# ПО для геномики

## Технические характеристики


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Ставрополь (8652)20-65-13
Сургут (3462)77-98-35
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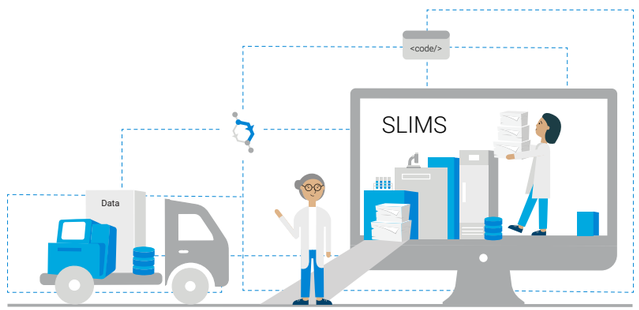
# What is Agilent SLIMS?

Agilent SLIMS combines a laboratory information management system (LIMS) and electronic laboratory notebook (ELN) in a single system, enabling comprehensive workflow management. SLIMS is flexible and configurable, helping you increase your lab's productivity. The system is designed to support the requirements of ISO17025, 21 CFR Part 11, HIPAA, and CLIA.




## Domains

SLIMS can be applied within various fields to facilitate data collection and record keeping, improving reproducibility and compliance and streamlining processes.

### Analytical

- Track complete request lifecycle from analysis to results
- Use SOPs to generate and follow worklists
- Provide product specification testing management
- Integrate with chromatography data systems

### Research

- Take notes interactively and follow workflow steps
- Flexibly manage protocol features
- Integrate sample data, experiments, users, and more
- Optimize sample repository management

### NGS

- Pool libraries and assign lanes
- Design NGS plates with drag-and-drop functionality
- Track external barcodes or assign plate layout indexes
- Export sample sheets directly to integrated sequencers

### Biobanks

- Automate external lab instruments
- Design complete, detailed studies
- Collect, schedule, and send samples to workflows
- Register subjects and restrict personal data access

# Enhancing the Everyday Life of Labs

## Time-saving SLIMS Store

When installed, SLIMS is ready to adapted to your lab. The SLIMS Store maintains a collection of preconfigured packages that are ready to install and will get you fully functional quickly. Additionally, you can customize any of the packages after they are installed in your SLIMS deployment.

## Flexible deployment

SLIMS offers flexible installation options, deploying to either a virtual or physical server. Using Amazon's ECS technology, SLIMS can be used in the cloud on a scalable, powerful, secure virtual server—or installed on a server within your IT infrastructure.

## Easy integration

SLIMS generates the sample sheet and returns results for many NGS sequencing machines (such as BGI, and others), QC machines (such as Agilent TapeStation, Fragment Analyzer, and Bioanalyzer systems), analytical instruments including LC, GC, MS, ICP, and Chromatography Data Systems (CDS) systems such as Agilent OpenLab CDS and others.

It can also be connected to other Agilent and non-Agilent laboratory software systems, SAP, and bioinformatics platforms.

SLIMS fully interfaces your instruments and software. It features three APIs (REST, Java, and Python), which allow communication with third-party systems.

## Multiple features

SLIMS includes features and modules that can be tailored to meet the needs of your lab.

### Sample management

- Digitally track samples and retain lineages
- Record results for reporting
- Maintain data integrity

### Dashboard

- Display graphs, tables, and text on one screen
- Access different parts of system simultaneously
- Use shortcuts to simplify repetitive tasks

### Workflows

- Visualize workflows with Workflow Management module

### Electronic laboratory notebook

- Replace paper lab book with electronic record
- Organize experiments by project name and create SOPs
- Connect sample and reagent information with test results
- Add lab notes and attachments

### Order management

- Provide access to track orders
- Create, manage, and monitor test requests
- Review and validate results

NGS Software

# AGeNT

RUO

The Agilent Genomics NextGen Toolkit (AGeNT) is a Java-based software module that processes the read sequences from targeted high-throughput sequencing data generated by sequencing Agilent SureSelect and HaloPlex libraries.

The Trimmer utility of the AGeNT module processes the read sequences to identify and remove the adaptor sequences and extracts dual molecular barcodes (for SureSelect XT HS2).

The LocatIt utility of the AGeNT module processes the Molecular Barcode (MBC) information from HaloPlex HS, SureSelect XT HS, and SureSelect XT HS2 Illumina sequencing runs with options to either mark or merge duplicate reads and output in BAM file format.

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## Features

- Consists of flexible command line tools for NGS data processing, ready to be run on Linux shells as well as Windows and Mac command line with minimal configuration.
- Processes the read sequences of Agilent's Target Enrichment libraries to identify and remove the adaptor sequences
- Deduplicate reads using the Molecular Barcode (MBC) information from HaloPlex HS, SureSelect XT HS, and SureSelect XT HS2 Illumina sequencing runs.

## Specifications

| | | | |
|---|---|---|---|
| **Additional Software Requirements** | Java version 8 or later | | |
| **Current Software Version** | 2.0.5 | | |
| **Memory** | ≥8RAM GB | | |
| **Operating System Requirements** | RedHat Enterprise Linux 8.0 | Windows 10 Enterprise | macOS Mojave |

# Alissa Align & Call

## The Next Evolution of NGS Data Analysis

**Alissa Align & Call Delivers:**

- Faster time-to-results
- Optimized algorithms for Agilent assays
- Greater efficiency than internal pipelines
- Seamless analysis pipeline and variant assessment integration
- Comes with a team of experts
- Secure, ISO 27001 certified environment

## Make your Data Analysis Flow

**Alissa Align & Call ushers in the next generation of NGS data analysis on the Agilent Alissa Clinical Informatics platform to deliver bioinformatic accuracy and speed, from raw data to draft report.**

With optimized algorithms for samples enriched by Agilent SureSelect, HaloPlex, and OneSeq libraries and reagents, Align & Call unlocks complex data and accelerates time-to-results. In an integrated NGS workflow, Align & Call's upstream process to align and call variants for detection, annotation, and visualization is scalable and its QC assessment and VCF files easily flow downstream on the Alissa platform to data interpretation and reporting.

### Designed for NGS Data Management Ease

Alissa Align & Call is designed with the routine lab user in mind. Navigating big genomics data using Align & Call's analysis pipeline — from raw data to variant identification — does not require complex IT infrastructure or special hardware. As a fully-hosted workflow, Align & Call is easily deployed and comes with Agilent's team of experts to help your lab quickly setup and scale volumes.

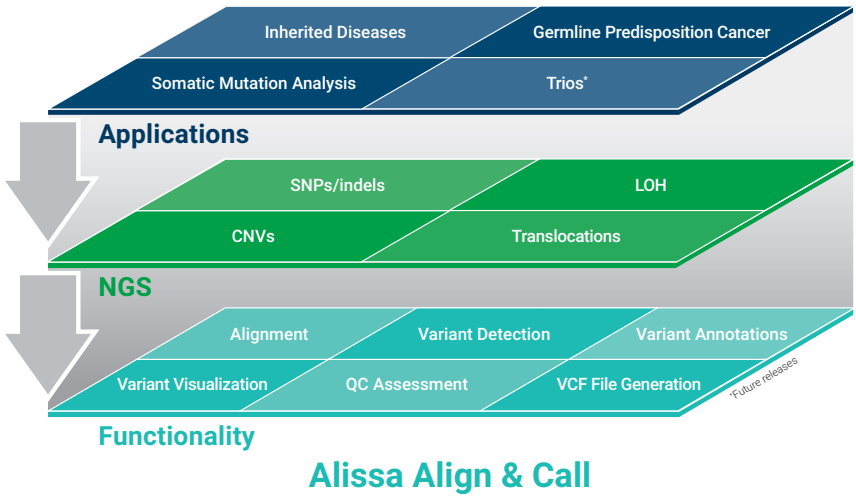



**Figure 1.** A 3D view of how the tools and functionality provided by Alissa Align & Call deliver data analysis across NGS application areas and genomic events.

## Analysis, Interpretation, and Workgroup Integration

Alissa Align & Call seamlessly integrates downstream with the variant assessment and reporting module on the Alissa Clinical Informatics platform, making QC reports and VCF files easy to export and navigate among all users within the same workgroup, when accounts are fully subscribed.

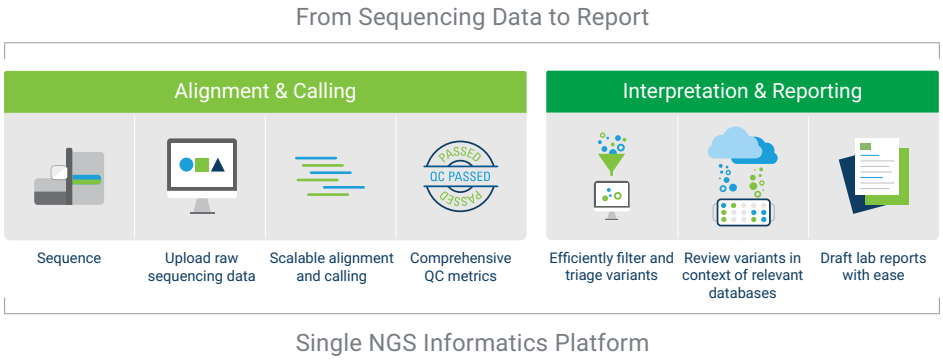



**Figure 2.** Shared access to data, files, and results fosters collaboration across the platform, increasing operational efficiency, and establishing higher industry standards throughout the lab.

## Speed, Quality, and Accuracy

Comprehensive QC metrics of Align & Call ensure NGS data quality at a robust workflow level. The quality performance of Align & Call is fueled by algorithms optimized for Agilent's industry leading Target Enrichment solution, yielding robust coverage metrics for SNPs, indels, CNV and cnLOH variant analysis, which increases the speed of analyses without sacrifice of quality or accuracy.

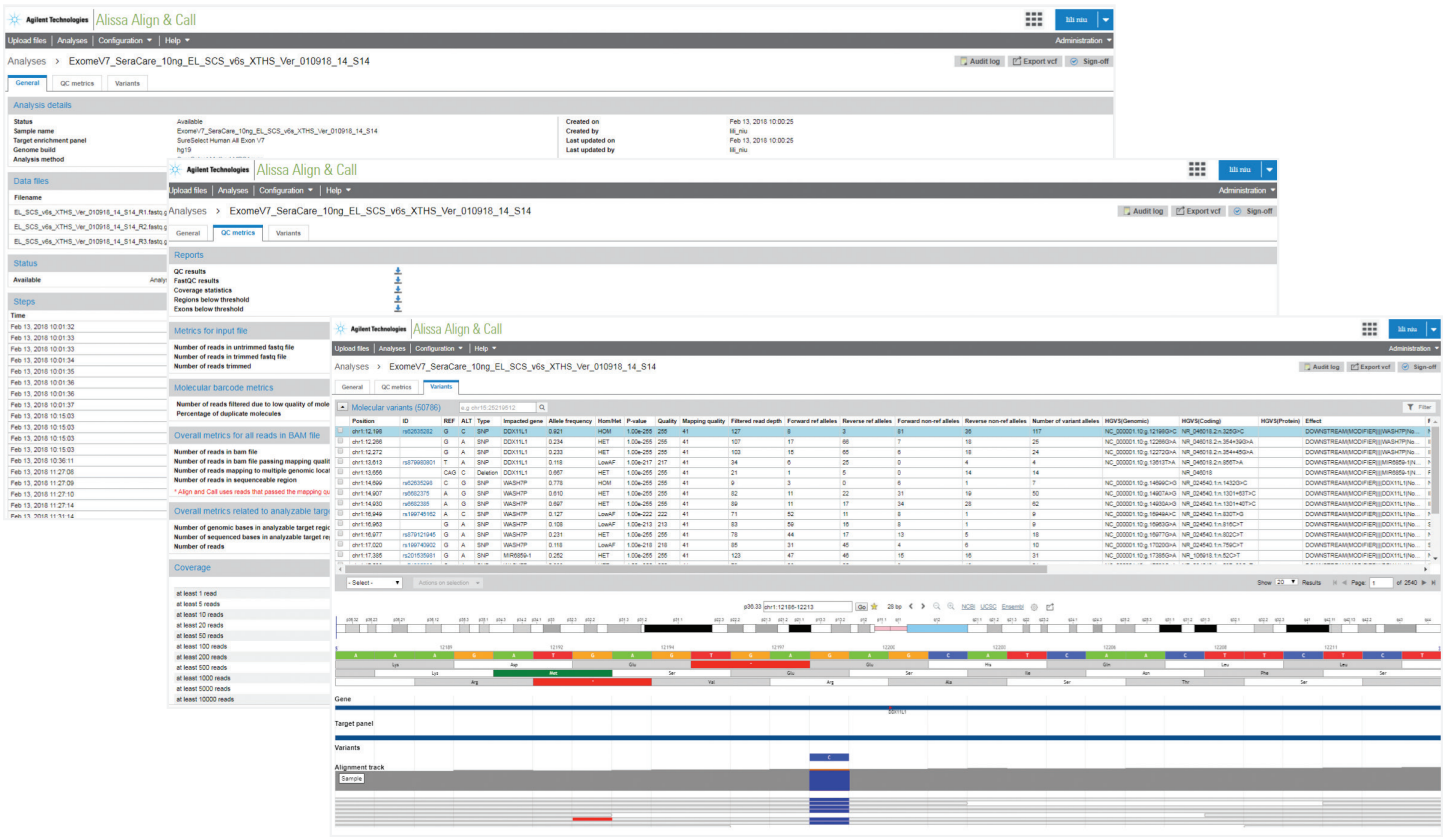



**Figure 3.** All expected SNPs and indels were identified and presented by Align & Call when analyzed using SureSelect Human All Exon V7 in a single day exome workflow from DNA to captured libraries.

# Alissa Interpret Research

Clinical-grade workflows and knowledgebases

## Make your Variant Assessment Flow

Alissa Interpret Research allows clinical research labs to efficiently triage, curate and report genomic variants. Whether from NGS or arrays, this solution automates genomics data management from variant filtration and annotation, through curation and classification, to draft lab report. Rely on a team of experts who enable you to deploy your assays quickly and ramp up your research as your lab grows.

### Designed for Clinical Research

Alissa Interpret Research is built with the clinical research lab in mind. The web-based solution provides access to a wealth of annotation sources and databases, including direct access to JAX-CKB*, the most current information on actionable variants. It also supports building a bespoke curated variant database, and features a wide range of in-depth analytic tools for constructing inheritance modes, phenotype contexts, and variant effect reviews.

### A Single Platform for all Applications Across NGS and CGH

Alissa Interpret Research integrates your application workflows from somatic to inherited disease, your variants from molecular to structural, and your data from secondary to tertiary analysis—all on a single platform. It combines SNVs, CNVs and translocations in an integrated workflow, unlocking efficient triage, databasing, and reviewing across variant types.

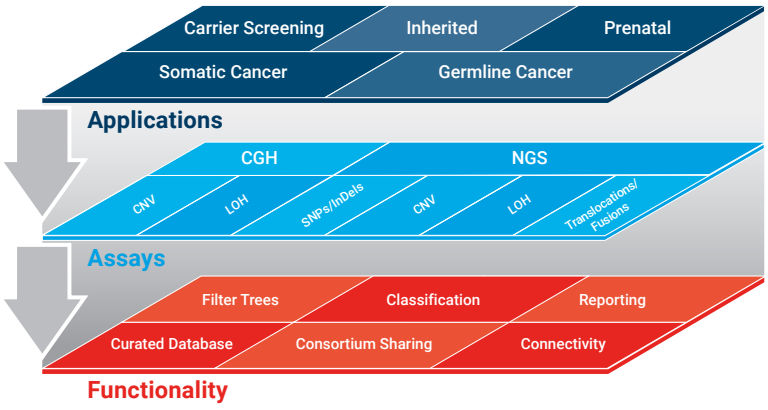



**Figure 1.** A 3D rendering illustrating how the tools and functionality provided by Alissa delivers informative variant assessment across different application areas and genomic events.

### Alissa Interpret Research Delivers

- Inherited and somatic sample workflows
- Molecular and structural variant classification and curation
- Clinical-grade standard operating procedure (SOP) implementation
- Database access and lab report drafting with ease
- Rely on a team of experts

** Somatic gene variant annotations and related content have been powered by JAX-CKB, a database of The Jackson Laboratory Clinical Knowledgebase (JAX-CKB™).*

## Scale Your Assays

Labs that implement their standard operating procedures on Alissa Interpret Research free up time for their for clinical researchers to focus on curating variants and checking hypotheses. This fast and precise variant assessment and reporting solution comes with support from our field application scientists and product specialists to enable labs to run efficiently and scale to high throughput across different research applications. It can also be seamlessly integrated with existing lab BioIT pipelines and LIMS systems for an even greater efficiency gain, either as a service or by using the available APIs.

## Advance Your Filtration System and Decision Trees

Automate your lab's variant assessment workflow in configurable, versioned pipelines. Slice and dice to quickly drill down to your variants of interest for further manual review. Store and version your pipelines to support increasing volumes and scale your sample throughput with ease.

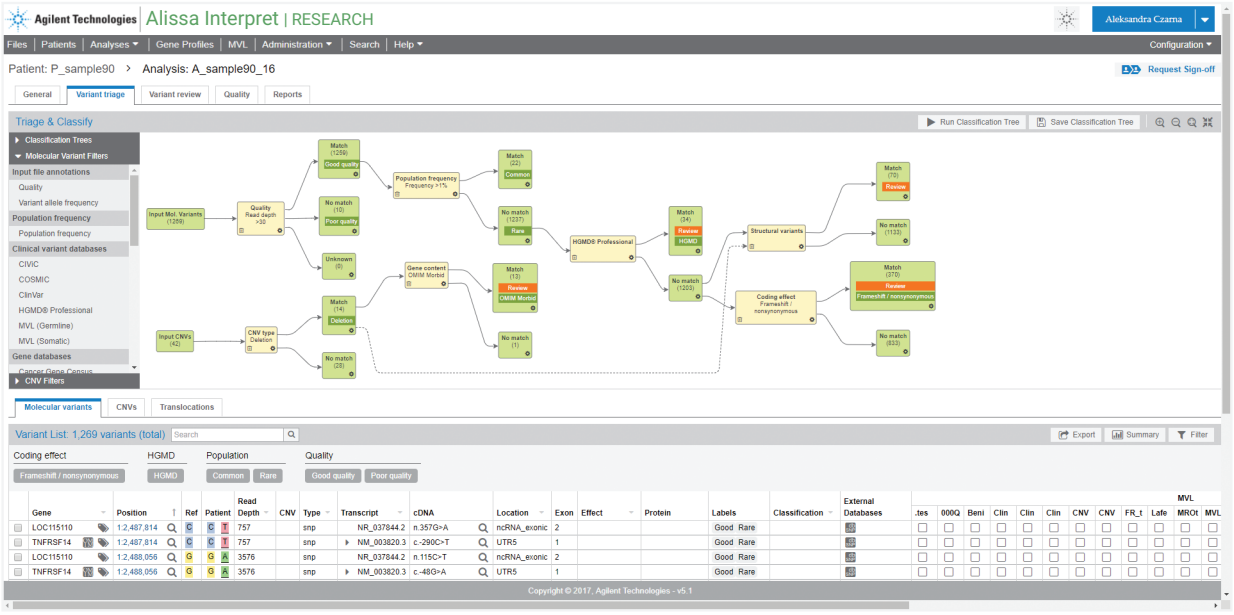



**Figure 2.** A variant filtration system featuring the integration of a CNV type decision tree.

## Build and Access Your Curated Variant Databases

Curate your internal knowledgebase by tapping into an expansive array of public databases and variant classification information. Enhance your variant information and effect annotations, frequency databases, clinically relevant peer-reviewed findings, and many others.

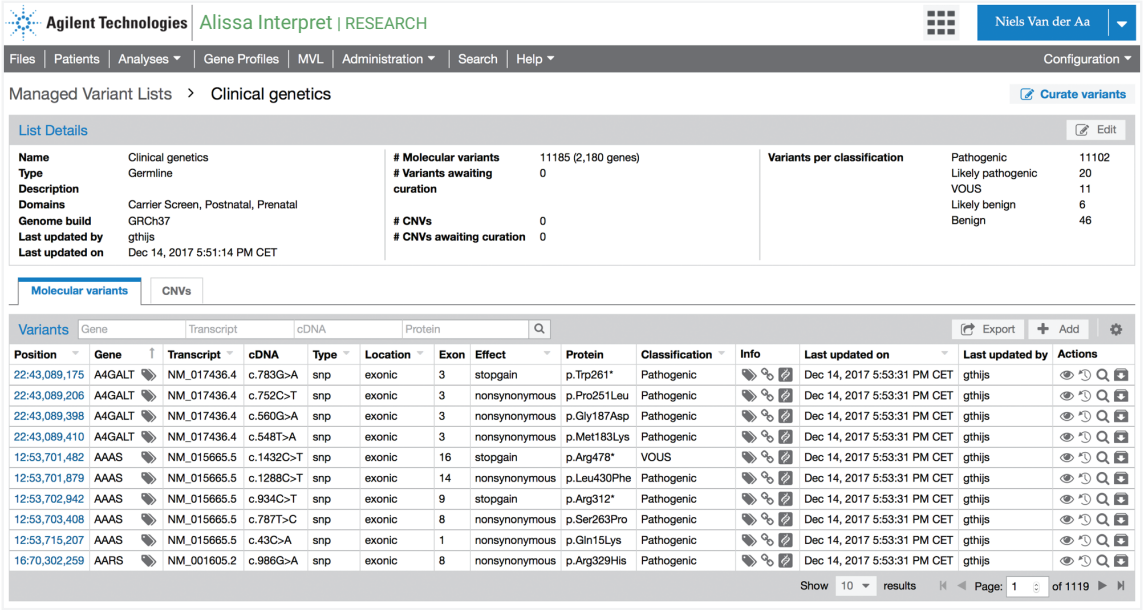



**Figure 3.** A curated list of CNVs stored in the Managed Variant List with classification and relevant findings for future reference.

## Generate Powerful Cohort Analyses

With Alissa Interpret Research, you can easily group a set of cases according to phenotype, assay characteristics, affected vs. non-affected status, and more. The platform allows you to compare these groups, and to annotate and compare all variants in the cohort with the full suite of tools also available for index, trio and single sample analyses.

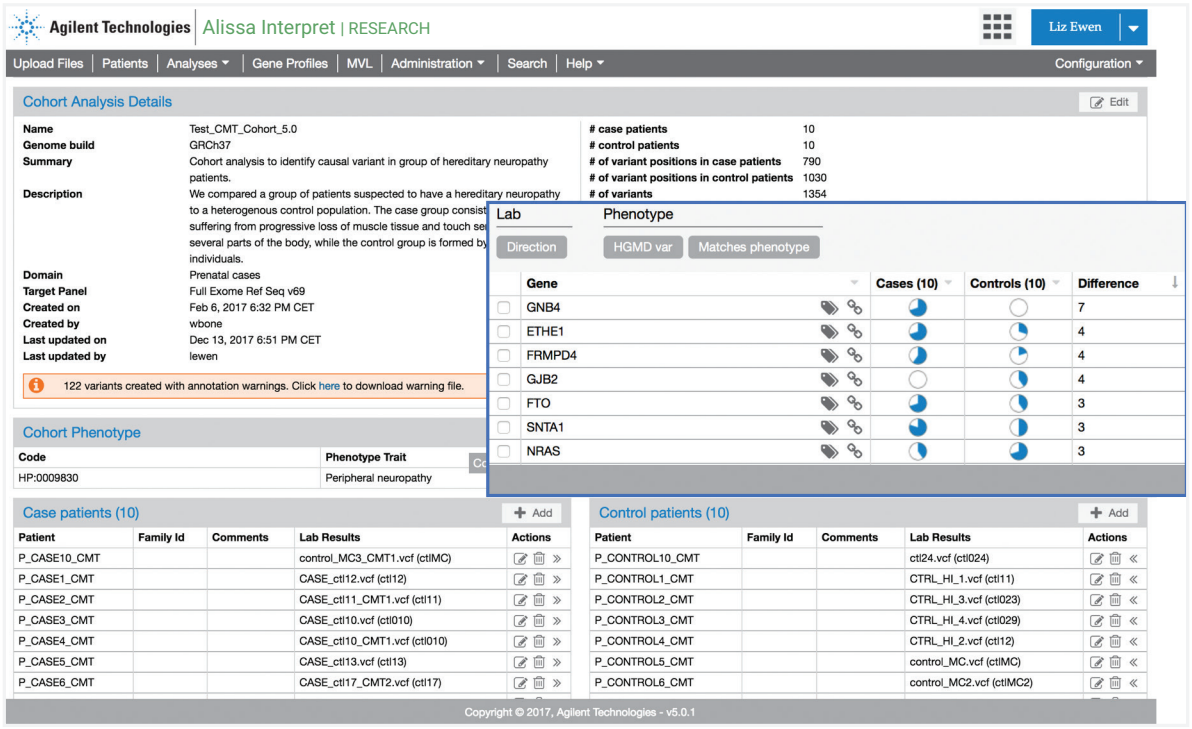



**Figure 4.** An example of a cohort analysis report. The insert demonstrates the overview of gene mutational burden in the cohort.

## A Fully Traceable Environment

The Alissa Interpret Research platform supports full traceability of all versions of databases, pipelines, and workflows. Keep track of what databases are used, and for example, identify which research scientist has annotated each piece of information to specific variants. This traceability enables you to build a truly reproducible variant assessment pipeline.

# One Source

## The Agilent Advantage

Agilent promises to deliver trusted answers to your critical questions and challenges -- helping achieve excellent outcomes in your laboratory, clinic, organization, and in the world we seek to improve.

| Streamlined | Complete | Trusted |
| --- | --- | --- |

- Inventory management
- End-to-end ordering
- Cost savings with bulk purchases
- Troubleshooting and support

# MASTR Reporter for SureMASTR Assays

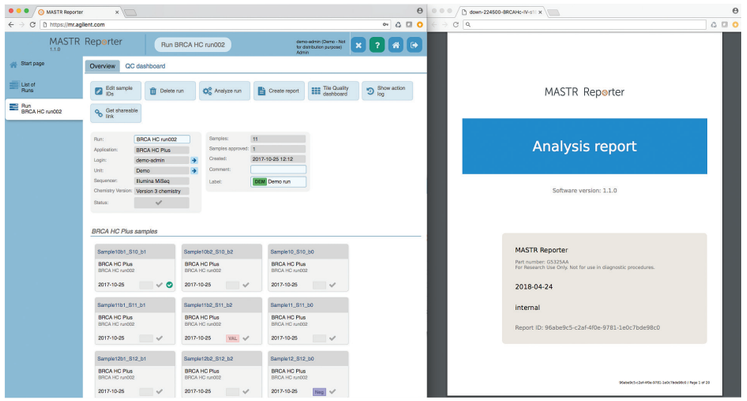
The quality of NGS results depends on a wide range of factors, from the quality of the initial sample to the way results are interpreted. MASTR Reporter was developed with exactly this knowledge in mind. It not only ensures the correct analysis of results, it also enables optimized, simultaneous variant calling of SNVs, indels and CNVs including quality control of the entire workflow. MASTR reporter is available for both somatic and germline applications.

## MASTR Reporter benefits

- **Simple and more complete workflow:** from DNA sample to analysis report.
- **Easy-to-use software:** intuitive, user-friendly interface with pop-up help texts to guide you through the workflow.
- **High quality data:** integrated quality control to measure, monitor and optimize the complete workflow.
- **Reliable variant calls:** all software parameters are optimized specifically for SureMASTR assays enabling fast and reliable variant calling (SNVs, indels and CNVs).
- **Transparent data analysis:** layered information from variant to sequencing reads, which allows for deep analysis of the data.
- **Safe data:** stringent data security. Developed with IEC62304 compliance. You own your data.
- **Metrics and analytics:** for traceability and audits.
- **Automation of the analysis and interpretation:** Automatic upload from the sequence server to MASTR Reporter and from MASTR Reporter to Alissa Interpret is possible.

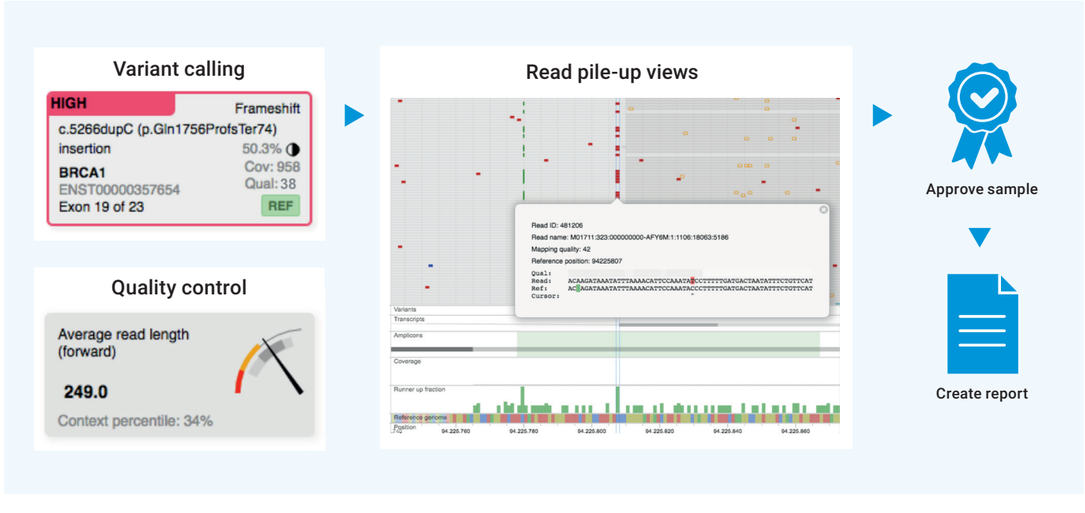
## Understand your data and optimize your performance

The integrated quality control features of MASTR Reporter help you monitor and optimize your complete workflow. The transparent, layered information obtained with MASTR Reporter enables deep analysis of your data. All software parameters are optimized specifically for SureMASTR assays to ensure fast and reliable variant calling (SNVs, indels and CNVs). MASTR Reporter now also includes a stutter correction algorithm for homo- and heteropolymer regions. Furthermore, MASTR Reporter comes with the option to customize your gene and variant filtering to allow adjustments that meet country-specific requirements. Variant annotation can further be performed with information provided by Alissa interpret.



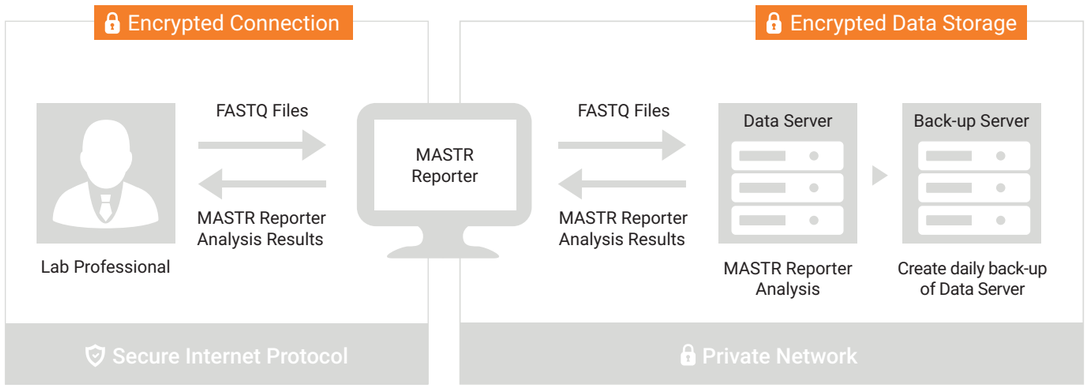

## Simple & complete workflow

Thanks to its intuitive and user-friendly interface, MASTR Reporter offers a simple and complete workflow for tracking and analysis. Various metrics and analytic views ensure traceability and help during audits. Results are presented in the form of a customizable PDF report. You can even choose to automatically upload the sequencing server to MASTR Reporter and to Alissa Interpret in order to automate your analysis.




## Secure and traceable results

MASTR Reporter is IEC62304 compliant, ensuring robustness and reliability. Your results can be stored for up to two years on the private, secure server. You can effortlessly consult earlier tests and results. It is even possible to set up an internal approval system for the clinical interpretation of the results and to define users and their rights. All data entries are safely logged and effortlessly traced.



NGS Software

# SureCall RUO

SureCall is a research desktop application combining both novel and widely accepted opensource algorithms for end-to-end NGS data analysis from alignment to categorization and annotation of mutations, supporting Agilent Target Enrichment applications.

SureCall provides four different types of analysis: Single, Pair, Trio, and OneSeq CNV and Mutation analysis. The SNPPET SNP caller is an Agilent algorithm, which is optimal for detecting low-frequency variants with high sensitivity and specificity.

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## Features

- From alignment of raw data to categorization and annotation of mutations in three simple steps
- Supports four different types of analysis: Single Sample, Tumor-Normal, Trio and OneSeq CNV and Mutation Analysis
- Supports variant annotation from many public sources, including NCBI, COSMIC, PubMed, ClinVar and custom annotation
- Utilize single/duplex molecular barcodes (MBC) to remove false positives and accurately detect variants down to ≤1% variant allele frequency
- Addresses the needs of clinical researchers from analysis to reporting out of their target enrichment NGS data, eliminating data analysis as a bottleneck

NGS Software

# SureDesign RUO

SureDesign is a web-based application that harnesses the flexibility of SurePrint oligo manufacturing technology for the creation of custom NGS target enrichment libraries, CGH microarray designs, and FISH probes.

SureDesign, free to all registered users, has an intuitive design wizard that creates custom panels specific to research needs, as well as for cross-validation using multiple applications.

To create a custom design, you can access the SureDesign Portal below in the 'Tools' section.

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## Features

- NGS Target Enrichment: Create custom SureSelect or HaloPlex target enrichment library designs based on the targets you want to sequence.
- Define regions of interest and select probes based on target genes, genomic coordinates, or selection parameters.
- CGH, ChIP-on-chip, DNA Methylation: Create custom CGH designs with various layouts, from 8 x 15 K up to 1 x 1 M.
- CRISPR Guide RNAs: Find gRNAs that target CRISPR sites within any sequence.
- Identify potential target candidate sites in the input or selected background.
- Download ready to order DNA sequence templates.
- FISH Probes: Input gene names, accession IDs, or genomic coordinates to create custom break apart, dual fusion or single probes.
- Rapidly validate results by creating the same assay on a FISH probe and an array or target enrichment library.

CGH & CGH+SNP Microarray Software

# Agilent Genomic Workbench

RUO

Agilent Genomic Workbench (AGW) software provides powerful analysis of key microarray applications, including CGH, CGH+SNP, ChIP-on-Chip, and DNA Methylation on both human and model organisms. With AGW, scientists can change filters, thresholds, and other settings to optimize the real-time visualization effects.

Analyzing multiple DNA microarray data in a single system helps streamline genomic workflows. In addition, the system features the ability to easily alter analysis settings, test different filters and thresholds, and visualize the effects in real-time.

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## Features

- Suitable for many different aspects of DNA microarray research, including CGH, CGH+SNP, ChIP-on-chip and DNA Methylation
- Can carry out basic research on both human and non-human samples
- Features the ability to change analysis settings, such as filters and thresholds
- Real-time visualization effects
- A single powerful, intuitive and integrated software package suitable for a range of genomic data analysis processes

CGH & CGH+SNP Microarray Software

# CytoGenomics Software RUO

Agilent CytoGenomics software provides advanced data analysis tools for cytogeneticists. The system features a streamlined workflow from data upload to final report and is capable of processing CGH and CGH+SNP data from both constitutional and hematological cancer samples.

This multi- analysis software is designed specifically for cytogenetic research, to give biological context to recorded data. The intuitive cytogenetic analysis workflow can accurately detect copy-number changes and copy-neutral variations, including LOH and UPD, and output the results in a range of convenient formats.

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## Features

- Provides cytogeneticists with the capability to carry out effective analysis and triage of their CGH and CGH+SNP data from both constitutional and cancer samples.
- A streamlined workflow that is automation-enabled from data upload to analysis and report.
- The software contains optimized algorithms for the accurate detection of copy-number changes and copy-neutral variations, including LOH and UPD.
- Software includes functions used to suppress, classify, edit, and annotate aberrations and report generation.
- Convenient input and output support, allowing for integration with LIMS, is provided.
- CytoGenomics is designed specifically for cytogenetic research, to put data into biological context.
- Support for direct upload of results to Agilent Alissa Interpret for further interpretation and triage of sample aberrations.

# Agilent Feature Extraction Software

## Automated Image Analysis Paired with QC Tools

## Product Note

One of the big challenges in microarray data analysis is generating reliable, high-quality image-analysis results. Agilent's Feature Extraction (FE) software reads and processes up to 100 raw microarray image files in an automated, walkaway mode. It finds and places microarray grids, rejects outlier pixels, accurately determines feature intensities and ratios, flags outlier features, and calculates statistical confidences. Application-specific QC reports summarize multiple analyses. FE is a key component of Agilent's comprehensive informatics platform that integrates complementary technologies and multidisciplinary approaches. It produces output files compatible with Agilent's GeneSpring GX, GeneSpring Workgroup, and DNA Analytics software, as well as Rosetta® Resolver and other microarray data analysis applications.

"Fantastic tool! The QC Tool and Metric Sets have enabled us to improve our microarray protocols and ensure optimal quality. It has become an essential component of our microarray processing pipeline."

—Dr. Alan A. Dombkowski
Assistant Professor and Director,
Microarray & Bioinformatics
Facility Core
Wayne State University

The Application Note titled "Enhanced Quality Assessment Using Agilent Feature Extraction QC Metric Sets, Thresholds, and Charting Tools" (5989-5952EN) overviews new quality control outputs and tools — metric sets, thresholds, and the QC tool — for Agilent Feature Extraction

### Features-at-a-Glance

- **Extended dynamic range** – Quantify low-abundance transcripts without saturating high-abundance transcripts (using an Agilent scanner
- **Multiple application usage** – Analyze gene expression (GE), CGH, miRNA, and ChIP-on-chip data
- **Multiple format and density compatibility** – Process both 244K and Agilent's new SurePrint G3 density arrays as well as 1, 2, 4, and 8 microarrays per slide with the click of the mouse.
- **Output file compatibility** – Analyze with Agilent integrated informatics or public domain programs
- **Convenient yet flexible workflows** – Take advantage of preloaded, user-modifiable default protocols already optimized for individual applications
- **Integration with eArray** – automatically update microarray annotation and image analysis protocols
- **Improved gridding** – Automatically grid single and multiplex microarrays with minimal manual intervention
- **QC Charting Tools** – Efficiently monitor microarray processing performance of hundreds of extractions and create new metrics and thresholds for your own workflow
- **QC Metric Sets with thresholds** – Guidance on identifying key metrics and establishing normal metric ranges (for Agilent Gene Expression two-color microarrays)
- **Software updates** – Be automatically notified of new software releases
- **Convenient QC report PDF** – Easily share QC Reports and QC Charts

## Accurate Data Extraction

Feature Extraction software delivers the maximum amount of high-quality data from each and every microarray run. When used in conjunction with a high-density Agilent microarray and an Agilent Microarray Scanner, it extends the dynamic range to accurately measure both very high- and very low-intensity features. Feature Extraction identifies the highest quality pixels in each feature for intensity quantitation, flags outlier features, and detects and removes spatial gradients and local backgrounds. Data is normalized using a combined rank consistency filtering with LOWESS intensity normalization. Output data includes summary statistics for each microarray and feature, including initial, intermediate, and final intensity values, optional log ratio values, automated flagging information, statistical confidence values, and Spike-in regressions.

## Application-Specific QC Reports

QC reports are tailored to specific microarray applications and document processing quality and reproducibility of sample preparation, labeling, hybridization, and working conditions for gene expression (both one- and two-color) as well as CGH and miRNA applications. A typical QC report like the example shown in Figure 1 contains values and graphs that include general microarray processing metrics, application-specific quality metrics, and Spike-in probe set metrics (for GE platforms).

Built-in QC features detect, disclose, and document data quality issues arising from technical sample preparation and hybridization issues including sample degradation, wash artifacts, and ozone exposure. Feature Extraction reports also provide a visual display of spot finding on all four microarray image corners, and document replicated probes, log ratios, and spatial distributions of statistically significant features.

The optional QC Charting tool can generate QC metric sets tailored to your experimental conditions (Figure 2). These metric sets can be imported into Feature Extraction and implemented to monitor processing and overall data quality. It allows customized sorting, color- and shape-by attributes and is a powerful tool for visualizing and highlighting trends and patterns.

## Keep Current with eArray

Feature Extraction ensures that you have the latest microarray annotation and image analysis protocols through integration with eArray. Simply input your eArray login information and whenever Feature Extraction runs, it will check for updated information. See Figure 3.

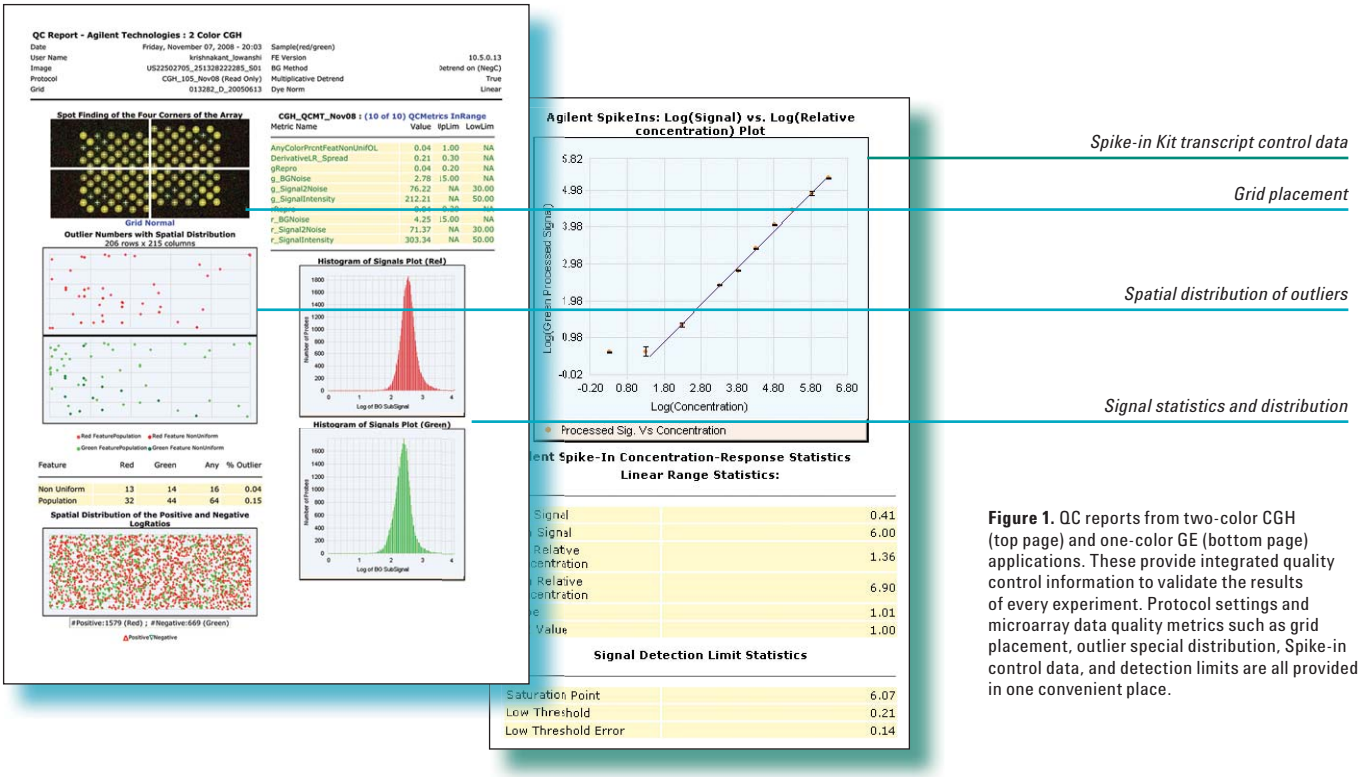



**Figure 1.** QC reports from two-color CGH (top page) and one-color GE (bottom page) applications. These provide integrated quality control information to validate the results of every experiment. Protocol settings and microarray data quality metrics such as grid placement, outlier special distribution, Spike-in control data, and detection limits are all provided in one convenient place.

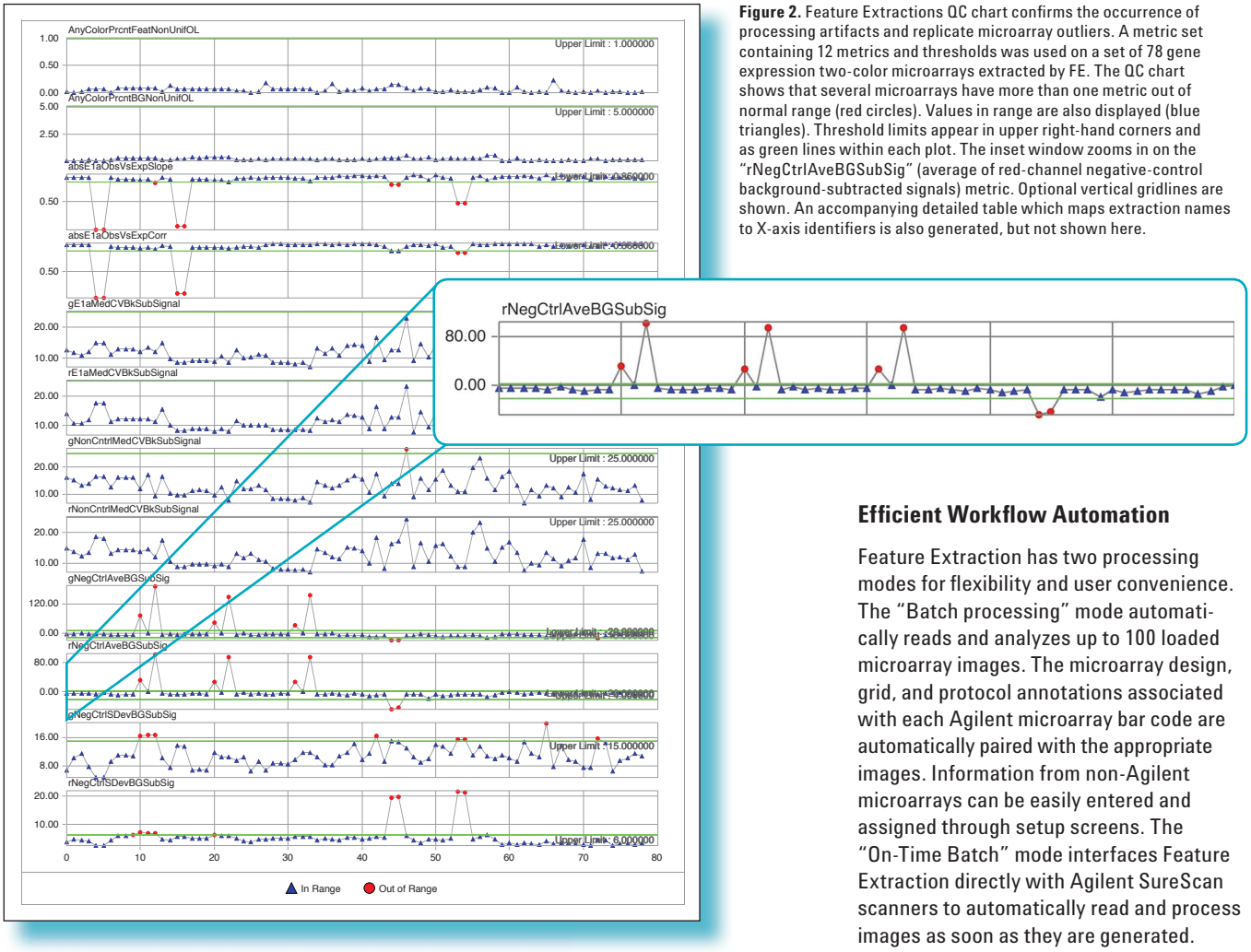



**Figure 2.** Feature Extractions QC chart confirms the occurrence of processing artifacts and replicate microarray outliers. A metric set containing 12 metrics and thresholds was used on a set of 78 gene expression two-color microarrays extracted by FE. The QC chart shows that several microarrays have more than one metric out of normal range (red circles). Values in range are also displayed (blue triangles). Threshold limits appear in upper right-hand corners and as green lines within each plot. The inset window zooms in on the "rNegCtrlAveBGSubSig" (average of red-channel negative-control background-subtracted signals) metric. Optional vertical gridlines are shown. An accompanying detailed table which maps extraction names to X-axis identifiers is also generated, but not shown here.

## Efficient Workflow Automation

Feature Extraction has two processing modes for flexibility and user convenience. The "Batch processing" mode automatically reads and analyzes up to 100 loaded microarray images. The microarray design, grid, and protocol annotations associated with each Agilent microarray bar code are automatically paired with the appropriate images. Information from non-Agilent microarrays can be easily entered and assigned through setup screens. The "On-Time Batch" mode interfaces Feature Extraction directly with Agilent SureScan scanners to automatically read and process images as soon as they are generated. Automated FTP uploads save your data to a specified server or workstation.

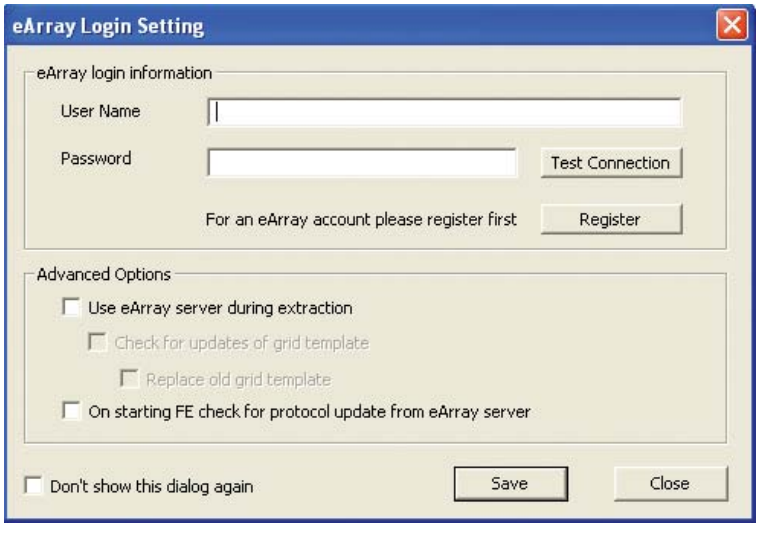



**Figure 3.** By entering your e-array login information and selecting the desired Advanced Options, Feature Extraction can automatically check and apply updates to grid templates and extraction protocols.

## Output Files Compatible with Industry Standard Analysis Applications

Images and data are saved in JPEG, GEML, MAGE, tab-delimited text, and other universal file types. Disk space and network bandwidth can be conserved through options to reduce and compress the output files. The data is compatible with a wide variety of informatics packages. The data flow has been tested and optimized for import into Agilent's integrated informatics products including Agilent's GeneSpring GX, GeneSpring Workgroup, and DNA Analytics software, as well as Rosetta® Resolver.

| Microarray Format | Scan Resolution |
|---|---|
| Agilent High-Density | 5 µ |
| Agilent High-Density Multiplex | 5 µ |
| Non-Agilent | Varies |
| Agilent SurePrint G3 | 3 µ |

## Recommended System Requirements

| | |
|---|---|
| CPU | Pentium® III 1.5 GHz or higher (Pentium IV 2.0 GHz or higher recommended) |
| Operating Systems | Microsoft Windows® XP 32-bit, Windows Server 2003 SP1, Windows Vista 32-bit, Windows Vista X64, Windows XP X64 |
| RAM | 2 GB (4 GB recommended for high-density 244K microarrays) |
| Hard Disk Space | 40 GB |

PC must be able to load MSDE 2000 Release A version 8.0

## Ordering Information

| | |
|---|---|
| Feature Extraction Software Commercial 1-year Perpetual Upgrade License* | G4460AA |
| Feature Extraction Software Commercial 2-year Perpetual Upgrade License | G4461AA |
| Feature Extraction Software Commercial 3-year Perpetual Upgrade License | G4462AA |
| Feature Extraction Software Not-for-profit 1-year Perpetual Upgrade License | G4463AA |
| Feature Extraction Software Not-for-profit 2-year Perpetual Upgrade License | G4464AA |
| Feature Extraction Software Not-for-profit 3-year Perpetual Upgrade License | G4465AA |
| Agilent DNA Microarray Scanner Bundle (includes two 1-year Perpetual Upgrade Licenses for FE) | G2565CA |

*A Perpetual Upgrade License is a permanent license that allows for software updates for the specified time period.

### About Agilent's Integrated Workflows

Agilent Technologies is a leading supplier of life science research systems that enable scientists to understand complex biological processes, determine disease mechanisms, and speed drug discovery. Engineered for sensitivity, reproducibility, and workflow productivity, Agilent's integrated workflows include instrumentation, microfluidics, software, microarrays, consumables, and services for genomics, proteomics, and metabolomics applications.

Gene Expression Microarray Software

# eArray RUO

The Agilent eArray provides advanced data analysis software for microarray designs and oligo libraries. The system enables analysts to harness the flexibility of Agilent SurePrint oligo manufacturing technology in the creation of custom arrays. Many different array formats are available.

The system enables analysts to create assays with web-based application technology quickly and easily. Array designs and libraries can be developed for Gene Expression, microRNA, Model Organisms as well as designs for Oligo Library Synthesis (OLS) and Mutagenesis. The system also enhances collaboration be enabling analysts to work better together online by sharing and publishing custom designs.

*For Research Use Only. Not for use in diagnostic procedures.*

## Features

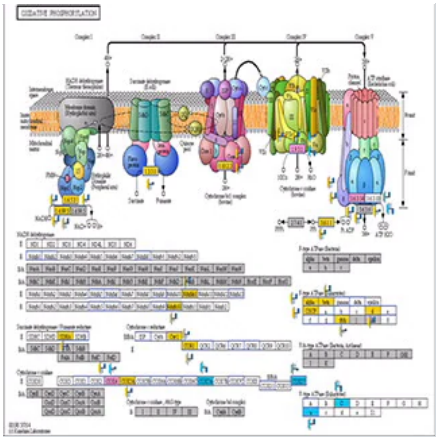
- Create custom microarray designs for Gene Expression, microRNA, Model Organisms as well as designs for Oligo Library Synthesis (OLS) and Mutagenesis.
- Design your own format with a range of different available layouts, from 8 x 15K up to 1 x 1M.
- Enable collaborations by sharing and publishing designs with other researchers.

Gene Expression

# GeneSpring GX

Agilent's GeneSpring provides powerful, accessible statistical tools for intuitive data analysis and visualization. Designed specifically for the needs of biologists, GeneSpring offers an interactive environment that promotes investigation and enables understanding of Transcriptomics, Genomics, Metabolomics, Proteomics and NGS data within a biological context.

GeneSpring allows you to quickly and reliably identify targets of interest that are both statistically and biologically meaningful. For Research Use Only. Not for use in diagnostic procedures.



## Features

- Transcriptomic analysis
- Statistical tools for testing differential expression
- Intuitive graphical displays
- Multi-omic analysis with Agilent's GeneSpring Bioinformatics Suite
- Platform for integrated data analysis and biological contextualization
- Extensible functionality with Python and R
- Report Generation Capability
- Downstream analysis of processed NGS data/ Variant analysis using vcf files
- Genome-wide association analysis
- Built-in ID browser automates database and spectral library searches
- Agilent CGH data NGS data visualization and Integration
- Genomic copy number analysis
- Support for NGS data visualization

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