

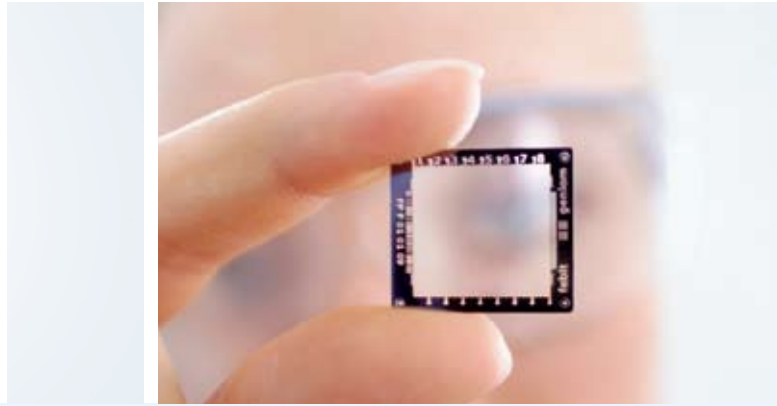


GENOME EXPLORATION. SIMPLIFIED. AUTOMATED.

HybSelect™

SEQUENCE CAPTURE FOR NEXT GENERATION SEQUENCING





HYBSELECT

For Convenient Targeted Re-Sequencing

■ HYBSELECT

is a microarray based sequence capture application. It represents an accurate method for highly efficient enrichment of genomic target regions prior to sequencing on next generation sequencing systems. HybSelect features outstanding sequence coverage for statistically robust determination of biological variation including SNPs, point mutations or indels. It is ideally suited for mutation detection in disease related genes of the human genome.

HybSelect has successfully been applied to human, mouse and microbial samples in combination with the Applied Biosystems SOLiD™ 3plus.*

HybSelect takes advantage of febit's microfluidic Biochip platform, wherein the fluidics of the Geniom Biochip and the HybSelector instrument provide a robust, easy to use and highly automated sequence capture environment for DNA fragments.

Validated protocols and HybSelect performance data from the Applied Biosystems SOLiD™ 3plus are available.*

We offer exciting HybSelect options:

HybSelect Sequence Capture Service

HybSelect & Sequencing Service

Sequence Capture and Next Generation Sequencing

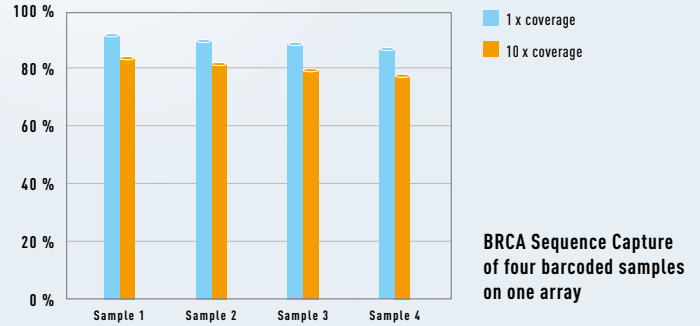
HybSelect on febit's instruments in your lab

*For other NGS platforms, please inquire.

- **AUTOMATED SEQUENCE CAPTURE ON MICROFLUIDIC BIOCHIPS**
- **EXCELLENT COVERAGE, ENRICHMENT AND THROUGHPUT**
- **EXCELLENT SNP DETECTION AND PROVEN ABSENCE OF ALLELIC BIAS**
- **FLEXIBLE AND FAST SCIENTIFIC BIOINFORMATICS FOR DESIGN AND ANALYSIS**
- **PARALLEL SEQUENCE CAPTURE WITH BARCODED SAMPLES**



HybSelector



HYBSELECT

The Power of Detection

■ THE FIRST FULLY AUTOMATED SEQUENCE CAPTURE SOLUTION

It's easy to capture your region of interest automatically using the HybSelector in your laboratory. The HybSelect protocol only takes 30 minutes of hands-on time using the HybSelector and is simple to implement.

The entire HybSelect sequence capture process is enabled by febit's microfluidic Biochips. Just insert your Biochip, inject your samples, and walk-away. Sample loading, hybridization, washing and temperature control are fully automated in the HybSelector.

You can work with our catalog Biochips, or with Biochips custom-designed to capture your region of interest. Customized HybSelect Biochips are promptly designed by our bioinformatics team.

■ POWER OF DETECTION

The HybSelect technology offers an excellent depth of coverage of your genomic region of interest: typically several hundred-fold for targets up to 2Mb. This capability can be used for accurate detection of mutations in disease-related genes. For example 98.1% (455/464) of heterozygous SNP's were detected and called correctly from a 1.5 Mb region of interest in a HapMap CHB reference sample (NA18561). HybSelect gives you an excellent power of detection for finding the mutations in your region of interest.

■ ECONOMICAL SEQUENCE CAPTURE BY PROCESSING POOLED BARCODED SAMPLES DURING ENRICHMENT

febit is the premium supplier for highly economical sequence capture using barcoding to reduce cost and increase throughput in your targeted Next Generation Sequencing projects. febit protocols allow pooling of at least 4 barcoded samples prior to enrichment on the capturing array for prevalidated genomic regions. Pooling of up to 16 samples was demonstrated for major cancer genes including the BRCA 1 and 2, employing febit's Cancer Exon Catalog Content. Customer selected loci can be rapidly qualified to test applicability of pooled barcoding. Please contact febit to receive an updated list of validated genomic regions or to discuss how your regions of interest can be qualified for a pooled processing assay.

■ FLEXIBLE AND FAST BIOINFORMATICS DESIGN AND ANALYSIS

We have the fastest and most flexible bioinformatics support available for targeted sequence capture. Just specify the genes that you want to capture and we will design and synthesize a customized HybSelect Biochip for you within days.

If you choose our HybSelect Service, you will also receive a concise and complete Bioinformatics Report. We can assist in the analysis and interpretation of your sequencing data. If you need additional bioinformatics support, please contact us.

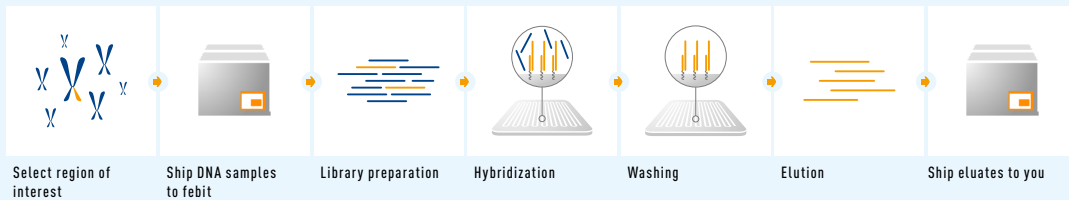


HYBSELECT

Options for Sequence Capture

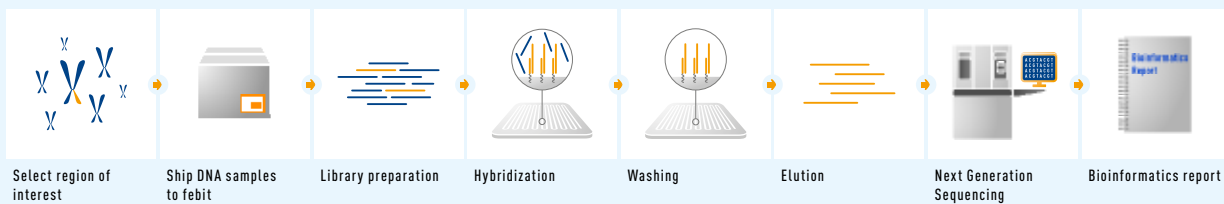
HYBSELECT SEQUENCE CAPTURE SERVICE

Specify the genes you want to capture, and ship your genomic DNA samples to febit. febit's experts will capture your region of interest and send back the captured DNA to you with hints and tips for the sequencing run.



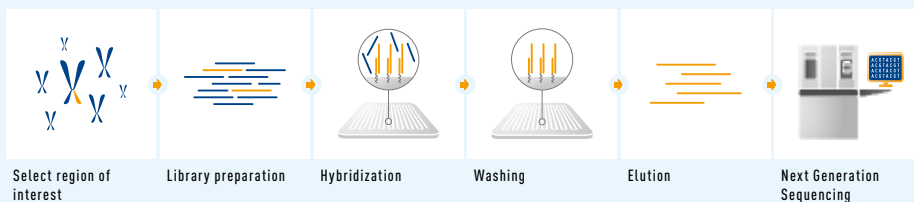
HYBSELECT SEQUENCE CAPTURE & SEQUENCING SERVICE

After specifying the region of interest and shipping your genomic DNA to febit, we will capture the interesting sequences and perform next generation sequencing. We will provide you a clear and publishable bioinformatics report based on the sequencing results.



HYBSELECT IN YOUR LAB

With HybSelect and a HybSelector, you can easily perform sequence capture in your own laboratory. Our platform sets a new standard for ease-of-use and sequence capture workflow automation.





HYBSELECT

Unmatched Depth of Coverage

TARGETED CAPTURE OF SNP REGIONS USING HYBSELECT

One thousand 500 bp regions with a centrally located SNP were HybSelected from a HapMap reference sample. The ranked average depth of coverage for the 1000 individual 500 bp regions is shown in the figure below. The average depth of coverage was 469 fold.

Depth of Coverage Across 1,000 SNP regions (500 bp)
(500 kb Total Target Region)



HYBSELECT DETECTION PERFORMANCE

The table below shows results of the sequence capture of 1000 HapMap SNPs out of a 1.5 Mb region of interest. The results demonstrate HybSelect's detection power. 91.2% of the 1000 SNP positions were covered at $\geq 20x$, and 98.6% of those were concordant with the reference sequence. There was no evidence of allelic bias, and 98.1% of the heterozygotes were detected and called correctly.

HYBSELECT	PERFORMANCE
Region of Interest	1.5 Mb
Target	0.5 Mb
Average Target Coverage	469 fold
Percent Target Covered	97.5 %
Percent Target Covered at $\geq 10x$	90.5 %
Percent Target Covered at $\geq 20x$	88.5 %
Enrichment	1062
SNP calling rate	98,6 %

Bioinformatics Definitions

REGION OF INTEREST (ROI)

The summed length (bp) of specific locations within the genome from which the researcher wants sequence information.

TARGET

The summed length (bp) of the ROI for which the HybSelect Biochip is designed to capture minus the regions (bp) that are deliberately excluded (e. g., repetitive elements).

AVERAGE TARGET COVERAGE

Number of base pairs from sequence reads within the target divided by the total number of base pairs of the target.

PERCENT TARGET COVERED

Percentage of the target for which there is at least 1 x Depth of Coverage.

ENRICHMENT

Percentage of filtered bases from NGS which map to the target, divided by the percentage of the genome represented by the target. (number of bases mapped to target/number of filtered bases from NGS)/(size of target in bp/size of genome in bp).

HybSelect and Sequencing Services

HYBSELECT LIBRARY PREPARATION

HYBSELECT SEQUENCE CAPTURE

SEQUENCING SERVICE ON SOLID™ 50 BASE SINGLE END

HYBSELECT & SEQUENCING SERVICE

LIBRARY PREPARATION & HYBSELECT & SEQUENCING SERVICE

For every HybSelect Service you can choose your Bioinformatics support: Saver, Gold or Platinum.
Choose also whether your order is processed as priority or standard.

For research use only.

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