# Advanced Targeted Depletion by CRISPR

Wasting sequencing capacity on commonly known content is not necessary anymore. Deplete rubbish sequences precisely with IAB.

Introduction

Saving on sequencing costs is one of the main drivers in library prep innovations. For example, total RNA comprise mainly rRNAs and housekeeping genes mRNAs that drown out the sequencing signal of less abundant but more exciting transcripts. Ribodepletion nor poly-A selection solve the issue of these overabundant sequences at once. CRISPRClean technology does! Moreover, it does not matter whether the overabundant sequences are rRNAs, housekeeping mRNAs, repetitive sequences in the genome, or host DNA/RNA. CRISPRClean solves it all.

Method

Using CRISPR/Cas9 and synthetic guide RNA panel, CRISPRClean depletes defined content from ready-to-sequence libraries. Although the technology allows for unlimited customisation, there are several main applications that can be combined.
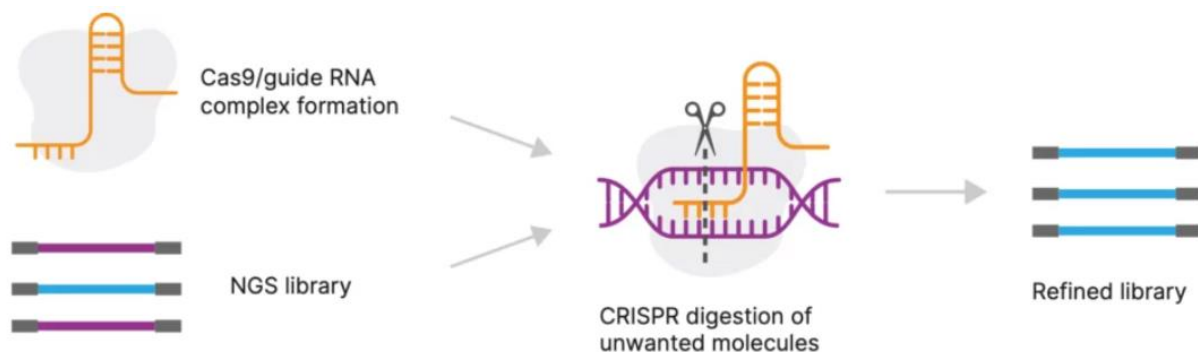
- Mitochondrial and nuclear rRNAs (human, mouse, rat)
- Prokaryotic and eukaryotic rRNAs in mixed samples
- Highly expressing transcripts in mammals
- Specialised panel for abundant sequences in liver tissue
- Globin and insulin panel
- Single-cell analysis
- Repetitive sequences in plant genomes

Simple 3-step protocol integrated into 10x Genomics® Chromium™ Next GEM Single Cell 3' workflow
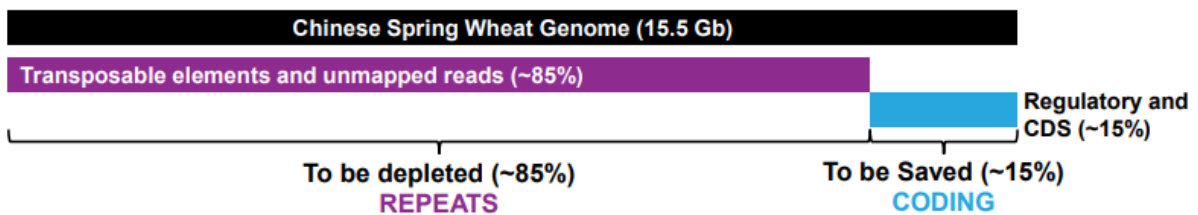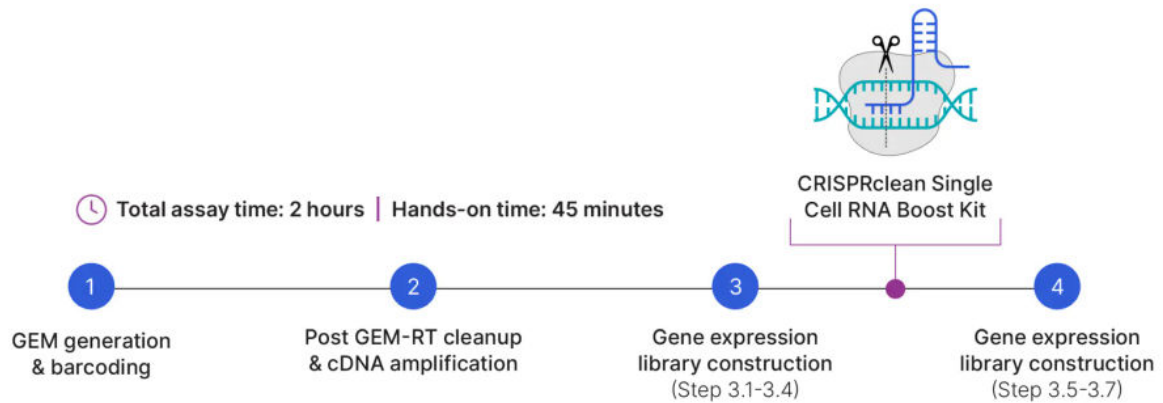
Conclusion

IAB includes CRISPRClean in its portfolio as a perfect customisable tool for cost-effective sequencing. The CRISPRClean technology has been adopted for whole transcriptome profiling, single-cell analyses, microbiome research, infectious disease surveillance, plant whole genome sequencing and other agri-genomics applications, but the use is unlimited.