Agilent

Trusted Answers

Next Generation Sequencing

Target Enrichment

Your Partner in Every Step – from Sample to Data

NGS: Revolutionizing Genetic Analysis with Single-Molecule Resolution

Next generation sequencing has revolutionized variant analysis by providing single molecule sensitivity, enabling detection of rare alleles and those of low frequency even within highly heterogenous samples. This single molecule detection in a massively parallel manner allows you to overcome the inherent limitations of Sanger sequencing such as throughput, scalability, speed and resolution.

Sensitivity doesn't come without a cost and a more cost-effective solution to analyze specific targets by next generation sequencing is still a need. Target enrichment is a solution that provides exactly that—a way to focus reads on only those regions that matter.

The Leader in Target Enrichment

In 2009, Agilent introduced SureSelect, the first target enrichment solution for next generation sequencing. It enabled cost-effective analysis of thousands of targets, a paradigm shift in the elucidation of genes involved in disease pathogenesis. Since then, Agilent has become the leader in target enrichment solutions making major strides towards providing the complete solution from library prep, enrichment, sample QC, automation and data analysis.

Enabling Success, Advancing Clinical Research

Agilent offers a full range of catalog and custom target enrichment solutions that enable a streamlined workflow tailored to meet specific needs for target coverage, throughput and turn-around time for comprehensive profiling

SureSelect is a proven hybridization-based technology that has been instrumental in advancing NGS. With workflows that provide the fastest hybridization times and different pooling strategies, highly sensitive and accurate variant calling performance is achieved with either large exome captures or highly targeted panels.

HaloPlex^{HS} is a high sensitivity amplicon-based targeted sequencing method based on the HaloPlex^{HS} technology that incorporates molecular barcodes in the DNA library, allowing for the identification of duplicate reads hence significantly improving base calling accuracy even at low allelic frequencies compared to conventional NGS methods.

A Complete NGS Solution
For All Major NGS Platforms
Manual or Automated

MANUAL PROCESSING OR BRAVO-AUTOMATED

Content Definition

- **Catalog Designs**
  - -Exomes
  - -Panels
- **Create your own custom panel in SureDesign**

Library Prep

- **SureSelect**
  - -XT HS (low input with molecular barcode)
  - -XT (post-capture)
  - -XT2 (pre-capture)
  - -QXT (transposase-based)
  - -Strand Specific RNA
  - -MethylSeq
- **HaloPlex^{HS}**

Two Technologies, Infinite Possibilities

The Gold Standard in Target Enrichment — SureSelect

Great for:

- Detection of mutations, LOH and copy number
- Large custom captures (500 kb - 24 Mb)
- Highly sensitive and accurate variant calling
- DNA and RNA Target Enrichment

Next Generation PCR for NGS — HaloPlex^{HS}

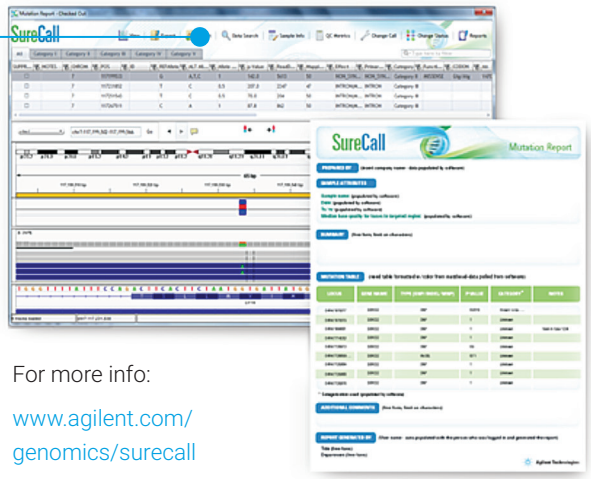
Great for:

- Small custom captures (1 kb - 500 kb)
- High specificity
- High sensitivity
- Streamlined workflow

SureCall–Data Analysis Bottleneck Resolved!

SureCall addresses the critical needs of clinical researchers. The free-of-charge software incorporates the most widely accepted open source algorithm optimized for accurate variant detection, including finding low allele frequency variants in cancer samples, and copy number changes.

- Easy-to-use and faster time-to-results
- Streamlined workflow for analysis
- Reduce the need for complex bioinformatics
- Integrated data analysis of SNPs, LOH, and genome-wide CNVs



For more info:

www.agilent.com/genomics/surecall

MANUAL PROCESSING OR BRAVO-AUTOMATED

Enrichment
- OneSeq
- ClearSeq Disease-focused Research Panels
- Clinical Research or Research Exomes
- Custom Designs (DNA/RNA)

Library QC
- 2100 Bioanalyzer System
- 2200 TapeStation System

Data Analysis
- Integrated copy number and mutation data analysis in SureCall
- RNA and Methylation workflows in GeneSpring

Proven Technology You Can Trust

Pave the Way to Constitutional Research

In the last 5 years, SureSelect and HaloPlex have played major roles in the identification of disease-associated genes by providing flexible solutions that couple expert-optimized designs with quick and easy workflows. This has addressed the need for deep target coverage, comprehensive and accurate variant calling and faster sample-to-data.

More Mendelian Disease Genes uncovered by SureSelect

Efforts to provide streamlined solutions for constitutional research has led to the introduction of three highly optimized designs that enable compatibility with both high output and benchtop sequencers that pave the way to definitive identification of disease-associated variants: **SureSelect Clinical Research Exome**, **SureSelect Focused Exome**, and **SureSelect Inherited Disease**. Coupled with the accelerated workflow of **SureSelect^{QXT}**, sequencing-ready libraries are generated in a day enabling faster sample to answers. Increased interest in analyzing copy number variants from NGS has led to Agilent's latest innovation – **OneSeq**, a combined detection of CNVs, SNPs, and LOH, allowing clinical researchers to investigate the role of CNVs in addition to mutations in many genetic disorders.

			Product Name	Features
Baits	Target Enrichment for SNPs, LOH, and genome-wide CNV detection		OneSeq Constitutional Research Panel	-Combined genome-wide CNV backbone, LOH, plus targets from SureSelect Focused Exome enabling mutation detection within disease-associated genes.
			OneSeq CNV Backbone + Custom	-Create designs with OneSeq CNV Backbone plus custom mutation panels up to 12 Mb using SureDesign.
	Capture baits for hybridization-based enrichment	NEW!	SureSelect Clinical Research Exome V2	-Comprehensive analysis of whole exome, with deeper coverage of disease-associated regions, ideal for the study of rare disorders.
			SureSelect Human All Exon V6, SureSelect Human All Exon V6 + UTR	-Most comprehensive exome capture design optimized for breadth and depth of coverage for highly sensitive and accurate variant calling as well as data uniformity for minimal sequencing.
			SureSelect Focused Exome	-Design targeted only on disease-associated regions, enabling compatibility with high-output or benchtop sequencers.
			SureSelect Inherited Disease	-Highly focused design that targets only the ~2,800 genes known to cause inherited diseases. -Ideal for deep sequencing or trio analysis on a benchtop sequencer.
			SureSelect Custom	-Create custom designs targeting regions of interest from 1 kb - 24 Mb using SureDesign.
	NGS disease research panels		ClearSeq Connective Tissue Disorders	-Focus on 40 genes known to play an important role in inherited forms of connective tissue disorder, including Marfan syndrome, Ehlers-Danlos syndrome, Loeys-Dietz syndrome, thoracic aortic aneurysm and dissection (TAAD), Stickler syndrome and Osteogenesis imperfecta.
		NEW!	ClearSeq Cardiomyopathy^{HS}	-Designed specifically for inherited forms of cardiomyopathy, including hypertrophic cardiomyopathy, dilated cardiomyopathy and arrhythmogenic right ventricular cardiomyopathy.
			ClearSeq Arrhythmia	-Targets genomic regions in 20 genes known to be linked to four inherited arrhythmia-related heart disorders.
Library Prep	Next Gen PCR		HaloPlex^{HS}	-Create custom designs targeting regions of interest from 1 kb - 5 Mb using SureDesign.
	Library prep for hybridization-based target enrichment		SureSelect^{QXT}	-Accelerated 90-minute hyb coupled with transposase-based library prep for sample-to-sequencing in a single day.
			SureSelect^{XT}	-High complexity target-enriched libraries for rare variant detection.

Unlocking the Cancer Genome

SureSelect and HaloPlex[HS] are key players in efforts to catalog mutations in cancer by enabling the identification of key low allele frequency mutations, indels, CNVs, gene fusions and translocations in many solid and hematological cancers. Optimized catalog and custom designs coupled with efficient SureSelect and HaloPlex[HS] workflows provide deep coverage for confident variant detection.

More Cancers Profiled using SureSelect & HaloPlex[HS]

To enable the accurate and comprehensive identification of somatic variants in solid tumors and hematological cancers, Agilent offers expert-defined focused panels. **ClearSeq Comprehensive Cancer**, **ClearSeq AML[HS]** and **ClearSeq Cancer[HS]** allows for deep coverage of disease-associated targets. For high sensitivity identification of low allele frequency variants in heterogenous cancer samples, **HaloPlex[HS]** incorporates unique molecular barcodes into each DNA library fragment. Combined with low input FFPE-compatible workflows and **SureCall** data analysis software, Agilent provides a rapid and complete sample-to-data solution ideal for the cancer clinical researcher.

			Product Name	Features
Baits	Capture baits for hybridization-based enrichment		SureSelect Human All Exon V6 + COSMIC	-Leverages the most comprehensive exome design with the addition of targets relevant to cancer research.
			SureSelect Human Methyl-Seq	-Comprehensive target enrichment for focusing on the regions where methylation is known to impact gene regulation.
			SureSelect RNA Capture	-Create custom designs targeting regions of interest from 1 kb - 24 Mb using SureDesign.
	NGS disease research panels		ClearSeq Comprehensive Cancer	-Enables genetic analysis of 151 key genes associated with a wide range of cancers.
		NEW!	ClearSeq AML[HS]	-Enables deep coverage of 20 genes frequently mutated in acute myeloid leukemia.
		NEW!	ClearSeq Cancer[HS]	-Identify somatic variants in 47 genes targeting known COSMIC hotspots found to be associated with a broad range of cancer types as well as published drug targets.
			ClearSeq Kinome	-Enables analysis of the human kinome including untranslated regions (UTRs).
Library Prep	Library prep for hybridization-based target enrichment	NEW!	SureSelect[XT HS]	-Generate high-sensitivity libraries with molecular barcodes from as little as 10 ng of input from intact or highly fragmented FFPE DNA.
			SureSelect[XT]	-Ligation-based library prep that enables generation of libraries of maximal complexity, ideal for analysis of highly heterogenous samples with variants of low frequency.
	Next Gen PCR		HaloPlex[HS]	-Unique molecular barcodes are incorporated into each DNA library fragment enabling de-duplication of reads and low allele frequency variant detection.
	Library prep for whole transcriptome sequencing	NEW!	SureSelect[XT] RNA Direct	-RNA target enrichment without ribosomal depletion bias for FFPE samples.
	Input Sample QC		Agilent NGS FFPE QC Kit	-qPCR-based assay for upfront sample prequalification and quantitation of amplifiable DNA prior to NGS library prep. Quality scores tie in to recommended modifications to the SureSelect[XT] Low Input Target Enrichment workflow to maximize target coverage and library complexity

Customize Your Genes for a Perfect Fit

Unparalleled Flexibility, Unmatched Performance

Agilent allows you to create any panel suitable to your specific field of interest by harnessing the flexibility of Agilent's proprietary SurePrint oligo manufacturing technology in the creation of custom NGS target enrichment libraries.

- Proven platform: More than 30,000 custom target enrichment designs created
- Flexibility to produce capture libraries from 1 kb to 24 Mb
- Easily leverage validated bait designs from catalog panels

Unrivaled Ease: SureDesign Custom Design Tool

SureDesign is a web-based application allowing you to create custom NGS target enrichment libraries that are specific to your research needs within minutes.

- Intuitive design wizard allows you to create designs based on target genes, genomic coordinates or selection parameters
- Comprehensive design report and target files are generated for easy review
- Collaborative Custom Design Service available for any organism

Welcome to the Agilent NGS Resource Center!

Looking for information regarding Agilent's NGS portfolio, cancer and constitutional applications, related literature, webinars, technical support and more? We have a wide array of tools to answer your Next Generation Sequencing questions.

We have you covered

For more info: www.agilent.com/genomics/NGSResource

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www.agilent.com/genomics/NGS

U.S. and Canada
1-800-227-9770
agilent_inquiries@agilent.com

Europe
info_agilent@agilent.com

Asia Pacific
inquiry_lsca@agilent.com

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