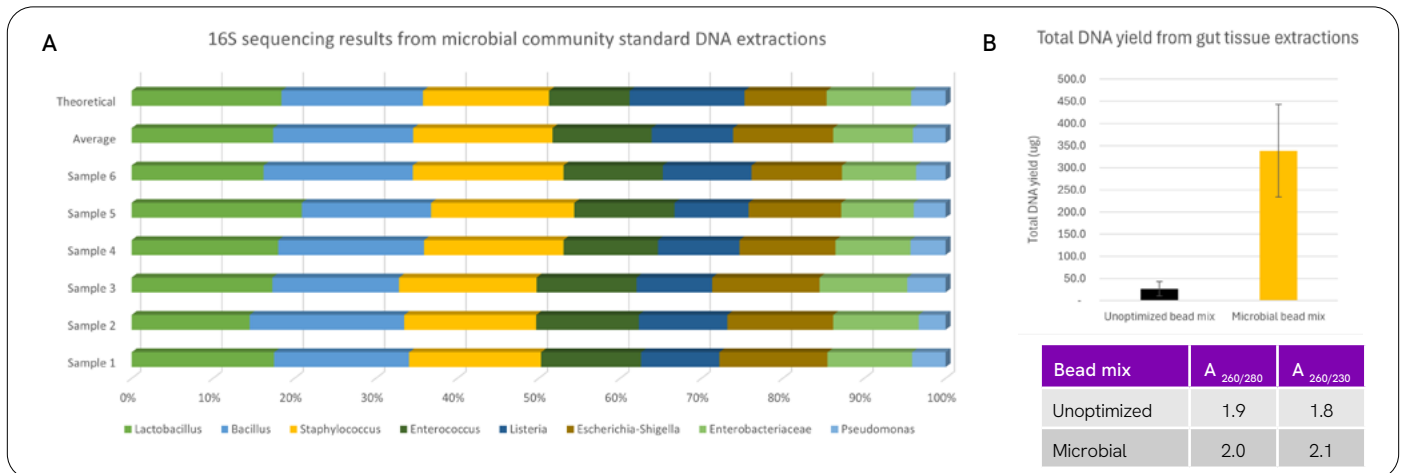




# Great science from the first step.

For microbial studies, the reliability of data is largely contingent on the completion of lysis and recovery of the nucleic acids that feed into downstream genomic applications, such as NGS.



(A) 16S sequence alignment of contrived sample replicates vs theoretical values from a community standard. (B) Importance of optimized bead mixes in total DNA yields from murine GI tracts.

# Optimized recovery of microorganisms



## Generate meaningful data

- Avoid bias and misrepresentation of populations
- Automation-enabled consistency in homogenization, lysis, and recovery of biological analytes vs manual prep
- Don't let sample processing throughput limit your experimental designs

*"These technologies work, and my lab depends on them day to day."*

- Dr. Charlie Johnson, Dir of TxGen

## Ordering information

Product description	Ordering
Omni Bead Ruptor Elite™ bead mill homogenizer*	19-042E
Bead Ruptor Elite 2 mL Tube Carriage (24 tube positions)	19-373
Microbiome Homogenizing Bead Mix (50 x 2 mL tubes)	19-636D
chemagic 360 instrument	2024-0020
chemagic 96 rod head set	CMG-370
chemagic DNA stool 200 kit H96 or chemagic DNA soil 250 kit H96	CMG-1076 or CMG-1054

\* We offer a range of bead-beating tubes and lysing matrices. We also offer higher throughput solutions. Contact us.

## Additional resources

- [Jones, A, et al. \(2020\) Choice of Laboratory Tissue Homogenizers Matters When Recovering Nucleic Acid From Medically Important Ticks. Journal of Medical Entomology. doi:10.1093/jme/tjaa006](#)
- [Homogenization and DNA extraction for 16S sequencing application note](#)



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