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Impact Report

Exploring the innovations, breakthroughs, applications of genomics and multi-omics research powered by Genotypic Technology

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Reading the Genome Before Diabetes Begins

How Genotypic's Nanopore long-read methylome sequencing enabled a landmark Indian longitudinal study - linking blood DNA methylation patterns to Type 2 Diabetes risk, years before any clinical symptom appears

PUBLISHED IN

Clinical Epigenetics, 2026

PARTNER INSTITUTION

BRIC-Rajiv Gandhi Centre for Biotechnology

PLATFORM

Oxford Nanopore PromethION P24

GENOTYPIC TECHNOLOGY ROLE

NGS Sequencing & Data Analysis

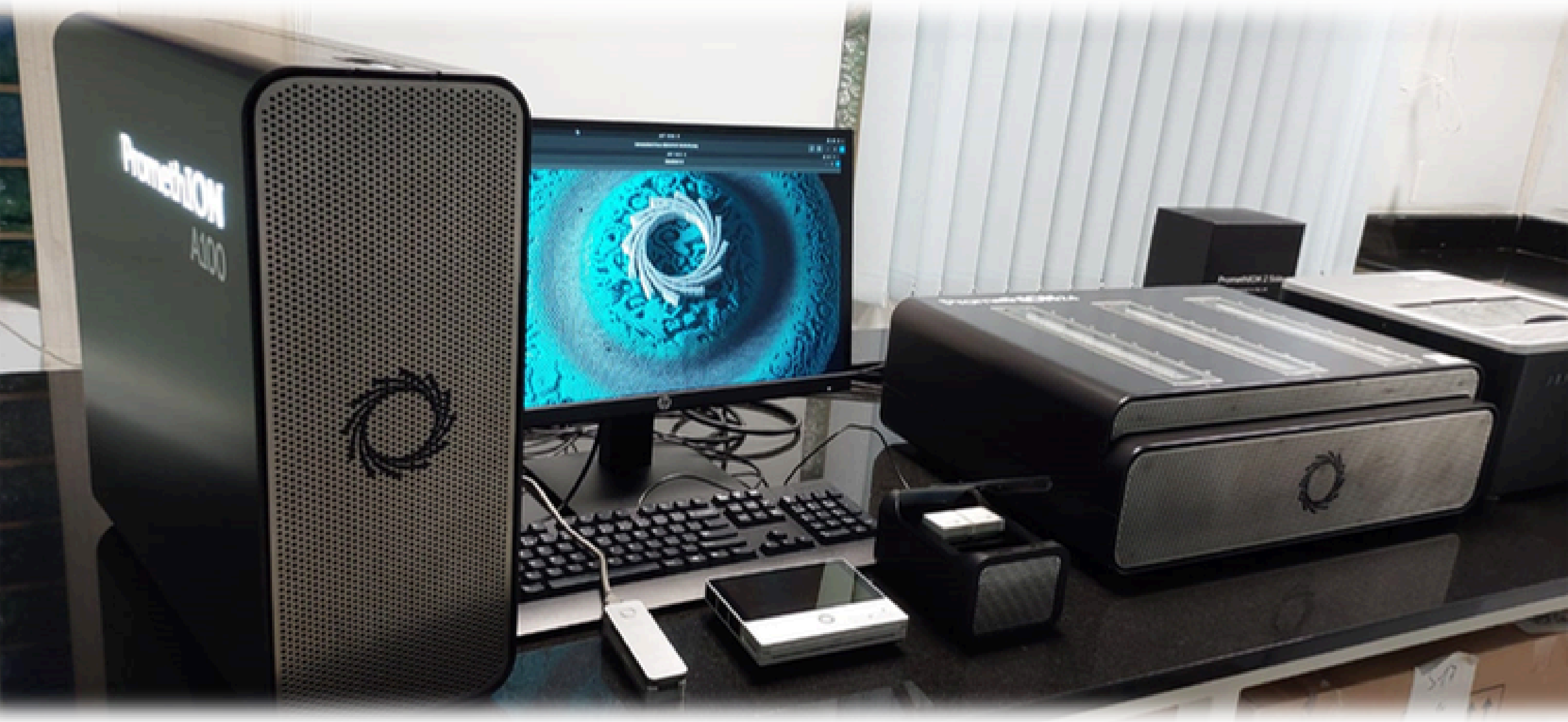

Fig: Oxford Nanopore Sequencing facility at Genotypic Genomics lab

THE RESEARCH CHALLENGE

India's Diabetes Burden Needs Earlier Molecular Signals

Researchers at BRIC-Rajiv Gandhi Centre for Biotechnology posed an ambitious question: could disease risk be detected years before symptoms appear, encoded within the methylation patterns of blood cells? Can such Biomarkers contribute to enabling people to make lifestyle changes to prevent/delay onset ? Their initial plan was to study methylation using conventional Illumina array-based methods. However, after evaluating the project goals, we recommended transitioning to Nanopore long-read sequencing to generate richer and more comprehensive datasets with substantially greater discovery potential.

> *"No longitudinal cohort studies in India had profiled DNA methylation prior to the development of Type 2 Diabetes. This study addresses that gap directly."*
> *- Satheesh et al., Clinical Epigenetics (2026) 18:64*

GENOTYPIC'S TECHNICAL CONTRIBUTION

We worked closely with the team to identify the most appropriate sequencing strategy and demonstrated that long-read sequencing could match and in several areas potentially outperform traditional array-based approaches for methylation analysis. Beyond methylation profiling alone, the long-read workflow enabled a far more integrated genomic analysis, allowing simultaneous detection of structural variants, haplotype phasing, tandem repeat variation, and native epigenetic modifications within a single experimental and analytical framework.

24
Samples

5.4M
CpG Sites identified

This unified approach not only expanded the biological insights obtainable from each sample but also created opportunities for future biomarker discovery that would be difficult to achieve using array-only technologies.

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