

## **Advanced microbiome tools for metagenomics**

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Metagenomics is broadly used in microbiome research to identify and create an extensive catalogue of microbial DNA sequences from a given sample. While gut samples were the leading sample type in the beginning of microbiome research, scientists are now turning their attention towards more challenging and unique microbiome samples.

Analyzing new types of samples comes with a price as using standard microbiome tools and workflows may not always produce accurate metagenomics results. Some of the challenges that are encountered include a low amount of DNA, fragmented/low quality DNA and hard to lyse microorganisms.

Emerging sequencing technologies such as the long-read Nanopore sequencing and single cell transcriptomics also pose new challenges to standard metagenomics tools, thus requiring specialized, high quality reagents.

Here we present some of the metagenomics reagents and tools that we developed at MilliporeSigma to help address the gaps in the microbiome workflows that accompany the research of unique and challenging samples. These include a kit which allows to multiplex the 16S rRNA gene when DNA is fragmented or in low amounts, DNA free reagents that allow a bias-free analysis of low DNA samples and lytic enzyme mixtures to lyse a variety of microbes.