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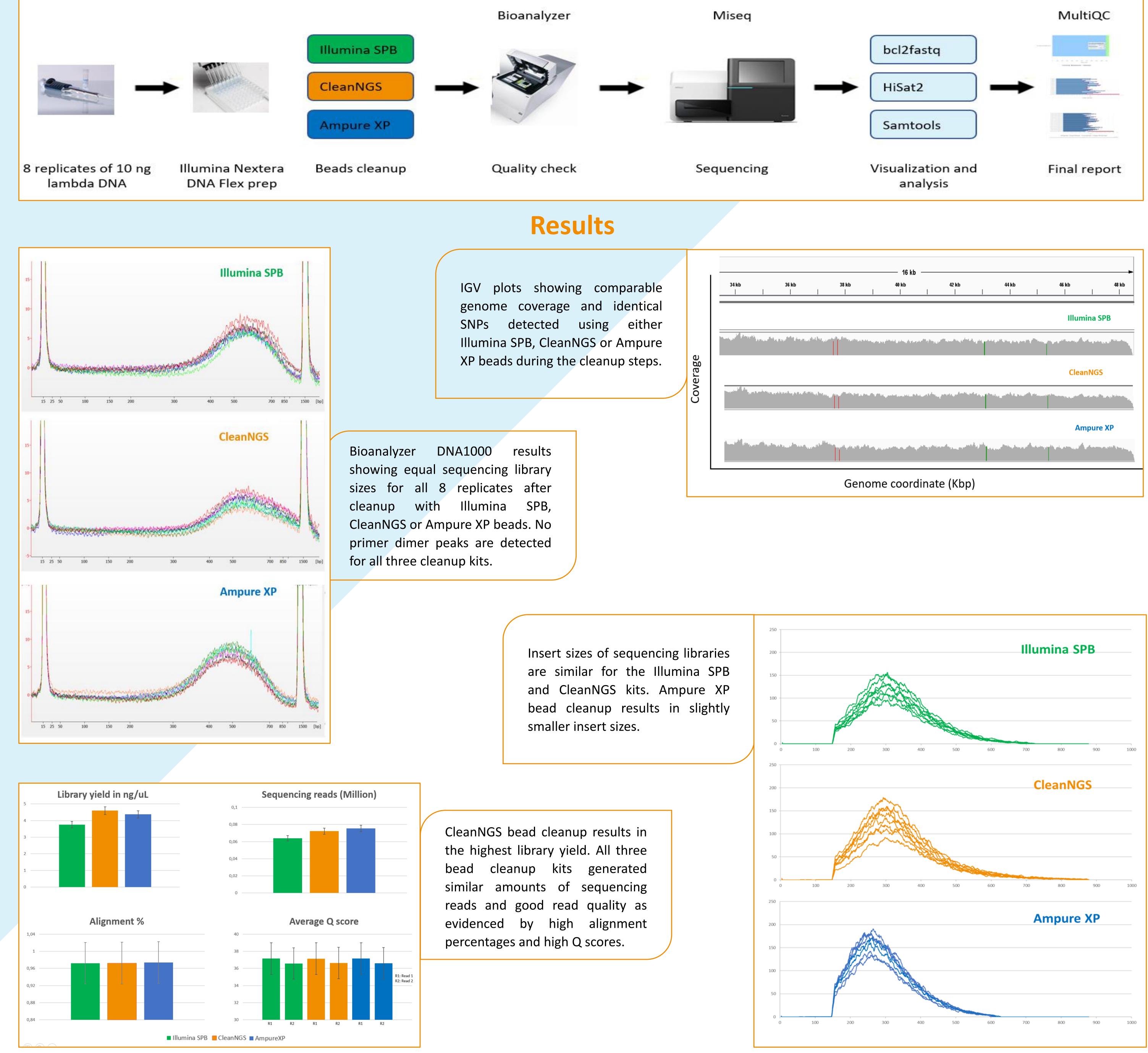
# **Introduction and Objective**

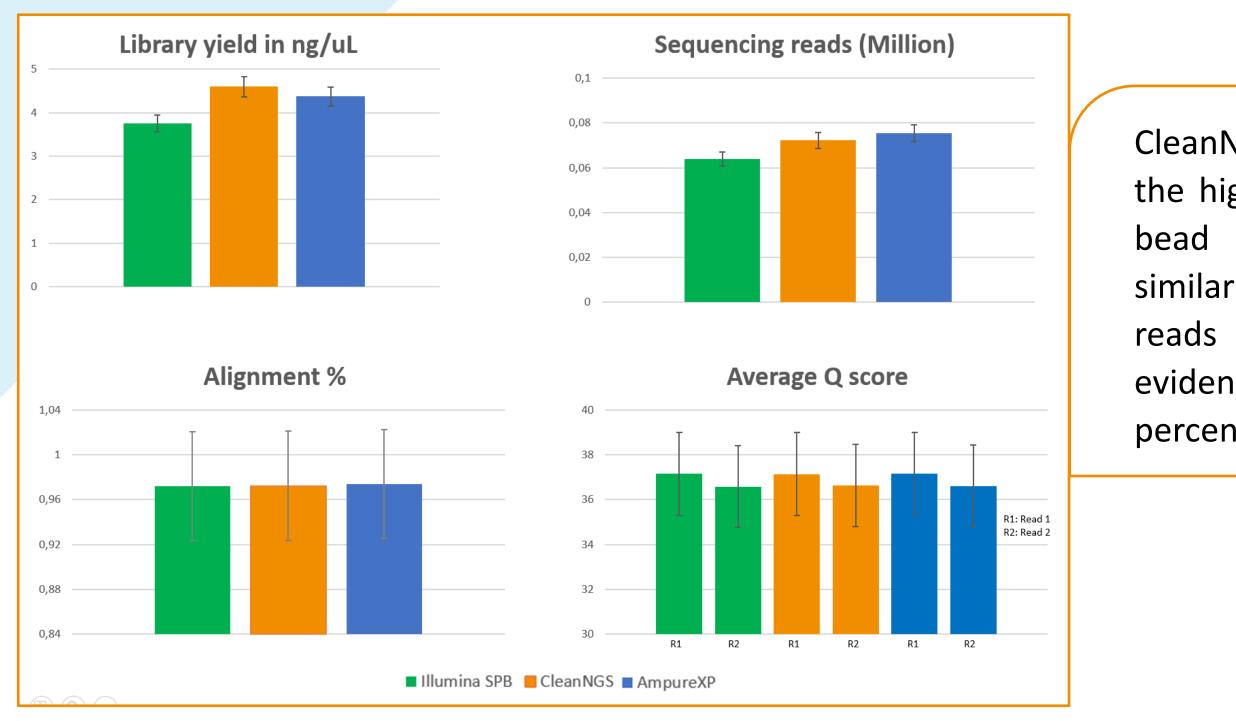
Next generation sequencing (NGS) allows for the generation of robust information on the genetic diversity of organisms at the single cell, organ, species or population level. NGS, sometimes also referred to as massively parallel or deep sequencing, is a DNA sequencing technology which has revolutionised genomic research. It's become an important technology for a wide range of applications ranging from single cell to whole-genome population sequencing. To perform an NGS experiment, users must prepare a sequencing library from a purified nucleic acid sample.

Magnetic beads have many uses within NGS workflows. In addition to nucleic acid isolation, magnetic beads are also used for size selection in NGS library preparation and library normalization. With emerging NGS technologies, there is an increased need for NGS library purification methods providing accurate results starting from low input amounts of DNA and/or RNA. Since CleanNGS (CleanNA) can be used both manually as well as automated it can be adopted in any NGS laboratory independent of sample throughput.

The aim of our study was to compare the performance of CleanNGS in DNA cleanup versus two equivalent magnetic beads based kits.

## Workflow





## Conclusion

The CleanNGS bead cleanup performs equally compared to the Illumina SPB or Ampure XP competitor kits.