

RELIABLE CALLING BY ARCHER™ ASSAYS SEQUENCED WITH THE AVITI™ SYSTEM

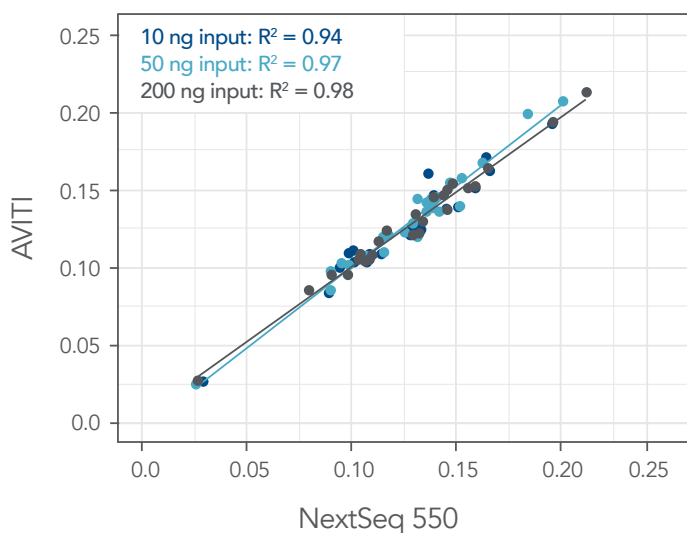
Determining reliable calling and comparable metrics

- To determine reliability of variant and fusion calling with Archer assays on the recently-released AVITI platform from Element Biosciences, nucleic acid isolated from SeraCare reference materials was prepared for sequencing with small to large VARIANTPlex™ and FUSIONPlex™ library prep panels and data was analyzed with Archer Analysis.
- VARIANTPlex panels and inputs analyzed were Core Myeloid—50 ng; Core Solid Tumor—10 ng, 50 ng, 200 ng; Solid Tumor Focus v2—50 ng, 200 ng; Complete Solid Tumor—50 ng. FUSIONPlex panels and inputs analyzed were Pan Solid Tumor—10 ng, 50 ng, 200 ng; Lung v2—10 ng, 50 ng, 200 ng; Heme v2—50 ng. Libraries were sequenced with the AVITI and compared to those sequenced on the Illumina® NextSeq 550.

Reliable variant and fusion detection calling with highly correlated key metrics

- All variants (97/97) and fusions (43/43) present in reference materials were detected by Archer assays sequenced with the AVITI system across all VARIANTPlex and FUSIONPlex panels tested, including at low input quantities (10 ng).
- Key metric values (allelic frequency and variant depth for VARIANTPlex panels, fusion supporting reads and start sites for FUSIONPlex) for libraries sequenced with the AVITI were highly correlated with the same libraries sequenced on the Illumina® NextSeq 550, with R^2 values ranging from 0.92–1.

A. Allele frequency



B. Fusion supporting reads

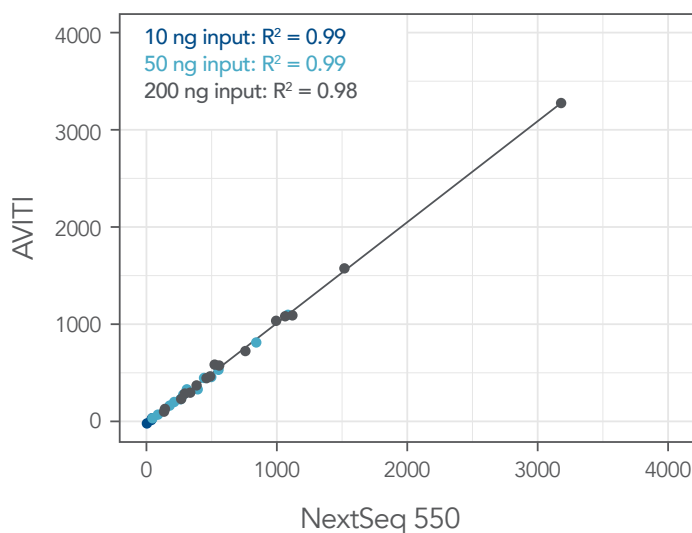


Figure 1. Correlation of allele frequency for samples analyzed with VARIANTPlex Core Solid Tumor (A) and correlation of fusion supporting reads for samples analyzed with FUSIONPlex Pan Solid Tumor (B). Input materials and corresponding R^2 values demonstrate the high correlation of these metrics between libraries sequenced by the AVITI and the NextSeq 550.

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