



Long Read



Methylation Arrays



Targeted



WES



WGS

Whole Genome Sequencing (WGS)

The most comprehensive sequencing analysis with the widest coverage

Whole Genome Sequencing (WGS) provides the most comprehensive genetic blueprint of an organism. WGS is often conducted in exploratory analysis, for example in the investigation of rare diseases of unknown causes. GenomeScan offers an accredited (ISO/IEC 17025) WGS service across a multitude of diagnostics, therapeutics and research applications. WGS not only provides unique insights into disease mechanisms, but it also generates genome wide information opposed to Whole Exome Sequencing (WES) generating data for only 1-2%

of the genome. It offers the ability to identify copy number variations, insertions-deletions (indels), rearrangements and other structural variations. It helps you make an educated decision for the next step of your research project and offers you the advantage of reanalyzing and reinterpreting your data at any time.

By using unique dual-indexed sequencing adaptors, we are able to analyze hundreds of samples in parallel delivering the least bias and highest reproducibility, making WGS a very powerful and cost-effective tool for genetic profiling.

Input material

Isolated genomic DNA

- Required input:
 - without PCR ≥ 25 ng / sample*
 - with PCR ≥ 1 ng / sample
- Minimum volume: 20 μ l / sample
- Quality: High Molecular Weight DNA
- Optional: FFPE repair available

Sequencing on Illumina NovaSeq (PE 150)

- PCR free library preparation (≥ 25 ng)
- Unique Molecular Identifiers for samples with PCR
- Unique dual indexed sequencing adaptors

Deliverables

- FastQ files
- Quality score Q30 of $\geq 80\%$
- Optional data analysis with comprehensive report

*Higher input is required (> 100 ng) for deep sequencing

NGS Laboratory workflow



