

SureSelect

Target Enrichment for 454 Sequencing...Made Surely Better Agilent SureSelect Target Enrichment System

The leading target enrichment platform is now optimized and validated for all major second-generation sequencing platforms. Precisely direct your search for genetic variants with the Agilent SureSelect Target Enrichment System for 454 Sequencing. With protocols that are fast and easy to use, you receive superior on-target performance and read-depth uniformity.

Address your specific requirements with a variety of products optimized for 454 Sequencing systems. Enrich for the human exome or kinome with our off-the-shelf kits — or develop your own custom capture product with eArray, which allows you to easily design your own targets from <200 Kb up to 6.8 Mb. Our state-of-the-art, high-fidelity SurePrint long oligo printing facility delivers your order quickly so you can get your research moving faster than with other target enrichment products.

- Fully validated and compatible with 454 GS FLX Titanium and GS Junior sequencers
- 5-10 times less DNA required than for other protocols
- Fast, 24-hour hybridization

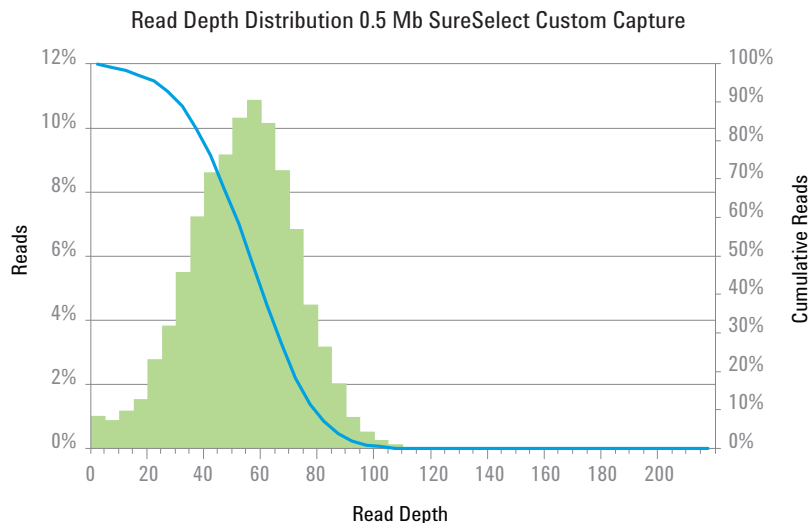
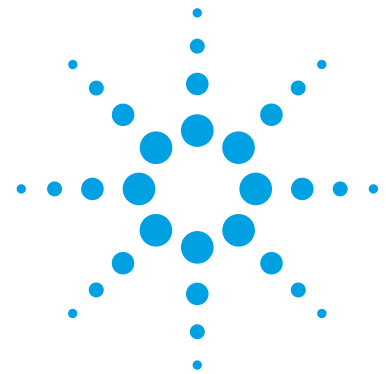
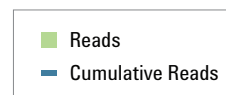


Figure 1. Read-depth distribution plot for DNA enriched with a SureSelect Custom Target Enrichment Kit (0.5 Mb capture) and sequenced on a GS FLX System. 67 Gb of sequence data was obtained, with an average read length of 360 bases. The percentage of on-target reads was 60 percent and the target enrichment delivered a high degree of read-depth uniformity. Average read depth was 53X and 95 percent of targeted bases were covered at 20X or greater, enabling high-confidence SNP calling.



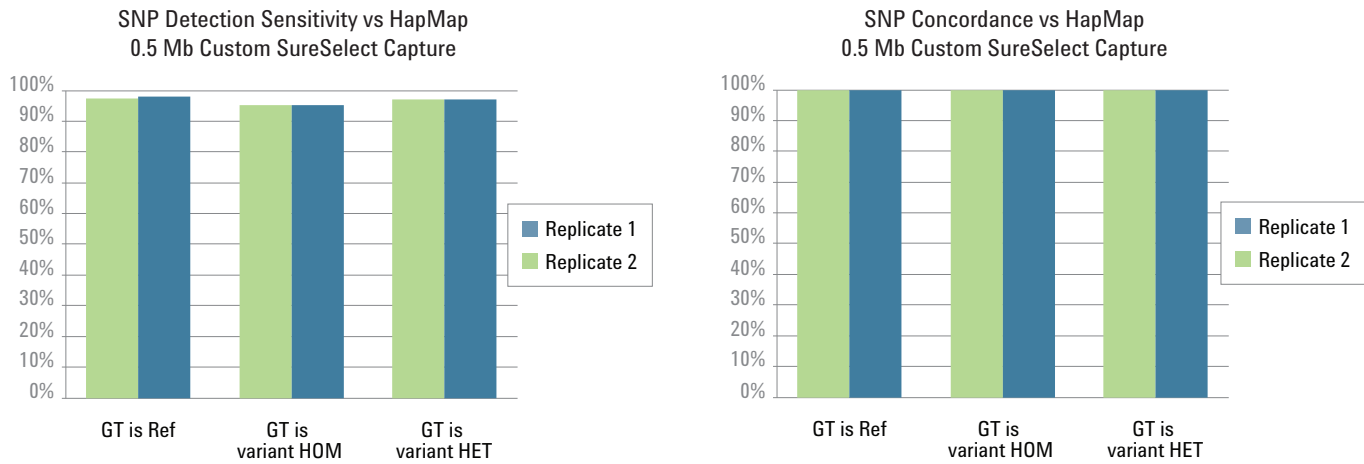


Figure 2. SNP detection with 454 Sequencing after SureSelect target enrichment was highly sensitive and SNP calls were highly concordant with HapMap. 343 known SNPs from HapMap were assayed in replicate samples (NA10831) using SureSelect library preparation and target enrichment with a 0.5 Mb custom capture. The resulting libraries were sequenced on the 454 FLX platform and over 90 percent of the capture was sequenced at a depth of 20X or greater. a) Sensitivity of SNP detection relative to HapMap was very high with the SureSelect/454 platform, with 98 percent of reference SNPs detected. Variant homozygous SNPs and heterozygous SNPs were also detected at high rates — 95 and 97 percent, respectively. b) Of the SNPs detected, concordance with HapMap was 100 percent for reference SNPs as well as for homozygous and heterozygous variants.

SureSelect Custom Kits

Reactions/Kit	<200 Kb	200 Kb - 499 Kb	500 Kb - 1.49 Mb	1.5 Mb - 2.99 Mb	3.0 Mb - 6.8 Mb	Roche 454 option code
10	G3360A	G3360A	G3360A	G3360A	G3360A	003
25	-	-	-	-	G3360B	003
50	-	-	-	-	G3360C	003
100	G3360K	G3360O	G3360S	G3360W	G3360D	003
250	G3360L	G3360P	G3360T	G3360X	G3360E	003
500	G3360M	G3360Q	G3360U	G3360Y	G3360F	003
1000	G3360N	G3360R	G3360V	G3360Z	G3360G	003
2000	-	-	-	-	G3360H	003
5000	-	-	-	-	G3360J	003

SureSelect Catalog Kits

Reactions/Kit	Human X Chromosome (3.1 Mb)	Human Kinome (3.2 Mb)	Human All Exon (38 Mb)	Human All Exon v.2 (44 Mb)	Human All Exon Plus (38 + 6.8 Mb)	Human All Exon (50 Mb)	Roche 454 option code
5	G4459A	G3365A	G3362A	G3353A	G3363A	G3370A	003
10	-	G3365B	G3362B	G3353B	G3363B	G3370B	003
25	-	G3365C	G3362C	G3353C	G3363C	G3370C	003
50	-	G3365D	G3362D	G3353D	G3363D	G3370D	003
100	-	G3365E	G3362E	G3353E	G3363E	G3370E	003
250	-	G3365F	G3362F	G3353F	G3363F	G3370F	003
500	-	G3365G	G3362G	G3353G	G3363G	G3370G	003
1000	-	G3365H	G3362H	G3353H	G3363H	G3370H	003
2000	-	G3365J	G3362J	G3353J	G3363J	G3370J	003
5000	-	G3365K	G3362K	G3353K	G3363K	G3370K	003
10000	-	G3365L	G3362L	G3353L	G3363L	G3370L	003

www.agilent.com/genomics/sureselect

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