CUTANA™ ChIC/CUT&RUN Kit

Catalog No. 14-1048

Lot No. 12270001

Pack Size 48 samples

Product Description:

The CUTANA ChIC/CUT&RUN Kit contains sufficient materials for 48 CUT&RUN samples and is designed for multi-channel sample pipetting in order to realize the increased experimental throughput advantage of CUT&RUN. The kit includes positive (H3K4me3) and negative (IgG) control antibodies. A panel of bead immobilized H3K4 methyl designer nucleosomes (dNucs™) are spiked-in to control samples to directly monitor experimental success and aid troubleshooting (**Figure 2**). *E. coli* DNA is added to samples after pAG-MNase cleavage to enable experimental normalization. The kit is compatible with cells and nuclei, including cryopreserved and cross-linked samples. It is recommended to start with 500,000 cells, however comparable data can be generated using as few as 5,000 cells. The inclusion of controls and compatibility with diverse target types, sample inputs, and low cell numbers make the CUTANA ChIC/CUT&RUN Kit ideal for a variety of research applications.

Kit Contents:

Kit contains buffers, enzymes, magnetic beads, control antibodies, spike-in controls, 8-strip tubes, and spin columns necessary to prepare and purify CUT&RUN DNA starting from cells or nuclei. See kit manual for additional materials and equipment required for the protocol.

Storage and Stability:

DO NOT FREEZE ENTIRE KIT. Upon receipt, store individual components at room temperature, 4°C and -20°C (see manual for full instructions).

Instructions for use:

See kit manual for complete instructions.

References:

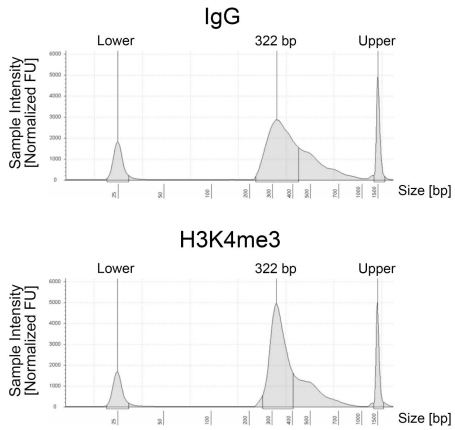

Figure 1: CUT&RUN DNA Fragment Size Distribution Analysis. CUT&RUN was performed using the CUTANA ChIC/CUT&RUN Kit starting with 500,000 K562 cells. CUT&RUN DNA isolated from IgG Negative Control (13-0042k) and H3K4me3 Positive Control (13-0041k) antibodies was used to prepare paired-end Illumina sequencing libraries. Library DNA was analyzed by Agilent Tapestation®. This analysis confirmed that mononucleosomes were predominantly enriched in CUT&RUN (~300 bp peak represents 150 bp nucleosomes + sequencing adapters).

		CUTANA Spike-in dNuc			
		Unmodified	H3K4me1	H3K4me2	H3K4me3
anti-IgG	Rep 1	20.1	32.3	26.1	21.6
	Rep 2	20.2	32.6	25.7	21.5
	Rep 3	19.7	32.8	26.2	21.3
anti-H3K4me3	Rep 1	2.1	3.8	2.9	100.0
	Rep 2	2.3	4.1	3.1	100.0
	Rep 3	3.0	5.2	3.6	100.0

Figure 2: CUTANA H3K4 MetStat Spike-in Controls. DNA-barcoded unmodified and H3K4-methylated dNucs were immobilized to Streptavidin Beads and spiked-in to CUT&RUN samples prior to the addition of either IgG (top) or H3K4me3 (bottom) control antibodies. The shell script available on the product page was used to count instances of each barcoded dNuc in the CUT&RUN sequencing data. The proportion of read counts normalized to on-target (H3K4me3) are shown. The spike-ins confirmed that the control antibody specifically recovered the target dNuc.

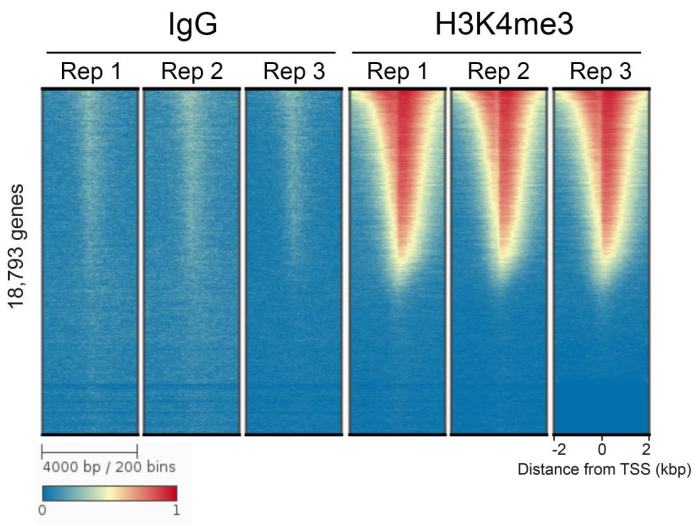

Figure 3: CUT&RUN genome-wide heatmaps. CUT&RUN data was generated using CUTANA ChIC/CUT&RUN Kit with 500,000 K562 cells. Three replicates ("Rep") of IgG (left) and H3K4me3 (right) antibodies are shown in a heatmap. CUT&RUN signal (from an average of 5.9 million paired-end reads) aligned to the transcription start site (TSS, +/- 2kb) are presented for 18,793 genes. High and low signal are ranked by intensity (top to bottom) and reflected by red and blue colors, respectively. Gene rows in each heatmap are aligned and sorted from high to low signal relative to H3K4me3 Rep 3 (far right), demonstrating the reproducibility of the kit workflow.

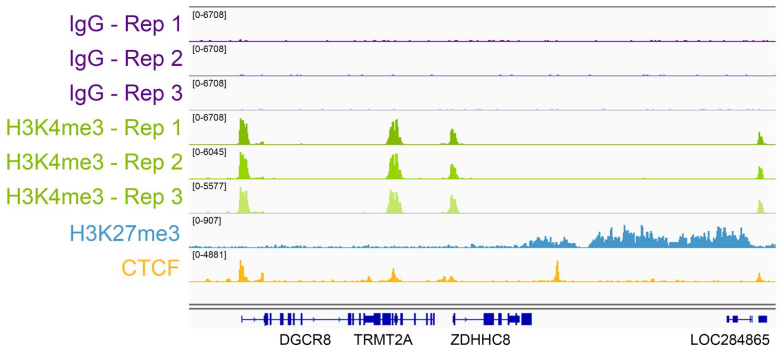

Figure 4: Representative gene browser tracks. CUT&RUN data was generated as described above. A representative 150 kb window at the TRMT2A gene is shown for three replicates ("Rep") of IgG and H3K4me3 antibody controls (included in the kit). Representative tracks are also shown for H3K27me3 (EpiCypher Catalog No. 13-0030) and the transcription factor CTCF (EMD Millipore Catalog No. 07-729) antibodies. The CUT&RUN kit produced the expected genomic distribution for each target. Images were generated using the Integrative Genomics Viewer (IGV, Broad Institute).