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Nextera® Rapid Capture Exomes

A rapid workflow and comprehensive exome content, with unparalleled flexibility.

Highlights

- **Rapid exome preparation and enrichment**
  Prep and enrich 96 exomes in only 1.5 days with less than 5 hours hands-on time
- **Comprehensive exome coverage**
  Two different exome designs are available to access core exonic content or expanded content
- **Kit configurations designed to fit your needs**
  Choose the optimal fit for your system, samples, and study, with more flexible options than ever before
- **Complete support for entire process from library preparation to sequencing**
  All-in-one kit for prep and enrichment from the world's leading sequencing provider

Overview

Nextera Rapid Capture Exomes are all-in-one kits for library preparation and exome enrichment that allow researchers to identify coding variants up to 70% faster than other methods. Nextera Rapid Capture Exome delivers 37 Mb of expertly selected exonic content, including challenging regions excluded from other exome designs.

Rapid Exome Prep and Enrichment

Nextera Rapid Capture Exomes provide library prep and exome enrichment in only 1.5 days. Sequencing with the HiSeq® 2500 or NextSeq™ 500 system enables experiments to go from DNA sample to data in as little as 2.5 days. The speed of Nextera Rapid Capture Exomes enables you to complete projects faster, return results faster, and ultimately publish faster.

Focused Exonic Content

Nextera Rapid Capture Exome has been optimized to provide uniform and specific coverage of 37 Mb of expert-selected exonic content. The probe set was designed to enrich 214,405 exons (Table 1). This focused design, paired with uniform and specific enrichment, enables the most comprehensive exome sequencing available and reliable identification of true, coding variants (Table 2).

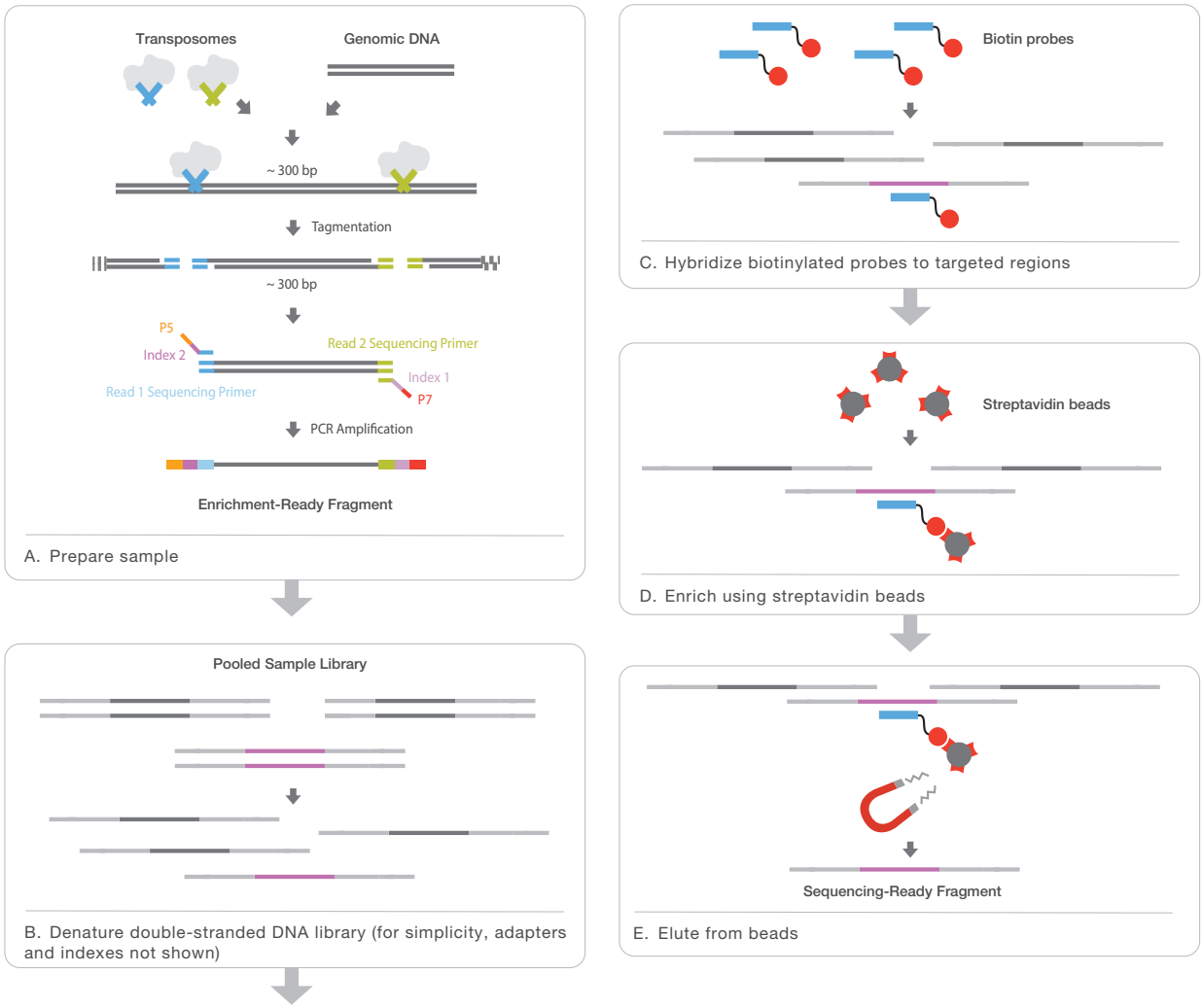
Table 1: Coverage Details

	Nextera Rapid Capture Exome	Nextera Rapid Capture Expanded Exome
Coverage Specifications		
Number of target exons	214,405	201,121
Target content	Coding exons	Exons, UTRs, and miRNA
Percent of Exome Covered (by Database)		
Refseq	98.3%	95.3%
CCDS	98.6%	96.0%
ENSEMBL	97.8%	90.6%
GENCODE v12	98.1%	91.6%

Table 2: Comparison of Rapid Capture Exomes

Specification	Nextera Rapid Capture Exome	Nextera Rapid Capture Expanded Exome
Target size	37 Mb	62 Mb
Genomic DNA input	50 ng	
Hands-on time	5 hours	
Total time	1.5 days	
Batch size	1–96 exomes	

Figure 1: Nextera Rapid Capture Workflow



The Nextera Rapid Capture Exome Kit provides a fast, simple method for isolating the human exome. The streamlined, automation-friendly workflow combines library preparation and exome enrichment steps, and can be completed in 1.5 days with minimum hands-on time.

Greater Coverage with Expanded Exome

Nextera Rapid Capture Expanded Exome features a highly optimized probe set that delivers broad coverage of exons as well as expanded content, such as UTRs and miRNA binding sites. Genome-wide association studies suggest that > 80% of disease-associated variants fall outside coding regions[1]. Analysis of these regions enables researchers to discover variants that affect gene function, at a more affordable price than whole-genome sequencing. The kit includes >340,000 95mer probes, each constructed against the human NCBI37/hg19 reference genome (Table 1). Nextera Rapid Capture Expanded Exome targets a genomic footprint of 62 Mb.

Unmatched Ease

Nextera Rapid Capture Exomes allows researchers to maximize the productivity of their lab personnel and Illumina sequencing technology. The simplicity and speed of the Nextera Rapid Capture assay enables a single technician to prepare and enrich 96 samples in only 1.5 days.

The process starts with rapid Nextera-based library prep to convert input genomic DNA into adapter-tagged libraries (Figure 1A). This rapid prep requires only 50 ng of input DNA and takes less than 3 hours for a plate of 96 samples. Nextera tagmentation of DNA simultaneously fragments and tags DNA without the need for mechanical shearing.

Table 3: Nextera Rapid Capture Throughput by Illumina Sequencing Systems

Pooling Plexity	Exome Samples per Run				
	MiSeq	NextSeq 500—Mid Output	NextSeq 500—High Output	HiSeq 2500—Rapid Run Mode	HiSeq 2500—High Output
1	Up to 1	–	–	–	–
3	–	Up to 3	–	–	–
6	–	–	Up to 6	Up to 24	Up to 96
9	–	–	Up to 9	Up to 24	Up to 115
12	–	–	Up to 12	Up to 24	Up to 115

Table 3 helps identify which options provide optimal alignment across three vital study design considerations: sequencing instrument, number of exome samples sequenced per run, and the number of exome samples pooled together before enrichment (pooling plexity).

Integrated sample barcodes then allow the pooling of up to 12 samples for a single exome Rapid Capture pull down. Next, libraries are denatured into single-stranded DNA (Figure 1B) and biotin-labeled probes specific to the targeted region are used for the Rapid Capture hybridization (Figure 1C).

The pool is enriched for the desired regions by adding streptavidin beads that bind to the biotinylated probes (Figure 1D). Biotinylated DNA fragments bound to the streptavidin beads are magnetically pulled down from the solution (Figure 1E). The enriched DNA fragments are then eluted from the beads and hybridized for a second Rapid Capture. This entire process is completed in only 1.5 days, enabling a single researcher to efficiently process up to 96 exomes at one time—all without automation.

Summary

Nextera Rapid Capture Exomes provide a fully integrated, rapid solution for exome library prep and enrichment. Available in a wide range of kit configurations (Table 3), as well as two unique designs, Nextera Rapid Capture Exomes provide unparalleled flexibility to optimally align with your specific needs.

References

1. Manolio TA, Collins FS, Cox NJ, Goldstein DB, Hindorff LA, et al. (2009) Finding the missing heritability of complex diseases. Nature 4618: 747–753.

Ordering Information

Kit Description	Catalog No.
Nextera Rapid Capture Exome (8 rxn x 1 plex)	FC-140-1000
Nextera Rapid Capture Exome (8 rxn x 3 plex)	FC-140-1083
Nextera Rapid Capture Exome (8 rxn x 6 plex)	FC-140-1086
Nextera Rapid Capture Exome (8 rxn x 9 plex)	FC-140-1089
Nextera Rapid Capture Exome (2 rxn x 12 plex)	FC-140-1001
Nextera Rapid Capture Exome (4 rxn x 12 plex)	FC-140-1002
Nextera Rapid Capture Exome (8 rxn x 12 plex)	FC-140-1003
Nextera Rapid Capture Expanded Exome (2 rxn x 12 plex)	FC-140-1004
Nextera Rapid Capture Expanded Exome (4 rxn x 12 plex)	FC-140-1005
Nextera Rapid Capture Expanded Exome (8 rxn x 12 plex)	FC-140-1006

Illumina • 1.800.809.4566 toll-free (U.S.) • +1.858.202.4566 tel • techsupport@illumina.com • www.illumina.com

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Pub. No. 770-2013-002 Current as of 16 May 2015

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