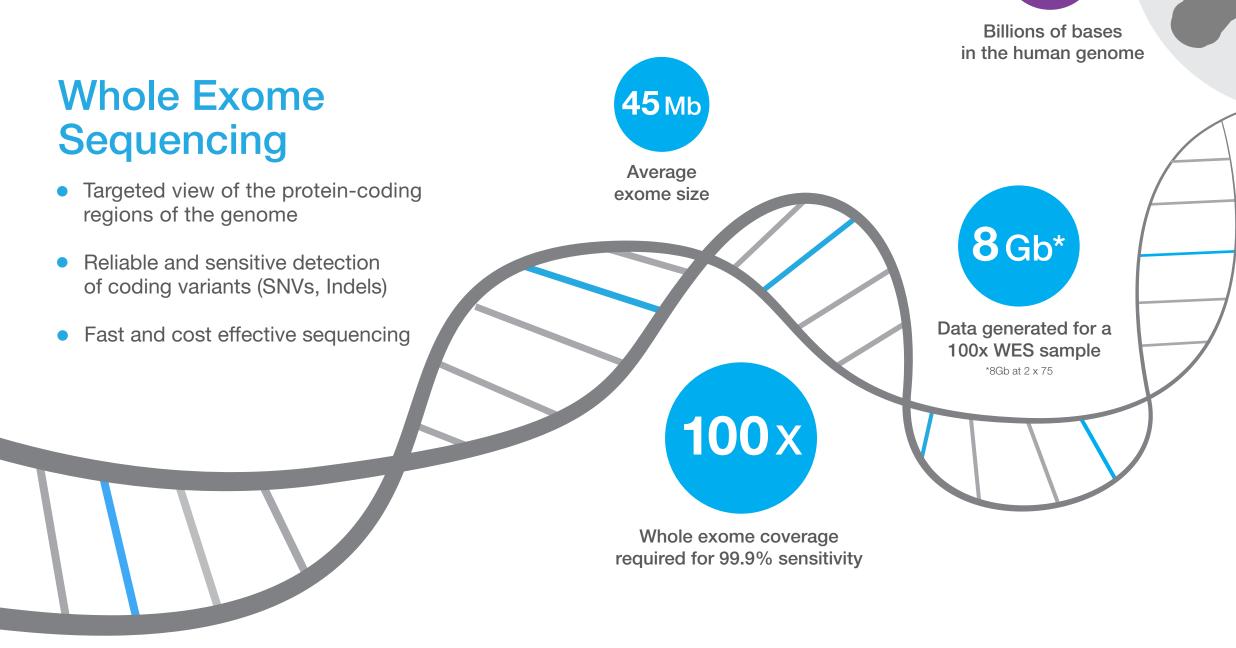
Find the method that's right for your research

Next-generation sequencing (NGS) allows researchers to explore genetic variations like never before – down to single nucleotide resolution. Whether you need to identify specific variants from a focused set of regions, or look more broadly for potential causative variations, whole exome sequencing (WES) or whole genome sequencing (WGS) both offer effective solutions.

Explore the benefits of these approaches to understand which method is best for your research.



3.2в



Data generated from 30x WGS

Whole genome coverage required for 99.9% sensitivity

30x

Whole Genome Sequencing

- Comprehensive view of the genome (coding, non-coding and mtDNA)
- Reliable and sensitive detection of all variant types (SNVs, Indels, SVs, CNVs)
- Low cost, fast library preparation

