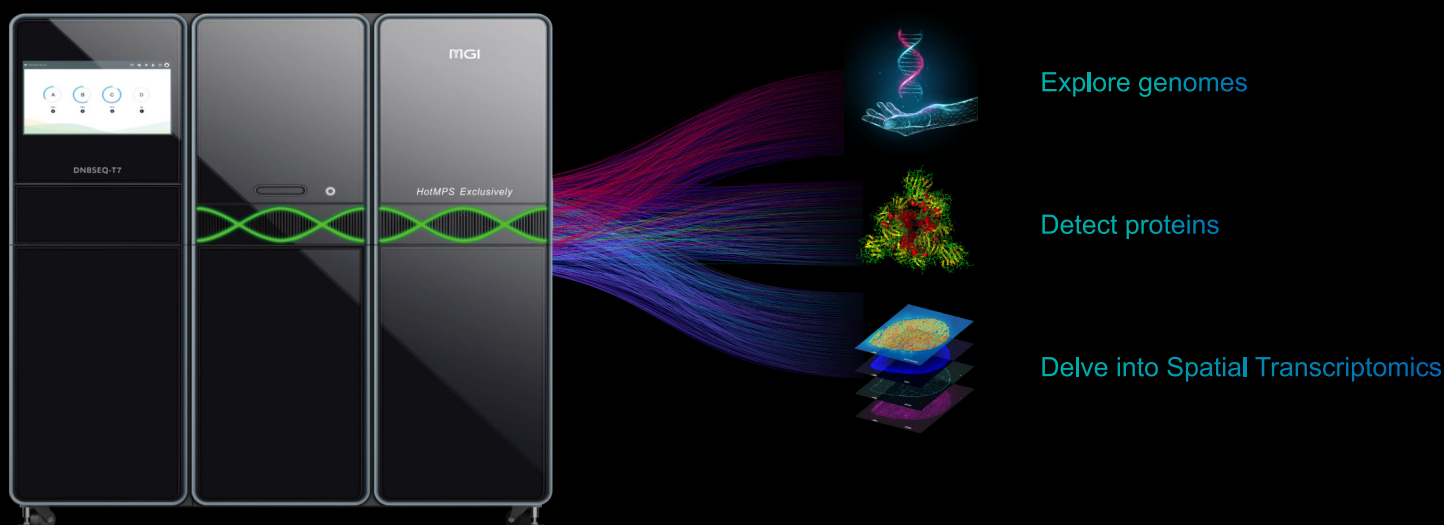


# What if

## Your Platform Could Explore Beyond the Genome with All in One Platform

The DNBSEQ-T7's scalability makes it ideal for national and global initiatives looking to generate multi-layered biological data at a lower cost per sample.

Explore the genetic, proteomic, single-cell and spatial transcriptomic layers of disease and health across populations, with one platform.



### ***Ultra-high Throughput for Large-scale Studies***

With 4 independent loadable flow cells the T7 provides up to 15 000 genomes per year.

### ***A Single Platform for Multi-Omics Capabilities***

A multi-omics powerhouse: With support for whole-genome sequencing (WGS), spatial transcriptomics, single-cell sequencing and proteomics, the T7 allows you to seamlessly integrate multiple omics layers.

### ***Cost-effective, Scalable and High-Speed to Accelerate Discovery in Population and Multi-Omics Research with 30X Coverage***

The T7 can process up to 60 human genomes in 24 hours or run extensive transcriptomic and proteomic analyses quickly, allowing you to accelerate discoveries.

# A single tool for many breakthroughs

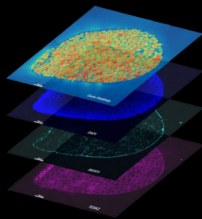
Unlock the full potential of **population genomics** and **multi-omics integration** with the T7, the ultimate platform for researchers aiming to uncover new insights into genetic diversity, health, and disease.



## WGS

Samples/run	60
Flow cells	4 independent
Data output/sample	1-7 Tb

## Spatial Transcriptomics

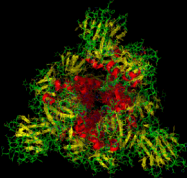


Resolution	0.5 $\mu$ m
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Sample type	FFPE	Fresh frozen
Capture method	Random probes	Poly-A
Recommended reads	3 billion	1.5 - 2 billion
Samples/run	4*	8*

\*This is recommended samples/run. Based on sample type and quality, deeper sequencing (less sample/run) might be needed

## Proteomics



Samples/run	344
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Number of proteins	5 400
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