

Shotgun Metagenomics of iNPH Stool Samples Powered by Zinexts MagPurix[®] Extraction

MagPurix[®] reaches the expectations for high-quality nucleic acids ready for direct sequencing

Executive Summary

In a multicenter shotgun metagenomics study of idiopathic normal pressure hydrocephalus (iNPH), researchers processed 168 stool samples with the **MagPurix[®] Bacterial DNA Extraction Kit** on an automated Zinexts system, enabling high-quality libraries and deep sequencing for species- and pathway-level insights. The MagPurix[®] workflow delivered robust, automation-ready DNA that supported an average of ~28.5 million raw reads per sample on NovaSeq platforms and only one library failure across the cohort—demonstrating reliability for demanding microbiome discovery and clinical-research pipelines.

Key Findings

Automated, reproducible extraction at scale. DNA was extracted “using the MagPurix[®] Bacterial DNA Extraction kit on an automated Zinexts system,” integrating bead-beating pre-lysis and standardized handling—ideal for multi-site studies and tech transfer to partners.

- **High sequencing performance supported by MagPurix[®] DNA quality**
Libraries prepared from MagPurix[®]-extracted DNA achieved 28.53 ± 7.25 million raw reads per sample (2×150 bp), targeting ~3.5 GB per sample on NovaSeq 6000 DX / NovaSeq X Plus—ample depth for species-level profiling (MetaPhlAn 4) and functional pathway calling (HUMAN 3).
- **Exceptional reliability across a large cohort**
From 168 recruited participants, only one sample failed to yield an adequate sequencing library (in an evHC subject), underscoring extraction consistency for downstream library construction.
- **Species-level resolution and biomarkers made feasible by high-quality inputs**
Powered by deep, clean reads, the study identified 43 bacterial species differing in iNPH and/or enlarged-ventricle groups vs. controls; 14 species were confirmed by two independent DA methods (Maaslin2, ANCOM-BC). Example: *Enterocloster bolteae* showed strong enrichment (log-fold change 6.6 in iNPH).
- **Functional pathway discoveries (clinical relevance)**
Robust functional profiling revealed enrichment of methionine/S-adenosyl-L-methionine (SAM) metabolism pathways in iNPH—hypotheses that touch inflammation and epigenetic regulation—made possible by sufficient depth and uniformity from MagPurix DNA.
- **Confounder-aware analytics enabled by consistent data quality**
With uniform inputs, beta-diversity differences (Aitchison) were resolved between iNPH / enlarged-ventricle groups and healthy controls, while sequencing read count

did not drive the signal—supporting true biological separation rather than technical noise.

Why MagPurix® for Microbiome Partners

- End-to-end automation minimizes hands-on time and variability while scaling to hundreds of samples.
- Proven downstream success in shotgun metagenomics: high-depth libraries, species-level calls, and functional pathway detection.
- Reliability: >99.4% Success reported in the cohort (1/168 library failure).
- Flexible to real-world operations: compatible with routine home collection and mixed freezer conditions, with covariates modeled in analysis.

Conclusion

The Park *et al.* study demonstrates that Zinexts MagPurix® provides the DNA quality, consistency, and throughput required for modern microbiome programs from discovery to translational research. Partners can confidently adopt MagPurix to:

1. Standardize extractions across sites
2. Achieve deep, clean datasets for species-level and pathway-level insights
3. Reduce failure rates that inflate time and cost.

In short, MagPurix® turns complex stool cohorts into reliable, decision-ready metagenomic data.

Reference

Park, R., Chevalier, C., Kieser, S., et al. (2025). Gut microbiome signatures in iNPH: Insights from a shotgun metagenomics study. *PLOS ONE*, 20(9), e0330251. <https://doi.org/10.1371/journal.pone.0330251>