CUTANA™ CUT&RUN Library Prep Kit with Primer Set 1

Catalog No 14-1001
Lot No 22010001-81
Pack Size 48 Reactions

EpiCypher®
www.epicypher.com

Product Description:

The CUTANA™ CUT&RUN Library Prep Kit offers high fidelity library generation for Illumina® sequencing by harnessing the power of New England Biolabs® best-in-class NEBNext® reagents. The kit offers a streamlined protocol specifically optimized for high sensitivity CUT&RUN applications, including those with low cell inputs. Included are all necessary reagents to perform end repair, adaptor ligation, combinatorial dual indexing for multiplexing up to 48 samples, and DNA cleanup with SPRIselect reagent from Beckman Coulter, Inc.* If additional multiplexing is desired, this kit can be used in tandem with Primer Set 2 (EpiCypher 14-1002) for up to 96 samples. Pairing this kit with the EpiCypher CUT&RUN Kit (EpiCypher 14-1048) affords users a cells-to-sequencing solution for chromatin mapping experiments with all the necessary controls and validated reagents to ensure confidence in obtaining high quality data.

Kit Contents:

Kit contains all buffers, enzymes, DNA purification beads, multiplexing primers, and 8-strip tubes necessary to prepare dual-indexed Illumina sequencing libraries from CUT&RUN DNA. See user manual for additional materials and equipment required for the protocol.

Storage and Stability:

DO NOT FREEZE KIT. Remove SPRIselect reagent and 0.1X TE buffer, which should be stored at RT. The remainder of the components should be stored at -20°C. Kit components stable for 6 months from date of receipt.

Instructions for use:

See the included manual and quick card or find them in "Documents & Resources" at epicypher.com/14-1001

References:

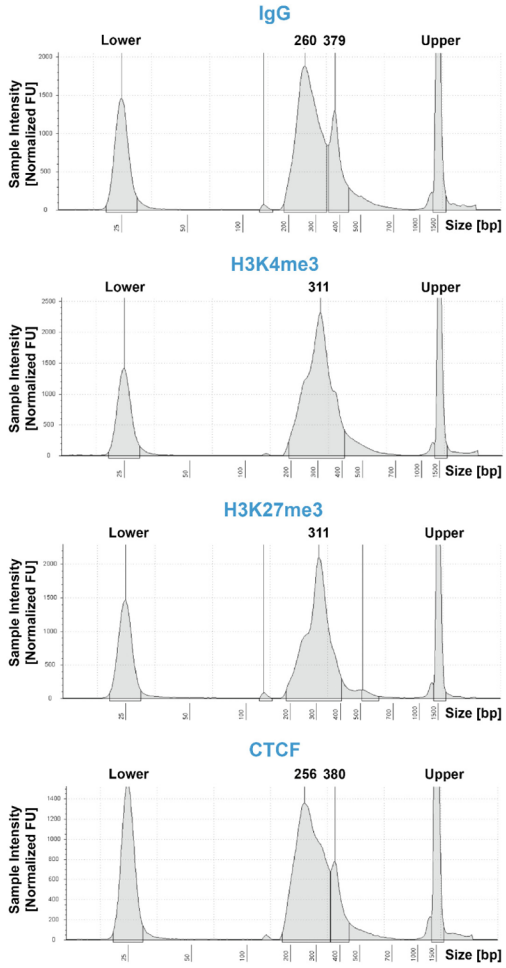

Figure 1: CUT&RUN DNA Fragment Size Distribution Analysis. CUT&RUN was performed using the CUTANA ChIC/CUT&RUN Kit (EpiCypher 14-1048) starting with 500k K-562 cells. Five nanograms of CUT&RUN output DNA from reactions utilizing IgG (EpiCypher 13-0042), H3K4me3 (EpiCypher 13-0041), H3K27me3 (ABclonal A16199), and CTCF (EpiCypher 13-2014) antibodies were prepared for paired-end Illumina® sequencing with the CUTANA CUT&RUN Library Prep Kit. Library DNA was analyzed by Agilent TapeStation®, which confirmed that mononucleosomes were predominantly enriched in CUT&RUN (~300 bp peaks represent 150 bp nucleosomes + sequencing adapters). Peaks at ~380 bp correspond to the SNAP-CUTANA™ K-MetStat Panel of spike-in controls (EpiCypher 19-1002).

This product is for *in vitro* research use only and is not intended for use in humans or animals.

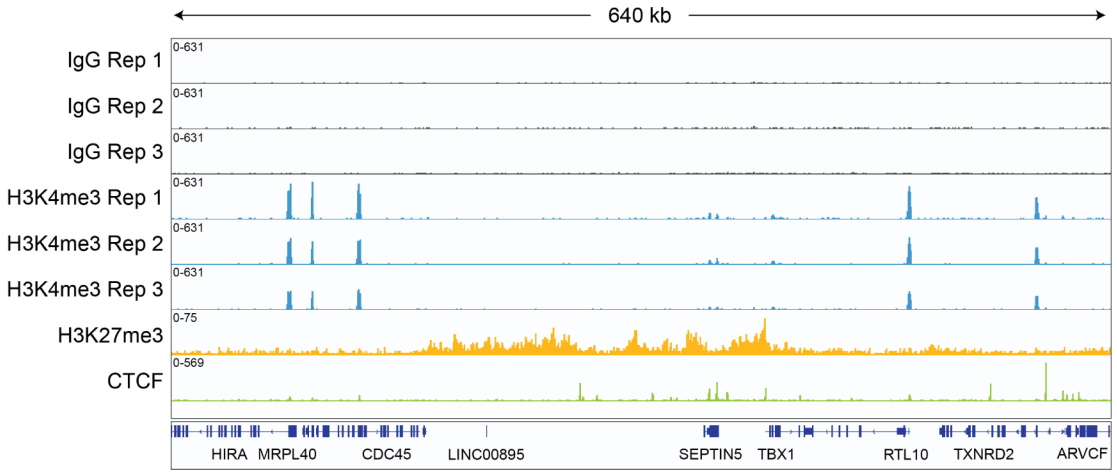

Figure 2: Representative gene browser tracks. CUT&RUN sequencing libraries described in Figure 1 were sequenced on an Illumina NextSeq 2000 with a P3 cartridge (paired-end 2x50 cycle). Data were aligned to the hg19 genome using Bowtie2. Data were filtered to remove duplicates, multi-aligned reads, and blacklist regions. A representative 640 kb window at the SEPTIN5 gene is shown for three replicates ("Rep") of IgG and H3K4me3 antibodies, as well as individual tracks for H3K27me3 and the transcription factor CTCF, demonstrating the robustness and reproducibility of the workflow with a variety of targets. Sequencing libraries prepared with the CUTANA CUT&RUN Library Prep kit produced the expected genomic distribution for each target. Sample sequencing depth was as follows (millions of reads): IgG Rep 1 (20.1), IgG Rep 2 (16.6), IgG Rep 3 (16.1), H3K4me3 Rep 1 (7.3), H3K4me3 Rep 2 (17.2), H3K4me3 Rep 3 (13.8), H3K27me3 (13.4), CTCF (16.2). Images were generated using the Integrative Genomics Viewer (IGV, Broad Institute).