Agilent
Trusted Answers

SureSelect Clinical Research Exome V2

Optimized for Rare Diseases

SureSelect Clinical Research Exome V2
Definitive Answers Where It Matters Most

The SureSelect Clinical Research Exome V2 is the newest version of the Clinical Research Exome, both developed in collaboration with researchers at Emory University and The Children's Hospital of Philadelphia. Disease-relevant content were highly curated and added to the Human All Exon V6 as a base, making it the most comprehensive medical exome solution in the market today. In addition to deeper coverage of the most relevant disease-associated targets, the CRE V2 will be the only exome on the market to come with a list of included genes and their evidence for disease-relevance.

More information than any other exome on the market today!

A gene list is provided to help guide the analysis of your genomic data!

- **Superior coverage:** Excellent overall exonic coverage with enhanced coverage of genes associated with disease; increased coverage of HGMD, OMIM, ClinVar, and ACMG targets.
- **More relevant information:** Expert-driven curation of newly added disease-relevant content by Emory University and the Children's Hospital of Philadelphia; list of genes and their evidence for disease association is provided.
- **Complete and flexible solutions:** Accelerate discoveries and advance clinical research with the complete solution from sample to data – customizable target enrichment content, automatable workflow, along with data analysis and interpretation solutions.

Frequently Asked Questions

What differentiates CRE V2 from V1?

The CRE V2 is comprised of the SureSelect Human All Exon V6, as well as enhanced coverage of 1,099 disease-associated genes; in excess of 75,000 splice sites of non-coding exons; more than 12,000 previously reported deep intronic variants; over 800 previously reported variants in promoter regions, and non-coding RNAs. 71 breakpoint spanning probes have also been included for common deletions. The 67.3 Mb CRE V2 design enables deeper reach into regions of the genome not previously accessible through standard WES.

What are the disease-associated targets and how are they defined?

Disease-associated targets are genes linked to disorders. These were identified through the gene curation effort led by Emory University and CHOP, with data aggregated through large-scale literature and database curation efforts, deep sequencing of genes, functional validation of disease causality of gene variants through cDNA sequencing and breakpoint sequencing of variants.

When should I use CRE V2 instead of V6?

With its optimized bait selection and the newest curated disease-associated content, CRE V2 focuses additional sequencing power where it matters most, providing the most comprehensive coverage of clinical targets.

Which library prep solutions are CRE V2 compatible with?

The Clinical Research Exome V2 is compatible with best in class SureSelect library prep options (XT, XT2, and QXT).

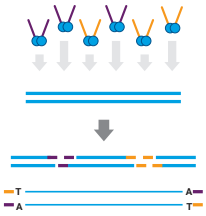
Fastest Workflow, Enriched Libraries in 1 Day

Complement the best content with the accelerated enrichment workflow of SureSelect^{QXT} which enables a 90-minute hybridization for faster sample to answers.

1 Ordering a Catalog Bait Library or Creating a Custom Panel

Order an NGS catalog panel or easily design a custom panel in minutes using Agilent's SureDesign web application

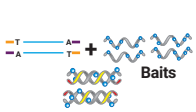
2 Preparation of DNA Libraries



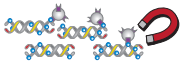
Genomic DNA is enzymatically fragmented and tagged with the adaptors

Adaptor-tagged fragments are amplified to generate the pre-capture libraries

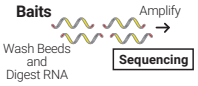
3 Hybridization and Capture



a. DNA library is allowed to hybridize with biotinylated SureSelect RNA baits (90 min for QXT)



b. DNA-RNA hybrids are pulled down using streptavidin-coated magnetic beads



c. Stringent washes are applied to eliminate non-specific targets

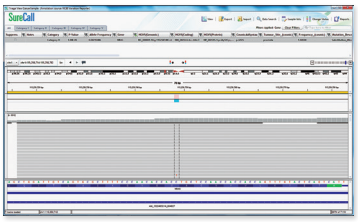
4 Amplification of Enriched Libraries

Indexes are added to the enriched library using on-bead PCR

5 QC Final Library

Quantify and QC prepared libraries using a 4200 TapeStation System or 2100 Bioanalyzer System

6 Sequencing & Data Analysis



Sequence libraries, analyze and obtain report of mutations using Agilent SureCall Software

Did You Know

Streamline your NGS data analysis and variant assessment workflows with our integrated software platform, **Agilent Alissa Clinical Informatics**!

The Most Comprehensive Clinical Research Exome, with a Flexible Workflow

The SureSelect platform provides a flexible workflow with different library prep options for your diverse needs. Our highly proven SureSelect^{XT} library prep with mechanical shearing provides a very robust solution for highly accurate results. For labs with enzymatic shearing needs or a need for faster turnaround time, the SureSelect^{QXT} library prep offers the solution with a 90-minute hybridization, with comparable performance to SureSelect^{XT}.

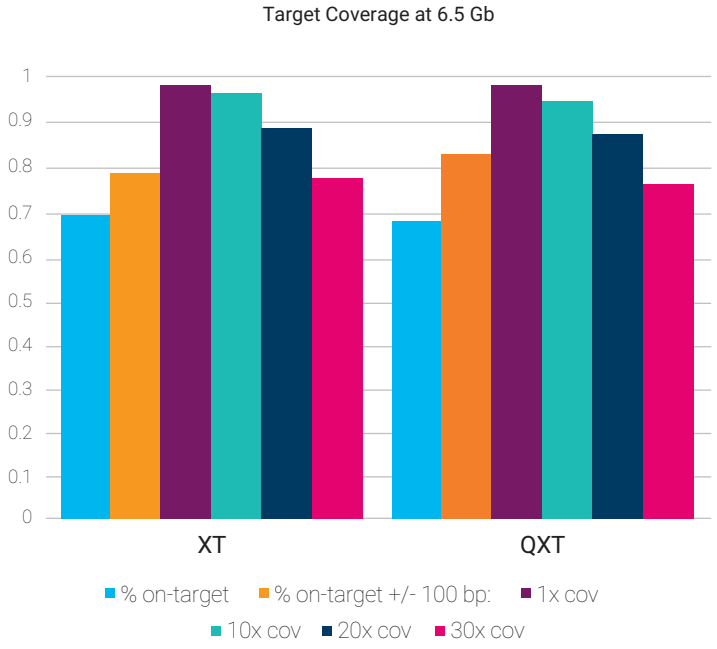


Figure 1. Comparison of sequencing performance between target enrichment with SureSelect Clinical Research Exome V2 using SureSelect XT and QXT library preps. Data averaged for 8 different HapMap DNA samples, with 6.5 Gb sequencing output.

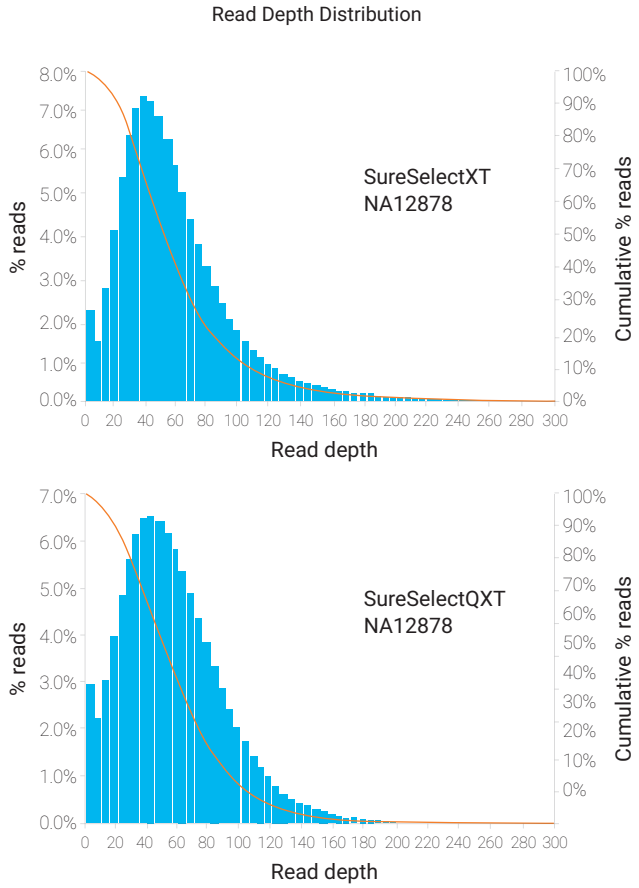


Figure 2. Read depth distribution for SureSelect Clinical Research Exome V2 using the SureSelect XT and QXT library prep. Sample HapMap NA12878 is shown.

Confidence Where it Matters

The SureSelect Clinical Research Exome V2 utilizes the Human All Exon V6 as its core design with boosted coverage in disease-associated regions, enabling more comprehensive coverage of highly curated databases (Table 1) and facilitating more confident variant calling within these targets. This design consists of targets included in databases such as the Online Mendelian Inheritance in Man (OMIM), the Human Genome Mutation Database (HGMD) and NCBI's ClinVar, along with additional targets to disease-relevant regions as defined by Emory University and the Children's Hospital of Philadelphia.

Coverage Across Select Annotation Sources

	CRE V2	Competitor I	Competitor R
Database*	**Percent of database covered**		
CCDS	99.77%	99.27%	97.99%
GENCODE-v17	99.69%	97.86%	97.44%
UCSC Known Genes	99.60%	96.04%	94.79%
RefSeq	99.63%	98.56%	97.52%
Vega	99.66%	97.57%	96.97%
HGMD coding regions	99.86%	99.23%	98.31%
OMIM coding regions	99.76%	99.12%	97.95%
ClinVar	97.63%	96.86%	93.71%
COSMIC	99.76%	98.96%	99.02%

**Data pulled May 2016*

Table 1. The SureSelect Clinical Research Exome V2 design shows superior bait coverage across select annotation sources compared to other disease-focused exome solutions on the market. Percent coverage of databases (intersect of baited regions with the databases) is shown.

SureSelect Clinical Research Exome V2 Has Superior Content…That Matters!

The CRE V2 enables better gene coverage in more difficult exonic regions, typically left out of designs due to high GC content and problematic sequencing. Also, researchers are able to detect more pathogenic ClinVar variants when compared with using competitor exomes.

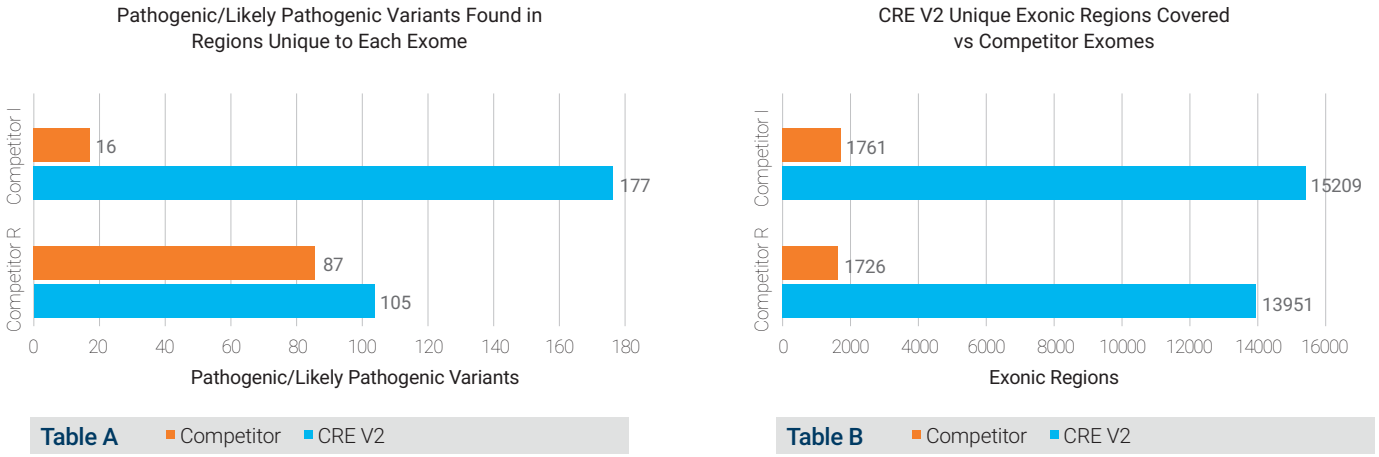


Figure 3. Comparison of the CRE V2 vs competitor exomes, using their respective design .bed files. Table A shows significantly more Pathogenic/Likely Pathogenic ClinVar variants found in regions unique to CRE V2 when compared with Competitor R and Competitor I. Table B shows that the CRE V2 design covers substantially more unique exonic regions than competitor designs.

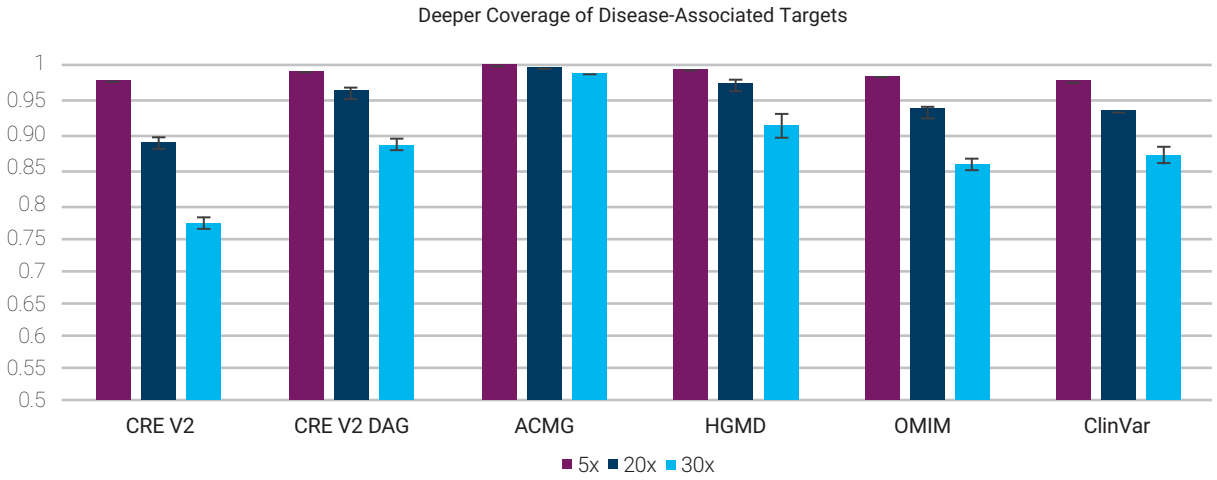


Figure 4. The SureSelect Clinical Research Exome V2 enables deep coverage of genes associated with disease. Coverage performance for CRE V2 with all baited regions , CRE V2 DAG (disease-associated genes as defined by Emory University and CHOP) and databases: ACMG (target list from *Green R.C. et al. Genet Med. 2013 Jul;15(7):565-74),* HGMD, OMIM, and ClinVar. All coverage statistics based on 6.5 Gb of sequencing at 2x100 bp. Shown is the average of 8 HapMap samples.

Product Description	16 Rxn	96 Rxn	96 Rxn Auto
SureSelectXT Clinical Research Exome V2	5190-9491	5190-9492	5190-9493
SureSelectXT Clinical Research Exome V2 Plus 1	5190-9494	5190-9495	5190-9496
SureSelectXT Clinical Research Exome V2 Plus 2	5190-9497	5190-9498	5190-9499
SureSelectXT2 Clinical Research Exome V2	5190-9500	5190-9501	5190-9502
SureSelectXT2 Clinical Research Exome V2 Plus 1	5190-9503	5190-9504	5190-9505
SureSelectXT2 Clinical Research Exome V2 Plus 2	5190-9506	5190-9507	5190-9508

For access to the SureSelect Clinical Research Exome V2 gene list and associated evidence for disease relevance, please contact your regional Technical Support.

Find an Agilent customer center in your country:
www.agilent.com/genomics/contactus

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