Powerful NGS Data Analysis Software for Clinical Researchers

Agilent SureCall improves next generation sequencing workflows with time-saving, customizable features for genomic data alignment, visualization, annotation, and report generation, all from your Windows or Mac operating system.

All-in-one application

- Align raw data, identify mutations, and categorize and annotate mutations in a simple 3-step workflow.
- Analyze, visualize, and contextualize NGS data using a single application without the need for coding or special bioinformatics training.
- Speed up clinical research by analyzing and reporting from Agilent target enrichment NGS data, eliminating additional data analysis bottlenecks.
- Take advantage of rich annotation, with information from custom and public sources, including NCBI Variation Reporter, COSMIC, PubMed, and ClinVar.

Versatile

- Perform four different types of analysis: Single Sample, Tumor-Normal, Trio, and OneSeq CNV and Mutation Analysis.
- Perform simultaneous detection of genome-wide copy number changes, copy-neutral LOH, SNP, and Indel mutations in one workflow with OneSeq Target Enrichment.
- Generate reports with multiple supported file formats to maximize flexibility.
- Customize features such as aligner, variant caller, filtration criteria, annotation, and more.

Accurate

- Use best-in-class open source algorithms, including BWA-MEM, BWA, SamTools, SIFT, and Polyphen.
- Use our proven in-house developed SNPPET variant caller optimized for cancer samples.
- Analyze HaloPlex<sup>®</sup> data with the incorporation of molecular barcodes, significantly improving base calling accuracy even at low allelic frequencies compared to conventional NGS methods.
- Reliably identify SNPs, Indels, CNVs, LOH, somatic mutations and de novo mutations.

Fast time-to-results

- Reduce time-to-results from days to minutes without complex IT infrastructure or special hardware.
- Speed up the process with software that is streamlined to work with Agilent’s Target Enrichment portfolio.
- Get familiar with the software quickly using tutorial videos with step-by-step guidance for new users.

From Raw Data to Categorization of Mutations in 3 Simple Steps

SureCall’s 3-step workflow addresses the critical need for an easy-to-use analysis tool that incorporates the most widely accepted open source algorithms. Analysis begins with raw reads from Illumina HiSeq/MiSeq or aligned Ion Torrent sequencing of genomic DNA enriched with Agilent’s SureSelect, OneSeq, or HaloPlex Target Enrichment (Figure 1).

![SureCall Workflow Diagram](image-url)

**Read Alignment**
- Adapter removal
- Bam file generation

**Post Alignment Processing**
- Mutation identification
- Mutation impact analysis
- QC Reports

**Report Generation**
- Categorization
- Table output
- Visualization
- Links to database

Figure 1. Agilent SureCall’s end-to-end solution eliminates the need to outsource bioinformatics resources.
QC Metrics and Triage View

The SureCall Triage View (Figures 2A and 2B) allows researchers to suppress the reporting of mutations, change mutation categorization assignments, look up annotation information in external databases, filter mutations, and add notes to the analysis. You can also compare mutations in a sample with those present in other samples. An audit trail is kept of all changes that are made to the analysis of a sample.

Reporting Options in SureCall

SureCall’s flexible, customized reporting functionality offers multiple options to present information based on your requirements, including a mutation report, CNV/LOH report, QC report, or your own custom report (Figure 3).

FOR MORE INFORMATION
www.agilent.com/genomics/surecall

© Agilent Technologies, Inc. 2015
Published in USA, July 13, 2015
5991-6003EN

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