CUTANA™ Concanavalin A-Conjugated Paramagnetic Beads

Catalog No	21-1401	**Pack Size**	550 µL
Lot No	25007015-81	**Concentration**	5 mg/mL

DESCRIPTION

This product contains Concanavalin A (ConA) conjugated to paramagnetic microspheres. ConA is a lectin (carbohydrate-binding protein) that binds specifically to mannosyl- and glucosyl-containing extracellular glycoproteins. The ConA magnetic beads are therefore useful to immobilize cells or nuclei presenting these glycans in their extracellular matrices.

TECHNICAL INFORMATION

Storage	DO NOT FREEZE!! Stable for 12 months at 4°C from date of receipt.
Formulation	Concanavalin A conjugated to 1 µm paramagnetic microspheres in 10 mM PBS, 0.1% sodium azide.

APPLICATION NOTES

Magnetized immobilization of intact cells or nuclei is a key feature of CUT&RUN and CUT&Tag assays that enables scalable sample processing and efficient recovery of target DNA. For more information, see our CUTANA protocols: www.epicypher.com/protocols.

**Note: It is recommended to use 10 µL ConA beads per reaction (500,000 cells or less) for ChIC/CUT&RUN and 10 µL ConA beads per reaction (100,000 nuclei or less) for CUT&Tag. CUTANA™ Concanavalin A-Conjugated Paramagnetic Beads are compatible with Magnetic Separation Racks (EpiCypher 10-0008/10-0012).*

VALIDATION DATA

CUT&RUN Methods

CUT&RUN was performed using CUTANA™ Concanavalin A-Conjugated Paramagnetic Beads (10 µL with 500k K562 cells), 0.5 µg of either IgG negative control (EpiCypher 13-0042), H3K4me3 positive control (EpiCypher 13-0060), or H3K27me3 positive control (EpiCypher 13-0055) antibodies, and the CUTANA™ ChIC/CUT&RUN Kit v5 (EpiCypher 14-1048). Library preparation was performed with 5 ng of DNA (or the total amount recovered if less than 5 ng) using the CUTANA™ CUT&RUN Library Prep Kit (EpiCypher 14-1001/14-1002). Libraries were run on an Illumina NextSeq2000 with paired-end sequencing (2x50 bp). Sample sequencing depth was 10.1 million reads (IgG), 11.1 million reads (H3K4me3), and 14.0 million reads (H3K27me3). Data were aligned to the hg19 genome using Bowtie2. Data were filtered to remove duplicates, multi-aligned reads, and ENCODE DAC Exclusion List regions.

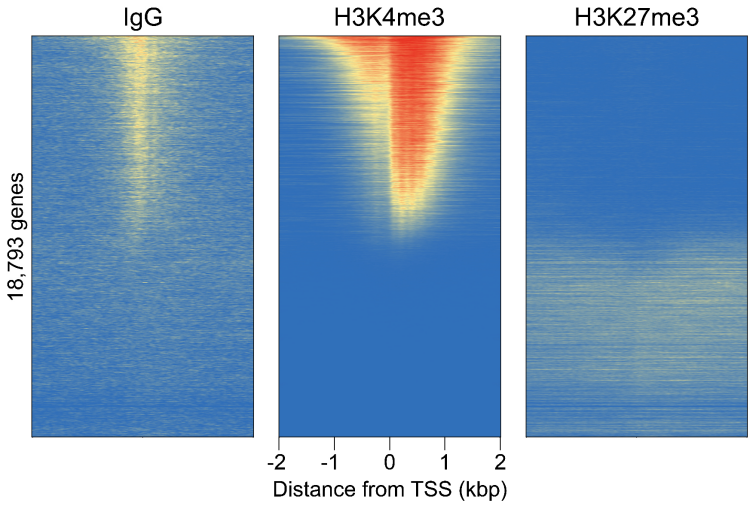

FIGURE 1 CUT&RUN genome wide enrichment. CUT&RUN was performed as described above. Sequence reads were aligned to 18,793 annotated transcription start sites (TSSs, ±2 kbp). Signal enrichment was sorted by intensity (top to bottom) and colored such that red indicates high localized enrichment and blue denotes background signal. All rows were aligned relative to H3K4me3 antibody. H3K4me3 antibody displayed strong enrichment around the TSS, while H3K27me3 showed oppositional enrichment to H3K4me3, as expected. The IgG control showed minimal background.

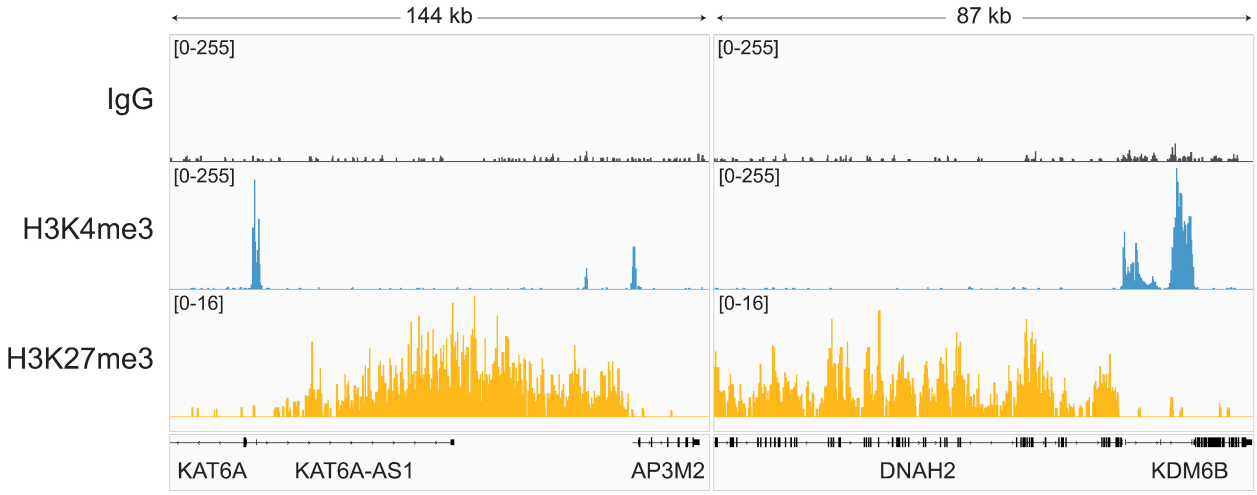

FIGURE 2 CUT&RUN representative browser tracks. CUT&RUN was performed as described above. Gene browser shots were generated using the Integrative Genomics Viewer (IGV, Broad Institute). Two representative loci are shown.