
Wobble GENOMICS

UKRI Biotechnology and Biological Sciences Research Council

ROSLIN INNOVATION CENTRE

# Academic Consultancy Supporting Translation of RNA Normalisation Technology to Metagenomic and Microbiome Sequencing

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**Wobble Genomics** is a biotechnology company developing innovative sample normalisation technologies designed to improve sequencing data quality by enhancing the representation of low-abundance nucleic acids. Its flagship products reduce bias caused by highly abundant sequences, enabling more accurate transcriptome analysis, genome annotation, and downstream biological insight.

Based at the **Roslin Innovation Centre**, Wobble Genomics benefits from access to specialist laboratory facilities and close proximity to the world-leading genomics expertise at the Roslin Institute. This environment supports rapid technology development, robust validation, and effective translation of new methods into research, clinical, and applied genomics markets

**Metagenomic sequencing** is fundamentally challenged by extreme differences in species abundance within microbiome samples. Highly abundant organisms dominate sequencing reads, while low-abundance species receive insufficient coverage to be reliably detected, identified, or assembled into genomes. This bias means that sequencing data often fails to capture the true diversity and functional potential of complex microbial communities., Rare but important organisms, including potential pathogens, can be missed entirely. Existing metagenomics workflows offer limited practical solutions to address this imbalance without substantially increasing sequencing depth, cost or the need for multiple sequencing runs.

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The **Campus Innovation Award (CIA)** funded a collaborative project partnership between Wobble Genomics and an academic consultant at the Roslin Institute to modify its RNA normalisation technology for use with metagenomic DNA, addressing a major challenge in microbiome sequencing.

The project explored whether the existing normalisation approach could be adapted for this new sample type. This required developing a method to shear DNA and ligate adapters that mimic cDNA libraries, alongside optimising the protocol for the markedly different abundance profiles seen in microbiome samples. The adapted workflow was first tested on mock microbial communities containing known species at defined abundances, allowing clear assessment of performance.

Sequencing results demonstrated effective normalisation across a broad range of species abundances, with improved representation of low- and mid-abundance organisms and reduced dominance of highly abundant species. Although extremely rare species remained difficult to recover, the overall shift towards more even coverage was clear, confirming that the technology can be applied beyond RNA.

The academic consultant played a critical role by contributing metagenomics expertise, experimental design, and access to appropriate samples, enabling rapid protocol development and rigorous evaluation. The CIA grant de-risked this exploratory collaboration, allowing validation of a new application without diverting core commercial resources.

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**“The academic consultant and collaborative support were critical in enabling this work, providing expertise, resources, and experimental insight needed to adapt our technology to a new application and demonstrate its scientific and commercial potential.”**

***Richard Kuo, CEO of Wobble Genomics Ltd.***