

Reclaim sequencing capacity from mitochondrial-derived fragments for ATAC-seq.

NEXTFLEX™ Cas9-gRNA Mito Depletion Enzyme (Human)

The NEXTFLEX Cas9-gRNA Mito Depletion Enzyme (Human), Powered by Jumpcode™ DepleteX™ technology, is a cost effective standalone CRISPR-Cas9 module added at the dsDNA library stage to reduce mitochondrial background in human ATAC-seq libraries, freeing sequencing capacity for nuclear targets.

Free sequencing capacity

- Reduce mitochondrial background so more reads land on nuclear targets.

Fast add-on step

- One-hour reaction time with about 5 minutes hands-on work.

Workflow-independent

- Slots into any existing ATAC-seq workflows at the dsDNA stage.

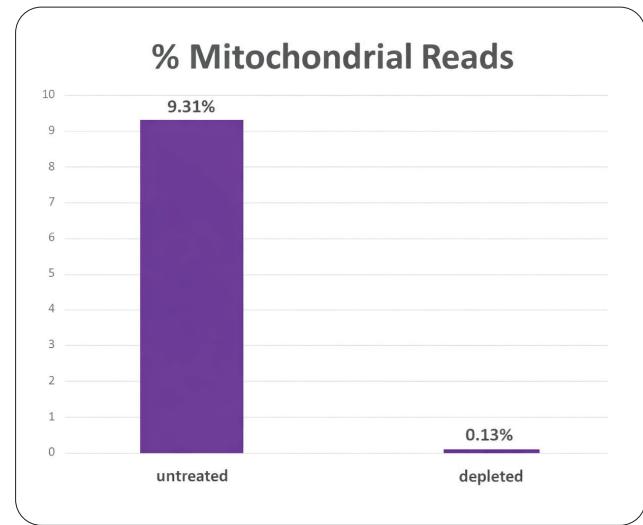


Figure 1. Percent of reads mapped to the mitochondrial genome in an untreated library compared with the same library after depletion, showing a drop from 9.31% to 0.13% and freeing sequencing capacity for nuclear targets.

Workflow



Cleavage plus cleanup prevents mtDNA-derived fragments from carrying through to sequencing so more reads land on nuclear content.

Technical overview

What it is

A pre-complexed Cas9-guide RNA mixture designed for targeted cleavage of human mitochondrial-derived fragments in dsDNA sequencing libraries, including ATAC-seq.

Guide pool design

The guide RNA pool contains 657 unique guides targeting 17 mtDNA-encoded genes and selected nuclear mitochondrial pseudogenes.

How it works

DASH-style depletion at the dsDNA library stage: Cas9-gRNA complexes cleave targeted mitochondrial-derived library molecules, followed by cleanup and sequencing.

Recommended workflow placement

Add the depletion step wherever your workflow has converted material to double-stranded DNA and can accommodate a one-hour incubation followed by cleanup.

What's in the box

- Ready to use: provided as a Cas9-gRNA complex with integrated RNase inhibitor and 10X Cas9 Buffer.
- Powered by Jumpcode™ DepleteX™ technology.

Compatibility

- Species: Human
- Library stage: dsDNA libraries
- Applications: ATAC-seq; DNA-seq; RNA-seq; single-cell workflows at the dsDNA stage
- Sequencing: short-read and long-read
- Automation: manual or automated workflows

Ordering: NOVA-803100 and NOVA-803500

Reference: Gu et al., *Genome Biology* (2016), DASH: Depletion of Abundant Sequences by Hybridization (CRISPR-Cas9 depletion in sequencing libraries).



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