CUTANA™ Concanavalin A-Conjugated Paramagnetic Beads

Catalog No	21-1401	**Pack Size**	550 µL
Lot No	23283012-01	**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 six 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 slurry per sample (500,000 cells or less) for ChIC/CUT&RUN. Compatible with Magnetic Separation Racks (EpiCypher 10-0008/10-0012).*

REFERENCES

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) or H3K4me3 positive control (EpiCypher 13-0041) antibodies, and the CUTANA™ ChIC/CUT&RUN Kit v3 (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). Both kit protocols were adapted for high throughput Tecan liquid handling. Libraries were run on an Illumina NextSeq2000 with paired-end sequencing (2x50 bp). Sample sequencing depth was 11.9 million reads (IgG) and 13.2 million reads (H3K4me3). Data were aligned to the hg19 genome using Bowtie2. Data were filtered to remove duplicates, multi-aligned reads, and ENCODE DAC Exclusion List regions.

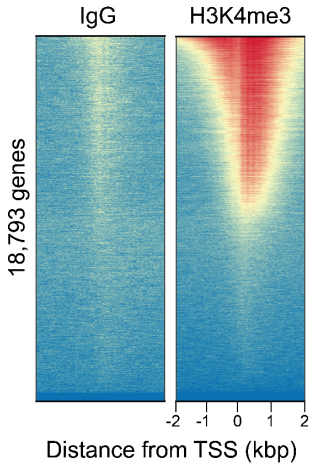

FIGURE 1 CUT&RUN genome wide enrichment. CUT&RUN was performed as described above. Sequence reads were aligned to 18,793 annotated transcription start sites (TSSs, ± 2 kbp). Signal enrichment was sorted by intensity (top to bottom) and colored such that red indicates high localized enrichment and blue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

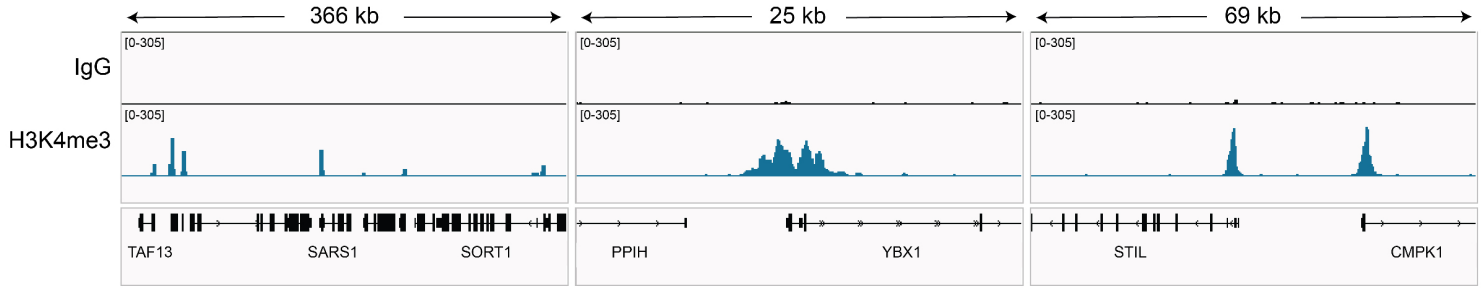

FIGURE 2 CUT&RUN representative browser tracks. CUT&RUN was performed as described above. Gene browser shots were generated using the Integrative Genomics Viewer (IGV, Broad Institute). Three representative loci are shown.