SureSelect
Human All Exon V7
Data Sheet

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Sleek Design, Best-in-Class Coverage, Minimal Sequencing

SureSelect Human All Exon V7 is a sleek exome targeting 35.7 Mb of content with design size of only 48.2 Mb. A novel machine learning based bait design approach reduces sequencing cost while providing superb coverage of coding regions from key databases such as RefSeq, CCDS, GENCODE etc.

Best-in-class coverage with minimal sequencing

% of Databases Targeted

	RefSeq	GENCODE v24	CCDS	UCSC Known Genes
SureSelect Human All Exon V7	**99.3%**	**99.6%**	**99.6%**	**99.6%**
Vendor ID	97.3%	97.1%	98.3%	94.5%
Vendor R	96.9%	97.2%	97.5%	96%
Vendor I	98.8%	99.1%	99.5%	98.3%
Vendor T	96.9%	97.1%	99.9%	93.7%

Percent Databases Covered at 20x

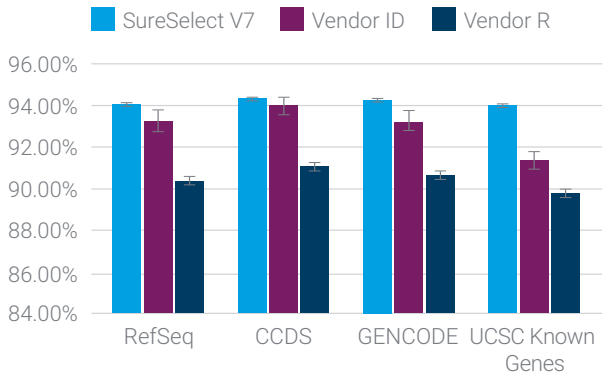
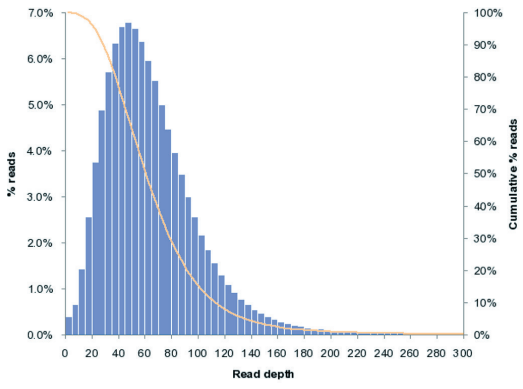
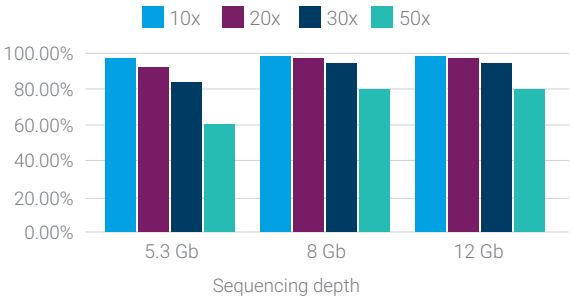


Figure 1. SureSelect Human All Exon V7 is a comprehensive exome that targets coding regions from 4 key databases. With just 5.3 Gb of sequencing, it provides excellent coverage of these databases. Exome sequencing was performed on 8 hapmap samples. Each vendor's protocol was followed for target enrichment. Data shown is average of 8 samples.



Percent Targeted Bases Covered with Increasing Sequencing Depth



Duplicate Rate	Percent on target +/- 100bp
2.1%	80%

Figure 2. SureSelect Human All Exon V7 provides uniform coverage across targeted regions in combination with low duplicate rates and high percent on-target.

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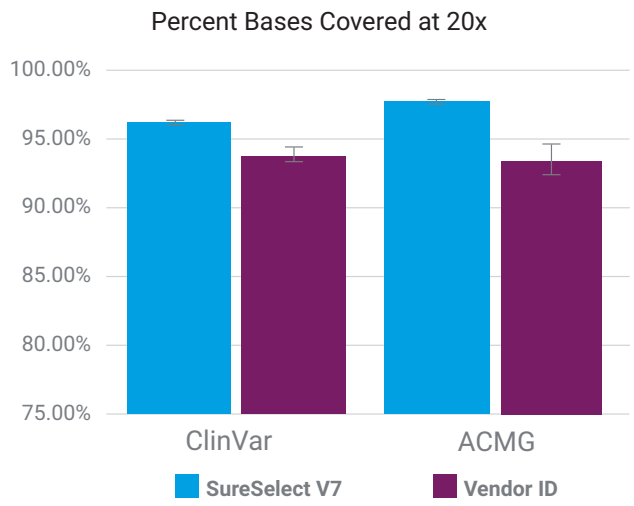
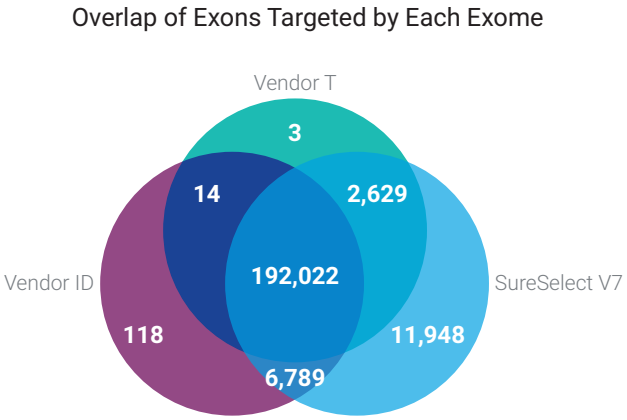
The most comprehensive variant detection platform

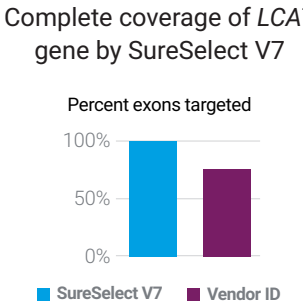
	SureSelect Human All Exon V7	Vendor ID	Vendor T
Percent coding exons targeted*	99.7%	92.9%	90.0%
Number of disease associated genes with incomplete coverage	51	1,377	1,574
Number of ClinVar pathogenic variants missed**	1	93	192

*Total number of coding exons = 213,994; Sources = RefSeq, GENCODE v24, CCDS, UCSC Known Genes

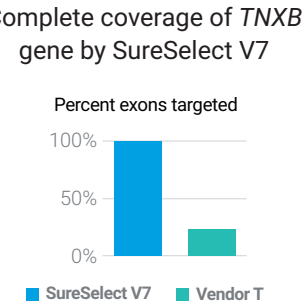
**Pathogenic/likely pathogenic variants from ClinVar occurring within coding regions were intersected with each vendor's targets







Mutations in the *LCAT* gene are associated with Norum and fish-eye diseases.



Mutations in the *TNXB* gene are associated with Ehlers-Danlos syndrome.

Figure 3. SureSelect Human All Exon V7 provides a highly comprehensive variant detection platform. Targeting >99% of coding exons from 4 key databases, SureSelect V7 provides the most comprehensive coverage of ClinVar. Incomplete coverage of disease-associated genes by other exomes results in multiple pathogenic variants to be missed by these exomes.

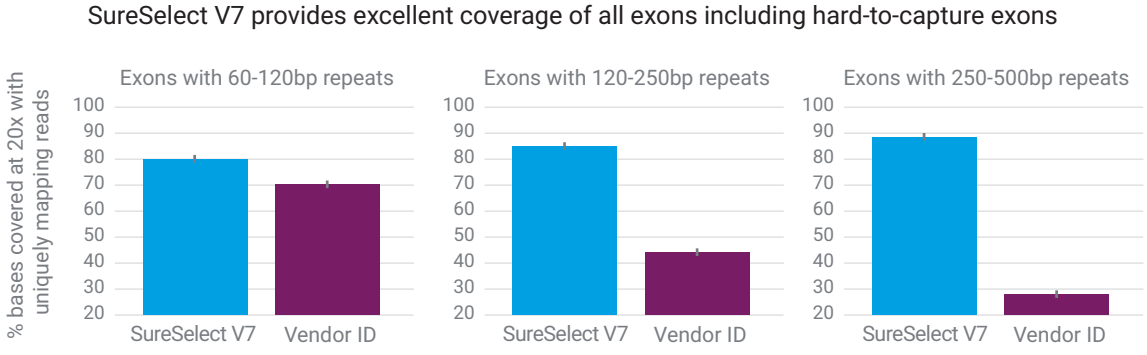


Figure 4. SureSelect Human All Exon V7 targets and provides excellent coverage of exons with repetitive elements, thus enabling robust variant calling in these regions. Only uniquely mapping reads were used for the analysis.

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PR7000-1841

Published in the USA, February, 2018
5991-9040EN

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