
## Illumina Whole Exome Sequencing and Bioinformatic Methods

Illumina whole exome sample enrichment was prepared using the Twist Exome 2.0 Plus Comprehensive Spike-in and the Twist Mitochondrial panels. Prepared libraries were then loaded onto an Illumina NovaSeq X Plus sequencer in one or more multiplexed shared-flow-cell runs, producing 2x151bp paired-end reads.

Demultiplexing, quality control and adapter trimming was performed with bcl-convert[1] (v4.2.4). Sequencing statistics are included in the '*DNA Sequencing Stats.xlsx*' file.

Additional resources

- Exome enrichment reference: Twist Exome 2.0 hg38 reference
- Sample data sets and run outputs: https://basespace.illumina.com/s/GBEdTs1IKRCM
- Example Baseline files: https://basespace.illumina.com/s/X8j2Lr7cKJXu
- TruSight Oncology Analysis Files: https://basespace.illumina.com/s/CXP94TyjB9Tr

[1] bcl-convert: A proprietary Illumina software for the conversion of bcl files to basecalls.

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