

NGS 討論會

KAPA 文庫製備介紹

NGS 討論會申請專線

02-2758-5928



只要 30 分鐘

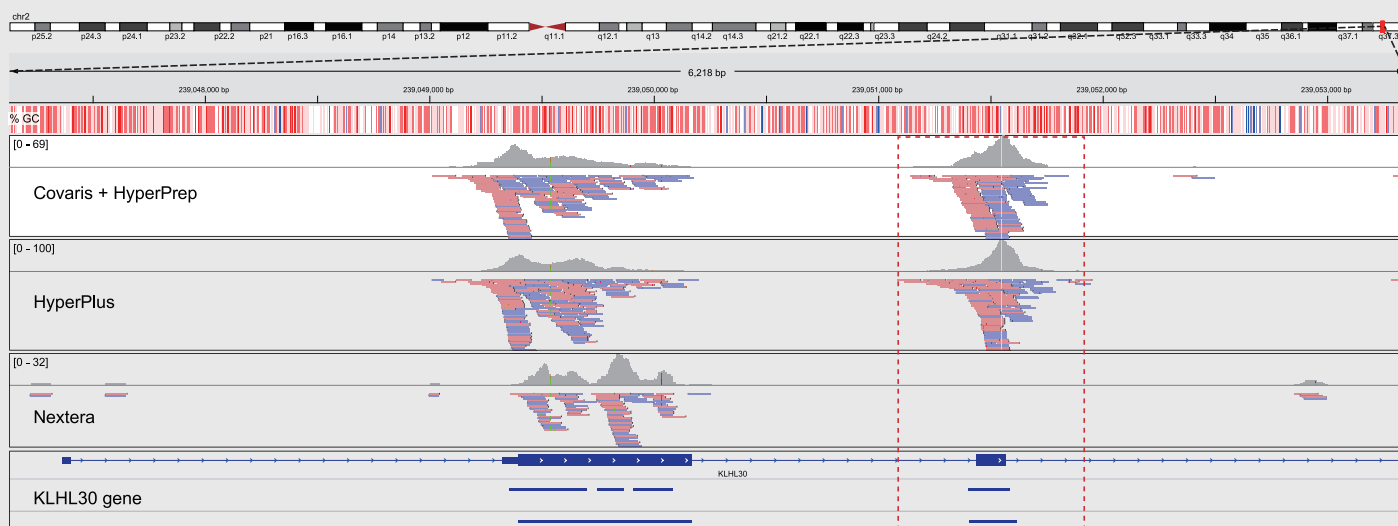
提供 NGS 實驗更好的選擇！

特定細菌基因組
無法定序？

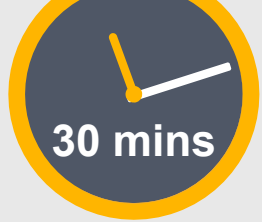
某些片段
無法定序？

KAPA NGS Library Preparation Kit

Superior coverage uniformity and improved coverage of "difficult" regions



Thirty million reads from each library were aligned to the hg19 reference sequencing, using BWA. The Integrative Genomics Viewer (IGV) was used to visualize reads aligning in the 5' region of the human KLHL30 gene, which includes exons 1 and 2. Vertical lines depict the genomic GC content in a 20 bp sliding window (red = high %GC and blue = low %GC). Libraries were prepared from Covaris-sheared or enzymatically fragmented DNA. The KAPA HyperPrep chemistry exhibits good coverage in this GC-rich region. The Nextera data displays less uniform coverage of exon 1 and has no coverage for exon 2 (outlined in red), which contains a SNP of interest (yellow vertical line). Lower coverage uniformity requires more sequencing to cover all targets to the requisite depth, whereas gaps in coverage may have to be filled with alternative methodologies to obtain data for all variants of interest.



只要 **30** 分鐘 提供 **NGS** 實驗更好的選擇！

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空前優惠價 / 再送超值好禮

1



KAPA HyperPlus 24 rxns (07962401001) \$ 52,000

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KAPA mRNA Hyper Prep 24 rxns (08098115702) \$ 55,000

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6



KAPA mRNA HyperPlus 96 rxns (08098123702) \$ 188,000

KAPA Dual Indexed Adapter (15 μ M) 96 rxns (08278555702-2)

即日起至 2018 12 月底止



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