Data Sheet

Agilent
Trusted Answers

High-Performance Exome Sequencing Panels Tailored to Your Specific Needs

Key Advantages

Versatile and relevant content for every application

- Updated and comprehensive core content from major databases for more complete coverage
- Wide selection of predesigned content, such as UTRs, non-coding clinical variants, CNV backbone, pan-cancer biomarkers, and the mitochondrial genome for rapid customization
- Easy addition of custom content to augment or enhance regions of interest

Complete and flexible solutions from sample to report

- Native automation support for increased productivity
- Seamless integration with cloud-based informatics solutions for faster time-to-answers

Introduction

Exome sequencing offers a cost-effective approach to interrogate the protein coding portion of the human genome, which contains approximately 85% of known disease-causing mutations.[1] The Agilent SureSelect Human All Exon V8 features a slim and efficient design, powered by machine learning-based probe selection and placement. The panel provides comprehensive and updated coverage of human protein-coding regions from major public databases, such as RefSeq, CCDS, and GENCODE. It also covers the *TERT* promoter and hard-to-capture exons that are omitted by other exome sequencing panels on the market. Most importantly, the panel delivers excellent enrichment performance and sequencing economy, making it ideal for routine exome sequencing.

The SureSelect Human All Exon V8 exome panel is fully customizable. For applications that require augmentation or enhancement of the exome, Agilent provides a suite of predesigned content that can be leveraged and combined with the core exome content offered by SureSelect Human All Exon V8 to quickly create a customized exome panel. Examples of predesigned content include designs such as untranslated regions (UTRs), non-coding clinical variants (NCVs), copy number variations (CNVs) backbone, pan-cancer biomarkers, and the mitochondrial genome. Custom content can also be easily created using the Agilent SureDesign web-based custom design portal, or with the help of the Agilent SureSelect panel design team.

The SureSelect Human All Exon V8 exome enrichment workflow is natively supported on the Agilent Bravo Automated Liquid Handling platform for high-throughput sample preparation and the Agilent Magnis NGS Prep system for complete, walkaway automation. The sequencing data can be readily analyzed using the Agilent Alissa Interpret software for efficient variant interpretation and reporting, providing an end-to-end exome sequencing solution.

Easily Customizable with Custom or Predesigned Content

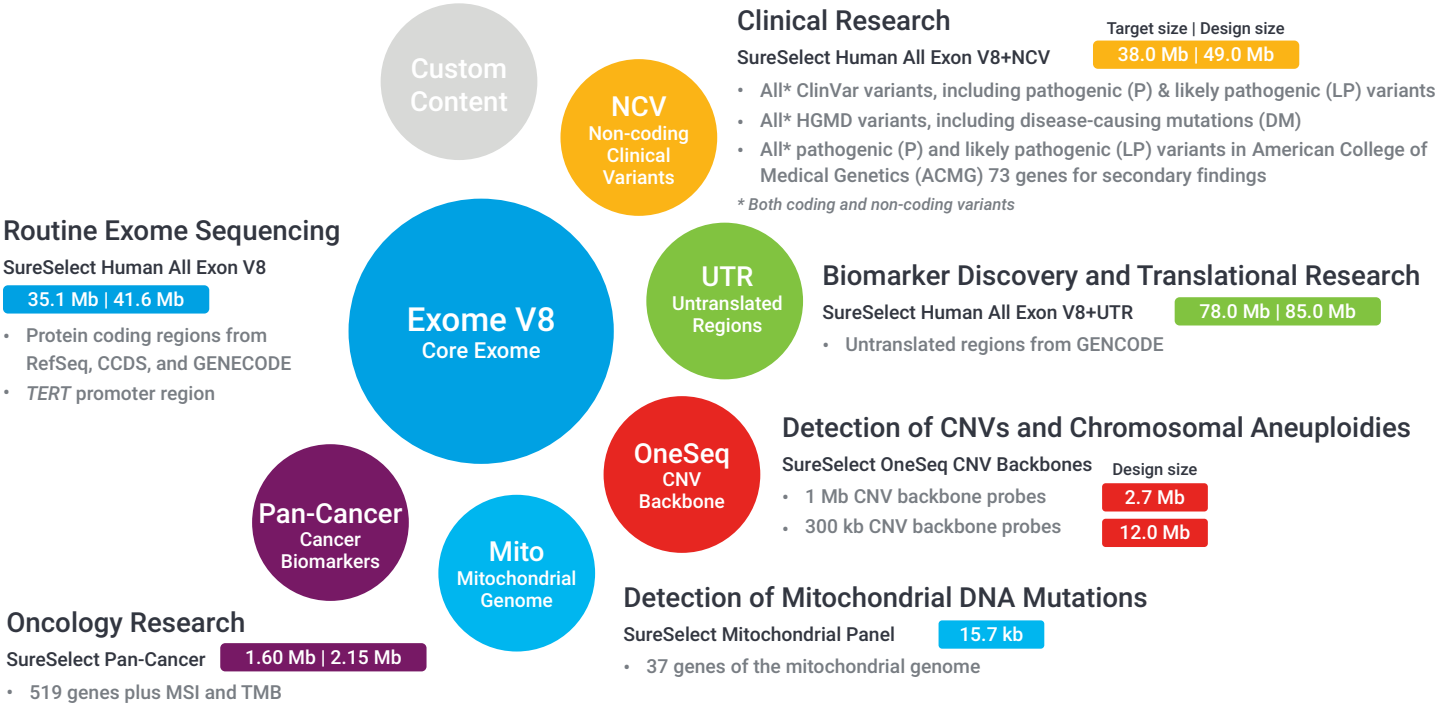

Figure 1. Customizable exome content. The SureSelect Human All Exon V8 exome panel can be rapidly customized via the wide selection of predesign content offered by Agilent to meet specific needs in exome sequencing. User-defined custom content can also be easily created using the SureDesign web-based portal, or with the help of the SureSelect panel design team.

Up-to-Date and Clinically Relevant Content

Table 1. Clinically relevant exome content for any application. The SureSelect Human All Exon V8 exome panels target up-to-date content from relevant databases, such as coding sequences from CCDS, RefSeq, and GENCODE, pathogenic variants in ACMG, ClinVar, and HGMD, untranslated regions (UTR) defined by GENCODE, and genes recommended by the National Comprehensive Cancer Network (NCCN). The table summarizes design coverage compared to other commercially available exome panels. The ACMG variants are pathogenic (P) and likely pathogenic (LP) variants in the 73 genes that ACMG recommends reporting secondary findings for in clinical exome sequencing. SureSelect Human All Exon V8+Pan-Cancer provides boosted coverage of 143 NCCN genes from the 13 most prevalent cancers according to the National Cancer Institute.

	SureSelect Human All Exon V8	SureSelect Human All Exon V8+NCV	SureSelect Human All Exon V8+UTR	SureSelect Human All Exon V8+Pan-Cancer	Vendor ID	Vendor R	Vendor T
Target Size	35.1 Mb	38.0 Mb	78.0 Mb	35.2 MB	34.1 Mb	35.8 Mb	36.5 Mb
Design Size	41.6 Mb	49.0 Mb	85.0 Mb	42.3 Mb	42.3 Mb	43.0 Mb	42.1 Mb
Coding Content	% Database Covered						
CCDS Release 22	**100%**	100%	100%	100%	99.8%	97.9%	97.6%
RefSeq Release 95	**100%**	100%	100%	100%	97.2%	97.4%	97.2%
GENCODE V31	**100%**	100%	100%	100%	99.7%	97.7%	97.3%
Non-coding Content							
ACMG variants	43.2%	**100%**	44.3%	43.8%	43.2%	70.7%	78.0%
ClinVar P/LP variants	12.4%	**100%**	14.3%	14.3%	12.8%	64.5%	98.9%
HGMD DM variants	8.7%	**100%**	12.2%	9.0%	9.2%	38.4%	54.0%
UTR Content							
GENCODE V33	0%	0.31%	**100%**	3.0%	0%	0.33%	0.88%
NCCN Guidelines							
Enhanced coverage of NCCN genes	No	No	No	**Yes, 143 NCCN genes**	No	No	No

V8+NCV Offers Deep Coverage of Clinically Relevant Variants

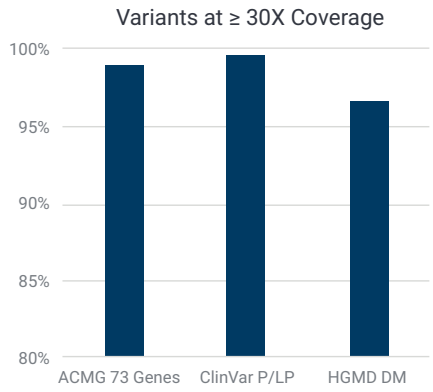

Figure 2. Comprehensive coverage of both coding and non-coding content for clinical research. The SureSelect Human All Exon V8+NCV exome panel expands coverage beyond the human protein-coding regions to include non-coding clinical variants from major databases. The 49 Mb panel provides excellent (>30X) coverage across pathogenic (P) and likely pathogenic (LP) variants in the ACMG 73 genes and the ClinVar database, as well as the disease-causing mutations (DM) in the HGMD database. Exome-enriched libraries were generated using the Agilent SureSelect XT Low Input Reagent kit with 200 ng of mechanically-sheared HapMap genomic DNA from the Coriell Institute and enriched as 1-plex captures using a 90 min hybridization. Samples were sequenced using 2x150bp reads and downsampled to 9 gigabases (Gb) for analysis.

V8+UTR Provides Robust Coverage of Untranslated Regions

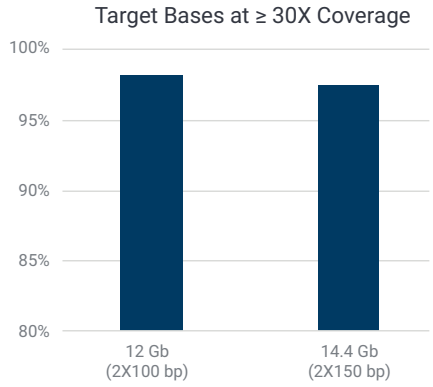

Figure 3. Robust coverage of untranslated regions for translational research and biomarker discovery. The SureSelect Human All Exon V8+UTR exome panel expands coverage beyond the human protein-coding regions to include untranslated regions (UTRs) defined by GENOCODE V33. The 85 Mb panel provides excellent (>30X) coverage across the protein-coding regions and UTRs. Exome-enriched libraries were generated using the SureSelect XT Low Input Reagent kit with 200 ng of mechanically-sheared HapMap genomic DNA from the Coriell Institute and enriched as 1-plex captures using a 90 min hybridization. Samples were sequenced using 2x100bp and 2x150bp reads and downsampled to 12 Gb and 14.4 Gb, respectively, for analysis.

V8+Pan-Cancer Delivers Tunable and Enhanced Coverage of Cancer Biomarkers

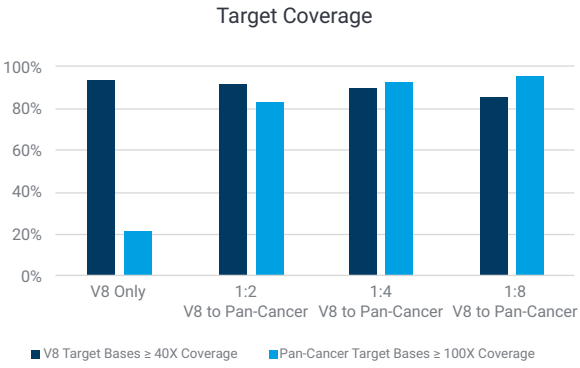

Figure 4. Enhanced coverage of cancer biomarkers for oncology research. The SureSelect Human All Exon V8 exome panel augmented with a custom SureSelect pan-cancer panel provides improved coverage of important cancer biomarkers. This enhanced exome panel allows confident calling of low-frequency somatic variants in tumor sequencing. The pan-cancer panel targets somatic variants including single nucleotide variants (SNVs), insertions and deletions (indels), CNVs, and translocations in 519 genes, as well as genomic loci for determining tumor mutational burden (TMB) and microsatellite instability (MSI) status. The blend ratio of the V8 exome panel and the pan-cancer panel can be customized to provide the desired target coverage. Exome-enriched libraries were generated using the SureSelect XT Low Input Reagent kit with 10 ng of HD799 moderately formalin-compromised DNA from Horizon Discovery and enriched as 1-plex captures using a 90 min hybridization. The capture probes consisted of just the SureSelect Human All Exon V8 exome panel (V8 only), or with the Pan-Cancer panel as a spike-in at different ratios (1:2, 1:4, and 1:8). Samples were sequenced using 2x150bp reads and downsampled to 15 Gb for analysis.

References

1. Choi, M.; Scholl, U. I.; Ji, W.; Liu, T.; Tikhonova, I. R.; Zumbo, P.; Nayir, A.; Bakkaloğlu, A.; Ozen, S.; Sanjad, S.; Nelson-Williams, C.; Farhi, A.; Mane, S.; Lifton, R. P. Genetic Diagnosis by Whole Exome Capture and Massively Parallel DNA Sequencing. *Proc. Natl. Acad. Sci. U. S. A.* **2009**, *106* (45), 19096–19101. https://doi.org/10.1073/pnas.0910672106.

Ordering Information

Compatible with SureSelect XT HS/LI/HS2 and QXT			
Product Description	**16 Rxns**	**96 Rxns**	**96 Rxns Auto**
SureSelect XT HS Human All Exon V8	5191-6873	5191-6874	5191-6875
SureSelect XT HS Human All Exon V8+UTR	5191-7401	5191-7402	5191-7403
SureSelect XT HS Human All Exon V8+NCV	5191-7407	5191-7408	5191-7409
Compatible with SureSelect XT HS/LI/HS2			
Product Description	**2 Hybs**	**12 Hybs**	**12 Hybs Auto**
SureSelect XT HS PreCap Human All Exon V8	5191-6876	5191-6877	5191-6878
SureSelect XT HS PreCap Human All Exon V8+UTR	5191-7404	5191-7405	5191-7406
SureSelect XT HS PreCap Human All Exon V8+NCV	5191-7410	5191-7411	5191-7412
Compatible with SureSelect XT			
Product Description	**16 Rxns**	**96 Rxns**	**96 Rxns Auto**
SureSelect XT Human All Exon V8	5191-6879	5191-6891	5191-6892
SureSelect XT Human All Exon V8+UTR		Contact Sales	
SureSelect XT Human All Exon V8+NCV		Contact Sales	
Compatible with Magnis NGS Prep system			
Product Description	**32 Rxns**	**96 Rxns**	
Magnis SSEL XT HS Human All Exon V8, Rev B	G9772C	G9772D	
Product Description			
SureSelect Human All Exon V8+Pan-Cancer	Contact Sales		
SureSelect Human All Exon V8+Mitochondrial Genome	Contact Sales		
SureSelect Human All Exon V8+OneSeq CNV Backbone	Contact Sales		
Alissa Interpret	Contact Sales		

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Alissa Interpret is a USA Class I Exempt Medical Device, Europe CE IVD, Canada and Australia Class I IVD Device.
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