



Runtime Summary

Step	Description	Duration
1	FX Fragmentation	56m
2	Adapter Ligation + Cleanup	1hr 49min
3	Amplification + Cleanup	58m
Total	—	3h 43m

Setup takes ~30 minutes, after which the run proceeds without user intervention. (*Based on 48 sample run)

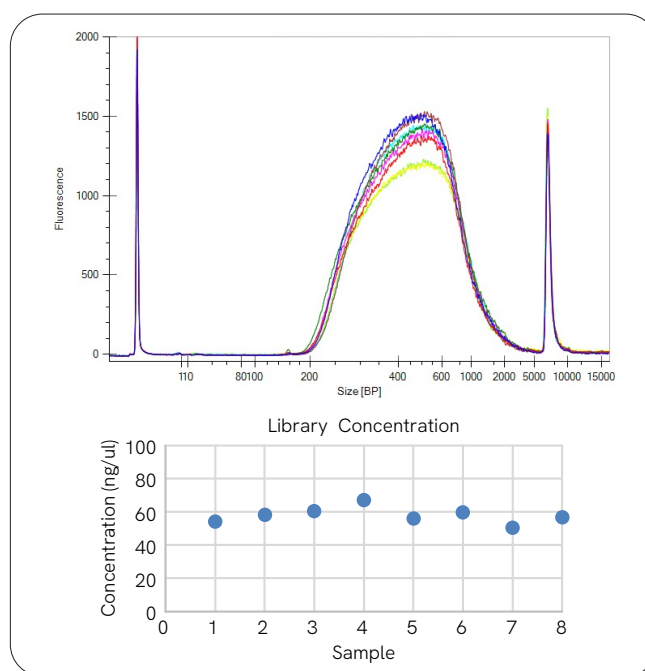
Key Features

- Processes 1–96 samples
- High library complexity and uniform coverage
- 384 Unique Dual Index (UDI) adapters for multiplexing
- DNA input range: 10 ng – 1 µg
- Compatible for various sequencing instruments

Experimental Design

48 Libraries were prepared from Promega G304A using QIAseq® FX DNA Library Kit and UDI Y-Adapter Kit A on the Fontus system. Each sample used 100 ng starting input. Final library concentrations were measured by Qubit HS and library size was evaluated via Revvity lab chip. Final libraries were primer dimer free with yields within the acceptable range. Libraries were normalized to 4nM using QIAseq® Library Normalizer Kit. A random selection of 8 libraries were selected for sequencing on the Illumina® Nextseq 2000 with 2 x 151 bp paired read length. FASTQ files were analyzed with QIAGEN® CLC Genomics Workbench for mapping and quality control of reads.

Results



- Library Quality: 470 ± 20 bp fragments, adapter free
- Median Library quantification: 57.50 ng/ul
- Sequencing Yield: 452.02 Gbp
- Q30 Score: 93.60%
- Reads passing filter: 84.89%
- Median read mapping to reference: 99.12%

Conclusion

The automated workflow using QIAseq® FX DNA Library Kit on the Fontus NGS System delivers high-quality, sequencing-ready libraries, as demonstrated by the experimental results. Libraries showed optimal library profiles, free of adapter dimers with high concentrations. Sequencing metrics further demonstrate robust performance, indicating exceptional accuracy and sensitivity. The data shows consistency that is ideal for scalable whole genome sequencing applications, reducing variability and limiting human error.

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