Comparative evaluation of MGI DNBSEQ-E25 and Illumina MiSeq for HIV-1 genomic surveillance using QCMD Panels

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Introduction

Next-generation sequencing (NGS) platforms are increasingly central to HIV-1 drug resistance monitoring and minority variant detection. While Illumina MiSeq remains the reference standard in clinical genomics, alternative platforms such as MGI DNBSEQ-E25 emerge as cost-competitive options. However, their comparative performance for HIV-1 genomic surveillance under standardized conditions has not been systematically evaluated. We aimed to compare sequencing performance, coverage depth, and resistance mutation detection between MGI DNBSEQ-E25 and Illumina MiSeq using standardized HIV-1 QCMD panels processed through a unified DeepChek® workflow.

Methods

HIV-1 QCMD panel samples were amplified and sequencing libraries constructed using DeepChek® HIV kits (ABL Diagnostics), followed by parallel sequencing on MGI DNBSEQ-E25 and Illumina MiSeq. Raw FastQ files were analysed with MicrobioChek® software (ABL) for quality control, reference mapping, and mutation calling across protease, reverse transcriptase, and integrase regions. Performance metrics included mapping rate, mean sequencing depth, and concordance of resistance-associated mutation profiles.

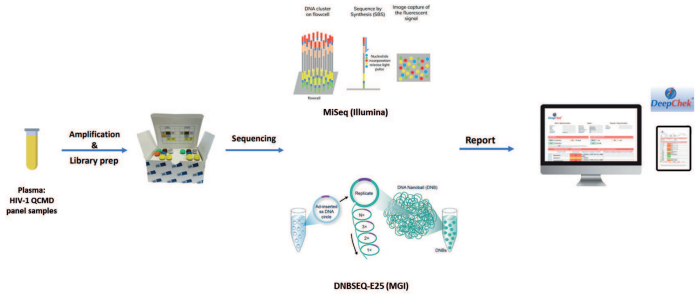

Figure 1. Standardized DeepChek® workflow applied to HIV-1 QCMD panels on MiSeq and MGI DNBSEQ-E25

Results

Both platforms achieved high mapping rates (>80%), confirming robust read quality across all samples. MiSeq showed marginally higher alignment accuracy (mean mapping rate: 82.6% vs. 82.1%), while MGI DNBSEQ-E25 delivered significantly greater sequencing depth (~113,000 vs. ~95,000 reads per sample), enhancing sensitivity for minority variant detection. Resistance mutation profiles were highly concordant for major markers (M46I, I54V, V82A, M184V, G190A). MGI DNBSEQ-E25 additionally detected low-frequency substitutions below the 10% allele frequency threshold in pooled samples, not consistently identified on MiSeq.

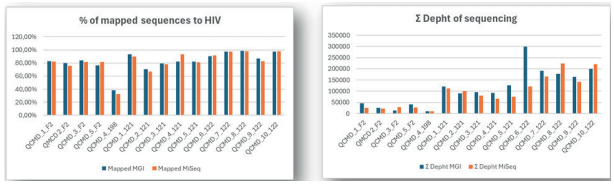

Figure 2. Sequencing performance comparison of MiSeq and DNBSEQ-E25 on HIV-1 QCMD samples

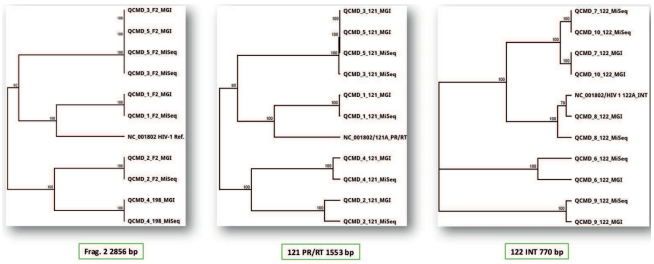

Figure 3. High phylogenetic concordance between MiSeq and DNBSEQ-E25 across HIV-1 genomic regions

Conclusions

MGI DNBSEQ-E25 and Illumina MiSeq deliver comparable performance for routine HIV-1 genomic surveillance when combined with the DeepChek® workflow. MGI DNBSEQ-E25 offers a specific advantage for minority variant detection owing to its higher sequencing depth, while MiSeq retains a marginal edge in mapping accuracy. These findings provide a practical basis for informed platform selection in clinical and public health HIV surveillance settings.