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Comparative Analysis of Essential NGS Panel Data on MGI DNBSEQ-G50 and NextSeq 550

Abstract

This white paper presents comparative analysis of the AmoyDx® Essential NGS Panel on two major sequencing platforms: MGI DNBSEQ-G50 (MGI G50) and Illumina NextSeq 550. The study analysed 32 FFPE DNA samples and 22 cfDNA samples to assess sequencing quality, as well as SNV/InDel, gene fusion, CNV (FFPE DNA only) detection performance. The findings confirm that the MGI G50 platform demonstrates accuracy and reliability comparable to the NextSeq 550 making it an alternative sequencer for the Essential NGS Panel mutation analysis in clinical diagnosis.

Introduction

Lung cancer, mainly non-small cell lung cancer (NSCLC) often involves driver mutations in genes like EGFR, KRAS, and ALK, influencing targeted therapy outcomes. Similarly, colorectal cancer (CRC) frequently harbors KRAS, NRAS, PIK3CA, and BRAF mutations, affecting responses to anti-EGFR treatments. Clinical guidelines recommend multi-gene testing to guide precision oncology.

The AmoyDx® Essential NGS Panel is designed for qualitative detection of common mutations in 10 key solid tumor genes, and has been optimized for use on the Illumina sequencing platforms including NextSeq 550. With the growing demand for more flexible and efficient sequencing options, this study aims to validate the performance of AmoyDx® Essential NGS Panel on the MGI G50 platform. By comparing key performance metrics between the two platforms including sequencing quality, mutation detection and CNV consistency, this white paper explores the potential for expanding the use of AmoyDx® Essential NGS Panel beyond Illumina systems to the MGI G50 platform.

Methodology

1. Sample Collection

In total 32 FFPE DNA samples and 22 cfDNA samples were used for performance testing of the MGI G50 & Nextseq 550 in this report.

1) FFPE DNA Samples:

- 20 clinical FFPE DNA samples with negative results within the detection range of the kit;
- 8 clinical FFPE DNA samples with known mid-positive variants, including 4 SNVs, 3 InDels, 1 fusion and 1 CNV in 7 genes (*KRAS, PIK3CA, EGFR, ERBB2, MET, ALK, RET*).
- 4 reference DNA samples with known low-positive variants, including 32 SNVs, 7 InDels, and 3 fusions in 9 genes (*EGFR, MET, ROS1, RET, PIK3CA, BRAF, KRAS, NRAS, ALK*).

2) cfDNA Samples:

- 20 clinical cfDNA samples with negative results within the detection range of the kit;
- 2 commercial cfDNA reference samples with multiple SNV/InDel/fusion variants, including 14 SNVs, 4 InDels and 2 fusions in 7 genes (*PIK3CA, EGFR, BRAF, ROS1, ALK, NRAS* and *KRAS*).

2. Extraction & Library Preparation

FFPE DNA and cfDNA extraction was conducted using the AmoyDx® DNA/RNA Extraction Kit and AmoyDx® Circulating DNA Kit. Library preparation was performed according to the AmoyDx® Essential NGS Panel protocol. Sequencing was carried out on both the MGI G50 and NextSeq 550 platforms for comparative analysis.

3. Data Processing and Analysis

Variant calling was conducted using the ADXLC10 module. Key metrics including quality control parameters, sequencing depth and variant frequency were evaluated to assess performance.

Results

Sequencing Performance Comparison

Metric FFPE DNA	MGI G50	NextSeq 550
Sequencing Quality (Q30)	≥75%	≥75%
Coverage	≥ 98%	≥ 98%
MeanDepth	≥ 10000×	≥ 10000×
SSBCDepth	≥ 500×	≥ 500×

Metric Plasma cfDNA	MGI G50	NextSeq 550
Sequencing Quality (Q30)	≥75%	≥75%
Coverage	≥ 98%	≥ 98%
MeanDepth	≥ 10000×	≥ 10000×
SSBCDepth	≥ 1500×	≥ 1500×

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FFPE DNA

Comparison and Statistical Analysis of Illumina NextSeq 550 and MGI G50 Platforms for FFPE DNA SNV/INDEL/Fusion/CNV Detection

MGI G50	Illumina NextSeq 550		Total	Positive percent agreement (PPA)	Negative percent agreement (NPA)	Overall percent agreement (OPA)
	Positive	Negative				
Positive	12	0	12	100%	100%	100%
Negative	0	20	20			
Total	12	20	32			

Plasma cfDNA

Comparison and Statistical Analysis of Illumina NextSeq 550 and MGI G50 Platforms for Plasma cfDNA SNV/INDEL/Fusion Detection

MGI G50	Illumina NextSeq 550		Total	Positive percent agreement (PPA)	Negative percent agreement (NPA)	Overall percent agreement (OPA)
	Positive	Negative				
Positive	2	0	2	100%	100%	100%
Negative	0	20	20			
Total	2	20	22			

Discussion

The comparative analysis highlights several key findings:

Sequencing Quality:

Both platforms demonstrated high sequencing quality, with Q30 values exceeding 75%. The coverage of the FFPE DNA samples is 100%; MeanDepth＞10000×; SSBCDepth＞500×, and the coverage of the plasma cfDNA samples is 100%; MeanDepth＞10000×; SSBCDepth＞1500×. This indicates that both the MGI G50 and NextSeq 550 can generate accurate sequencing data suitable for clinical analysis. The consistency in Q30 values between the platforms suggests comparable base-calling accuracy, reinforcing the reliability of the MGI G50 for mutation detection within the target region of the 10 key solid tumor genes from the AmoyDx® Essential NGS Panel.

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Detection Performance:

Both platforms achieved a 100% detection rate for single nucleotide variants (SNVs) and insertions/deletions (InDels), gene fusions, MET copy number variation (CNV). The overall percent agreement (OPA) was 100%, with a positive percent agreement (PPA) of 100%, a negative percent agreement (NPA) of 100% These data confirm the high accuracy and consistency of the MGI G50 platform in mutation detection and MSI detection, positioning it as a reliable alternative to the NextSeq 550.

Conclusion

The study confirms that the AmoyDx® Essential NGS Panel performs exceptionally well on both MGI G50 and NextSeq 550 platforms. The MGI G50 demonstrated superior sequencing quality and depth while maintaining comparable accuracy, mutation frequency detection, and detection performance. These findings validate MGI G50 as a robust and reliable platform for detecting the target region of the 10 key solid tumor genes from the panel in both clinical and research applications.