Oxford Nanopore Technologies

Go with the gold standard in methylation sequencing

Comprehensive biology in one run

Oxford Nanopore provides gold-standard methylation sequencing and comprehensive variant calling in a single run — without chemical conversion.

Get all you need in one dataset and save preparation time so you can focus on discovery.

- Gain best-in-class methylation accuracy, with a false-positive rate of just 0.1%
- Call ~10% more CpG sites than short-read sequencing
- Comprehensively capture the variant landscape
- Leverage digital panels for targeted sequencing, powered by Adaptive Sampling*

	Oxford Nanopore	PacBio HiFi	Illumina 5-base	EM-seq v2	WGBS
Genome-wide methylation	✓	✓			
High-accuracy 5mC	✓		✓	✓	✓
High-accuracy 5hmC	✓				
All-context 5mC	✓		✓	✓	✓
SNVs / SVs / CNVs	✓	✓	✓	C/T variants lost	C/T variants lost
Complex SVs	✓	✓			
			Short-read sequencing		

Get high-accuracy 5mC calling with Oxford Nanopore

Take your research to the next level with gold-standard methylation sequencing.

Oxford Nanopore sequencing delivered the highest accuracy 5mC calling of all methods compared in benchmarking, achieving both low false-positive and low false-negative rates.

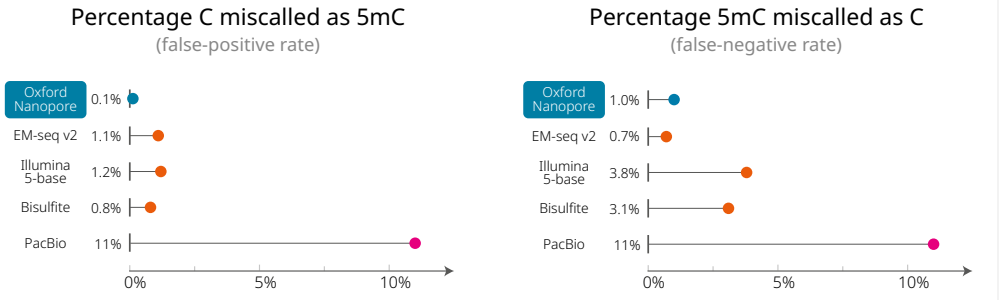


Figure 1. Oxford Nanopore methylation sequencing showed both a low false-positive rate (FPR) and low false-negative rate (FNR). We determined FPR (left) and FNR (right) for Oxford Nanopore and short-read sequencing technologies by sequencing a diverse mix of synthetic ground-truth benchmark oligonucleotide standards with either C or 5mC at defined positions (~200 testing sites). We basecalled Oxford Nanopore data using Dorado v2 with high accuracy (HAC) v5.2 models. We obtained Pacific Biosciences (PacBio) FPR and FNR from publicly available PacBio data[1].

Call more CpG sites with Oxford Nanopore

See more biology with gold-standard methylation calls.

Oxford Nanopore sequencing provides gold-standard methylation calls across the whole genome, including for 'dark' regions where assembly of short reads often fails. In our benchmarking, the method confidently called ~10% more CpGs than Illumina bisulfite sequencing.

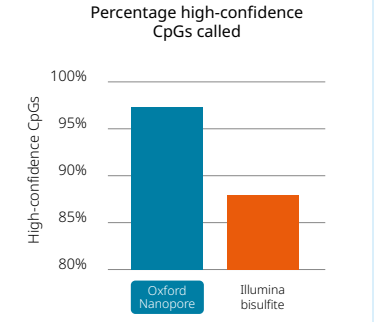
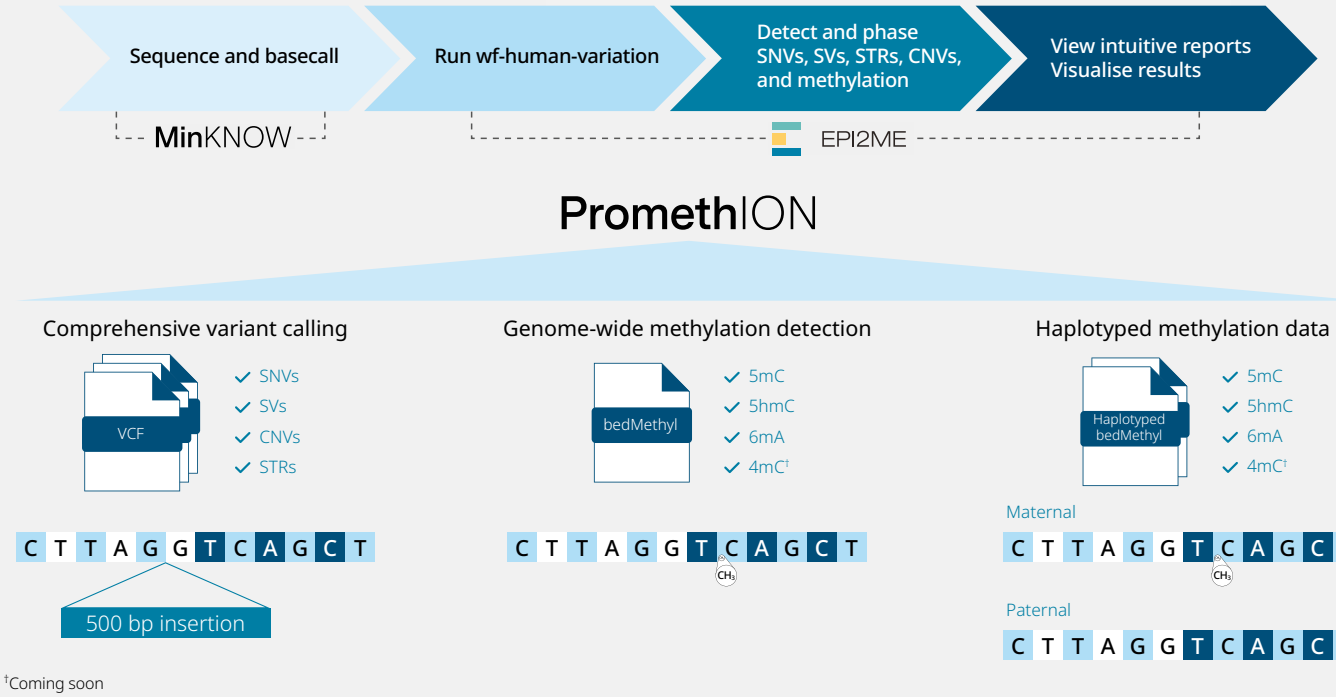


Figure 2. Oxford Nanopore methylation sequencing called 9.8% more high-confidence CpGs than Illumina bisulfite sequencing. Percentage of all CpG sites in HG002 that can be confidently called for 30x Illumina sequencing with bisulfite conversion and Oxford Nanopore methylation sequencing.

*Discover Adaptive Sampling: nanoporetech.com/adaptive-sampling-blog

The end-to-end human variation workflow



†Coming soon

View the workflow overview: **nanoporetech.com/human-variation-workflow-overview**

Sequencing at scale for population-level methylation insights

Population-scale whole-genome sequencing (WGS) is transforming our ability to uncover the genetic foundations of phenotypic traits and disease.

At the London Calling 2026 conference, Brynja Sigurpálsdóttir (Amgen deCODE genetics, Iceland) described how she and the team use high-throughput Oxford Nanopore sequencing to look at methylation across thousands of UK Biobank samples[2].

> 'the star of the show will be ... the methylation, both the 5mc and the 5hmC'

Combining WGS of native DNA with EPI2ME data analysis, the team have already sequenced samples from 5,000 UK Biobank participants to a depth of coverage of 30x and are on track to sequence a further 45,000 samples to 15x coverage by the end of 2026.

Brynja described how, as well as producing haplotyped whole-genome methylation data, they will identify and phase SVs and variants in previously inaccessible 'dark' regions of the genome[3].

Early findings are compelling: principal component analysis of CpG methylation is revealing ancestry-related clustering, while ongoing EWAS has identified a high number of associations between CpG methylation and specific traits. Crucially, both datasets will be made publicly available, providing extensive and comprehensive multiomic information to advance human genomic research.

Find out more about methylation detection with Oxford Nanopore: **nanoporetech.com/resources/epigenetics**

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References:

1. GitHub. Pacific Biosciences — jasmine. https://github.com/PacificBiosciences/jasmine/blob/main/ACCURACY.md [Accessed 06 July 2026]
2. Sigurpálsdóttir, B. Presentation. Available at: https://nanoporetech.com/resource-centre/oxford-nanopore-sequencing-of-the-uk-biobank-lc26 [Accessed 18 Jun 2026]
3. Ebbert, M.T.W. et al. *Genome Biol.* 20(1):97 (2019). DOI: https://doi.org/10.1186/s13059-019-1707-2

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