



Stop abundant RNAs from taking over your small RNA-seq data.

Maximize discovery with custom depletion of dominant species

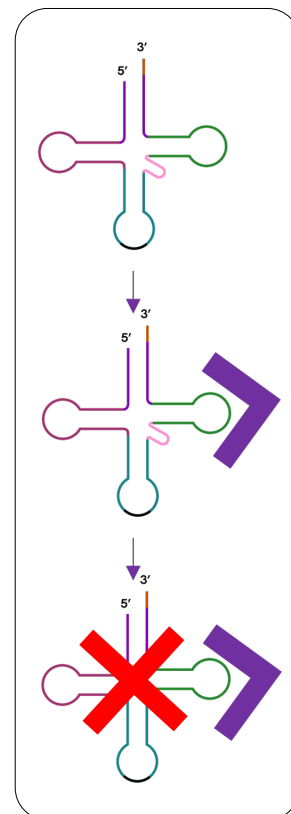
Small RNA sequencing captures a diverse landscape of RNA molecules under 200 nucleotides. Yet, in many samples, a handful of highly abundant species (tRNA fragments, Y RNA fragments, and a few overexpressed miRNAs) consume most sequencing reads. This reduces detection of rare RNAs that often provide the most meaningful insights.

NEXTFLEX™ Custom Small RNA Blockers enable you to selectively deplete up to 10 high-abundance sequences of your choice. The result: greater sequencing depth for transcripts that matter to your biology. Optimized for the NEXTFLEX Small RNA-Seq Kit v4, they support flexible design across species, tissues and study designs.

- Affordable and customizable.
- Targets up to 10 user-selected sequences.
- Reduce unwanted sequences without skewing data.
- Can be used in conjunction with the tRNA/Y RNA blockers and blood blockers.
- Free up sequencing capacity for low-abundance RNAs.

How it works

- Sequence-specific oligos hybridize to your chosen high-abundance RNAs.
- Hybridized targets are blocked at the very first step of library prep.
- Blocked RNAs cannot undergo 3' adapter ligation and are not amplified.



Get Started

Contact our team our team to design blockers tailored to your species, tissue, or project. Boost complexity, sensitivity, and discovery power in your small RNA-seq experiments today.

