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.

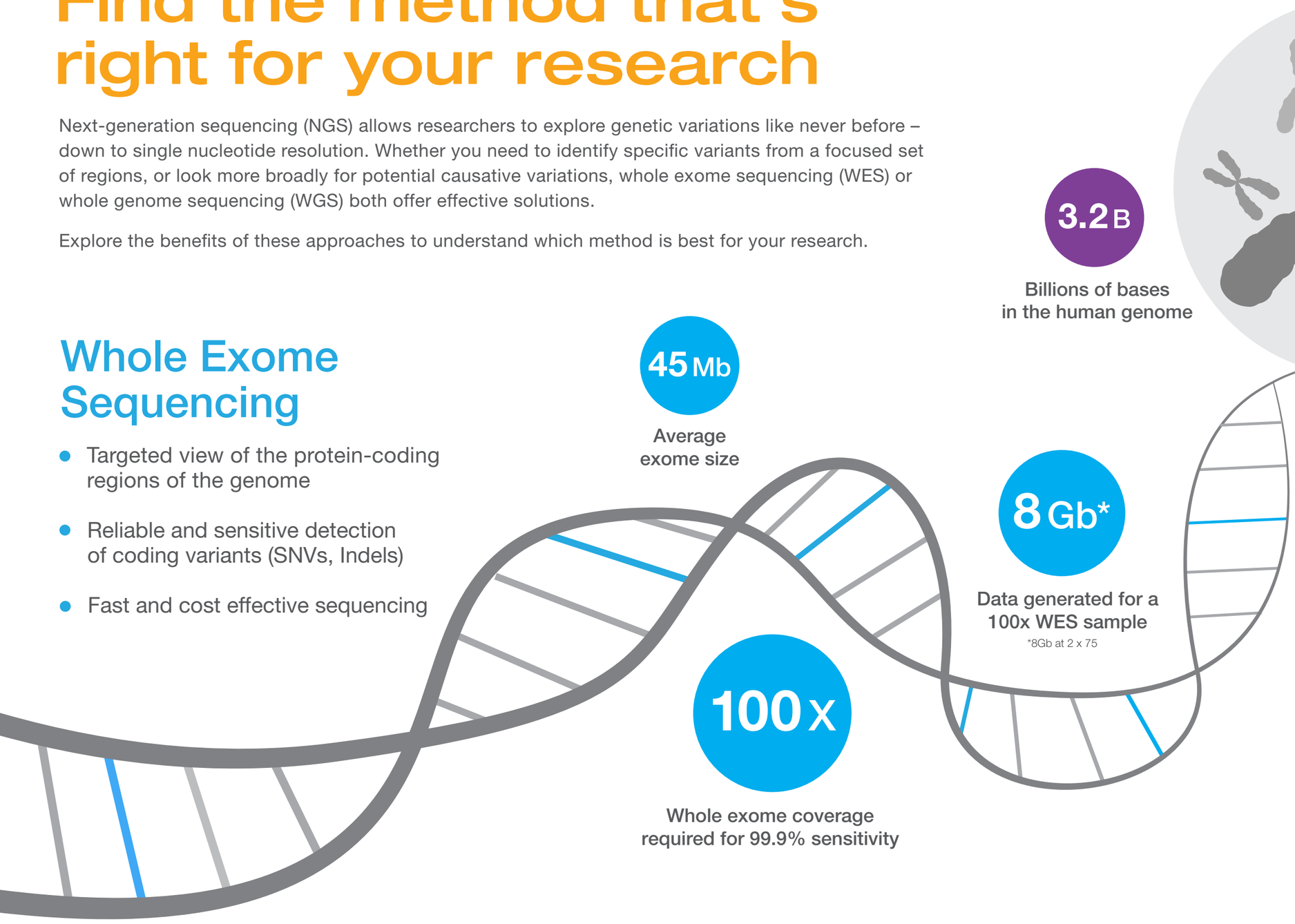
Explore the benefits of these approaches to understand which method is best for your research.

Whole Exome Sequencing

- Targeted view of the protein-coding regions of the genome
- Reliable and sensitive detection of coding variants (SNVs, Indels)
- Fast and cost effective sequencing

45 Mb
Average exome size

100 x
Whole exome coverage required for 99.9% sensitivity



8 Gb*
Data generated for a 100x WES sample
*8Gb at 2 x 75

3.2 B
Billions of bases in the human genome

120 Gb
Data generated from 30x WGS

30 X
Whole genome coverage required for 99.9% sensitivity

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

Learn more about sequencing methods at http://www.illumina.com/wes-wgs

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