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 VARIANT*Plex*™ and FUSION*Plex*™ library prep panels and data was analyzed with Archer Analysis.
- VARIANT*Plex* 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. FUSION*Plex* 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 VARIANT*Plex* and FUSION*Plex* panels tested, including at low input quantities (10 ng).
- Key metric values (allelic frequency and variant depth for VARIANT*Plex* panels, fusion supporting reads and start sites for FUSION*Plex*) 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.

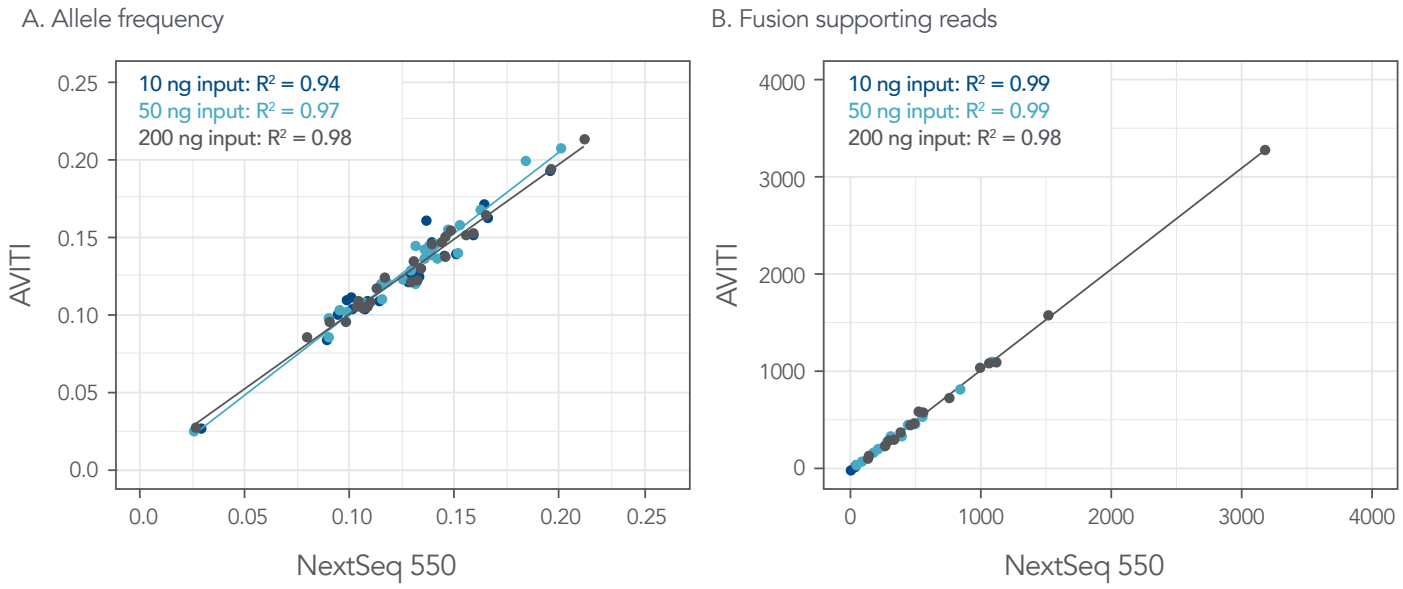

Figure 1. Correlation of allele frequency for samples analyzed with VARIANT*Plex* Core Solid Tumor (A) and correlation of fusion supporting reads for samples analyzed with FUSION*Plex* Pan Solid Tumor (B). Input materials and corresponding R^2 values demonstrate the high correlation of these metrics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

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