Performance of CleanNGS in Next-Generation Sequencing

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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.
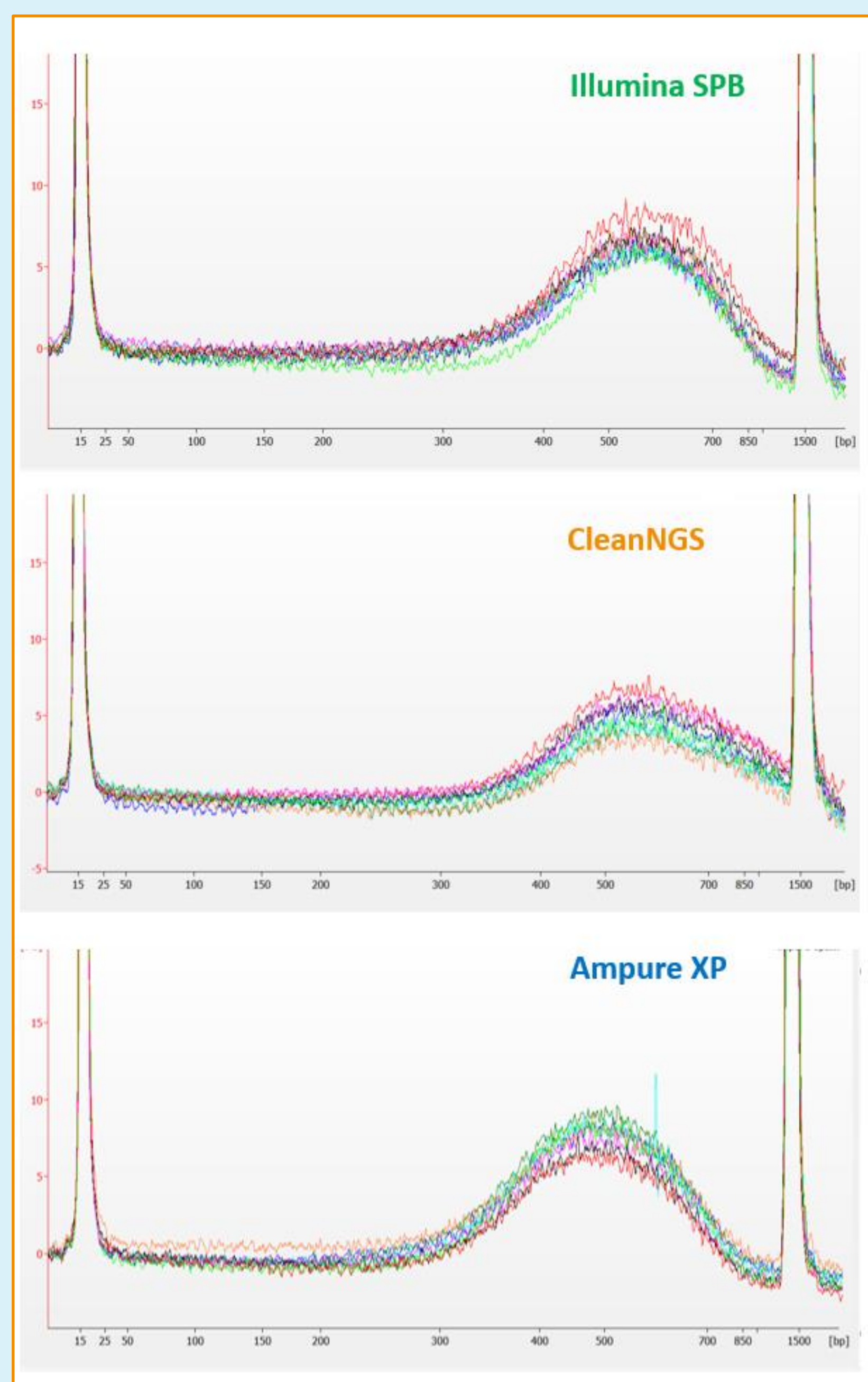
Magnetic beads have many uses within NGS workflows. In addition to nucleic acid isolation and purification, magnetic beads are also used for size selection in NGS library preparation and library normalization. With emerging NGS technologies, there is an increased need for NGS library purification methods 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.
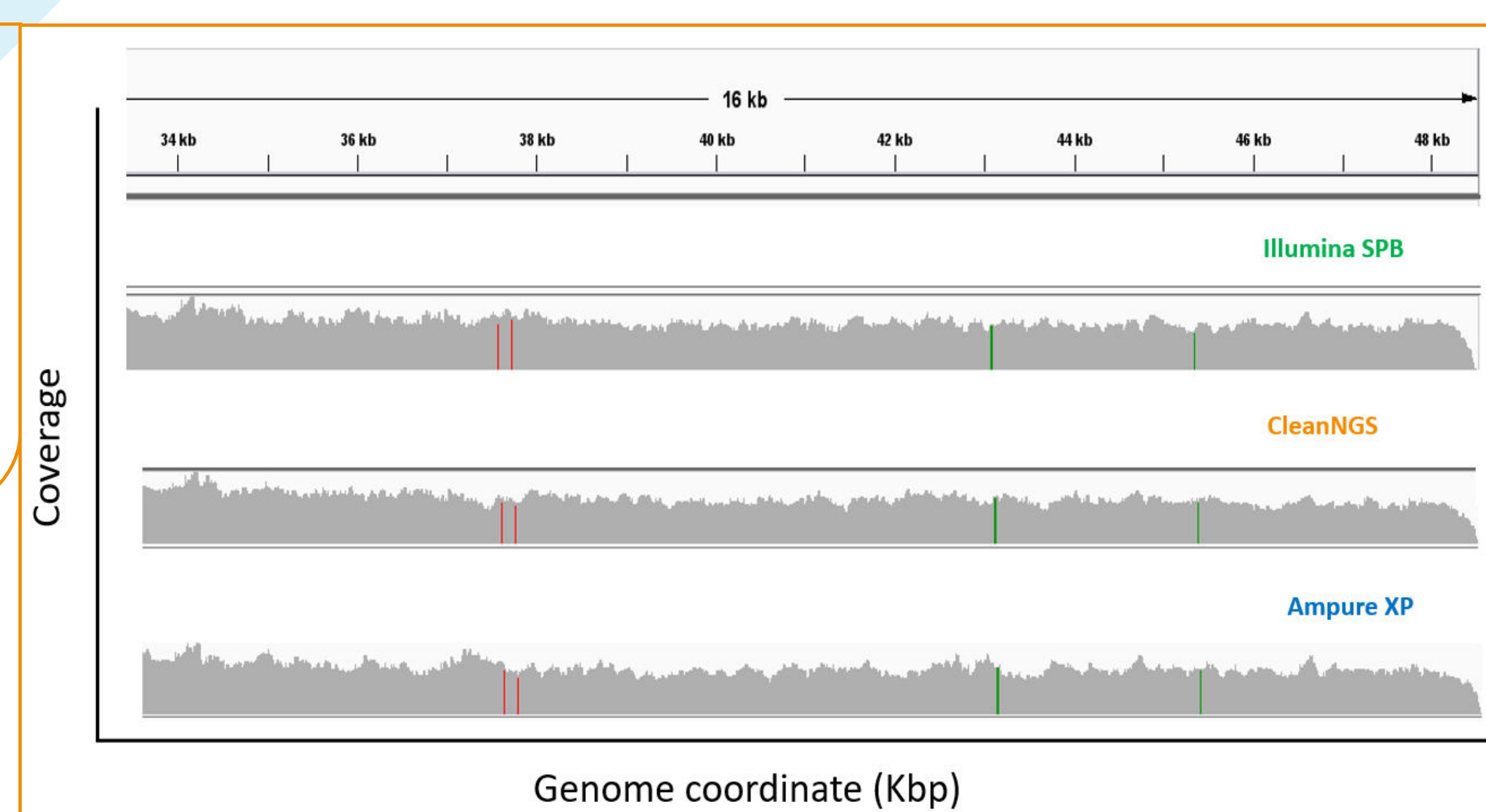
Workflow

| 8 replicates of 10 ng lambda DNA | Illumina Nextera DNA Flex prep | Beads cleanup | Quality check | Sequencing | Visualization and analysis | Final report |

Results

IGV plots showing comparable genome coverage and identical SNPs detected using either Illumina SPB, CleanNGS or Ampure XP beads during the cleanup steps.

Bioanalyzer DNA1000 results showing equal sequencing library sizes for all 8 replicates after cleanup with Illumina SPB, CleanNGS or Ampure XP beads. No primer dimer peaks are detected for all three cleanup kits.

Insert sizes of sequencing libraries are similar for the Illumina SPB and CleanNGS kits. Ampure XP bead cleanup results in slightly smaller insert sizes.
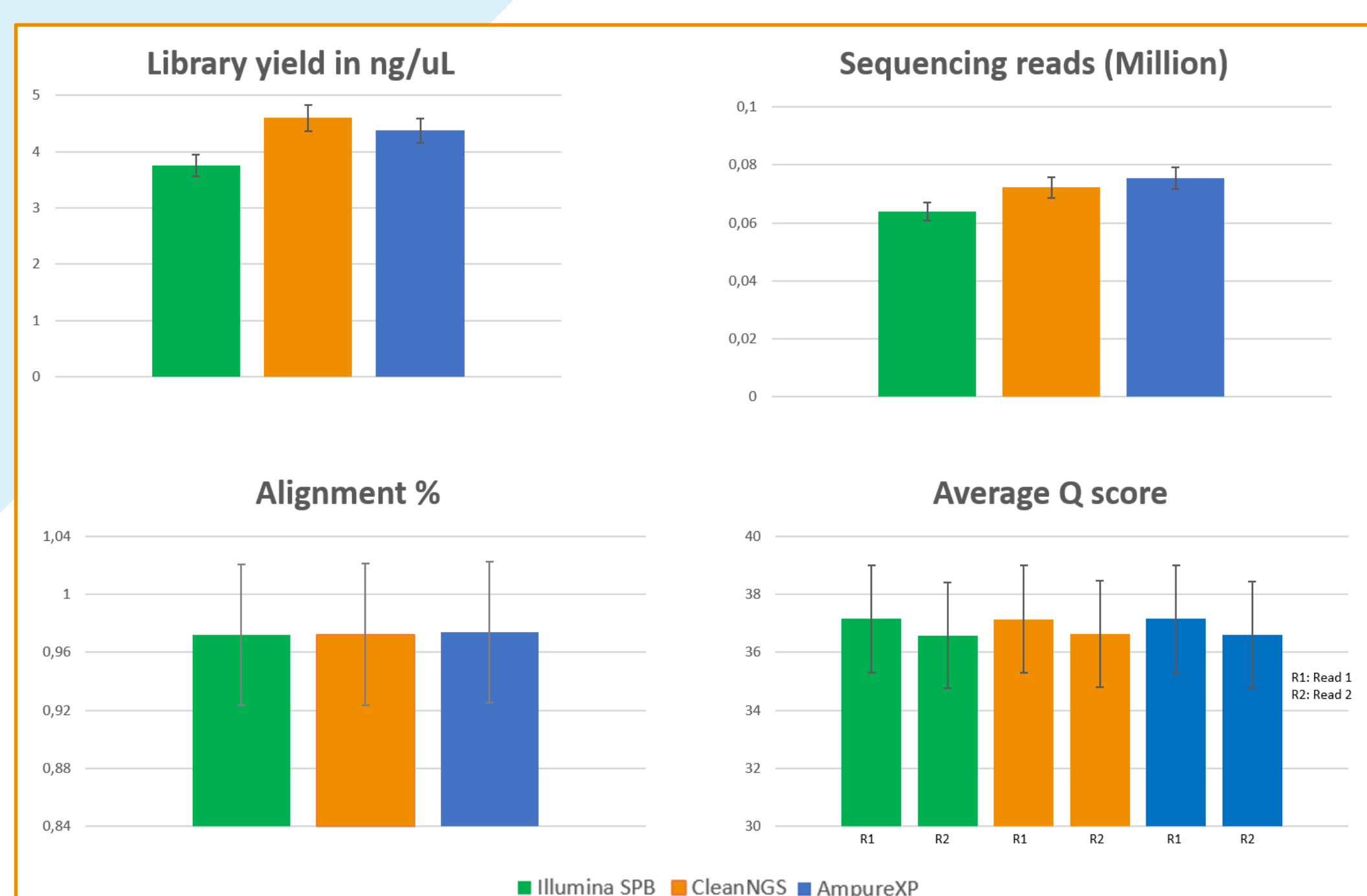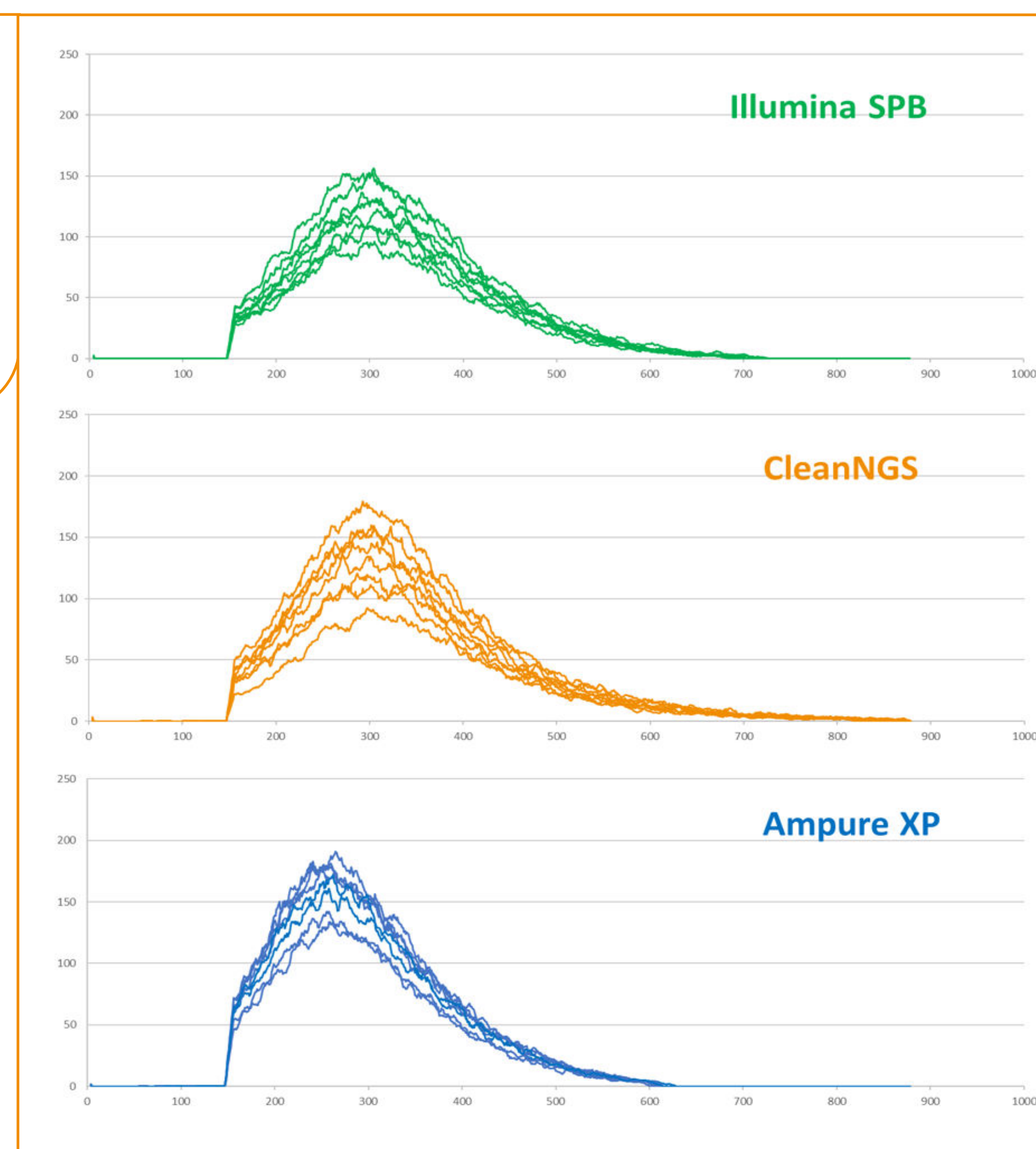
CleanNGS bead cleanup results in the highest library yield. All three bead cleanup kits generated similar amounts of sequencing reads and good read quality as evidenced by high alignment percentages and high Q scores.

Conclusion

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