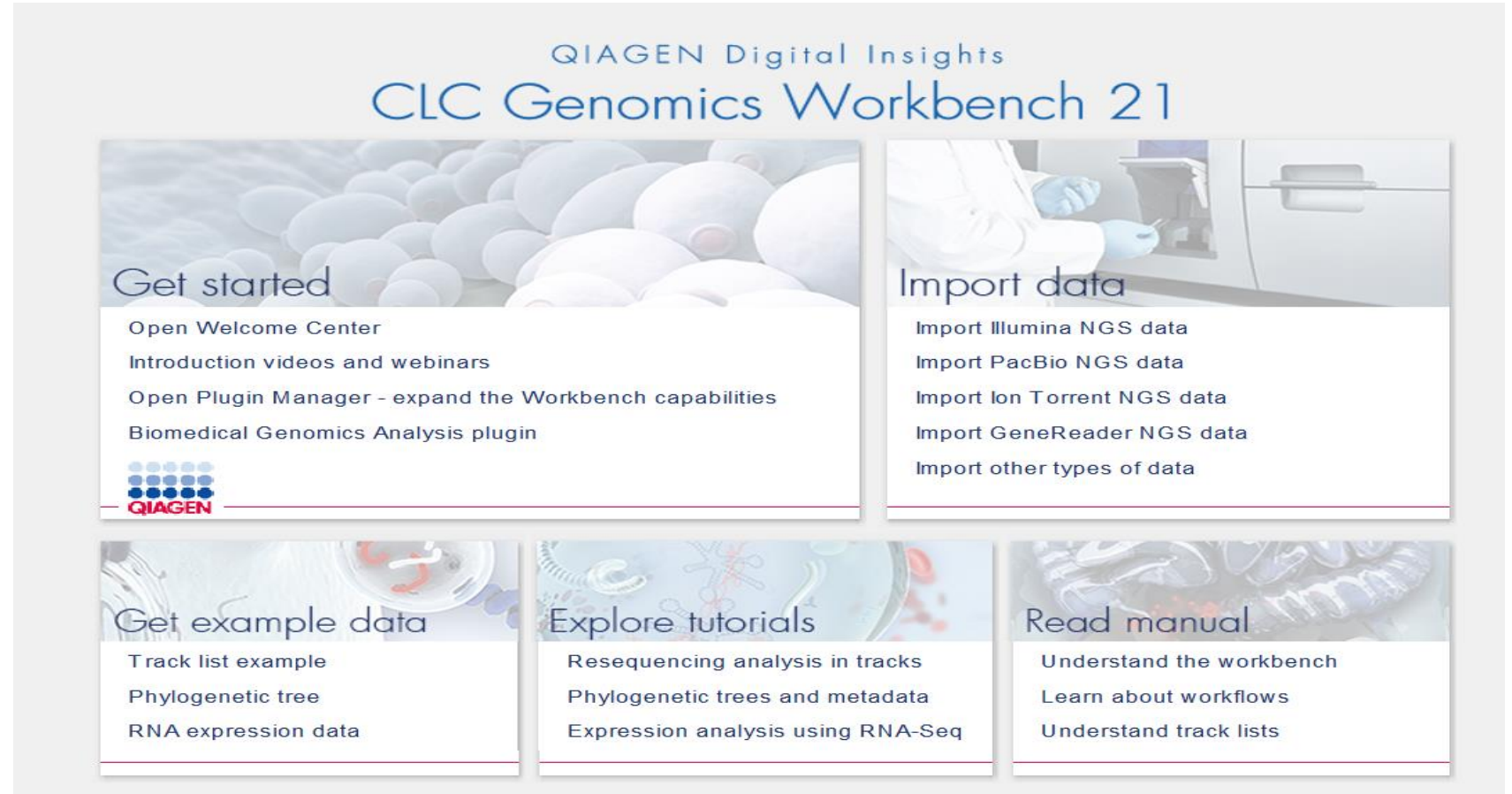
QIAGEN CLC Genomics Workbench

Q&A: <https://qiagen.secure.force.com/KnowledgeBase/KnowledgeGemomicWorkbench>

Tutorial: <https://digitalinsights.qiagen.com/support/tutorials>

# The new CLC Genomics Workbench 21

- **Cloud Plugins**
- Single Cell Analysis Plugins
- Biomedical Workflow
  - SARS-CoV-2 Workflow
  - TSO500 Panel Workflow
- RNA-Seq Analysis
  - Long Reads
- MGM
  - Functional Database



QIAGEN Digital Insights  
CLC Genomics Workbench 21

**Get started**

- Open Welcome Center
- Introduction videos and webinars
- Open Plugin Manager - expand the Workbench capabilities
- Biomedical Genomics Analysis plugin

**Import data**

- Import Illumina NGS data
- Import PacBio NGS data
- Import Ion Torrent NGS data
- Import GeneReader NGS data
- Import other types of data

**Get example data**

- Track list example
- Phylogenetic tree
- RNA expression data

**Explore tutorials**

- Resequencing analysis in tracks
- Phylogenetic trees and metadata
- Expression analysis using RNA-Seq

**Read manual**

- Understand the workbench
- Learn about workflows
- Understand track lists

# CLC Cloud Engine on BaseSpace

**Illumina High-Throughput Sequencing Import**

1. Choose where to run
2. **Import files and options**
3. Result handling
4. Save location for new elements

Select files of types Illumina (.txt/.fastq/.fq)

Location **BaseSpace** Access BaseSpace...

**General options**

- Paired reads
- Discard read names
- Discard quality scores

**Paired read information**

- Paired-end (forward-reverse)  Mate-pair (reverse)
- Minimum distance  Maximum distance

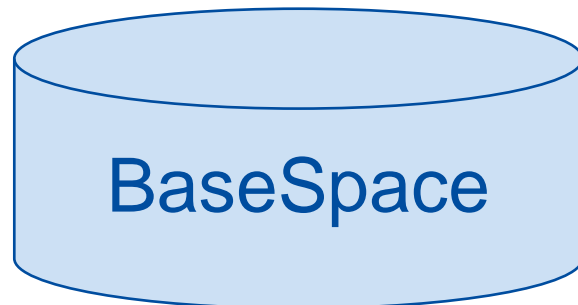
**Illumina options**

- Remove failed reads Quality scores **NCBI/Sanger or Illumina Pipeline 1.8 and later**
- MiSeq de-multiplexing
- Trim reads
- Join reads from different lanes

Buttons: Help, Reset, Previous, Next, Finish, Cancel

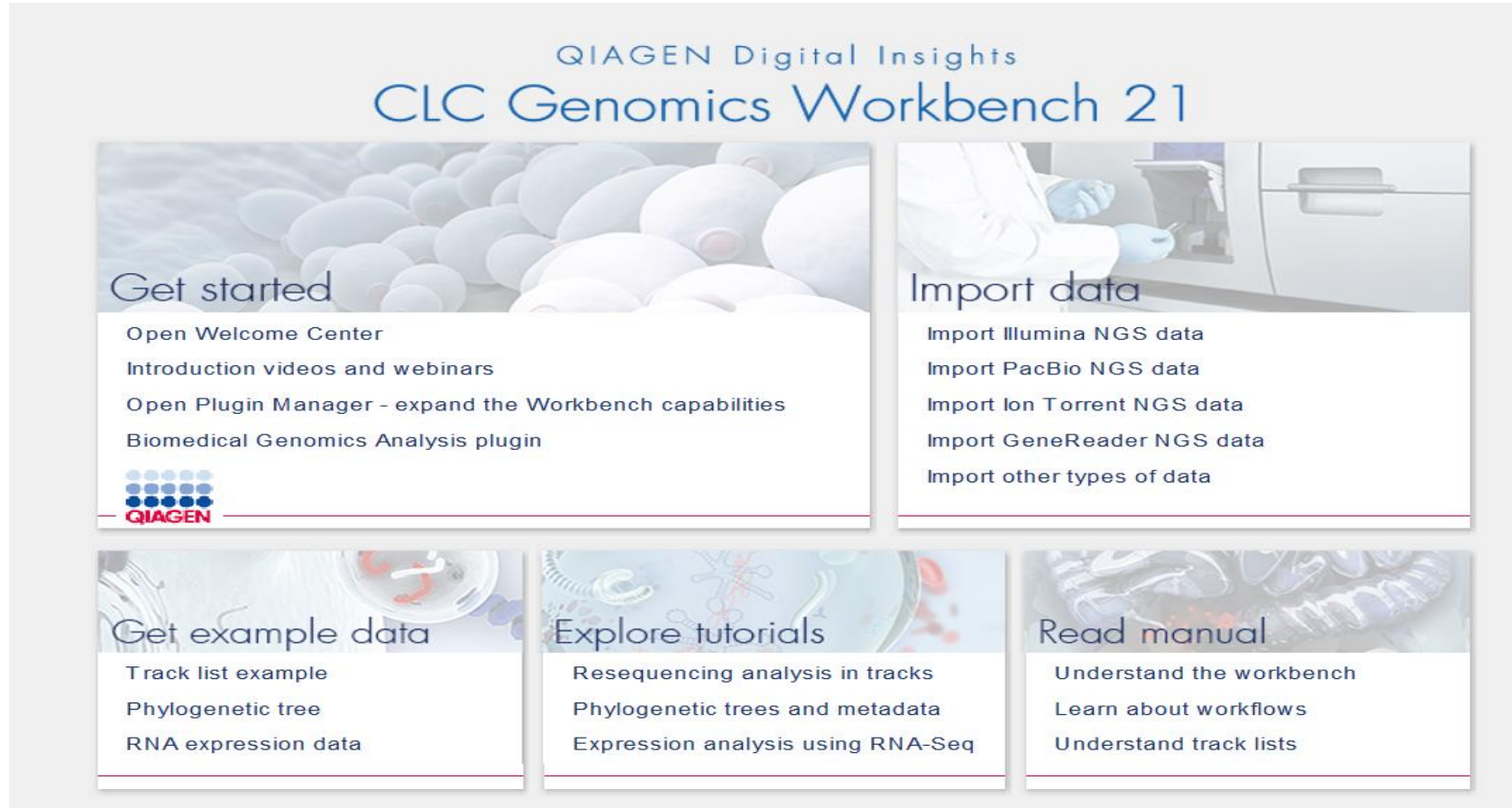
Select files of types Illumina

Location **BaseSpace** File system BaseSpace



# The new CLC Genomics Workbench 21

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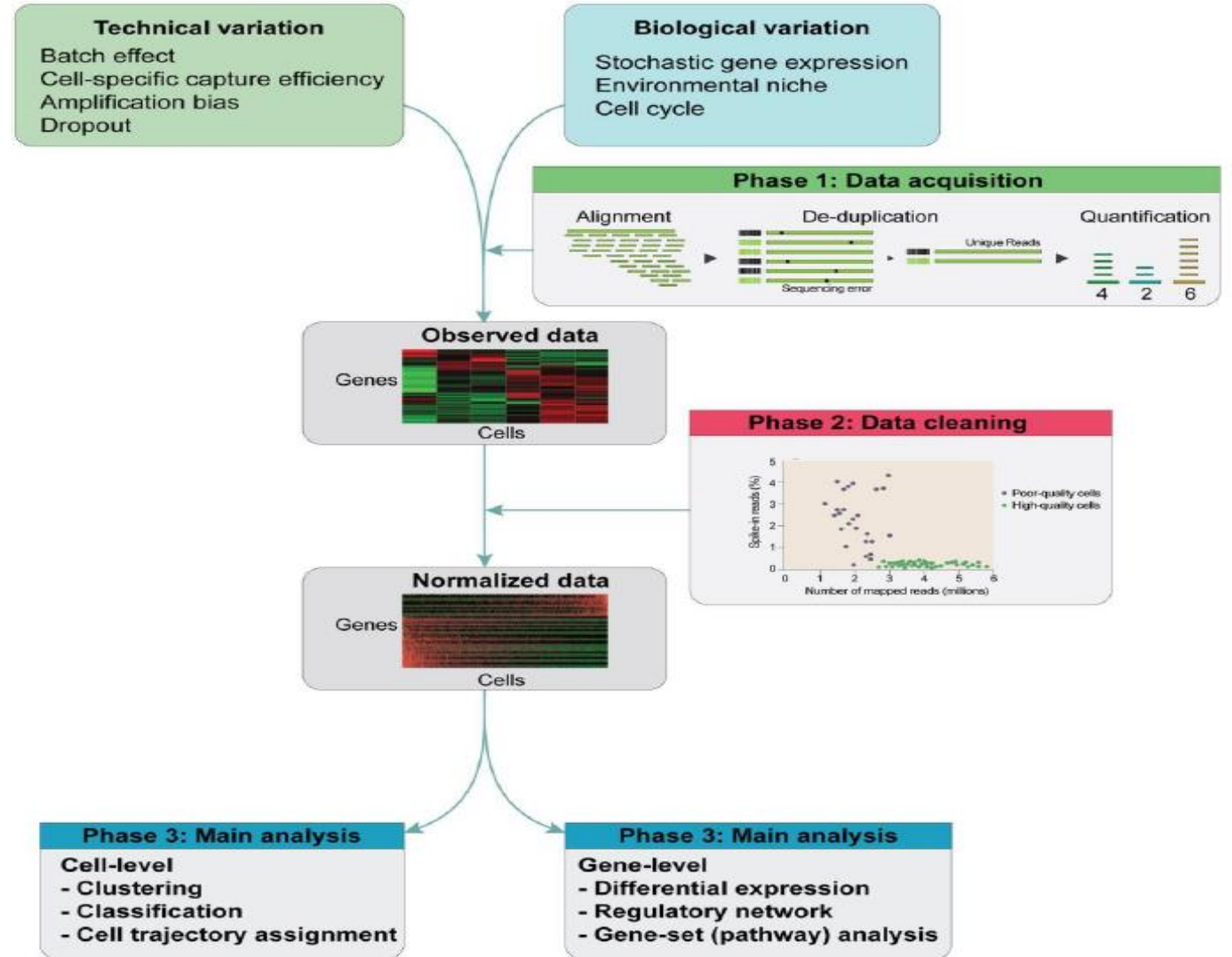
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**Read manual**

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# Single Cell Analysis

1. Raw sequencing data QC
2. Alignment to genome
3. Cellular barcode and UMI process
4. Generate gene expression matrix (zero-inflated matrix)
5. Cell QC and clean
6. Normalization
7. Estimate confounding factors
8. Cell-level and gene-level analysis



# Single Cell Analysis

## Tools

- ▼ Single Cell Analysis
  - ▼ Cell Preparation
    - Annotate Reads with Cell and UMI
    - Single Cell RNA-Seq Analysis
    - QC for Single Cell
    - Normalize Single Cell Data
    - Combine Cell Annotations
    - Combine Cell Clusters
    - Convert Metadata to Cell Annotations
  - ▼ Cell Annotation
    - Predict Cell Types
    - Train Cell Type Classifier
    - Cluster Single Cell Data
  - ▼ Dimensionality Reduction
    - UMAP for Single Cell
    - tSNE for Single Cell
    - Add Information to Plot
  - ▼ Expression Analysis
    - Differential Expression for Single Cell
    - Create Expression Plot
  - ▼ Workflows
    - Perform Single Cell Analysis from Expression Matrix
    - Perform Single Cell Analysis from Reads

## Importers

- Import Cell Annotations...
- Import Cell Clusters...
- Import Expression Matrix
  - Import Expression Matrix in Cell Ranger HDF5 Format...
  - Import Expression Matrix in Loom format...
  - Import Expression Matrix in MEX format...
  - Import Expression Matrix in MEX format (archive)...
  - Import Expression Matrix in CSV/TXT Format...

## Exporters

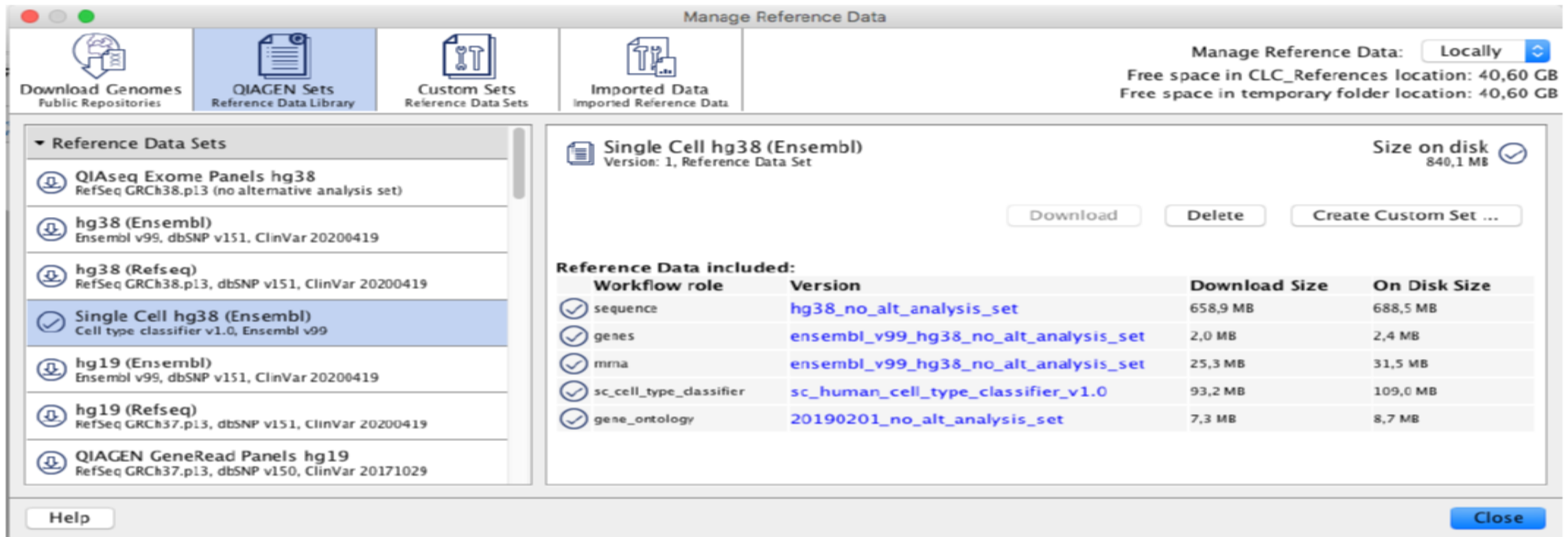
The screenshot shows a dialog box titled "Select export format" with a search bar containing "expression matrix". Below the search bar is a table with the following data:

Name	Description	Extension	Supported format
10x HDF5	Export Expression Matrix in Cell Ranger HDF5 Format	[h5]	No
Loom Expression Matrix	Export Expression Matrix in Loom Format	[loom]	No
MEX	Export Expression Matrix in Cell Ranger Feature-Barco...	[tar.gz]	No

At the bottom right of the dialog box are "Cancel" and "Select" buttons.

# Single Cell Analysis

- Limitation on installed version: Human, Mouse



Manage Reference Data

Manage Reference Data: Locally

Free space in CLC\_References location: 40,60 GB  
Free space in temporary folder location: 40,60 GB

**Reference Data Sets**

- QIAGEN Exome Panels hg38  
RefSeq GRCh38.p13 (no alternative analysis set)
- hg38 (Ensembl)  
Ensembl v99, dbSNP v151, ClinVar 20200419
- hg38 (Refseq)  
RefSeq GRCh38.p13, dbSNP v151, ClinVar 20200419
- Single Cell hg38 (Ensembl)**  
Cell type classifier v1.0, Ensembl v99
- hg19 (Ensembl)  
Ensembl v99, dbSNP v151, ClinVar 20200419
- hg19 (Refseq)  
RefSeq GRCh37.p13, dbSNP v151, ClinVar 20200419
- QIAGEN GeneRead Panels hg19  
RefSeq GRCh37.p13, dbSNP v150, ClinVar 20171029

**Single Cell hg38 (Ensembl)**  
Version: 1, Reference Data Set  
Size on disk: 840,1 MB

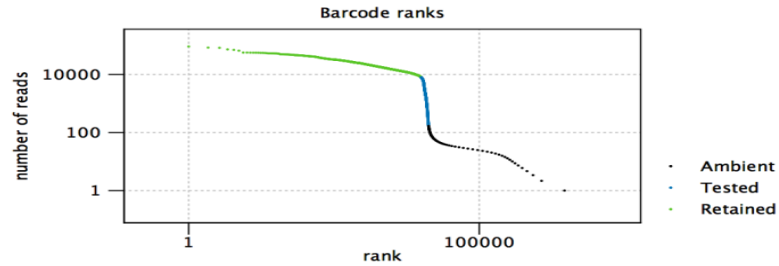
Download Delete Create Custom Set ...

**Reference Data included:**

Workflow role	Version	Download Size	On Disk Size
sequence	hg38_no_alt_analysis_set	658,9 MB	688,5 MB
genes	ensembl_v99_hg38_no_alt_analysis_set	2,0 MB	2,4 MB
mna	ensembl_v99_hg38_no_alt_analysis_set	25,3 MB	31,5 MB
sc_cell_type_classifier	sc_human_cell_type_classifier_v1.0	93,2 MB	109,0 MB
gene_ontology	20190201_no_alt_analysis_set	7,3 MB	8,7 MB

Help Close

# QC for Single Cell Report

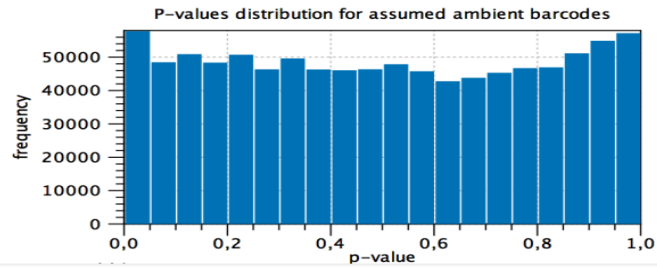


## 2 Cell calling for droplet data for 5k\_pbmc\_v3\_S1\_L001\_R1

### 2.1 Summary

Minimum number of reads for retaining barcodes	3.225
Maximum number of reads for ambient barcodes	100
Estimated number of cells	4.989
Sufficient simulations	Yes
Number of barcodes with significant FDR-corrected p-value	1.008
Fraction of reads in cells	89,27
Median number of reads per cell	4.605,00
Median genes per cell	1.545,00

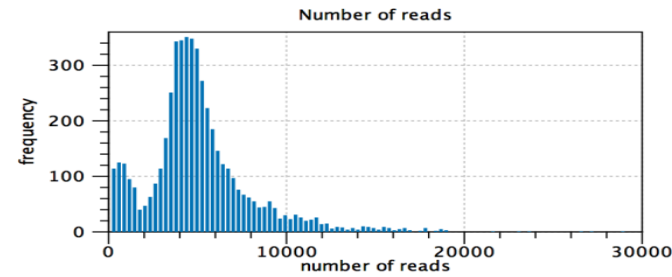
### 2.2 P-values distribution for assumed ambient barcodes



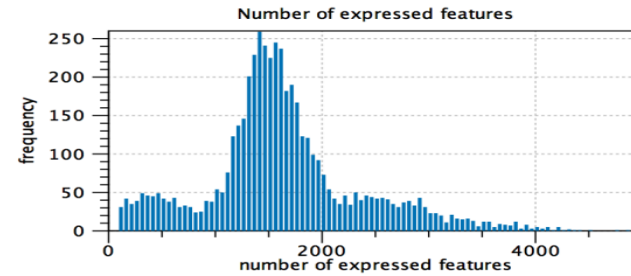
### 3.1 Summary

Input cells	4
Retained cells	4
Known retained cells	
Maximum mitochondrial reads (%)	
Cells with too many mitochondrial reads (%)	

### 3.2 Number of reads

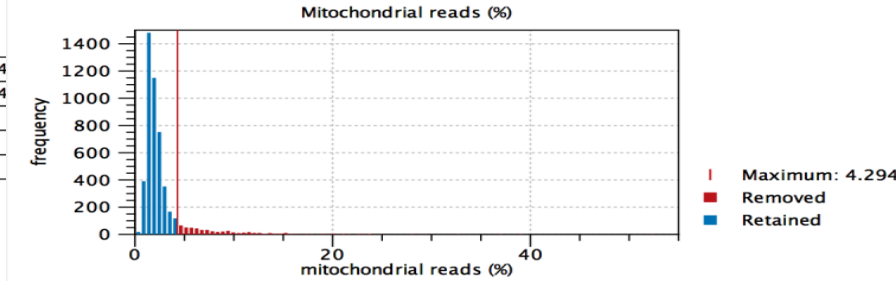


### 3.3 Number of expressed features



### 3.4 spike-in reads (%)

### 3.5 Mitochondrial reads (%)



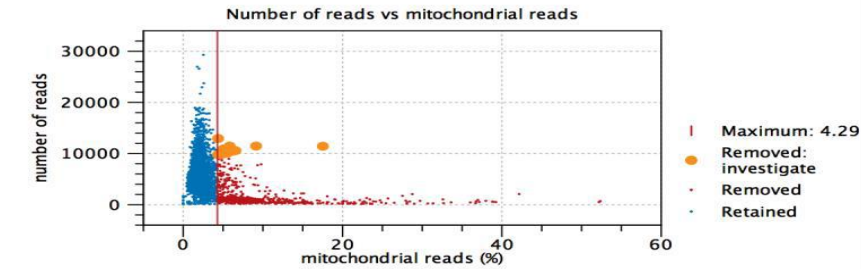
### 3.6 QC metrics relations

The relation between the mitochondrial reads (%) and the other QC metrics highlight if there are cells with both:

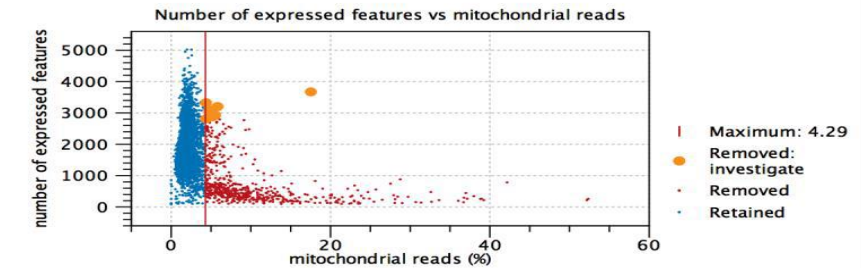
- many number of reads / expressed features and large mitochondrial reads, indicative of high-quality cells that are highly metabolically active;
- few spike-in and many mitochondrial reads (%), indicative of undamaged cells that are metabolically active.

These cells are highlighted in orange and should not necessarily be removed.

#### 3.6.1 Number of reads vs mitochondrial reads

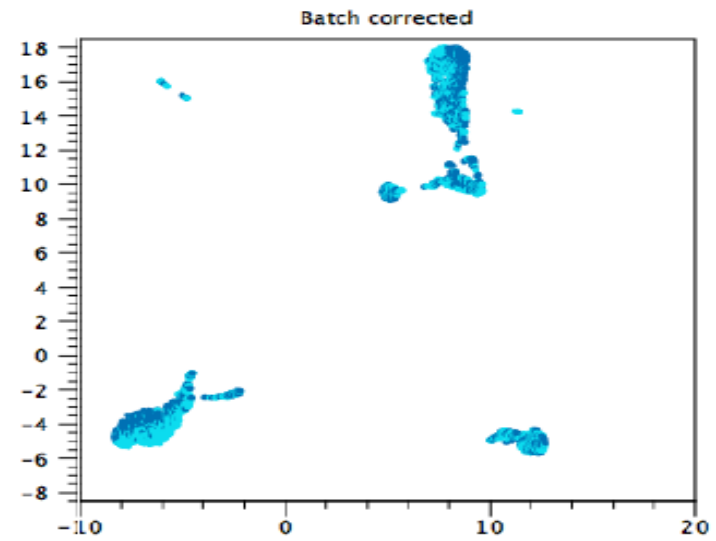
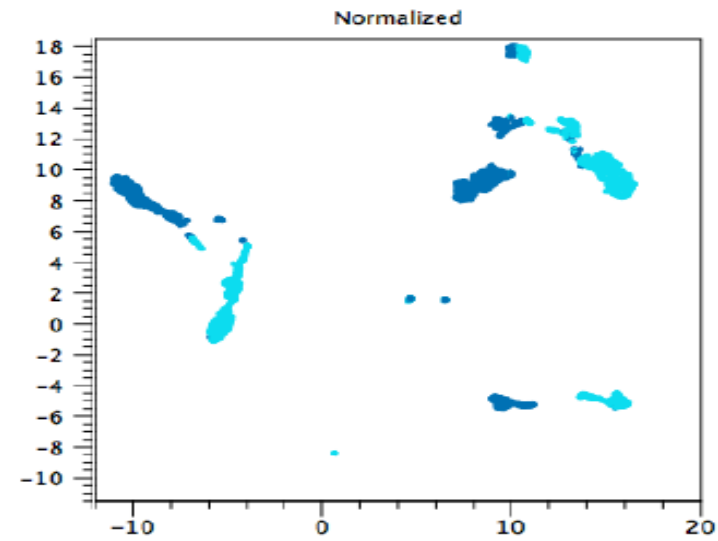
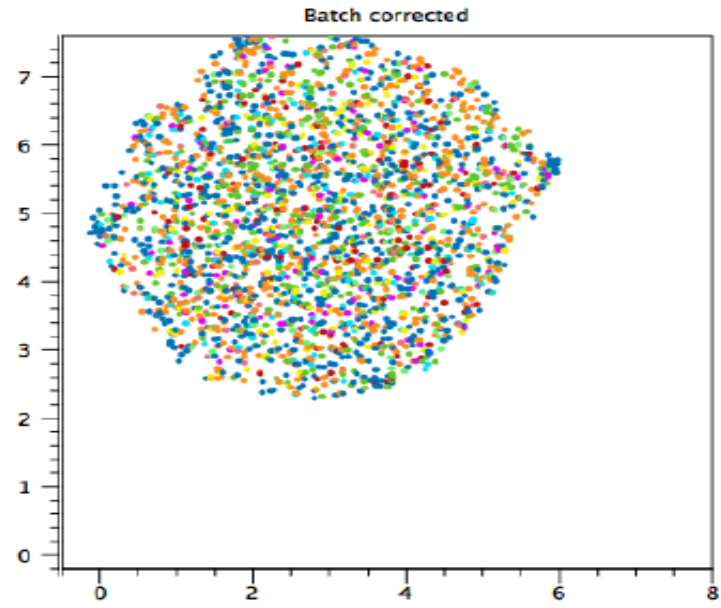
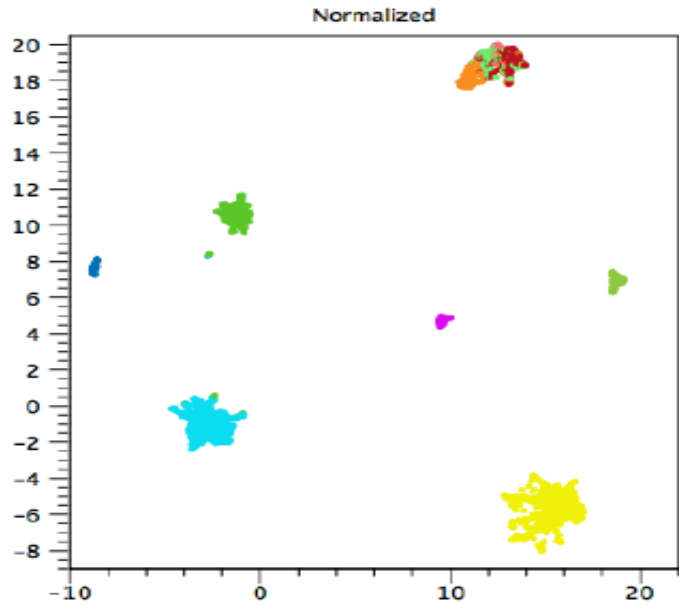


#### 3.6.2 Number of expressed features vs mitochondrial reads

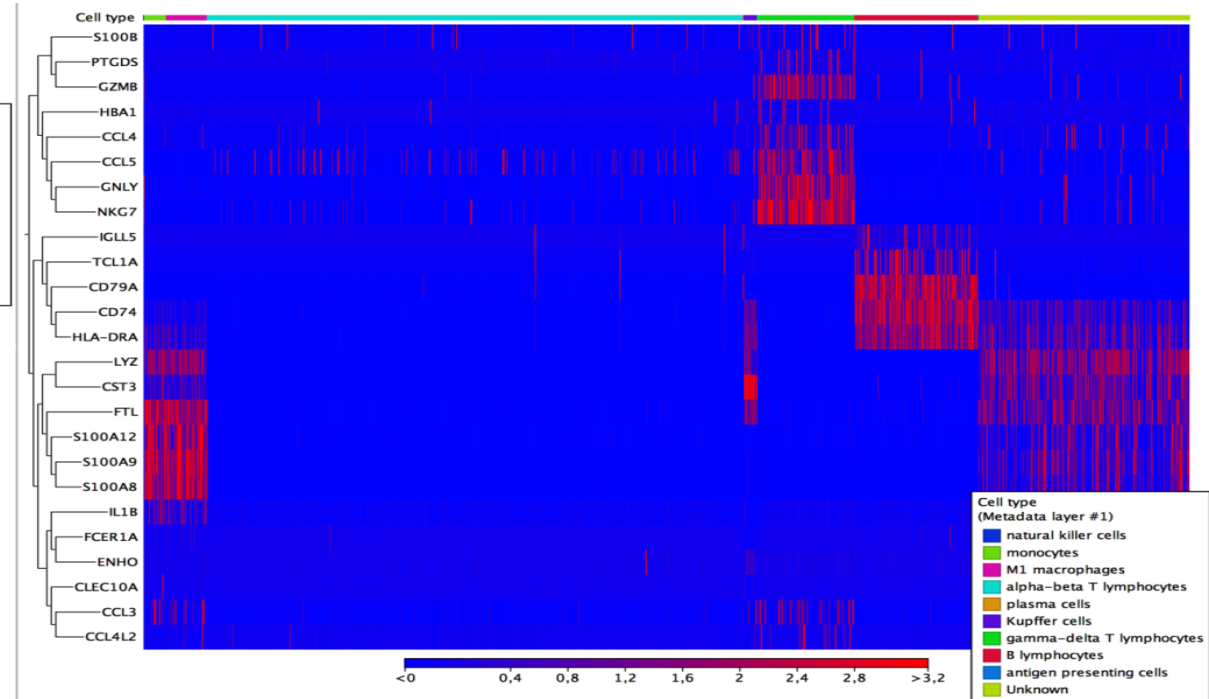
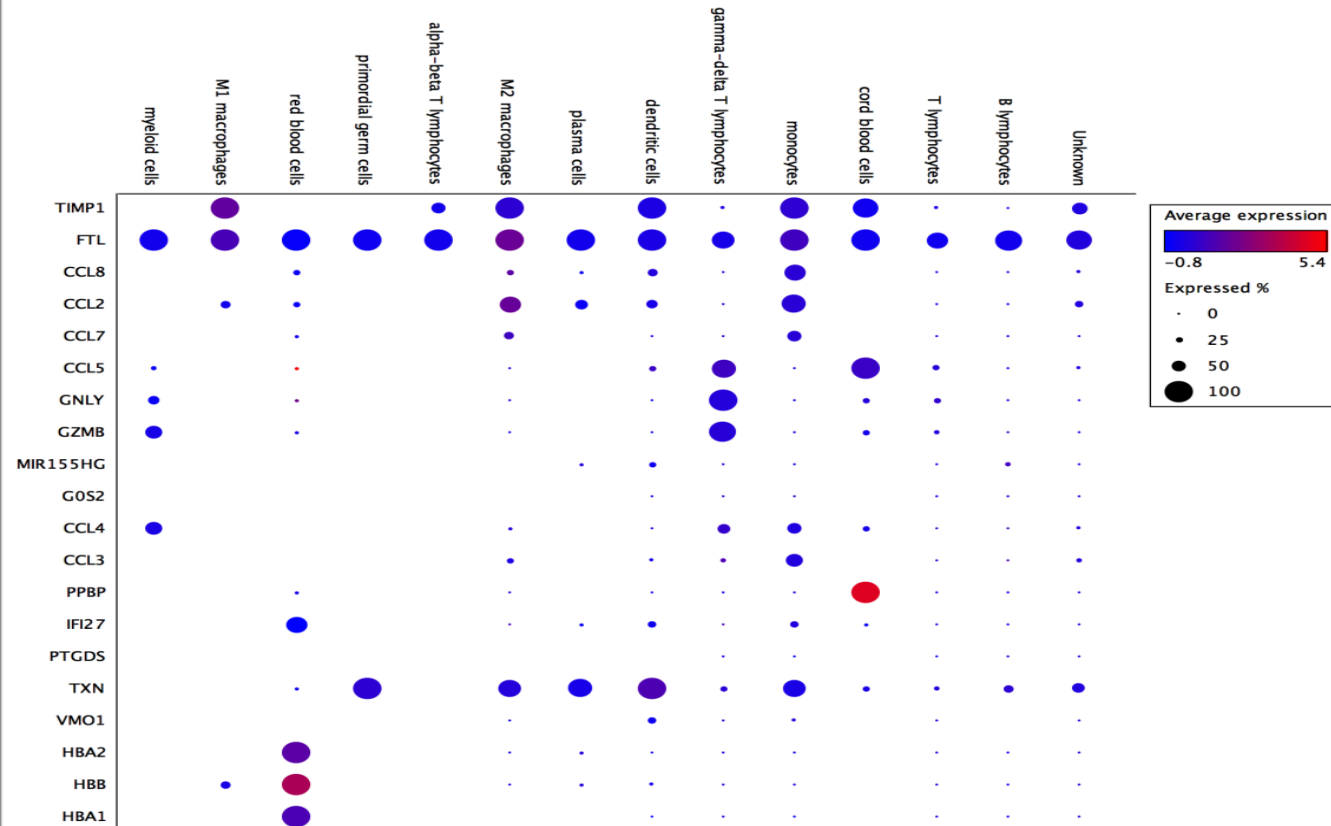




# Normaliz



# Expression Analysis on Single Cell



# The new CLC Genomics Workbench 21

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**Read manual**

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## Biomedical Tools and Workflows

### ➤ New tools

- **Structural Variant Caller**
- **Compare Immune Repertoires**
- **Extract Reads with Primer**
- **Remove Marginal Reads**
- **Target Region Coverage Analysis**
- **CNV and LOH Detection**

### ➤ New workflows

- **SARS-CoV-2**
- **TruSight Oncology 500 bundle**
- **QIAseq**
- **Reference data**

### Ready-to-Use Workflows

- ▼ SARS-CoV-2 Workflows
  - Identify Ion AmpliSeq SARS-CoV-2 Low Frequency and Shared Variants (Ion Torrent)
  - Identify QIAseq SARS-CoV-2 Low Frequency and Shared Variants (Illumina)
- ▶ Preparing Raw Data
- ▼ QIAseq Panel Analysis
  - Analyze QIAseq Panels
    - ▶ QIAseq Analysis Workflows
- ▼ TSO500 Panel Analysis
  - Perform TSO500 DNA Analysis (Illumina)
  - Perform TSO500 RNA Analysis (Illumina)
- ▶ Whole Genome Sequencing
- ▶ Whole Exome Sequencing
- ▶ Targeted Amplicon Sequencing
- ▶ Whole Transcriptome Sequencing
- ▶ Small RNA Sequencing

# Structural Variant Caller

- Can be used for whole genome or targeted analysis
- Better performance compared to old tools in CLC
- Detects germline as well as somatic variants

## 1 Variants

Chromosome	Length	Reads	Left breakpoints	Right breakpoints	Variants
1	248,956,422	1,272,783	202	186	3
2	242,193,529	1,255,428	229	211	2
3	198,295,559	1,075,417	193	170	3
4	190,214,555	563,830	125	125	1
5	181,538,259	795,898	141	124	2
6	170,805,979	1,050,319	219	190	8
7	159,345,973	753,297	131	141	0
8	145,138,636	688,069	126	149	1

## 2 Summary

Chromosome	Total # variants	Insertion	Deletion	Tandem Duplication	Inversion	CNV Loss	CNV Gain
1	3	0	0	2	1	0	0
2	2	0	0	1	1	0	0
3	3	0	2	1	0	0	0
4	1	0	1	0	0	0	0
5	2	0	2	0	0	0	0

Chromosome	Region	Type	Score	Subtype	Complexity	Evidence	Left breakpoint	Right breakpoint
19	57018308...57018310	Deletion	28	Deletion	13	Single Breakpoint	57018307^57018308	
19	57174102...57174145	Deletion	44	Deletion	18	Single Breakpoint	57174101^57174102	
19	57499556...57499621	Deletion	48	Deletion	20	Single Breakpoint		57499621^57499622
19	245876...245978	Deletion	103	Deletion	30	Paired Breakpoints	245900^245901	245971^245972
19	245971^245972	Insertion	30	Insertion	23	Paired Breakpoints	245999^246000	245971^245972
19	269761...269826	Deletion	66	Deletion	20	Paired Breakpoints	269825^269826	269819^269820
19	302692^302693	Insertion	87	Tandem Dupli...	26	Paired Breakpoints	302778^302779	302692^302693
19	365492...365545	Deletion	79	Deletion	41	Paired Breakpoints	365541^365542	365545^365546

# Compare Immune Repertoires

## Outputs

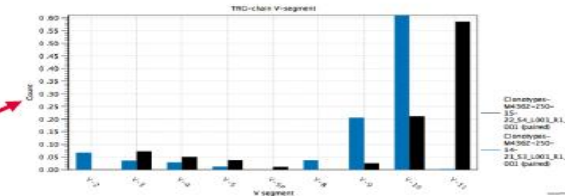
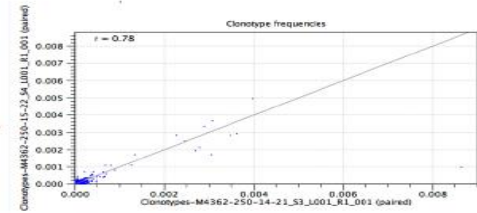
## Report

- Table of Contents
- 1 Summary
- 2 Diversity indices
  - 2.1 TRA diversity indices
  - 2.2 TRB diversity indices
  - 2.3 TRG diversity indices
  - 2.4 TRD diversity indices
- 3 Scatter plots
  - 3.1 TRA scatter plot
  - 3.2 TRB scatter plot
  - 3.3 TRG scatter plot
  - 3.4 TRD scatter plot
- 4 Rarefaction
  - 4.1 TRA rarefaction
  - 4.2 TRB rarefaction
  - 4.3 TRG rarefaction
  - 4.4 TRD rarefaction
- 5 CDR3 length
  - 5.1 TRA
  - 5.2 TRB
  - 5.3 TRG
  - 5.4 TRD
- 6 V and J usage

**2 Diversity indices**

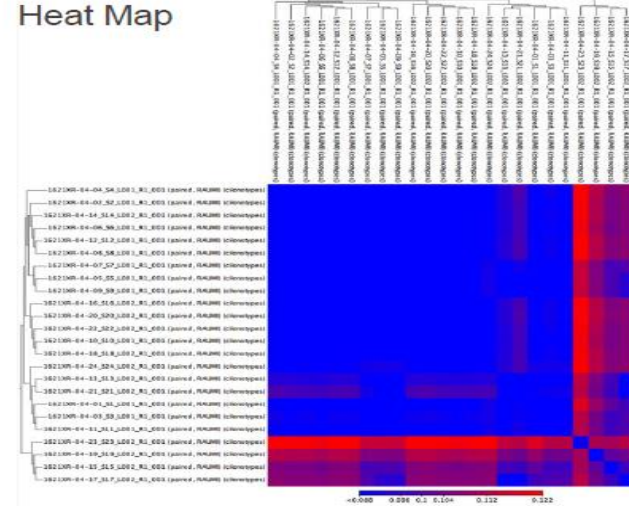
**2.1 TRA diversity indices**

Sample	Observed diversity	Extrapolated diversity (jack10)	Extrapolated Shannon-Wiener index (shann10)	Incorporated to total sample diversity
Clonotypes-M4362-250-14-21_S4_L001_R1_001 (pair)	31,277.00	37,693.33	10.30	37,693.33
Clonotypes-M4362-250-14-21_S4_L001_R1_001 (pair)	30,033.00	36,519.04	10.31	36,519.04



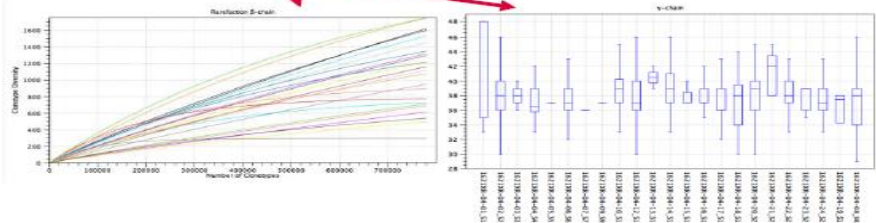
2 samples

## Heat Map



Sample	1621XR-04-01_S1_L...	1621XR-04-02_S2_L...	1621XR-04-03_S3_L...	1621XR-04-04_...	1621XR-04-05_S5_L...	1621XR-04-06_S6_L...
1621XR-04-01_S1_L...	1.00	0.92	0.91	0.92	0.92	0.92
1621XR-04-02_S2_L...	0.92	1.00	0.91	0.93	0.93	0.93
1621XR-04-03_S3_L...	0.91	0.91	1.00	0.91	0.92	0.91
1621XR-04-04_S4_L...	0.92	0.93	0.91	1.00	0.92	0.93
1621XR-04-05_S5_L...	0.92	0.93	0.92	0.92	1.00	0.94
1621XR-04-06_S6_L...	0.92	0.93	0.91	0.93	0.94	1.00

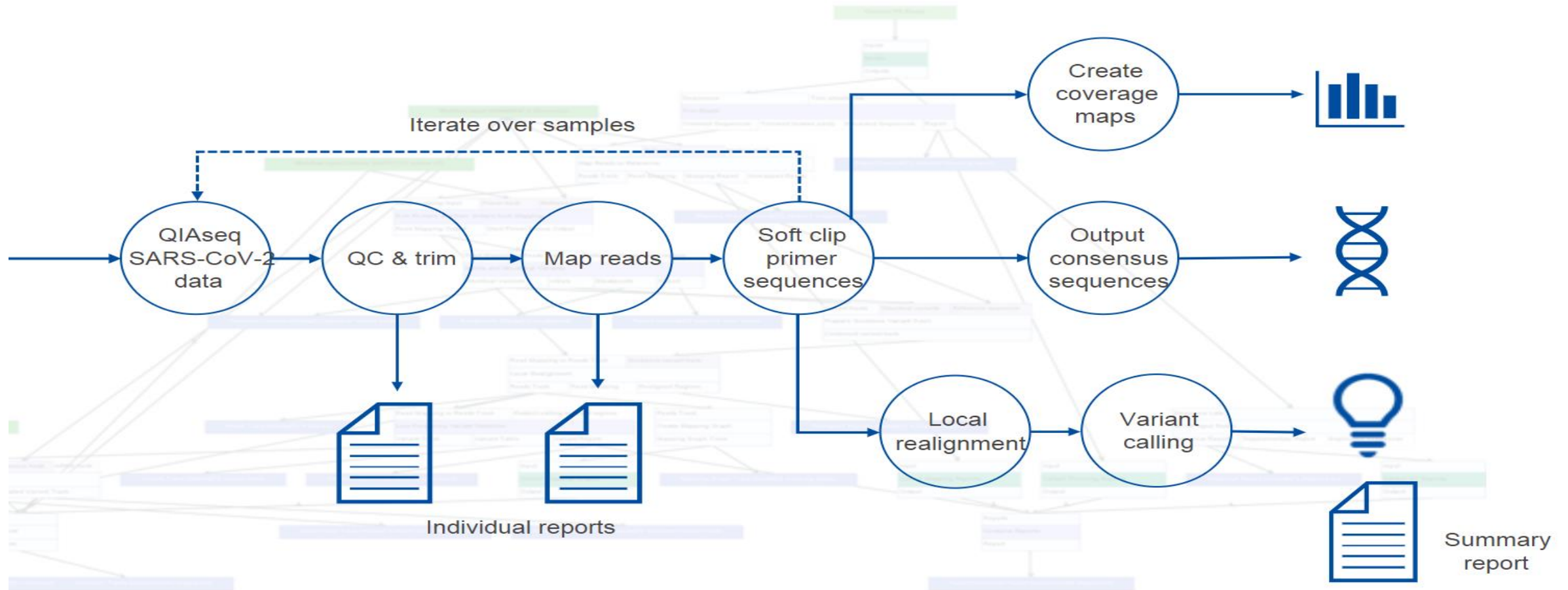
Similarity table



Multiple samples



# SARS-CoV-2 Workflow





# TSO500 Panel Analysis

- ▼ TSO500 Panel Analysis
  - Perform TSO500 DNA Analysis (Illumina)
  - Perform TSO500 RNA Analysis (Illumina)

Manage Reference Data

Imported Data  
Imported Reference Data

Manage Reference Data: Locally

Free space in CLC\_References location: 22.26 GB  
Free space in temporary folder location: 22.26 GB

TSO500 hg38

Version: 1.0, Reference Data Set

Size on disk  
837.2 MB

Copy from server
Download
Delete
Create Custom Set ...

Reference Data included:			
Workflow role	Version	Download Size	On Disk Size
<input checked="" type="checkbox"/> sequence	hg38_no_alt_analysis_set	658.9 MB	688.5 MB
<input checked="" type="checkbox"/> genes	refseq_GRCh38.p13_no_alt_analysis_set	3.4 MB	4.1 MB
<input checked="" type="checkbox"/> mrna	refseq_GRCh38.p13_no_alt_analysis_set	13.2 MB	16.0 MB
<input checked="" type="checkbox"/> cds	refseq_GRCh38.p13_no_alt_analysis_set	27.6 MB	36.5 MB
<input checked="" type="checkbox"/> target_regions	tso500_v1.0_hg38_no_alt_analysis_set	97 KB	296 KB
<input checked="" type="checkbox"/> fusions	qiagen_v1_hg38_no_alt_analysis_set	28 KB	55 KB
<input checked="" type="checkbox"/> gene_pseudogene_track	tmb-large_v1.0_hg38_no_alt_analysis_set	104 KB	23 KB
<input checked="" type="checkbox"/> masking_regions	tmb-large_v1.0_hg38_no_alt_analysis_set	8 KB	15 KB
<input checked="" type="checkbox"/> dbsnp_tmb	tmb-large_151_refseq_hg38_no_alt_analysis_set	21.0 MB	91.7 MB

Close

## Outputs

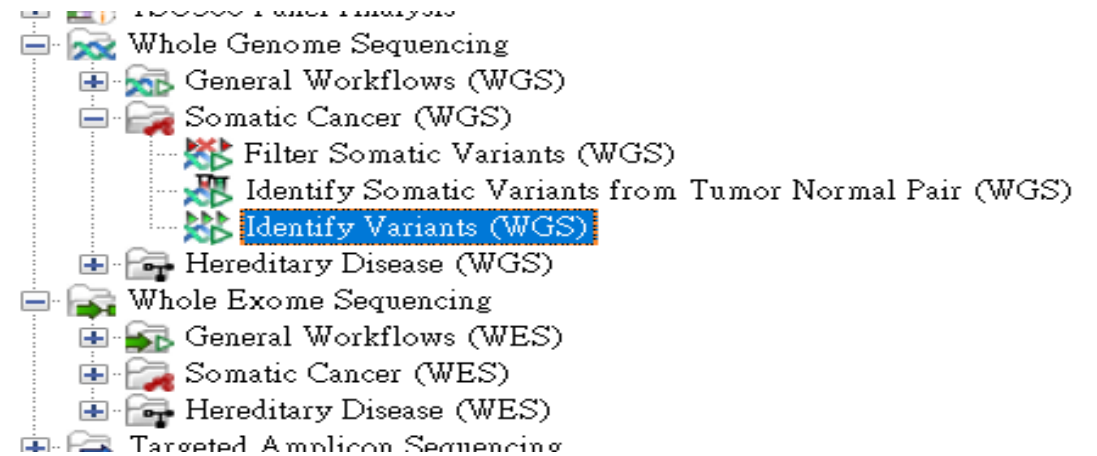
- ▼ TSO500\_DNA
  - Workflow Result Metadata
  - ▶ QC & Reports
  - ▼ Tracks
    - Mapped\_UMI\_reads-DL017-UP01-19MAY20-ABU\_S1\_L001\_R1\_001 (paired)
    - Per-region\_statistics\_track-DL017-UP01-19MAY20-ABU\_S1\_L001\_R1\_001 (paired)
    - Unfiltered\_variants-DL017-UP01-19MAY20-ABU\_S1\_L001\_R1\_001 (paired)
    - Amino acid track
    - TMB\_somatic\_variants-DL017-UP01-19MAY20-ABU\_S1\_L001\_R1\_001 (paired)
  - ▼ VCF Exportable Tracks
    - Variants\_passing\_filters-DL017-UP01-19MAY20-ABU\_S1\_L001\_R1\_001 (paired)
  - DNA\_combined\_report-DL017-UP01-19MAY20-ABU\_S1\_L001\_R1\_001 (paired)
  - Track List
  - Perform TSO500 DNA Analysis (Illumina) log
- ▼ TSO500\_RNA
  - Workflow Result Metadata
  - ▶ QC & Reports
  - Gene\_expression-RL008-UP16-19MAY20-SA\_S16\_L001\_R1\_001 (paired)
  - ▼ Tracks (WT)
    - RNA\_read\_mapping (WT)-RL008-UP16-19MAY20-SA\_S16\_L001\_R1\_001 (paired)
    - Fusion\_genes\_unaligned\_ends (WT)-RL008-UP16-19MAY20-SA\_S16\_L001\_R1\_001 (paired)
    - Fusion\_genes (WT)-RL008-UP16-19MAY20-SA\_S16\_L001\_R1\_001 (paired)
    - Read\_mapping\_refined (WT)-RL008-UP16-19MAY20-SA\_S16\_L001\_R1\_001 (paired)
  - RNA\_combined\_QC\_report-RL008-UP16-19MAY20-SA\_S16\_L001\_R1\_001 (paired)
  - ▶ Tracks (fusion)
  - ▼ VCF Exportable Tracks
    - Final\_fusion\_genes (WT)-RL008-UP16-19MAY20-SA\_S16\_L001\_R1\_001 (paired)
  - Genome Browser View (Fusions)
  - Genome Browser view (WT)
  - Perform TSO500 RNA Analysis (Illumina) log

## Summary

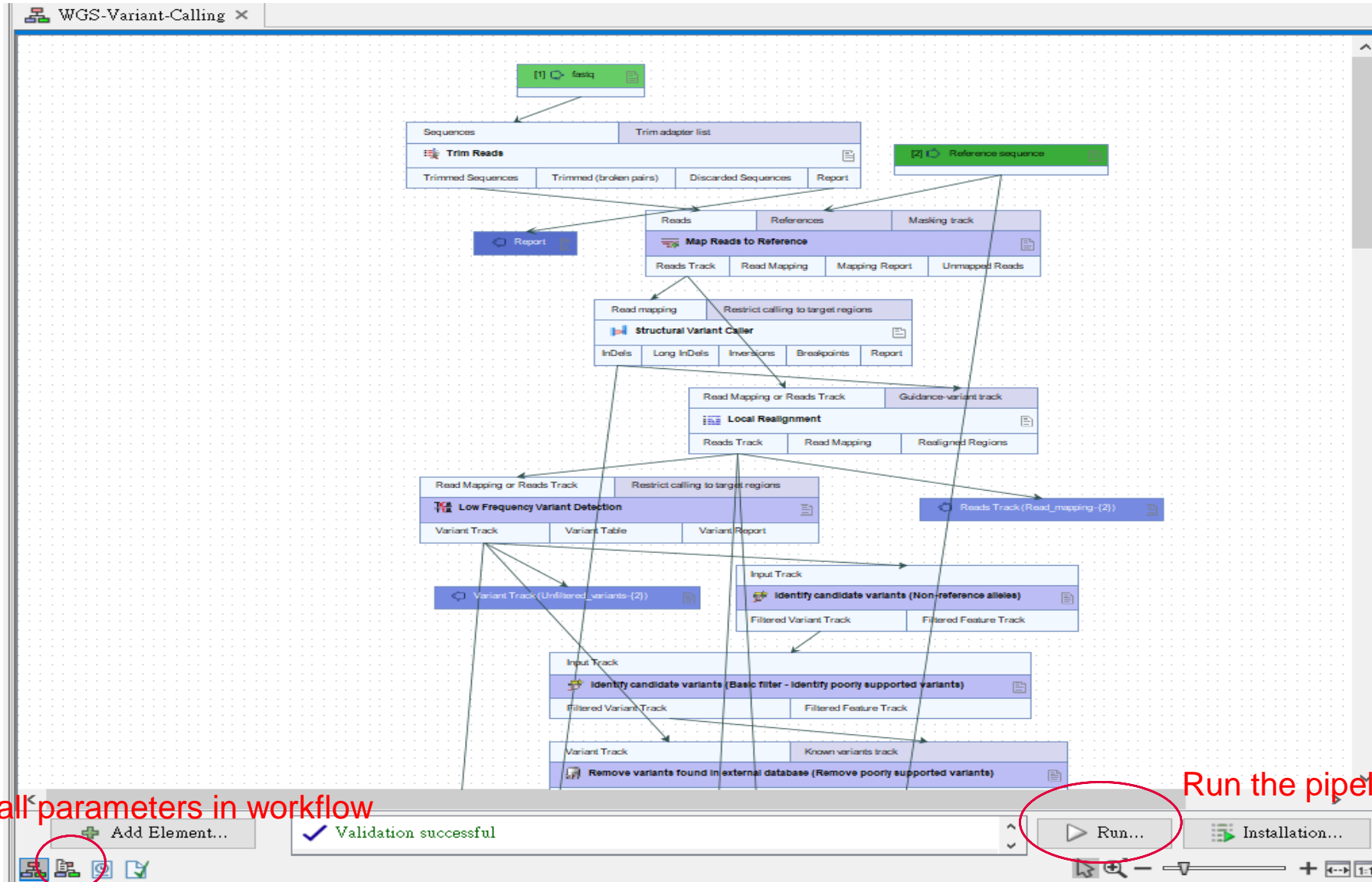
- One solution for genomics application with GUI
  - User-friendly interface
  - Interactive visualization to facilitate analysis
  - Ready-to-use and customizable workflows
    - For automated processing
    - For sharing with colleagues
  - Modular design to add plugins
  - Works with reads from most platform
    - Illumina, Ion Torrent, Oxford Nanopore, PacBio, BGI/MGI
  - Fully documented and supported

# Workflow Methods

- The whole workflow is design when you have FASTQ files
  - Previous work: DNA-Seq Analysis for all your sample
  - Input:
    - FASTQ data
    - Metadata
  - Output:
    - VCF files with filtering variants



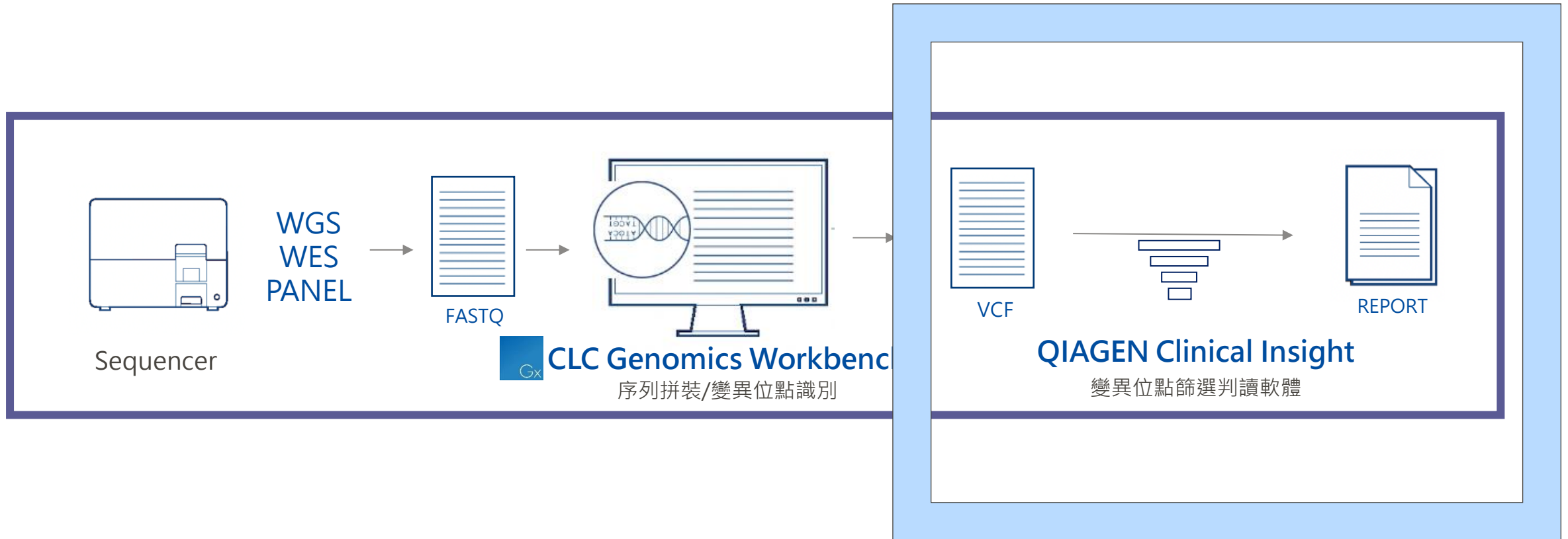
# Customized full workflow



Change all parameters in workflow

Run the pipeline

# QIAGEN Clinical Insight System



# NGS Variant Analysis Service

Variants  
number

1: sequencing & base call [FastQ]

```

@PCC078PAC00:2:1101:1184:3385#ACTCAA0/2
GGGGCATCAATGATAGTCACATAGTACTTCTGCTCAAAATTCACAAAGGAGATCAATGATACCACGCTTACGCTTC
+
_||_eeeeegfgfgehhgfghhhfsgihiiiiiihhchfhiisihhiiiiiddegfhdfghihfdddfgdshdgtgpeddcdbddcd
@PCC078PAC00:2:1101:1162:3439#ACTCAA0/2
CTGCTTTCCTTCCTTCATATTCGGAATCCAGCAGTTCTTCTGTTTTGCGAGGACACAGATTATCTTATTTGGTACCACCA
+
[ _ccccceecog'beadf'gbg'chf@bbbihihd_'cefbbbe]aYaefffthafff[ 'cdgd@bd]decdccc' ]Z'bbbbBB
@PCC078PAC00:2:1101:1210:3447#ACTCAA0/2
GGCCCGCATCACTGTGCTGCTTGAAGTATAAGCCGCTGAATCCCGGAGTGAAGACATGGCCCTGACTGCACCTCAATCTGGATGCCCG
+
a_bcececeppghaeethff]]ebcf"bggfthie]fafh[beghi fgg0'ZZZ_'Z'dbdecc"jbbcbjbc]bbb@bY_"ba_
:
  
```

2: Variants calling[VCF]

#CHROM	POS	ID	REF	ALT	QUAL	FILTER	INFO	FORMAT
chr1	978603	rs3588118	CCT	C	2883.6	PASS	AC=1;AF=GT;AD:DP:GQ:PL	
chr1	1163811	rs1476947	G	GGACA	2118.64	PASS	AC=1;AF=GT;AD:DP:GQ:PL	
chr1	1177918	rs3835300	CT	C	1614.6	PASS	AC=1;AF=GT;AD:DP:GQ:PL	
chr1	1223465	rs5808105	GC	G	375.6	PASS	AC=1;AF=GT;AD:DP:GQ:PL	
chr1	1247578	.	T	TGG	13	PASS	P=0.9462 GT:VR:RR:DP:GQ	

3: variants  
annotation

[annotation file]

Gene	Type	Position	AChange	dbSNP	AlleleFreq	gnomAD_e	gnomAD_c	primaryACMGEvid	primaryACMGL
TSHR	nonsynony	chr14:816	NM_000369.3:exon9:c.	rs1895064	0.0019230	0 22	0 3	pm1 pm2 pm5 pp3	Likely pathogeni
LZTR1	nonsynony	chr22:213	NM_006767.4:exon14:c.	rs1331354	5.57165e-4	0 1	.	pm1 pm2 pm5	Likely pathogeni
C7	frameshift	chr5:4095	NM_000587.4:exon11:c.	rs7458262	0.0006426	0 5	0 1	pvs1 pm2	Likely pathogeni
CACNA1A	nonsynony	chr19:133	NM_001127221.1:exon.	rs5741943	0.0008409	0 15	.	pp2 pm1 pm2 pp3	Likely pathogeni
CACNA1A	nonframes	chr19:133	NM_001127222.2:exon.	.	.	.	.	pm2 bp3	VUS
HSD17B4	nonsynony	chr5:1188	NM_000414.4:exon4:c.	rs5444551	0.0006524	0 12	.	pm1 pm2 pp3	VUS
COL11A1	nonsynony	chr1:1035	NM_001854.4:exon3:c.	rs1158320	.	.	.	pm1 pm2 bp4	VUS
KMT2C	stopgain	chr7:1519	NM_170606.3:exon18:c.	rs5852856	.	.	.	pvs1 pm2	Likely pathogeni

4: Clinical  
report

Gene	Position	Transcript	HGVS(c) (Exon)	HGVS(p)	Type	dbSNP	MAF	Heterozygosity	Clinical Level	Disease and Inheritance
MYH7	chr14:2390286 5-23902865	NM_00025 7.3	c.77C>T (exon3)	p.A26V	nonsynony mous SNV	rs186964 570	0.0069	het	Likely path ogenic	Cardiomyopathy, hypertrophic, 1 AD

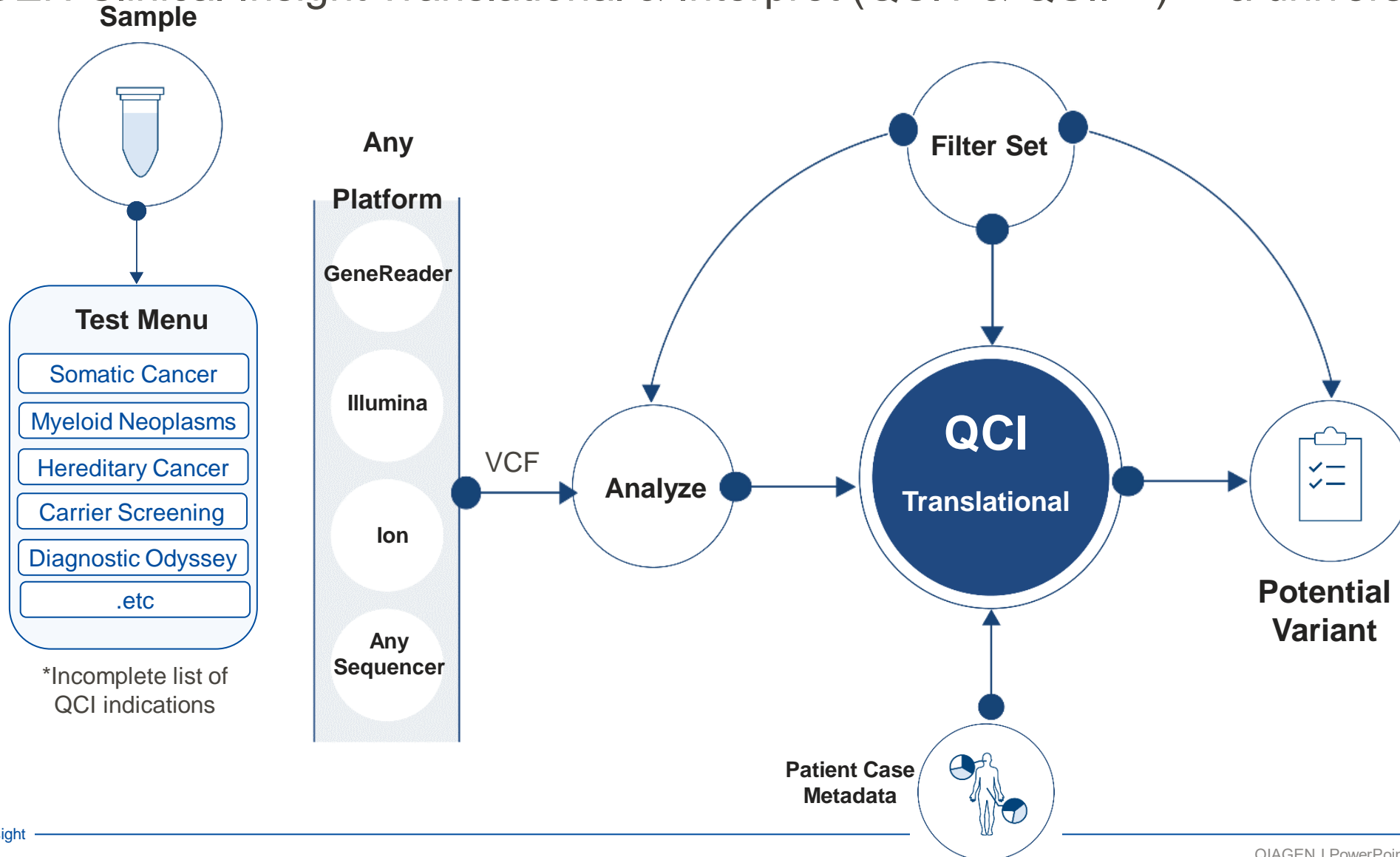


## Database in QCII/QCIT (Free access in QCII/QCIT software)

Public Databases	Licensed Databases	QIAGEN Databases	Clinical Guidelines	Others
TCGA		Clinical Cases	<b>ACMG</b>	CADD
Clinvar		Clinical & Functional Studies	AMP	Polyphen
dbSNP	<b>COSMIC</b>	<b>HGMD</b>	NCCN	SIFT
1000 Genome	ICGC	PGMD	ASCO	
ESP	OMIM	Curated variants	CAP	PhyloP
gnomAD	BIC	Pathway and causal network	ESMO	Blosum
ExAC	<b>CentO MD</b>	Allele Frequency Community	FDA	MaxEntScan
Clinical Trials			EMA	Mutation Taster



# QIAGEN Clinical Insight Translational & Interpret (QCIT & QCII™) – a universal solution



## QCII/QCIT difference

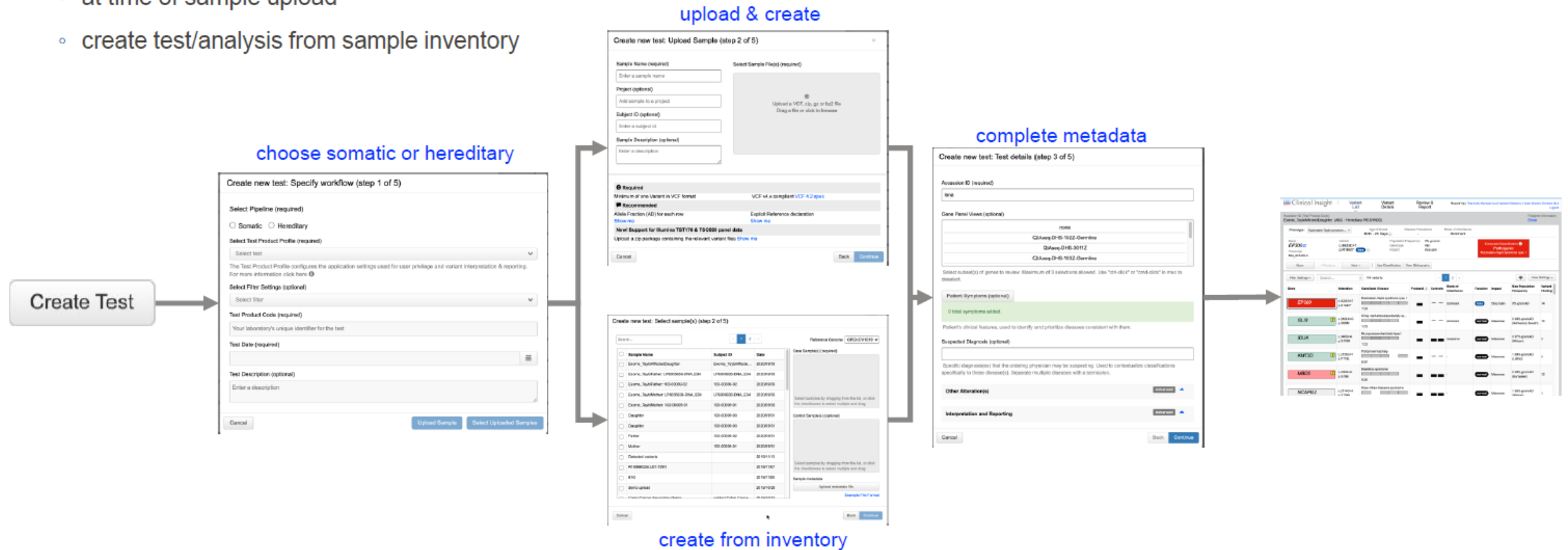
	QCIT(偏研究使用)	QCII(偏臨床使用)
功能	註解工具與篩選位點	註解工具與篩選位點 臨床與藥物資料提供臨床判讀使用
應用	<ul style="list-style-type: none"> <li>• 可單一或多樣本分析，或是家族(trio)分析</li> <li>• 可做群組分析(cohort study)</li> </ul>	<ul style="list-style-type: none"> <li>• 出具臨床報告</li> </ul>
優勢	<ul style="list-style-type: none"> <li>• Qiagen內建database(含ACMG guideline)</li> <li>• 有權限管理系統</li> <li>• 可設定多種分析流程</li> </ul>	<ul style="list-style-type: none"> <li>• Qiagen內建database(含ACMG&amp;AMP guideline)</li> <li>• 可客製報告模板</li> <li>• 有權限管理系統</li> <li>• 可設定多種分析流程(TPP)</li> <li>• 可設定報告簽核系統</li> </ul>
輸出	Excel表格(註釋資料)	Excel表格與檢測報告

# Create Your Variant Analysis Strategically

New Create Test button to start test creation workflow

Create new test/analysis

- at time of sample upload
- create test/analysis from sample inventory



# QIAGEN Clinical Insight Interface

Pathogenic

Likely Pathogenic

VUS

Likely Benign

Benign

## Actionability

### AMP/ASCO/CAP Guidelines – Somatic Testing\*\*

Tier 1A Strong clinical significance  
Tier 1B

Tier 2C Potential clinical significance  
Tier 2D

Tier 3 Unknown clinical significance

Tier 4 Likely benign or benign

Clinical Insight

Variant List

Variant Details

Review & Report

Gene Chen | Test List | Sample List | Variant Directory | User Guide

Accession ID (Test Product Code)  
TestA: A4 (ABC - Somatic)

## 1 Variant Basic Information

Sex  
Female

Ethnicity  
-

Phenotype: Breast cancer | Age of Onset: 61 Years | Gene Prevalence: 20% | Disease Prevalence: 1/77

Gene: **PIK3CA** | Variant: c.1624G>A p.E542K gain | Somatic Frequency: 2.53% | Population Frequency: 0% gnomAD | Allele Fraction: 35% (of 60 reads) | Impact: missense

## 2 ACMG & AMP Guideline

Computed Classification  
Tier 1A  
Pathogenic  
Breast cancer

New Assessment  
Tier 1A  
**Pathogenic**  
for Breast cancer  
Reportable

## 3 Filter Setting

## 4 View Variant List

## 5 View Setting

Filter Settings | Search... | 39 variants

Biomarker	Alteration	Function	Impact	Case - Quantity	Somatic Frequency	Max Population Frequency
<b>PIK3CA</b> 1A Pathogenic	c.1624G>A p.E542K	gain	Missense	35% (of 60 reads)	2.53%	0% gnomAD
<b>ESR1</b> 1B Pathogenic	c.1610A>C p.Y537S	gain	Missense	24% (of 74 reads)	0.30%	0% gnomAD
<b>2C FANCD2</b>	c.1278+3_1278+6delAAGT	loss	-	14% (of 74 reads)	0%	0.001% gnomAD (European)
<b>2C ATRX</b>	c.2671G>C p.E891Q	loss	Missense	72% (of 50 reads)	0%	0% gnomAD
<b>3 CYP2D6</b>	c.1457G>C p.S486T	loss	Missense	63% (of 40 reads)	0%	0% gnomAD
<b>3 HLA-DRB1</b>	c.115C>T p.Q39*	loss	Stop Gain	26% (of 39 reads)	0%	0% gnomAD
<b>3 PRSS1</b>	c.47C>T p.A16V	loss	Missense	32% (of 44 reads)	0%	4.32% gnomAD (African)

## Test Performed: Somatic Panel

Report Date Nov 8, 2020  
Status -

Patient		Client		Specimen	
Patient Name	Michelle Doe	Client	General Hospital	Specimen ID	TestA: A4
Date of Birth		Client ID	ABC123	Specimen	biopsy
Age		Physician	Dr. E Smith	Collection	Nov 9, 2020
Sex	Female	Pathologist	Dr. R Jones	Accession	Nov 9, 2020
Ethnicity		Primary Tumor Site	Breast		
Diagnosis	Breast Cancer				

Result: **Positive**

<b>2</b> Clinically Significant Variants	<b>5</b> Therapies Associated with Resistance	<b>8</b> Therapies with Potential Clinical Benefit	<b>22</b> Clinical Trials
---	--	---	------------------------------

## Report Summary

PIK3CA E542K was identified and is associated with an available treatment. One alteration is associated with resistance to aromatase inhibitor therapy.

#####

## Actionable Variants With Associated Therapies

Gene / Variant	Allelic Fraction	Approved Therapies			Clinical Trials
		Breast Cancer	Other Indications	Associated With Resistance	
<b>PIK3CA</b> c.1624G>A p.E542K g.179218294G>A Tier 1A Pathogenic	35.0% (of 60 reads)	alpelisib alpelisib /fulvestrant lapatinib /letrozole letrozole	-	-	19
<b>ESR1</b> c.1610A>C p.Y537S g.152098788A>C Tier 1B Pathogenic	24.0% (of 74 reads)	fulvestrant neratinib tamoxifen toremifene	-	anastrozole aromatase inhibitor fulvestrant letrozole tamoxifen	3

Gene / Variant	Trial Title Trial ID	Treatments	Trial Phase	Location / Contact
<b>ESR1</b> p.Y537S g.152098788A>C Tier 1B Pathogenic	A Phase 1 Study of SY 5609, an Oral, Selective CDK7 Inhibitor, in Adult Patients With Select Advanced Solid Tumors <a href="#">NCT04247126</a>	SY-5609 fulvestrant	Phase 1	United States: MI, OK, PA, TN, TX Kimberley Caliri; kcaliri@syros.com; 617-674-9053;
<b>ESR1</b> p.Y537S g.152098788A>C Tier 1B Pathogenic	INTERACT- Integrated Evaluation of Resistance and Actionability Using Circulating Tumor DNA in HR Positive Metastatic Breast Cancers <a href="#">NCT04256941</a>	anastrozole letrozole ribociclib abemaciclib /letrozole letrozole /palbociclib palbociclib abemaciclib fulvestrant letrozole /ribociclib	Phase 2	United States: TX Senthilkumar Damodaran; sdamodaran@mdanderson.org; 713-792-2817;

## Individual Variant Interpretations

Gene <b>PIK3CA</b> Exon 10 Nucleotide NM_006218.4: g.179218294G>A c.1624G>A Amino Acid p.E542K Function gain Allelic Fraction 35.0% (of 60 reads) Classification <b>Tier 1A</b> Assessment <b>Pathogenic</b>	<b>Interpretation</b> PIK3CA encodes the protein p110-alpha, which is the catalytic subunit of phosphatidylinositol 3-kinase (PI3K). The PI3K pathway is involved in cell signaling that regulates a number of critical cellular functions, including cell growth, proliferation, differentiation, motility, and survival [16, 6]. PIK3CA mutations are not mutually exclusive with EGFR or KRAS or BRAF mutations, and are associated with increased PI3K signaling and increased activation of Akt [22, 10]. Activating missense mutations in PIK3CA, including the E542K, E545K, and H1047R hotspot mutations, predominantly occur in the helical (exon 9) and kinase (exon 20) domains [17, 2].
Gene <b>ESR1</b> Exon 10 Nucleotide NM_001122742.1: g.152098788A>C c.1610A>C Amino Acid p.Y537S Function gain Allelic Fraction 24.0% (of 74 reads) Classification <b>Tier 1B</b> Assessment <b>Pathogenic</b>	<b>Interpretation</b> ESR1 encodes estrogen receptor alpha (ER-alpha), one of the major estrogen receptor isoforms in humans; binding of estrogen to ER-alpha promotes its translocation to the nucleus and the transcriptional activation of genes involved in cell cycle progression and survival [14]. Mutation or amplification of ESR1 and activation of ER-alpha may result in the upregulation of genes involved in cell cycle progression and survival, and ER-alpha signaling has been implicated in a number of cancer types [14, 12, 4, 21, 15]. However, ER-alpha may act as a tumor suppressor in some cancers [23, 3, 1, 5].

# MyQCI – Test Product Profile (TPP) Configuration

Create a new Test Product Profile ✕

Workflow (required)  
Somatic

Workflow Pipeline (required)  
Interpret

User Group (required)  
2019August

Copy from  
--- Available TPP ---

- Available TPP ---
- QIAGEN Test Product Templates**
- Illumina® TruSight™ Oncology 500
- Illumina® TruSight™ Tumor 170**
- QCI Interpret Somatic Default
- QCI Interpret (Somatic) Default + ReportingPolicy
- QIAact-AIT-Basic-FFPE\_QIAGEN
- QIAact-AIT-Basic-Plasma\_QIAGEN
- QIAact-AIT-UMI-FFPE\_QIAGEN
- QIAact-BRCA-1\_2-Basic-FFPE\_QIAGEN
- QIAact-BRCA-UMI-FFPE\_QIAGEN



myQCI Test Product Profiles Reports API Explorer Admin Tool Contact U

Search by Test Product Profile... Import Create New

Test Product Profile	User Group Name	Workflow Type	Last Updated	Updated By
HopeSeq Heme Research Panel	QIAGENOfTheShellTPP	Somatic	19/05/2020 15:02	myqci super_admin
SomaticBare	QIAGENOfTheShellTPP	Somatic	18/05/2020 22:45	myqci super_admin
tpp-ds-auto-LhbrpAWdwkPtjzXRmPNC	QIAGENOfTheShellTPP	Somatic	18/05/2020 06:30	myqci super_admin
tpp-ds-auto-aNQdRHZPAffPSzkJPzde	QIAGENOfTheShellTPP	Somatic	18/05/2020 06:30	myqci super_admin
testngb0fa6b0a-060a-425b-900c-69312a8b0b61	QIAGENOfTheShellTPP	Hereditary	18/05/2020 04:24	myqci super_admin
testngd8fed7d7-627e-4fa3-8575-d9dae7803a60	QIAGENOfTheShellTPP	Somatic	18/05/2020 03:16	myqci super_admin
tppDefaultiUR	QIAGENOfTheShellTPP	Somatic	17/05/2020 21:03	dstestuser qci-a

Details

- Name: HopeSeq Heme Research Panel
- Workflow type: Somatic
- Workflow Pipeline: QCI Interpret One Pre-curated
- State: STAGING
- User Group Name: QIAGENOfTheShellTPP
- Code: COH-HSRP
- Report Template: QCII-One\_DemoReport
- Variant Pre-filter: hopeseq\_prefilter
- Automated Flow: false
- Reporting Method:

# MyQCI - Report

myQCI Test Product Profiles Reports API Explorer Admin Tool

Contact Us User Guide

Manage Signatures Create New

Report Name	Base Report	Last Updated ^	Updated By
Onco report	Somatic Demo v2.1.0	24/11/2020 16:28	Mariana Satrova

1 selected / 1 total

Details

**Report Name**  
Onco report

**Based on**  
Somatic Demo v2.1.0

**Created**  
24/11/2020 16:28




**Created by**  
Mariana Satrova

**Last updated**  
24/11/2020 16:28


**Updated by**  
Mariana Satrova

Delete Copy Preview Export Edit

# MyQCI – Customize Your Report Style

« Back  Save  Settings  Styling ▶ Preview
Editing report: TESTGRSomaticDemo
</> Advanced edit

**Warning:** The purpose of this sample report is to illustrate report components and not accuracy or completeness of scientific evidence.



**YOUR LAB**

Your Lab  
1700 Lincoln Blvd, Suite 20, Redwood City, CA 94063  
labxyz.com / (650) 484 4040  
Additional Information

Page 1 of 6

**Test Performed: Somatic Panel**

Report Date **Nov 25, 2019**  
Status -

**Specimen Information**

Date of Birth Jan 29, 1990	Accession ID NSCLC demo
Age 29	Specimen biopsy
Sex Male	Collection Aug 7, 2019
Ethnicity Caucasian	Accession Aug 1, 2019
Diagnosis Lung adenocarcinoma	Primary Tumor Site Lung
Diagnosis Stage IB	

**Result: Positive**

<b>3</b>	<b>1</b>	<b>1</b>	<b>1</b>
Clinically Significant Variants	Therapies Associated with Resistance	Therapies with Potential Clinical Benefit	Clinical Trials

**Report Summary**

This is a customizable sample report. The purpose of this sample report is to illustrate report components and not accuracy or completeness of scientific evidence.



# MyQCI - API Explorer (**Another License Required**)

**Test Endpoints**

Search for Tests

[Submit a New Test](#)

[Check Status of Submission](#)

[Share Test with Others](#)

[Export Test Results](#)

[Update assessment](#)

**Profile Endpoints**

[Get All Test Product Profiles](#)

[Get Test Product Profile by Name](#)

**Metadata Prep**

**Select SDK version to Download**

SDK 1.14 ▼

Download

GET /v1/clinical Search for submitted tests satisfying user-supplied criteria

### Parameters

Parameter	Value	Description	Parameter Type	Data Type
<b>state</b>	<input type="text"/>	Limit search results to tests in a specific state.	query	string
<b>startReceivedDate</b>	<input type="text" value="YYYY-MM-DD"/>	Beginning of the range of dates to search format: yyyy-mm-dd	query	date
<b>endReceivedDate</b>	<input type="text" value="YYYY-MM-DD"/>	Beginning of the range of dates to search format: yyyy-mm-dd	query	date
<b>sort</b>	<input type="text"/>	Order for the list of results. ( <i>receivedDateDesc</i> - default)	query	string

**bold red**= required

Run Query

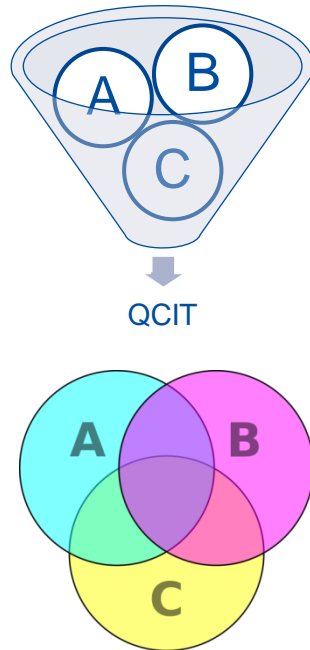
**Response Class (status 200)**

Model Schema

# CASE STUDY

## 1. 針對不同表型之癌症病患篩選位點並提供用藥資訊

- Characterizing the variants specific to the different subtypes
  - Samples
    - Subtype A: 9 samples
    - Subtype B: 9 samples
    - Subtype C: 9 samples



Gene	Alteration	Phenotype	Cases	Mode of Inheritance	Function	Impact	Max Population Frequency	Variant Findings
ACTN3	c.1726C>T p.R577*	ACTN3 deficiency	█	-	-	Stop Gain	0% gnomAD	242
CSTF9	c.235C>T p.R82*	Familial 45, XY disorders of sex.	█	-	-	Stop Gain	1.54% gnomAD (East Asian)	6
CYP2D6	c.1437G>C p.S481*	Schizophrenia	█	-	-	Missense	0% gnomAD	156
CYP2D6	c.480G>C p.V136V	Schizophrenia	█	-	-	Synonymous	0% gnomAD	17
DPYD	c.261A>C p.C59R	Dihydropyrimidine dehydrogenase	█	recessive	-	Missense	0% gnomAD	325
ESR1	c.1618A>C p.Y537S	Hemiblast breast and/or ovarian.	█	dominant	-	Missense	0% gnomAD	342
FANCD2	c.1278-3_1278-18delAGGT	Fanconi anemia	█	recessive	-	-	0.001% gnomAD (European)	8

## 2. 以Trio家族性遺傳性分析評斷多表型遺傳症狀之變異位點

- Heredity: Trio Analysis on multiple-phenotypes genetic disease
  - Samples
    - Proband
    - Father
    - Mother
  - Goal:
    - To find the genetic-linkage variants on specific phenotypes on case children

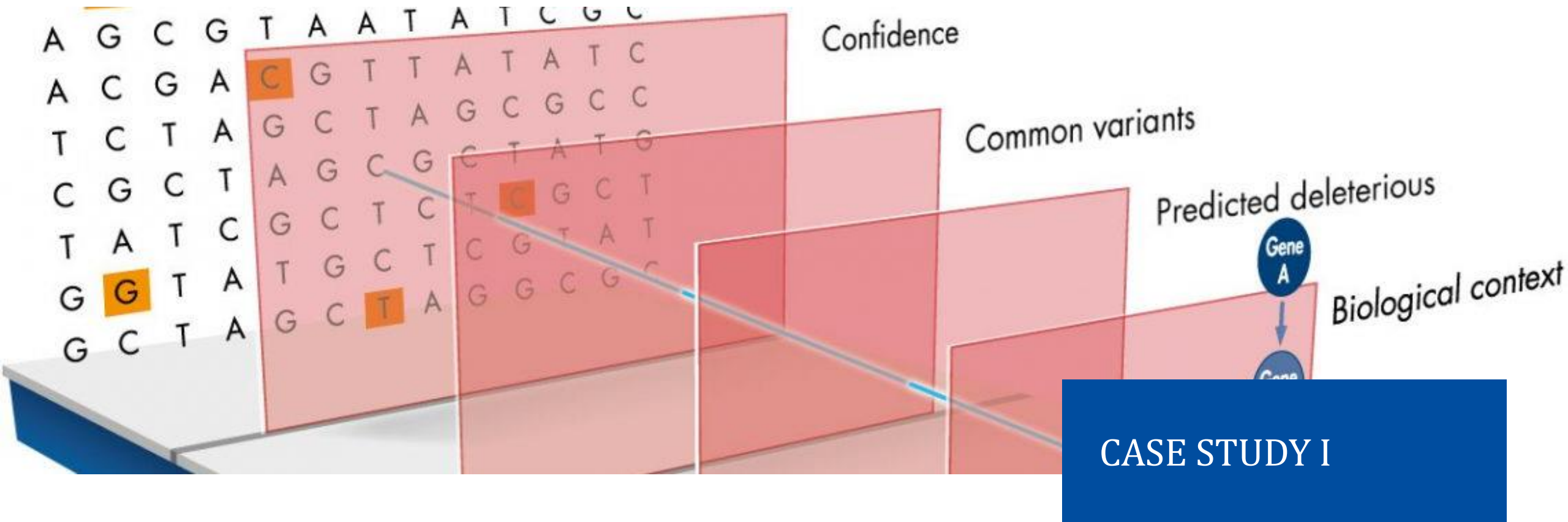
**Patient Symptoms**

Ranks candidate genes by computing semantic similarity between supplied phenotypes and known disease-gene associations.

- Multiple congenital anomalies (Multiple congenital anomalies)
- Fetal akinesia (Fetal akinesia)
- Hypotonia (Hypotonia)
- Pena-shokeir syndrome type I (Pena-shokeir syndrome type I)
- Failure to thrive (Failure to thrive)
- Encephalopathy (Encephalopathy)
- Muscle spasticity (spasticity)
- Disorder of sex development (Disorder of sex development)
- Macrocephaly (Macrocephaly)
- Hearing loss (Hearing loss)

Upload file with HPO IDs

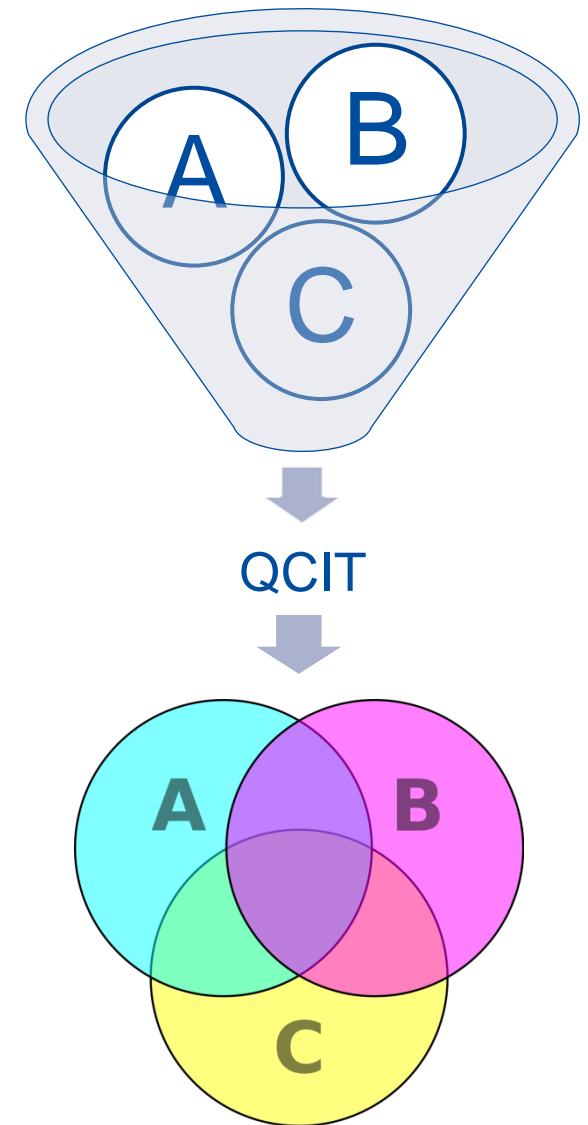
# LIVE DEMO



針對不同表型之癌症病患篩選位點並提供用藥資訊

## Case Studies I: 針對不同表型之乳癌病患篩選位點並提供用藥資訊

- Characterizing the variants specific to the different subtypes
  - Samples
    - Subtype A: 9 samples
    - Subtype B: 9 samples
    - Subtype C: 9 samples
  - Goal:
    - To find the specific variants between different subtypes
  - Ways:
    - Filter out the false positive variants – **Confident Filter**
    - Filter out common variants – **Common Variant Filter**
    - Search for reportable pathogenic variants by ACMG guideline – **Predict Deleterious**
    - Pool all potential variant and find the intersection and specific variants



## Step III: Change Filter Settings

A ANALYSIS x

Filtered Variants

102836

↓

**X** Confidence

71899

↓

**X** Common Variants

6061

↓

**X** Predicted Deleterious

84

Advanced ▾ Add Filter ▲ Apply



Edit Filter x

Name (required)

Exclude  variants that are observed in any of these populations with an allele frequency of

≥  % of  in the [Allele Frequency Community](#) (includes [gnomAD](#) and [CGI](#))

≥  % of  in [gnomAD](#)

≥  % of  in [ExAC](#)

≥  % of  [NHLBI ESP exomes](#)

≥  % in the [1000 Genomes Project](#)

are present in  [dbSNP](#) or  [DGV](#)

unless an [established Pathogenic common variant](#)

Cancel Save

# Step IV: View the Variant Results AND Report

Phenotype: ACTN3 deficiency Age of Onset: - Disease Prevalence: -

Gene: **ACTN3** Variant: c.1729C>T p.R577\* **loss** Population Frequency: 0% gnomAD  
 Transcript: NM\_001104.4 Genotype: - Impact: stop gain

**Computed Classification**  
**Pathogenic**  
 ACTN3 deficiency

Open < Previous Next > Use Classification View Bibliography

Filter Settings Search... 84 variants < 1 > View Settings

Gene	Alteration	Phenotype	Cases	Mode of Inheritance	Function	Impact	Max Population Frequency	Variant Findings
<b>ACTN3</b>	c.1729C>T p.R577*	ACTN3 deficiency		-	-	Stop Gain	0% gnomAD	242
<b>CST9</b>	c.259C>T p.R87*	Familial 46, XY disorders of sex...		-	-	Stop Gain	1.54% gnomAD (East Asian)	6
<b>CYP2D6</b>	c.1457G>C p.S486T							
<b>CYP2D6</b>	c.408G>C p.V136V							
<b>DPYD</b>	c.85T>C p.C29R							
<b>ESR1</b>	c.1610A>C p.Y537S							
<b>FANCD2</b>	c.1278+3_1278+6del							

▼ Assessment

▼ Criteria

Criteria	Criteria ID	Strength	Evidence	Rationale
x Null variant (nonsense, frameshift, canonical +/-1 or 2 splice sites, initiation codon, copy number loss, single or multi exon deletion) in a gene where loss of function (LOF) is a known mechanism of disease (Very Strong)	PVS1	Very Strong	-	<a href="#">Add</a>
x The prevalence of the variant in affected individuals is significantly increased compared with the prevalence in controls [odds ratio = 86615.75; 95% confidence interval = (5404.82, 1388072.72); FET 2-tail p-value < 0.0001; affected individual count = 401] (Strong)	PS4	Strong	5	<a href="#">Add</a>
x Absent from controls (or at extremely low frequency if recessive) in gnomAD [In these sources of population frequency data, this variant's frequency is 0% or <= 0.001%] (Moderate)	PM2	Moderate	-	<a href="#">Add</a>
x Variant found in a case with an alternate molecular basis for disease (Supporting)	BP5	Supporting	1	<a href="#">Add</a>
x Reputable source recently reports variant as benign, but the evidence is not available to the laboratory to perform an independent evaluation (Supporting)	BP6	Supporting	1	<a href="#">Add</a>

[+ Add Criterion](#)

Set Pathogenicity Assessment: Pathogenic Reportability: Not Reportable [Set Assessment](#)

[View/Add notes](#) | [Remove assessment](#) | [Set Validation Status](#)

# Step V: Further Analysis on Your Own Pipeline

## A subtype specific variant lists (Pathogenic Variant)

Chromosome	Position	End Position	Reference Allele	Sample Allele	Variation Type	Gene Region	Gene Symbol	Protein Variant	Variant Findings	Translation Impact	ACMG
1	45332088	45332088	T	C	SNV	Splice Site; Intronic	MUTYH	-	195	-	Pathogenic
3	75737893	75737894	-	CTT	Insertion	Promoter; Exonic; Intronic	ZNF717; MIR4273	p.F577delins*V; p.F527delins*V	1	in-frame	Pathogenic
3	1.79E+08	1.79E+08	G	A	SNV	Exonic	PIK3CA	p.E542K	3679	missense	Pathogenic
3	1.79E+08	1.79E+08	C	A	SNV	Exonic	PIK3CA	p.Q546K	762	missense	Pathogenic
3	1.79E+08	1.79E+08	G	A	SNV	Exonic	PIK3CA	p.E726K	430	missense	Pathogenic
6	1.52E+08	1.52E+08	A	C	SNV	Exonic; Intronic; 3'UTR	ESR1	p.Y536S; p.Y537S; p.Y276S; p.Y539S	364	missense	Pathogenic
8	1.33E+08	1.33E+08	G	A	SNV	Exonic; ncRNA; Intronic	LRRC6	p.R60*; p.R180*; p.R98*	2	stop gain	Pathogenic
10	8073787	8073787	C	T	SNV	Exonic	GATA3	p.R367*; p.R366*	39	stop gain	Pathogenic
12	1.03E+08	1.03E+08	T	C	SNV	Exonic	PAH	p.Y204C	537	missense	Pathogenic
17	7674179	7674179	A	C	SNV	Splice Site	TP53	-	19	-	Pathogenic
17	31352348	31352348	C	T	SNV	Exonic	NF1	p.R2517*; p.R2496*	66	stop gain	Pathogenic
M	12338	12338	T	C	SNV	Exonic	MT-ND5	p.M1T	10	start loss	Pathogenic



# ESR1 Treatment Info from QCII

Phenotype: Breast cancer

Age of Onset  
61 Years i

Gene Prevalence  
8.42% i

Disease Prevalence  
1/77 i

Gene  
**ESR1**  
Transcript  
NM\_001122742.1

Variant  
c.1610A>C  
p.Y537S gain i

Somatic Frequency: 0.30% i  
Population Frequency: 0% gnomAD  
Allele Fraction: 24% (of 74 reads)  
Impact: missense

Computed Classification i  
**Tier 1B**  
**Pathogenic**   
Breast cancer

Variant List | 
 < Previous | 
 Next > | 
 Use Classification | 
 View Bibliography

## ▼ Treatment Information

Treatments [Report All Showing](#) | [Unreport All Showing](#)

Change Phenotype To: [All Cancers](#) 1 treatment(s) ineligible i

Treatment	Response <small>i</small>	Evidence <small>i</small>	Specificity <small>i</small>	Indication	References
aromatase inhibitor	Resistant	1B	exact variant	Breast cancer	<a href="#">Clinical Studies</a>
anastrozole	Resistant	2D	exact variant	Ductal breast carcinoma	<a href="#">Clinical Studies</a>
fulvestrant	Resistant	2D	exact variant	Breast cancer	<a href="#">Clinical Studies</a>
letrozole	Resistant	2D	exact variant	Ductal breast carcinoma	<a href="#">Clinical Studies</a>
tamoxifen	Resistant	3	same position p.Y537N	Breast cancer	<a href="#">Clinical Studies</a>



以Trio家族性遺傳性分析評斷多表型遺傳症狀之變異位點

## Case Studies II:以Trio家族性遺傳性分析評斷多表型遺傳症狀之變異位點

- Heredity: Trio Analysis on multiple-phenotypes genetic disease
  - Samples
    - Proband
      - Father
      - Mother
  - Goal:
    - To find the genetic-linkage variants on specific phenotypes on case children
  - Ways:
    - Heredity Analysis
    - Filter out the false positive variants – **Confident Filter**
    - Filter out common variants – **Common Variant Filter**
    - Search for reportable pathogenic variants by ACMG guideline – **Predict Deleterious**

## Step II: Patient Phenotypes (Optional)

### Patient Symptoms

Ranks candidate genes by computing semantic similarity between supplied phenotypes and known disease-gene associations.

Multiple congenital anomalies (Multiple congenital anomalies)

Fetal akinesia (Fetal akinesia)

Hypotonia (Hypotonia)

Pena-shokeir syndrome type I (Pena-shokeir syndrome type I)

Failure to thrive (Failure to thrive)

Encephalopathy (Encephalopathy)

Muscle spasticity (spasticity)

Disorder of sex development (Disorder of sex development)

Macrocephaly (Macrocephaly)

Hearing loss (Hearing loss)

Upload file with HPO IDs

Cancel

Apply Symptoms

# Step III: View and Interpret

Phenotype: IFAP syndrome    Age of Onset: Birth - 2 Years    Disease Prevalence: 40 Individuals    Mode of Inheritance: X-Linked

Gene: **GJB2**    Variant: c.109G>A p.V37I **loss**    Population Frequency: 8.35% gnomAD (East Asian)    Computed Classification: **Pathogenic** IFAP syndrome

Transcript: NM\_004004.6    Genotype: Het - transmitted    Impact: missense

Buttons: Open, < Previous, Next >, Use Classification, View Bibliography

The "transmitted" tag will be displayed on the genotype when the variant is present in the case and at least 1 control (parent).

Filter Settings Search... 11 variants < 1 > View Settings

**Phenotype driven ranking system**

Gene	Variant	Phenotype	Score	Mode of Inheritance	Impact	Classification	Prevalence	Count
<b>GJB2</b>	c.109G>A p.V37I	IFAP syndrome	1.5	X-linked	loss	Missense	8.35% gnomAD (East Asian)	1220
<b>HBB</b>	c.52A>T p.K18*	Beta-thalassemia major	0.68	recessive	loss	Stop Gain	0.08% gnomAD (East Asian)	514
<b>CYP1B1</b>	c.319C>G p.L107V	Anterior segment dysgenesis	0.59	-	loss	Missense	0.45% gnomAD (East Asian)	29
<b>CYP21A2</b>	c.1179C>G p.H393Q	Congenital adrenal hyperplasia	0.51	recessive	loss	Missense	2.01% gnomAD (East Asian)	7
<b>HYDIN</b>	c.1466G>A p.G489D	Kartagener syndrome	0.46	recessive	normal	Missense	0% gnomAD	12

## Step IV: Change View by Viewing Settings

Phenotype: Cancers and Tumors Age of Onset Disease Prevalence

Gene  
**CDC27**  
Transcript  
NM\_001293089.3

Variant  
c.761T>G  
p.L254\* **loss**

Population Frequency: 0% gnomAD  
Genotype: Het  
Impact: stop gain

Computed Classification **Pathogenic**  
Cancers and Tumors

Open < Previous Next > Use Classification View Bibliography

Filter Settings Search... 4 variants < 1 > View Settings

Gene	Alteration	Phenotype	Proband	Controls	Mode of Inheritance	Function	Impact	Ma
<b>CDC27</b>	c.761T>G p.L254*	Cancers and Tumors		— —	-	<b>loss</b>	Stop Gain	0%
<b>CDC27</b>	c.778A>C p.N260H	Cancers and Tumors		— —	-	<b>normal</b>	Missense	0%
<b>FRG2C</b>	c.464G>A p.G155E	Ataxia-ocular apraxia 2		— —	-	<b>normal</b>	Missense	0%
<b>KMT2C</b>	c.2578C>T p.P860S	Cancers and Tumors		— —	-	<b>normal</b>	Missense	0%

View Settings x

Sort By Pathogenicity (group by gene) v

- Phenotype Driven Ranking (246)
- Denovo (49)
- Sex-Linked (23)
- Homozygous (30)
- Truncating (25)
- Other (667)

Status

- Not Assessed (1009)

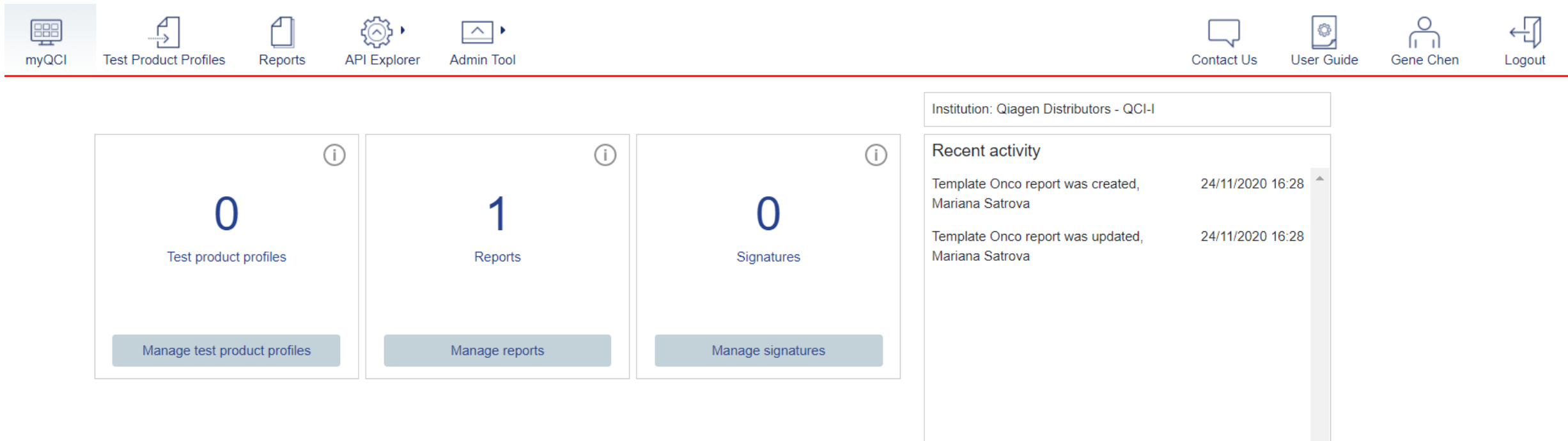
Classification

- Pathogenic (7)
- Likely Pathogenic (26)

# LIVE DEMO

# MyQCI – An Administrative Application for QCI Product

- MyQCI is an administrative application for QCI products providing a flexible and easy-to-use platform for managing, configuring, and customizing key components of your test menu including test configuration, PDF report template, and electronic signature.

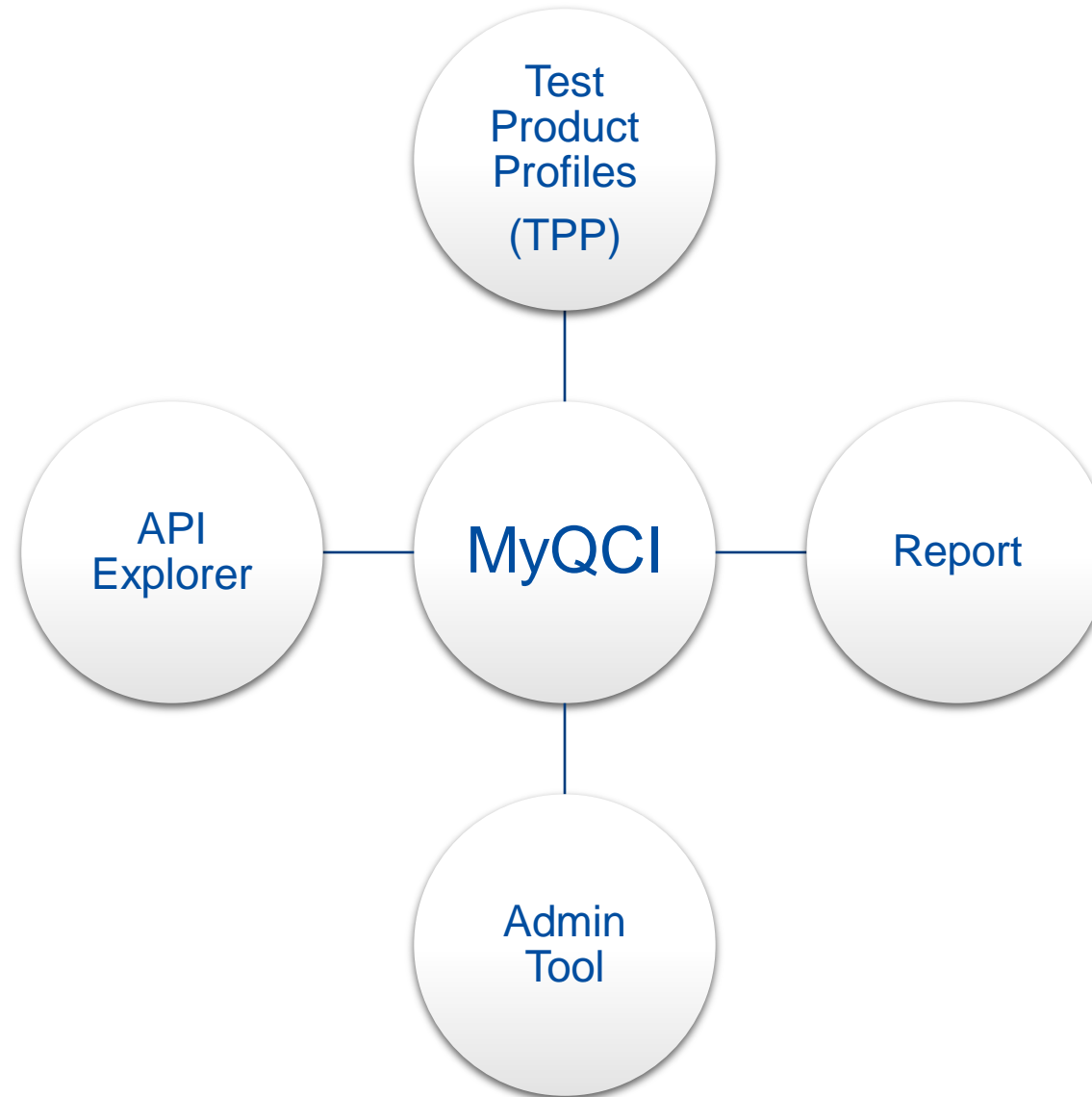


The screenshot displays the MyQCI administrative application interface. At the top, there is a navigation bar with icons for 'myQCI', 'Test Product Profiles', 'Reports', 'API Explorer', and 'Admin Tool'. On the right side of the navigation bar, there are links for 'Contact Us', 'User Guide', 'Gene Chen', and 'Logout'. The main content area features three large cards: 'Test product profiles' with a count of 0, 'Reports' with a count of 1, and 'Signatures' with a count of 0. Each card has a corresponding 'Manage' button. To the right of these cards is a sidebar with the text 'Institution: Qiagen Distributors - QCI-I' and a 'Recent activity' section listing two events: 'Template Onco report was created, Mariana Satrova' and 'Template Onco report was updated, Mariana Satrova', both dated 24/11/2020 16:28.

**Need to activate the function for any account**



## Applications on MyQCI



# MyQCI – Test Product Profile (TPP) Configuration

Create a new Test Product Profile ✕

Workflow (required)  
Somatic

Workflow Pipeline (required)  
Interpret

User Group (required)  
2019August

Copy from  
--- Available TPP ---

- Available TPP ---
- QIAGEN Test Product Templates**
- Illumina® TruSight™ Oncology 500
- Illumina® TruSight™ Tumor 170**
- QCI Interpret Somatic Default
- QCI Interpret (Somatic) Default + ReportingPolicy
- QIAact-AIT-Basic-FFPE\_QIAGEN
- QIAact-AIT-Basic-Plasma\_QIAGEN
- QIAact-AIT-UMI-FFPE\_QIAGEN
- QIAact-BRCA-1\_2-Basic-FFPE\_QIAGEN
- QIAact-BRCA-UMI-FFPE\_QIAGEN



myQCI Test Product Profiles Reports API Explorer Admin Tool Contact U

Search by Test Product Profile... Import Create New

Test Product Profile	User Group Name	Workflow Type	Last Updated	Updated By
HopeSeq Heme Research Panel	QIAGENOfTheShellTPP	Somatic	19/05/2020 15:02	myqci super_admin
SomaticBare	QIAGENOfTheShellTPP	Somatic	18/05/2020 22:45	myqci super_admin
tpp-ds-auto-LhbrpAWdwkPtjzXRmPNC	QIAGENOfTheShellTPP	Somatic	18/05/2020 06:30	myqci super_admin
tpp-ds-auto-aNQdRHZPAffPSZkJPzde	QIAGENOfTheShellTPP	Somatic	18/05/2020 06:30	myqci super_admin
testngb0fa6b0a-060a-425b-900c-69312a8b0b61	QIAGENOfTheShellTPP	Hereditary	18/05/2020 04:24	myqci super_admin
testngd8fed7d7-627e-4fa3-8575-d9dae7803a60	QIAGENOfTheShellTPP	Somatic	18/05/2020 03:16	myqci super_admin
tppDefaultiUR	QIAGENOfTheShellTPP	Somatic	17/05/2020 21:03	dstestuser qci-a

**Name**  
HopeSeq Heme Research Panel

**Workflow type**  
Somatic

**Workflow Pipeline**  
QCI Interpret One Pre-curated

**State**  
STAGING

**User Group Name**  
QIAGENOfTheShellTPP

**Code**  
COH-HSRP

**Report Template**  
QCII-One\_DemoReport

**Variant Pre-filter**  
hopeseq\_prefilter

**Automated Flow**  
false

**Reporting Method**

# MyQCI - Report

[myQCI](#)
[Test Product Profiles](#)
[Reports](#)
[API Explorer](#)
[Admin Tool](#)

[Contact Us](#)
[User Guide](#)

[Manage Signatures](#)
[Create New](#)

Report Name	Base Report	Last Updated ^	Updated By
Onco report	Somatic Demo v2.1.0	24/11/2020 16:28	Mariana Satrova

1 selected / 1 total

Details

**Report Name**  
Onco report

**Based on**  
Somatic Demo v2.1.0

**Created**  
24/11/2020 16:28




**Created by**  
Mariana Satrova

**Last updated**  
24/11/2020 16:28


**Updated by**  
Mariana Satrova

[Delete](#)
[Copy](#)
[Preview](#)
[Export](#)
[Edit](#)

# MyQCI – Customize Your Report Style

« Back  Save  Settings  Styling ▶ Preview
Editing report: TESTGRSomaticDemo
</> Advanced edit

**Warning:** The purpose of this sample report is to illustrate report components and not accuracy or completeness of scientific evidence.



**YOUR LAB**

Your Lab  
1700 Lincoln Blvd, Suite 20, Redwood City, CA 94063  
labxyz.com / (650) 484 4040  
Additional Information

Page 1 of 6

## Test Performed: Somatic Panel

Report Date **Nov 25, 2019**  
Status -

**Specimen Information**

Date of Birth Jan 29, 1990	Accession ID NSCLC demo
Age 29	Specimen biopsy
Sex Male	Collection Aug 7, 2019
Ethnicity Caucasian	Accession Aug 1, 2019
Diagnosis Lung adenocarcinoma	Primary Tumor Site Lung
Diagnosis Stage IB	

## Result: Positive

<b>3</b>	<b>1</b>	<b>1</b>	<b>1</b>
Clinically Significant Variants	Therapies Associated with Resistance	Therapies with Potential Clinical Benefit	Clinical Trials

## Report Summary

This is a customizable sample report. The purpose of this sample report is to illustrate report components and not accuracy or completeness of scientific evidence.

# MyQCI - API Explorer (**Another License Required**)

**Test Endpoints**

Search for Tests

[Submit a New Test](#)

[Check Status of Submission](#)

[Share Test with Others](#)

[Export Test Results](#)

[Update assessment](#)

**Profile Endpoints**

[Get All Test Product Profiles](#)

[Get Test Product Profile by Name](#)

**Metadata Prep**

**Select SDK version to Download**

SDK 1.14 ▾

Download

GET /v1/clinical Search for submitted tests satisfying user-supplied criteria

### Parameters

Parameter	Value	Description	Parameter Type	Data Type
<b>state</b>	<input type="text"/>	Limit search results to tests in a specific state.	query	string
<b>startReceivedDate</b>	<input type="text" value="YYYY-MM-DD"/>	Beginning of the range of dates to search format: yyyy-mm-dd	query	date
<b>endReceivedDate</b>	<input type="text" value="YYYY-MM-DD"/>	Beginning of the range of dates to search format: yyyy-mm-dd	query	date
<b>sort</b>	<input type="text"/>	Order for the list of results. ( <i>receivedDateDesc</i> - default)	query	string

**bold red**= required

Run Query

**Response Class (status 200)**

Model Schema

# The QIAGEN Knowledge Base System Support Full Variant Analysis

