

Roche

# Roche KAPA HyperCap Workflow v3.0

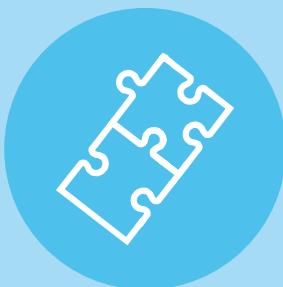
提供完整且高效率的建庫流程



## KAPA HyperExome

- 每反應探針捕捉高達 200 萬條
- 醫學相關資料庫皆有高覆蓋率 (CCDS, RefSeq, Ensembl, GENCODE, ClinVar...)
- KAPA HyperExome probe 僅 ~43Mb，減少定序分析時間及花費
- 實驗結果信賴度高

套組優惠方案實施中 請洽當區業務



## Custom Design

- 提供客製化探針設計 -HyperDesign 網站
- 原廠專家協助客製化 probe
- 網頁操作最直觀
- 影片教學輕鬆上傳資料

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**KAPA HyperExome**

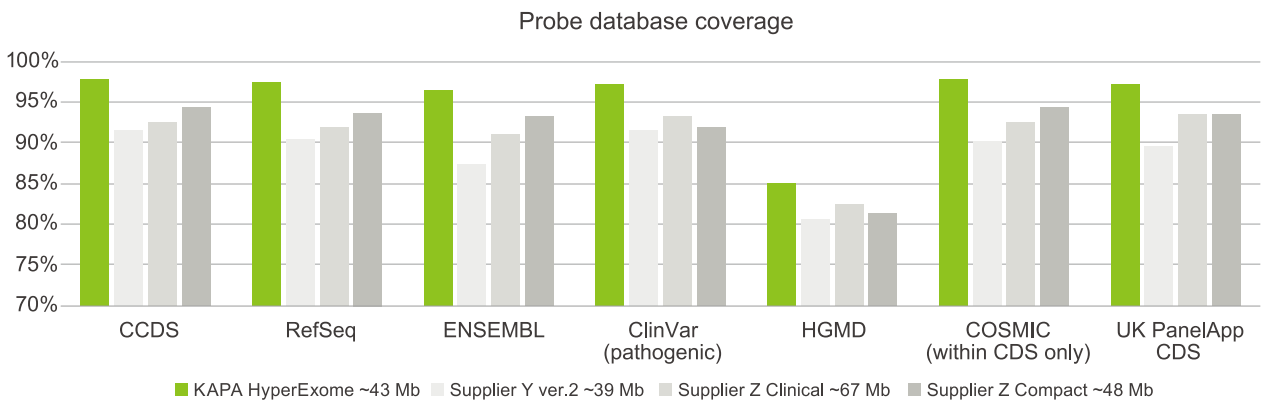




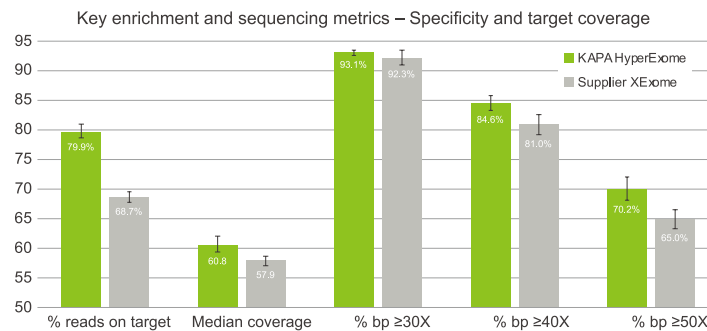
# Roche KAPA HyperExome Probes

精簡化的全外顯子 panel，減少測序成本、加入 SNP 探針建立樣本追蹤體系。捕獲區域為 ~ 43Mb，基於 GRCh38/ hg38 人類參考基因組並於多個資料庫 (CCDS、RefSeq...) 皆有高覆蓋度，提供更優異的 On-target rate 和覆蓋均一性。

## 覆蓋率在不同的資料庫中皆高於他牌



## 提供更優異的 On-target rate 不同深度皆有良好覆蓋率



客戶好評心得分享  
新竹 生物資訊公司

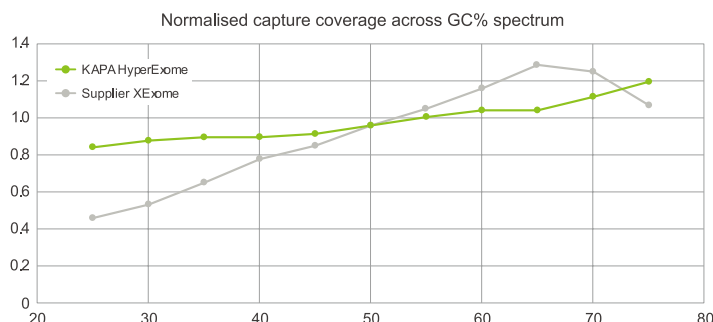
使用 KAPA HyperExome Probes 及 HyperCap Workflow v3.0 配套試劑進行建庫和外顯子基因擴增，分析數據結果平均覆蓋度及均勻度，皆優於其他品牌。



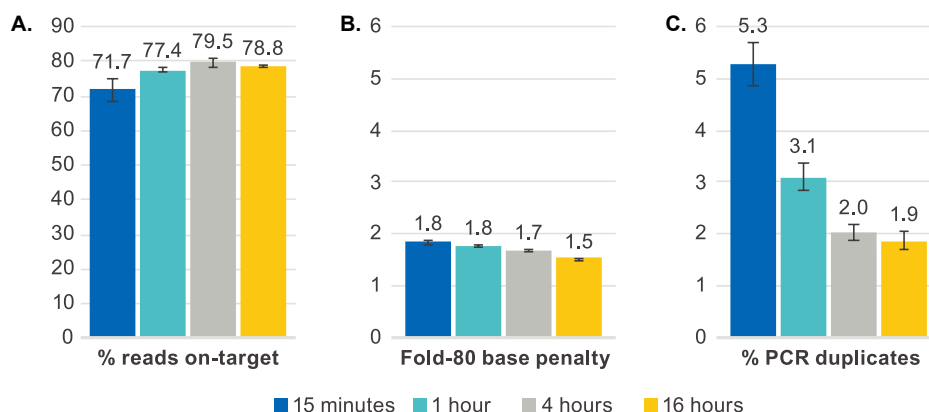


# Roche KAPA HyperExome Probes

覆蓋均一度佳，不因 GC bias 影響



雜合效率高，約 1 小時雜合即可達到和 O/N 相當的效果



Shorter hybridization times have minimal impact on capture efficiency but can affect library complexity.

(A) The percent of on-target reads refers to the percent of mapped, non-duplicate reads overlapping a target region by at least 1 base.

(B) Coverage uniformity expressed as fold-80 base penalty.

(C) Percent of duplicate reads, associated to the library complexity. Bars represent the mean from triplicate libraries and error bars indicate the standard deviation.

## 套組優惠方案實施中 請洽當區業務

192 samples

### KAPA HyperExome Prep Kit

人類外顯子套組

須另外加購 KAPA UDI Primer Mix  
(Rxn size : 96)

套組試劑及所含數量	Rxn size	數量
KAPA Hyper Prep (96rxn)	96	2
KAPA Universal Adapter, 15uM 960 uL	96	2
KAPA HyperPure Beads (5 mL)	5 mL	1
KAPA HyperPure Beads (30 mL)	30 mL	1
KAPA HyperExome, 24 rxn	24	1
KAPA Probes resuspension buffer, 1 mL	1 mL	1
KAPA HyperCapture Reagent kit, 24 rxn	24	1
KAPA HyperCapture Bead kit, 24 rxn	24	1

192 samples

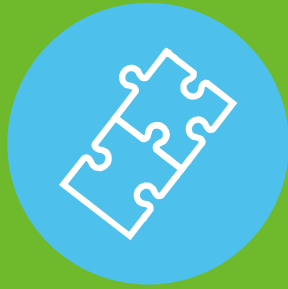
### KAPA HyperExome Plus Kit

人類外顯子套組

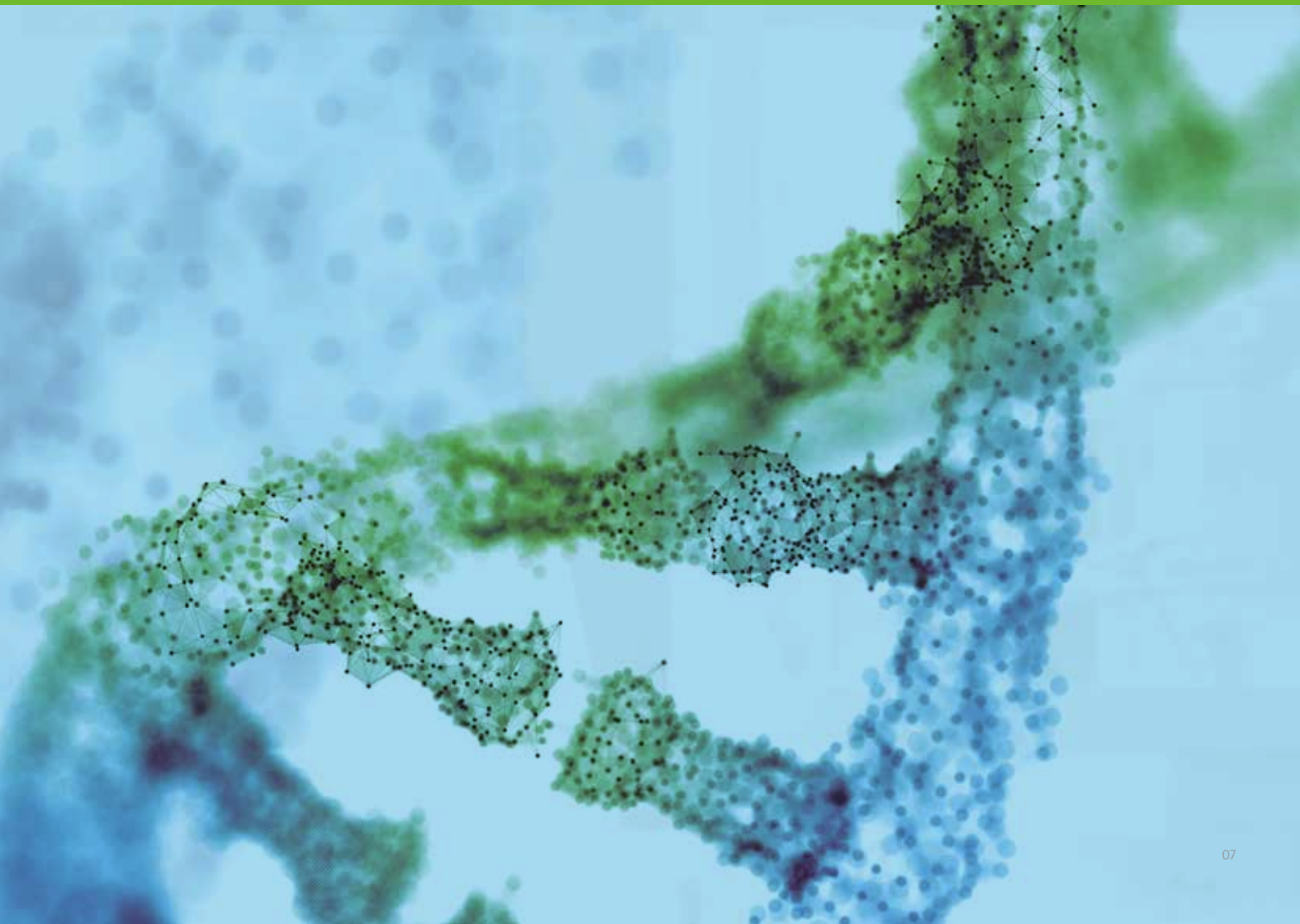
須另外加購 KAPA UDI Primer Mix  
(Rxn size : 96)

套組試劑及所含數量	Rxn size	數量
KAPA Hyper Plus (96rxn)	96	2
KAPA Universal Adapter, 15uM 960 uL	96	2
KAPA HyperPure Beads (5 mL)	5 mL	1
KAPA HyperPure Beads (30 mL)	30 mL	1
KAPA HyperExome, 24 rxn	24	1
KAPA Probes resuspension buffer, 1 mL	1 mL	1
KAPA HyperCapture Reagent kit, 24 rxn	24	1
KAPA HyperCapture Bead kit, 24 rxn	24	1

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Custom Design





# Roche KAPA HyperChoice and KAPA HyperExplore custom designs

- 提供 hyperdesign 網站，針對感興趣基因設計客製化探針
- 人類基因組及非人類基因組皆可設計捕捉高達 200Mb 的目標基因
- 高均勻度地抓取目標片段，提升定序精準度

HyperDesign

## 4 個步驟輕鬆設計客製化探針

1. 進入 HyperDesign 網站 (<https://hyperdesign.com/>)
2. 選擇您有興趣的物種
3. 加入目標基因資訊，方法任選
  - 直接輸入 Gene ID 或 Genomic coordinates
  - 上傳檔案，如：TXT.BED.FASTA 檔
  - 提供連結，如：NCBI 網頁
4. 提交資料，由專家為您設計



相同定序量中可得到更完整的資訊，增加經濟效益

### Performance of two KAPA HyperChoice designs

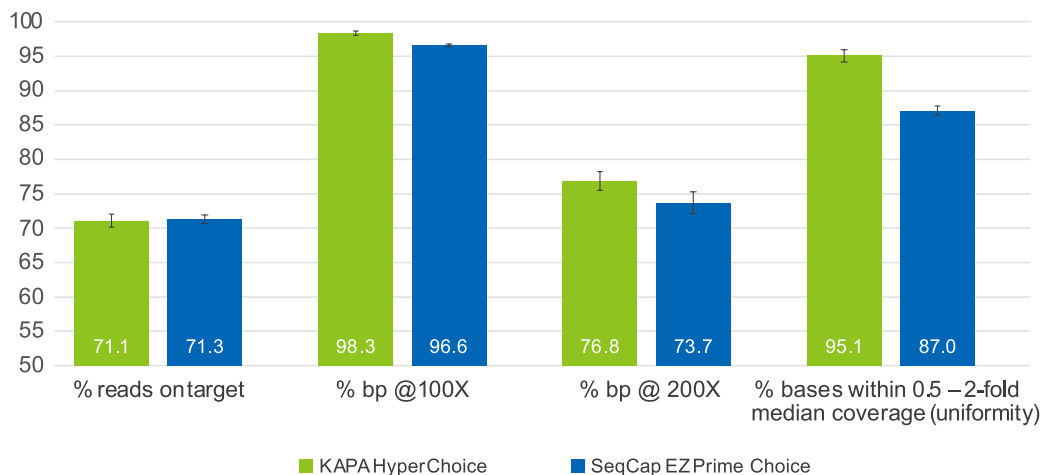
PCR duplication rate 低

覆蓋均一度佳

Design	Genes	Target size (capture)	HQ reads	System	% total duplicates	Fold 80 (uniformity)	% of bases $\geq 30X$
Neurodegenerative	>98	335 Kb	1,75 M	NovaSeq6000	2.78	1,38	99.83
Hereditary disease	>4100	12.3 Mb	20.00 M	NovaSeq6000	1,62	1,43	97.22

新一代客製化探針提供更優秀的覆蓋均一度

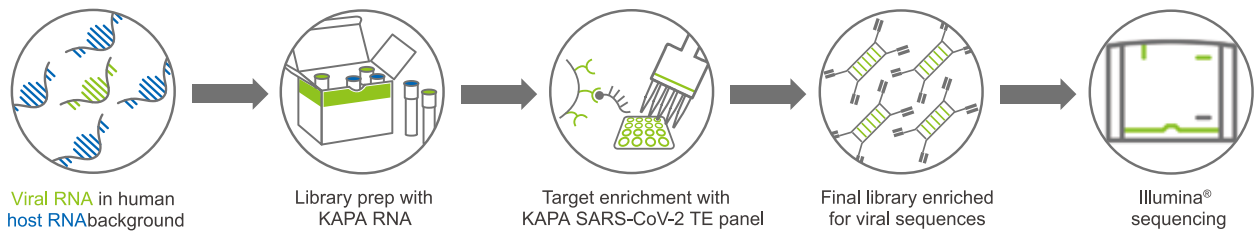
### Specificity and Uniformity deliver better target coverage



# Roche KAPA SARS-CoV-2 TE panel

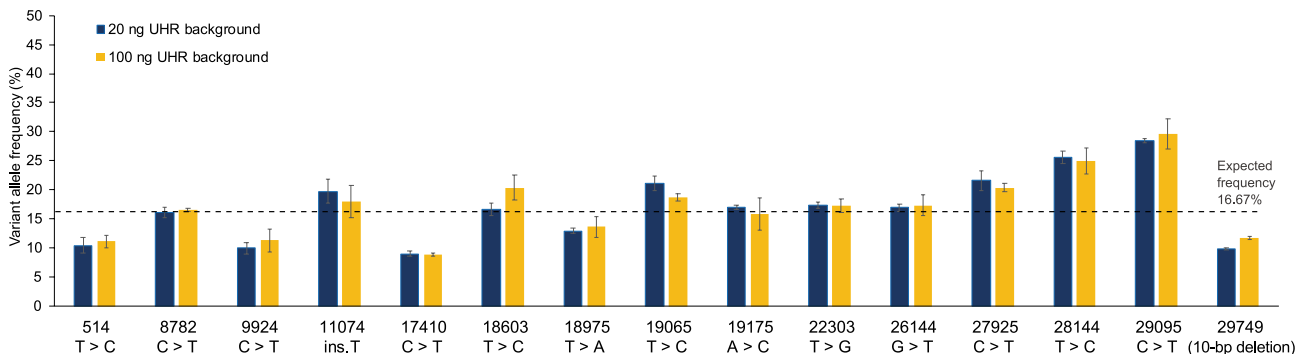
SARS-CoV-2 病毒造成 COVID-19 疫情嚴峻，藉由 KAPA SARS-CoV-2 TE panel 定序可追蹤變異株，研究病毒株基因序列及其變異進而了解病毒及其傳播能力。

- Roche 提供從建庫到上機一整套完整試劑
- 可容忍 10-20% 變異仍可抓取到 SARS-CoV-2 序列，有利於研究變異株序列分析。
- 雜交時間短至 1 小時，即可和 O/N 得到同樣良好的覆蓋率



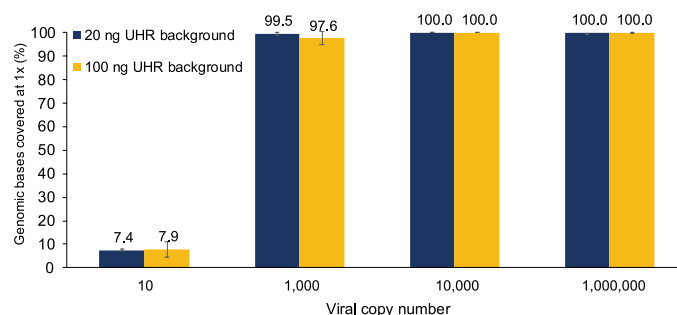
以 KAPA RNA HyperPrep Kit 建庫，使用 KAPA SARS-CoV-2 Target Enrichment Panel 針對 SARS-CoV-2 序列進行雜合 (Hybridization)，搭配 KAPA HyperCap Workflow v3 試劑，成功擴增 SARS-CoV-2 序列上機分析。

## 一次實驗可分析出多種變異點



Variants from six strains of SARS-CoV-2 are identified from within a single sample. A total of 1,000,000 SARS-CoV-2 genome copies from 6 different strains was combined with either 20 ng (dark blue) or 100 ng (yellow) of human RNA and processed in triplicate using KAPA RNA HyperPrep and the KAPA SARS-CoV-2 Target Enrichment Panel. Alternate allele frequency analysis shows that all expected variants from the six SARS-CoV-2 strains were identified at close to the expected frequency. Datasets downsampled to 1 million reads prior to analysis.

## 僅 1000 viral copies 也可有高達 97% 的覆蓋率 (1X)



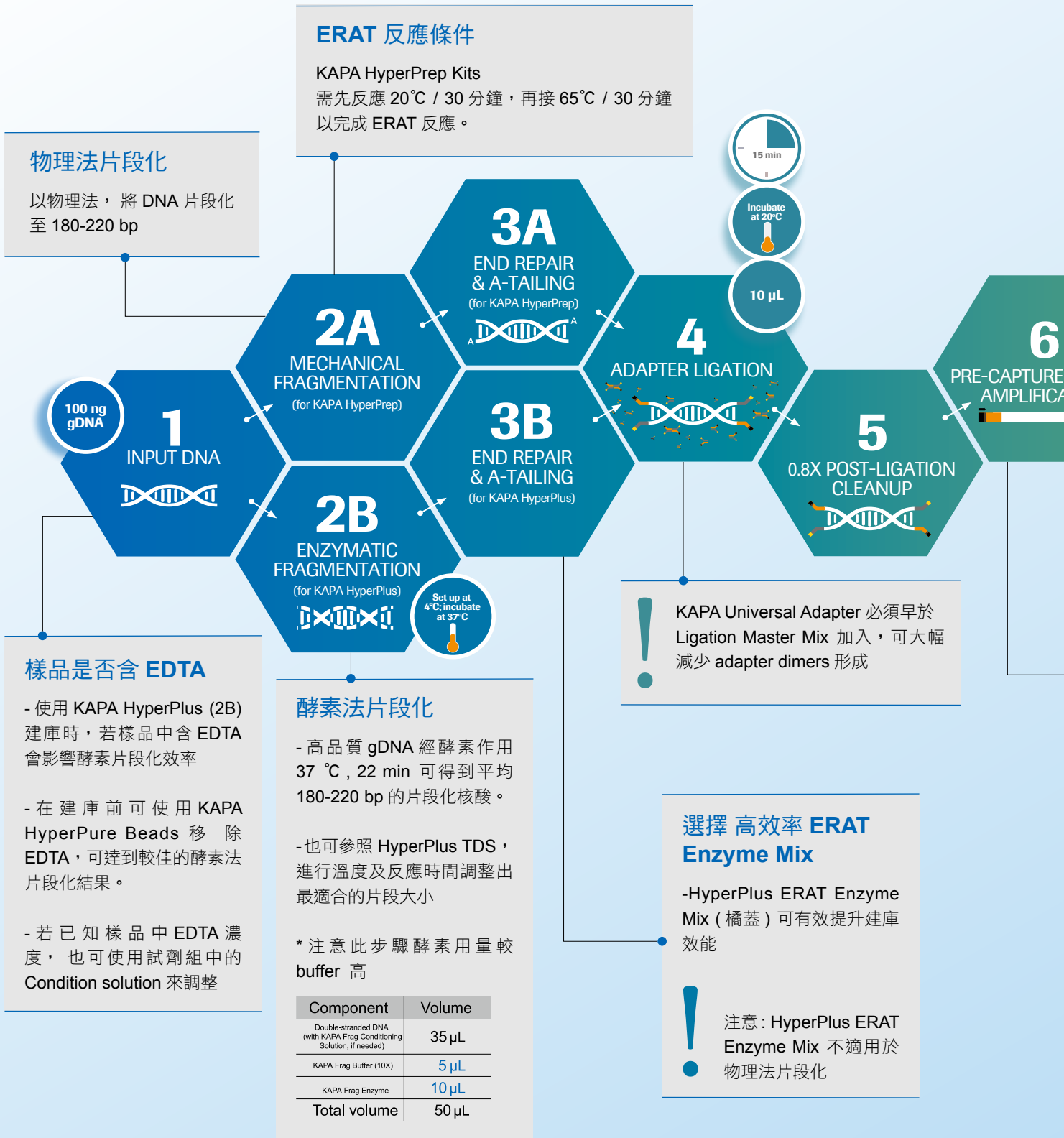
The KAPA SARS-CoV-2 Target Enrichment Panel achieves 1X coverage of >97% of the SARS-CoV-2 genome down to 1000 viral copies and genomic sequence from as few as 10 viral copies. Samples containing the indicated number of viral copies in a background of either 20 ng or 100 ng of human RNA were processed in triplicate using KAPA RNA HyperPrep and the KAPA SARS-CoV-2 Target Enrichment Panel. Datasets were downsampled to 1 million reads prior to analysis.

# Roche KAPA HyperCap Workflow v3.0

高效率的目標序列擴增

流暢的建庫流程

可選搭 **KAPA HyperPrep (物理法片段化)** **KAPA HyperPlus( 酵素法片段化 )**





# 掌握關鍵技巧 提升建庫效益



若都完成應注意事項，仍無法得到好的建庫結果，歡迎與我們連繫，由專員來協助您找出可能原因

## HyperDesign Tool

強調 user experience 直觀式操作及專家協助

輕鬆設計  
"符合實驗需求的探針"

[www.hyperdesign.com](http://www.hyperdesign.com)

### 確認建庫品質

- 確認核酸濃度及質量 (ex. Qubit)
- 確認片段分佈及品質 (ex. Agilent Bioanalyzer)

是否可得到優良的建庫結果？ YES Or NO

NO

YES

LIBRARY PREP

7

1.4X POST-AMP CLEANUP

### Pre-Capture PCR 建議擴增次數

KAPA HyperPrep Kit	8 cycles
KAPA HyperPlus Kit	6 cycles

8  
TARGET CAPTURE  
HYBRIDIZATION-BASED  
依據目標序列長度決定  
Hybridization Component H 加入體積

<40 Mbp Capture Target Size	12 µL
≥40 Mbp Capture Target Size	9 µL

Optional pre-capture multiplexing

1 µg (single-plex) or 1.5 µg (multiplex) input

95°C for 5min, 55°C for 16-20 hr

9  
WASH & RECOVERY

55°C for 5min

Hybridization 結束前  
先置備及預熱好 Wash Buffers 使其達到最好效能。

Capture Beads 體積  
依目標序列大小決定

<40 Mbp	50 µL per rxn
≥40 Mbp	100 µL per rxn

10  
POST-CAPTURE  
LIBRARY  
AMPLIFICATION

11  
1.4X POST-AMP  
CLEANUP

有效擴增目標序列，就可得到優良的建庫結果！

別忘了再與我們業務連繫訂購更多 Roche KAPA library prep kits

### Post-Capture PCR 建議擴增次數

<100 kb	18 cycles
100 kb – 2 Mb	16 cycles
>2 Mb – 40 Mb	10 cycles
>40 Mb	8 cycles