

Nimblegen Seqcap Ez Library Sr Users Guide V1 Roche

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~~Nimblegen Seqcap Ez Library Sr~~

describes the process for the capture of genomic DNA (gDNA) from specified regions of the human genome using the SeqCap EZ Exome Library and amplification of captured DNA by ligation-mediated PCR (LM-PCR) (Figure 1).

~~NimbleGen SeqCap EZ Exome Library SR User's Guide~~

This protocol is based on the Roche NimbleGen SeqCap EZ Exome Library SR platform, which enriches for ~44 Mb of the human exonic regions. The SeqCap system uses 55- to 105-base DNA probes to capture known coding DNA sequences (CDS) from the NCBI Consensus CDS Database, RefSeq, and Sanger miRBase.

~~Whole Exome Enrichment with the Roche NimbleGen SeqCap EZ ...~~

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~~Whole Exome Enrichment with the Roche NimbleGen SeqCap EZ ...~~

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Article. Whole-Exome Enrichment with the Roche NimbleGen SeqCap EZ Exome Library SR Platform. March 2015; Cold Spring Harbor Protocols 2015(7)

~~Whole Exome Enrichment with the Roche NimbleGen SeqCap EZ ...~~

NimbleGen®SeqCapEZ Library Preparation on the Sciclone NGS Workstation This application has only one step: The lyophilized library plate is placed onto the deck along with the Hybridization Mix/Probes Reagent Plate. The Hybridization Mix/Probes are added to the samples 1 column at a time and the shaker is used to mix.

~~NIMBLEGEN SEQCAPEZ - PerkinElmer~~

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The NimbleGen SeqCap EZ Choice kit is commonly used for the targeted enrichment of sequencing libraries comprising a target size up to 7 Mb. A major drawback of this commercially available method is the exclusive use of single-indexing, meaning that at most 24 samples can be multiplexed in a single reaction.

~~A Robust Protocol to Increase NimbleGen SeqCap EZ ...~~

The library is amplified by pre-capture LM-PCR (Linker Mediated-PCR) and hybridized to NimbleGen microarrays (385K or 2.1M features) or Seqcap EZ solution probe libraries. After washing, amplification by post-capture LM-PCR and a qPCR-based quality check, the successfully captured DNA is ready for SOLiD™ System sequencing.

~~Preparation of SOLiD™ System Fragment Libraries for ...~~

Sample prep and capture followed SeqCap EZ Library SR User's Guide v5.1. Competitor A kit data was generated by a 3rd party service provider following vendor's pre-capture multiplexing protocol. All reads were subsampled to 60 million for assessment. Performance was determined following the same bioinformatics pipeline

~~SeqCap EZ MedExome Target Enrichment Kit - Roche~~

The NimbleGen SeqCap EZ Library SR User's Guide (Version 5.1, September 2015) was followed for all steps with the modifications listed below. The dual size selection of the precapture libraries was adjusted to account for the larger shearing sizes. For Chinese Spring the volumes were 45 and 20 µl for right and left size selection, respectively.

~~Integrating genomic resources to present full gene and ...~~

Description: The same genetic sample was exome enriched using each of three major commercial exome-seq platforms: Agilent SureSelect Human All Exon (50M), Nimblegen SeqCap EZ-Exome Library SR v2.0 (44M), and Illumina TruSeq Exome (62M). These exome enriched samples were then sequenced with the Illumina HiSeq 2000 on one lane each. In addition, seven lanes of whole genome sequencing was ...

~~Studies : Browse : Sequence Read Archive : NCBI/NLM/NIH~~

SeqCap EZ Hybridization and Wash Kit (Roche NimbleGen, Cat. # 05634261001) SeqCap Pure Capture Bead Kit (Roche

NimbleGen; Cat. # 06977952001) SeqCap EZ Library; Other consumables as specified in the the SeqCap EZ Library SR User's Guide (version 5.0) under "Consumables Purchased from Other Vendors" Equipment

~~Targeted capture of ThruPLEX libraries with Roche ...~~

For instance, NimbleGen's SeqCap EZ exome library v2.0 targets approximately 44 Mb of genome, where as their next version EZ exome library v3.0 targets 64.1 Mb. The new Illumina Nextera capture technology has to the best of our knowledge not been tested extensively vis-à-vis other technologies.

~~Performance comparison of four exome capture systems for ...~~

One μ l of the ligated product was subsequently amplified in an enrichment PCR (10 cycles) for library quality assessment as recommended in the 'SeqCap EZ Library SR User's Guide' (Nimblegen, Roche). Thereafter, the pre-capture LM-PCR was performed on the samples for 8 cycles as prescribed in the SeqCap EZ library protocol. The concentration of each PCR product was determined using Quant-iT

~~Development and performance of a targeted whole exome ...~~

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Using these annotations, the custom NimbleGen SeqCap EZ Developer Library probe set was synthesized. 3.2 Library preparation, high-throughput sequencing, and sequence alignment We obtained over 12.4 million paired-end reads from the HTS MiSeq run (Table S5).

~~Development of a genotype by ... Wiley Online Library~~

The library preparation was performed as per the manufacturer's protocol (NimbleGen SeqCap EZ Library SR User's Guide v3.0, Roche, Inc.). Briefly, genomic DNA (5–10 μ g) of each cell culture was sonicated using a Covaris S2 instrument (Covaris, Inc.) to obtain fragments of approximately 200 bp. Then, sheared DNA samples were subjected to three enzymatic steps: end repair, A-tailing, and ...

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