

Tumour methylation profiling

Fast multiomic tumour profiling on one platform

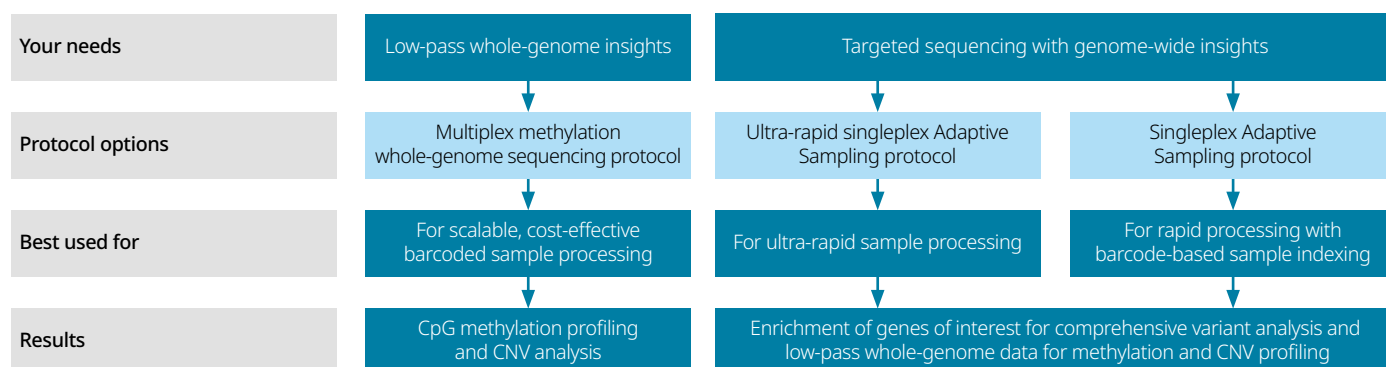
Comprehensively profile solid tumours using one of our three validated tumour methylation profiling protocols. One protocol provides low-pass whole-genome analysis, while two use the research-use-only Pan-Cancer digital panel, which is powered by Adaptive Sampling — an on-sequencer enrichment method that delivers high-coverage data across targets while simultaneously generating low-pass whole-genome data.

Achieve single-base methylation resolution and genetic variant detection from one sequencing experiment without additional library prep steps. Methylation outputs are compatible with widely used tumour methylation classifiers, including central nervous system (CNS) tumour and leukaemia classification frameworks.

Capture genomic and epigenomic data in one go

Choose a protocol to fit your needs:

- **Low-pass whole-genome sequencing protocol:** low-pass genome-wide tumour methylation profiling for CpG and copy number variant (CNV) analysis, with multiplexing of up to four samples per PromethION™ Flow Cell.
- **Adaptive Sampling whole-genome sequencing protocols:** comprehensive targeted analysis of small and complex genetic variants using the ready-to-use Pan-Cancer digital panel to target 723 cancer-associated genes alongside whole-genome data for methylation and CNV analysis. These protocols are available in an ultra-rapid format or with barcode-based sample indexing.



	Whole-genome sequencing protocol	Adaptive Sampling whole-genome sequencing protocols	
Protocol	Multiplex methylation whole-genome sequencing protocol	Ultra-rapid singleplex Adaptive Sampling protocol	Singleplex Adaptive Sampling protocol
Sample type	Fresh and frozen tissue		
Recommended DNA input	250 ng	1,000 ng	500–1,000 ng
Library prep kit	Native Barcoding Kit	Ligation Sequencing Kit	Native Barcoding Kit
Samples per PromethION Flow Cell	4	1	
Enrichment method	No enrichment	Adaptive Sampling	
Enriched genes	N/A	723 cancer-associated genes enriched using the Pan-Cancer digital panel	
Variants captured	Whole-genome methylation and CNVs	SVs, CNVs, indels, and SNVs across target regions, and whole-genome methylation	
Reference genome	N/A	GRCh38 (GIAB v3)	
Mean* coverage (Fold-80)	2x	>75x (1.18)	

*Median coverage for autosomal targets normalised for CNV.

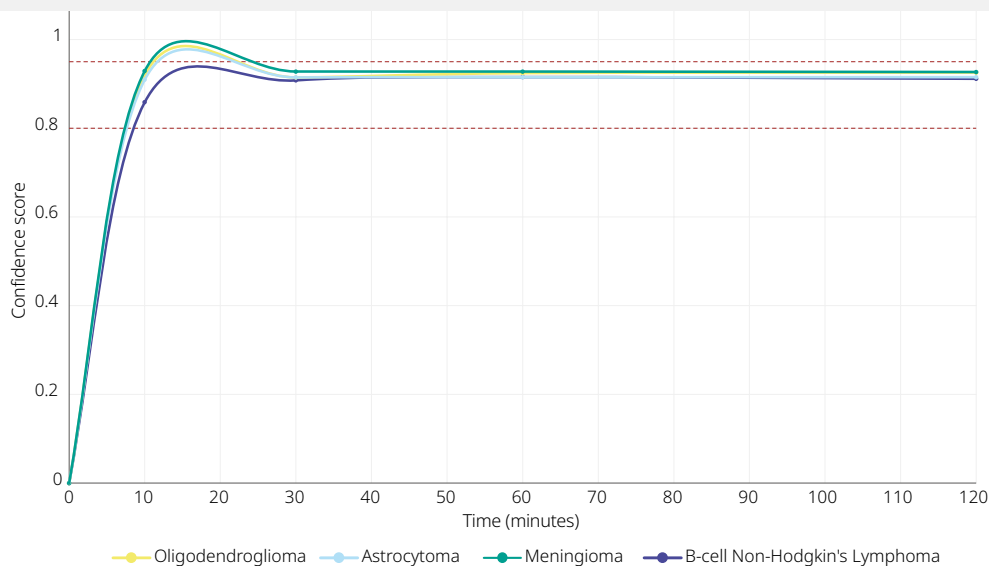


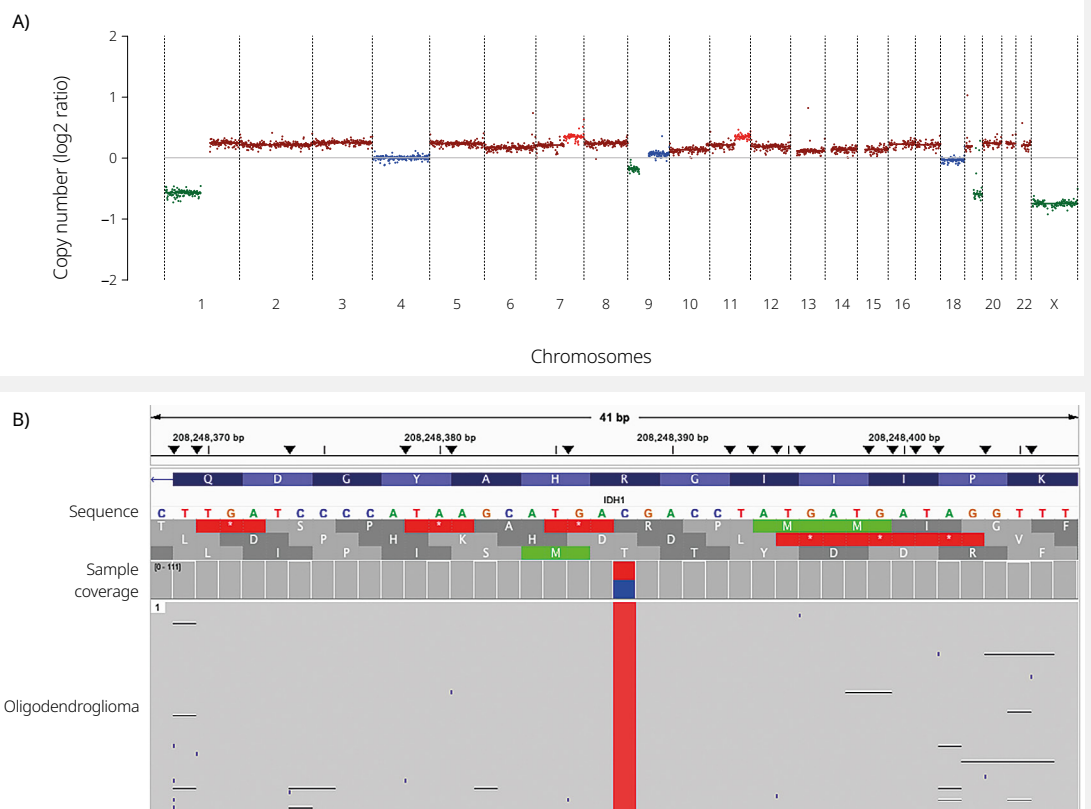
Figure 1. Ultra-rapid CNS tumour classification of four singleplex research samples (Avaden Biosciences) prepared using the ultra-rapid singleplex Adaptive Sampling protocol and analysed using Sturgeon¹, a CNS neural network methylation classifier.

All samples achieved the minimum recommended confidence threshold (>0.8) within 20 minutes and high-confidence classification (≥ 0.95) within 30 minutes of sequencing. This demonstrates the protocol's ability to generate accurate and reliable data for potential downstream tumour classification.

Figure 2. Integrated genomic characterisation of an oligodendroglioma sample (Avaden Biosciences) prepared using the ultra-rapid singleplex Adaptive Sampling protocol and analysed using the nanoDx² pipeline for CNS tumour-based classification.

A) Copy number profile demonstrating the characteristic 1p/19q co-deletion.

B) Detection of a pathogenic *IDH1* mutation, a defining molecular feature of oligodendroglioma. Together, these results highlight how the tumour methylation profiling protocol provides simultaneous methylation classification and detailed genomic variant analysis in a single assay.



Find out more: nanoporetech.com/methylation-profiling



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References

1. Vermeulen, C. and Pagès-Gallego, M. et al. *Nature* 622(7984):842–849 (2023). DOI: <https://doi.org/10.1038/s41586-023-06615-2>
2. Euskirchen, P. et al. *Acta Neuropathol.* 134(5):691–703 (2017). DOI: <https://doi.org/10.1007/s00401-017-1743-5>

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