Technical note

Performance evaluation of Olink™ Reveal on Element AVITI™ sequencing systems

Introduction

Accurate and comprehensive protein measurement is essential for understanding biology and disease. Modern proteomics platforms enable high-throughput protein profiling with the sensitivity, specificity, and multiplexing required for translational research.

Olink Reveal leverages Proximity Extension Assay (PEA™) technology to deliver scalable, NGS-based proteomics, measuring approximately 1,000 proteins from just 4 µL of sample.

When sequenced on AVITI or AVITI24™ systems from Element Biosciences™, Olink Reveal can support flexible throughput and efficient library processing while maintaining robust analytical performance. With low run costs and throughput that matches the sequencing requirements of the assay, AVITI Systems are an appealing complement to Olink Reveal.

This technical note evaluates the performance of Olink Reveal libraries when sequenced on the Element AVITI system, including run-to-run reproducibility, per-protein precision, and cross-platform concordance. The evaluation was jointly conducted by Olink and Element.

Methods

A diverse set of plasma samples was processed using Olink Reveal according to the standard protocol. The generated library was sequenced on the Element AVITI system. Sequencing data were processed using NPX™ Map to generate normalized protein expression (NPX) values.

Run-to-run reproducibility was evaluated using pairwise Pearson correlation and linear regression analysis of counts between three independent Element AVITI sequencing runs.

Precision was assessed by calculating the coefficient of variation (CV) across three independent sequencing runs.

For cross-platform comparison, the library was sequenced in triplicate on both the Element AVITI system and the Illumina™ NextSeq™ 2000 system.

Results

High run-to-run reproducibility on Element AVITI systems

Pairwise linear regression analyses between three independent Element AVITI sequencing runs showed slopes close to 1.0 and strong concordance across all measured proteins (Figure 1), indicating high agreement between sequencing runs with no observable systematic bias.

Consistent per-protein precision

Analysis of per-protein CV distributions showed tightly distributed

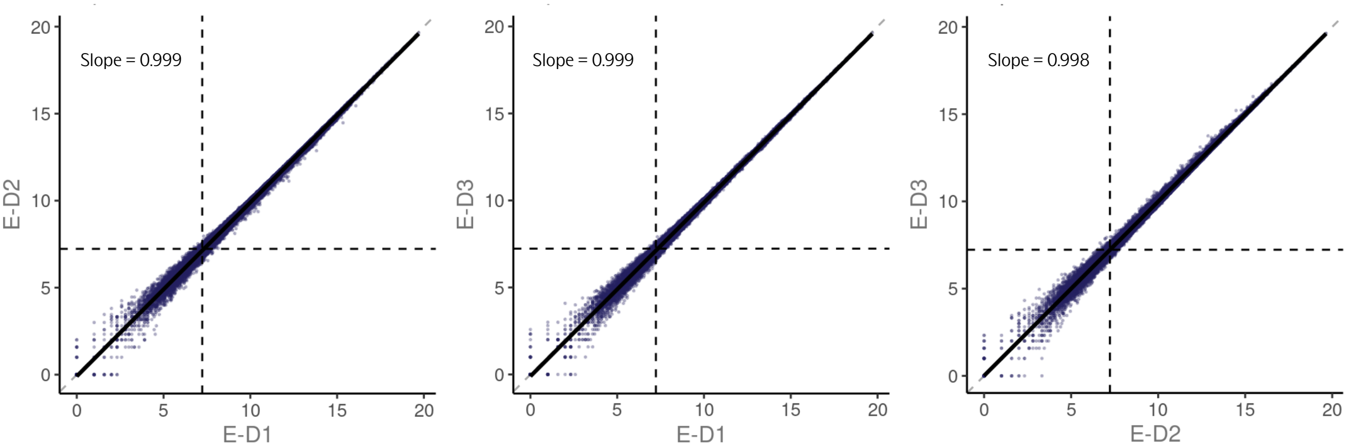

Figure 1. Pairwise comparisons of log2-transformed counts from three independent Element AVITI sequencing runs. Each point represents a measured protein. Linear regression analysis shows slopes close to 1.0, demonstrating strong agreement between runs and minimal proportional variation.

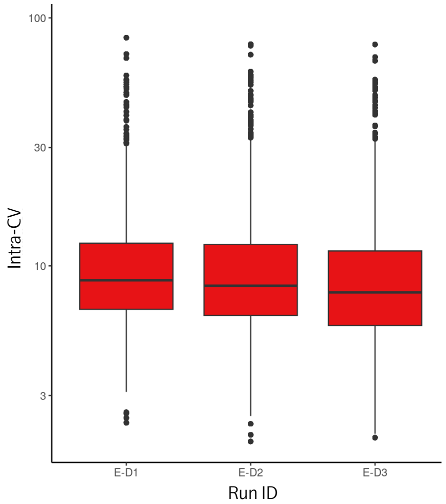

Figure 2. Distribution of intra-protein CV values calculated across three independent Element AVITI sequencing runs. Box plots show CVs derived from NPX values, and the tightly distributed CVs indicate consistent technical performance across sequencing runs. The y-axis is displayed on a log scale.

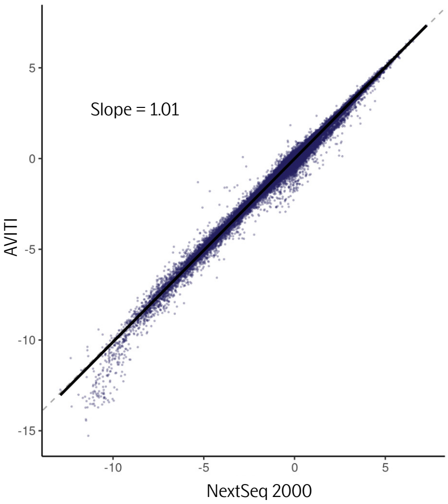

Figure 3. Cross-platform concordance of Olink Reveal libraries sequenced on the Element AVITI system and the Illumina NextSeq 2000 system. Strong agreement is demonstrated by a high median per-protein correlation (R = 0.985) on the NPX scale, indicating strong cross-platform concordance. Linear regression analysis shows a slope close to 1.0, further supporting concordance between platforms.

variability across sequencing runs (Figure 2), demonstrating low technical variation.

Strong cross-platform concordance with Illumina sequencing

Comparison of libraries sequenced on Element AVITI and Illumina NextSeq 2000 demonstrated high correlation of NPX values across all measured proteins (Figure 3). These results support cross-platform agreement and demonstrate compatibility of Olink Reveal libraries across sequencing technologies.

Conclusion

Element AVITI and AVITI24 systems provide reliable and reproducible sequencing solutions for Olink Reveal. Strong run-to-run reproducibility, stable per-protein precision, and high concordance with Illumina sequencing demonstrate robust analytical performance and support confident implementation of AVITI for sequencing Olink Reveal libraries. With dual independent flow cells, each producing throughput well-matched to Olink Reveal sequencing recommendations, AVITI systems create operational flexibility at a low cost per read.

Together, Olink Reveal and Element AVITI systems offer a flexible and cost-effective solution for scalable, high-quality NGS-based proteomic analysis.

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