

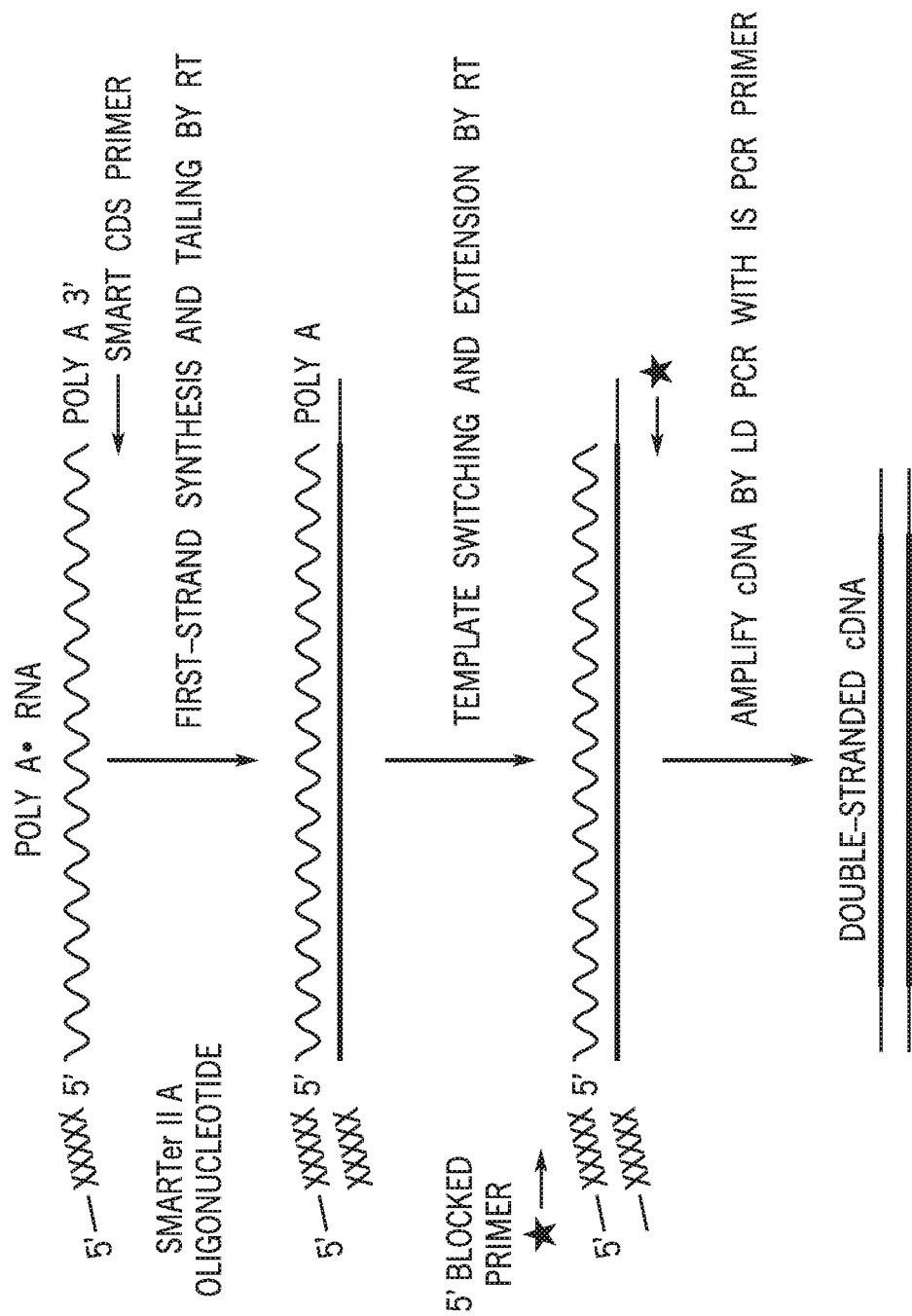


FIG. 1

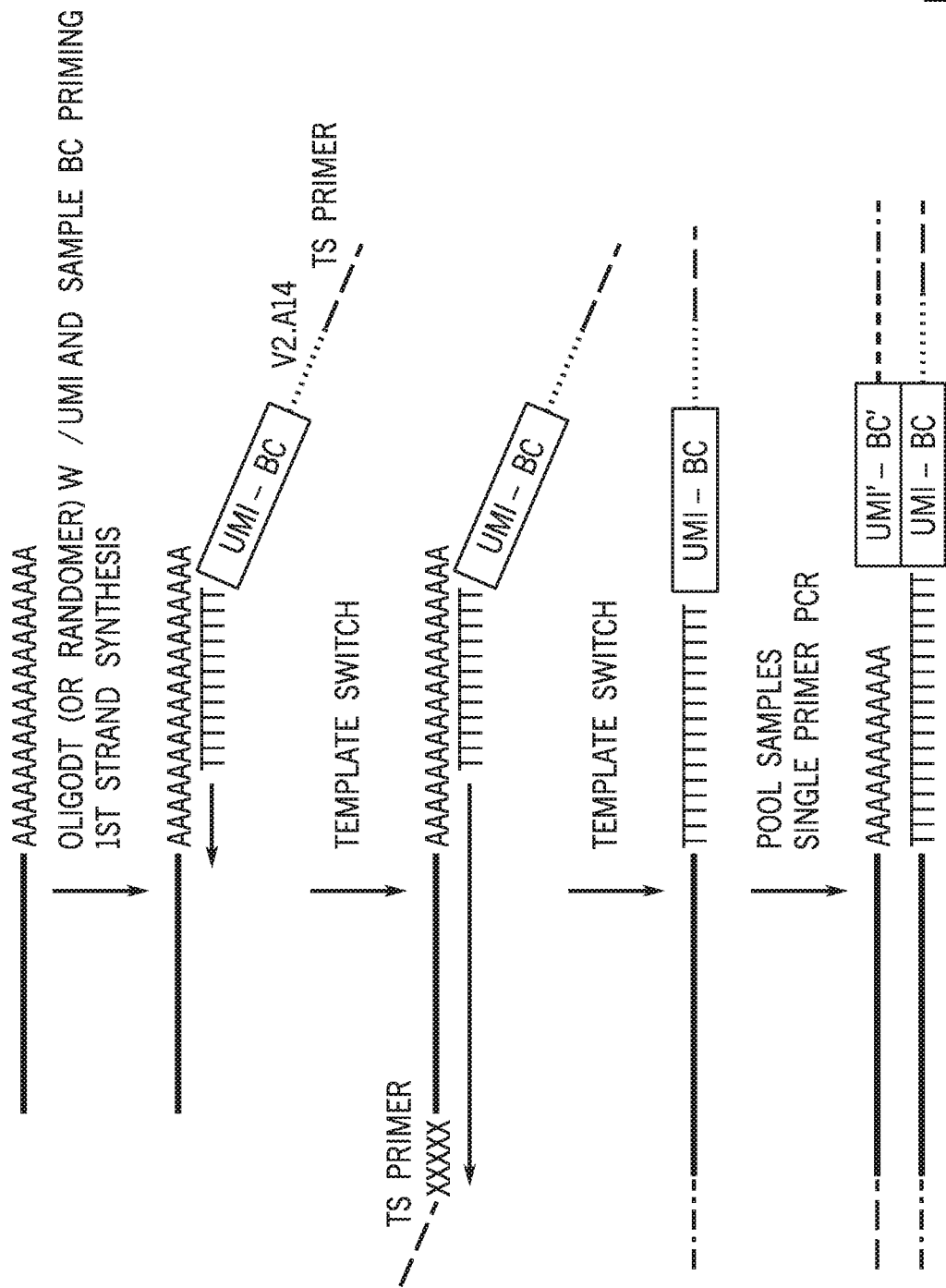


FIG. 2A

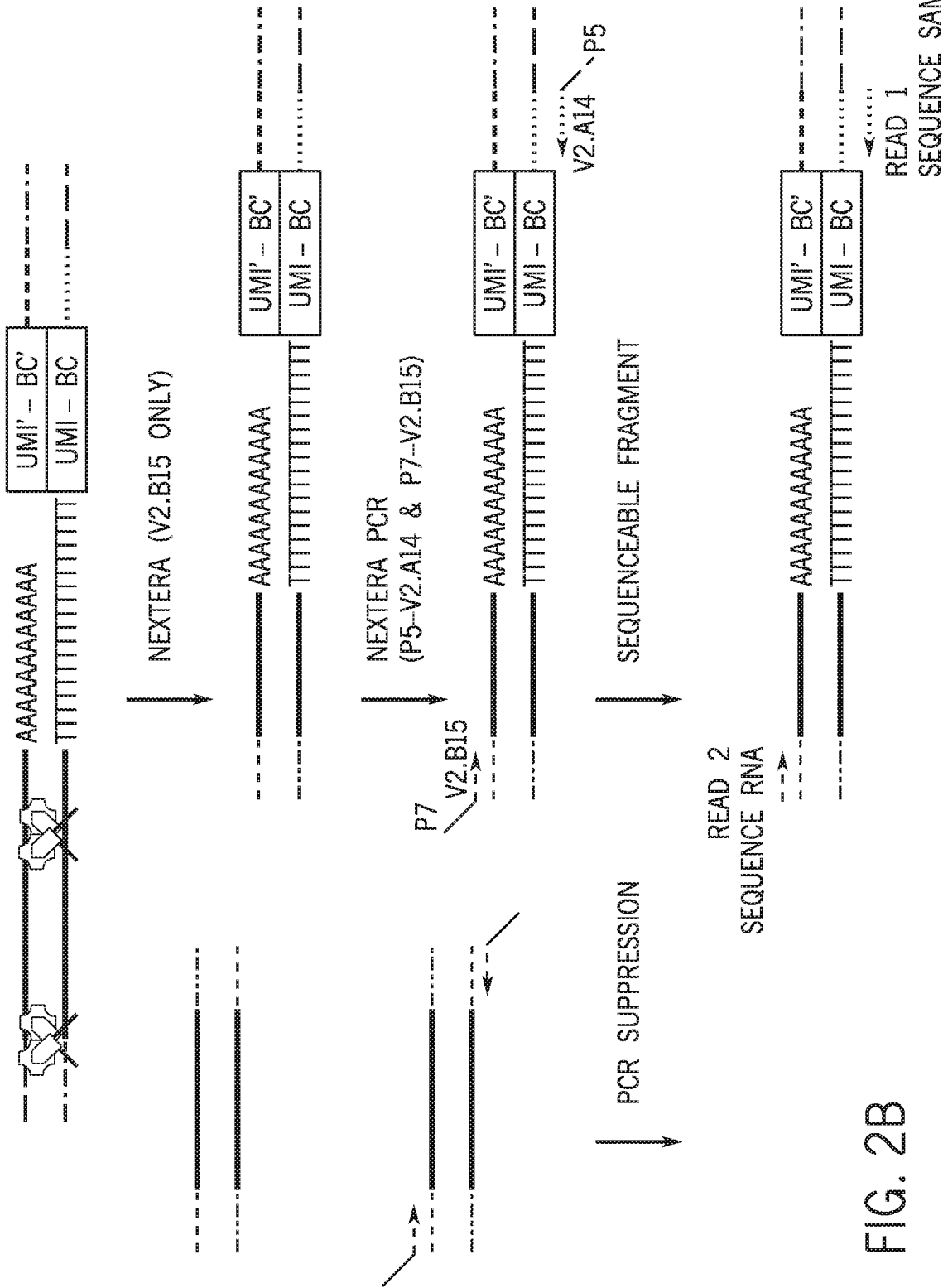


FIG. 2B

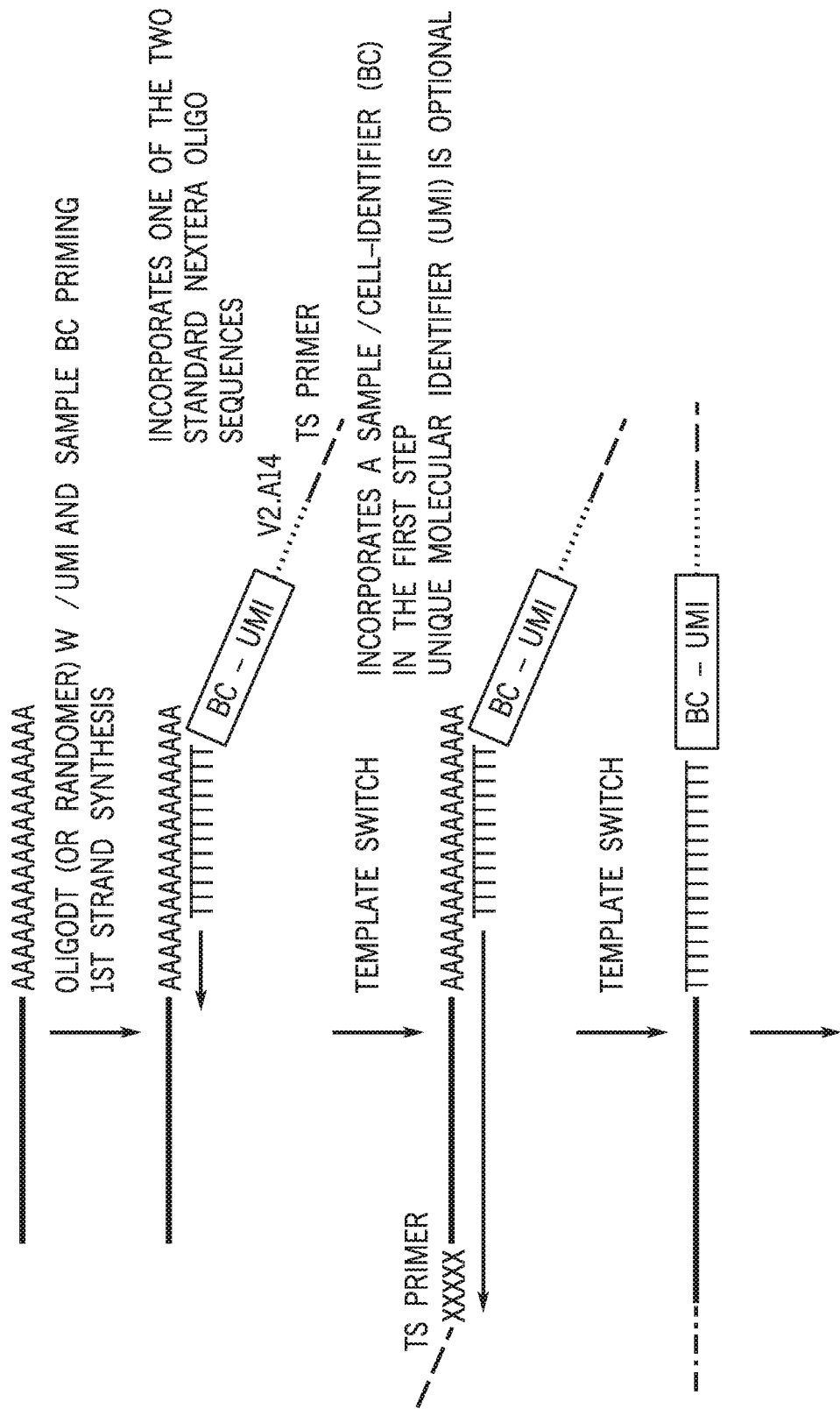


FIG. 3A

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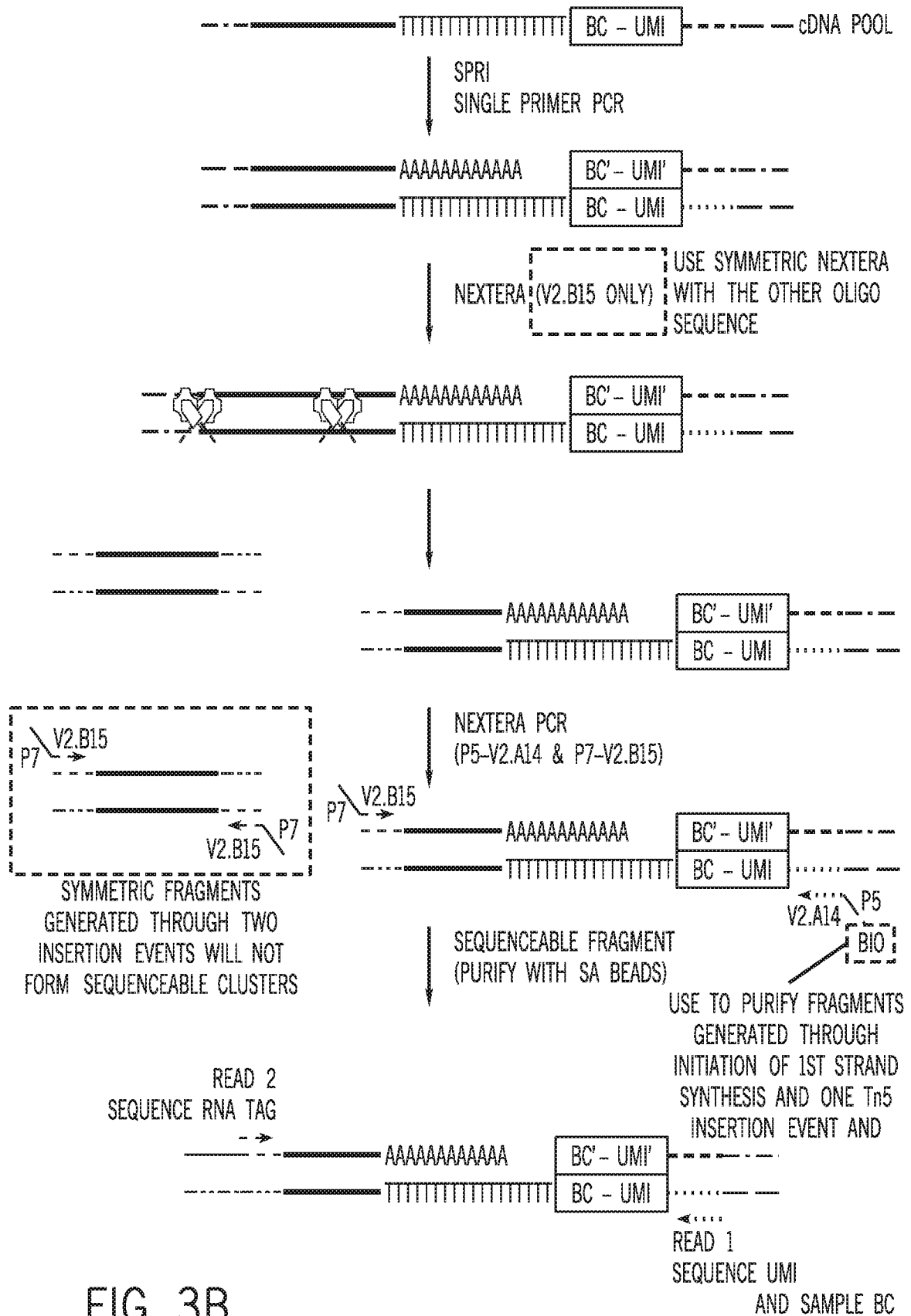


FIG. 3B

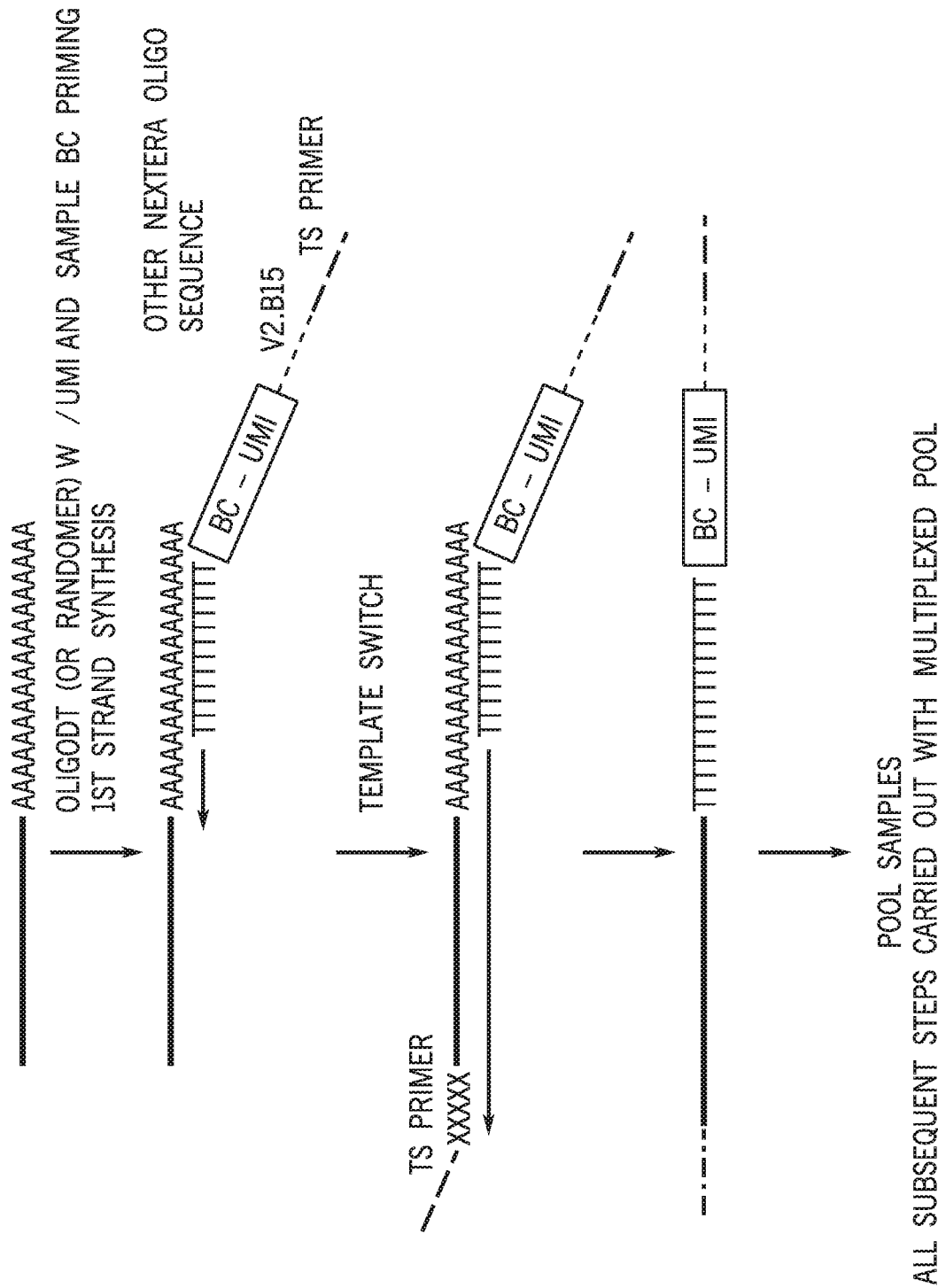


FIG. 4A

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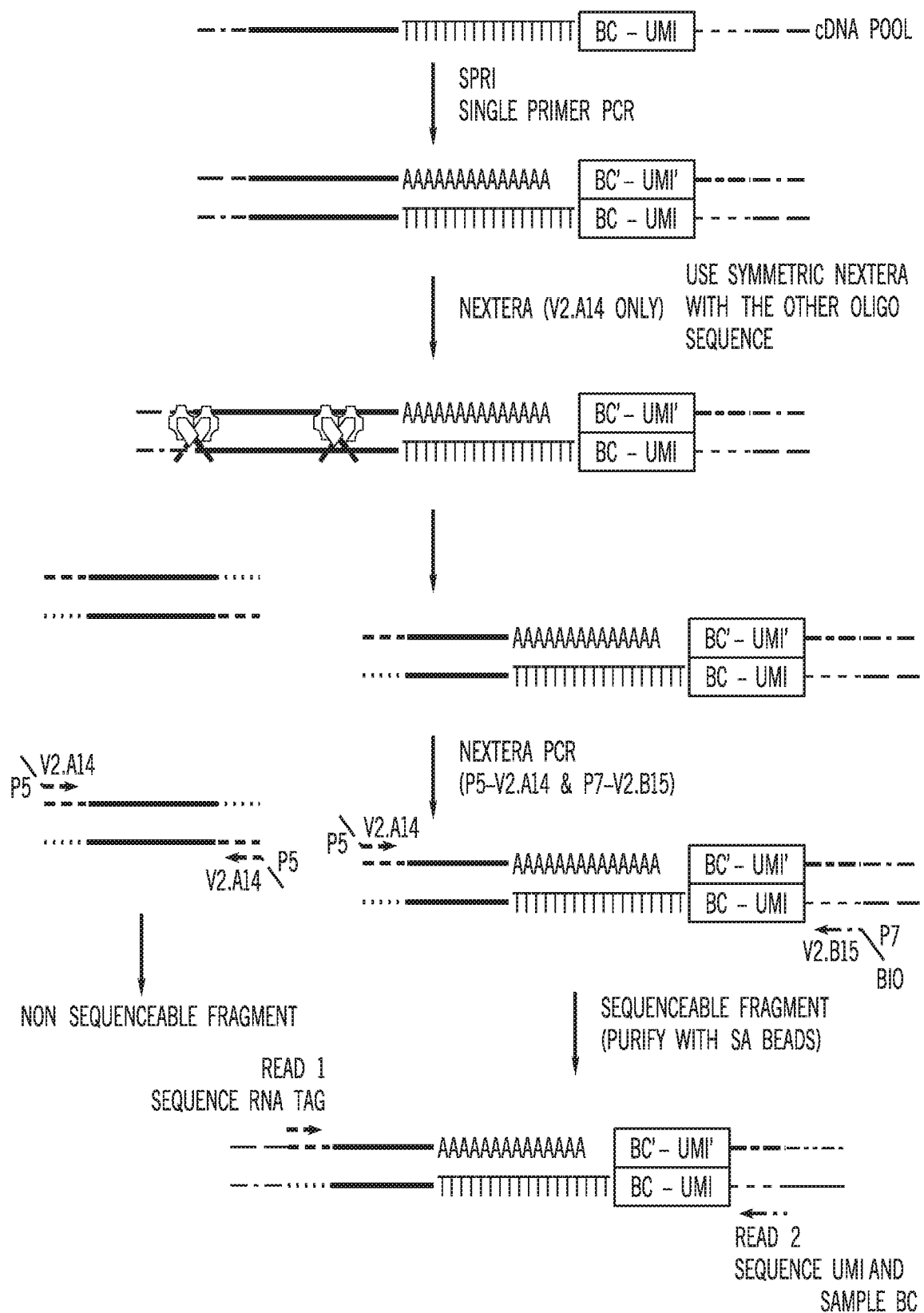
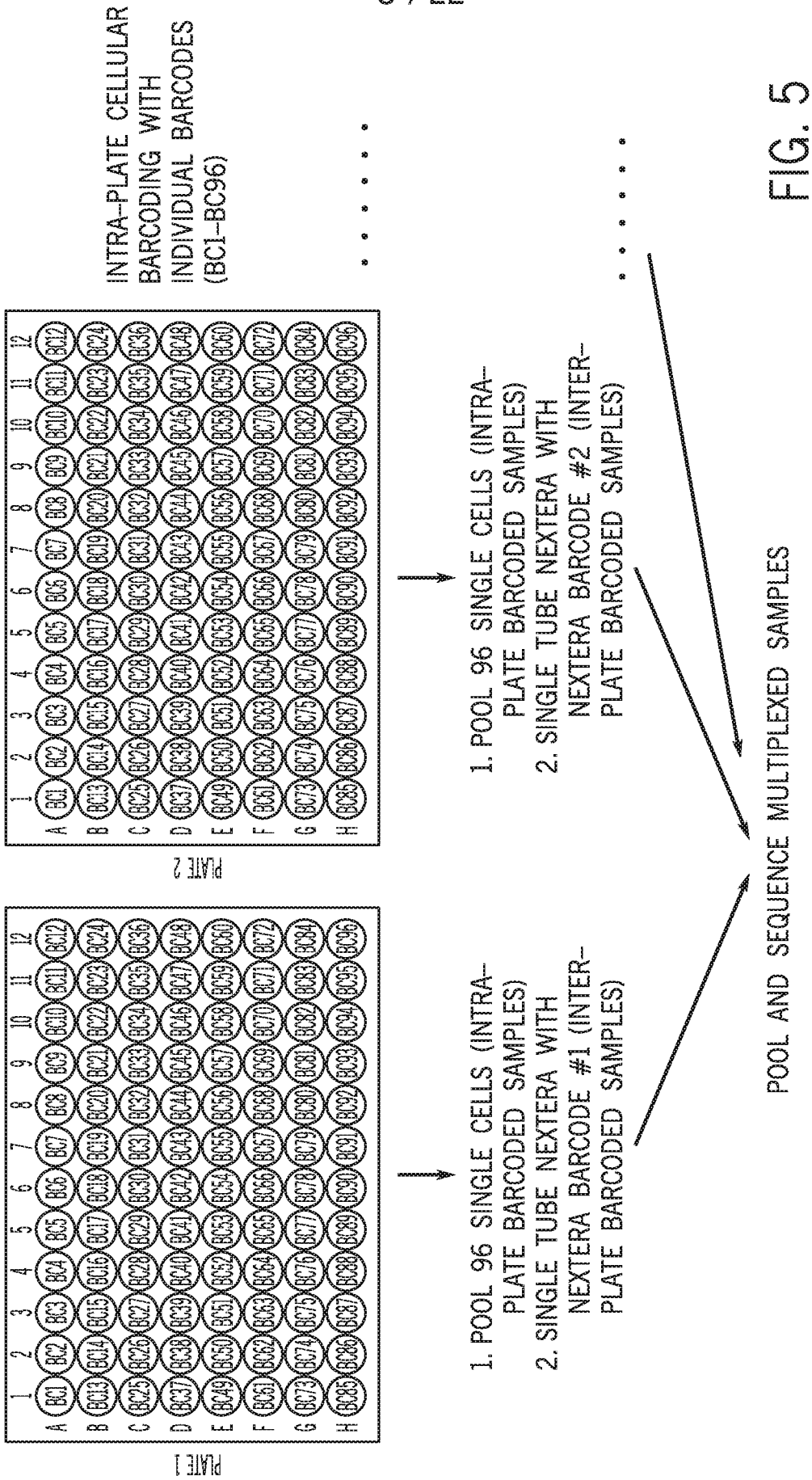


FIG. 4B



KEY SEQUENCE METRICS USING 100 pg HBR

SEQUENCE METRIC	STATISTICS			
	HIGH THROUGHPUT GEX	STRT	OLIGO-DT + RANDOMER	SMART
1 st STRAND PRIMING METHOD	OLIGO-DT	OLIGO-DT	OLIGO-DT + RANDOMER	OLIGO-DT
MAPPING RATE	ALIGNED TO HG19 TRANSCRIPTOME	63%	75%	78%
	RIBOSOMAL	1%	2%	1%
	MITOCHONDRIAL	15%	14%	12%
	OTHER	1%	0%	1%
CORRELATION OF GENE-EXPRESSION BETWEEN TECHNICAL REPLICATES (R)	UNALIGNED	20%	9%	8%
		0.9	0.85	0.94
NO. OF GENES DETECTED (FPKM > 1)	10,021	11,254	11,683	8,492

FIG. 6

INITIAL DATA FROM SINGLE CELLS				
SEQUENCE METRIC	STATISTICS			
	HIGH THROUGHPUT GEX		STRT	
1 st STRAND PRIMING METHOD	OLIGO-DT	OLIGO-DT	OLIGO-DT +	RANDOMER
NEXTERA VERSION	V2.B15	V2.B15 /V2.A14	V2.B15 /V2.A14	
MAPPING RATE	ALIGNED TO HG19 / MM10	69%	77%	80%
	RIBOSOMAL	1%	1%	5%
	MITOCHONDRIA	–	–	–
	OTHER	1%	1%	0%
	UNALIGNED	29%	21%	14%
CORRELATION OF GENE-EXPRESSION BETWEEN TECHNICAL REPLICATES (R)	0.95	0.94	0.60*	
NO. OF GENES DETECTED (FPKM>1)	6,904	7,789	8,727	
* UNUSUALLY LOW CORRELATION DUE TO ONE OUTLIER.				

FIG. 7

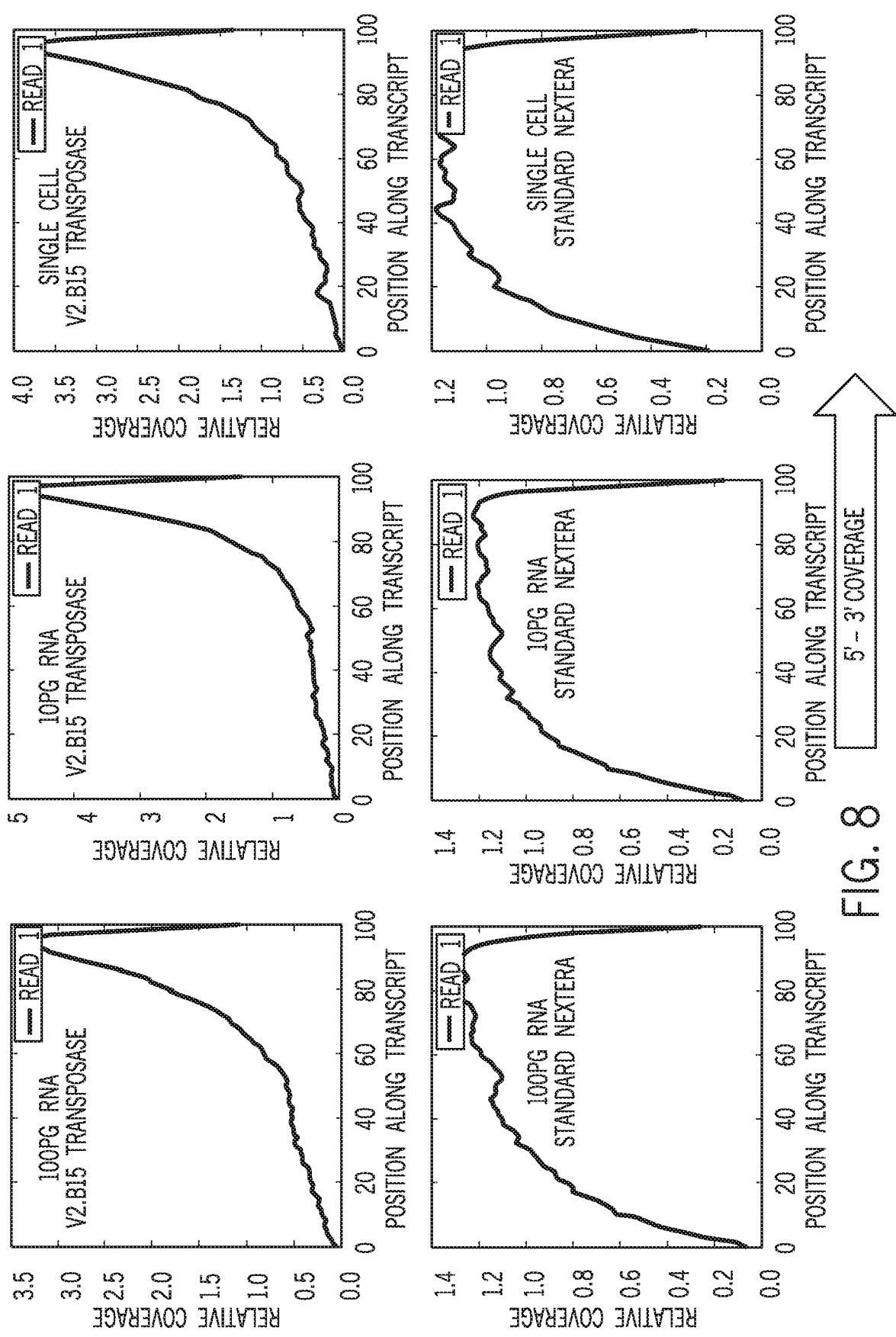


FIG. 8

RANDOMER AND OLIGO-DT PRIMING

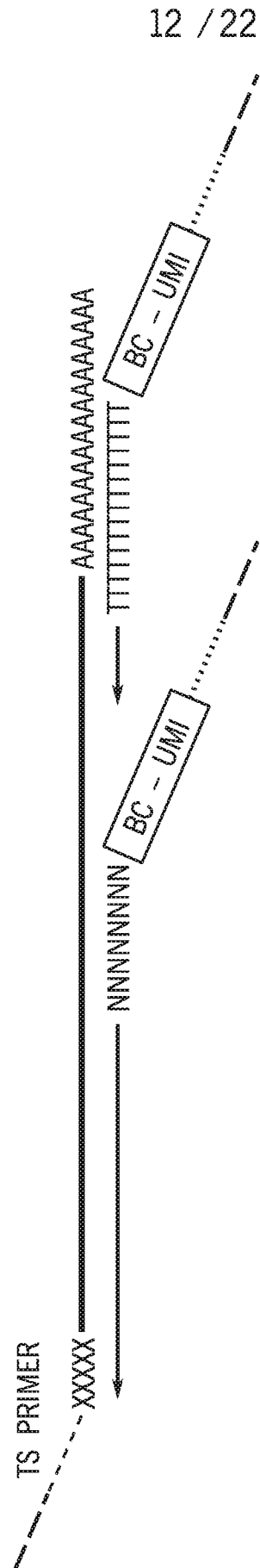


FIG. 9A

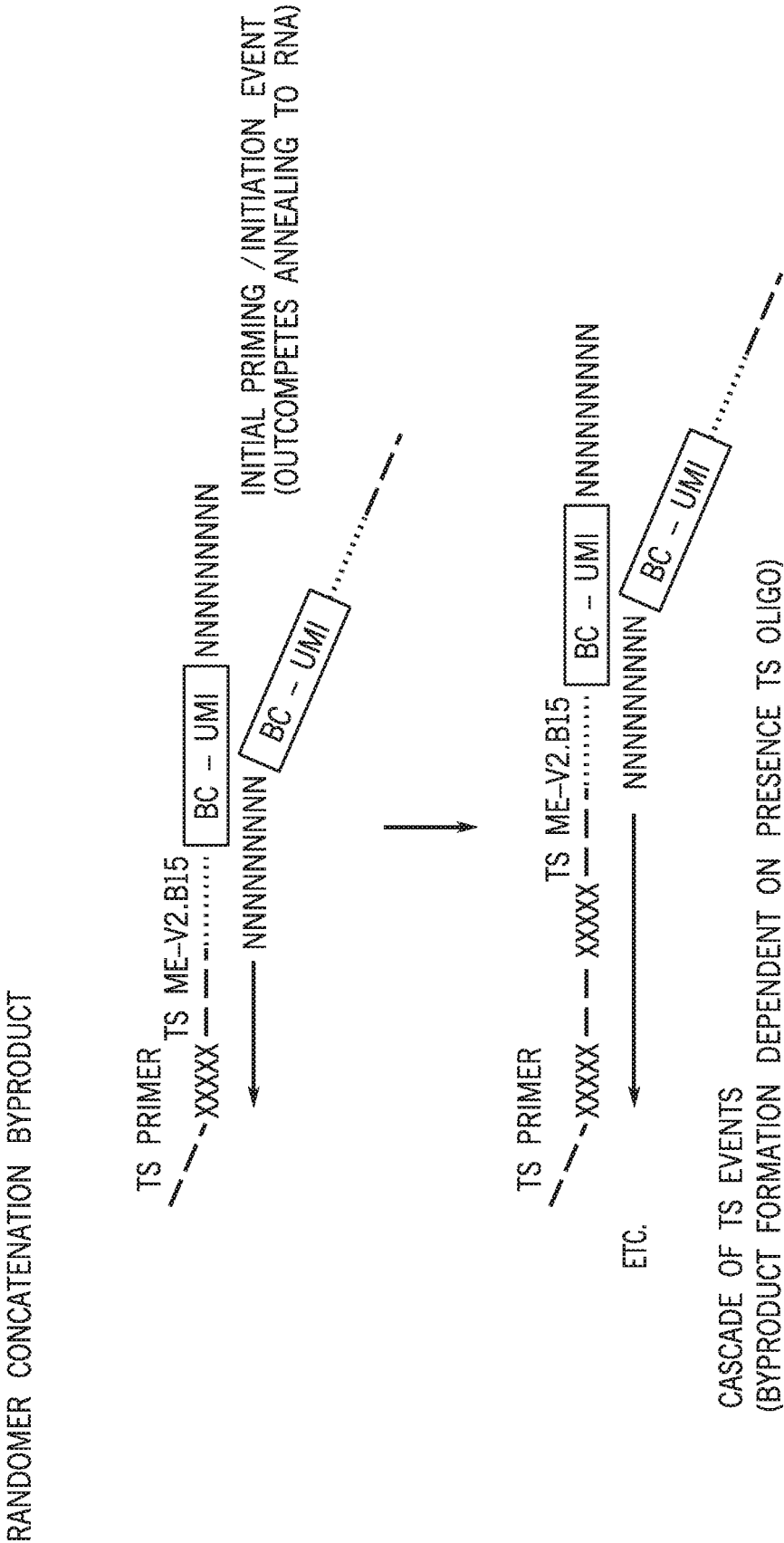


FIG. 9B

POSSIBLE STRATEGIES TO REDUCE CONCATENATION BYPRODUCT

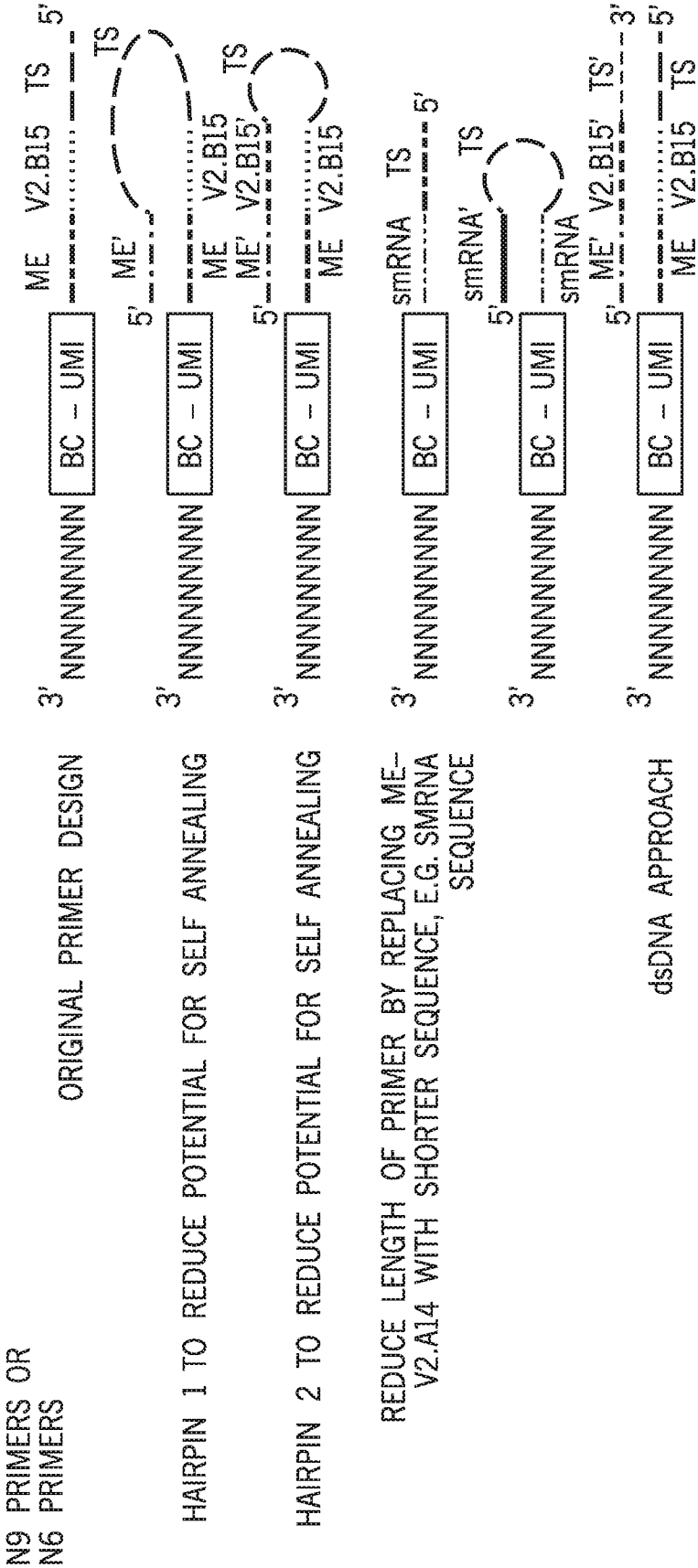


FIG. 10

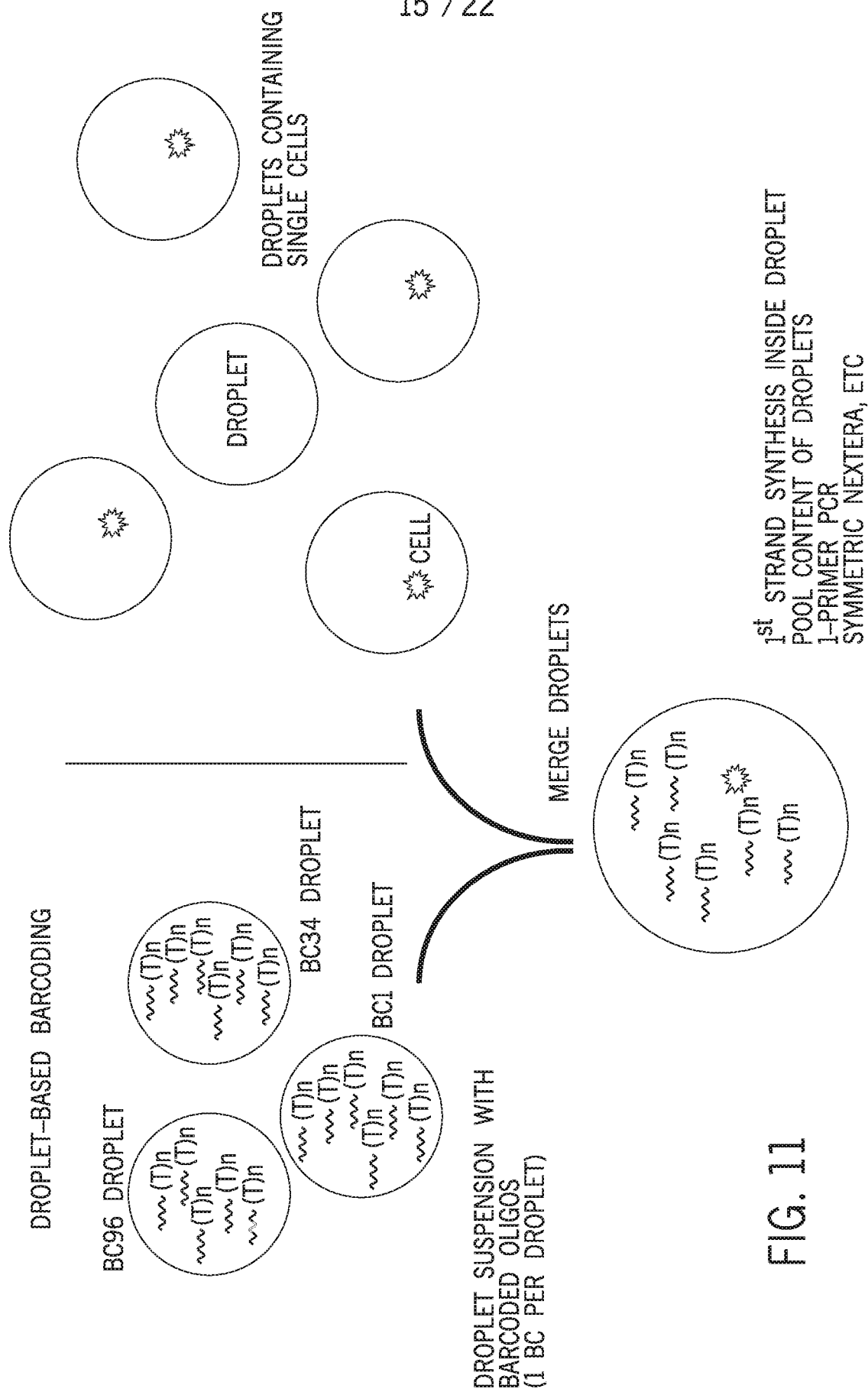
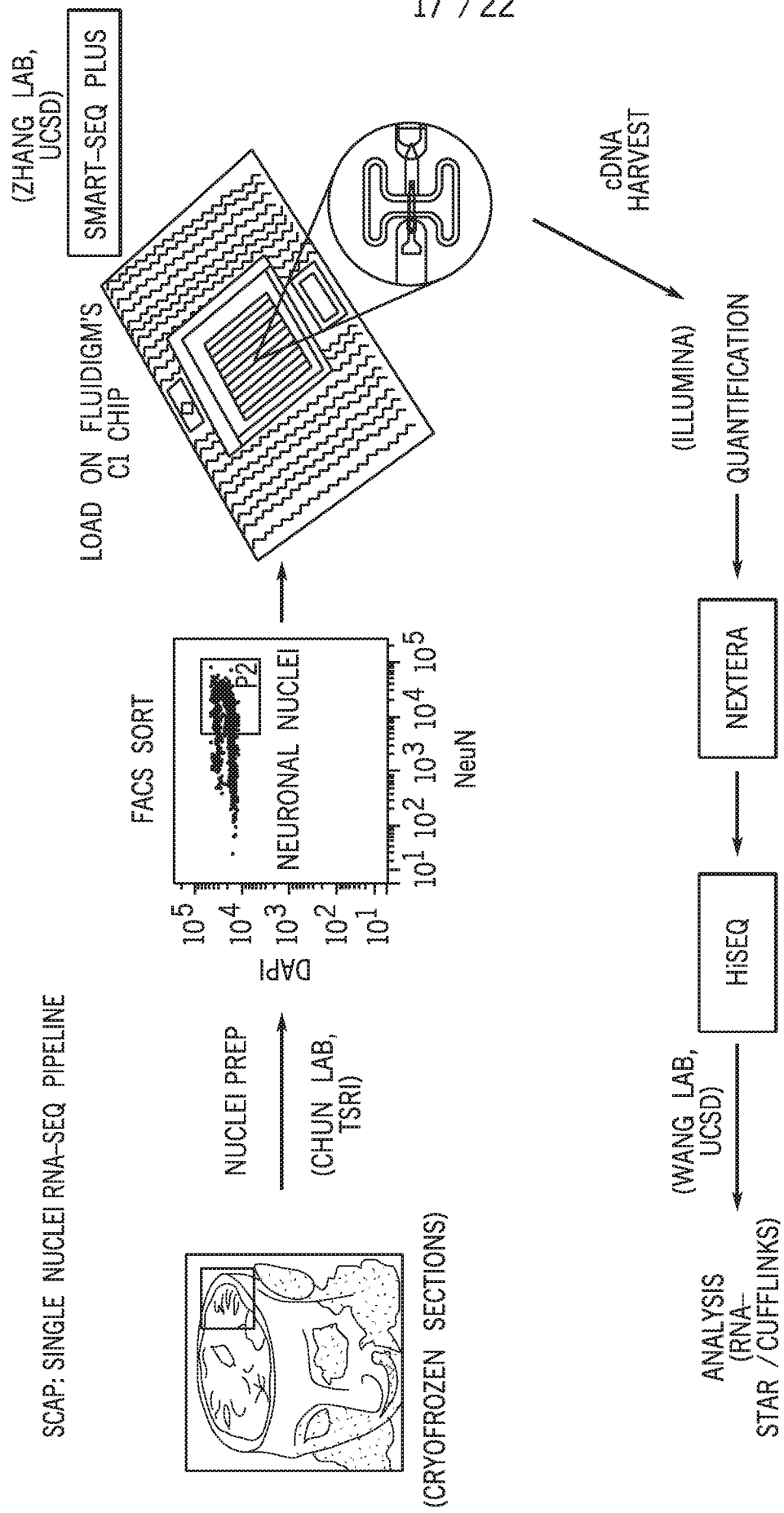


FIG. 11



• AROUND 7,000 SINGLE NUCLEI SEQUENCED

FIG. 13

- cDNA FROM SINGLE NUCLEI
- OVERVIEW OF FLUIDIGM'S C1 SYSTEM FOR RNA-SEQ
 - TRANSCRIPTOME PROFILING FROM NUCLEI RATHER THAN WHOLE NEURONS
 - TECHNICALLY DIFFICULT TO ISOLATE NEURONS IN HIGH THROUGHPUT
 - RNA CONTAMINATION FROM NEIGHBORING NEURONAL SYNAPTIC RNA
- C1 SYSTEM DESIGNED FOR 96 NANO-LITER REACTION VOLUMES
 - NUCLEI LOADING AND CAPTURE
 - WASH, LYSIS
 - cDNA SYNTHESIS
 - PCR AMPLIFICATION
 - cDNA HARVEST

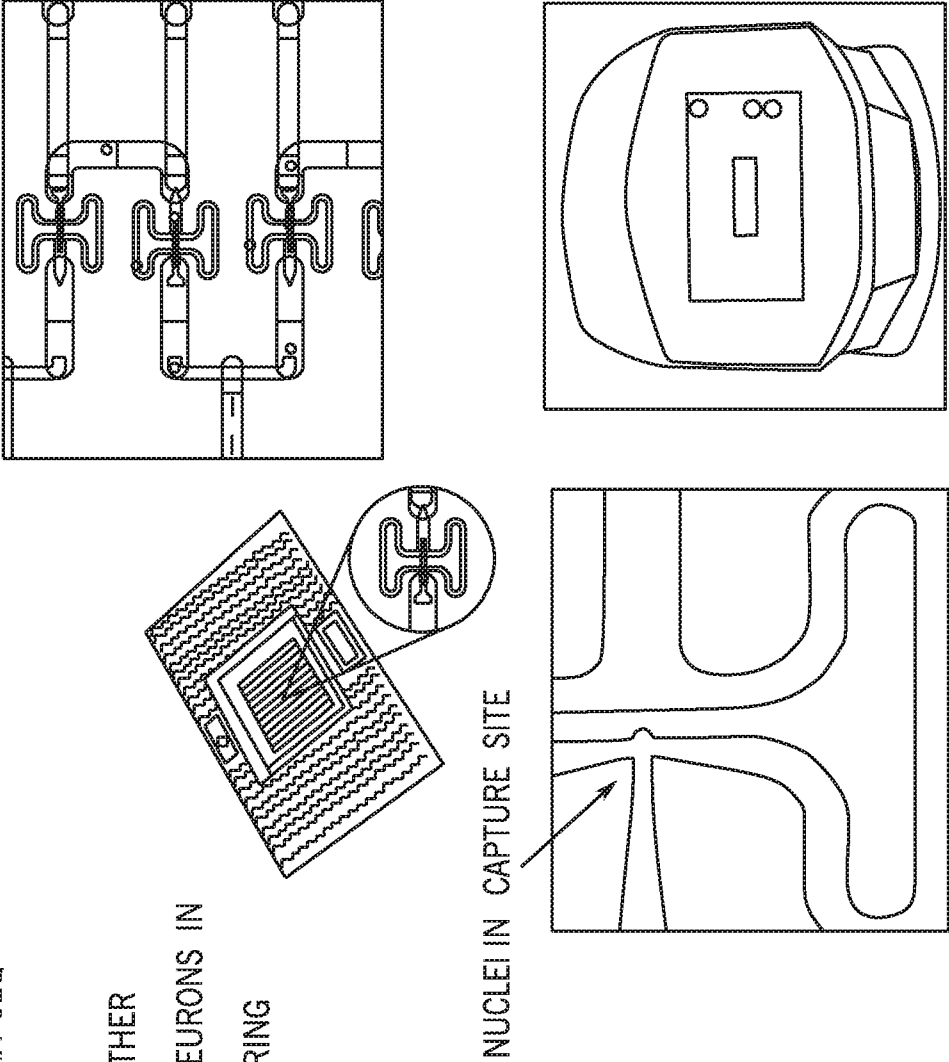


FIG. 14

OVERVIEW OF RNA-SEQ USING "TEMPLATE SWITCHING" APPROACH

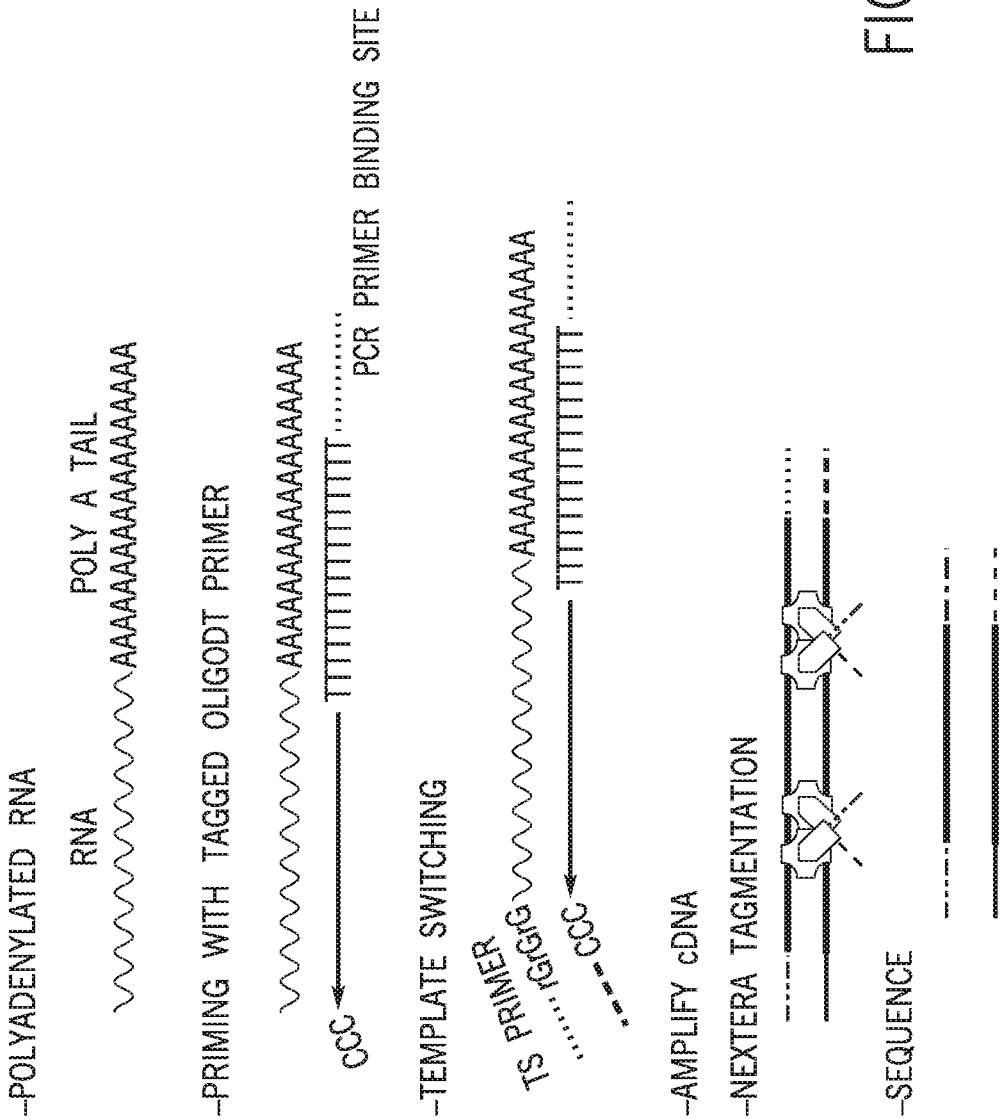


FIG. 15

SMART-PLUS: IMPROVING ASSAY SENSITIVITY AND GENE-BODY COVERAGE

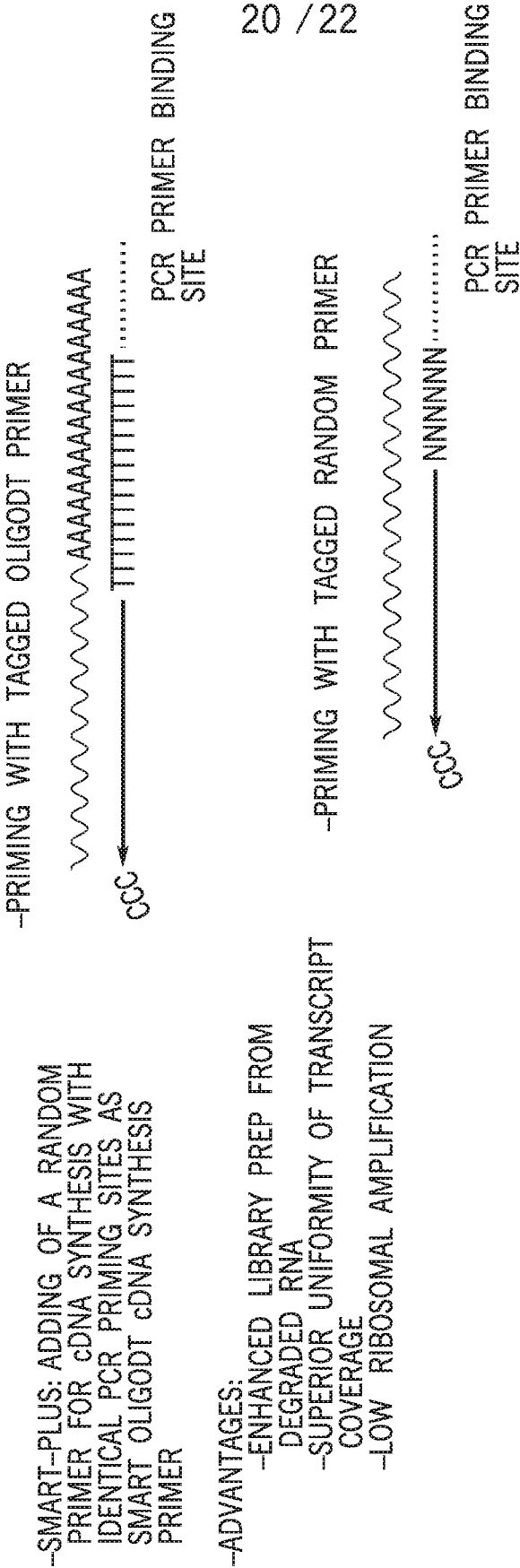


FIG. 16

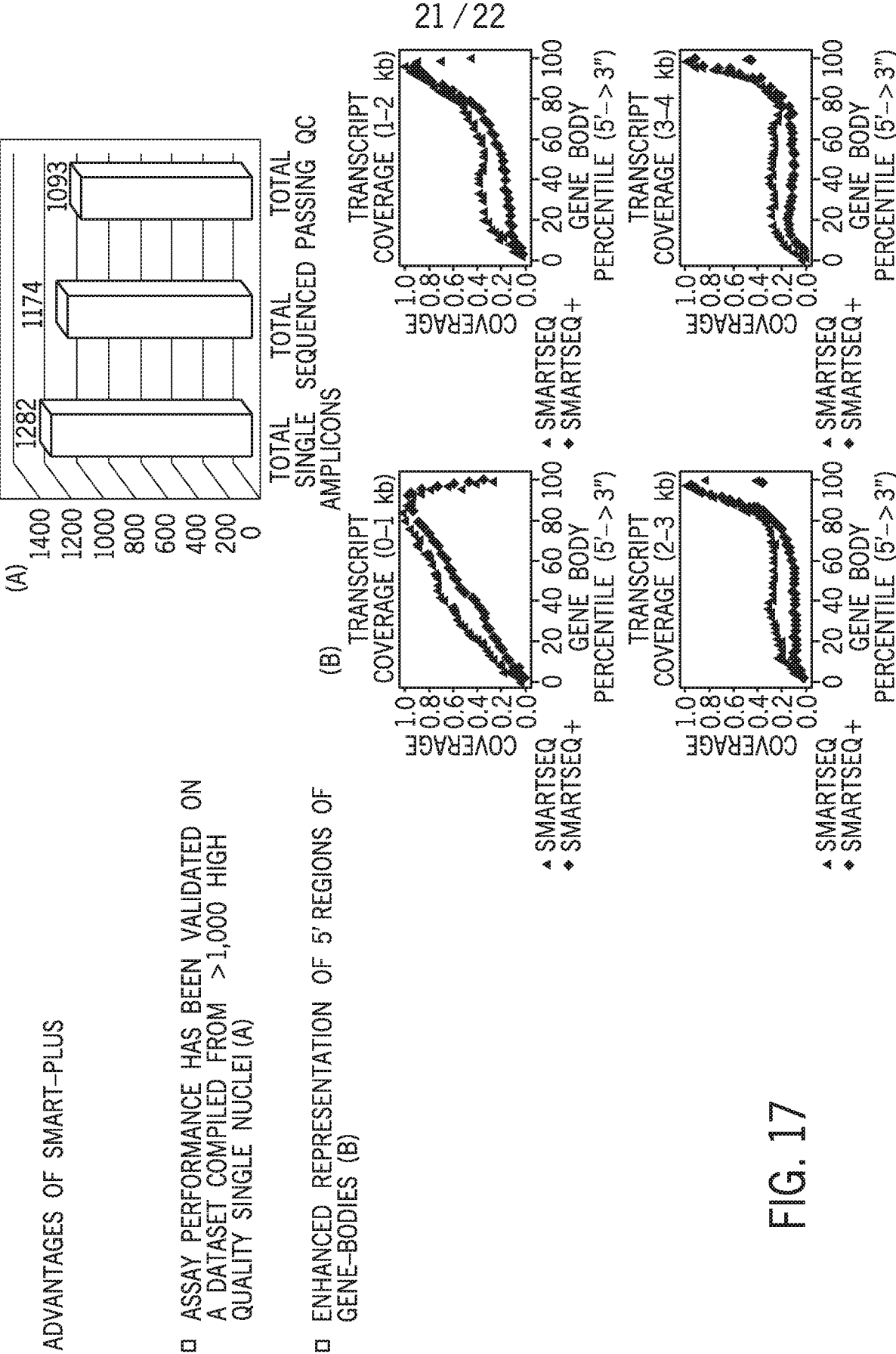


FIG. 17

SMART-SEQ PLUS: INCREASING ASSAY SENSITIVITY

□ APPROXIMATELY 1.5x INCREASE IN SENSITIVITY
(NUMBER OF GENES IDENTIFIED BY RNA-SEQ)
USING SMART-SEQ PLUS (FIG A)

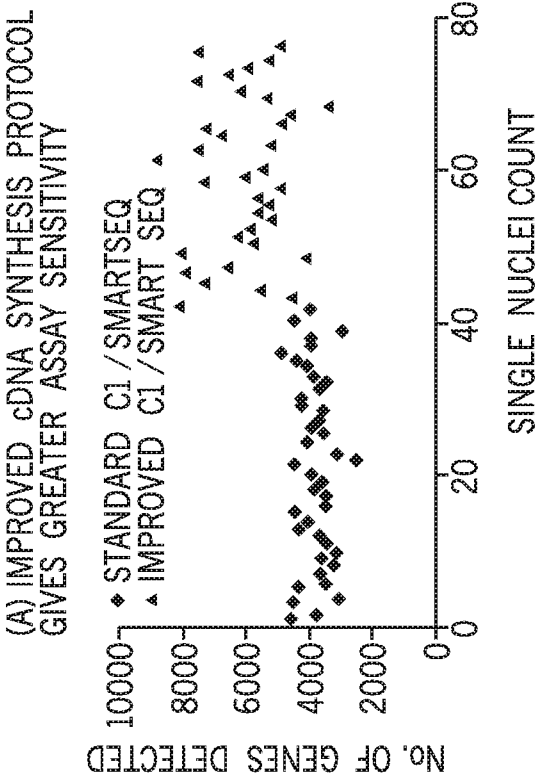


FIG. 18