Labor Cost Comparison between Ion Torrent Genexus Integrated Sequencer and Illumina MiSeq Workflows

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INTRODUCTION

Lab economics play a significant role in selection of a Next Generation Sequencing (NGS) platform for routine use. Outside of consumable costs, important attributes like ease of use, reproducibility of results, and operator hands-on time (HOT) have a direct impact on the overall operating costs of a lab. In this study, we compare labor costs of running equivalent assays on the Thermo Fisher Scientific Genexus Integrated Sequencer and the Illumina MiSeq System.

BACKGROUND

Biomarkers identified by sequencing can play an important role in diagnosis, prognosis and therapeutic selection for different cancers. These biomarkers represent a specific subset of relevant genes, so it is often more cost effective to perform "targeted" sequencing as opposed to whole genome sequencing. AmpliSeq is an amplicon-based library prep technology well suited for routine Oncology testing as it generates targeted sequencing libraries from minimal nucleic acid inputs. The Genexus Integrated Sequencer automates the entire NGS workflow from nucleic acid input to molecular biomarker report using amplicon based library prep. AmpliSeq is also available for Illumina platforms as a manual library prep workflow.

MATERIALS AND METHODS

Five operators with varying levels of experience sequenced eight purified nucleic acid samples on the Genexus Integrated Sequencer. Separately, the same operators prepared libraries from the same samples using the Ampliseq for Illumina workflow and sequenced on the MiSeqTM System. A Thermo Fisher Scientific auditor recorded operator HOT for every step of each respective workflow. Lab technician costs reported from jobs websites Glassdoor and Indeed of ~\$33/hour were then applied to extrapolate, model and compare FTE cost for both the Genexus Integrated Sequencer and Illumina MiSeq workflows.

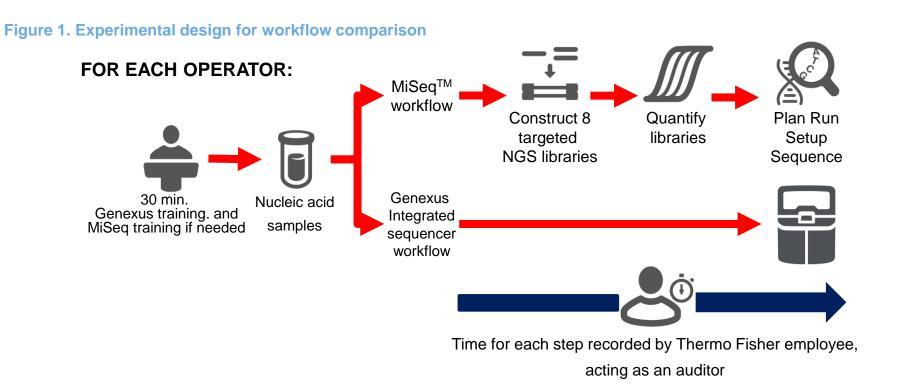
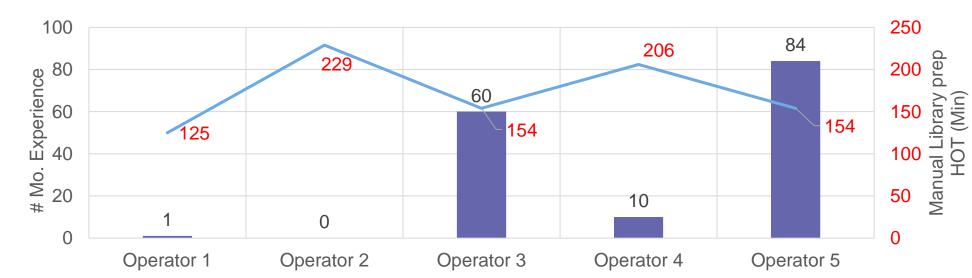
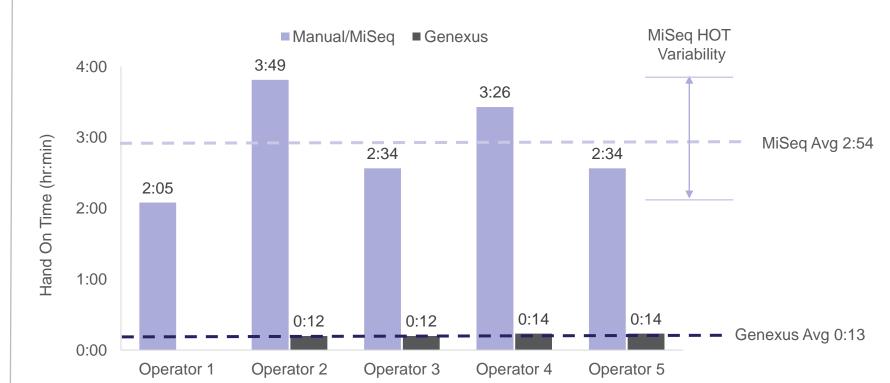


Figure 2. Variation of Operator Experience vs Manual Library Prep Time (minutes)



Results

Figure 3. Measured HOT per operator for each workflow



Operators 2-4 required an average of 13 minutes HOT with a standard deviation of 2 minutes to setup 8 nucleic acid samples on the Genexus Integrated Sequencer (Operator 1 finished internship before they could complete the study).

All five operators required an average of 2 hours 54 minutes to complete the Ampliseq for Illumina workflow with a standard deviation of 43 minutes. Modeled FTE expenses suggests that setting up a sequencing run for 8 samples on the Genexus Integrated Sequencer costs \$7.15 per run, while the equivalent workflow on the Illumina MiSeq costs \$95.70 in operator expense per run.

As the number of runs increases during routine testing, the modeled operator cost savings from using the Genexus Integrated Sequencer over the Illumina MiSeq increases from \$4,605 at 416 samples (1 run of 8 samples per week) to \$23,023 at 2080 samples (5 runs of 8 samples each per week).

Figure 4. Time and Cost Savings using Genexus Integrated Sequencer over Manual Lib Prep on MiSeq System Calculations of work days saved assume 1 sequencing run / day; 52 work days x 33% savings by the Genexus System = 17 work days saved (rounded down). FTE rate selected from Glassdoor and Indeed for USD. 33/hr. Calculations of cost savings = (Δ Cost of MiSeq HOT vs Genexus HOT per Sample) x # of samples

Sample Number	416	832	1248	1664	2080
Operator Hours Saved	139.5	279	418.6	558.1	697.6
Cost Savings	\$4,605	\$9,209	\$13,814	\$18,418	\$23,023

CONCLUSIONS

Use of the Genexus Integrated Sequencer demonstrated 2 hours 41 minutes time savings, or 33% of an 8-hour workday, compared to equivalent manual library preparation upfront of the MiSeq System. The time saved can increase productivity by freeing up operators to perform other tasks in the lab or help reduce headcount and thus reduce lab operational costs. Other considerations for lab efficiency include assay turn around time to result which should be evaluated in future studies.

The low variability in HOT on the Genexus Integrated Sequencer reflects the fewer steps in its setup, making it easy to train inexperienced lab technicians to perform the workflow. The high variability in the HOT for the manual library prep and MiSeq points to more operator steps in the workflow and highlights the need for more highly trained technicians which can increase lab operations costs for training and retention.

TRADEMARKS/LICENSING

Genexus™ and AmpliSeq™ are trademarks of Thermo Fisher Scientific. MiSeq™ is a trademark of Illumina.

References

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