

Performance advances and workflow simplifications for single cell RNA-Seq and DNA-Seq

Next-generation sequencing

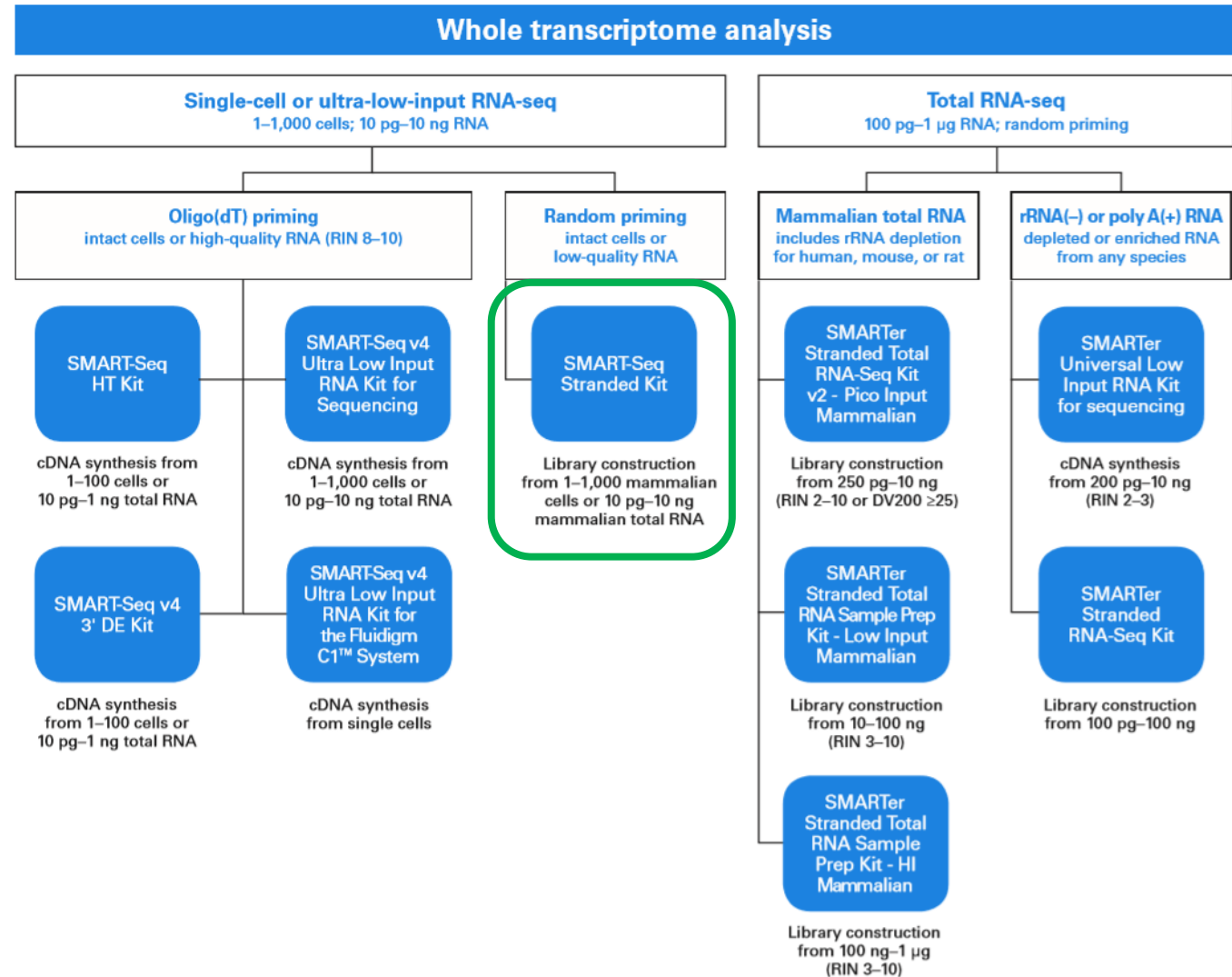


Breaking performance barriers

A complete portfolio for next-gen sequencing

- Sensitivity
- Reproducibility
- Reliability
- Ease of use
- Scalability

SMARTer Whole transcriptome analysis



SMART-Seq Stranded RNA-Seq

- Simple workflow from 1–1,000 intact cells or isolated total RNA
- High sensitivity, as determined by number of transcripts identified
- Reproducible chemistry enables confidence in your data
- Accurate detection of coding and noncoding transcripts

Experimental overview

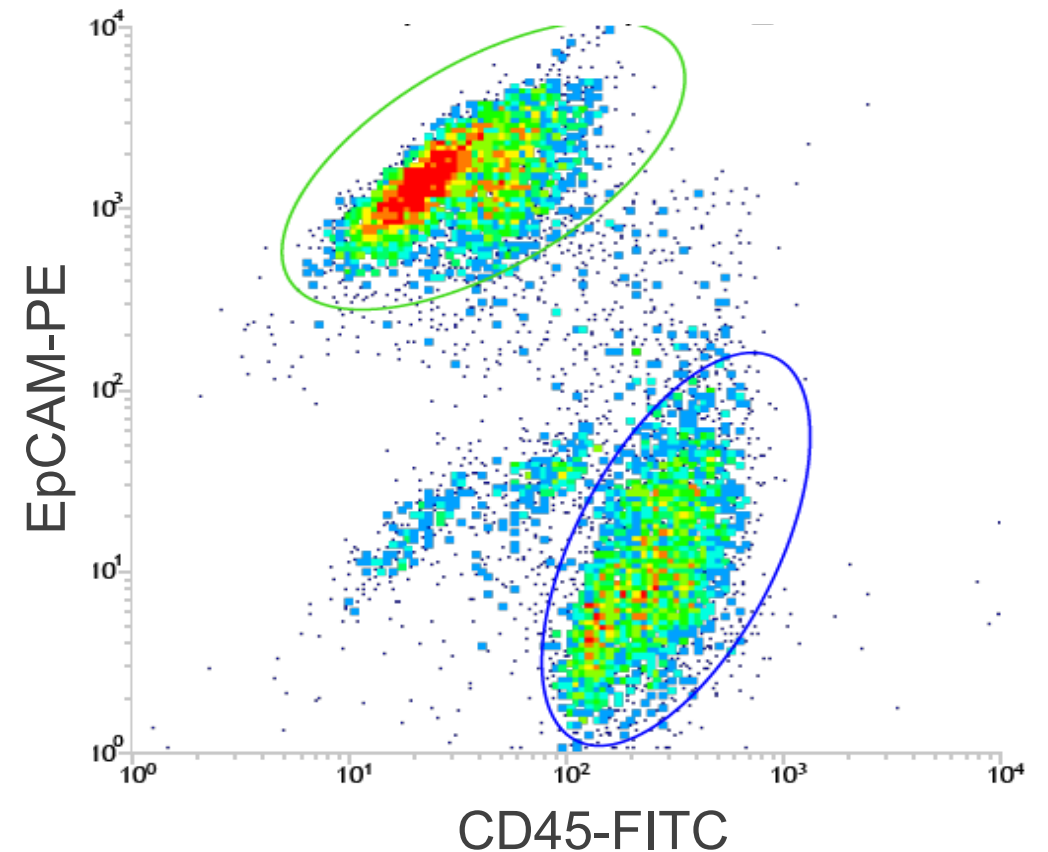
Tumor Cell Dissociation

Labeling and FACS

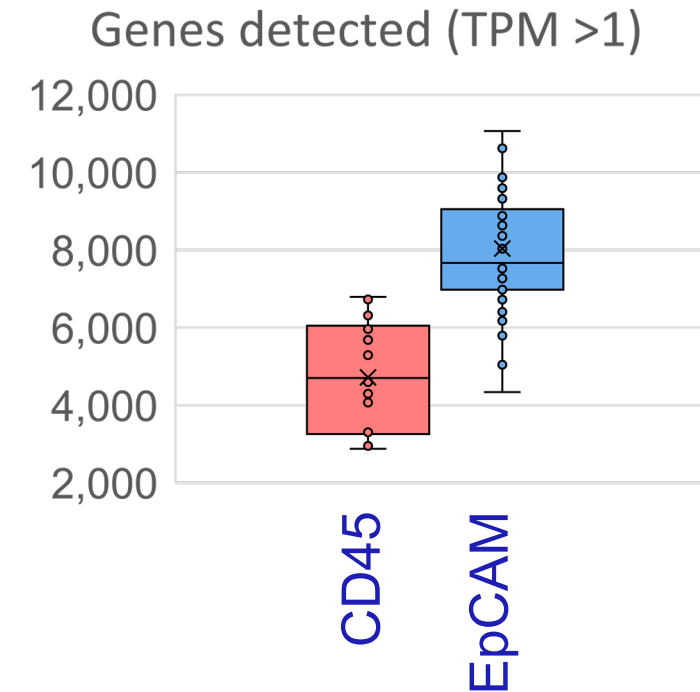
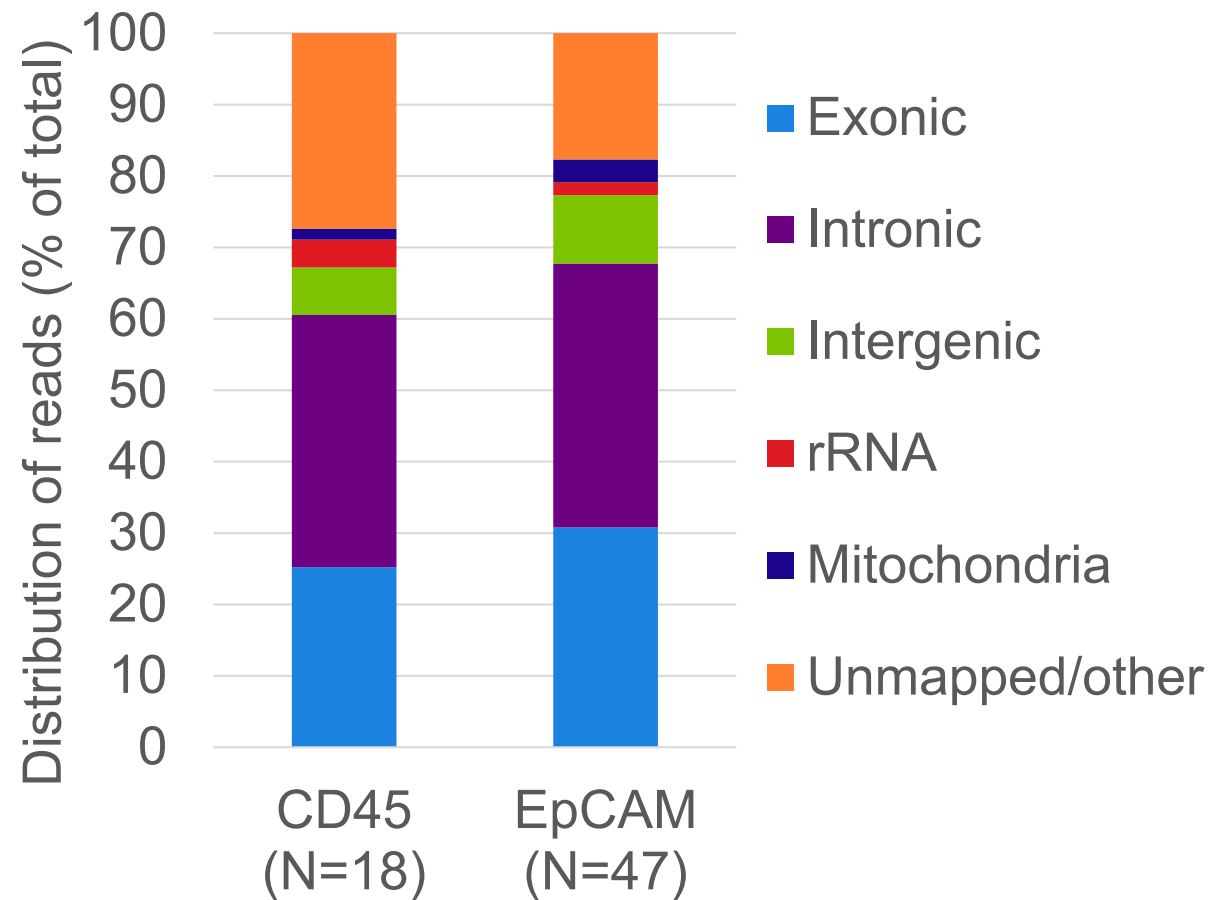
SMART-Seq Library
Prep

Sequencing & Analysis

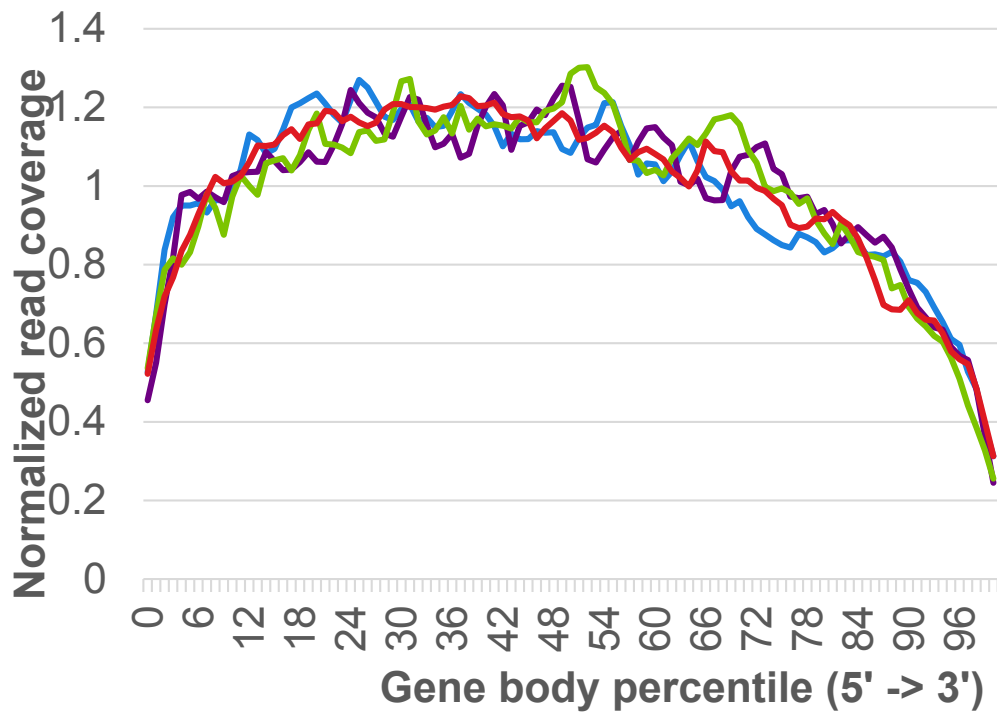
Tumor & immune cells



Excellent mapping statistics from cells with extremely low RNA content



Uniform gene-body coverage with the SMART-Seq Stranded Kit



ACTB (ENSG00000075624)

Chromosome 7 5,525,000 5,530,000 5,535,000 5,540,000 5,545,000 5,550,000 5,555,000 5,560,000 5,565,000 5,570,000



Homo sapiens
CRCh38 mRNA

CD69 (ENSG00000110848)

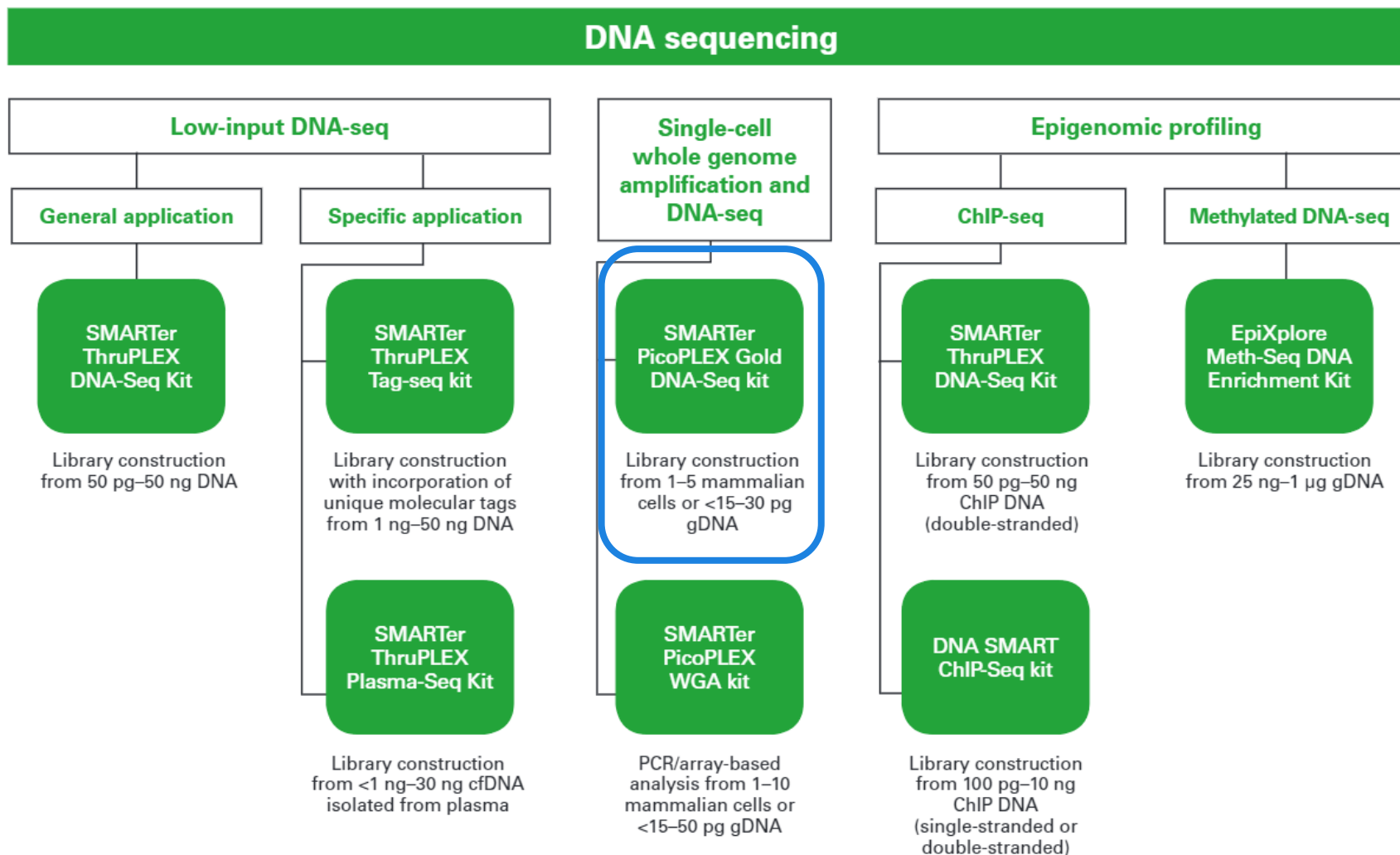
Chromosome 12 9,752,000 9,754,000 9,756,000 9,758,000 9,760,000 9,762,000



Homo sapiens
CRCh38 mRNA

- CD45⁺ cell C
- CD45⁺ cell D
- EpCAM⁺ cell C
- EpCAM⁺ cell B

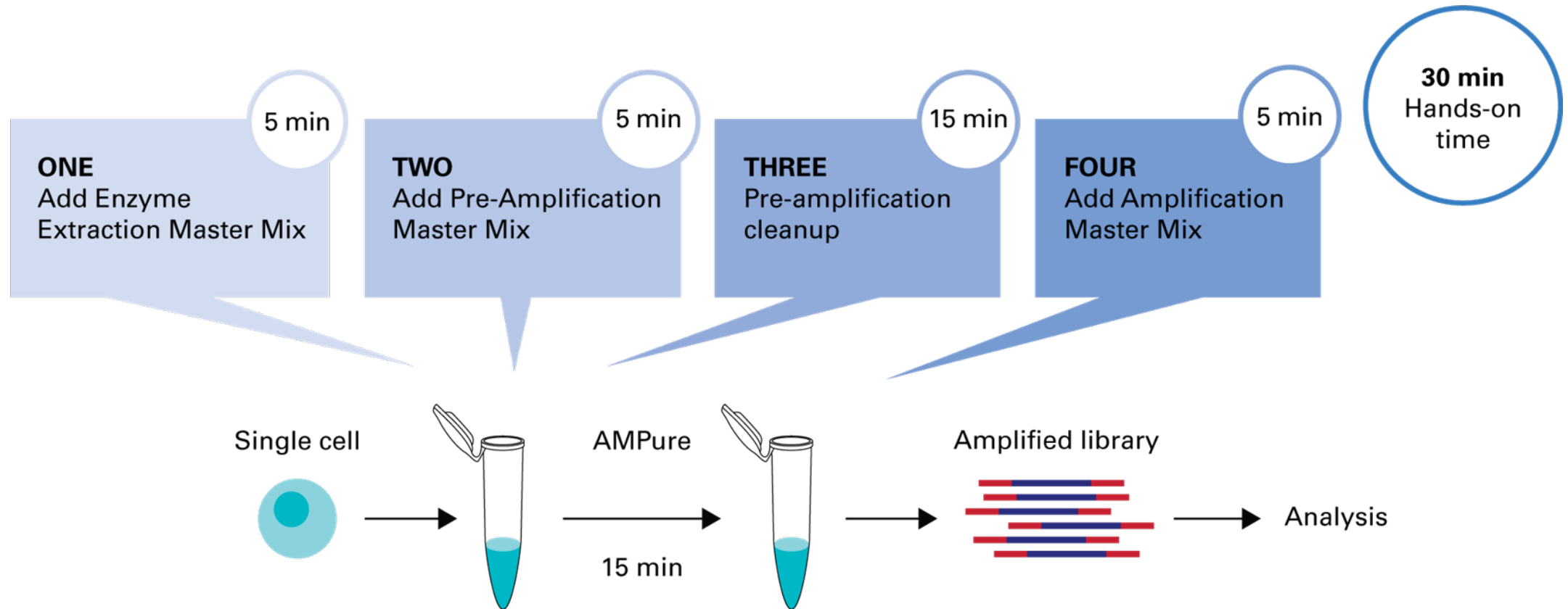
SMARTer DNA Sequencing



PicoPLEX Gold Single Cell DNA-Seq

- Fast, simple workflow: from cells to libraries in 3 hours, with minimal hands on time
- Best in class performance: superior reproducibility and sensitivity
- Flexible kit configuration: UDIs available for use on the NovaSeq

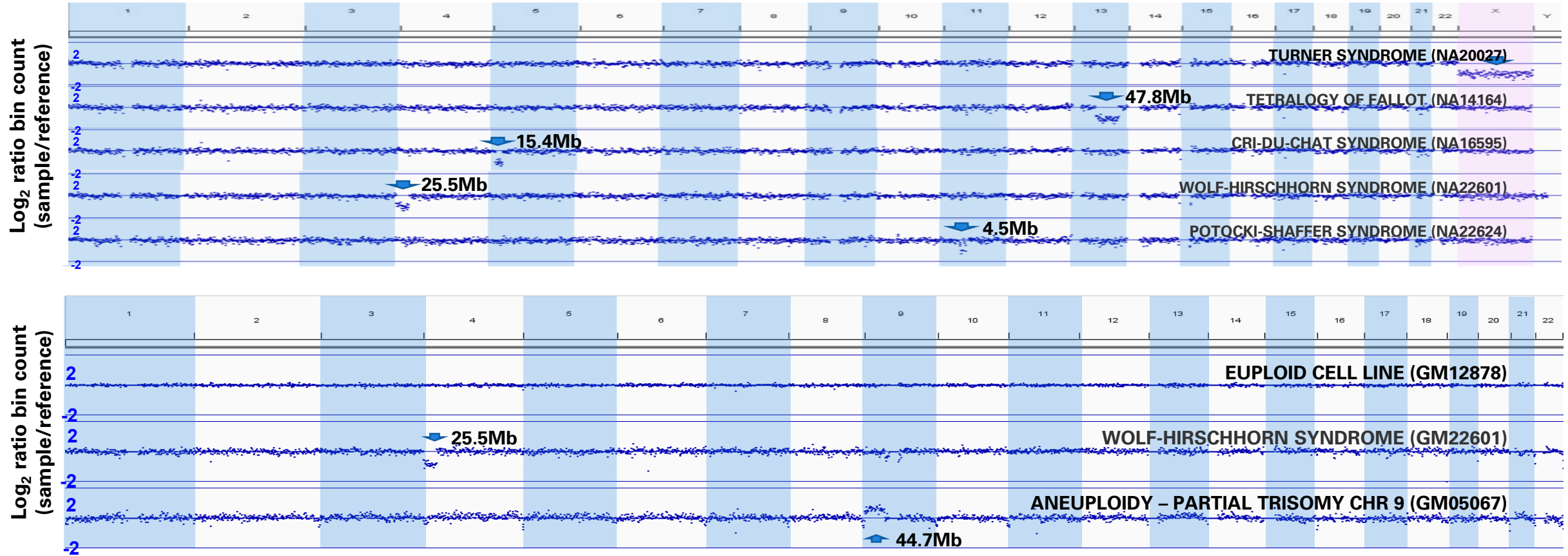
PicoPLEX Gold: fast, simple library prep



High-fidelity detection of single nucleotide variants

Depth of SNV position ≥ 10 Allele frequency $\geq 20\%$ Replicates n=2	PicoPLEX WGA v2				Kit D				Kit Q			
	1 cell		5 cells		1 cell		5 cells		1 cell		5 cells	
SNVs called (of 74 validated)	57	67	69	67	34	57	62	67	Failed	Failed	40	Failed
False positive calls	3	1	0	1	5	1	0	7	Failed	Failed	0	Failed
Call rate	78%	92%	95%	92%	47%	78%	85%	92%	Failed	Failed	55%	Failed
Average locus dropouts	16.2%		8.1%		38.5%		12.8%		Failed		45.9% Failed	
Average allele dropouts	7.8%		0.0%		25.6%		12.2%		Failed		71.1% Failed	

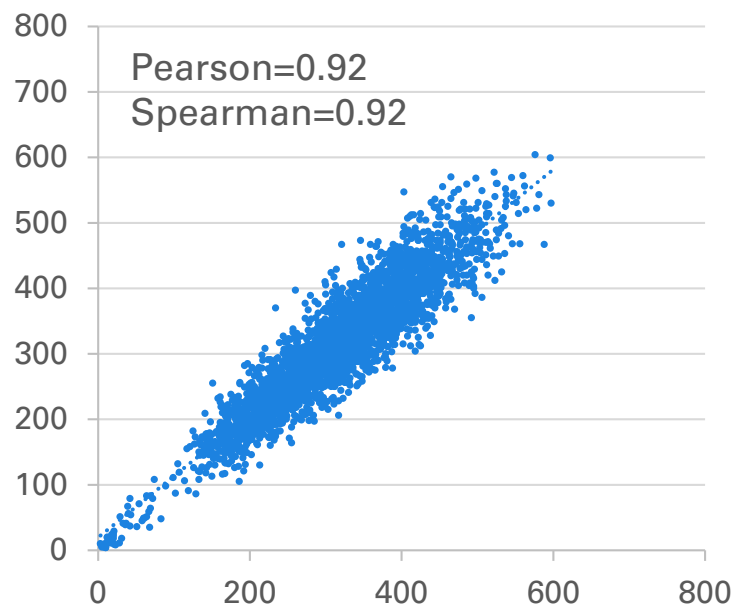
Accurate detection of segmental aneuploidies with low-pass sequencing



Best in class reproducibility

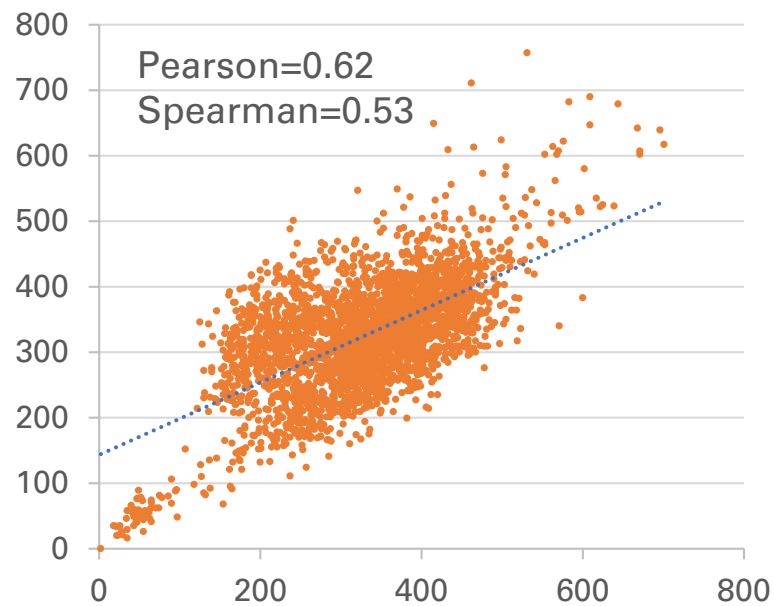
PicoPLEX WGA_{v2} single cell-to-cell reproducibility 0.5 M read pairs–1 Mb bin

Outliers excluded



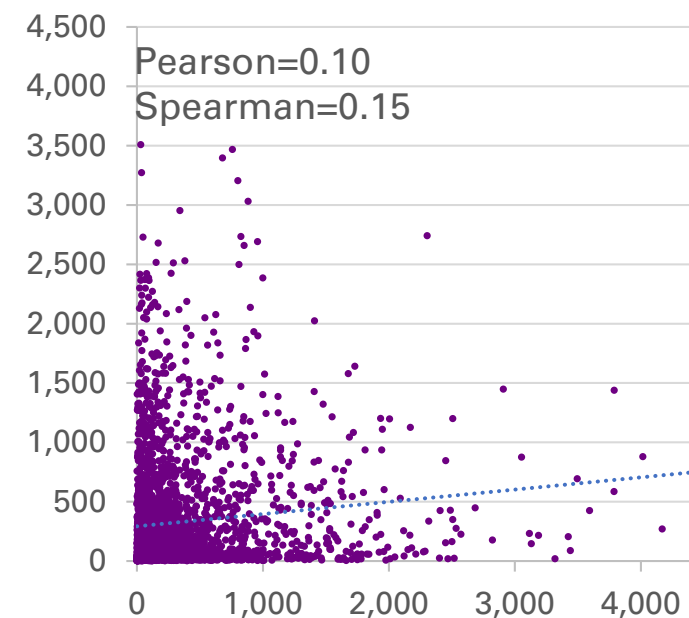
DOPlify single cell-to-cell reproducibility 0.5 M read pairs–1 Mb bin

Outliers excluded



REPLI-g single cell-to-cell reproducibility 0.5 M read pairs–1 Mb bin*

Outliers excluded





that's
GOOD
science!®

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