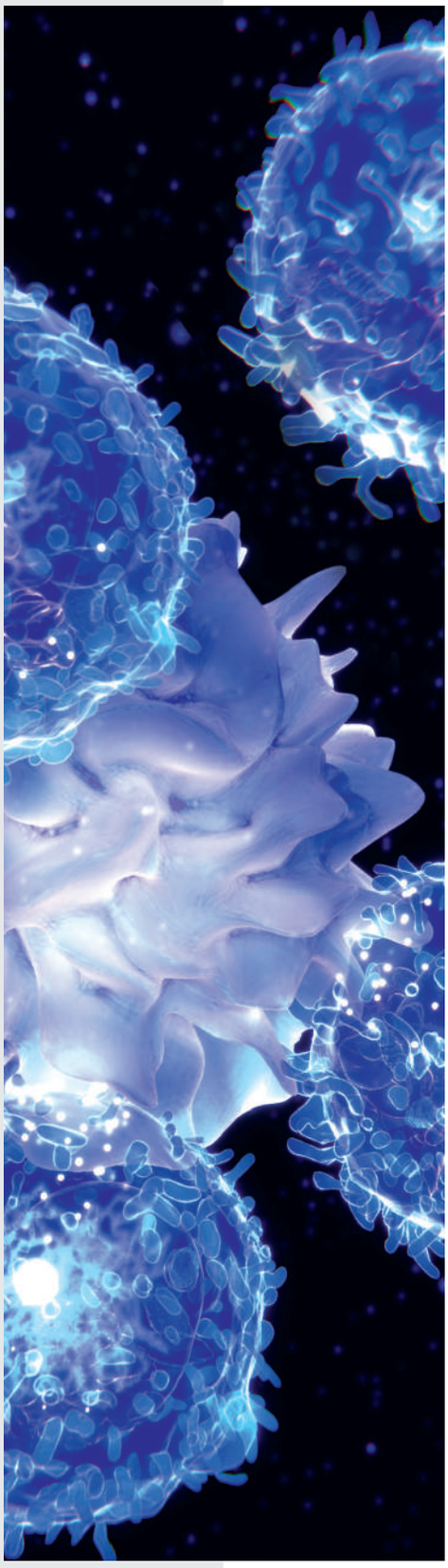
騰達行
UNIMED
0800-211-819

Recent advances in single-cell sequencing hold great potential for exploring biological systems with unprecedented resolution.

Single Cell Multi-omics

單細胞多體學研究



Single Cell Sequencing

2013 年，**單細胞定序**技術被 Science 評選為年度最值得關注的六大領域榜首。 隨著定序成本的降低，生殖細胞、胚胎發育及幹細胞、免疫細胞、癌症發展演化等方面的研究對**單細胞定序**的需求已日益增加，相關發表更從早期每年 2-30 篇，到現在 1-2000 篇的倍數成長，其中又以 scRNA-seq 最為熱門，隨著技術突破，更多的實驗室開始將目光投向 single cell multiomics 與 Spatial transcriptomics。

1 為何要研究 Single Cell ?

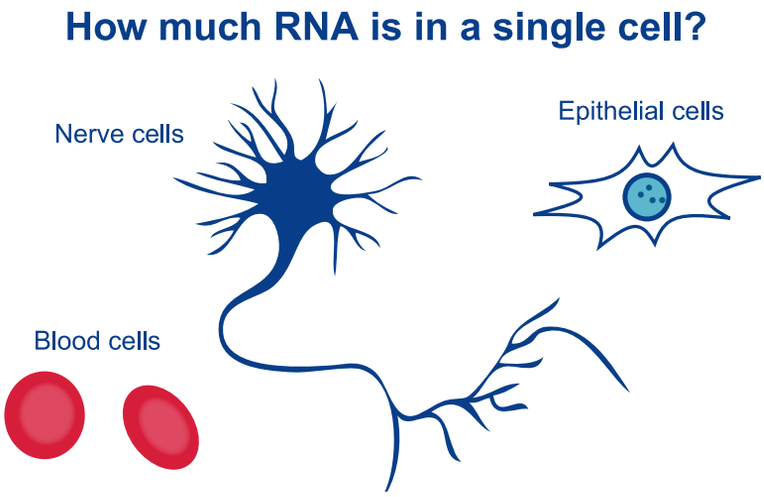
因為組織或細胞群內存在著的細胞異質性 (heterogeneity)，了解個別細胞間的差異與特性，有助深入探討各現象與細胞之間的關聯性，為疾病研究和臨床治療提供新線索。

2 為何要做 Single Cell RNA-Seq?

分析組成複雜的細胞群集
界定新的細胞類型

理解單細胞內的訊息路徑
改變與生物功能註釋

利用豐富的單細胞訊息
推動疾病和發育生物學的研究進展



3 想做 Single Cell RNA-Seq, 但 Single Cell 內有多少 RNA 呢 ?

一個細胞內的 RNA 含量強烈取決於細胞的大小以及其代謝狀態。在一般情況下，大多數體內細胞的 RNA 含量為 10-30 pg。

RNA-Seq 系列產品可進行單細胞 RNA 反轉錄，並建構單細胞 RNA 的 cDNA library 給您高品質的 RNA 定序結果，分析單一顆細胞 RNA 不再是難事！

Single-cell proteomics

IsoPlexis p.3

scRNA and protein

BD Rhapsody p.4

mRNA / total RNA

SMART-seq p.6

Immune profiling

BD Rhapsody p.4

SMARTer scTCR p.22

Single-cell WGA

PicoPlex p.24

DNA-Seq

ThruPLEX and Dual index p.28

Sample prep tools

Cell counter p.32

iMag p.34

Cell viability dye p.35

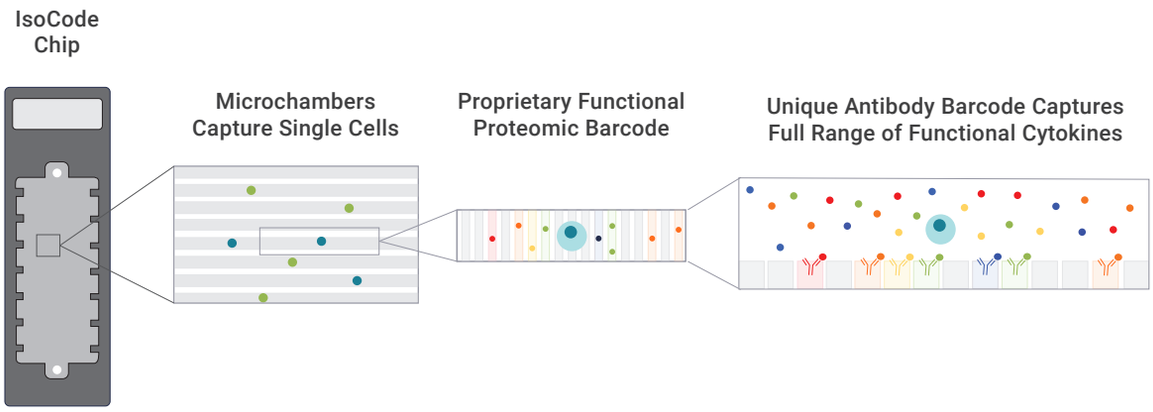
Washer p.36

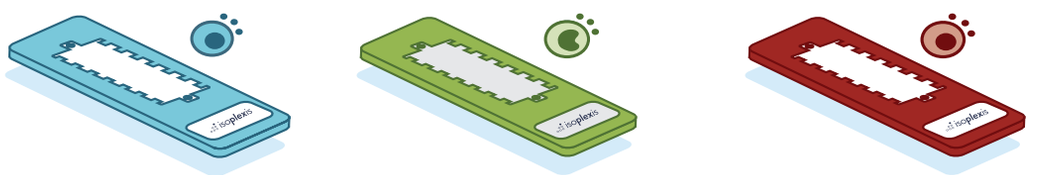
Cryopreservation p.37

Consumables p.38

isoplexis isoLight A Single-Cell Proteomics System

- 整合 CO_2 incubator、Auto Protein array system 與 single image 功能為一體的全自動分析設備
- 獨家專利的 Single-Cell Functional Technology，可在一個 microchamber 中同時分析單一細胞所分泌的 30 幾種功能性蛋白質多寡
- 整合單一細胞數據計算出多功能強度指數 (Polyfunctionality Strength Index, PSI) 藉此對細胞治療產品進行功能評估、品質監控或治療最佳劑量計算
- 國際各大細胞治療大廠皆已採用，並建立相關準則或申請專利





Single-Cell Adaptive Immune
T-cells, NK cells, CAR-T

Single-Cell Innate Immune
Monocytes, Macrophages, Fibroblast

Single-Cell Inflammation
T-cells, NK cells

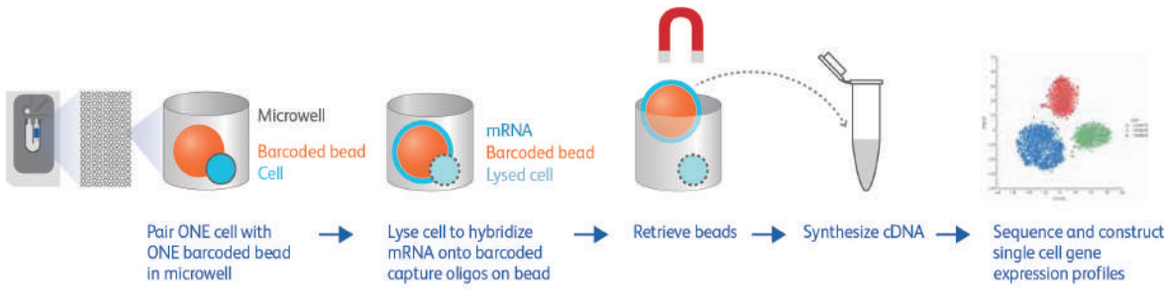
- Preinfusion polyfunctional anti-CD19 chimeric antigen receptor T cells are associated with clinical outcomes in NHL; Blood (2018) 132 (8): 804–814.
- Persistent Polyfunctional Chimeric Antigen Receptor T Cells That Target Glypican 3 Eliminate Orthotopic Hepatocellular Carcinomas in Mice; Gastroenterology, Volume 160, Issue 4, March 2021, Pages 1433
- TREATMENT USING CHIMERIC RECEPTOR T CELLS INCORPORATING OPTIMIZED POLYFUNCTIONAL T CELLS; WO/2018/187332

BD Rhapsody™ Single-Cell Analysis System

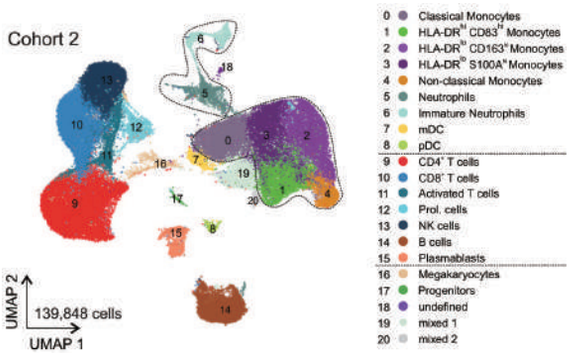
單細胞多體學分析平台

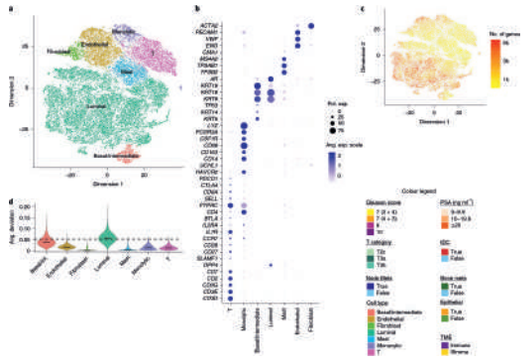
- Microwells 高效率補獲細胞， 不因管道堵塞丟失樣本。
- 可執行 100-40,000 大範圍單細胞實驗。
- 提供 scRNA-Seq, Targeted-RNA seq 與 VDJ 等應用。
- 多體學研究 : AbSeq 實現單細胞基因與蛋白同時分析。
- Sample Multiplexing kit 提供混樣上機。
- 88 萬組獨特 CL 序列標記單細胞、專利 UMI 計算真實基因表現。
- Seven Bridges Genomics 雲端平台，SeqGeq 視覺化分析軟體支援。

BD Rhapsody system workflow



BD Rhapsody Data





Severe COVID-19 Is Marked by a Dysregulated Myeloid Cell Compartment.Cell.2020;182(6):1419-1440

Single-cell analysis reveals transcriptomic remodellings in distinct cell types that contribute to human prostate cancer progression. Nat Cell Biol. 2021;23(1):87-98.

整合影像系統分析上機步驟效率

唯一即時提供 QC 的單細胞平台，為每個上機流程把關

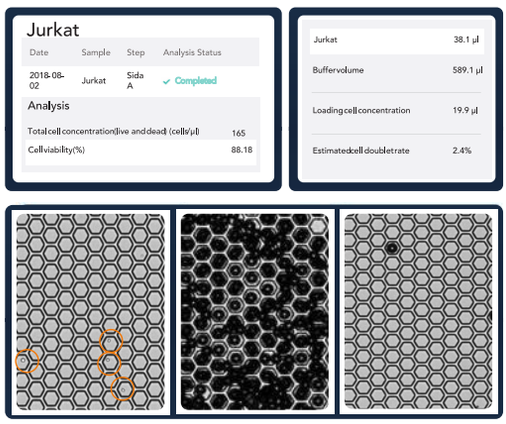
- Sample QC: 上機前細胞濃度與存活率
- Cartridge QC: 細胞與磁珠沉降效率、複數細胞及回收效率等

Sample QC

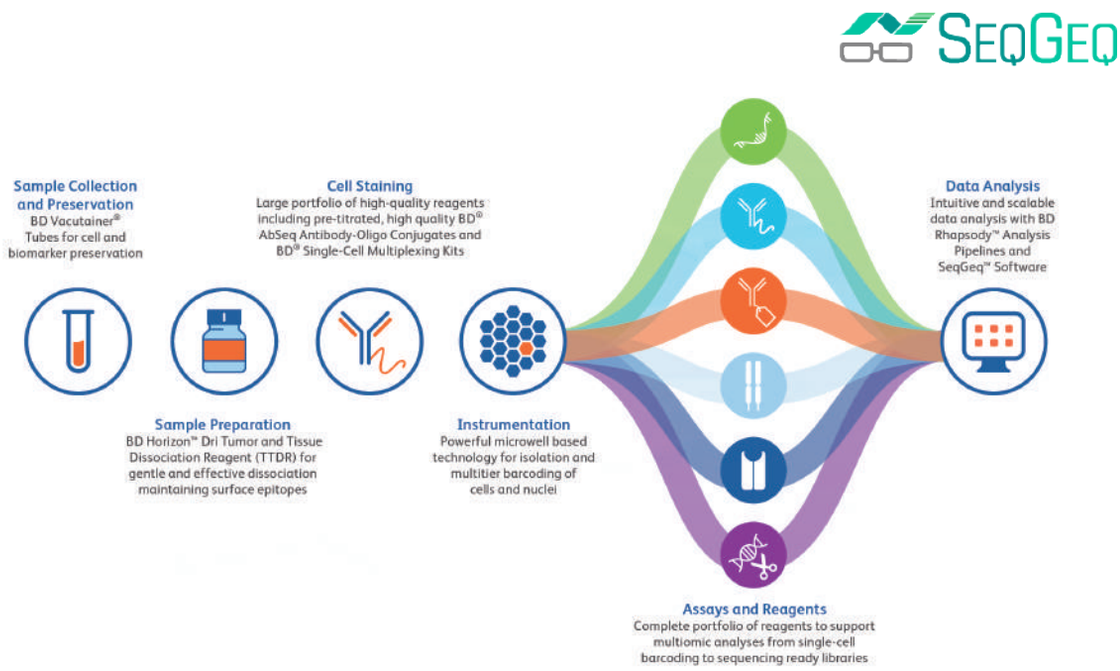
- Cell count
- Cell viability

QC Report

- Cell/Bead loading efficiency
- Cell retention rate
- Bead retrieval efficiency
- Number of retrieved beads with viable cells



BD 提供完整單細胞研究工具

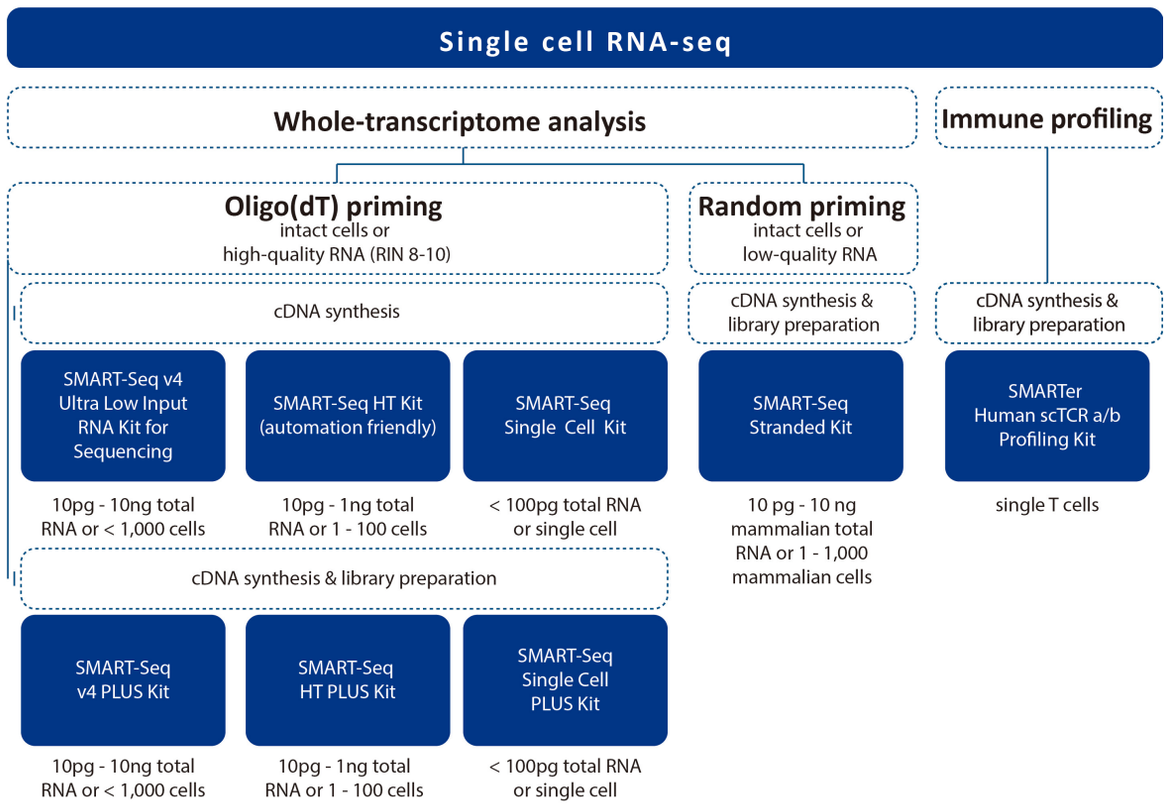


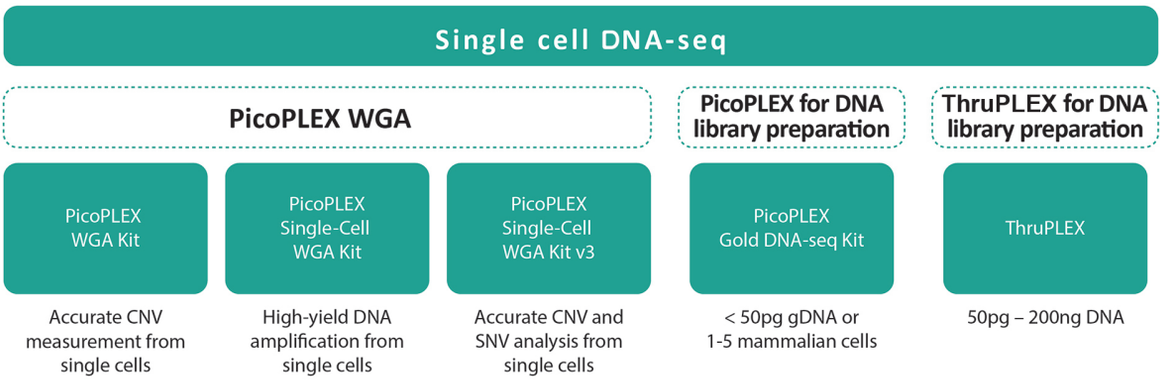
BD Rhapsody Publications

1. Modeling human adaptive immune responses with tonsil organoids. Nat Med. 2021;27(1):125-135.
2. Smc3 dosage regulates B cell transit through germinal centers and restricts their malignant transformation. Nat Immunol. 2021;22(2):240-253

TAKARA single-cell product portfolio

Quick selection guide

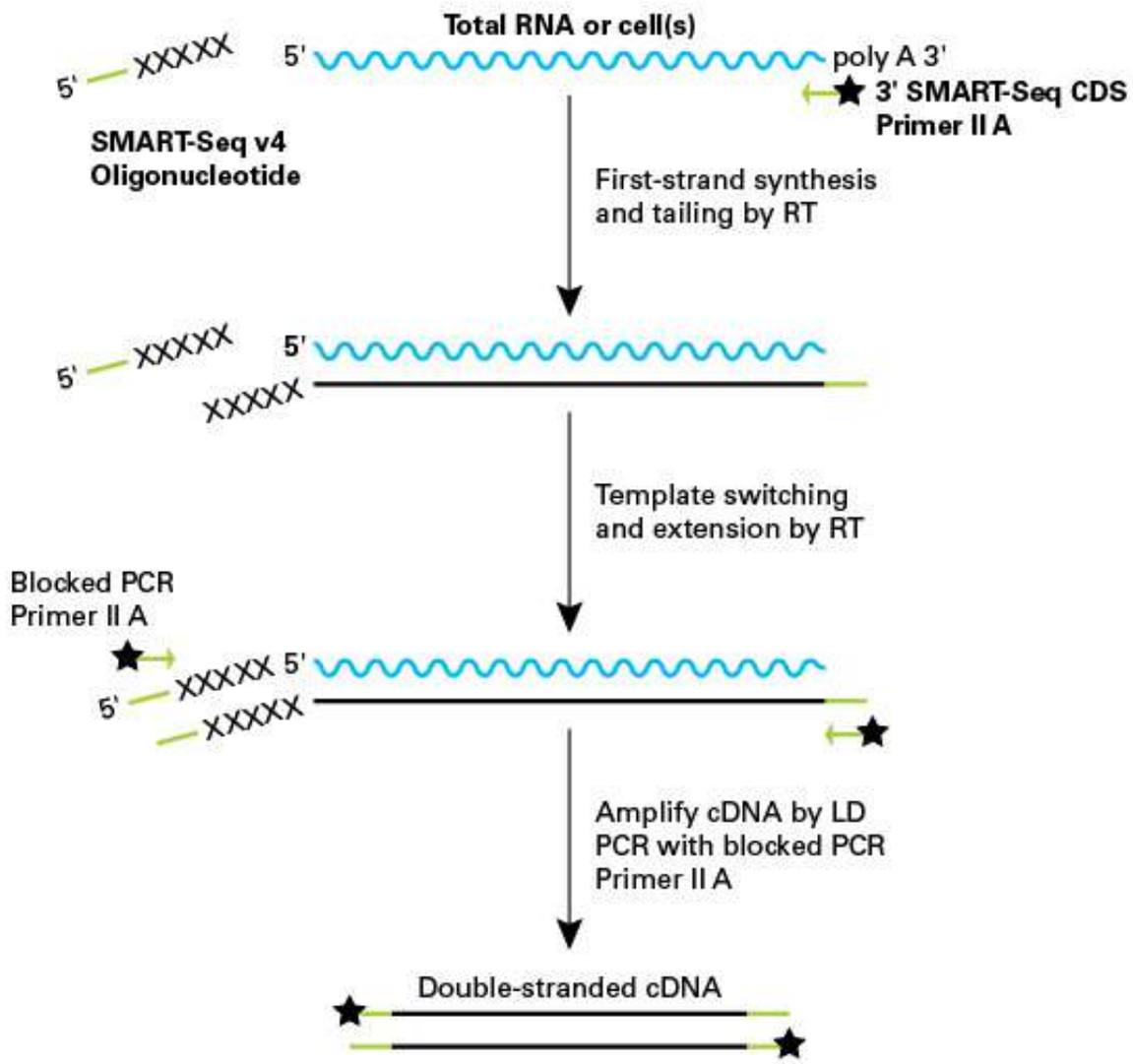




SMART-Seq® v4 Ultra® Low Input RNA Kit for Sequencing

- 嶄新技術： **SMART-Seq2** 和 **Locked Nucleic Acid (LNA)** 技術的結合
- 高靈敏度： **1–1,000** 顆細胞或 **10 pg–10 ng total RNA** (RIN>8)
- 操作簡便：直接以細胞起始的單管操作流程，有利於保留樣品的完整資訊，避免 handling errors
- 高品質定序數據：檢測更多基因、保留全長轉錄本資訊、低 rRNA 比例、真實呈現 GC-rich transcripts
- 使用彈性：後續可應用於 Illumina ® 或是 Ion Torrent NGS 平台

利用升級版 SMART 技術將 mRNA 反轉錄成全長 cDNA



SMART-Seq v4 於 RNA 濃度低至 10pg 條件下的表現

Sequencing metrics comparing different cDNA synthesis protocols							
RNA source		10 pg Mouse Brain Total RNA					
cDNA synthesis		SMARTer ultra-low v3		SMART-Seq v4		SMART-Seq2	
Yield (ng)		4.7	6.0	10.6	11.2	12.6	8.1
Number of transcripts	FPKM >0.1	11,647	10,885	14,731	14,813	12,080	12,039
	FPKM >1	9,729	9,105	12,501	12,591	10,270	10,058
Percentage of reads (%):							
Mapped to rRNA		0.8	0.4	6.5	6.1	6.9	3.8
Mapped to mitochondria		6.0	5.4	3.4	3.4	5.1	7.2
Mapped to genome		96	97	96	95	72	93
Mapped to exons		73	73	76	76	66	67
Mapped to introns		21	21	19	20	28	27
Mapped to intergenic regions		6.0	6.2	4.7	4.7	5.8	5.8

10 pg–10 ng of Human Brain Total RNA were used to generate cDNA libraries in duplicate with the SMART-Seq v4 Ultra Low Input RNA Kit for Sequencing. cDNA libraries were amplified using 17, 14, 10, or 7 PCR cycles for the 10-pg, 100-pg, 1-ng, or 10-ng libraries, respectively. RNA-seq libraries were generated using the Nextera XT DNA Library Preparation Kit and sequenced on an Illumina MiSeq instrument. Sequences were analyzed as described in the Methods.

三種技術的比較： SMART-Seq v4 是目前 Ultra Low Input Kit 的佼佼者

Sequencing metrics comparing different cDNA synthesis protocols							
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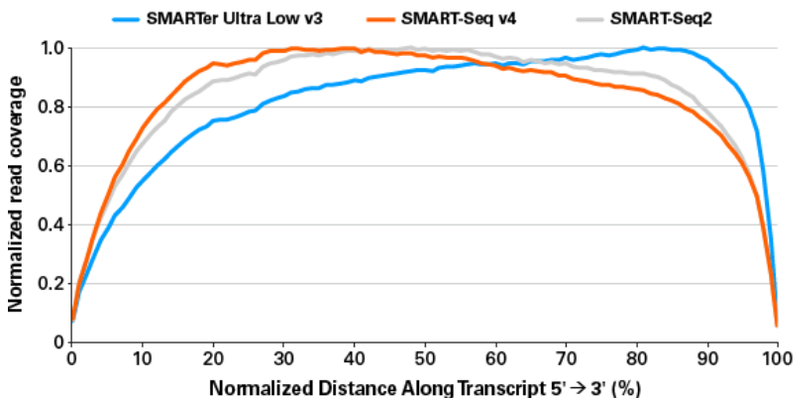
Mapped to exons		73	73	76	76	66	67
Mapped to introns		21	21	19	20	28	27
Mapped to intergenic regions		6.0	6.2	4.7	4.7	5.8	5.8

Replicate libraries were generated from 10 pg Mouse Brain Total RNA using the SMART-Seq v4 kit, the SMARTer Ultra low v3 kit, or the SMART-Seq2 method. 18 PCR cycles were used to amplify cDNA libraries with the SMART-Seq2 method and SMARTer ultra-low v3 kit; however, only 17 PCR cycles were needed for the SMART-Seq v4 libraries. RNA-seq libraries were generated using Nextera® XT DNA Library Preparation Kit and sequenced on an Illumina MiSeq® instrument.

1、100、1000 個 Hela Cells 以 SMART-Seq® v4 建構基因庫後的定序數據 (Illumina® MiSeq® platform)

Table I. Sequencing Data from Intact Cells									
Input	1 cell					100 cells		1,000 cells	
Number of reads (millions)	2.3 (paired-end)					2.0 (single-end)			
PCR cycles	17					11		8	
Replicate	1	2	3	4	5	1	2	1	2
Yield (ng)	8.3	6.3	3.3	31.6	13.7	26.9	18.4	20.6	23.3
Percentage of reads (%):									
rRNA	0.5	0.8	2.2	0.3	0.5	1.1	1.1	1.8	1.8
Mapped to genome	91	91	88	88	92	98	98	98	98
Mapped uniquely to genome	87	86	83	84	88	82	82	79	80
Exonic	94	94	88	89	87	76	77	74	75
Intronic	2.4	2.3	5	7	9	13	13	12	12
Intergenic	3.4	3.4	5	3.7	4.1	10	9	12	11
Transcripts with FPKM >0.1	8,888	8,532	7,302	10,967	10,856	13,417	13,219	13,348	13,324
Transcripts with FPKM >1	8,040	7,670	6,084	10,036	9,703	10,725	10,560	10,494	10,531

均一的基因覆蓋率



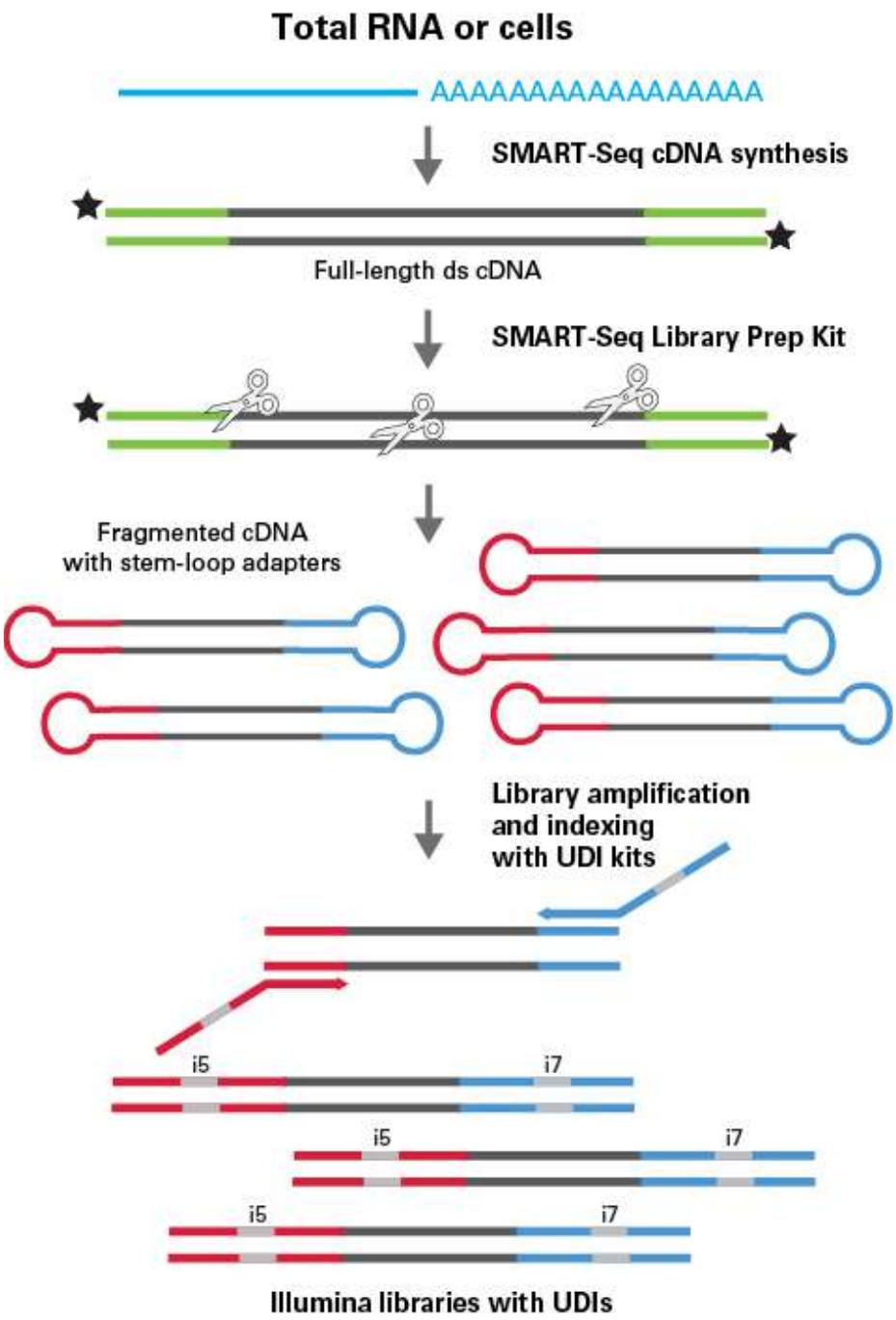
Gene body coverage shown is the average of two replicate libraries prepared from 10 pg Mouse Brain Total RNA using the three different cDNA synthesis methods. The SMARTer Ultra low v3 kit produced a slight 3' bias, and the SMART-Seq v4 kit produced a slight 5' bias; however, the overall coverage was fairly even.

產品	包裝	貨號
SMART-Seq® v4 Ultra® Low Input RNA Kit for Sequencing	12 Rxns	634888
	24 Rxns	634889
	48 Rxns	634890
	96 Rxns	634891
	192 Rxns	634892
	480 Rxns	634893
	960 Rxns	634894

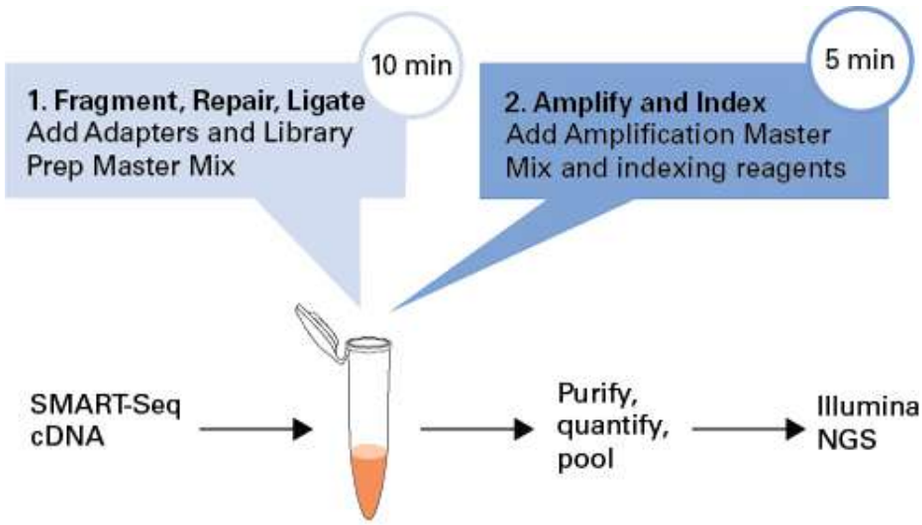
SMART-Seq® v4 PLUS Kit

完整版 SMART-Seq® v4 **PLUS** Kit ： 內含 Unique dual indexes，直接製備 Illumina-ready libraries

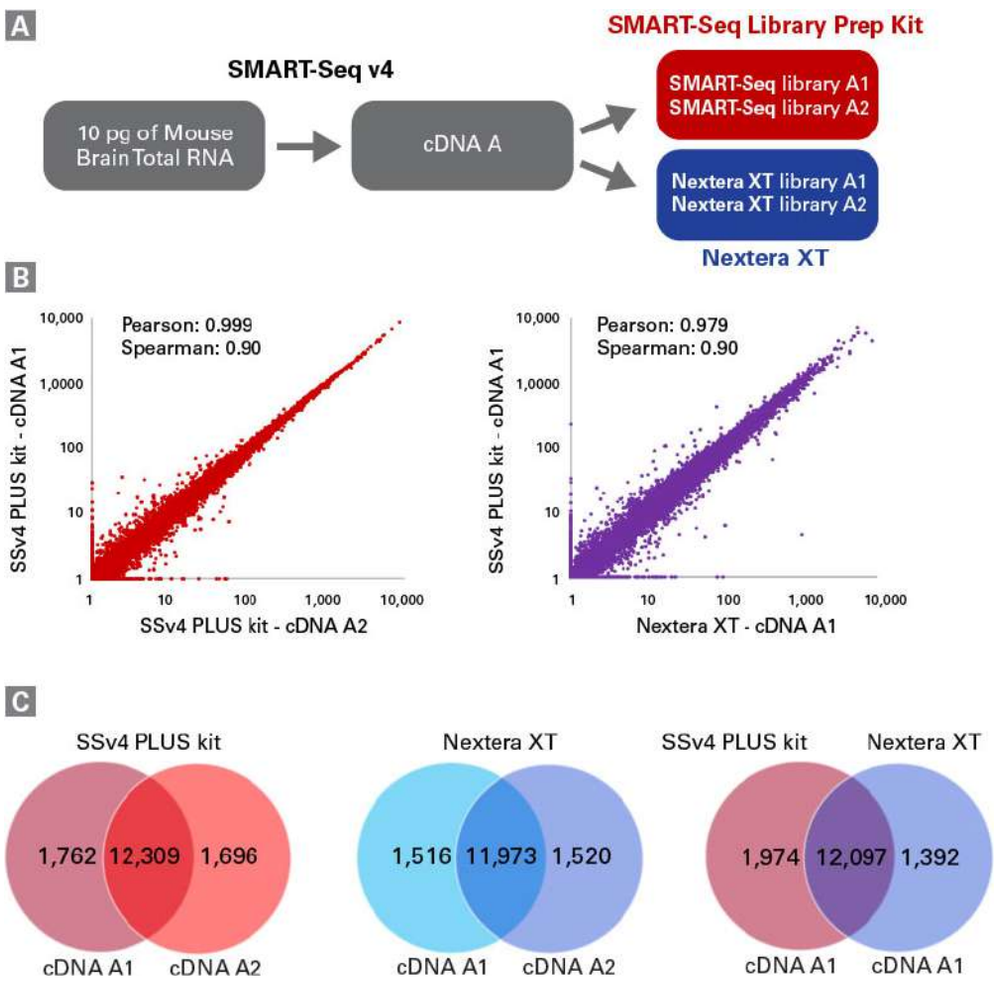
單管反應中達成片段化、加上 stem-loop adapters
完成 Illumina-compatible libraries



簡易操作步驟，hands-on time 最小化

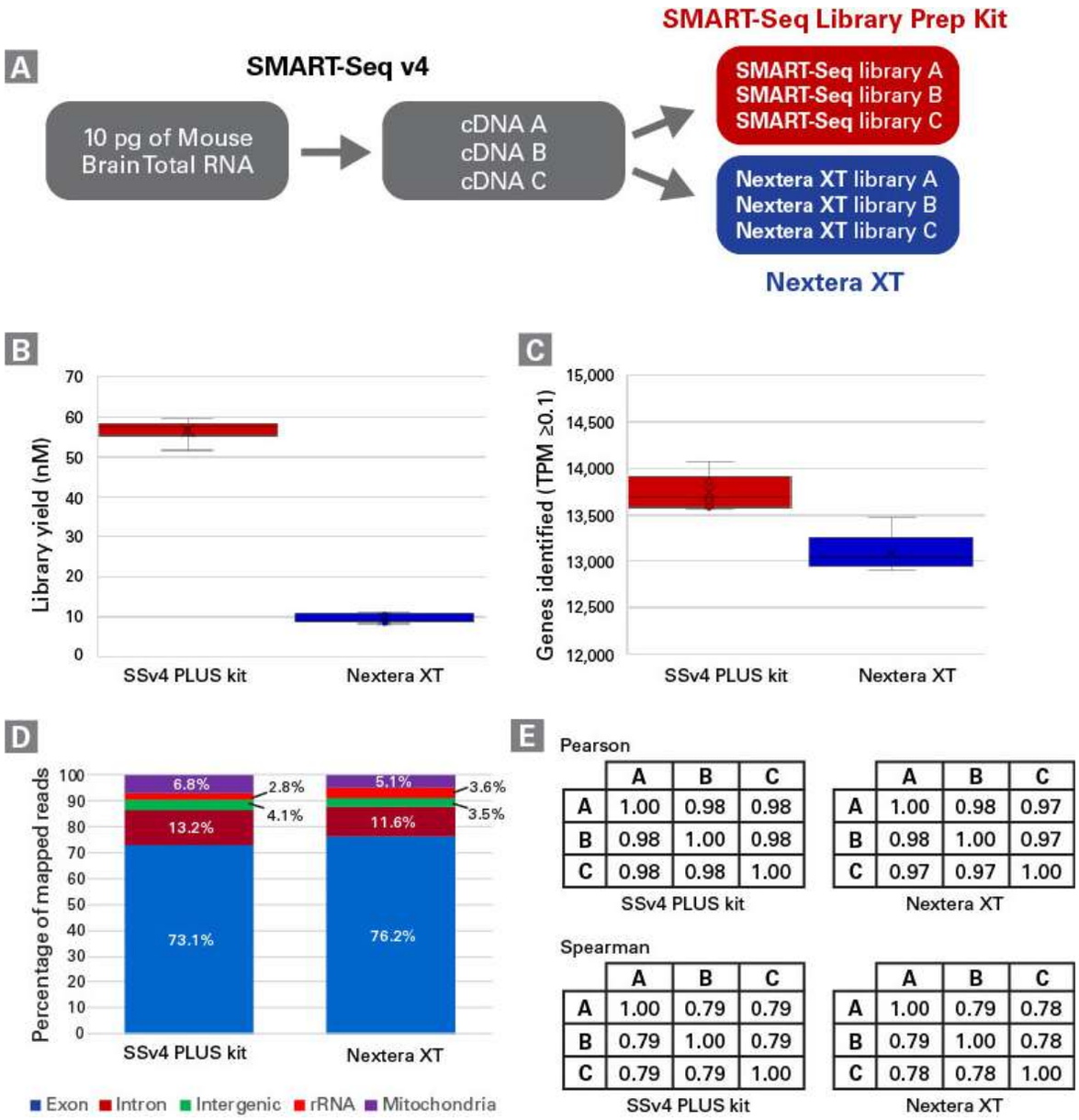


SMART-Seq v4 PLUS 結果一致性更高



Panel A. Libraries were prepared in duplicate from the same SSv4 cDNA using either the SMART-Seq Library Prep Kit portion of the SSv4 PLUS kit or Nextera XT. Panel B. Correlation plots between libraries made with SSv4 PLUS and Nextera XT kits. Pearson and Spearman's correlations were calculated from the TPM values obtained. Scatter plots showed the TPM values from all genes with a log10+1 scale. Panel C. Venn diagram showing the number of genes identified from the processed cDNA, in duplicate, with the SSv4 PLUS kit, Nextera XT, or between both chemistries.

SMART-Seq v4 PLUS Kit 建構更高品質的 libraries



Pearson	A	B	C
A	1.00	0.98	0.98
B	0.98	1.00	0.98
C	0.98	0.98	1.00

SSv4 PLUS kit

Pearson	A	B	C
A	1.00	0.98	0.97
B	0.98	1.00	0.97
C	0.97	0.97	1.00

Nextera XT

Spearman	A	B	C
A	1.00	0.79	0.79
B	0.79	1.00	0.79
C	0.79	0.79	1.00

SSv4 PLUS kit

Spearman	A	B	C
A	1.00	0.79	0.78
B	0.79	1.00	0.78
C	0.78	0.78	1.00

Nextera XT

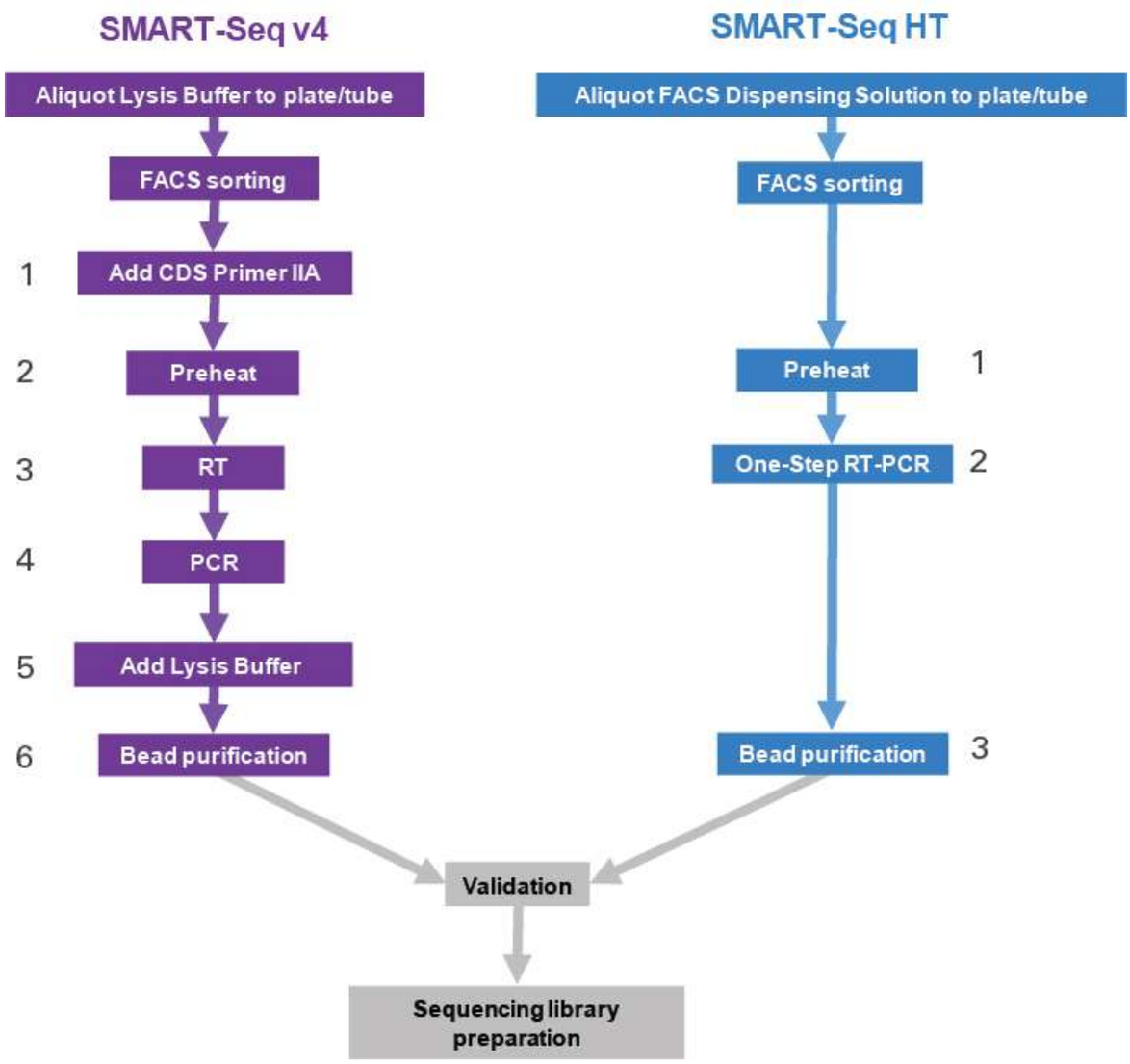
SSv4 chemistry was used to produce cDNA, in triplicate, from 10 pg of Mouse Brain Total RNA. Illumina-compatible libraries were then generated from 1 ng or 125 pg using the SMART-Seq Library Prep Kit portion of the SSv4 PLUS kit or Nextera XT, respectively, and sequenced on a NextSeq 500. The reads were normalized to 4M paired-end reads and analyzed as described in the methods. Panel B. The library yield obtained with the SSv4 PLUS kit is higher than the yield obtained when using Nextera XT. Panel C. The number of genes identified was also higher for the SSv4 PLUS kit compared to Nextera XT. Panel D. As expected, the distribution of the mapped reads is similar between the two library preparation methods. Panel E. Pearson and Spearman's correlations were calculated from the TPM values obtained from the triplicate cDNAs (A to C) processed with the SSv4 PLUS or Nextera XT kit.

產品	包裝	貨號
SMART - Seq® v4 PLUS Kit	48 Rxns	R400752
	96 Rxns	R400753

SMART-Seq® HT Kit
SMART-Seq®HT PLUS Kit

- 適用於自動化機器的簡易流程：在更短的時間內分析更多的樣品，並節省自動化平台的空間
- 超低樣本起始量： **1–100 顆細胞或 10 pg–1 ng total RNA**
- 高品質定序數據：檢測更多基因、保留全長轉錄本資訊、低 rRNA 比例、真實呈現 GC-rich transcripts
- 使用彈性：後續可應用於 Illumina ® 或是 Ion Torrent NGS 平台
- 完整版 SMART-Seq® HT PLUS Kit： 內含 Unique dual indexes，直接製備 Illumina-ready libraries
- 更高的 library 產量，便於使用高通量 Illumina 定序儀 (NovaSeq)，或能用於多次的定序

更簡易的操作流程，適合用於自動化機器

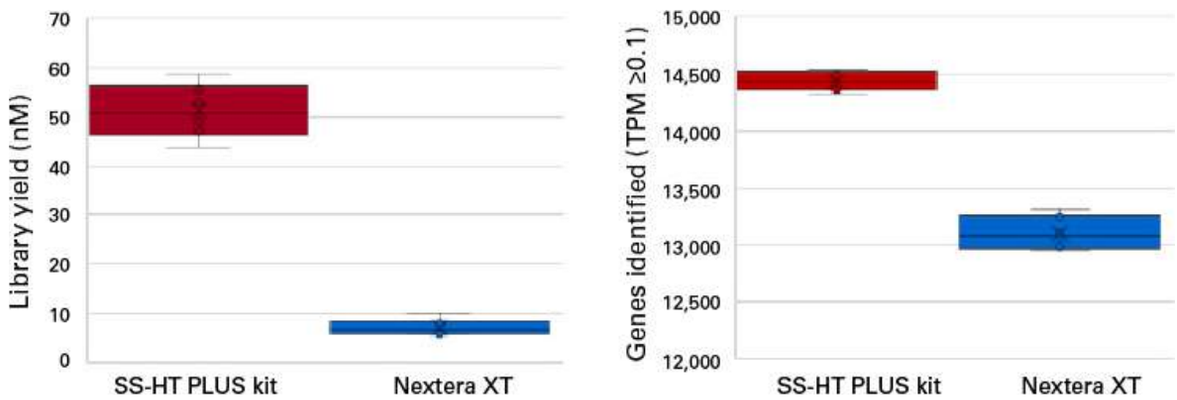


與 SMART-Seq® v4 的表現一致，皆具有高品質定序結果

Sequencing metrics comparing SMART-Seq v4 and SMART-Seq HT kits							
RNA source	10 pg Mouse Brain Total RNA						
cDNA synthesis	SMART-Seq v4			SMART-Seq HT			
Replicate	A	B	C	A	B	C	
Yield (ng)	7.3	8.5	9.4	9.5	9.9	9.2	
Number of transcripts	14,168	13,934	14,147	14,510	14,650	14,553	
	11,455	11,267	11,349	11,582	11,670	11,454	
Average Pearson/Spearman	0.97/0.67			0.97/0.68			
	0.96/0.66						
Proportion of reads mapped (%)							
rRNA	0.7	0.6	0.5	1.1	1.1	1.1	
Mitochondria	2.8	4.2	4.1	3.7	3.8	4.2	
Genome	92.3	90.8	86.6	89.1	89.0	87.8	
Exons	74.8	72.5	69.0	67.3	67.1	65.3	
Introns	13.3	14.1	13.3	16.9	16.9	17.4	
Intergenic regions	4.2	4.2	4.4	4.9	5.0	5.2	

Libraries were prepared from 10 pg of Mouse Brain Total RNA. The output cDNA was converted into RNA-seq libraries using the Illumina Nextera XT DNA Library Preparation Kit and sequenced on an Illumina NextSeq® instrument (2 x 75 bp). Sequences were analyzed as described in the methods after normalizing all the samples to 13

SMART-Seq HT PLUS Kit 建構更高品質的 libraries



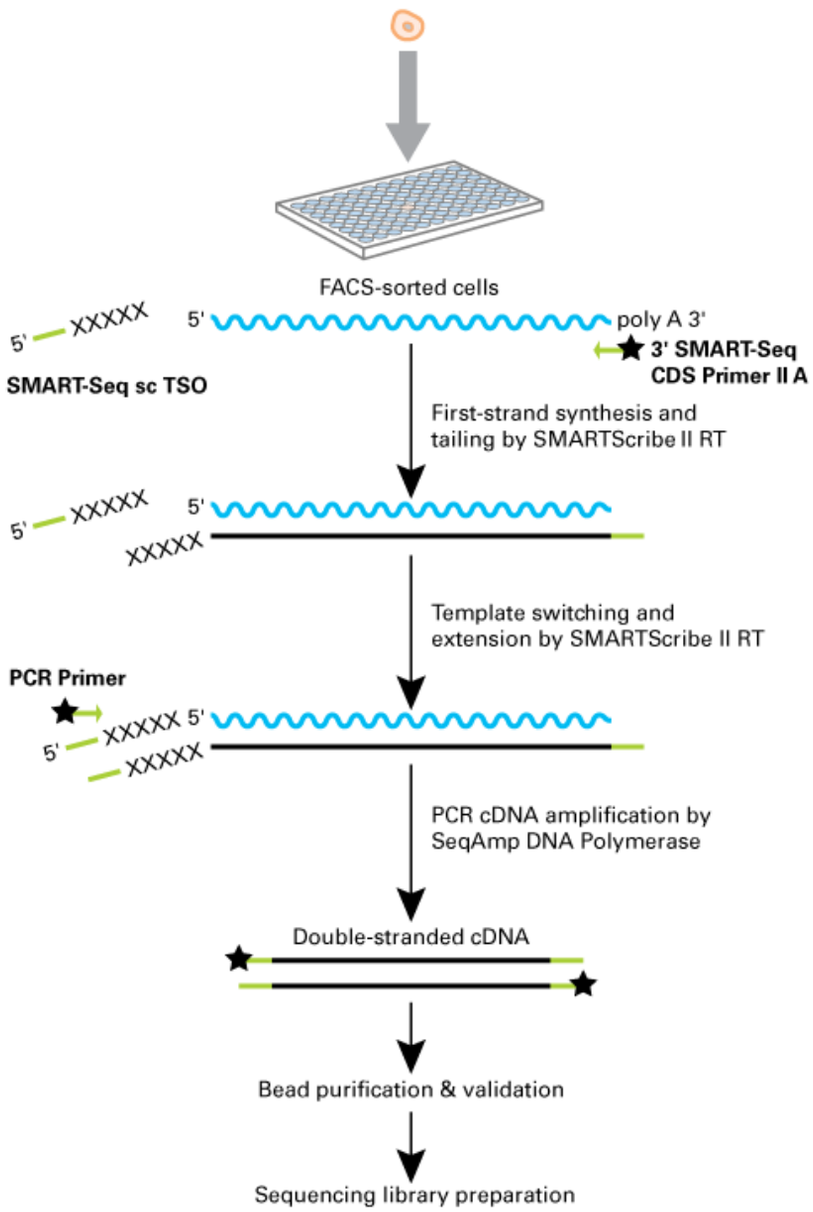
SMART-Seq HT was used to produce cDNA from 10 pg of Mouse Brain Total RNA in triplicate. Illumina-compatible libraries were generated using SMART-Seq PLUS or Nextera XT (Illumina) library prep kits, and sequenced on a NextSeq 500 system. The reads were normalized to 4M paired-end reads and analyzed as described in the technical note.

產品	包裝	貨號
SMART- Seq® HT Kit	12 Rxns	634455
	48 Rxns	634456
	96 Rxns	634437
	192 Rxns	634438
	480 Rxns	634436
SMART- Seq® HT PLUS Kit	48 Rxns	R400748
	96 Rxns	R400749

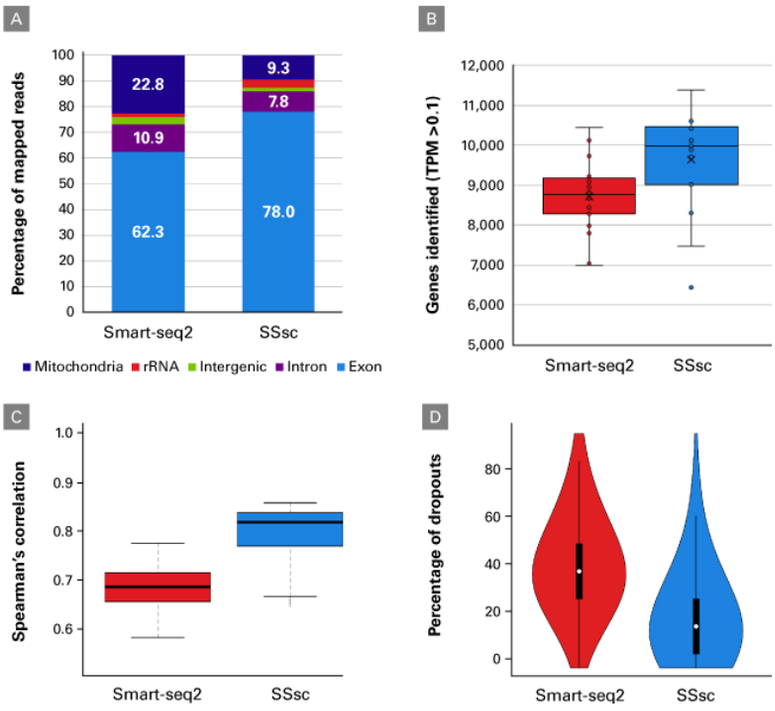
SMART-Seq® Single Cell Kit

- 簡單、plate-based 工作流程：利用 FACS（流式細胞儀）或其他方法分選的單細胞作為起始
- 極微量起始量：單細胞、< 100pg RNA
- 操作簡便：單管操作流程，有利於保留樣品的完整資訊，避免 handling errors
- 高靈敏度、高重複性：非常適於單細胞（尤其是 RNA 含量極低的細胞或細胞核，如 PBMCs）RNA-Seq 研究，可檢測更多基因
- 使用彈性：後續可應用於 Illumina ® 或是 Ion Torrent NGS 平台

利用升級版 SMART 技術
將單細胞之 mRNA 反轉錄成全長 cDNA



相較於 Smart-seq 2 代表現更卓越的靈敏度及再現性



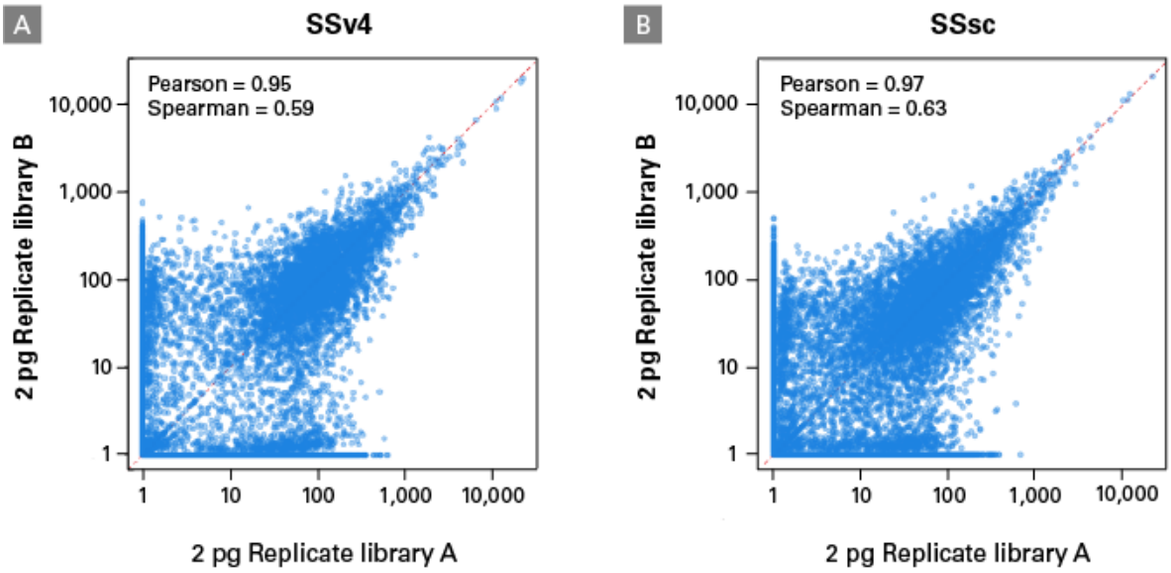
Single cells from the lymphoblastoid cell line GM12878 were processed with SSsc (18 cells) or the Smart-seq2 protocol (20 cells; Picelli et al. 2014) using 19 cycles of PCR. As described in the methods, RNA-seq libraries were generated and sequences analyzed (after normalizing all samples to 1.75 million paired-end reads).

相較 SMART-Seq v4 ，對於 2pg 的極微量 total RNA 的靈敏度更好

Sequencing metrics comparing the SMART-Seq v4 kit and SMART-Seq Single Cell Kit						
RNA source	2 pg UHR total RNA					
cDNA synthesis method	SSv4			SSsc		
Replicate	A	B	C	A	B	C
cDNA yield (ng)	7.8	6.9	5.5	14.8	14.9	9.6
Number of genes with TPM >1	7,412	7,522	7,487	8,774	8,614	8,406
Number of genes with TPM >0.1	8,660	8,868	9,240	10,319	10,276	10,285
Average Pearson/Spearman	0.95/0.59			0.97/0.63		
Proportion of reads mapped (%):						
Genome	92.7	92.5	92.5	80.1	80.9	80.6
Exon	79.3	78.7	76.6	63.4	64.1	62.0
Intron	10.5	10.9	12.5	13.0	12.8	14.0
Intergenic regions	2.9	3.0	3.4	3.7	4.0	4.6
rRNA	0.8	0.7	0.6	6.1	6.0	4.3
Mitochondria	3.5	3.6	3.9	9.3	8.4	10.2

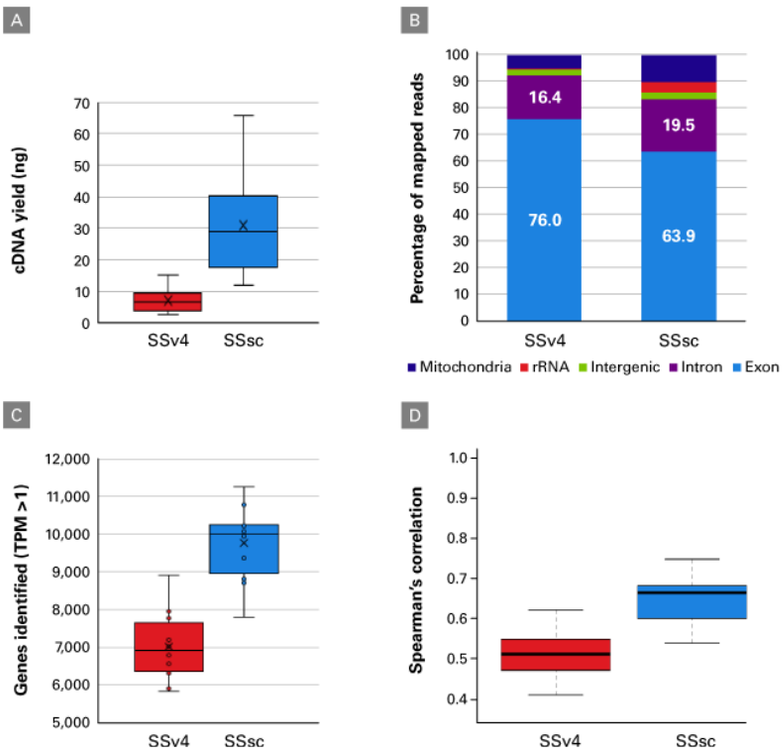
Replicate cDNA libraries were generated from 2 pg of Universal Human Reference (UHR) total RNA using the SMART-Seq v4 kit (SSv4) or the SMART-Seq Single Cell Kit (SSsc); all libraries were processed with 19 PCR cycles. As described in the methods, RNA-seq libraries were generated and sequences analyzed (after normalizing all samples to 1.6 million paired-end reads). SSsc identified about 15% more genes than SSv4

相較 SMART-Seq v4 ，對於 2pg 的極微量 total RNA 的再現性也更高



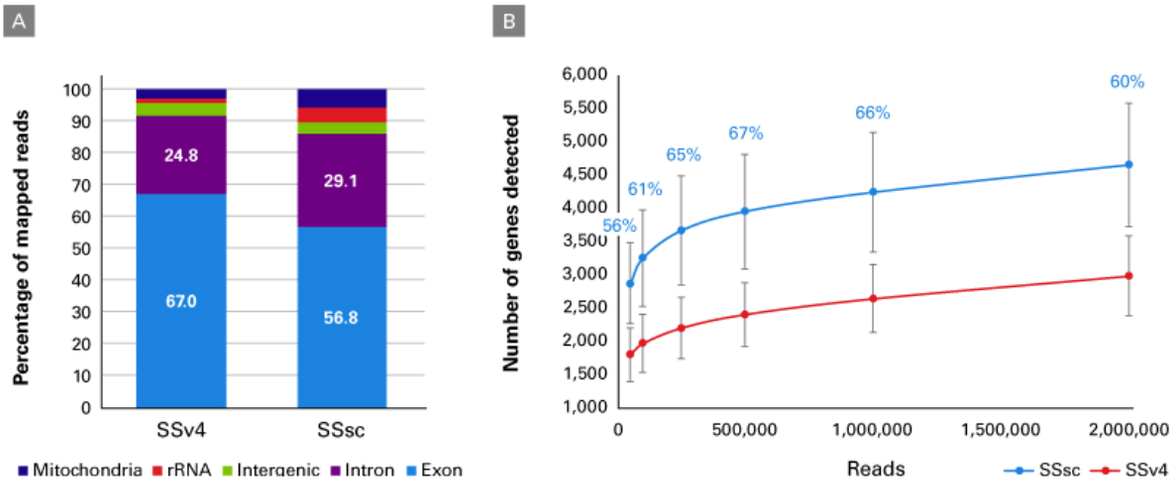
Libraries made from 2 pg of UHR total RNA (Table I) were analyzed using scatter plots to visualize the reproducibility between technical replicates (shown are TPM values from all genes with a log10+1 scale). SSv4 (Panel A) generated highly reproducible quantification, but SSsc (Panel B) produced superior reproducibility, as seen in the increased Pearson and Spearman correlations. In addition, SSsc was better at detecting low-expression genes.

增進 RNA 含量低單細胞的定序表現

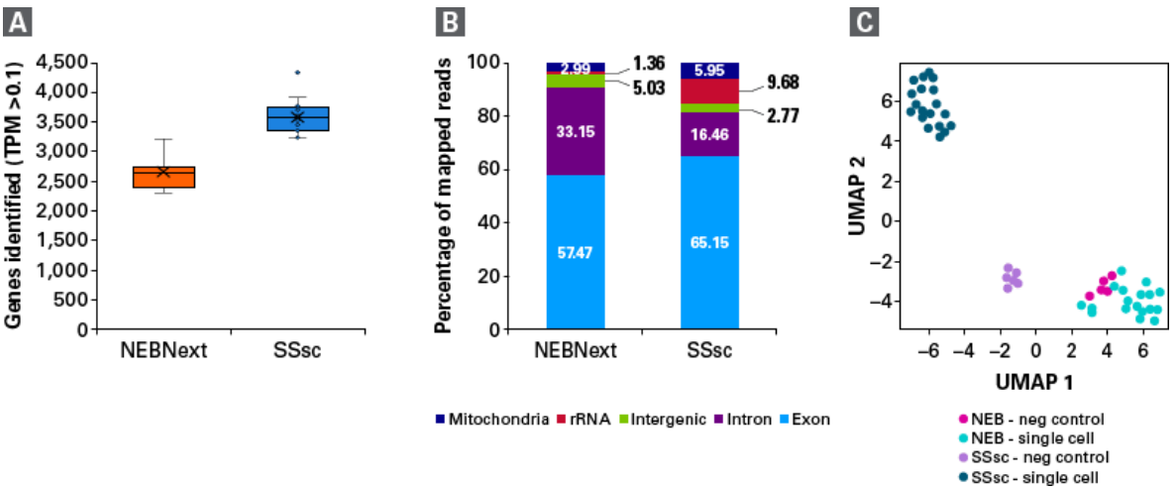


12 single cells from lymphoblastoid cell line GM22601 were processed with SSv4 or SSsc using 19 cycles of PCR. As described in the methods, RNA-seq libraries were generated and sequences analyzed (after normalizing all samples to 1.25 million paired-end reads). For all boxplots in this figure, the box denotes the interquartile range (IQR), i.e., the 25th and 75th quartiles; the whiskers are 1.5 x IQR from the median value and represent the extremes of the data.

增進 primary samples 的定序表現



PBMCs from a healthy donor were processed with the SSv4 or SSsc kit (~50 single cells per kit). RNA-seq libraries were generated as described in the methods. Panel A. The read distribution is fairly similar between the two chemistries. Panel B. About 60% more genes are detected in the cells processed with SSsc, regardless of the number of reads used for the analysis.



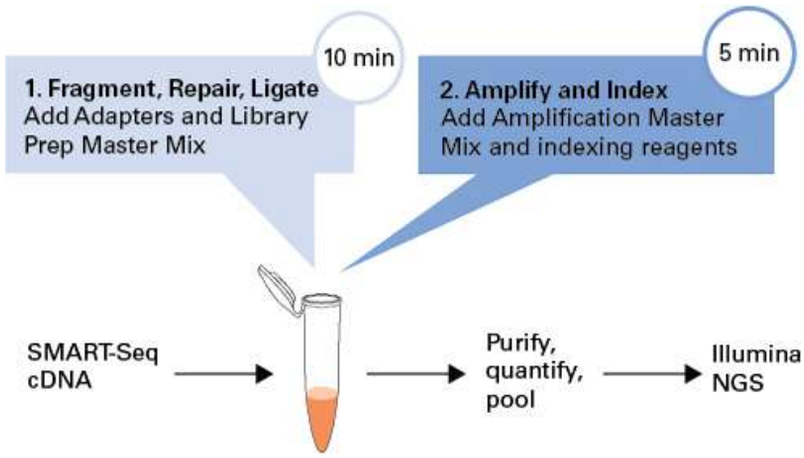
Libraries were prepared from T cells according to manufacturer's instructions with either SSsc or NEBNext Single Cell/Low Input RNA Library Prep Kit for Illumina. Panel A. In these boxplots, the box denotes the interquartile range (IQR), i.e., the 25th and 75th quartiles; the whiskers are 1.5 x IQR from the median value and represent the extremes of the data. The number of genes identified with a TPM >0.1 is higher (~40%) for SSsc (median = 3,591) than for NEBNext (median = 2,665). Panel B. The read distribution is different between the two chemistries, with more reads mapping to exon regions for SSsc. Panel C. The high number of cycles required to generate a library for the NEBNext protocol means that the negative controls for NEB (red) cluster strongly with the single-cell libraries (light blue), while the negative controls for SSsc (purple) are distinct from the single-cell libraries (dark blue).

產品	包裝	貨號
SMART-Seq® Single Cell Kit	12 Rxns	634470
	48 Rxns	634471
	96 Rxns	634472

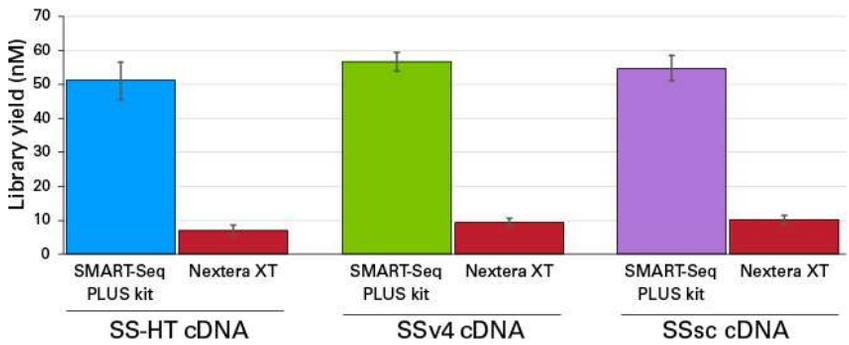
SMART-Seq® Single Cell PLUS Kit

- 完整版 SMART-Seq® Single Cell Kit： 內含 Unique dual indexes，直接製備 Illumina-ready libraries
- 更高的 library 產量，便於使用高通量 Illumina 定序儀 (NovaSeq)，或能用於多次的定序

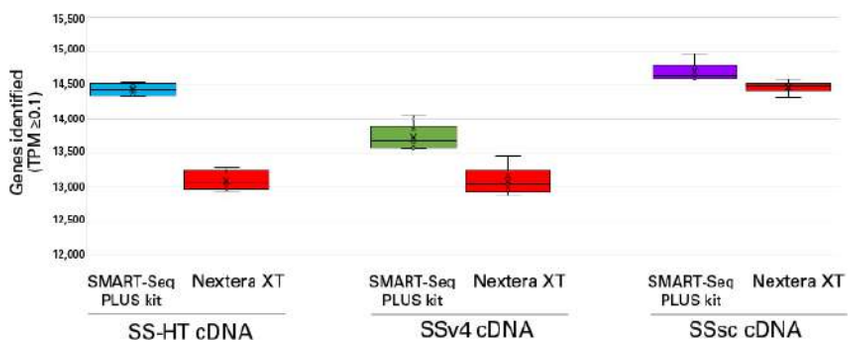
簡易操作步驟，hands-on time 最小化



三種微量 RNA-Seq PLUS kits 的 cDNA 產量比較



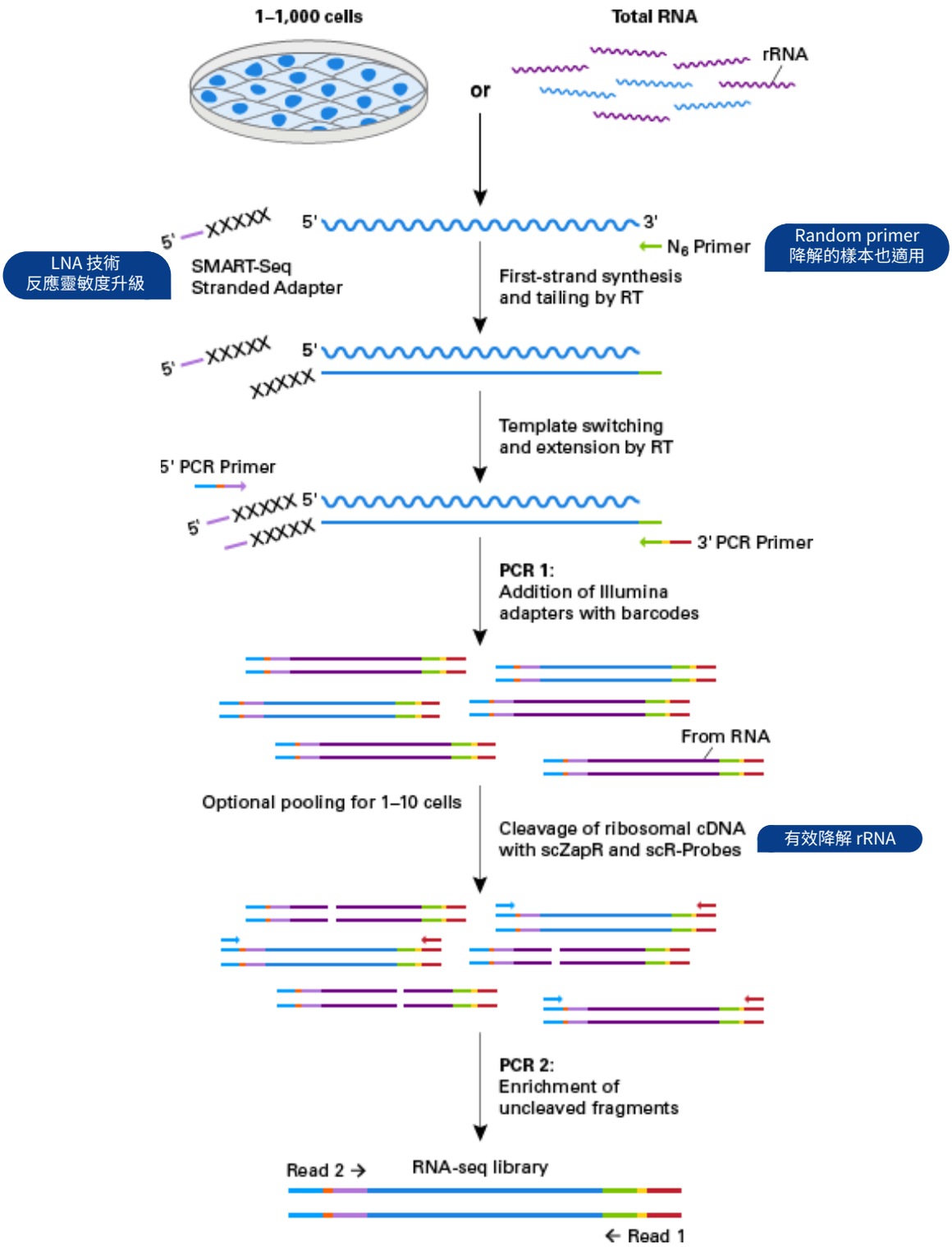
三種微量 RNA-Seq PLUS kits 的基因鑑別量比較



產品	包裝	貨號
SMART-Seq® Single Cell PLUS Kit	48 Rxns	R400750
	96 Rxns	R400751

SMART-Seq® Stranded Kit

- 超低樣本起始量： 1–1,000 顆細胞或 10 pg–10 ng 哺乳類動物 total RNA
- 用途廣泛：適用於人、小鼠、大鼠降解的樣本
- 簡易流程，可在 7 小時內製備 Stranded Illumina sequencing-ready libraries
- 保留 strand-of-origin 資訊，準確檢測包含 coding and noncoding transcripts 的全部轉錄組

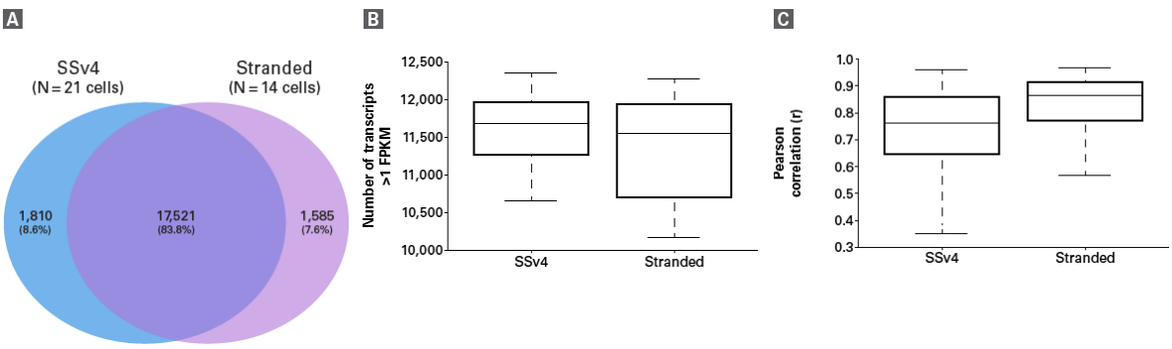


SMART-Seq Stranded Kit 彈性的樣本起始量

Sequencing alignment metrics for A375 total RNA and cells							
Input	**Total RNA**	**1,000 cells**	**500 cells**	**100 cells**	**10 cells**	**5 cells**	**1 cell**
Number of reads (pairs)	6,000,000	6,000,000	6,000,000	6,000,000	6,000,000	6,000,000	5,873,974
Number of transcripts >1 FPKM	13,260	13,294	13,583	13,520	12,726	12,602	11,540
Number of transcripts >0.1 FPKM	21,334	21,113	21,365	21,145	20,550	18,888	15,815
Proportion of reads (%):							
Exonic	34.7	36.4	39.2	42.7	36.7	36.2	37.3
Intronic	29.6	29.3	27.7	28.3	34.0	30.4	21.1
Intergenic	14.2	13.4	12.2	12.9	16.7	16.8	10.1
rRNA	7.0	11.4	11.5	6.3	3.6	4.9	7.1
Mitochondrial	4.1	3.5	3.7	4.9	3.8	4.4	4.6
Overall mapping (%)	89.6	93.9	94.3	95.1	94.9	92.7	80.2
Duplicate rate (%)	37.3	45.2	40.3	46.1	52.5	72.2	78.5
lncRNA mapping:							
Number of mapped reads (%)	7.2	10.4	10.8	9.4	8.7	8.6	7.3
lncRNA transcripts detected	5,395	4,687	4,565	5,439	5,440	4,983	2,802

A375 cells isolated by FACS were used to generate RNA-seq libraries with the SMART-Seq Stranded Kit. Input varied from 1 cell to 1,000 cells, with two replicates per input of 5–1,000 cells and 12 replicates for the single cells. For comparison, two aliquots of 1,000 cells were used for total RNA purification and then used for library preparation.

SMART-Seq Stranded Kit 與 SMART-Seq v4 Kit 具有一致性的靈敏度



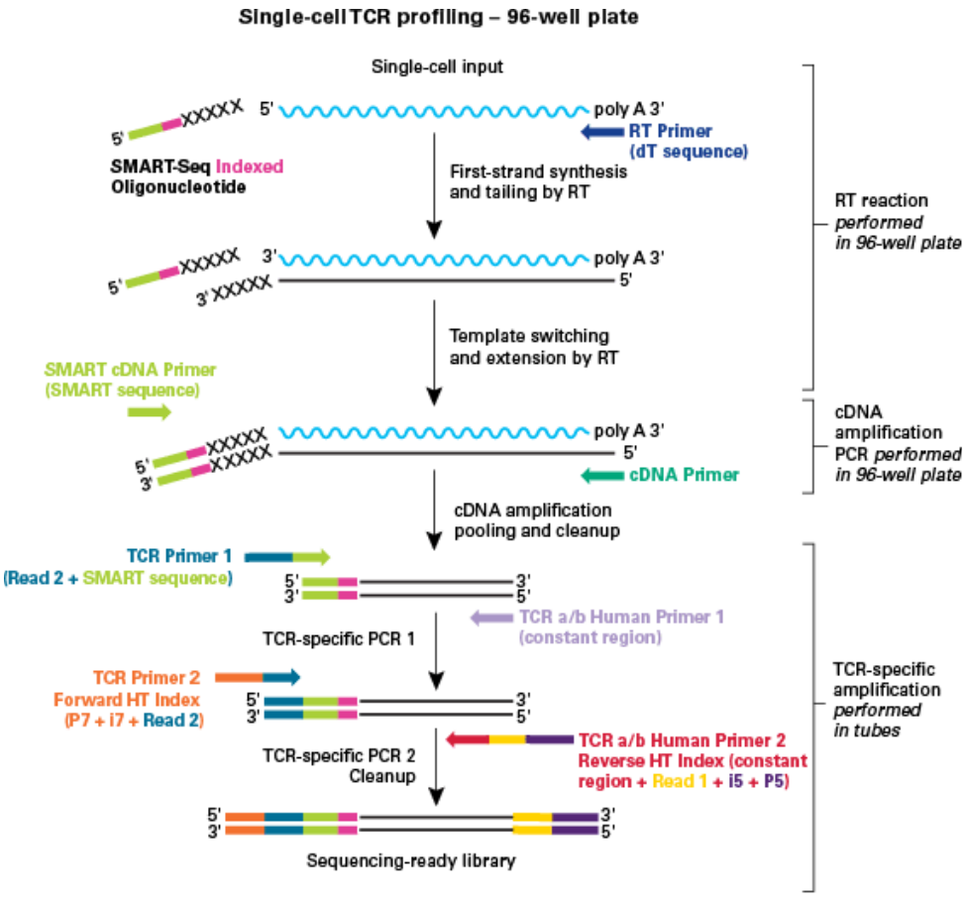
Single cells (K562) isolated by FACS were used to generate RNA-seq libraries with the SMART-Seq Stranded Kit (Stranded) and a SMART-Seq v4 Kit (SSv4; cDNA from this kit was further processed with a Nextera® XT DNA Library Preparation Kit). Panel A. The overlap in the total number of transcripts identified (FPKM >1) by each kit was analyzed and shown to be 83.8%. Panel B. The number of transcripts identified (FPKM >1) in individual cells was similar between the two kits, with a tighter range across cells processed with the SSv4 kit. Panel C. The reproducibility (Pearson correlation) of transcript expression levels across all cells from each kit was similar, although slightly higher and more consistent across cells processed with the Stranded kit.

產品	包裝	貨號
SMART-Seq® Stranded Kit	12 Rxns	634442
	48 Rxns	634443
	96 Rxns	634444

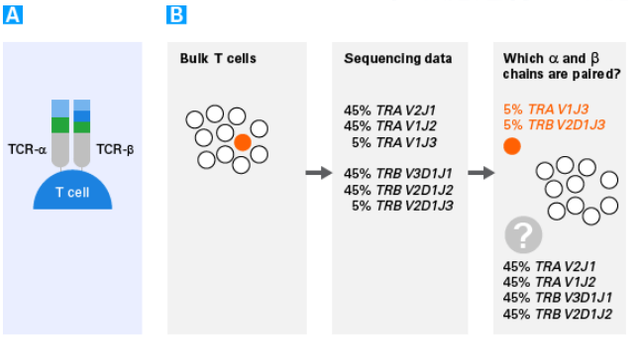
SMARTer® Human scTCR a/b Profiling Kit

- 靈活的工作流程： 可利用 FACS（流式細胞儀）或手動分選的細胞建構 Illumina sequencing-ready libraries
- 易於使用：升級版 index 可將 96 個樣本混合成 12 個 libraries，並可進一步混合，於 1 個 flow-cell lane 進行定序
- 高靈敏度：RACE-based 方法可以檢測低表現量 TCR variants
- 高特異性：full-length reads，多數 reads 可比對至目標區域並提供準確配對資訊

利用升級版 SMART 技術將 mRNA 反轉錄成 cDNA
特異性引子完整擴增 TCR alpha/beta chain

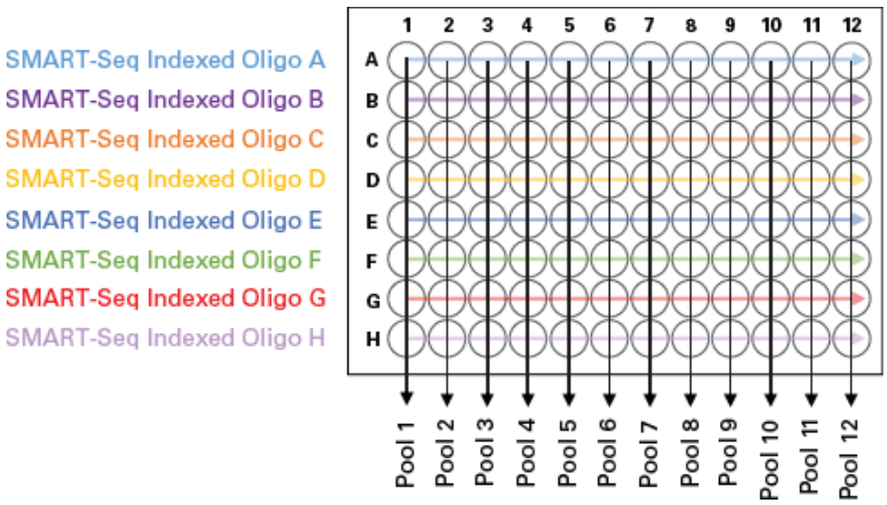


單細胞進行 T 細胞研究的優勢



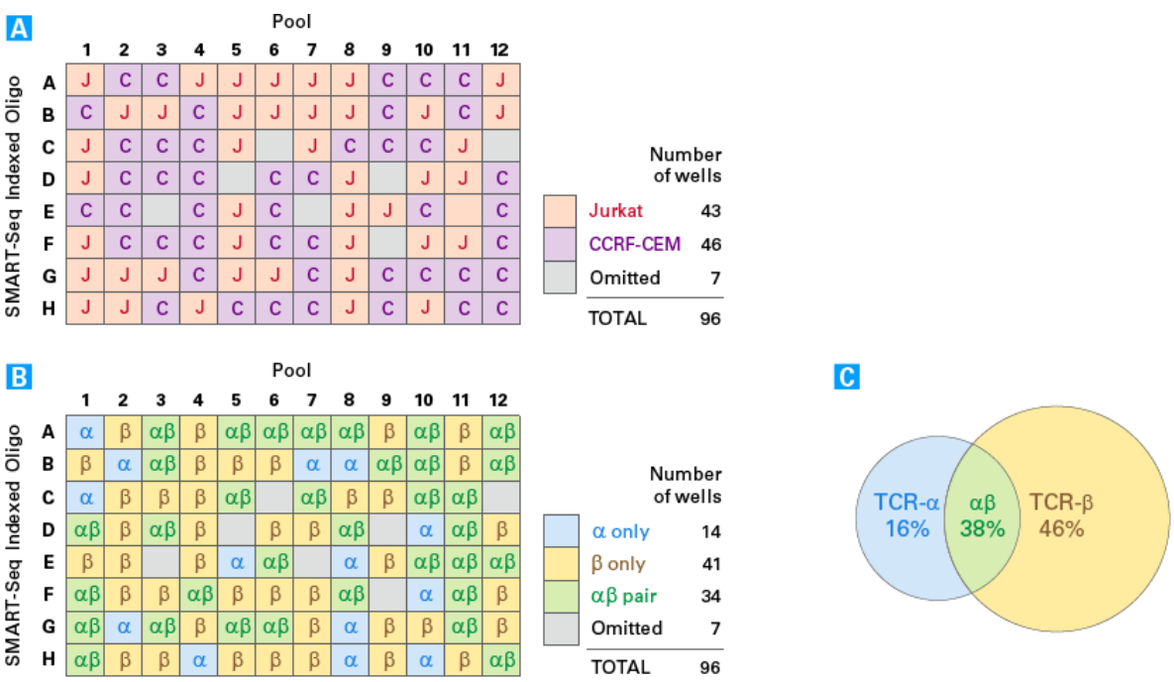
Panel A. Schematic of a T-cell receptor comprised of an alpha chain (TCR-α) and a beta chain (TCR-β). Panel B. Schematic representing the difficulties of obtaining pairing information for alpha and beta chains from bulk sequencing data. Rare clonotypes can allow for assessing the pairing of some cells (clonotypes in orange).

Pooling 策略



Samples are pooled by column, such that each pool contains eight cells, each with a differently indexed SMART-Seq Indexed Oligo. Different combinations of the Forward and Reverse HT indexes are used during PCR 2 to allow multiplexing of the samples into a single flow-cell lane (see the User Manual for more details).

分析 96 孔盤中的混和樣本



Panel A. Cell-type calling based on the identified clonotypes for each well. The seven omitted cells did not have clonotype calls for either TCR-α or TCR-β with read numbers that were above the threshold. Panel B. Analysis of pairing information. Paired TCR-αβ clonotypes were obtained for 34 cells in the plate. Panel C. The alpha, beta, or alpha-beta pairing information represented as a percent of cells analyzed. Omitted cells were not included in this analysis.

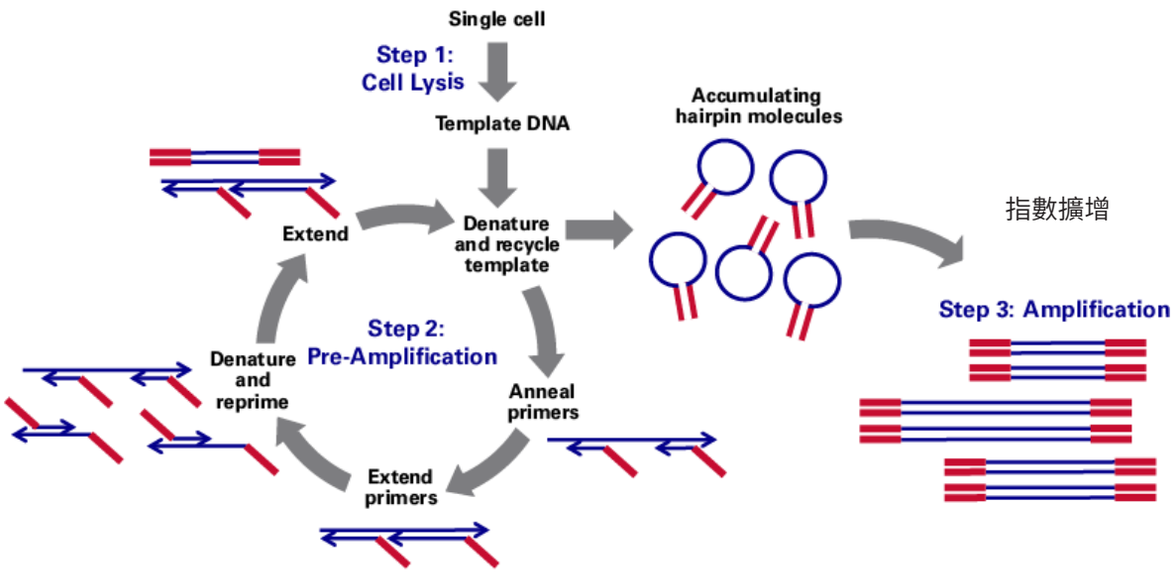
產品	包裝	貨號
SMARTer® Human scTCR a/b Profiling Kit	96 Rxns	634431
	480 Rxns	634432

PicoPLEX WGA family

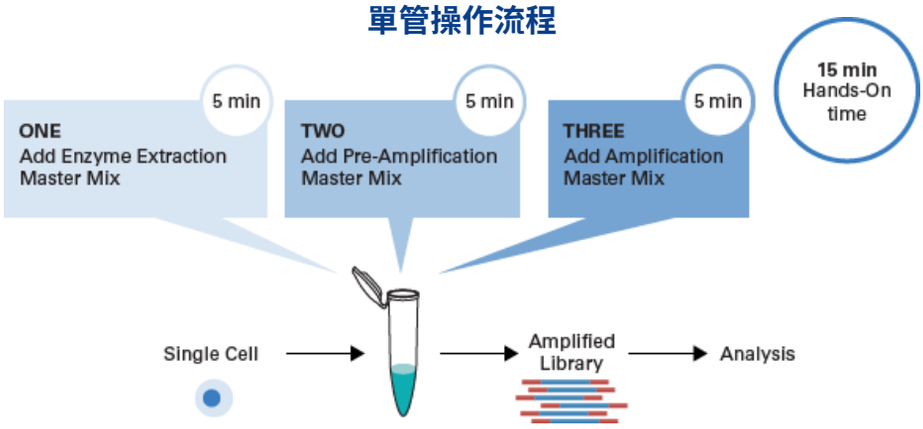
PicoPLEX 採用 quasi-random priming 技術進行全基因組擴增 (Whole Genome Amplification; WGA)，相較於 Multiple Displacement Amplification (MDA) 技術能更好偵測 SNV & CNV。

- 樣本：單細胞 或 起始量為 6 pg -50 pg DNA
- 卓越的等位基因再現性
- 易於使用和自動化，單管操作流程避免 handling errors
- 優良的實驗結果（例：array、PCR）

PicoPLEX 核心技術



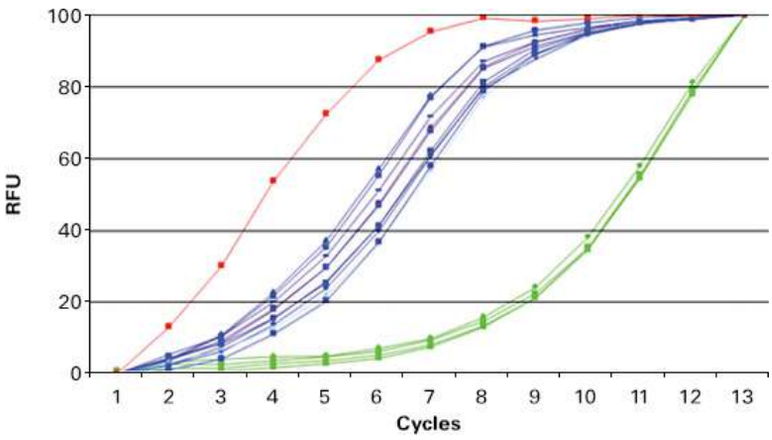
單管操作流程



產品	包裝	貨號
PicoPLEX® WGA Kit	50 Rxns	R30050
PicoPLEX® Single Cell WGA Kit	24 Rxns	R300671
	96 Rxns	R300672
	480 Rxns	R300673
PicoPLEX® Single Cell WGA Kit v3	24 Rxns	R300718
	96 Rxns	R300722
	480 Rxns	R300723

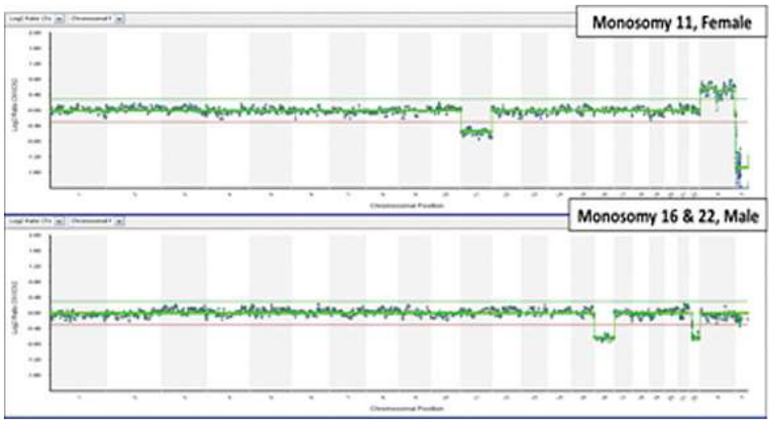
PicoPLEX® WGA Kit

單細胞擴增重複性分析



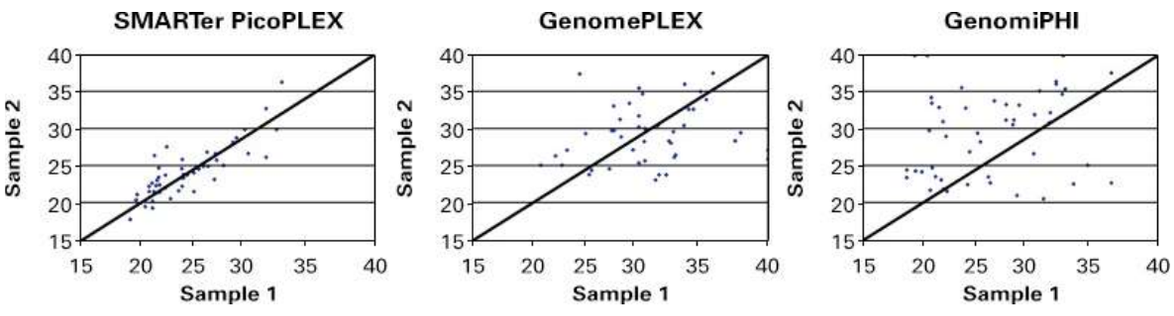
Flow-sorted cancer cells were amplified with PicoPLEX single cell WGA technology. Each of the cells (blue lines) amplified at the same rate and resulted in a similar, predictable yield. A pooled sample of five cells (red line) represents a positive control. Samples containing 0 cells (green lines; no template control) show very low background.

CNV 分析的良好準確性



Single-blastomere biopsies were amplified using PicoPLEX single cell WGA technology, labeled, and hybridized to BlueGnome's 24Sure arrays at Genesis Genetics Institute. Note the clear indication of CNVs. In 2011, ESHRE clinical trials confirmed accuracy of karyotyping using PicoPLEX technology.

優良的實驗再現性



Locus-specific qPCR was used to quantify 48 loci in independent single-cell libraries. Data shown compares results of DNA from two individual samples amplified with (left to right) PicoPLEX single cell WGA technology, GenomePLEX, and GenomiPhi using 10 pg of DNA. More than 90% of the product from the PicoPLEX single cell WGA technology produced identifiable, highly reproducible human sequences.

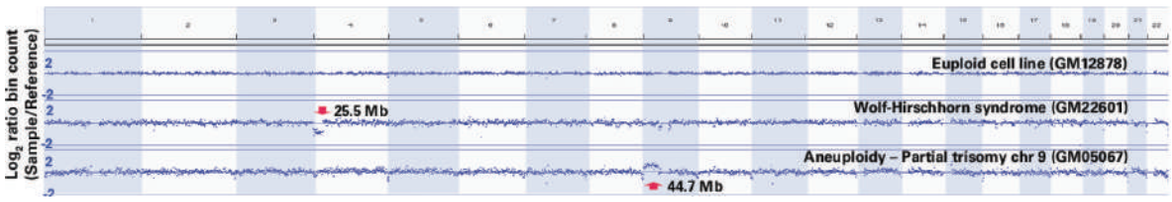
PicoPLEX® Single Cell WGA Kit v3

使用 PicoPLEX® Single Cell WGA Kit v3 及他牌進行 SNV 的檢測

The PicoPLEX WGA v3 system is more accurate at detecting SNVs when compared to DOPlify and REPLI-g technologies													
Depth of SNV position ≥10 Allele frequency ≥20%		PicoPLEX WGA v3 1 cell		PicoPLEX WGA v3 5 cells		DOPlify 1 cell		DOPlify 5 cells		REPLI-g 1 cell		REPLI-g 5 cells	
	Bulk	Rep1	Rep2	Rep1	Rep2	Rep1	Rep2	Rep1	Rep2	Rep1	Rep2	Rep1	Rep2
Number of SNVs called	74	57	67	69	67	34	57	62	67	Failed	Failed	40	Failed
Number of false positives		3	1	0	1	5	1	0	7	Failed	Failed	0	Failed
Average false positives		0.02%		0.005%		0.03%		0.035%		Failed		0	Failed
Call rate		78%	92%	95%	92%	47%	78%	85%	92%	Failed	Failed	55%	Failed
Average call rate		85%		93%		62%		88%		Failed		55%	Failed
Missed		17	7	5	7	40	17	12	7	Failed	Failed	34	Failed
Average locus dropouts		16.2%		8.1%		38.5%		12.8%		Failed		45.9%	Failed
Number of heterozygous SNVs called	45	45	38	45	45	36	31	38	41	Failed	Failed	32	Failed
Average allele dropouts		7.8%		0.0%		25.6%		12.2%		Failed		71.1%	Failed

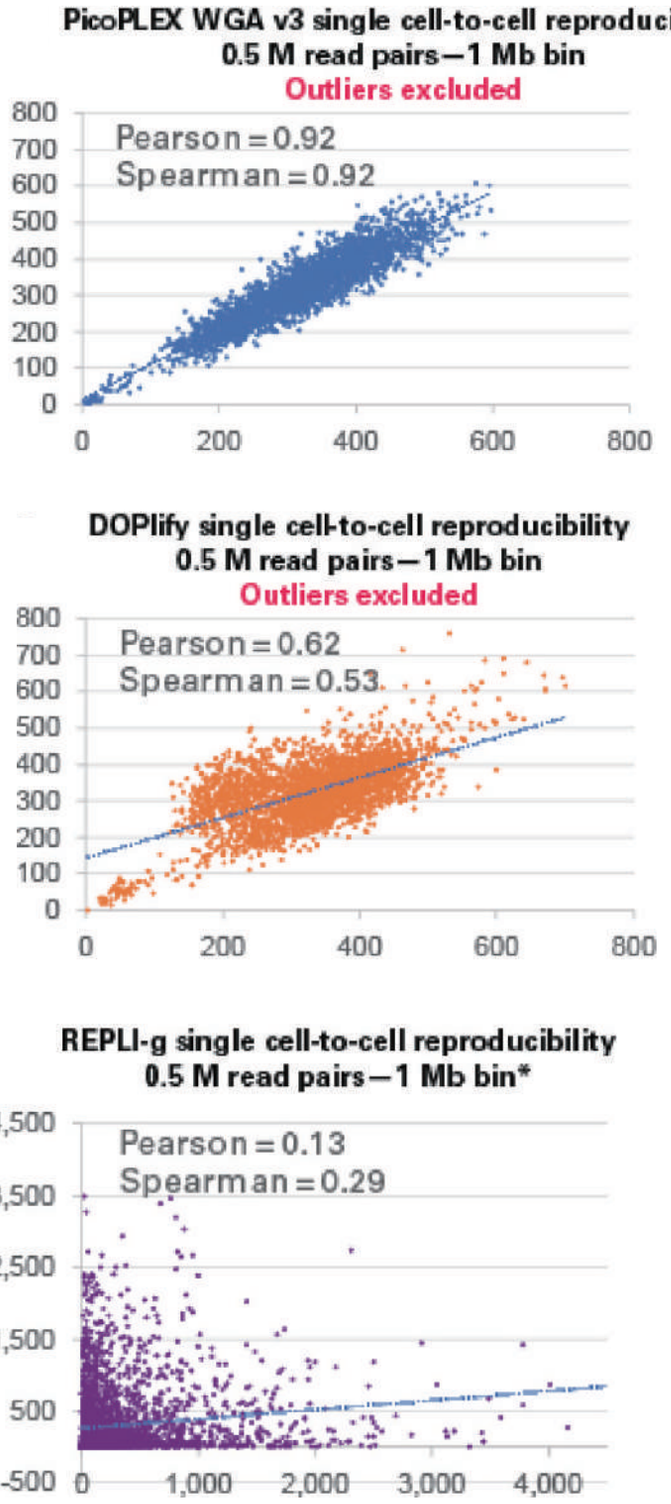
Whole genome amplification products from single- or five-cell samples of a GM12878 cell line (Coriell Institute) were prepared in replicates, and SNVs detected were reported as numbers and percentages. Although the REPLI-g system produced sufficient yield, only one of the five-cell samples contained enough amplicon material to sequence, and, therefore, no data is available for the other samples. An intersection of Genome In a Bottle (GIB) variants to hg19 (human genome assembly GRCh37, Ensembl) indicates that a total of 78 variants are expected to be present for the GM12879 cell line. Due to the amplicon design, paired-read lengths of 75 bp were too short to capture 4 out of the 78 SNVs; therefore, the total number of capturable SNVs was cut down to 74. VarDict was used to interpret SNVs from BAMfiles using the following criteria: depth of SNV position ≥ 10 reads (10X coverage), allele frequency ≥ 20%.

使用 PicoPLEX® Single Cell WGA Kit v3 及他牌進行 CNV 的檢測



Single cells from various cell lines (GM22601, GM05067, and GM12878) were amplified using a prototype of the PicoPLEXSingle Cell WGA Kit v3. 1 ng of the purified product was used as input for a Nextera® XT kit and sequenced on an Illumina MiSeq® platform at a read length of 2 x 75 bp. Fastq files were trimmed to remove adapters and then aligned to the human genome assembly GRCh37. Only autosomes are reported. For both panels, alignment was normalized to 1 million reads, and the number of reads per bin of 1 Mb was calculated using bedtools 2.25.0. The log2 ratio of the bin counts (Sample/Reference) was plotted using the Integrative Genomics Viewer.

優良的實驗再現性

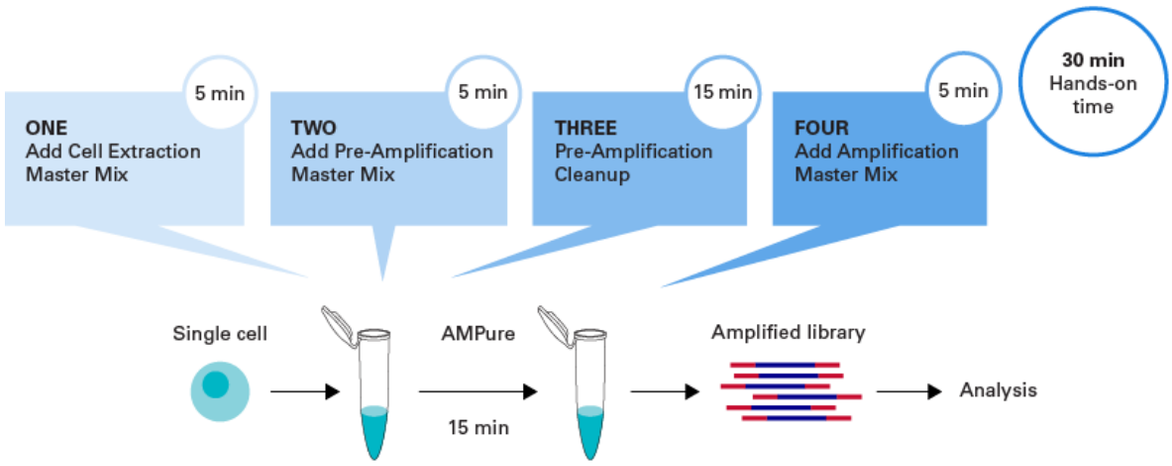


Whole genome coverage reproducibility of the prototype PicoPLEX Single Cell WGA Kit v3 in comparison to DOPlify and REPLI-g (MDA) kits. WGA products were prepared from single-cell samples of GM12878 in replicates, using a prototype of PicoPLEXWGA v3, DOPlify, and REPLI-g (MDA) kits.1 ng of amplified product was used as input for a Nextera XT kit, and the resulting libraries were sequenced on an Illumina MiSeq platform using a read length of 2 x 75 bp. After read alignment to human genome assembly GRCh37 and normalization to 1 million reads (0.5 million read pairs), the number of reads per bin of 1 Mb was calculated using bedtools 2.25.0. Total reads in each window from two single-cell libraries were plotted, with Pearson and Spearman correlations calculated and indicated on each graph

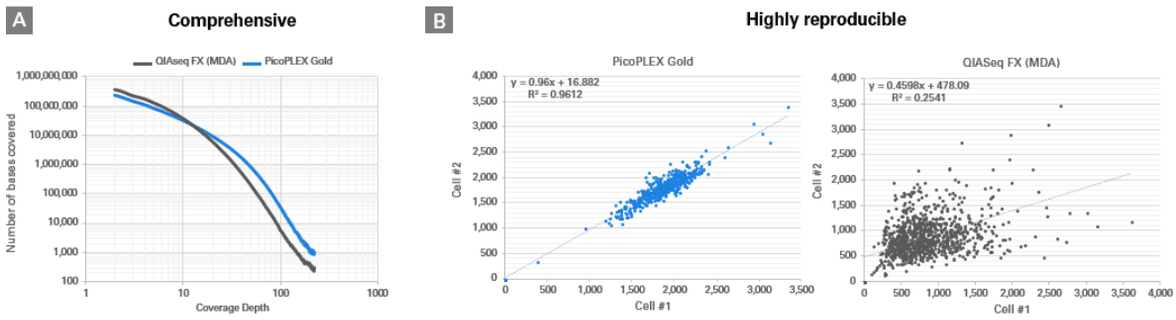
SMARTer® PicoPLEX® Gold Single Cell DNA-seq Kit

- 樣本：1–5 mammalian cells 或 等量的 gDNA 作為起始量
- Formalin 固定的細胞也可做！
- 需要搭配 SMARTer Index kits ，三小時製備成可以上機定序的基因庫
- 適用於準確且可重複的拷貝數變異 (Copy Number Variats; CNVs)、單核苷酸變異 (Single-nucleotide variants; SNVs)、 插入缺失 (InDels) 和小結構變異的偵測與分析

流線型操作流程，手動時間小於 30 分鐘

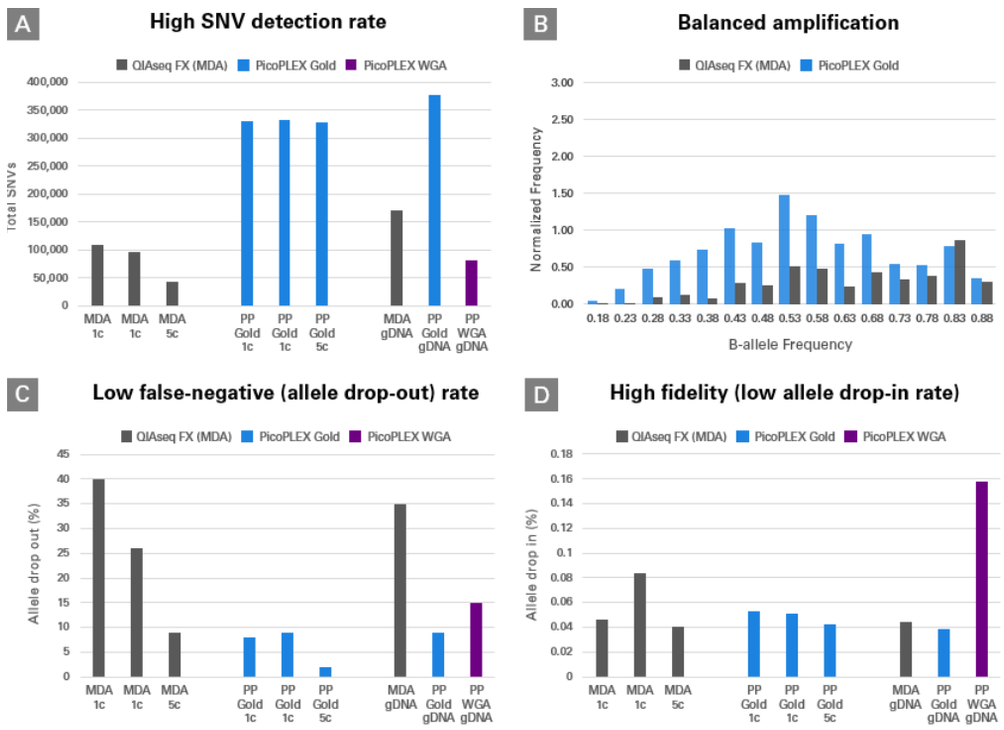


高覆蓋率、良好的一致性與再現性



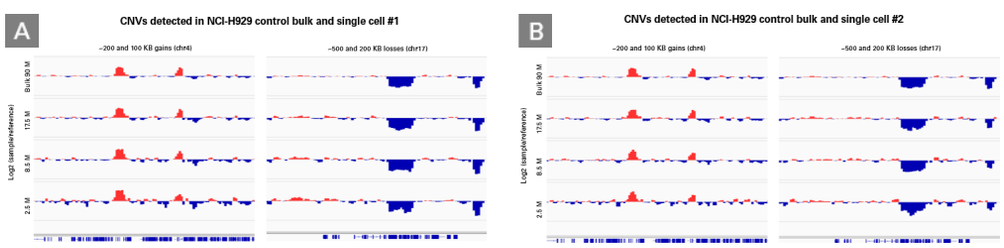
Panel A. A log-log plot showing the number of bases covered at various depths of sequencing (~35M read pairs, PE 2 x 150 bp). The coverage of PicoPLEX Gold was similar to QIAseq FX (MDA) at lower depths and greater at higher depths. Panel B. The reproducibility of coverage evaluated by comparing total reads in 100-kb bins. The consistency of the total reads in each window from the two single-cell libraries is significantly higher for PicoPLEX Gold (left), both in comparison to QIAseq FX (right) and to other technologies in the market (data not shown).

使用 SMARTer® PicoPLEX® Gold Single Cell DNA-seq Kit 進行 SNV 的檢測



Panel A. Comparison of SNV-detection rate between QIAseq FX (MDA), PicoPLEX Gold (PP Gold), and SMARTer PicoPLEX WGA (PP WGA) kits from one cell (1c), five cells (5c) or 15 pg of NA12878 gDNA inputs. Single and five cells were sequenced to a depth of ~35M read pairs, and gDNA samples to a depth of ~40M read pairs. The high fidelity and robust coverage of PicoPLEX Gold (blue bars) provide a clear advantage in detecting a greater (~2–9 fold) number of high-quality SNVs compared to QIAseq FX (gray bars) and PicoPLEX WGA (purple bar). Panel B. The symmetric distribution of the B-allele frequencies for PicoPLEX Gold (blue bars), centered around 0.5, indicating a balanced recovery of both alleles. PicoPLEX has better allele balance compared to QIAseq FX (MDA) (gray bars). Panel C. Unbiased amplification of PicoPLEX Gold results in the lowest allele drop-out (false-negative) rates among all single cell library-preparation technologies tested. Panel D. High fidelity of the polymerases used in PicoPLEX Gold kit (blue bars) leads to minimal allele drop-in rates that are comparable to QIAseq FX (gray bars) and significantly lower than PicoPLEX WGA (purple bar).

使用 SMARTer® PicoPLEX® Gold Single Cell DNA-seq Kit 進行 CNV 的檢測



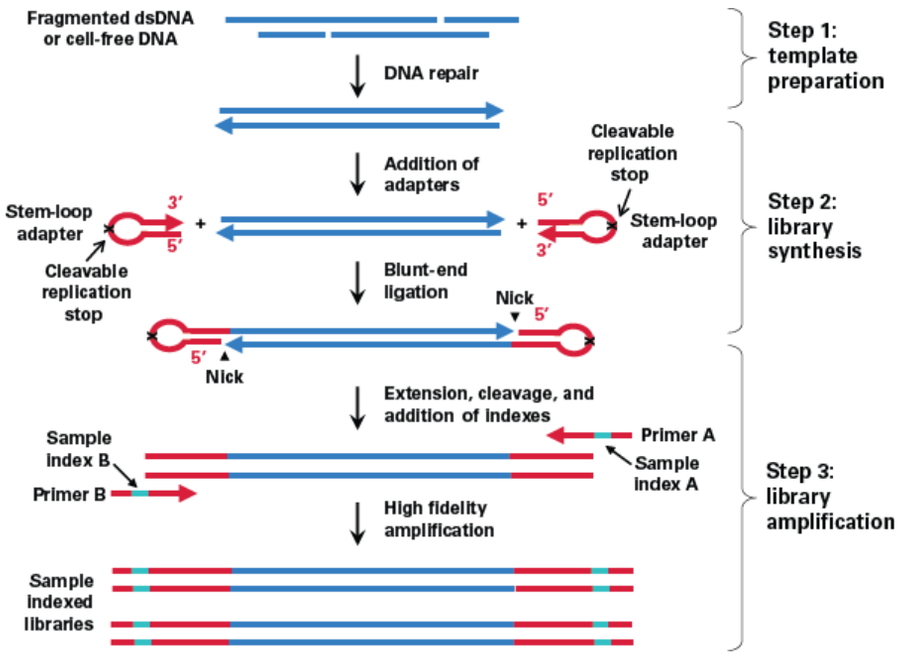
Log2 ratio of the total number of reads in 50-kb bins from single NCI-H929 cells, shown as one cell in Panel A and a second cell in Panel B. Red bars represent copy-number gains while blue bars represent losses. The top row of the graphs in each panel depicts the control bulk sample sequenced to a depth of 90 million read pairs. The highly reproducible coverage of the SMARTer PicoPLEX Gold kit enables the accurate detection of structural variants as small as 100 kb, even at shallow sequencing depths (2.5–8.5 million read pairs).

產品	包裝	貨號
SMARTer® PicoPLEX® Gold Single Cell DNA -s eq Kit	24 Rxns	R300669
	96 Rxns	R300670
	384 Rxns	R300698

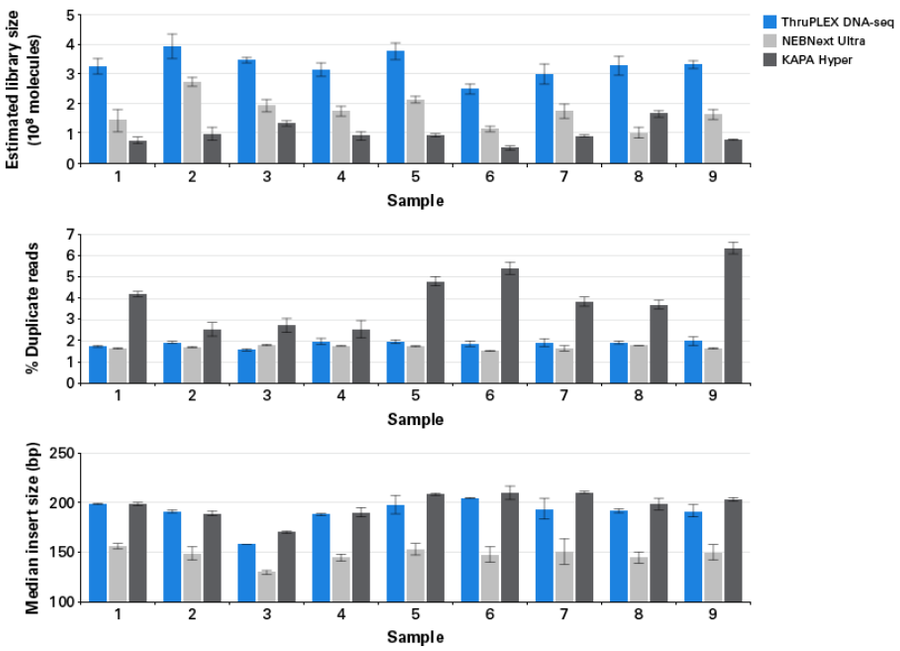
ThruPLEX DNA-Seq Kit

- 高靈敏度：50pg - 50ng DNA
- 簡單快速的作業流程：單管、3 步驟，2 個小時完成 libraries
- 與主流的 Target enrichment 平台相容—如 Agilent SureSelect、Roche Nimblegen SeqCap EZ 和 IDT xGen Lockdown probes

ThruPLEX 核心技術

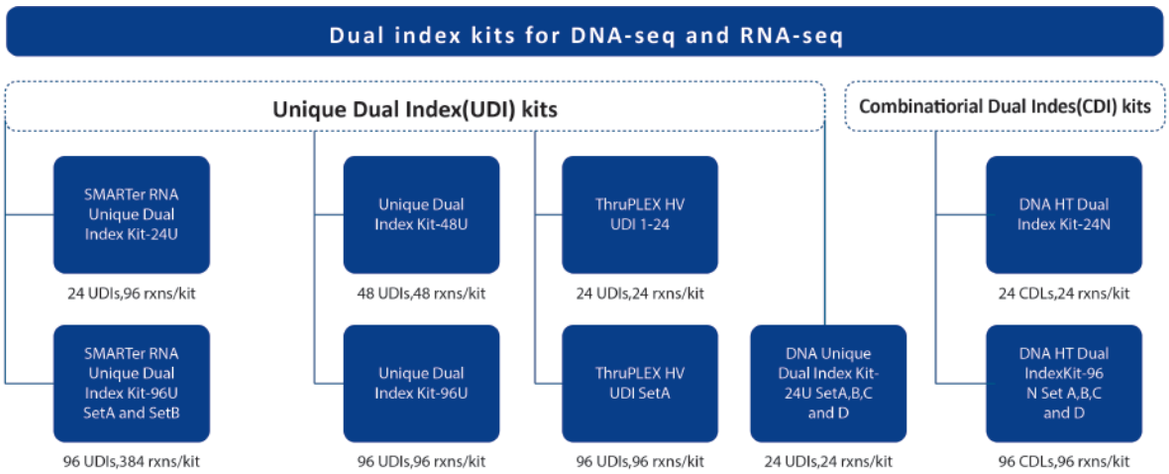


應用於 FFPE 樣本時，ThruPLEX DNA-Seq Kit 與他牌的比較



產品	包裝	貨號
ThruPLEX® DNA-Seq Kit	24 Rxns	R400674
	48 Rxns	R400675
	96 Rxns	R400676
	480 Rxns	R400677

Dual index kits



適用RNA- Seq

產品	版本	包装	貨號
Unique Dual Index Kit - 48U		48 Rxns	R400744
Unique Dual Index Kit - 96U		96 Rxns	R400745

適用DNA -S eq

產品	版本	包装	貨號
DNA HT Dual Index Kit - 24N		48 Rxns	R400664
DNA HT Dual Index Kit - 96N	Set A	96 Rxns	R400660
	Set B	96 Rxns	R400661
	Set C	96 Rxns	R400662
	Set D	96 Rxns	R400663
DNA Unique Dual Index Kit -2 4U	Set A	48 Rxns	R400665
	Set B	48 Rxns	R400666
	Set C	48 Rxns	R400667
	Set D	48 Rxns	R400668

Scepter™ 3.0 智能掌上型細胞計數器

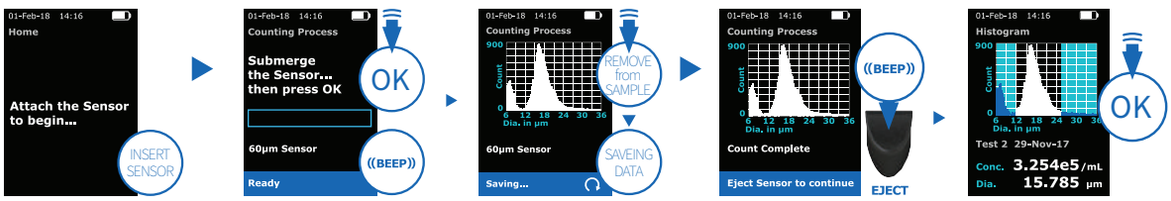
採用業界公認的 “計數標準” Coulter Coulter 電阻抗原理，避免發生圖像式傳統細胞計數方法常見的失真狀況。

30s OK　不須染色　3 重結果　細胞健檢

1. 長條圖顯示細胞計數結果，方便讀取。
2. 獨創人體工學設計，便於在無菌操作台內測量及存放。
3. 可簡單檢測細胞健康狀況 : 可通過監測細胞大小以及型態，獲得細胞健康狀態。
4. 便於攜帶。
5. 準確度高 : 一次計數上千的細胞，避免母群體過少造成誤差。
6. 三重結果 : 一次偵測可得到 細胞平均濃度， 細胞平均大小，以及細胞平均體積。
7. 操作簡單 : 使用方式如一般 pipet，人人都能快速上手
8. 多種細胞混合液也能偵測 : 藉由細胞的大小不同，可各別偵測不同族群細胞。

細胞計數三步驟

1 插入 Sensor　2 取樣及結果存取　3 移除 Sensor



可無線傳輸或 USB 匯出計數結果

可藍牙連接印表機即時列印結果

使用指南

Sensor tips 選擇指南

貨號	Sensor tip 規格	測量濃度範圍	適合測量顆粒直徑範圍(um)
PHCC340KIT	40 um	5 X 10^4-1.5 x10^6 cells/ml	5-15
PHCC360KIT	60 um	1 X 10^4-5 x10^5 cells/ml	8-25

CURIOSIS FACSCOPE B 全自動細胞計數器

- 全自動 XYZ 平台定位，對焦擷取細胞影像。
- 智能算法，卓越的識別技術，快速獲取細胞影像，精準計數各種形態細胞 (包含細胞團塊和不規則的細胞形態) 的數量。
- 全觸控面板，操作簡單。
- 偵測細胞濃度範圍最廣 : 1 x 10^4 至 1 x 10^7 cells/ mL 。
- 可偵測細胞大小 5-60 µm 。
- 具有 gating 功能。
- 搭配使用 4 通道 C-slide 細胞計數板，降低操作次數。
- C-slide 具 Neubauer Improved (NI) 網格，也可以用於手動計數。
- 全機韓國製造生產， 保固一年。

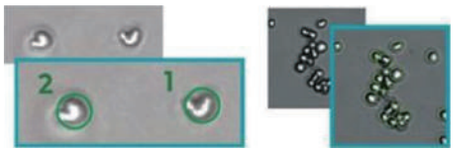
FACSCOPE B 儀器規格

- 螢幕顯示 : 觸控式彩色 LCD
- 光學系統 : 4 倍物鏡 / 高性能 CMOS 單色傳感器
- 外部尺寸 :
  163 mm（寬）x 293 mm（長）x 216 mm（高）
- 重量 : 5 公斤

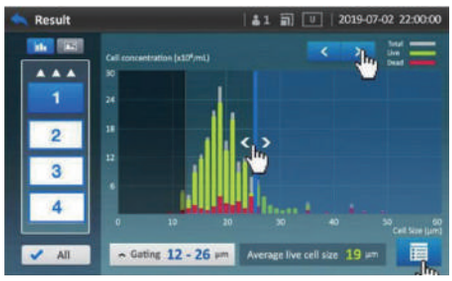
FACSCOPE B 儀器實機操作畫面

1 簡易操控介面 , 智能計算顯示細胞數量及細胞存活率

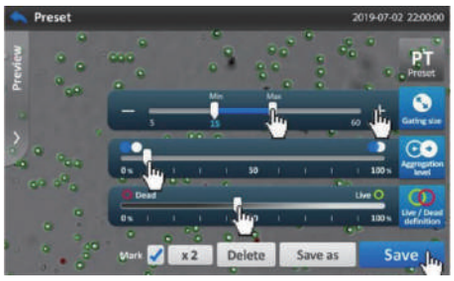
2 正確識別細胞團塊 / 不規則細胞形態



3 gating 功能調整偵測範圍

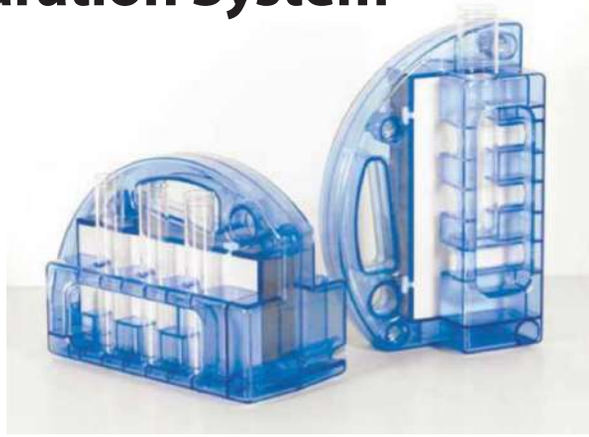


4 可依據細胞特性，最佳化計數條件

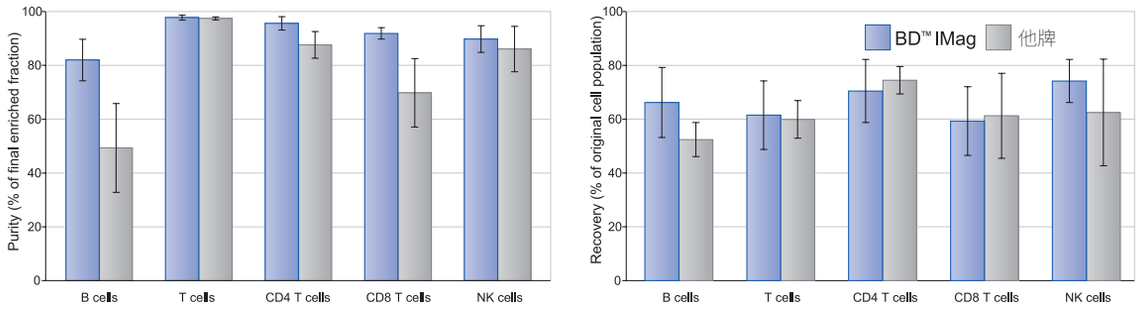


BD IMag Cell Separation System

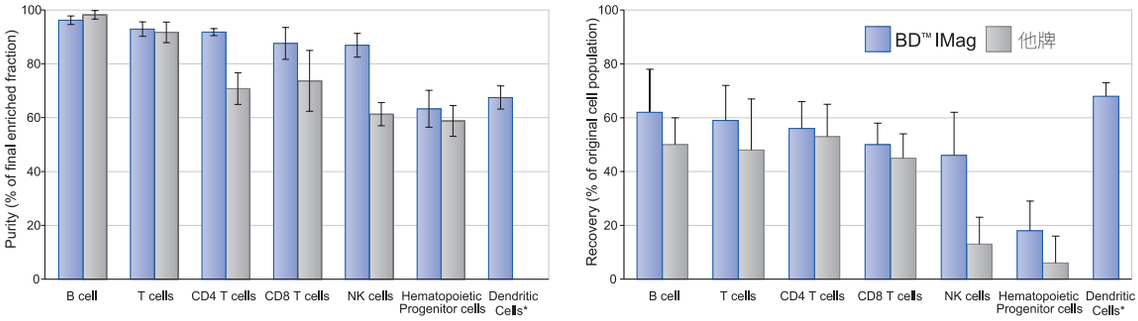
- 磁珠分離細胞系統。
- 簡單、快速分離特定細胞。
- 不需使用昂貴的 Column。
- 純度高、回收率高。



BD IMag™ Enrichment Set (Negative Selection 套裝試劑組) 之細胞純度與回收率比較



人類周邊血單核細胞 (PBMC) 當中，淋巴球亞型 (subtype) 細胞分別用 BD IMag™ Enrichment Set 及其他品牌試劑分離出來之後，比較最後收集細胞的純度及回收率。總體而言，BD IMag 效果較佳！



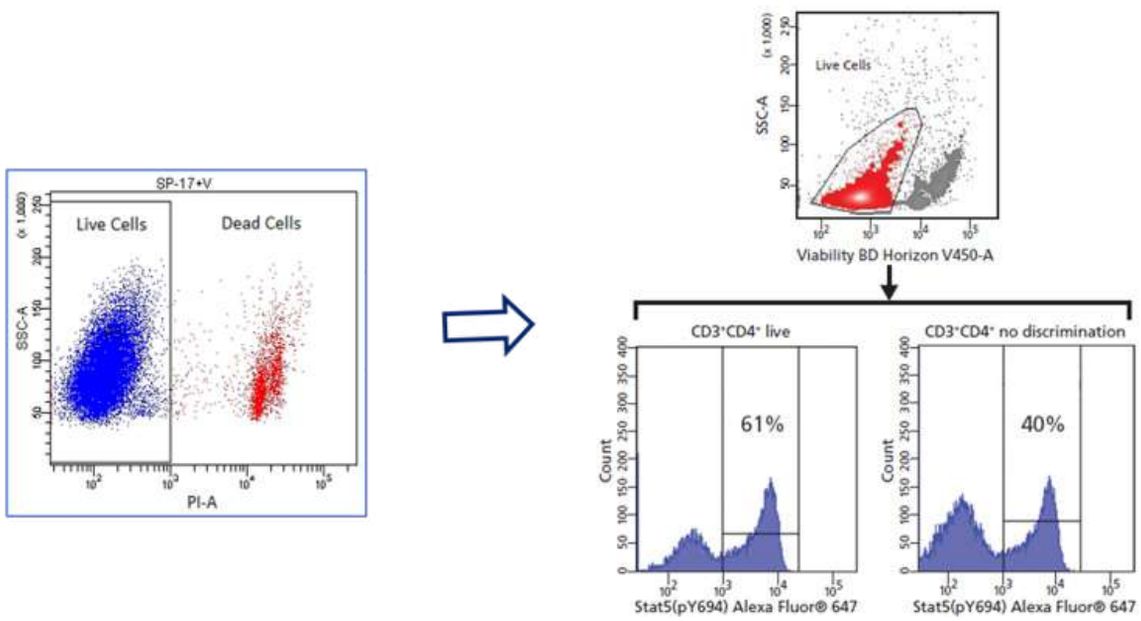
小鼠脾臟的淋巴球亞型 (subtype) 細胞或骨髓中的造血先驅細胞 (hematopoietic progenitor cell) 分別用 BD IMag™ Enrichment Set 及其他品牌試劑分離出來後，比較最後收集細胞的純度及回收率，由數據可知 BD IMag 效果較佳！

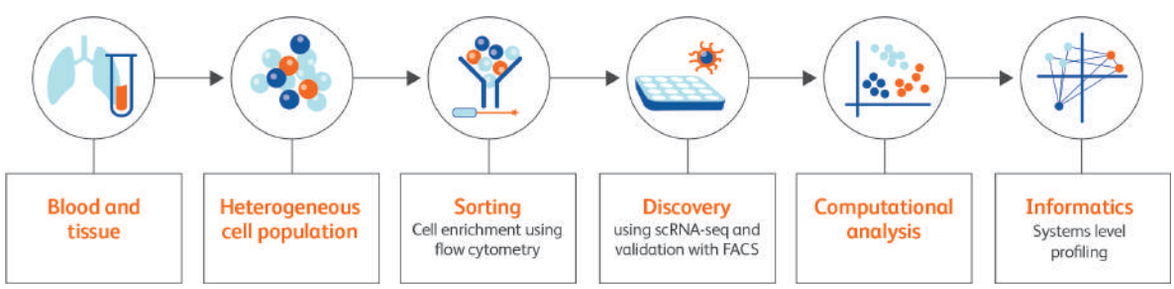
貨號	產品	包裝	分離細胞類型
Negtive selection			
557987	BD IMag™ Human NK Cell Enrichment Set - DM	1×10^9	NK
557874	BD IMag™ Human T Lymphocyte Enrichment Set-DM	1×10^9	T cell
558521	BD IMag™ Human Naive CD4 T Cell Enrichment Set - DM	1×10^9	T helper cell
557939	BD IMag™ Human CD4 T Lymphocyte Enrichment Set-DM	1×10^9	T helper cell
558569	BD IMag™ Human Naive CD8 T Cell Enrichment Set - DM	1×10^9	T cytotoxic cell
557941	BD IMag™ Human CD8 T Lymphocyte Enrichment Set-DM	1×10^9	T cytotoxic cell
558420	BD IMag™ Human Dendritic Cell Enrichment Set - DM	1×10^9	DC
560030	BD IMag™ Human Lineage Cell Depletion Set - DM	1×10^9	富集 stem cell, progenitor cells and dendritic cells
Postive selection			
552593	BD IMag™ Anti-Human CD3 Magnetic Particles - DM	1×10^9	T cell
557767	BD IMag™ Anti-Human CD4 Particles - DM	1×10^9	T helper cell
557766	BD IMag™ Anti-Human CD8 Magnetic Particles - DM	1×10^9	T cytotoxic cell
558705	BD IMag™ Anti-Human CD11c Particles - DM	1×10^9	DC
557775	BD IMag™ Anti-Human CD56 Magnetic Particles - DM	1×10^9	NK cell
558005	BD IMag™ Anti-Human CD25 Magnetic Particles - DM	1×10^9	Treg:Human CD4 T Lymphocyte Enrichment Set - DM, followed by the positive selection of the CD25+ population.

BD Cell viability dye

- PI , 7-AAD: 常用的 cell viability dye, 偵測 DNA 含量 , 但對於固定液和打洞液是無法耐受的。
- BD Horizon ™ Fixable Viability Stain (FVS) Reagents : FVS reagents 會與細胞表面或細胞內的 Amine 共價結合，活細胞的細胞膜沒有通透性，FVS 僅會存於細胞膜表面；但死細胞的細胞膜變得具有通透性，細胞表面及細胞內皆可偵測到 FVS 螢光，比活細胞的 FVS 螢光強度強 10-20 倍以上，因此便可以簡單辨別出細胞的死活。 最大的優點是對固定液和打洞液具耐受性。

圈出並去除死細胞 讓分析結果的統計更加精確





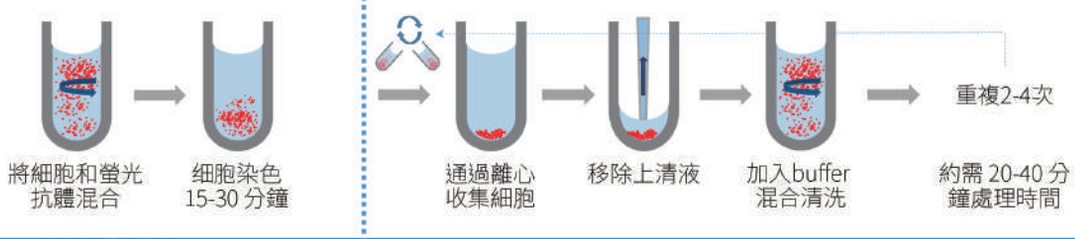
品名	貨號	功用
7-AAD	559925	stain the dead cells (red)
Calcein AM cell permanent dye	564061	stain the live cells (green)
Draq7™ , 0.3 mM	564904	stain the dead cells (red)
BD™ Stain Buffer (FBS)	554656	Antibody staining buffer
BD™ FC block	564219	Fc receptor block buffer

Laminar Wash™ System

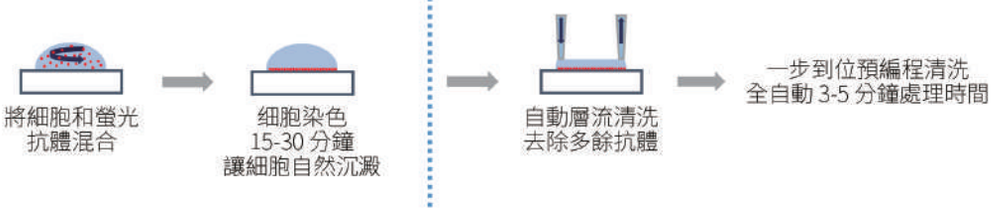
自動化無離心清洗平台 優化樣品處理步驟

- 一步驟完成清洗，大幅縮短流程至 3-6 分鐘。
- 非傳統離心洗滌，改善細胞的壓力與凋亡情況。
- 自動化實驗流程，增加數據再現性與一致性。
- 減少手動操作，降低人力成本。
- 層流 (laminar flow) 式清洗，大幅減少細胞流失 。
- 操作簡易，容易融入實驗室現有流程。

細胞離心清潔方式



DA-Cell清洗方式



Laminar Wash™System

MINI 1000

16 well 樣品自動清洗系統

HT2000

96 well 樣品自動清洗系統

AUTO 1000

全自動化樣品處理平台

ZENOGEN PHARMA STEM-CELLBANKER® 系列 & HSC-BANKER® 無血清細胞專用凍存液

簡介 & 特色

- 使用日 / 美 / 歐洲藥典最高等級原料，成分安全明確
- 完全不含血清和動物來源的成分，無動物衍生成分的污染風險，批次之間穩定性高
- 即開即用型完整配方，不需再加入 DMSO 或稀釋。操作簡單，無需繁瑣的製備流程
- 可直接將細胞凍存在 -80°C冰箱，無需程序降溫儀，也不需液態氮保存桶，可節省成本、時間、步驟
- 不會對凍存的細胞及組織內的 DNA 或 RNA 造成損害，細胞功能維持完整
- 解凍後可維持細胞活性，同時保持細胞多能性、正常核型（karyotype）和增殖能力
- 全系列產品遵循 JPN, EU, US, 和 PIC/S GMP 規範生產和品質控制
- 已完成 US FDA 與 Japan PMDA 的 Master File (MF) 登記申請

STEM-CELLBANKER®

20 mL / 100 mL

幹細胞 通用

Dr. Yamanaka 也愛用！ Nature SCIENTIFIC REPORTS | 4 : 3594 | DOI : 10.1038/srep03594

適合再生醫學研究
凍存幹細胞、免疫細胞、組織

STEM-CELLBANKER®

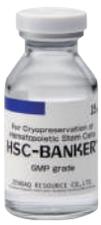
DMSO-free 20 mL / 100 mL

不含 DMSO

對細胞傷害降至最低

HSC-BANKER®

15 ml



造血幹細胞 通用

- 玻璃安瓶包裝，取用不容易汙染
- 1:1 等比添加
- 凍存效果優於傳統使用 DMSO &DEXTRAN 複合凍存液

安瓶包裝，取用不易汙染
1:1 等比添加

STEM-CELLBANKER® EX

100 ml

- 含有經過驗證的靜脈注射成分，適合作賦形劑使用
- STEM-CELLBANKER® EX 與 HSC-BANKER® 成分相同
- 已經過長期安定性評估，適合用於 ADSCs 凍存

凍存 HSC, ADSC, 其他來源幹細胞
已完成日本 PMDA 的 (MF) 登記

細胞保存在 STEM-CELLBANKER® DMSO Free GMP grade，

解凍後經測試，細胞活性為 80-90%。

Cell type	Description		
P3/x63-Ag8.U1	Murine myeloma cell	SK007	Human B-cell line
2D-8	Murine hybridoma	K562	Human caucasian chronic myelogenous leukaemia cell
YAC-1	Murine lymphoblast	HeLa	HUman uterine cervical carcinoma cell
NBM-Lu	Normal newborn murine fibroblast cell line	HepG2	Human hepatocellular carcinoma cell
129SV	Mouse ES cell	Caco-2	Human colonic adenocarcinoma cell
Feline PBMC	Feline peripheral blood mononuclear cells	UE6E7-16	Human Mesenchymal cell
Canine PBMC	Canine peripheral blood mononuclear cells	UE7T-13	Human Mesenchymal Stem cell
Jurkat	Human T-cell line	201B7	Human iPSc ell

! 另有一般細胞專用的凍存液，詳情請洽當區業務

PCR/qPCR Tube 與封膜

NEPTUNE Tools for Life Sciences　ANCELL Technology Inc.

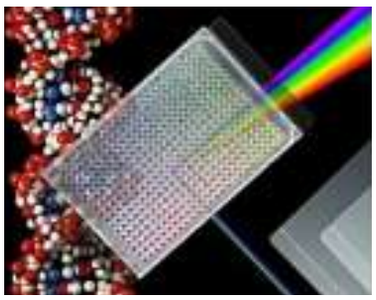
PCR & qPCR Tubes/ 8 連排/ Plate	品名	NEPTUNE	ANCELL	規格
單管	0.2ml (平蓋)	NEPTUNE 3423		1,000/ pack
	0.2ml (平蓋) (Sterile)	NEPTUNE 3423.S		1,000/ pack
PCR/qPCR 8 連排	0.2ml (無蓋)		ANCELL 3111-00	125/ pack
	0.2ml (管蓋分離 凸蓋)	NEPTUNE 3459.8		125/ pack
	0.1ml (管蓋分離 平蓋)		ANCELL 3145-00	125/ pack
	0.2ml (管蓋分離 平蓋)		ANCELL 3135-00	125/ pack
	0.1ml (管蓋相連 平蓋)		ANCELL 3248-00	120/ pack
	0.2ml (管蓋相連 平蓋)		ANCELL 3247-00	120/ pack
qPCR Plate	0.1ml (無裙邊)		ANCELL 3145-00	20/ pack
	0.2ml (無裙邊)	NEPTUNE 3730	ANCELL 3400C00	10/ pack
	0.1ml (半裙邊)		ANCELL 3421-00	10/ pack
	0.2ml (半裙邊)	NEPTUNE 3742	ANCELL 3420-00	10/ pack

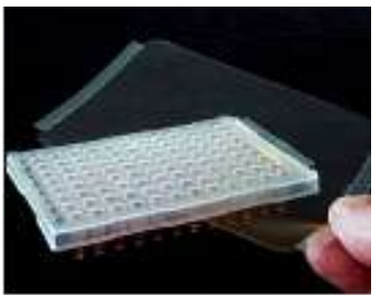

無裙邊款


半裙邊款

EXCEL SCIENTIFIC

品號	品名	功能	黏性	包裝
EXCEL F2-100	FoilSeal, Chemically Resistant (鋁膜)	PCR/ 儲存用	有	100片
EXCEL XTR-100	eXTReme™ Seal for Raised Rim Plates (透明膜)	PCR/ qPCR	有	100片
EXCEL TSS-RTQ-100	ThermalSeal® RTS, Silicone Adhesive (高光學透明度/ 透明膜)	PCR/ qPCR	無	100片





Filter Tip

S3 (Sample Saving Surface)

1 低殘留表面處理　　2 保留您的珍貴樣品　　3 精準化實驗數據

Pipette Tips – 三大特色

FlexFit ™
材質軟
契合度高
可輕鬆插入
符合人體工學

X-Resin ™
自然材質
降低樣品殘留
降低實驗誤差
增加精準度

Blade ™
前端特殊薄壁設計
防止水滴形成
可完全排出液體
降低樣品殘留於尖端處
增加精準度

Filter Tip 盒裝滅菌

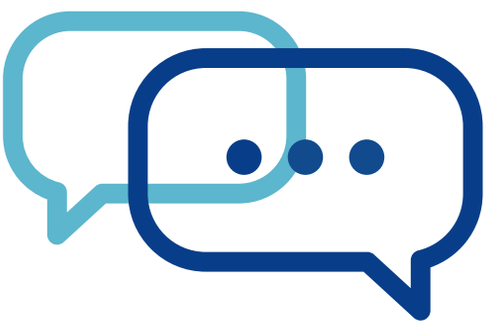
Biotix　NEPTUNE Tools for Life Sciences

Filter Tips(盒裝滅菌)	品號	品名	規格
BIOTIX	M-0010-9FC	10 ul, Filtered, Sterile	10 trays of 96/ pack
	M-0011-9FC	10 ul , Filtered, Sterile (加長型)	10 trays of 96/ pack
	M-0020-9FC	20 ul, Filtered, Sterile	10 trays of 96/ pack
	M-0100-9FC	100 ul, Filtered, Sterile	10 trays of 96/ pack
	M-0200-9FC	200 ul, Filtered, Sterile	10 trays of 96/ pack
	M-0300-9FC	300 ul, Filtered, Sterile	10 trays of 96/ pack
	M-1250-9FC96	1250 ul, Filtered, Sterile	10 trays of 96/ pack
NEPTUNE	BT10XLS3	10 ul , Filtered, Sterile (加長型)	10 trays of 96/ pack
	BT20	20 ul, Filtered, Sterile	10 trays of 96/ pack
	BT100	100 ul, Filtered, Sterile	10 trays of 96/ pack
	BT200	200 ul, Filtered, Sterile	10 trays of 96/ pack
	BT300	300 ul, Filtered, Sterile	10 trays of 96/ pack
	BT1000.96	1000 ul, Filtered, Sterile	8 trays of 96/ pack
	BT1250	1250 ul, Filtered, Sterile	8 trays of 96/ pack

Eppendroff 微量離心管

NEPTUNE Tools for Life Sciences　ANCELL Technology Inc.

品牌	品號	體積	耐-80℃	離心轉速	低殘留	滅菌	規格
NEPTUNE (好開)	NEPTUNE 4445.X	1.6mL	Yes	20,000g			500/ pack
	NEPTUNE 4445.S.X	1.6mL	Yes	20,000g		Yes	500/ pack
ANCELL (低殘留)	ANCELL 1260-00	1.5mL	Yes	20,000g	Yes		500/ pack



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