

DepleteX™ Human DNA Depletion Kit

Boost metagenomic samples by removing contaminating human DNA

Introduction

Metagenomic analysis of human samples for microbiome or infectious disease research can be contaminated with excessive amounts of host genomic DNA. This background host DNA reduces the depth of view into the microbes that are present. Current approaches to address this problem are either expensive (e.g. over-sequencing) or introduce the risk of biasing the microbial community readout.

Jumpcode Genomics has developed the DepleteX Human DNA Depletion Kit to remove contaminating host DNA prior to metagenomic sequencing and boost metagenomic studies. This technical note provides an overview of the kit's workflow, performance, and applications such as microbiome or infectious disease research.

Methodology

DepleteX utilizes a novel depletion strategy to selectively remove human DNA from samples, enriching the pool of non-human DNA for sequencing. First, adapters are ligated to the ends of DNA fragments in a sample, followed by CRISPR-based cutting of human specific repeat sequences (Figure 1). Finally, an exonuclease incubation removes any human fragments that were targeted by CRISPR for removal. Standard library prep and sequencing can be done downstream for either short or long read technologies.

Highlights

- Simple unbiased depletion of human DNA from metagenomic samples
- Boost microbial detection in difficult samples with high human content
- Compatible with short or long read sequencing workflows

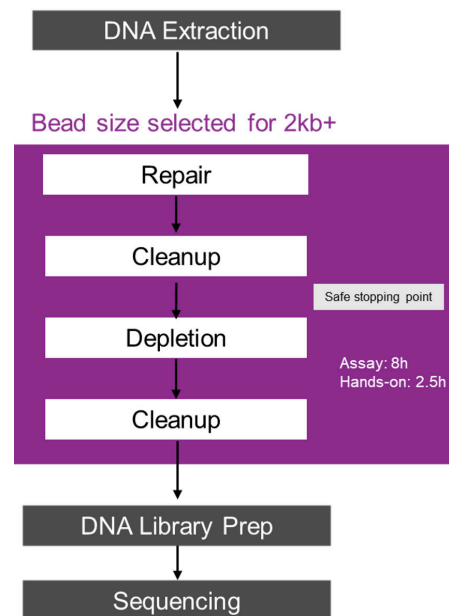


Figure 1. Simple workflow for depleting human DNA prior to metagenomic sequencing.

Boosting Bacterial Detection In Vaginal Samples

DNA from vaginal swab samples was extracted followed by depletion of the human content with the DepleteX Human DNA Depletion Kit. Libraries were prepared with Illumina DNA Prep and sequenced more than 50M reads per sample. Data were down sampled to 50M reads per sample for comparison of depletion benefit across conditions.

Control samples without depletion contained 98.55% human sequences and only 1.45% bacterial reads. After depletion, bacterial reads were increased over 16 fold to more than 24% of the total reads in a sample (Figure 2). This boost in sensitivity resulted in a doubling of bacterial species detected that were previously not seen due to the high contaminating human DNA (Figure 3). Importantly, depletion of human fragments does not introduce a biased readout of the microbial community with consistent read count correlation by bacterial species between depleted and control samples (Figure 4).

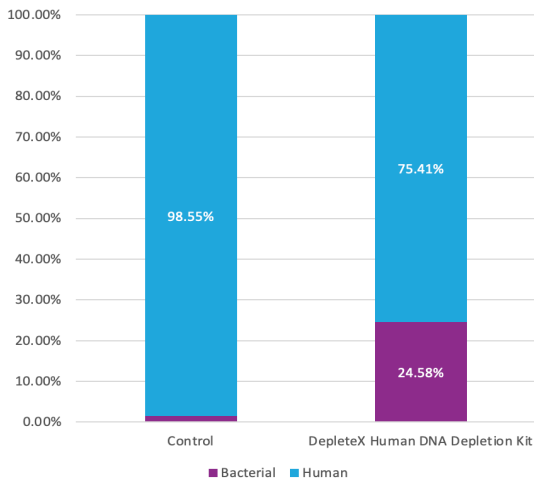


Figure 2: 16 fold increase in bacterial reads after human fragment depletion

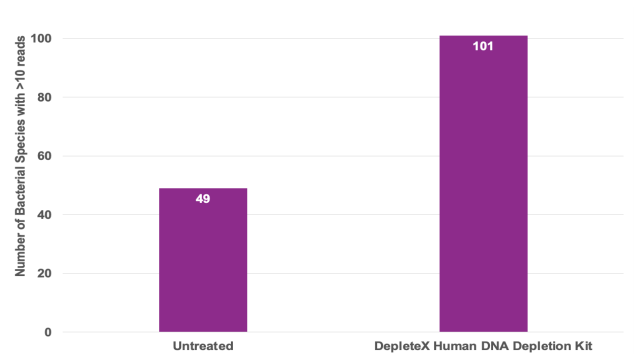


Figure 3: 2x improvement in bacterial species detected after depletion.

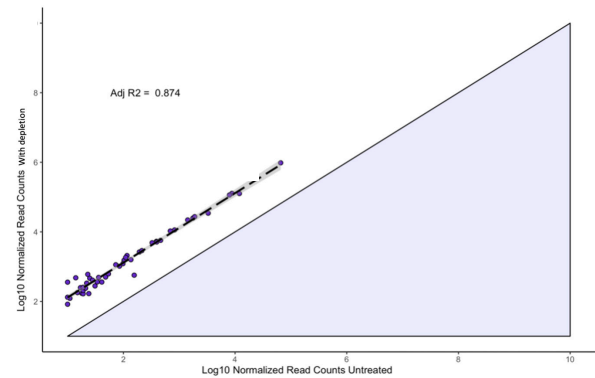


Figure 4: Unbiased boost in reads across bacterial species after human DNA depletion.

Summary

Metagenomic studies can be difficult with sample types containing a high percentage of contaminating human DNA. The DepleteX Human DNA Depletion Kit provides an unbiased and simple method for boosting microbial reads by targeting human fragments for removal.

To learn more, visit jumpcodegenomics.com

Ordering information

Catalog	Product name	Samples
KIT2020	DepleteX Human DNA Depletion Kit	24