Data Sheet

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Trusted Answers

High Performance Exome Built on Advanced and Proven Technology

Key Advantages

- Advanced technology that you can trust
- Superior performance for confident results and efficient sequencing
- Comprehensive content for more complete coverage
- Native automation support for increased productivity
- Seamless integration with cloud-based informatics solutions for faster time-to-answers

Introduction

The SureSelect Human All Exon V8 provides comprehensive content and the most up-to-date coverage of protein coding regions from RefSeq, CCDS, and GENCODE. It also covers the *TERT* promoter and hard-to-capture exons that are omitted by other exomes on the market. Powered by machine learning-based probe design and a new production process, the SureSelect Human All Exon V8 spans a 35.1 Mb target region of the human genome with an efficient end-to-end design size of only 41.6 Mb. The panel delivers excellent enrichment performance, as well as efficient and cost-effective exome sequencing. In addition, the panel is manufactured in large scale to provide consistent results for many years.

The SureSelect Human All Exon V8 is compatible with the legacy SureSelectXT target enrichment system, as well as the streamlined SureSelectXT HS2, SureSelectXT HS, SureSelectXT Low Input, and SureSelectQXT library preparation and target enrichment systems, which feature a fast, 90-minute hybridization protocol and a single-day workflow. The V8 exome workflow is natively supported by the Bravo Automated Liquid Handling platform for high-throughput sample preparation, and the Magnis NGS Prep system for complete, walkaway automation. The sequencing data can be readily analyzed using Alissa Interpret for efficient variant interpretation and reporting, providing an end-to-end exome sequencing solution.

Built on More Than 10 Years of Exome Technology

Figure 1. Superior by design. The new Human All Exon V8 is built on more then ten years of SureSelect technology and is now powered by machine learning for improved coverage and efficiency.

Excellent Target Coverage and Uniform Distribution for Confident Results

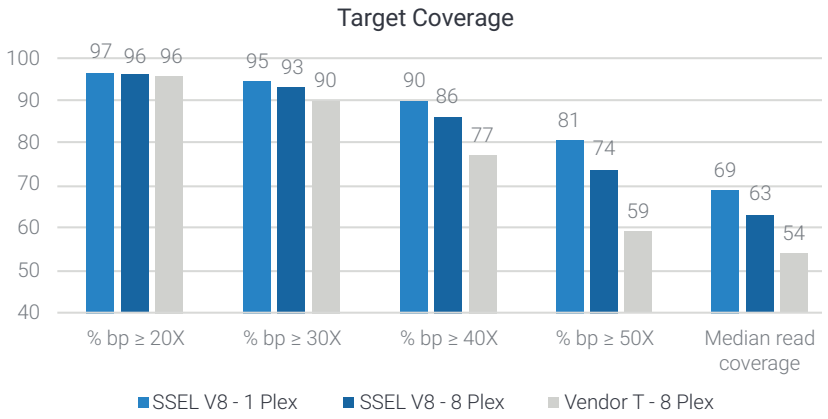

Figure 2. The SureSelect Human All Exon V8 delivers broader target coverage accross relevant depths and deeper median coverage for more confident variant detection. Exome-enriched libraries were generated following vendor protocols* and sequenced on an Illumina HiSeq 4000 instrument. All samples were downsampled to 5 Gb for analysis.

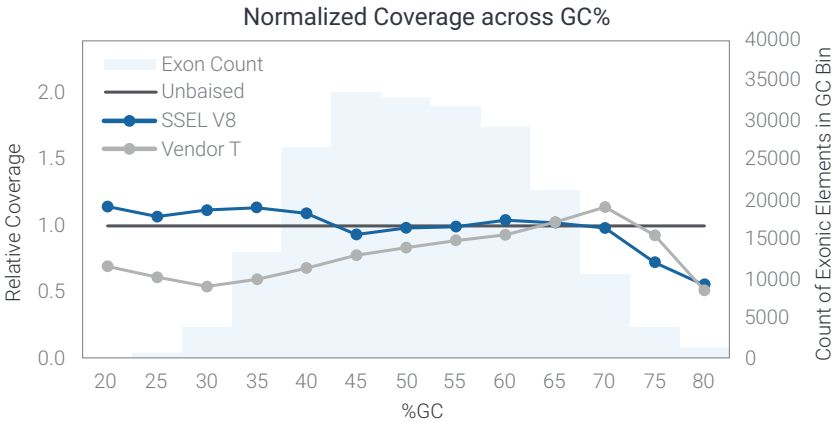

Figure 3. The SureSelect Human All Exon V8 provides more uniform distribution of coverage across the GC spectrum. Variants in GC-rich and GC-poor regions are better represented and less likely to be missed due to low coverage. Exome-enriched libraries were generated from 8-plex captures following vendor protocols* and sequenced on an Illumina HiSeq 4000 instrument. All samples were downsampled to 5 Gb for analysis.

Efficient Sequencing with High-Performance Enrichment

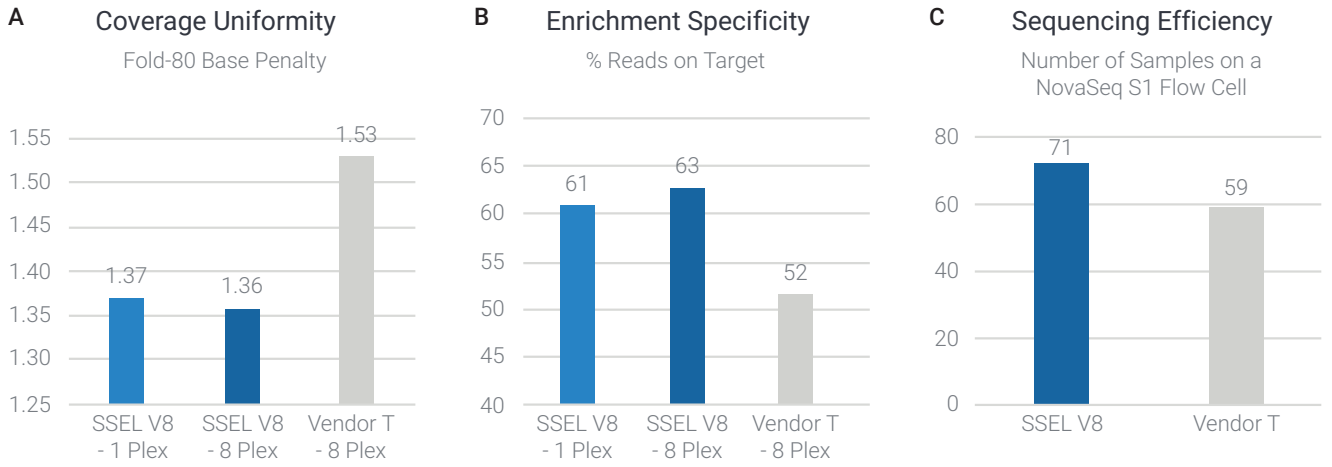

Figure 4. SureSelect Human All Exon V8 provides superior enrichment performance, resulting in lower sequencing costs. A) The SureSelect All Exon V8* delivers excellent coverage uniformity as measured by a lower fold-80 base penalty (lower is better). B) It also provides higher on-target rate, indicative of a highly specific enrichment of exonic sequences. C) SureSelect All Exon V8's high-performance exome enrichment, combined with an efficient design, reduces sequencing costs, allowing more samples to be sequenced together on a sequencing run. The number of reads required to achieve a 30X coverage of 90% from an 8-plex capture was calculated to determine the number of samples that can be sequenced together on a NovaSeq S1 flow cell.

** For both vendors, the respective protocol was followed without modification using NA12878 genomic DNA from the Coriell Institute (Camden, New Jersey). The starting DNA amount was 200 ng for samples prepared with the SureSelect Human All Exon V8 and 50 ng for Vendor T, as specified in Vendor T's protocol. For samples prepared with the SureSelect Human All Exon V8, libraries were constructed from Covaris-sheared DNA using the SureSelectXT Low Input Reagent kit and enriched as 1-plex or 8-plex captures, using 90-min hybridization. For Vendor T, DNA was enzymatically fragmented and libraries were generated and captured in 8-plex, using overnight hybridization. All samples were sequenced on an Illumina HiSeq 4000 instrument using 2x100bp reads and downsampled to 50 million reads or 5 Gb of data. Analysis was carried out using vendor provided target BED files. Fold-80 base penalty was reported from analysis with Picard HsMetrics (Broad Institute). The percentage of on-target reads was calculated as the total number of reads with at least 50% overlap with any base of the target, divided by the number of uniquely mapped reads.*

Ordering Information

Product Description	**16 Rxns**	**96 Rxns**	**96 Rxns Auto**
SureSelectXT HS Human All Exon V8	5191-6873	5191-6874	5191-6875
Sure SelectXT Human All Exon V8	5191-6879	5191-6891	5191-6892
Product Description	**2 Hybs**	**12 Hybs**	**12 Hybs Auto**
SureSelectXT HS PreCap Human All Exon V8	5191-6876	5191-6877	5191-6878
Product Description	**32 Rxns**	**96 Rxns**	
Magnis SSEL XT HS Human All Exon V8. Rev B	G9772C	G9772D	
Product Description			
Alissa Interpret	Contact Sales		

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