SWIFT HYBRIDIZATION CAPTURE KITS

Targeted Sequencing Panels for Human Exome, Pan-Cancer and Inherited Diseases

Highlights

- **Enables enrichment of the human exome or subsets of disease-related genes**
  Superior on-target performance and comprehensive coverage of human coding sequences from the RefSeq database, probes designed to version hg19
- **Saves sequencing costs**
  Pre-capture multiplexing facilitates orders of magnitude more efficient next generation sequencing by targeting genes of interest while conserving enrichment reagents
- **Provides high quality data**
  Probes achieve deep and uniform coverage even across GC-rich regions such as first exons

Introduction

Swift Hybridization Capture Panels offer probes for DNA hybridization capture-based target enrichment. The Swift panels consist of individually synthesized and quality-controlled probes designed to provide the highest level of performance and ready to hybridize to NGS libraries to enrich for targets of interest. The Swift Hyb, Wash and Universal Blocker kit completes the target enrichment workflow.

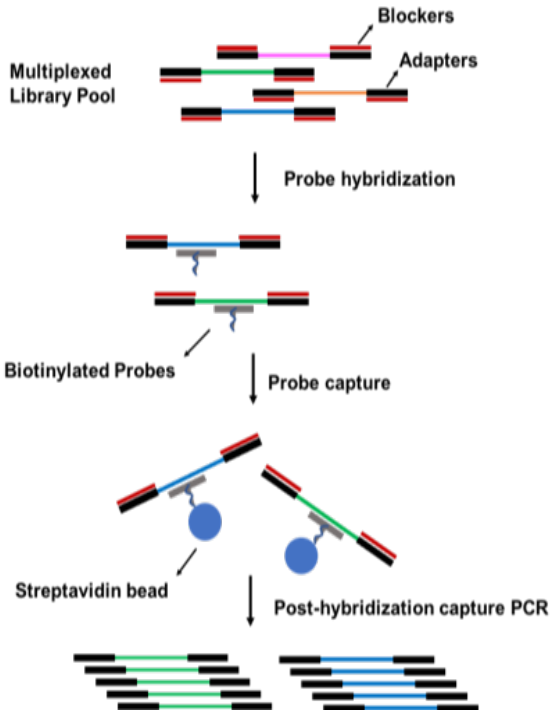

Figure 1. *Libraries are pooled and combined with blocking oligos and human Cot DNA. Next, the library pool is hybridized to Swift probes, captured using streptavidin beads, and washed to remove unbound fragments. Then, the enriched library pool is amplified by PCR and is ready for multiplexed Illumina® sequencing.*

	Swift Exome	Swift Pan-Cancer	Swift Inherited Diseases
Human Target Region	39 Mb	0.8 Mb	11.1 Mb
Genes Covered	Coding region of 19,396 coding genes*	127 oncology-related genes* implicated in 12 tumor types	4,503 genes* based on the Human Gene Mutation Database (HGMD®)
Numbers of Probes	429,826	7,816	116,355

**See complete gene lists at swiftbiosci.com and to access panel probe and target files.*

Applications and Sample Types

- Detection of germline inherited SNVs and Indels
- Low frequency somatic variant detection of SNVs and Indels
- Copy number variant detection

Compatible with the following DNA library prep kits:

- Swift 2S Turbo, for high quality genomic DNA and FFPE
- Accel-NGS® 2S Hyb for FFPE, cfDNA, and incorporation of molecular identifiers (MIDs) for ultra-low frequency variant detection
- Accel-NGS 1S Plus for heavily nicked or denatured samples

Highest On-Target Delivered by Swift Exome Hyb Panel

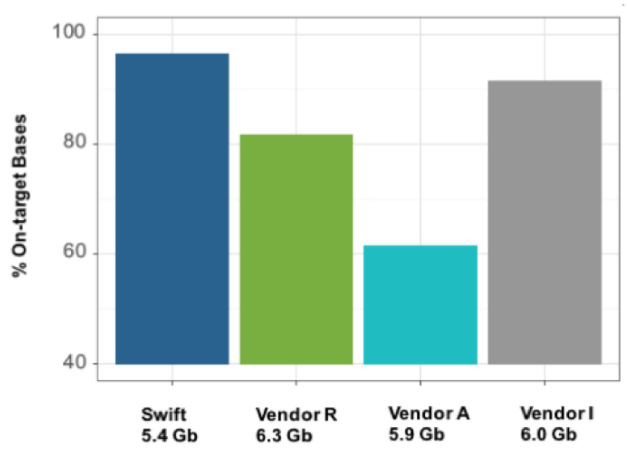

Figure 2. *An independent, large genome center compared the Swift Exome Hyb Panel to exome panels from other vendors. Sequencing libraries were prepared using standard shearing and ligation-based library preparation, and then pooled. The 12-plex pool was split into four 6 µg aliquots to assess each vendor's exome panel. Target capture was performed according to each vendor's recommended protocol. Enriched libraries were sequenced using 2 x 100 paired-ended reads. On-target bases were determined with Picard (selected bases), using 35M reads per library. Results demonstrated that the Swift Exome Hyb Panel had the highest on-target mapping of the exome panels tested. The percentage of bases on target for each vendor's panel was calculated across a 500 bp flanking region.*

Swift 2S Turbo with Swift Hyb Panels Produce Better Coverage Uniformity

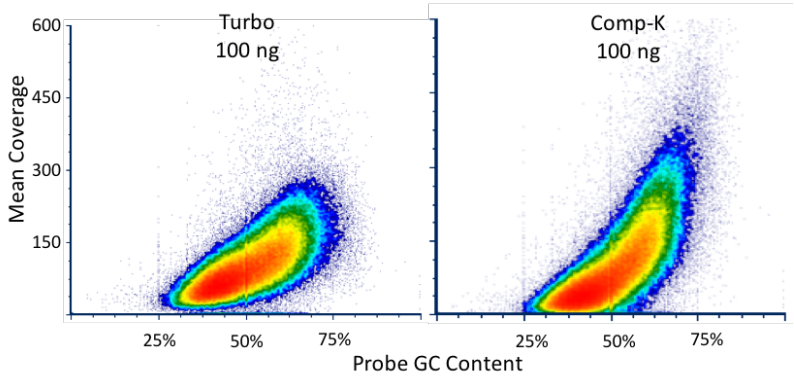

Figure 3. *Libraries produced with Swift 2S Turbo showed less Exome Panel probe base composition bias compared to competitor-K library prep kit in the probe dot plots. Libraries were constructed with 100 ng NA12878 DNA and sequenced on HiSeq4000 to 150x mean coverage.*

2S Turbo with Swift Hyb Panels Produce Better Uniformity at Low Input

Prep	Hyb Panel	Platform	Sample	Input (ng)	% Duplication	Mean Coverage	%Covered 20x	%Covered 50x	%Covered 100x	% Bases On-Target
Turbo	Exome	HiSeq4000	NA12878	100	18.2	154x	97.9	87.7	53.0	93.6
Turbo				50	17.5	151x	98.0	89.0	50.7	94.2
Turbo				25	17.4	146x	97.9	89.0	50.4	94.1
Comp-N				100	25.3	155x	97.7	88.1	47.9	94.2
Comp-K				100	14.8	155x	92.3	73.0	47.0	94.4
Turbo	Exome	HiSeq4000	NA12878	10	18.8	149x	98.0	87.5	51.5	94.2
Comp-N				10	19.1	149x	97.0	84.0	50.0	94.3
Comp-K				10	21.3	148x	92.3	70.2	44.3	94.4
Turbo	Exome	HiSeq4000	NA12878	1	47.6	151x	97.2	74.3	14.1	94.3
Comp-N				1	79.1	155x	74.1	1.01	0.03	93.9
Comp-K				1	73.1	147x	66.1	21.0	0.05	94.3

Table 1. *Swift 2S Turbo DNA Library Kit was evaluated for enrichment using Swift Exome Hyb Panel. Comprehensive target coverage and high complexity was observed with multiple input quantities. Coverage uniformity and complexity was higher with low input Turbo libraries compared to competitor library preparation kits (see highlighted region of table).*

Inherited Diseases and Pan-Cancer Panels Have High On-Target Coverage

Library	Sample Type	Sample Input	Mean Insert Size	%Duplication	Mean Bait Coverage	%Covered > 20X	%Covered > 40X	%Bases On-Target
Inherited Diseases_1	NA12878	50 ng	194.9	2.1	61x	99.3	60	95
Inherited Diseases_2			193.9	1.8	61x	99.3	61	95
Inherited Diseases_3			193.0	2.0	61x	99.3	60	95
Inherited Diseases_4			192.5	2.1	61x	99.3	60	95
PanCan_1			189.6	1.7	77x	98.9	96.2	78
PanCan_2		250 ng	196.5	2.1	79x	98.7	95.7	79

Table 1. *Swift 2S Turbo DNA Library Kit was evaluated for enrichment using Swift Inherited Diseases Panel and Pan-Cancer Panel. Comparable target coverage and complexity was observed with varied input Turbo libraries regardless of the panel size.*

MIDs Enable Ultra-Low Frequency Variant Detection using Pan-Cancer Panel

cfDNA Spike-in Variants

Chr: Position	ALLELE FREQUENCY					
	Sample 1		Sample 2		Sample 3	
	Expected	Observed	Expected	Observed	Expected	Observed
2: 212244718	1.0%	**1.05%**	1.0%	**0.87%**	1.0%	**0.77%**
12: 25361074	1.0%	**1.15%**	1.0%	**1.16%**	1.0%	**1.01%**
12:25361142	1.0%	**1.40%**	1.0%	**0.97%**	1.0%	**0.66%**
12: 25361646	1.0%	**1.39%**	1.0%	**1.40%**	1.0%	**0.59%**
12: 40688695	1.0%	**0.71%**	1.0%	**0.97%**	1.0%	**0.55%**
12: 115108136	1.0%	**0.90%**	1.0%	**1.96%**	1.0%	**0.70%**

gDNA Spike-in

Chr: Position	ALLELE FREQUENCY			
	Sample 4		Sample 5	
	Expected	Observed	Expected	Observed
2: 212243011	1.0%	**1.1%**	0.5%	**0.6%**
2: 212244761	1.0%	**0.9%**	0.5%	**0.3%**
2: 212245090	1.0%	**0.5%**	0.5%	**0.4%**
2: 212245489	1.0%	**1.3%**	0.5%	**0.7%**
3: 176738798	1.0%	**1.1%**	0.5%	**0.6%**
3: 176739663	1.0%	**1.2%**	0.5%	**0.7%**

Figure 3. *cfDNA was extracted from blood of four individuals with unique genetic background and Coriell gDNA samples from different genetic backgrounds were obtained. To determine the effect of MIDs on low frequency variant calling, sample spike-ins were performed at 1% or 0.5% frequency into 10 ng cfDNA or 100 ng gDNA. Libraries were prepared with the Swift Accel-NGS 2S Hyb Kit with MIDs, enriched with the Swift Pan-Cancer Panel and sequenced on an Illumina HiSeq to a minimum of 8000x coverage. A consensus sequence was generated for each MID family (BMFtools) and data were analyzed for homozygous SNPs present in the spike-in sample only. 6/6 known variants were present in all three 1% cfDNA samples and 27/27 known variants were present in both 1% and 0.5% gDNA samples depicting the power of MIDs for low frequency variant calling (only 6/27 variants shown). Refer to Swift MID Technical Note entitled, Increasing Specificity of Detecting Low Frequency Alleles with Molecular Identifier, for more information on experimental design and data analysis.*

Ordering Information

Product Name	Reactions	Catalog No.
Swift Exome Hyb Panel	16	83216
Swift Pan-Cancer Hyb Panel	16	83316
Swift Inherited Diseases Hyb Panel	16	83416
Swift Hyb and Wash Kit	16	88016
Swift Hyb, Wash, and Universal Blocker Kit	16	89016
Swift Library Amplification Primer Mix	96	88196

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