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NovaSeq™ X Plus Performance

Comparing the Performances of Our NovaSeq Instruments

The NovaSeq™ X Plus instrument employs the same general principles for sequencing libraries of short DNA molecules as the NovaSeq™ 6000 instrument. However, there are differences in the sequencing chemistry (e.g., modified nucleotides, polymerases) and the image acquisition system. These could impact the obtained sequencing data.

We conducted several tests with different datasets and specifications to show that the sequencing results are comparable between the NovaSeq™ X Plus and the NovaSeq™ 6000.

Subsequently, we compared the sequencing data with the following results:

- The NovaSeq™ X Plus instrument has a lower reported **error rate** than the NovaSeq™ 6000 instrument.
- The NovaSeq™ X Plus instrument does not introduce sequencing errors that negatively affect the **sensitivity and precision of variant calling** compared to the NovaSeq™ 6000 instrument.
- No difference can be detected between the **sequence error profiles** of the NovaSeq™ X Plus instrument and the NovaSeq™ 6000 instrument.

The NovaSeq™ X Plus instrument does not add bias due to sequence or GC content. Read sequences accurately reflect the molecular sequences in the libraries, allowing for highly accurate variant calling. Overall, the NovaSeq™ X Plus sequencer can replace the currently used NovaSeq™ 6000 instrument from a technical point of view.

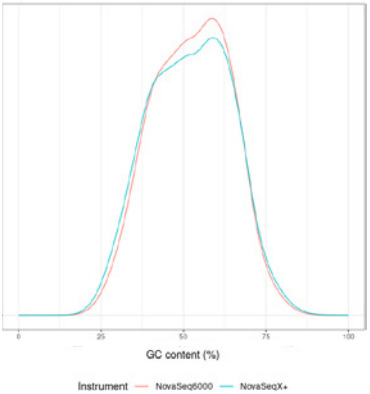

Figure: GC content distribution of sequencing reads from NovaSeq™ 6000 and NovaSeq™ X Plus sequencing of the same exome libraries shows no marked difference.

CeGaT GmbH
Research & Pharma Solutions
Paul-Ehrlich-Str. 23
72076 Tübingen
Germany

Phone: +49 7071 56544-333
Fax: +49 7071 56544-56
Email: rps@cegat.com
Web: www.cegat.com/rps

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