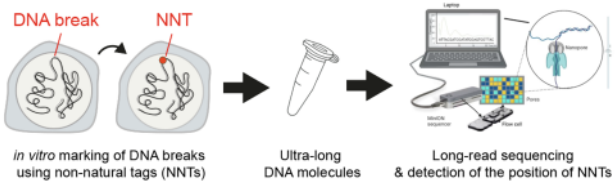
PROJECT NUMBER

23887

AnaLog-seq: An unbiased method for detecting DNA breakpoints throughout the whole genome

AnaLog-seq is a transformative technology that detects DNA breakpoints, including both single-strand (SS) and double-strand (DS) breaks, across the genome while preserving long-range genetic context.

Applications: Clinical diagnostics; research (e.g. into genome instability, immunity, reproduction, evolution and drug resistance in cancer)



Features	Benefits
Based on long-read sequencing	Precisely localises DNA breakpoints in repetitive and structurally complex genomic regions (where short-read sequencing fails). Quantifies DNA break frequency within individual long DNA molecules.
Detects and discriminates between SS and DS breaks	Provides complete information for diagnostic and research purposes
Elegantly simple method involving relatively few steps and reagents	Straightforward and inexpensive to apply
Current implementation on Oxford Nanopore Technology instrumentation	Widely used sequencing platform

Features	Benefits
Uses synthetic tags that do not occur naturally in biological systems	Simultaneously detects DNA breaks and other epigenetic modifications within the same DNA molecule
Relatively small amount of starting material required	Can be scaled up for the analysis of multiple samples

Patented and Available for

- Co-development
- Consulting
- Licensing

To find out more, contact enquiries@innovation.ox.ac.uk and quote the project number.