JUMPCODE GENOMICS

TECH OVERVIEW

Harnessing CRISPR to boost NGS sensitivity with CRISPRclean®

~66%
of human genome is made up of repetitive elements[1]

~90%
of reads from a single cell data are noise[2]

>90%
of reads from RNA seq data are abundant ribosomal, mitochondrial

Next-generation sequencing (NGS) technology has revolutionized the genomic research world. The ability to sequence genomes, transcriptomes, and epigenomes without a priori knowledge has yielded an unprecedented number of discoveries on genes and genetic variation. As NGS technology continues to advance with innovations to increase sensitivity and throughput while lowering costs, much of the sequencing data can be biologically uninformative.

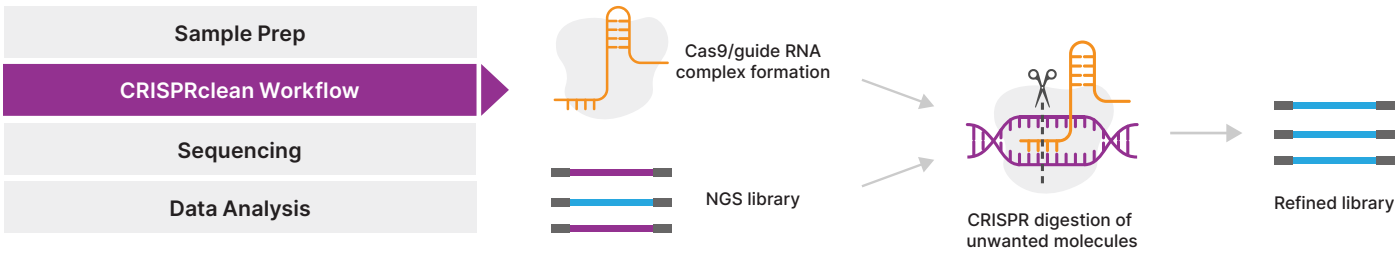
CRISPRclean technology harnesses the CRISPR system to refine NGS libraries by removing the noise or unwanted reads and shifting focus to informative reads. This results in increased sensitivity and lowered background noise to gain greater confidence in detecting differential gene expression and variant calling. Applying CRISPRclean technology may also save significantly on sequencing costs.

Legacy targeted resequencing approaches trade off the risk of introducing bias with the benefit of improved detection of desired genes or transcripts. CRISPRclean differs from these methods in that uninformative molecules are removed prior to sequencing, thus shifting sequencing to increase coverage across regions of interest that remain in a library. This maintains the ability to analyze more useful data without a priori knowledge of which transcripts or variants will be relevant in a given study.

Benefits of CRISPRclean technology

- Highly programmable
- Unbiased and efficient depletion
- Increased sensitivity
- Simple automatable workflow
- Sequencing platform agnostic

To learn more, visit **jumpcodegenomics.com**



References

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2. Qiu, P. Embracing the dropouts in single-cell RNA-seq analysis. Nat Commun 11, 1169 (2020). https://doi.org/10.1038/s41467-020-14976-9