

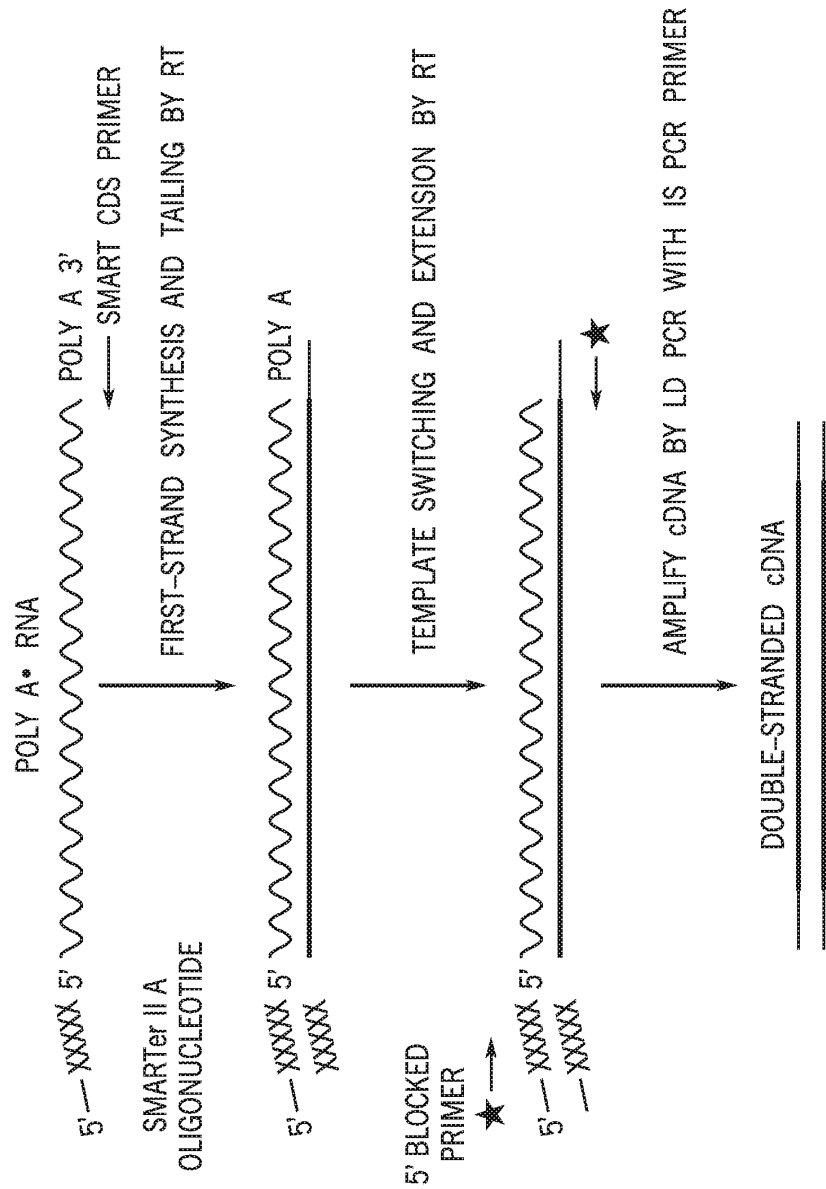


FIG. 1

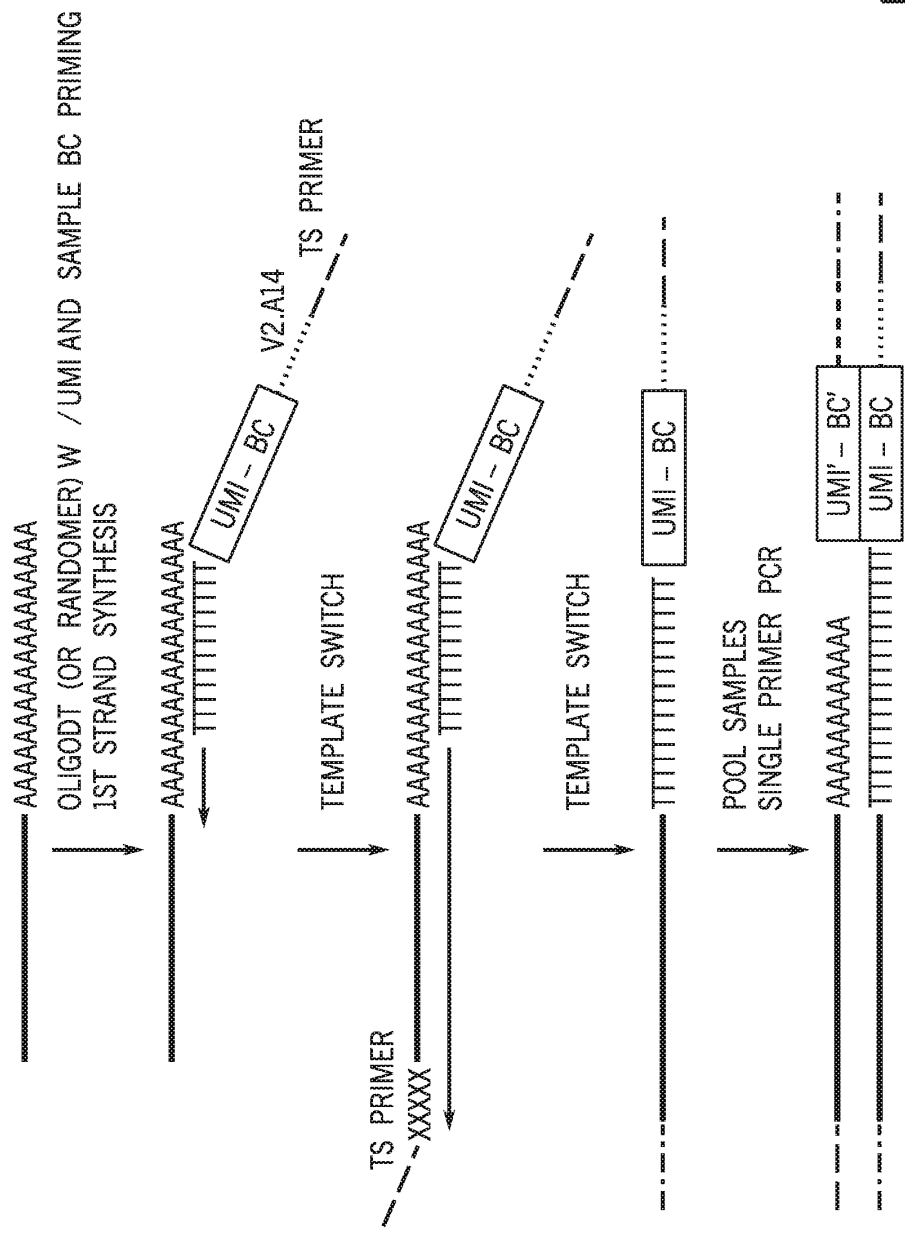


FIG. 2A

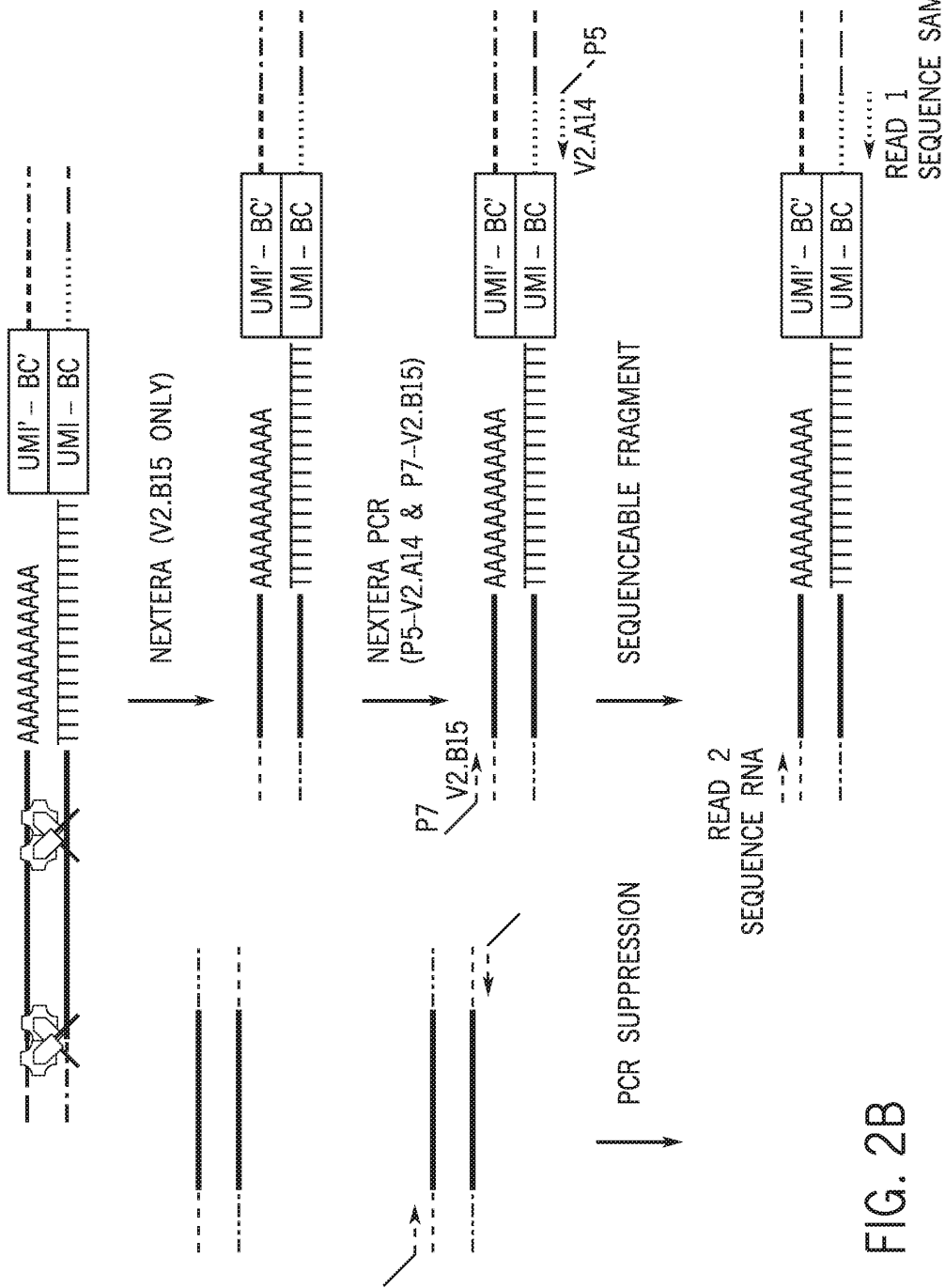


FIG. 2B

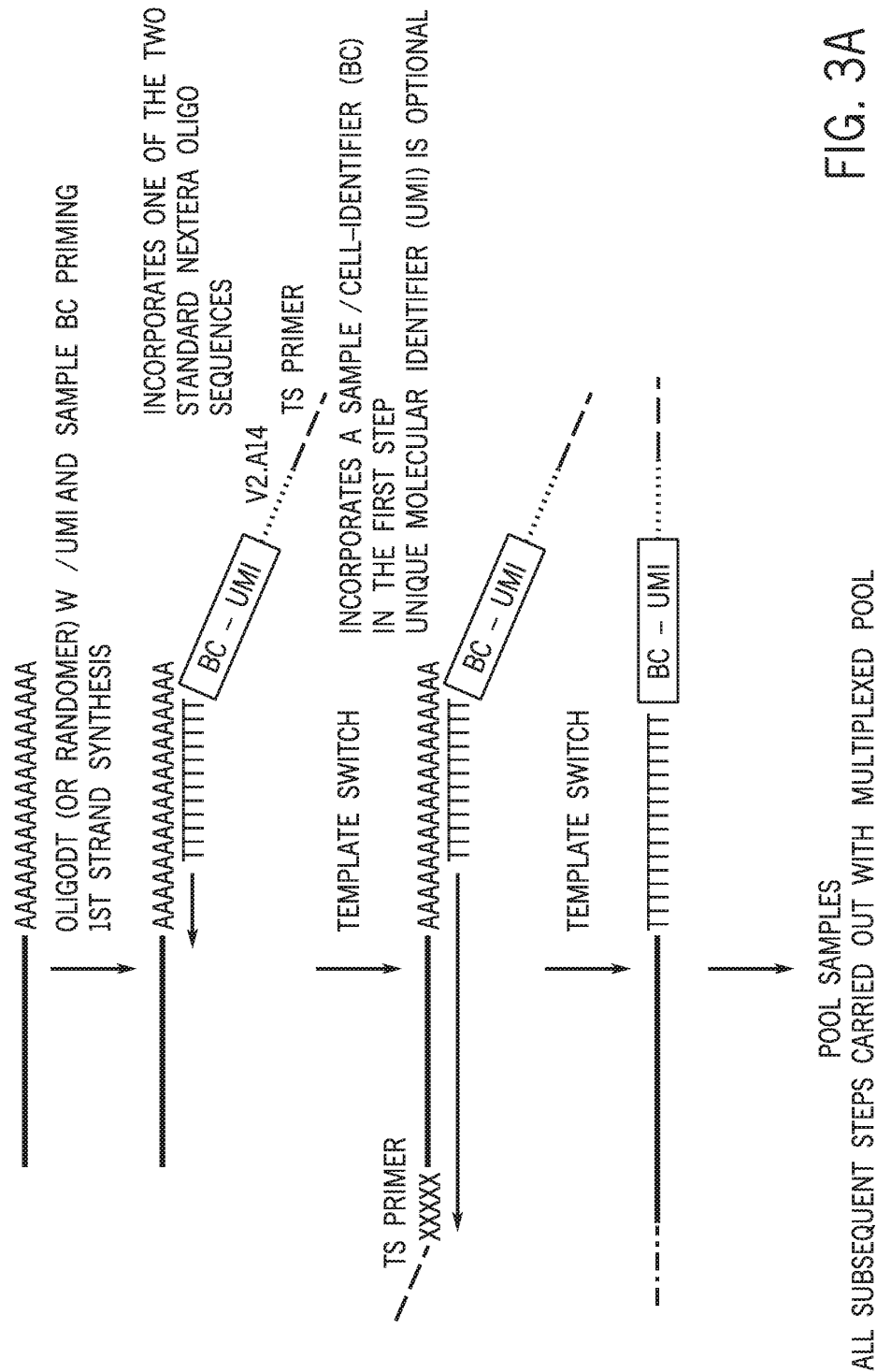


FIG. 3A

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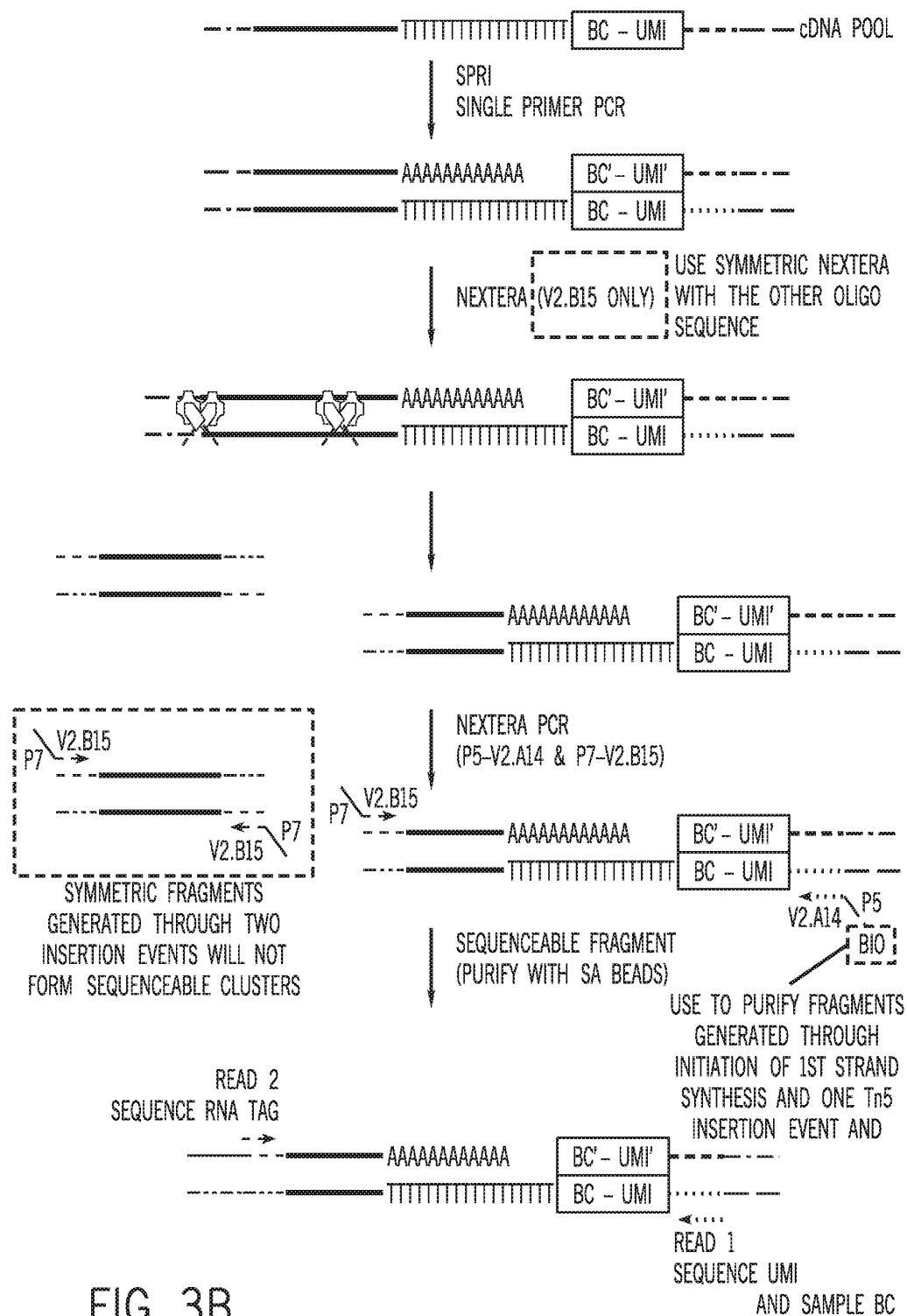
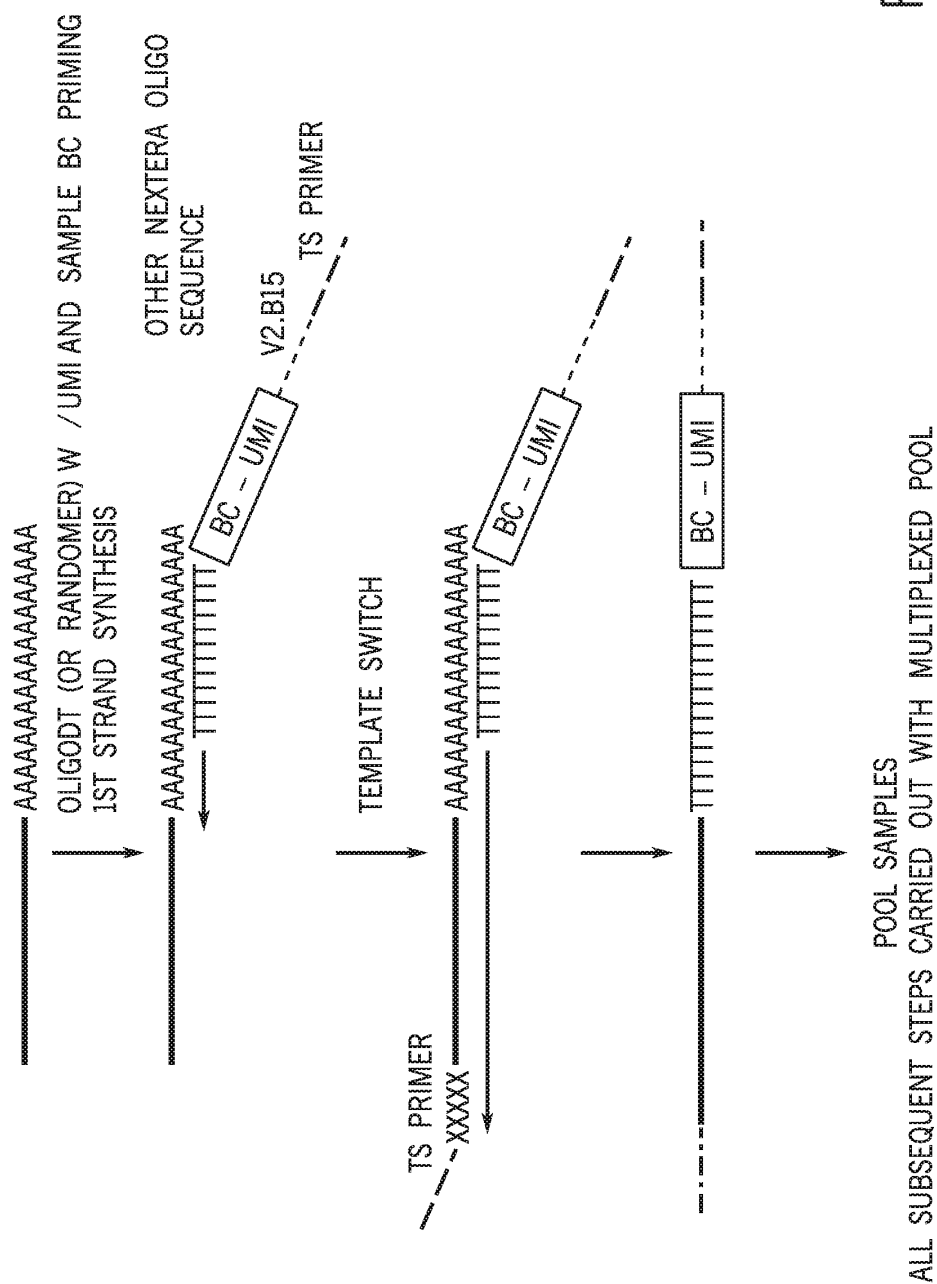


FIG. 3B



4A
4A
G²
E

7 / 22

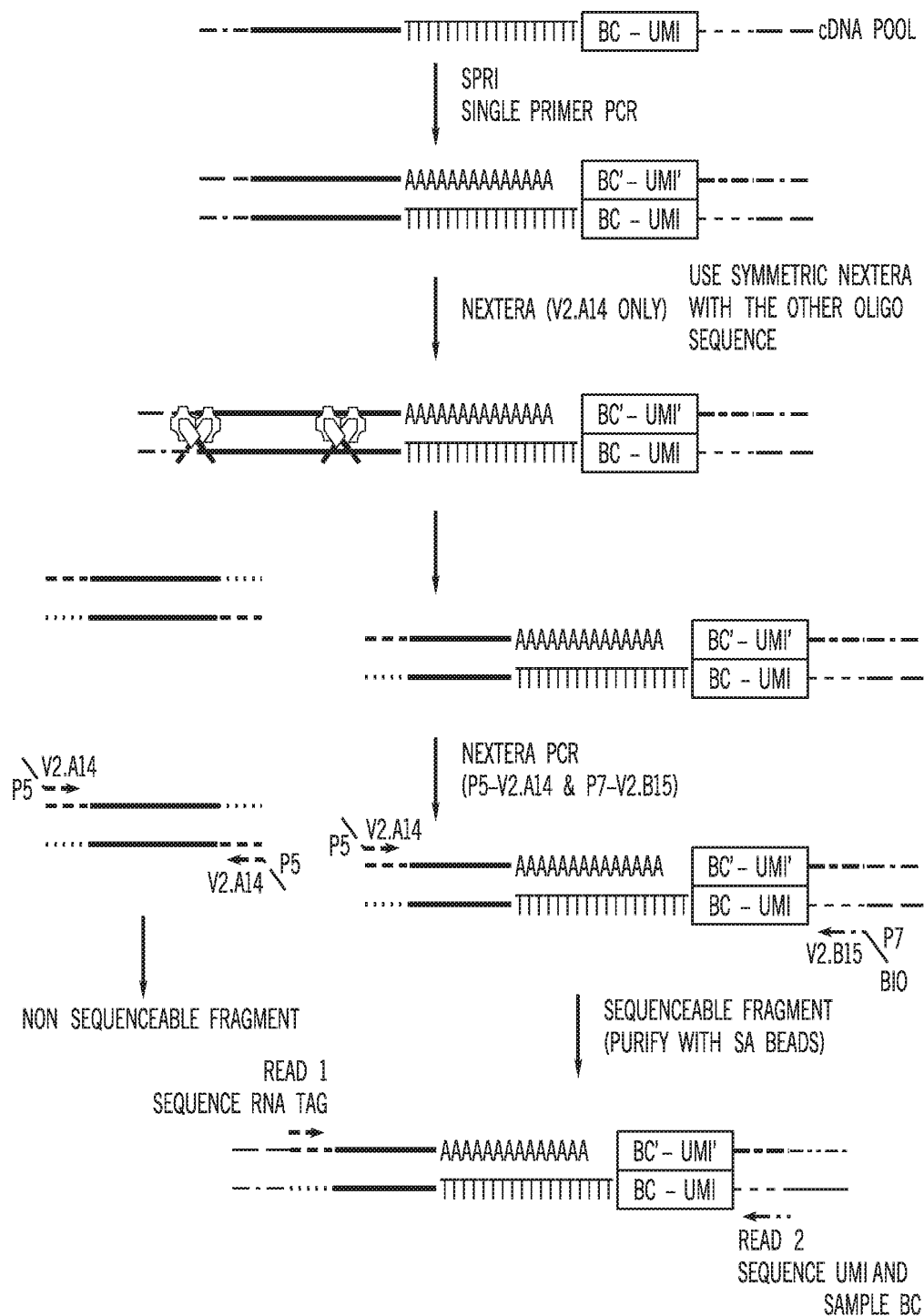
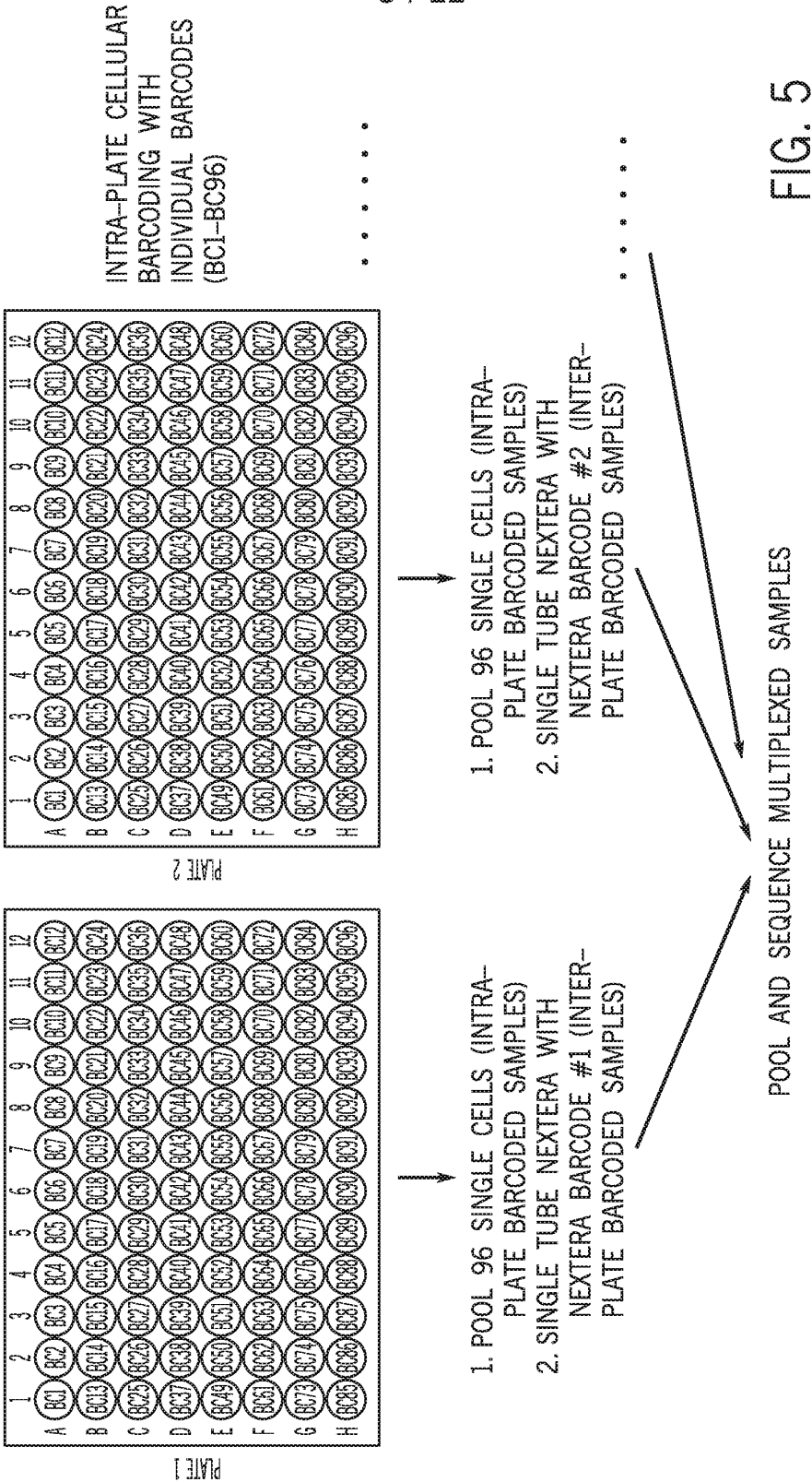


FIG. 4B



KEY SEQUENCE METRICS USING 100 pg HBR				
SEQUENCE METRIC	STATISTICS			
	HIGH THROUGHPUT GEX	STRT		
1 st STRAND PRIMING METHOD	OLIGO-DT	OLIGO-DT	OLIGO-DT + RANDOMER	OLIGO-DT
MAPPING RATE	ALIGNED TO HGL9 TRANSCRIPTOME	63%	75%	50%
	RIBOSOMAL	1%	2%	12%
	MITOCHONDRIAL	15%	14%	15%
	OTHER	1%	0%	0%
UNALIGNED		20%	9%	23%
CORRELATION OF GENE-EXPRESSION BETWEEN TECHNICAL REPLICATES (R)		0.9	0.85	0.72
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

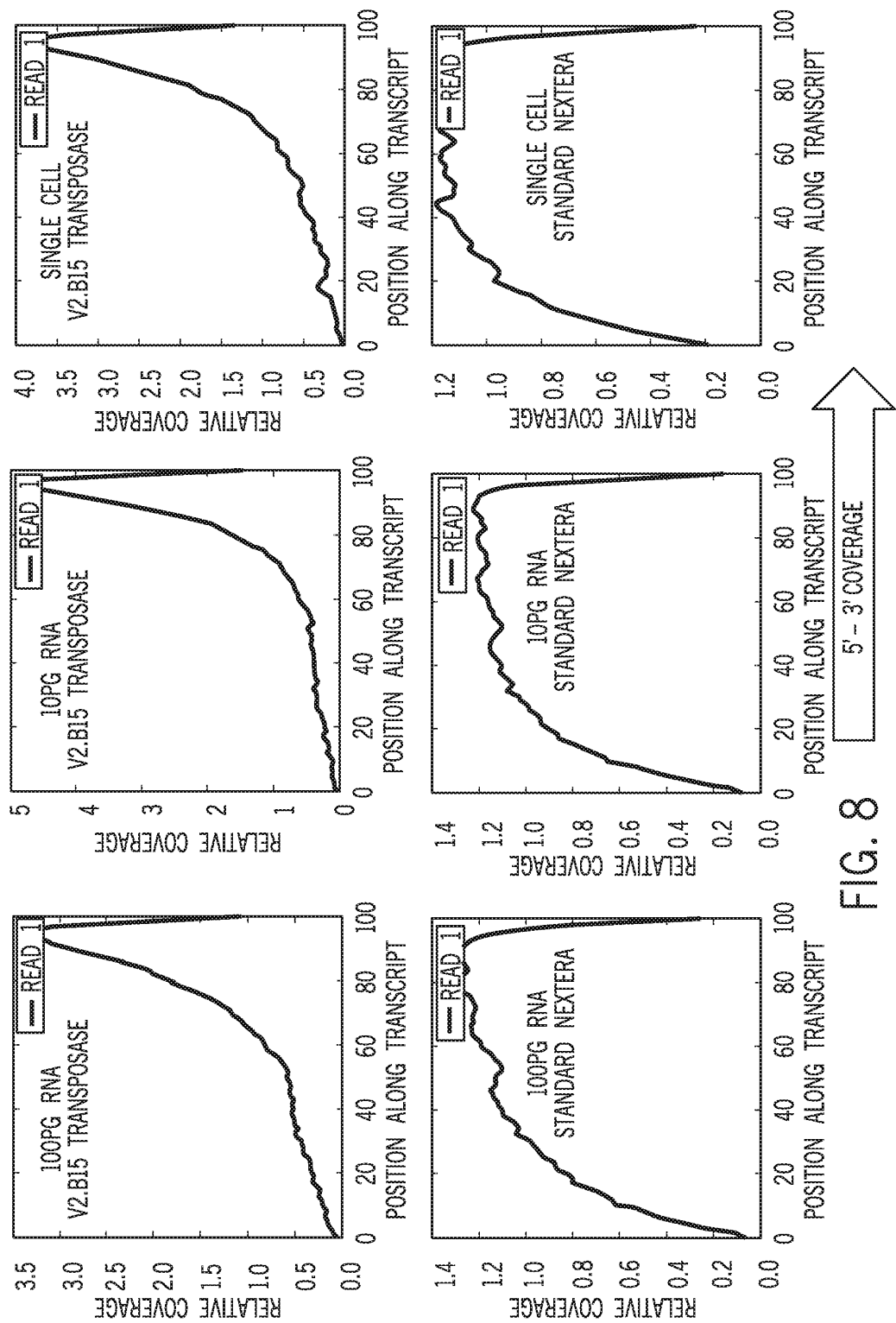


FIG. 8

RANDOMER AND OLIGO-DT PRIMING

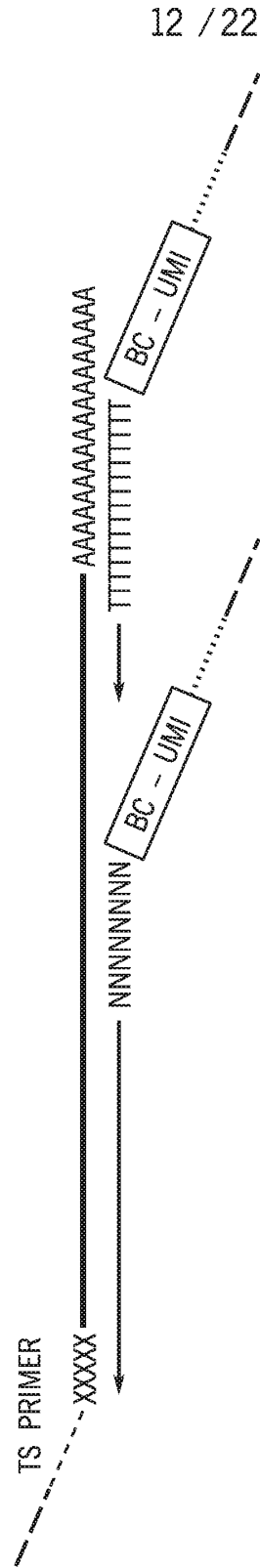


FIG. 9A

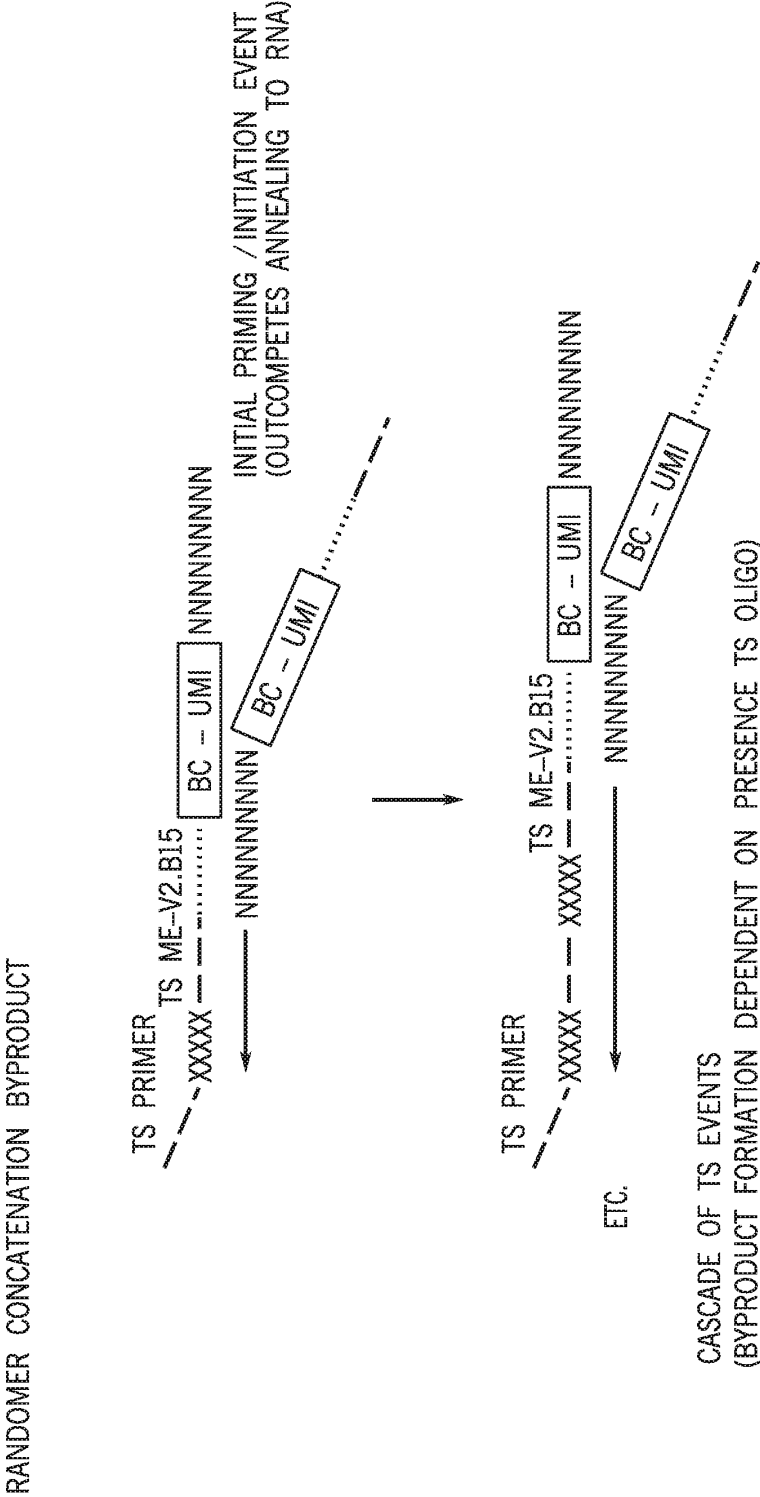


FIG. 9B

POSSIBLE STRATEGIES TO REDUCE CONCATENATION BYPRODUCT

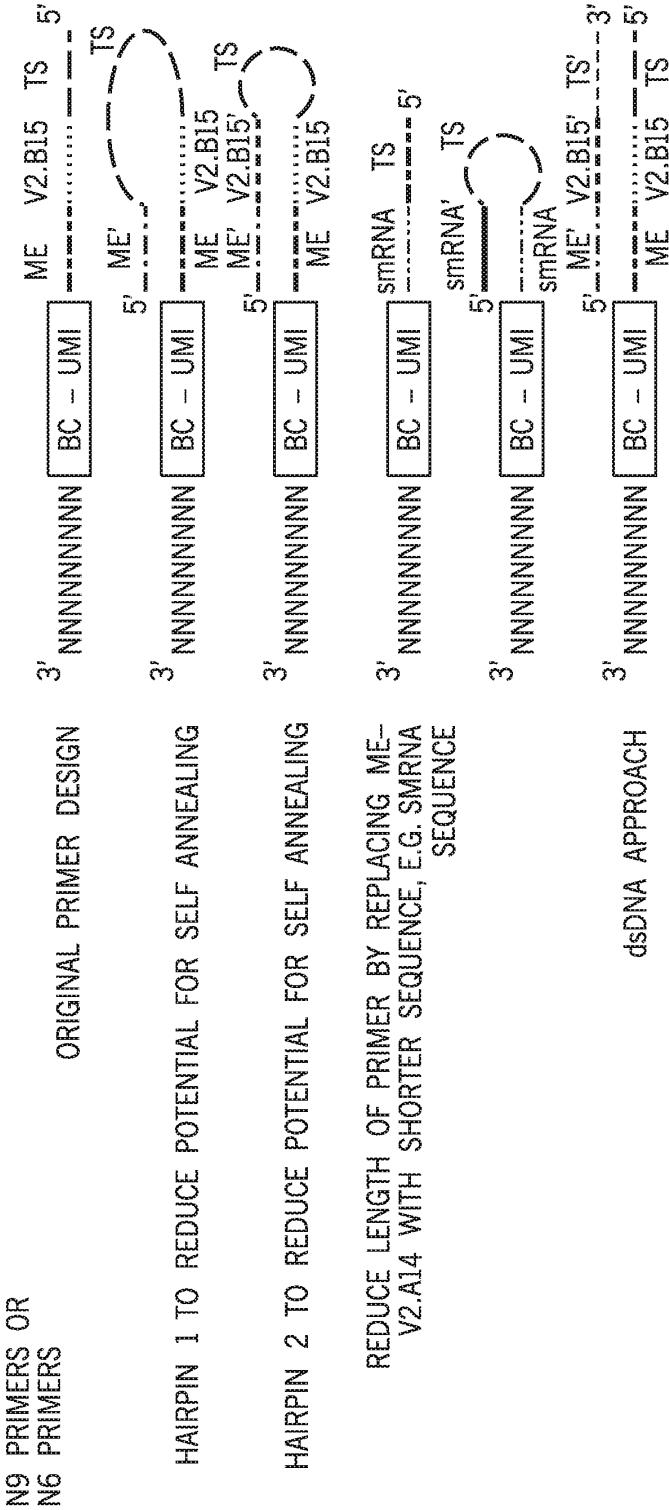


FIG. 10

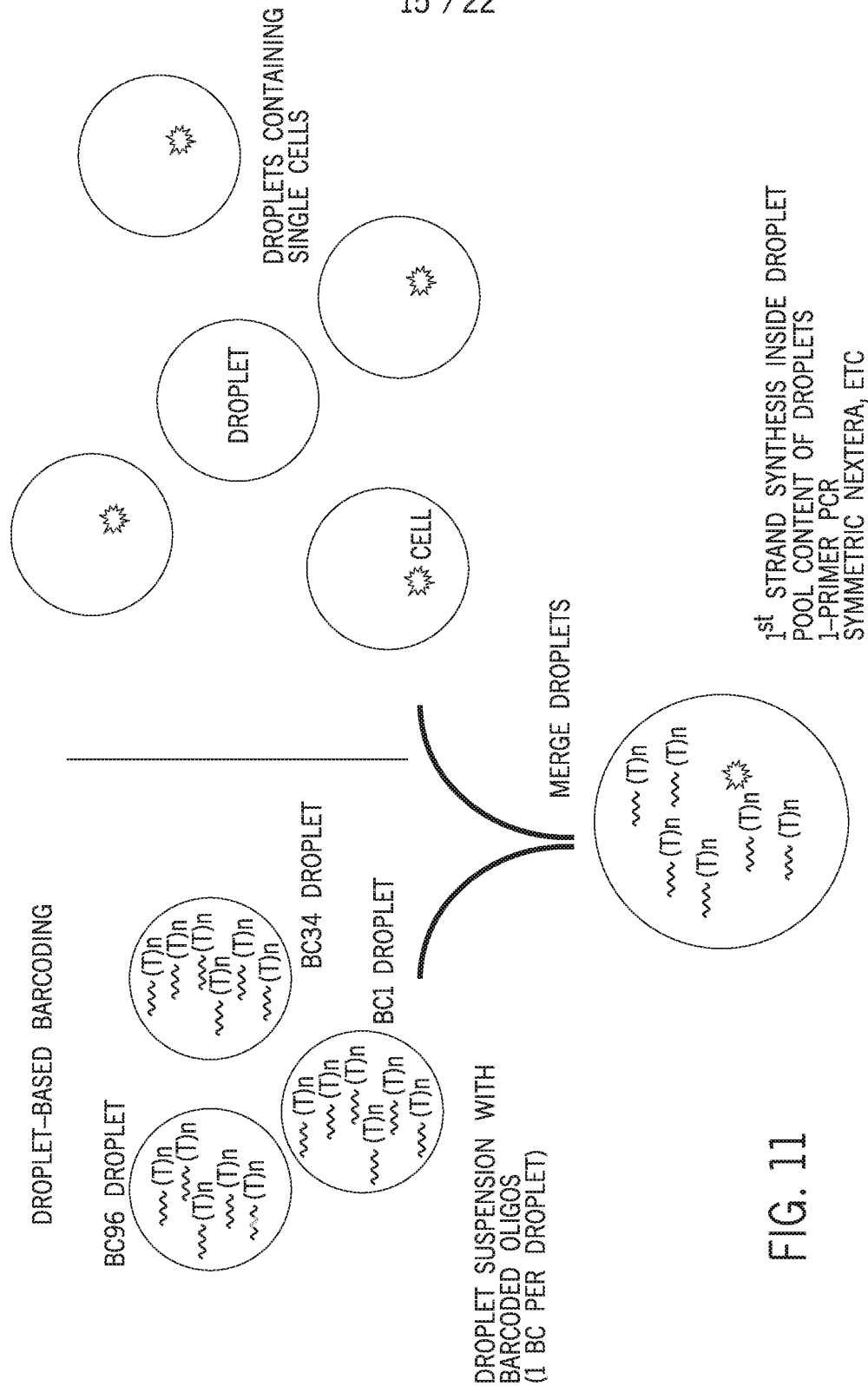


FIG. 11

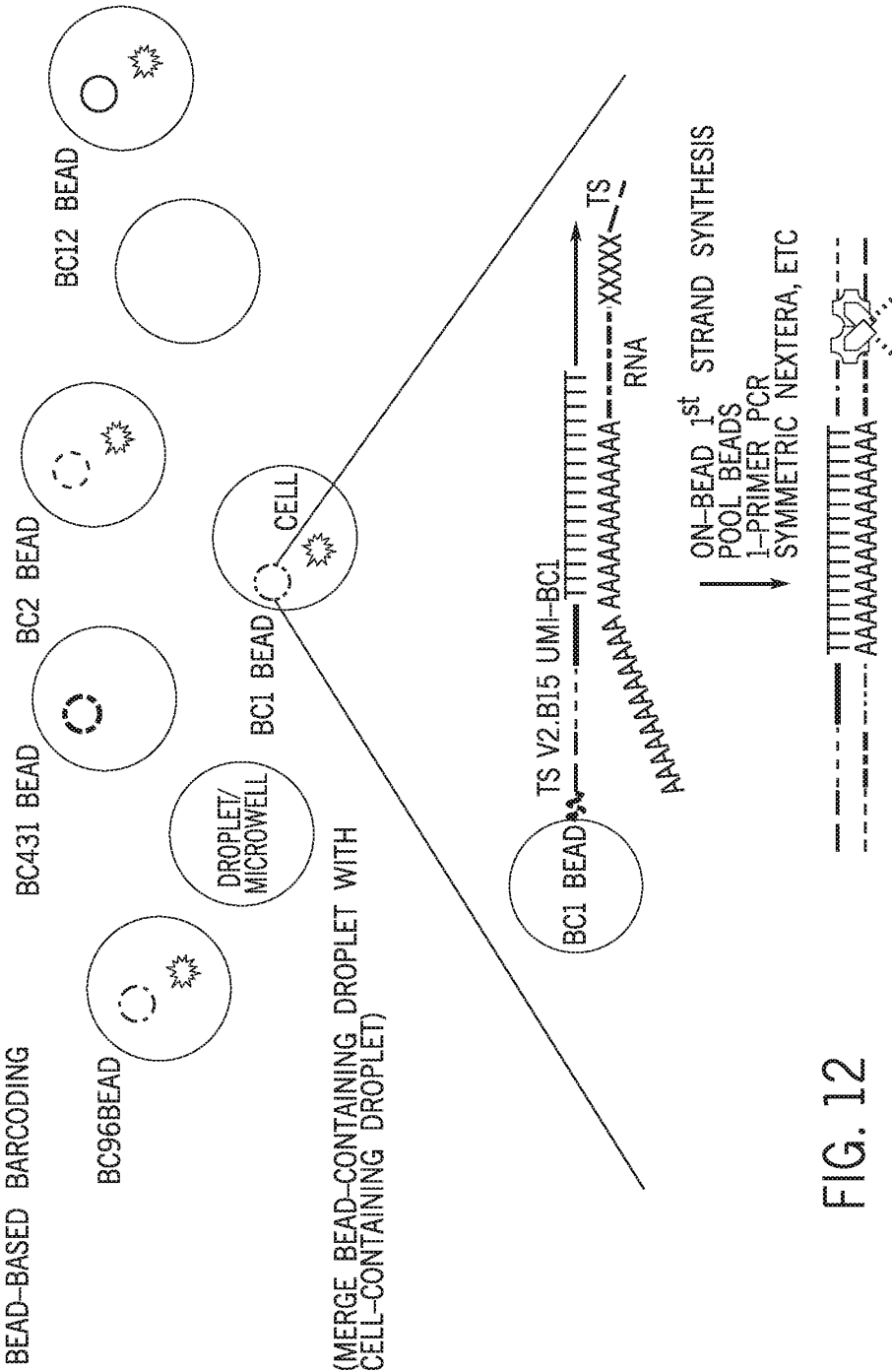


FIG. 12

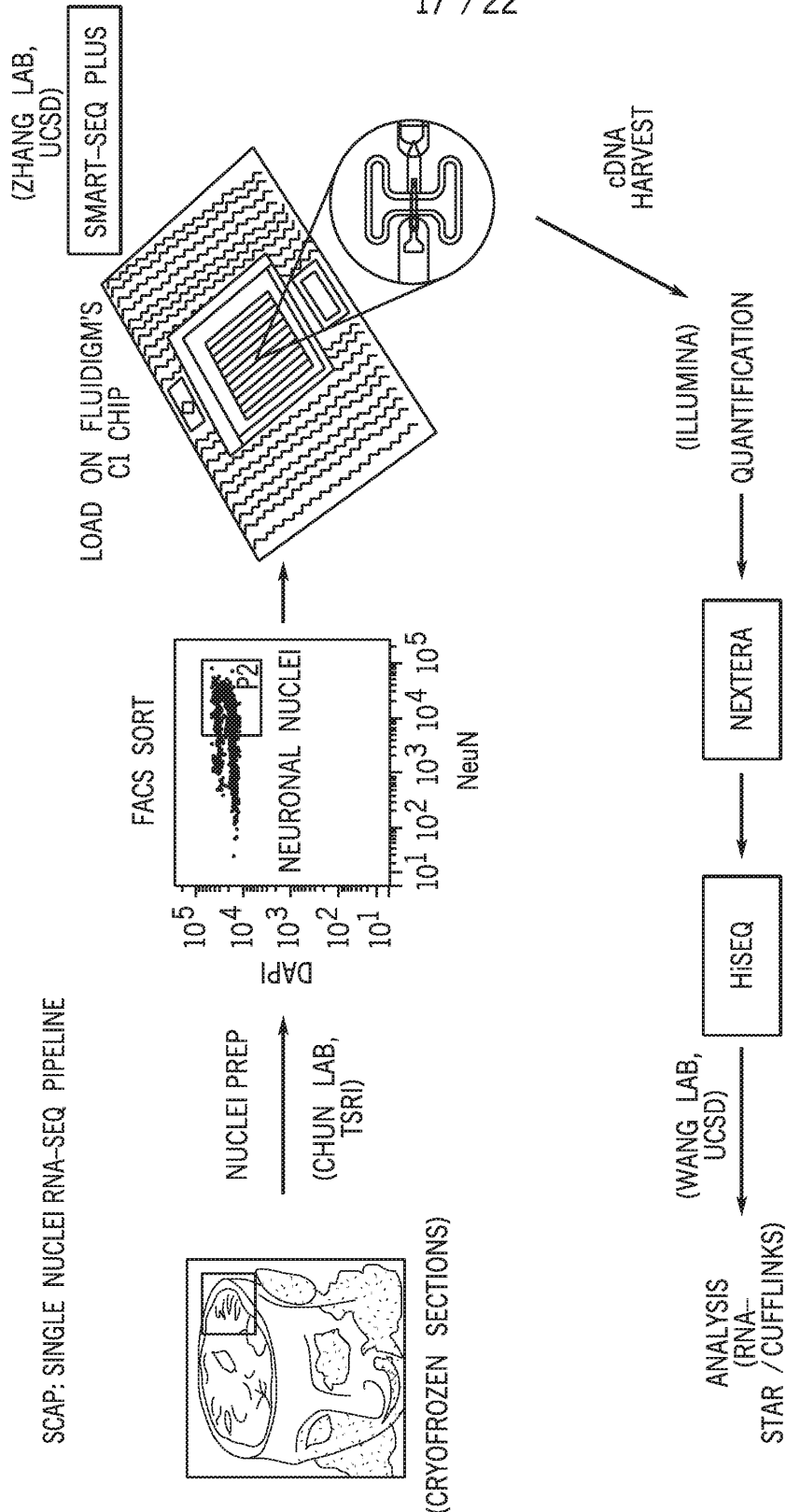


FIG. 13

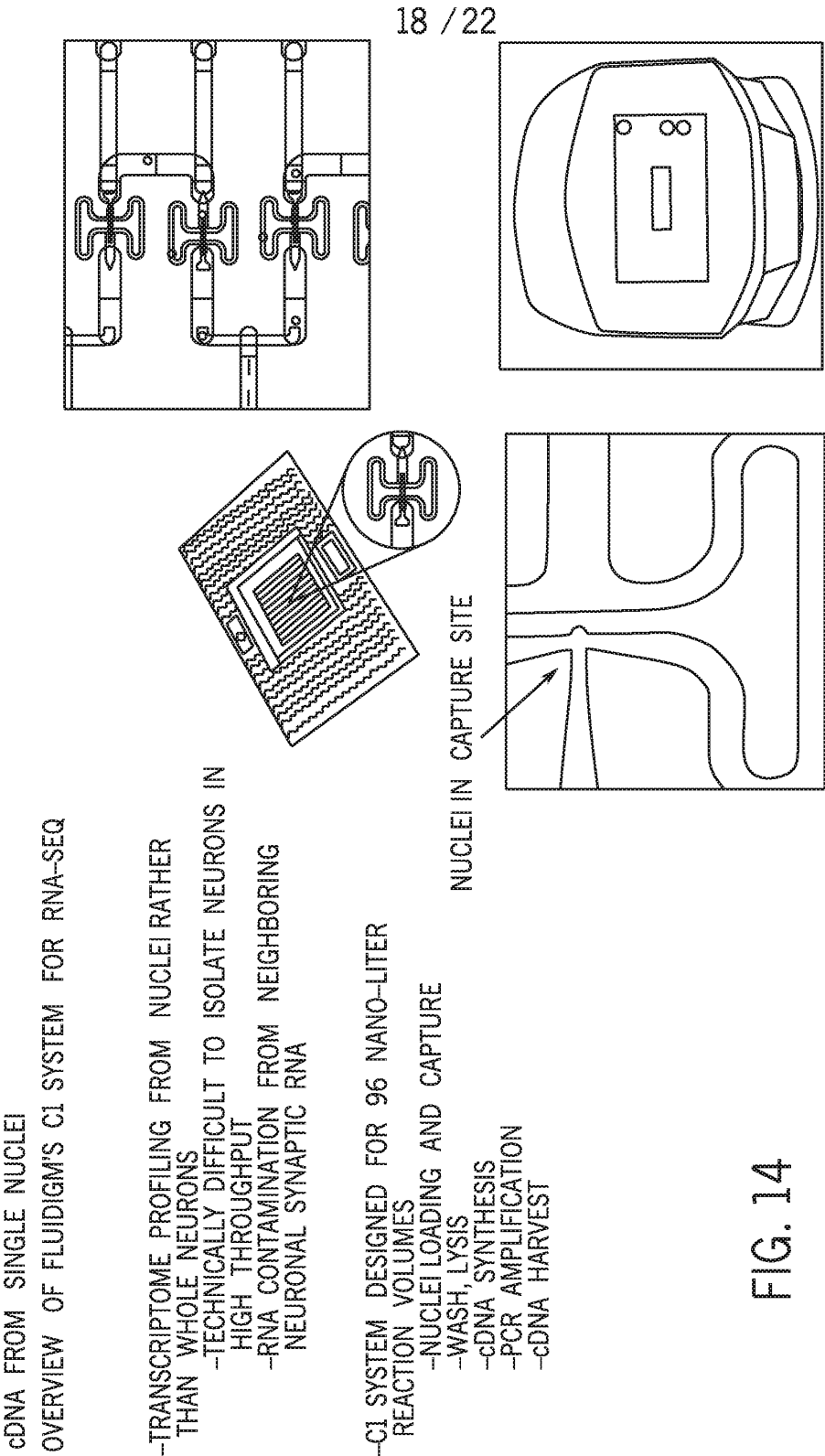


FIG. 14

OVERVIEW OF RNA-SEQ USING "TEMPLATE SWITCHING" APPROACH

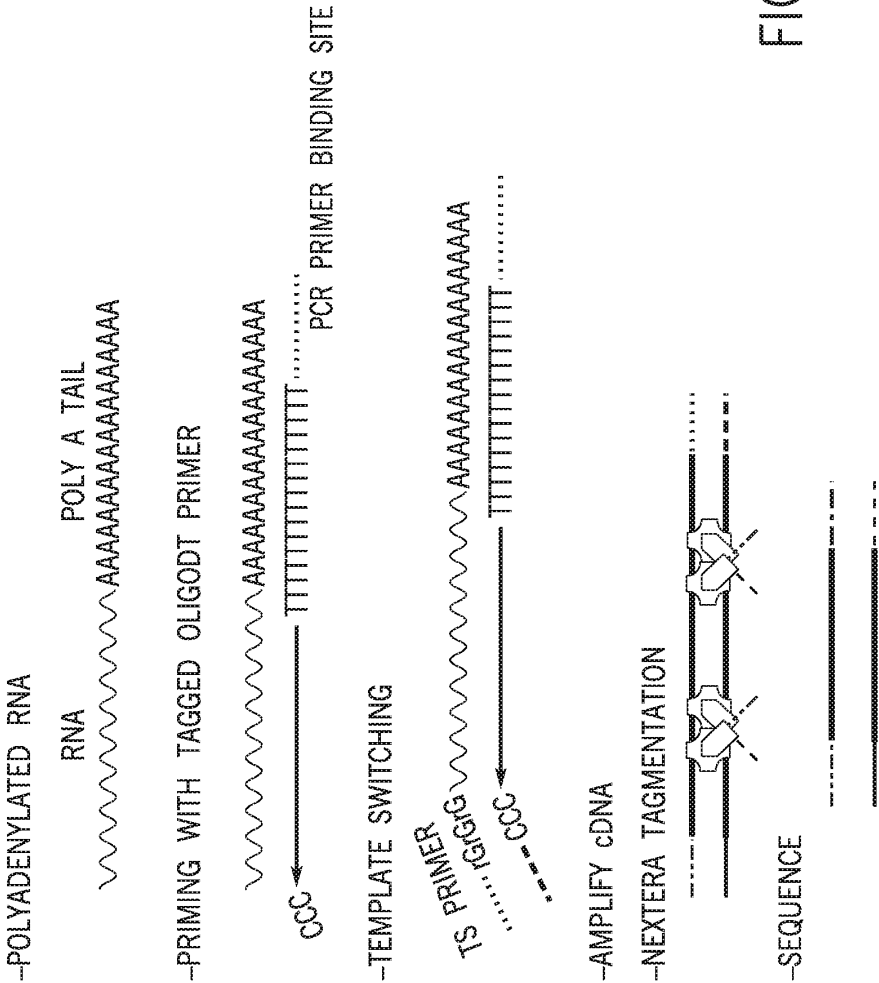


FIG. 15

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



FIG. 16

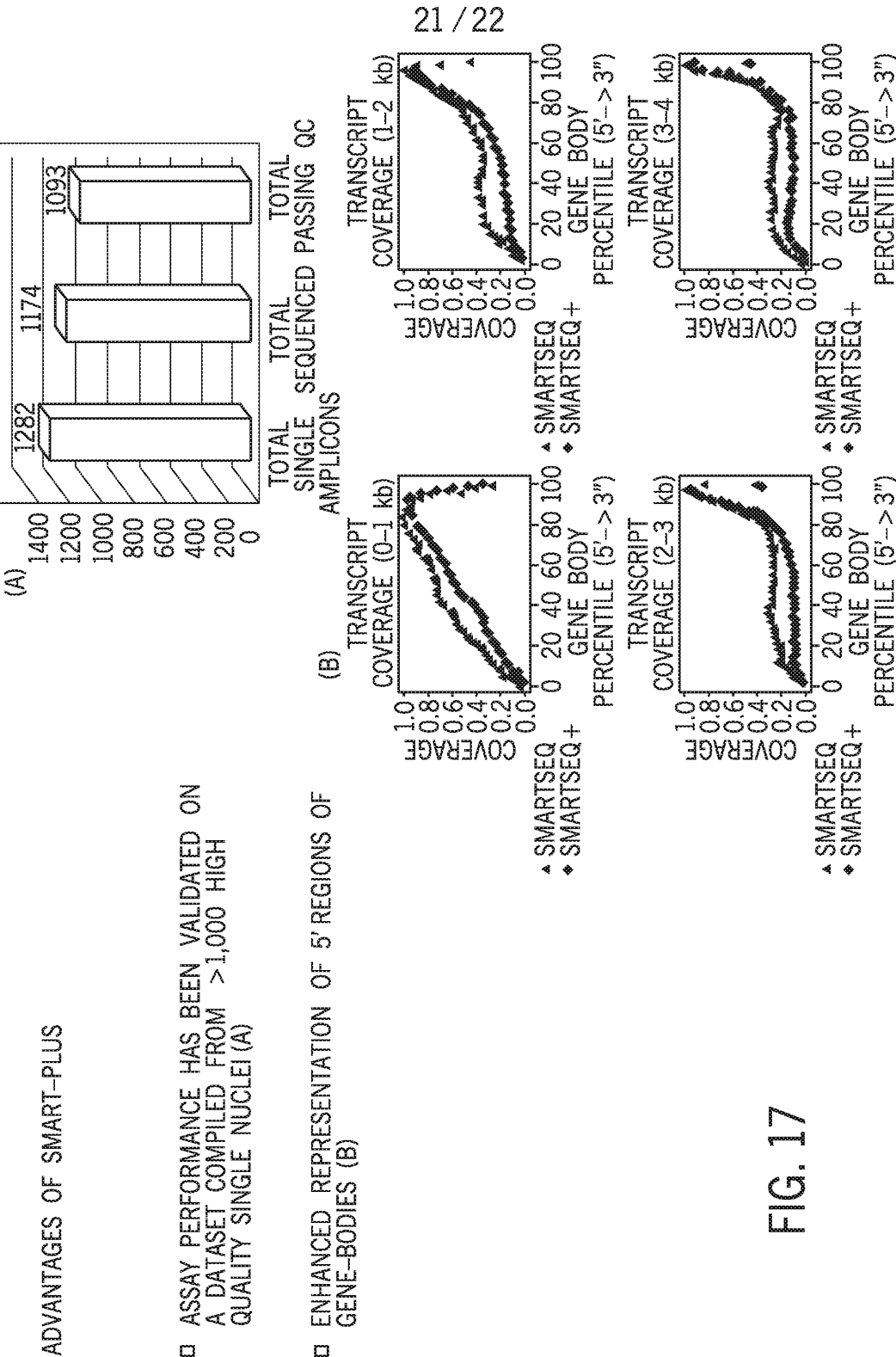


FIG. 17

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)

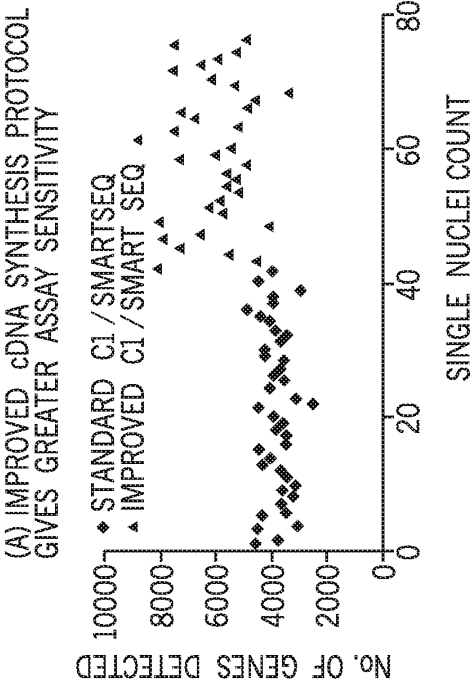


FIG. 18