

Customer feedback on products

Product Name: KAPA Library Amplification Kit (KK2611, KK2612)

Manufacturer : KAPA BIOSYSTEMS

Application : Effective sequencing of long amplicons containing AT-rich

regions targeting the PMS2 gene

(one of the genes responsible for hereditary colorectal cancer)

The following data were provided by the courtesy of Dr. Gou Yamamoto, Dr. Miho Kakuta and Dr. Kiwamu Akagi at Division of Molecular Diagnosis and Cancer Prevention, Saitama Cancer Center, Japan.

Experimental method

The problem in sequencing long amplicons targeting the PMS2 gene (one of the genes responsible for hereditary colorectal cancer) was the low coverage resulting from fewer reads particularly in the AT-rich regions due to library amplification bias. Here, in the "tagmented library prepared from long amplicons by Nextera XT" prepared by the current method, we attempted to solve the above problem by amplifying the library using KAPA Library Amplification Kit (KAPA HiFi HotStart ReadyMix).

■ Workflow Human genomic DNA PCR amplification of the target region: 3 kb to18 kb 5µl of input DNA at 0.2 ng/µl to 0.075 ng/µl was added, depending on the amplicon size Nextera XT DNA Sample Prep kit library preparation Library amplification Library amplification by KAPA Library by the current method Amplification kit* Next-generation sequencer illumina社 MiSeq Data analysis and visualization **CLC Genomics Workbench**

* Library amplification by KAPA Library Amplification Kit

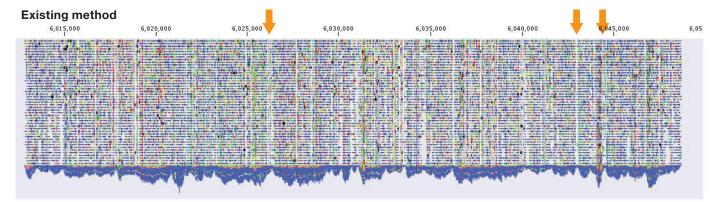
- ① After performing neutralization in the tagmentation step, 50µl (twice the volume of the reaction) of AMPureXP was added to 25µl of reaction, and cleanup was performed (washing twice with 80% ethanol)
- 2 Elution was carried out with 15µl of 10 mM Tris-HCl (pH 8) or PCR-grade water
- 3 Library amplification was performed under the following conditions

Reaction composition

	50ul RXN	
Library DNA	15µL	
Index 2 primer	5µL	
Index 1 primer	5µL	
2×KAPA HiFi HS ReadyMix	25µL	

PCR cycle

i Oil Oyolo			
Initial Extension	72°C	3min	
Denaturation	98℃	30sec	
Denaturation	98℃	10sec -	٦
Annealing	63°C	30sec	14cycles
Extension	72°C	3min -	J
Hold	10℃		

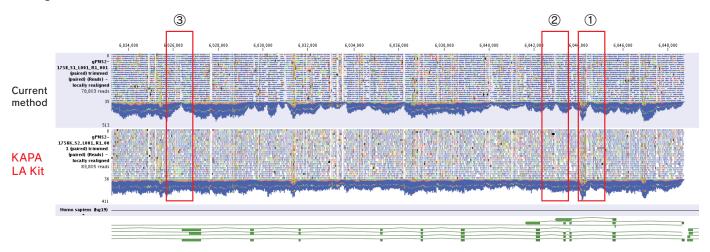


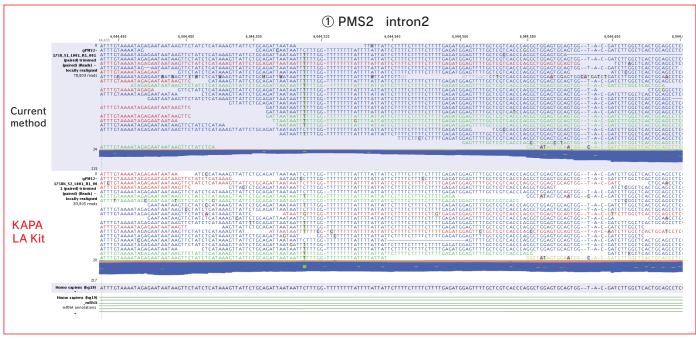
Sequencing results of long amplicons targeting the PMS2 gene Fewer reads in AT-rich regions (e.g. regions indicated by arrows) resulted in low coverage.

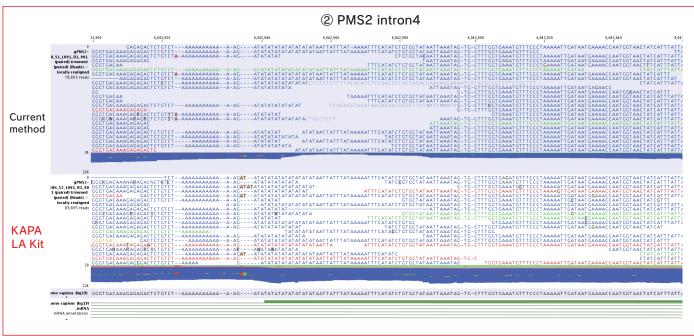


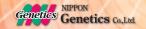
Results

Libraries amplified using KAPA Library Amplification (LA) Kit showed improved coverage in AT-rich regions, resulting in more uniform coverage.

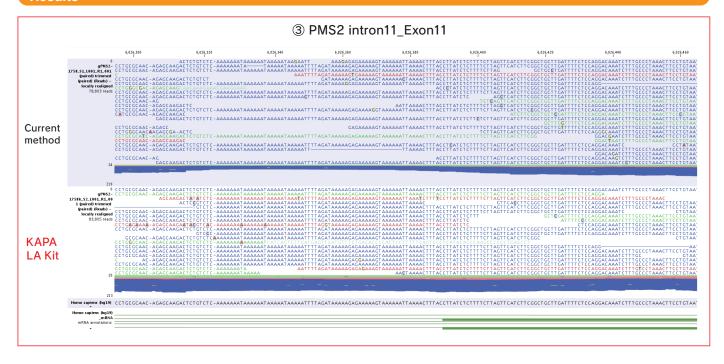








Results



The use of KAPA LA Kit also resulted in improvement of coverage in libraries amplified from a different sample (sample B at bottom).

PMS2 Exon1_Exon11

Sample A Current method **KAPA** LA Kit Sample B Current method **KAPA** LA Kit

<Customer's comments>

There was a substantial improvement in the results when using the KAPA Library Amplification Kit (KAPA HiFi HotStart ReadyMix) for amplification of AT-rich sequences.