SureSelect^{XT} Custom Kits...A Surely Better Workflow Solution

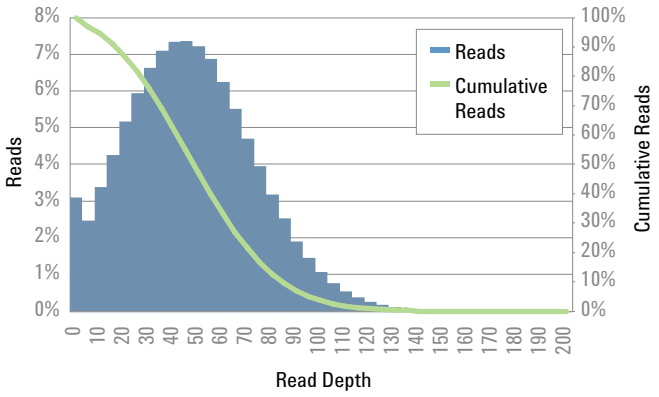
Agilent SureSelect Custom Target Enrichment System

Capture sizes available up to 34 Mb

Agilent's SureSelect^{XT} Custom Target Enrichment Kits now further expand the world's leading target enrichment technology by increasing the range of capture sizes from < 200 Kb, now up to 34 Mb — allowing for 5 times more sequence capture than ever before. SureSelect^{XT} kits include SureSelect Target Enrichment, optimized genomic DNA and library preparation kits.

- *Validated workflow fully compatible with Illumina and SOLiD next-generation sequencers*
- *Custom enrichment libraries for any species are easily designed in eArray*
- *Superior enrichment for targeting SNPs, indels and CNVs , providing richer, more comprehensive genetic information*
- *Single step 24-hour hybridization for faster time to results*
- *Kit configurations optimized for high-throughput automated workflows*

A. Read Depth Distribution for SureSelect^{XT} Custom Kit – 6.8 Mb



B. Read Depth Distribution for SureSelect^{XT} Custom Kit – 34 Mb

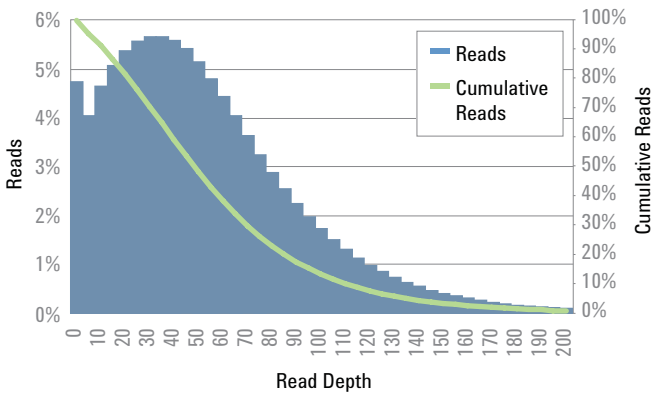
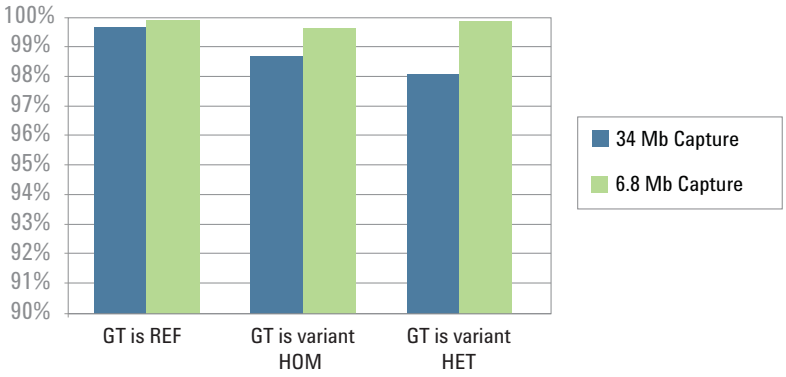


Figure 1. Read depth distribution plots for human genomic DNA enriched with SureSelect ^{XT} Custom Kit and sequenced on an Illumina HiSeq using 2x36 bp PE reads. A) 6.8 Mb custom target enrichment. 398 Mb of sequence was obtained with 85% on-target reads. 98% of targeted bases were covered at 1X or greater and average read depth was 49X. 87% of targeted bases were covered at 20X or greater. B) 34 Mb custom target enrichment. 2.3 Gb of sequence was obtained with 83% on-target reads. 98% of targeted bases were covered at 1X or greater, and average read depth was 56X. 81% of targeted bases were covered at 20X or greater.

A. Percent Sensitivity vs HapMap SureSelect^{XT} Custom Kits



B. Percent Concordance vs HapMap SureSelect^{XT} Custom Kits

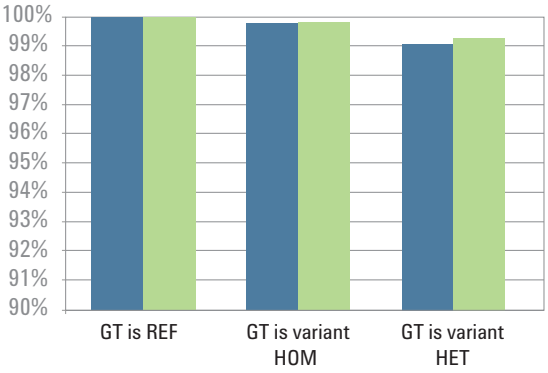


Figure 2. SNP data generated with both a 6.8 Mb capture and a 34 Mb capture after enrichment with SureSelect^{XT} Custom Library Kits and sequenced on an Illumina HiSeq. NGS libraries for HapMap sample NA10831 were prepared and enriched using two SureSelect^{XT} Custom Library Kits. 13,112 SNPs from the HapMap data set were assayed from the 6.4 Mb capture and 54,914 SNPs were assayed for the 34 Mb capture. Over 87% of targeted bases for the 6.8 Mb capture were sequenced at a depth of 20X or greater and over 83% of targeted bases for the 34 Mb capture were sequenced at 20X depth or greater. A) Sensitivity of SNP detection relative to the HapMap dataset was very high for the SureSelect^{XT} Custom Library / Illumina HiSeq platform, with over 99% of reference SNPs detected in both samples. Variant SNPs were also detected at high rates (> 98%) in both samples. B) Concordance with the HapMap SNP dataset for both samples was over 99%. This enabled high-confidence SNP calling in both experiments.

SureSelect^{XT} Custom Kits

Reactions Per Kit	<0.2 Mb (MP1)	0.2-0.49 Mb (MP2)	0.5-1.49 Mb (MP3)	1.5-2.9 Mb (MP4)	3.0-6.8 Mb (MP0)	Up to 13.6 Mb	Up to 20.4 Mb	Up to 27.2 Mb	Up to 34 Mb	Illumina Option Code	SOLiD Option Code
10	G7530A	G7531A	G7532A	G7533A	G7534A	G7535A	G7536A	G7537A	G7538A	001	002
25	G7530B	G7531B	G7532B	G7533B	G7534B	G7535B	G7536B	G7537B	G7538B	001	002
50	G7530C	G7531C	G7532C	G7533C	G7534C	G7535C	G7536C	G7537C	G7538C	001	002
100	G7530D	G7531D	G7532D	G7533D	G7534D	G7535D	G7536D	G7537D	G7538D	001	002
250	G7530E	G7531E	G7532E	G7533E	G7534E	G7535E	G7536E	G7537E	G7538E	001	002
500	G7530F	G7531F	G7532F	G7533F	G7534F	G7535F	G7536F	G7537F	G7538F	001	002
1000	G7530G	G7531G	G7532G	G7533G	G7534G	G7535G	G7536G	G7537G	G7538G	001	002
2000	G7530H	G7531H	G7532H	G7533H	G7534H	G7535H	G7536H	G7537H	G7538H	001	002
5000	G7530J	G7531J	G7532J	G7533J	G7534J	G7535J	G7536J	G7537J	G7538J	001	002

www.agilent.com/genomics/sureselect

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Published in USA, April 4, 2011
Publication Number 5990-7886EN

Agilent Technologies