COMPARATIVE ANALYSIS OF IMMUNOID NEXT™ AND ACE IMMUNOID™ NEXT GENERATION SEQUENCING PLATFORMS FOR INVESTIGATING TUMOR-IMMUNE INTERACTIONS TO ENABLE PRECISION ONCOLOGY DRIVEN BIOMARKER DISCOVERY

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Background ImmunoID NeXT is a comprehensive enhanced whole exome and whole transcriptome scale platform, that provides a multidimensional view of the molecular tumor microenvironment from a single tumor sample with augmented coverage and specific targeting.¹ As ImmunoID NeXT is based on Accuracy and Content Enhanced (ACE) technology to further supplement gaps in all 20,000 human genes and target unique genomic regions for immuno-oncology, we assessed key sequencing metrics between the platforms to assure smooth platform migration.

Methods Fifteen FFPE samples from late-stage, treatment-naive colorectal cancer patients were processed on both ACE ImmunoID and ImmunoID NeXT platforms. Specimens were evaluated using the same input criteria including the minimum 4 unstained slides per FFPE sample with 5–10 micro-meter thick sections, 25mm² surface area each section, ≥ 20% tumor content. ACE ImmunoID sequencing was performed using ACE enrichment including library preparation and 2x150bp sequencing on the NovaSeq. Whereas, ImmunoID NeXT exome sequencing was performed using NeXT enrichment including library preparation and 2x150bp sequencing on the NovaSeq. We assessed the concordance of the assays in overlapping features with respect to sequencing quality metrics, somatic variant calling, tumor mutational burden, and gene expression. Tumor mutation burden (TMB) from the two platforms was re-computed to align with the FOCR guidelines, counting exome-wide non-synonymous somatic variants over the coding sequence footprint of each assay.

Results The sequencing average base quality (Q score) is equivalent (exome-Seq: NeXT = 36.17 vs. ACE = 36.02; Transcriptome-Seq: NeXT = 35.79 vs. ACE = 35.90;) and alignment coverage consistent with the platform design. To look at somatic variant concordance, the ACE ImmunoID and ImmunoID NeXT .bed files were intersected, and the analysis was focused on the overlapping target region. The following filters were applied to the variants detected with ACE ImmunoID: allelic frequency of >10%, read depth of >50, and a population frequency filter where any variant over 1% was excluded. The same population frequency filter was also applied to variants detected with ImmunoID NeXT. We observed a concordance of 89–98% in high confidence calls between the two platforms. Focused on the overlapping coding region in the intersection of ACE and NeXT, the consistent TMB results were achieved with both platforms.

Conclusions It is demonstrated that both ImmunoID NeXT and ACE ImmunoID are high-performance platforms with consistently strong sequencing QC metrics. Collectively, ImmunoID NeXT, as the universal cancer immunogenomics platform, could provide end-to-end solution for immune/precision oncology clinical biomarker discovery.

REFERENCES

1. Zheng Feng, Danyi Wang, Mengyao Tan, Juergen Scheuenpflug. Whole-exome sequencing based immunogenomic profiling with potential clinical applicability in circulating cell-free DNA and tissue from advanced stage colorectal cancer patients [abstract]. In: Proceeding of the Annual Meeting of the Society for

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Ethics Approval The study protocol was in accordance with the tenets of the Declaration of Helsinki. Commercial samples used in this study were procured from BioIVT and BioChain following protocols approved by the local Institutional Review Board (IRB) committee. Informed consent forms were obtained from all the human subjects in this study.

Consent Written informed consent was obtained from the patient for publication of this abstract and any accompanying images. A copy of the written consent is available for review by the Editor of this journal.

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