

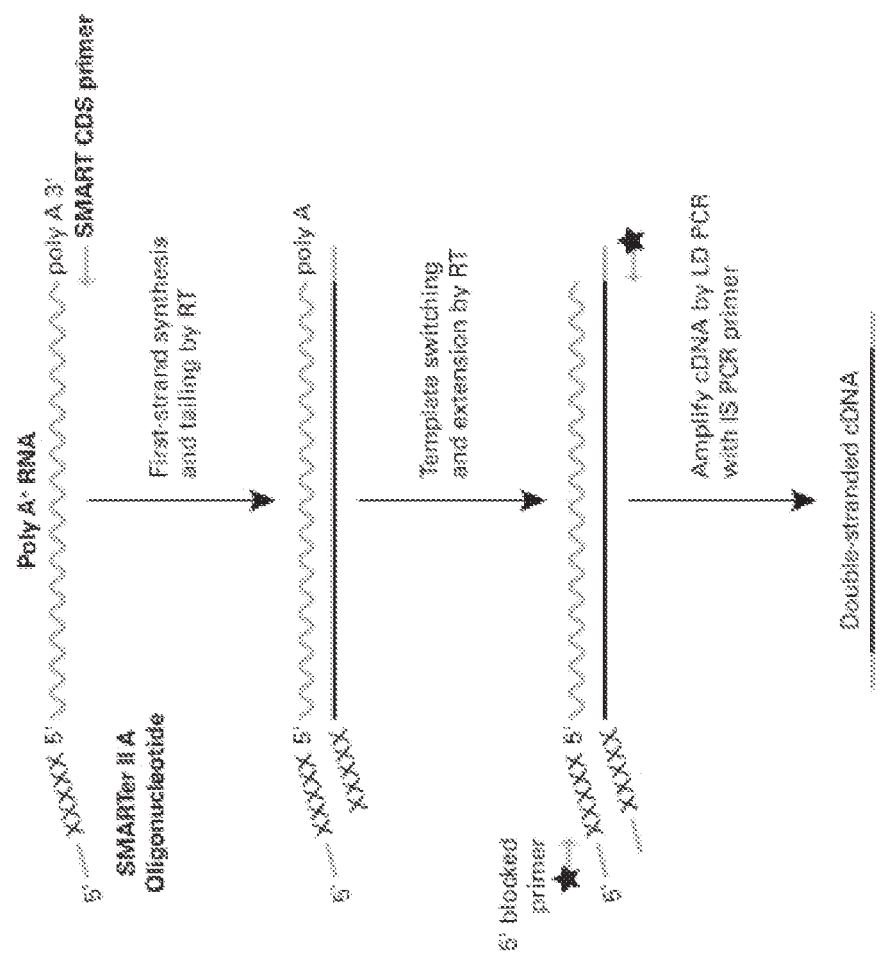


Fig. 1

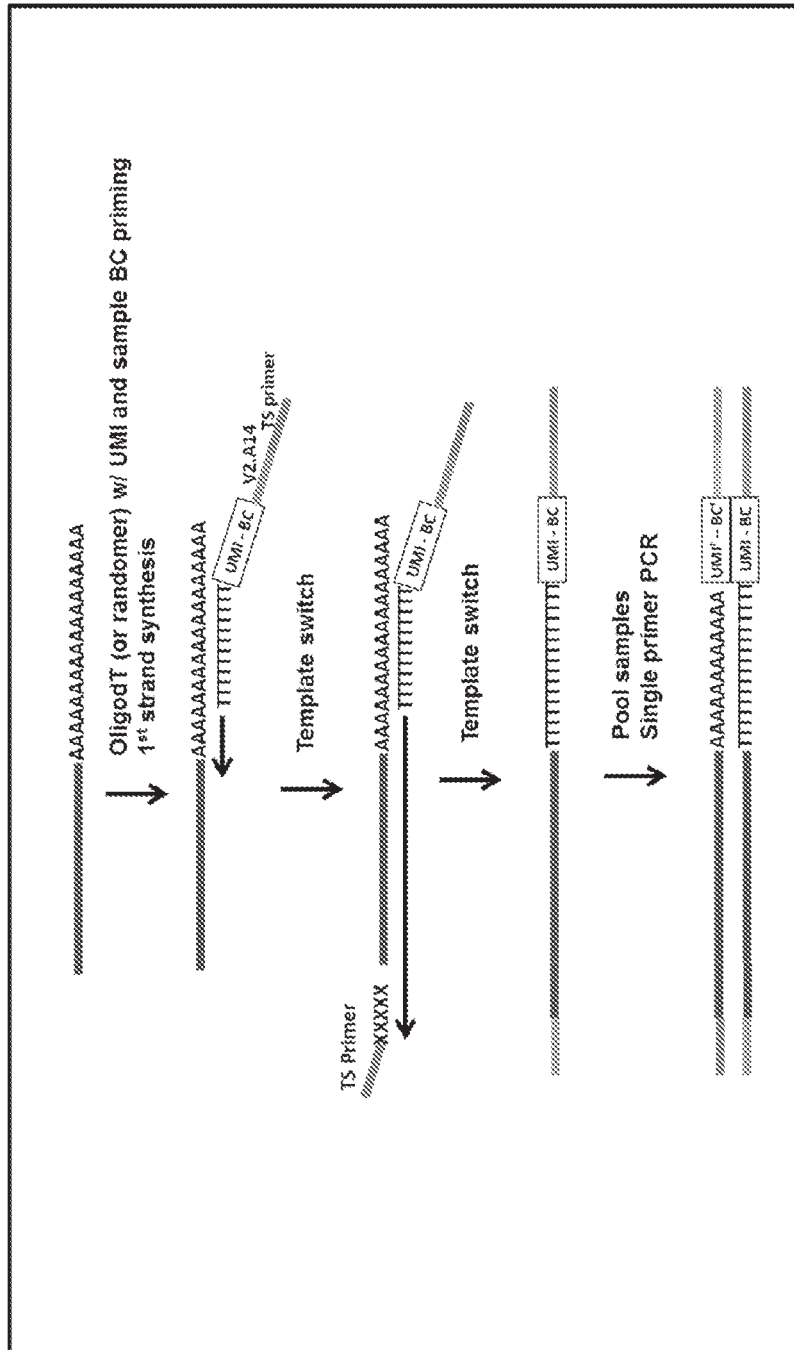


Fig. 2A

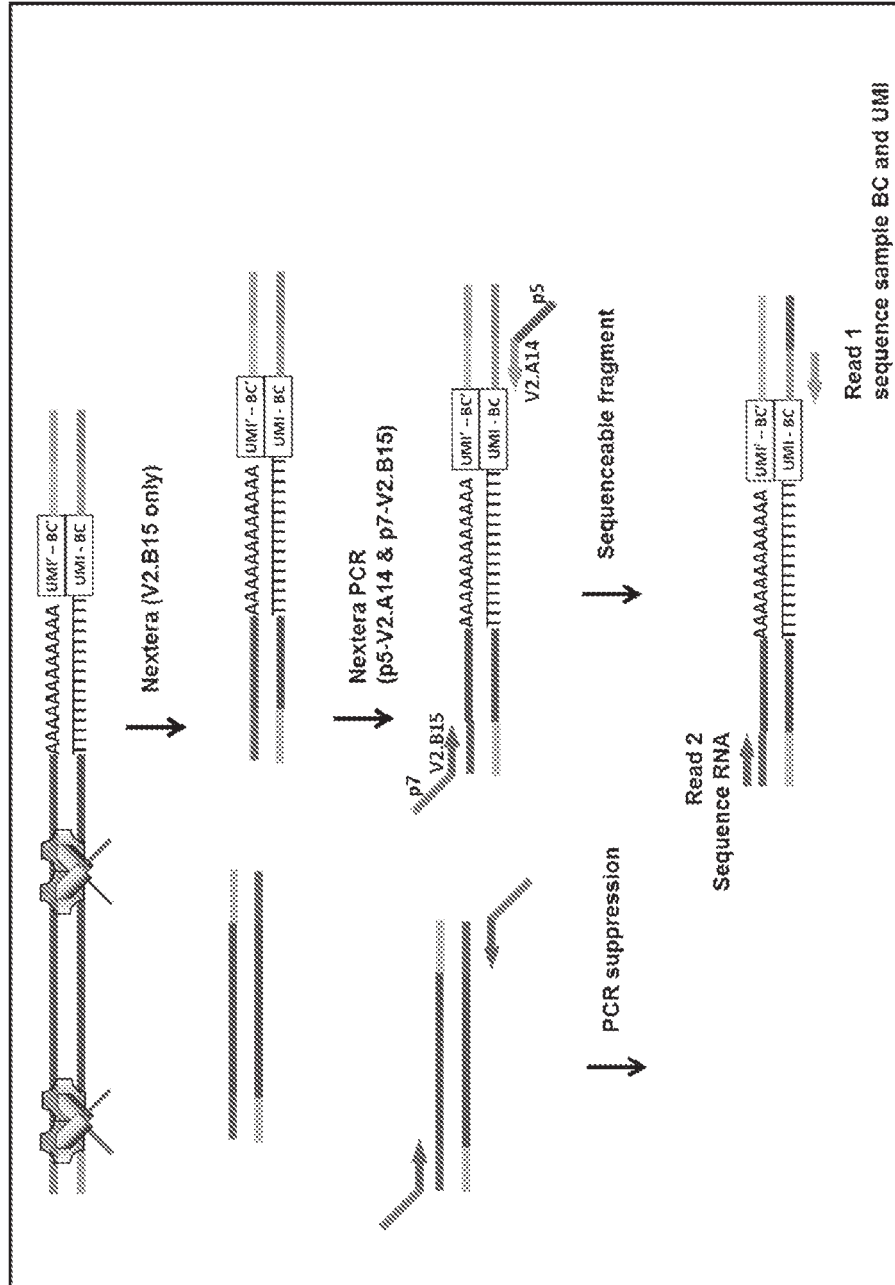


Fig. 2B

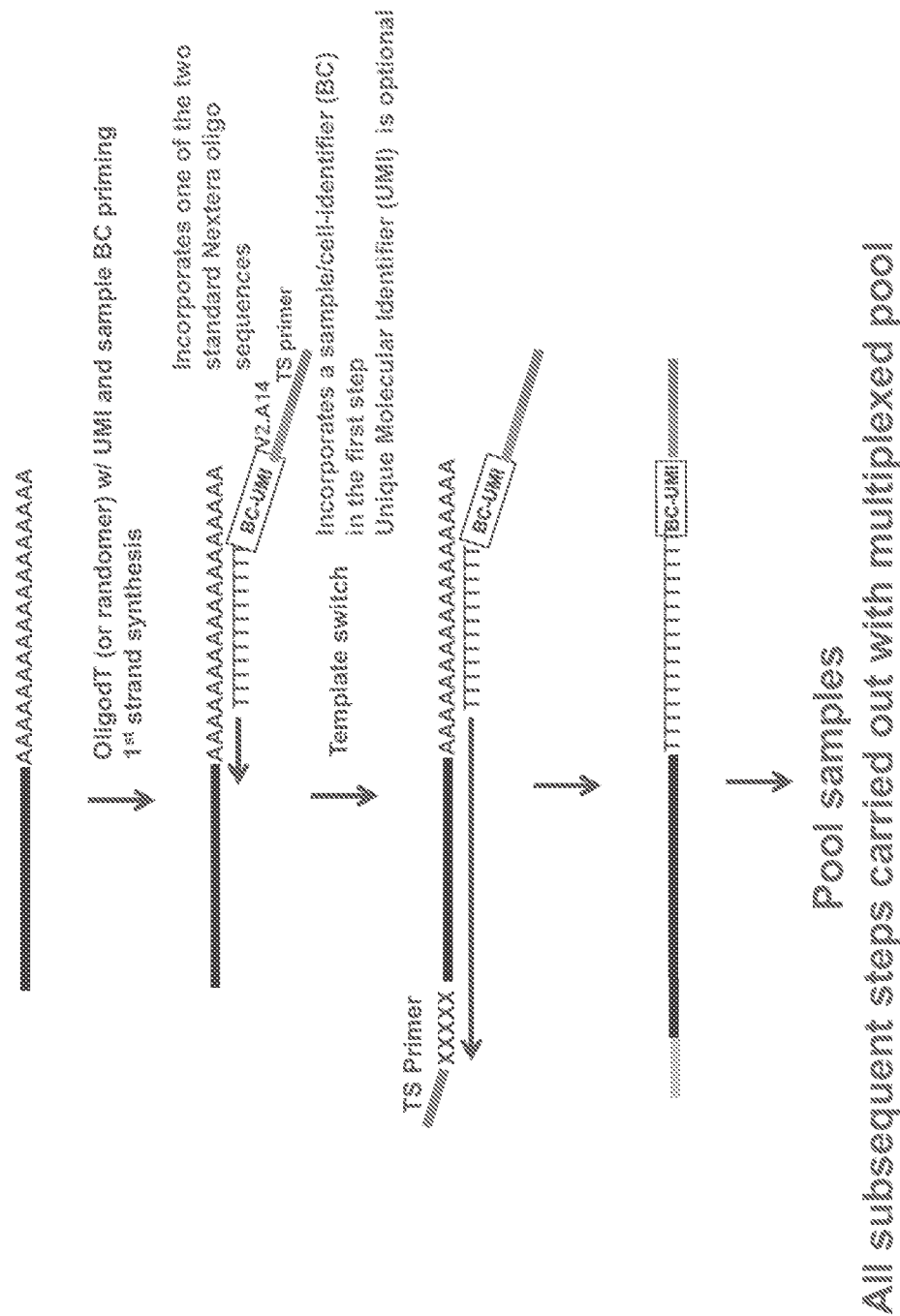
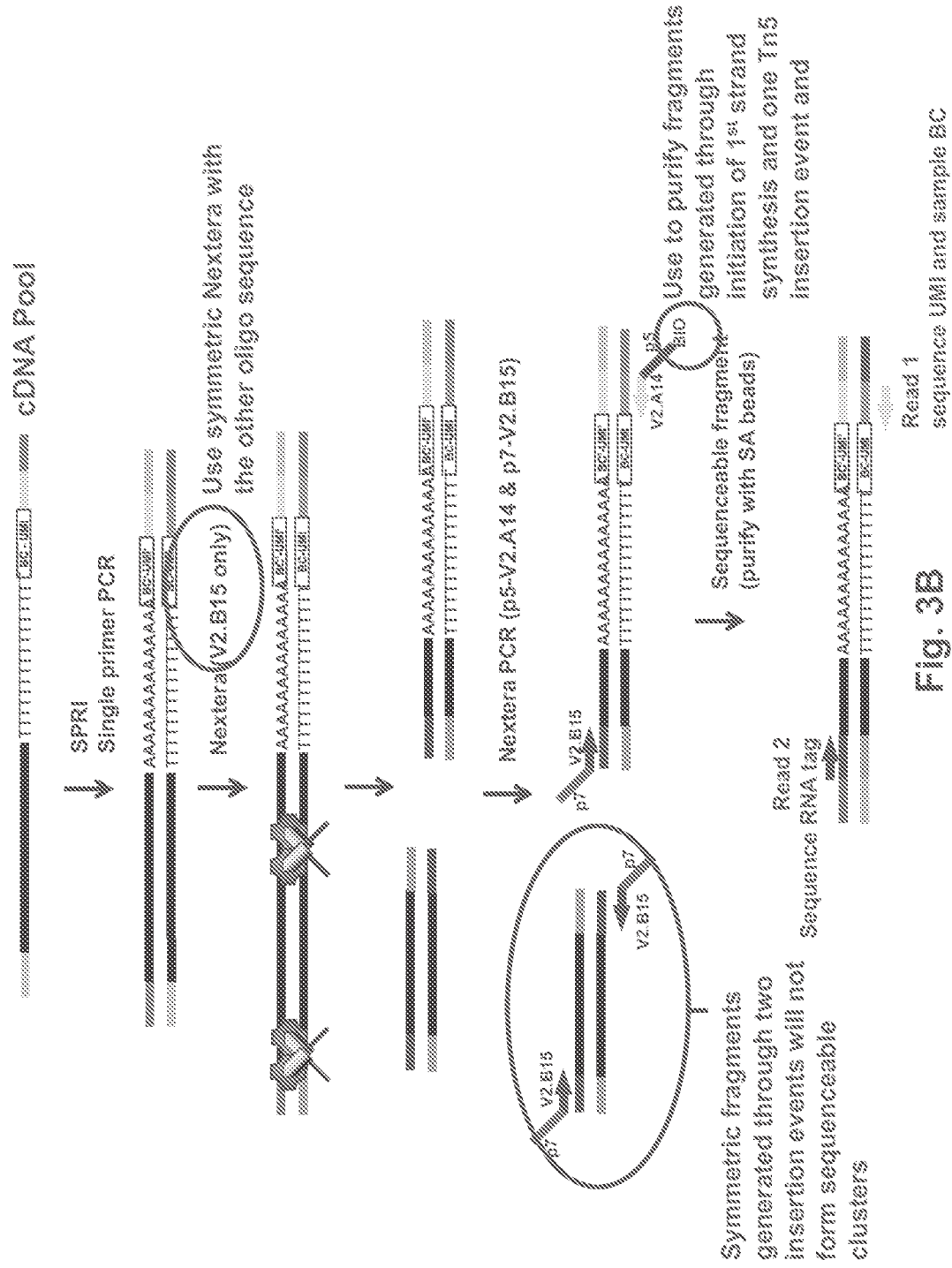


Fig. 3A



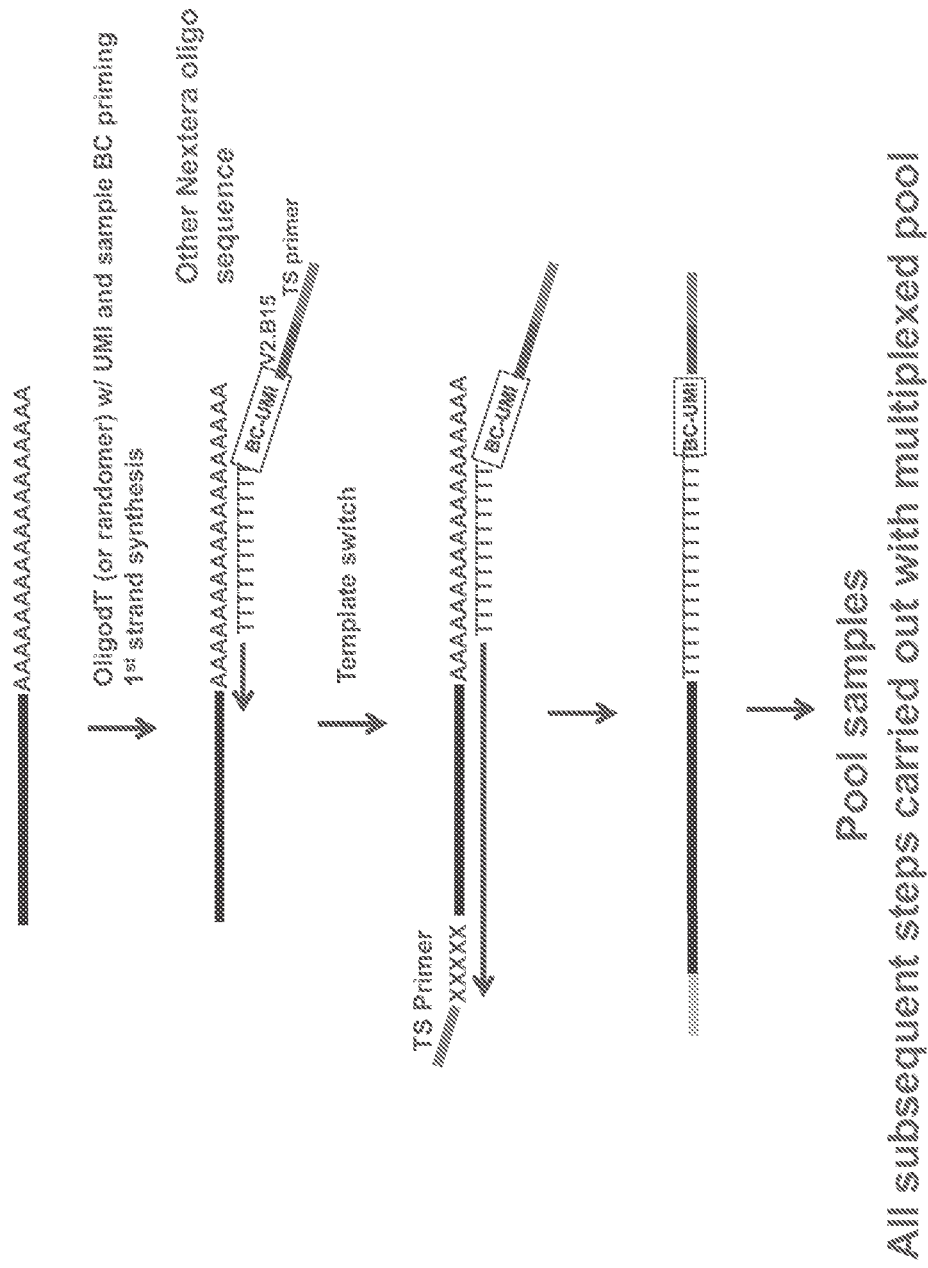


Fig. 4A

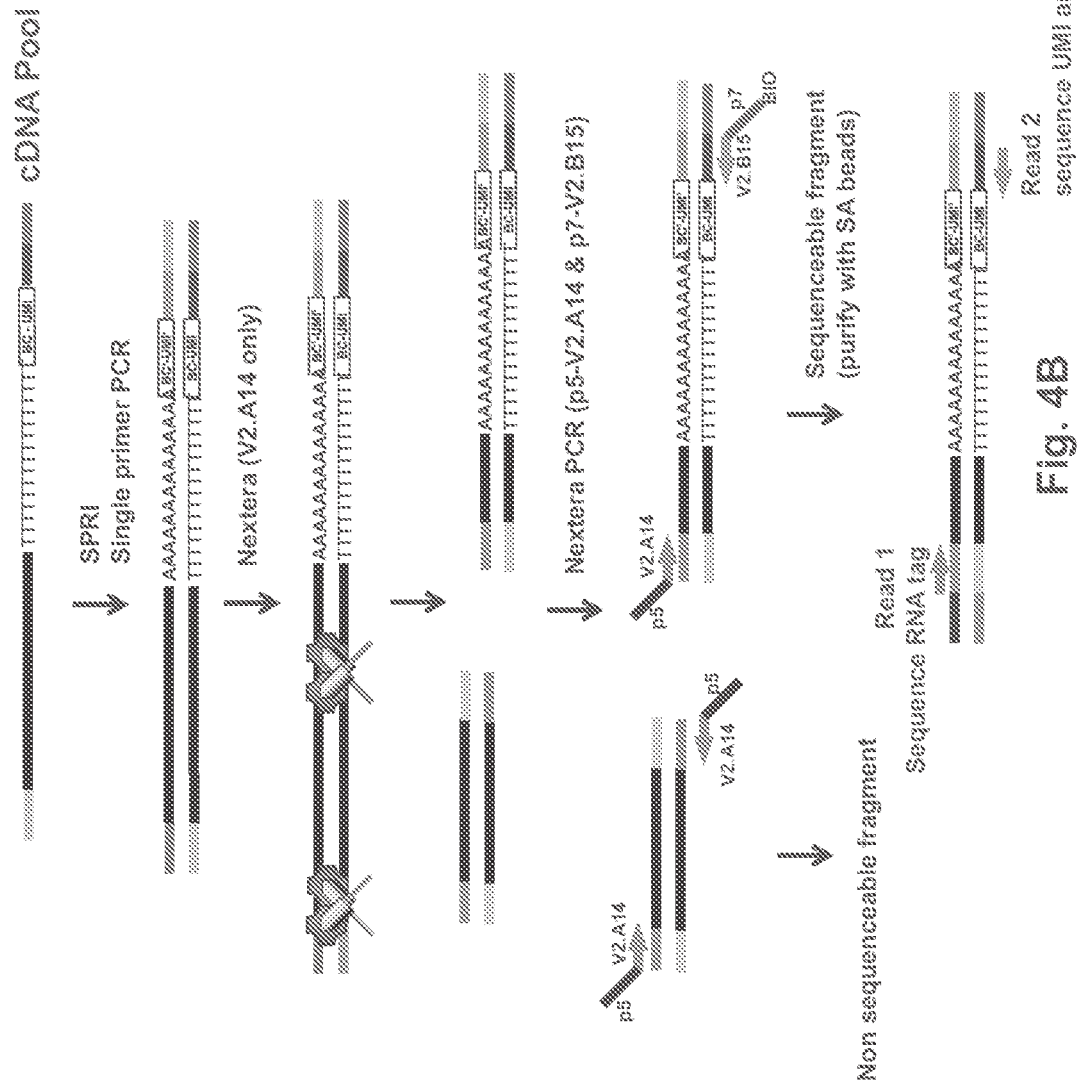


Fig. 4B

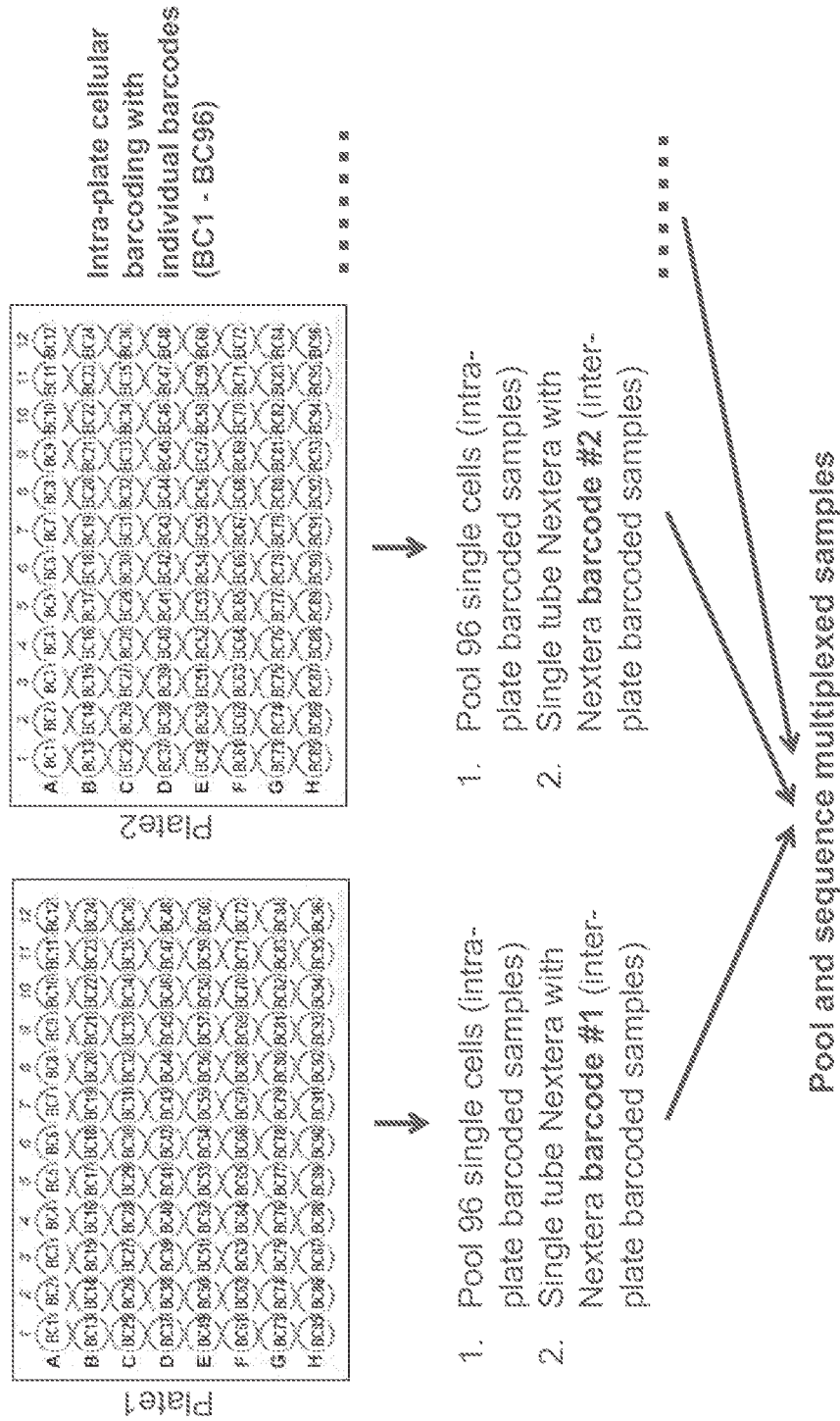


Fig. 5

Key sequence metrics using 100 pg HBR

Sequence Metric	Statistics			
	High Throughput GEX	SMART		
1 st Strand priming method	Oligo-dT	Oligo-dT	Oligo-dT + Randomer	Oligo-dT
Mapping rate	Aligned to Hg19 transcriptome	63%	75%	50%
	Ribosomal	1%	2%	12%
	Mitochondrial	15%	14%	15%
	Other	1%	0%	0%
Correlation of gene-expression between technical replicates (r)	Unaligned	20%	9%	23%
		0.9	0.85	0.72
No. of genes detected (FPKM>1)	10,021	11,254	11,683	8,492

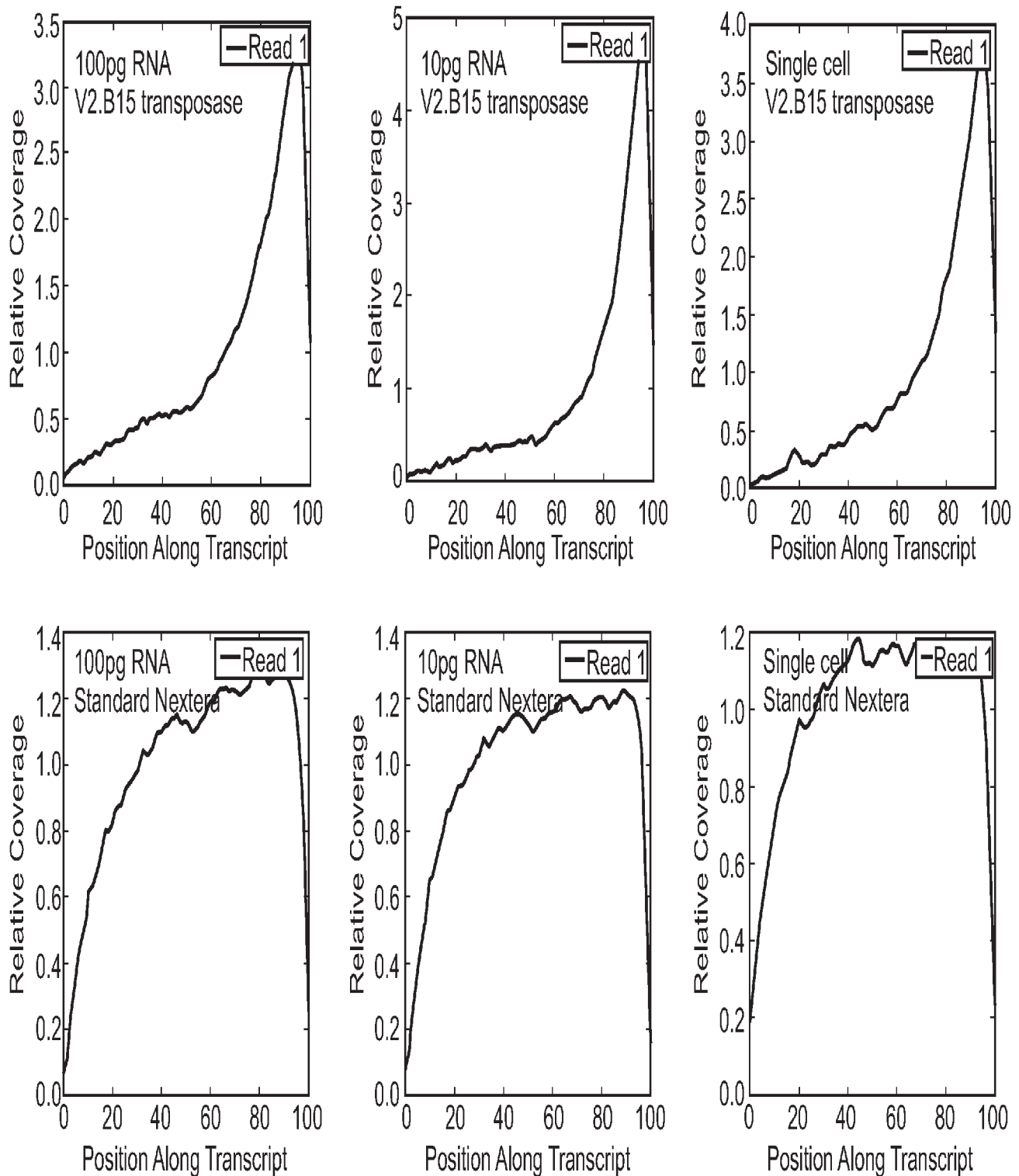
Fig. 6

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
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.

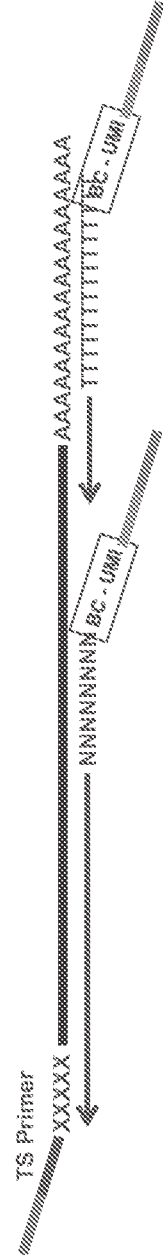
Fig. 7



5'-3' coverage

Fig. 8

Randomer and oligo-dT priming



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Fig. 9A

Randomer concatenation byproduct

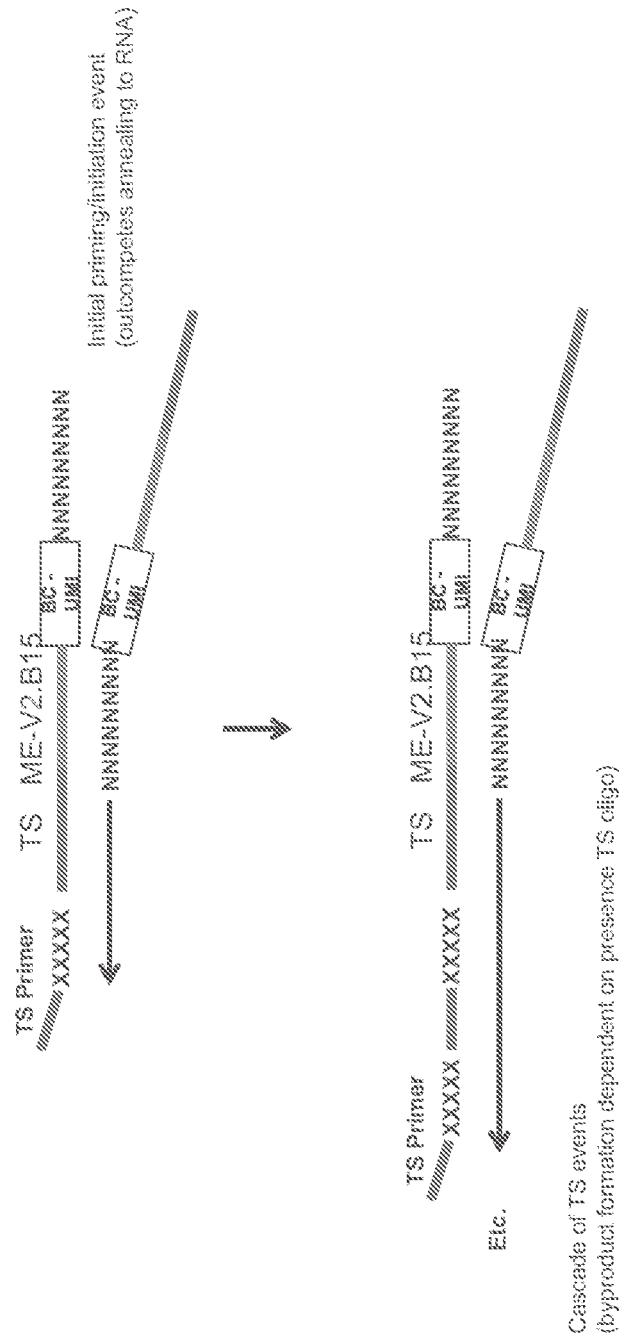


Fig. 9B

Possible strategies to reduce concatenation byproduct

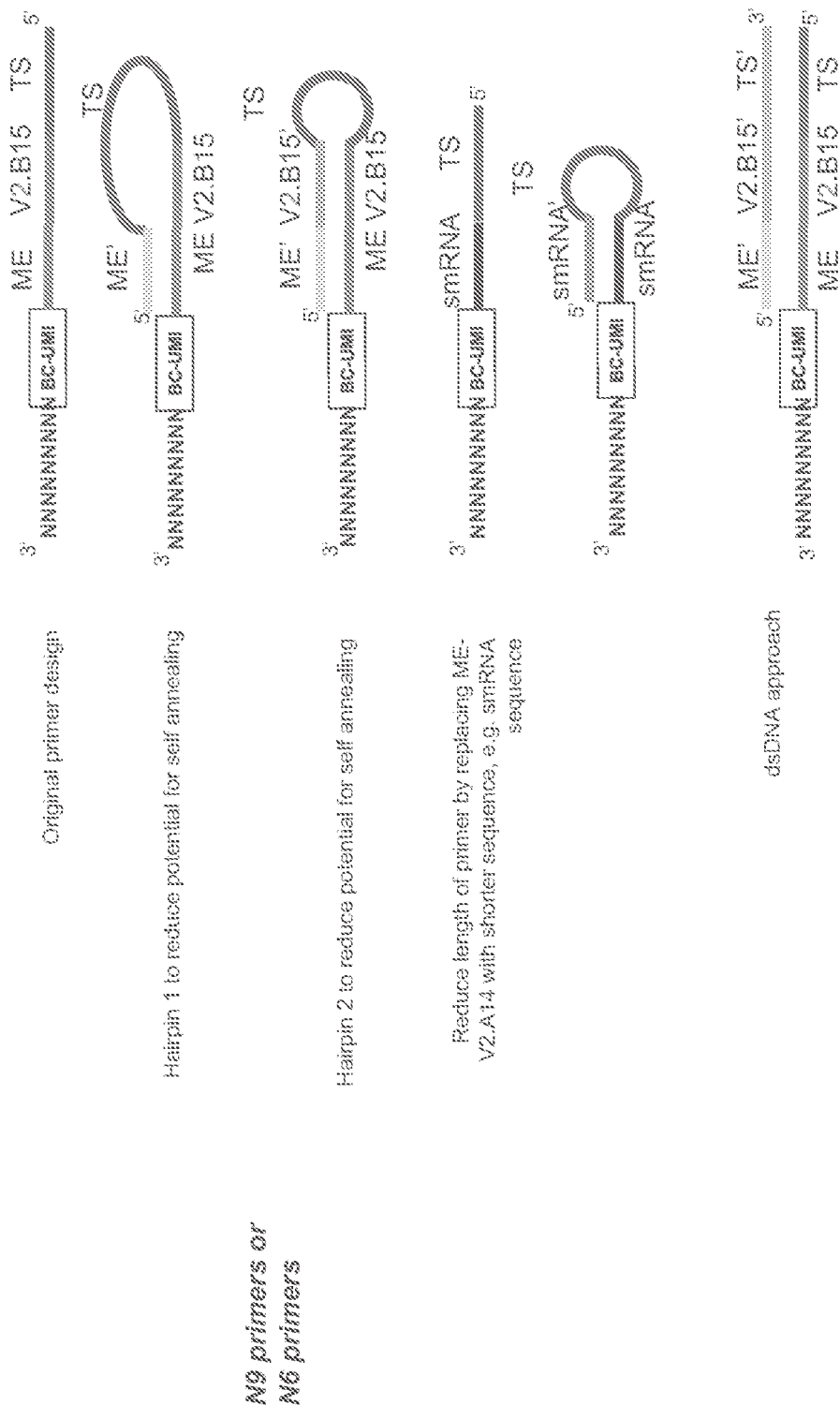


Fig. 10

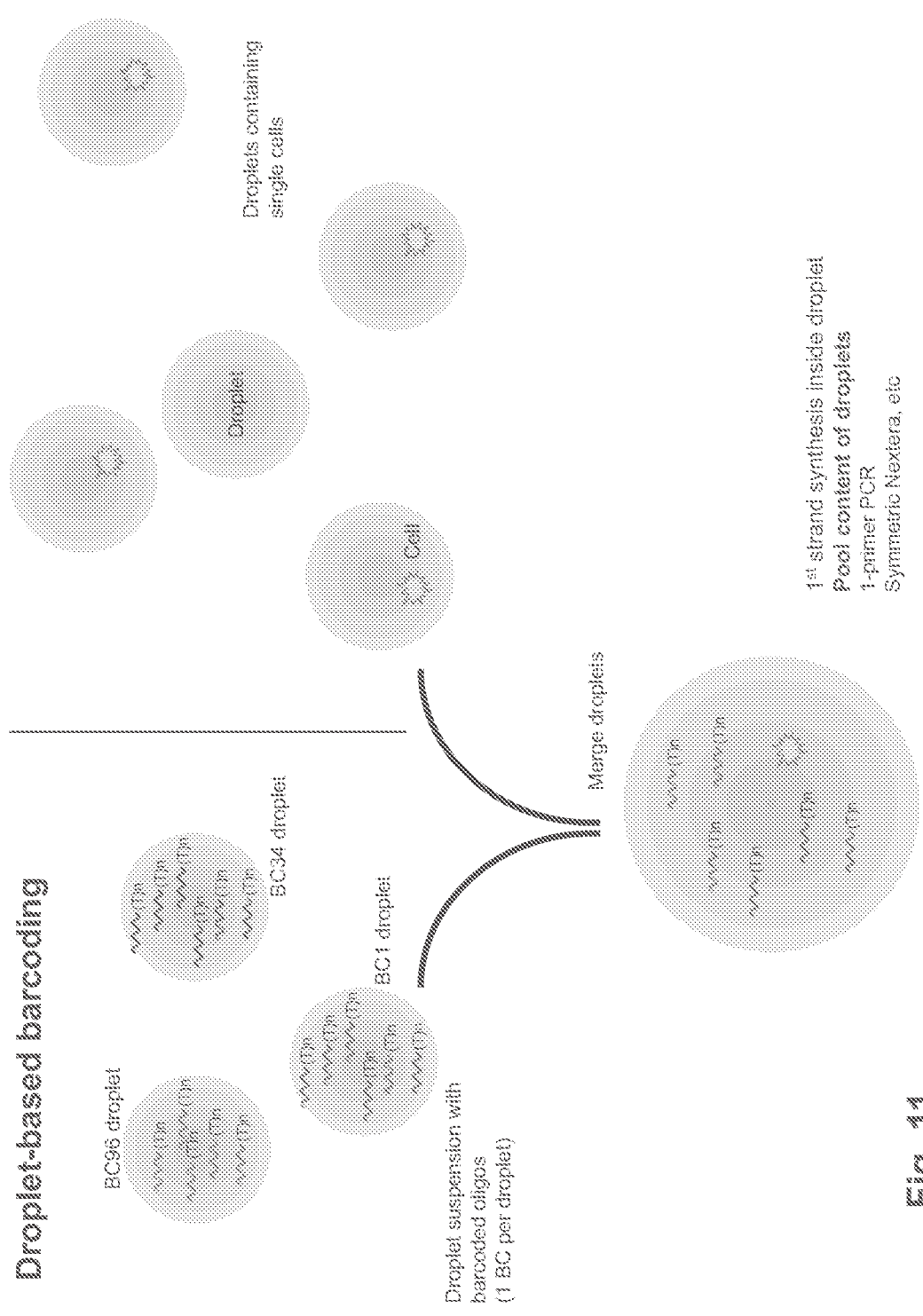
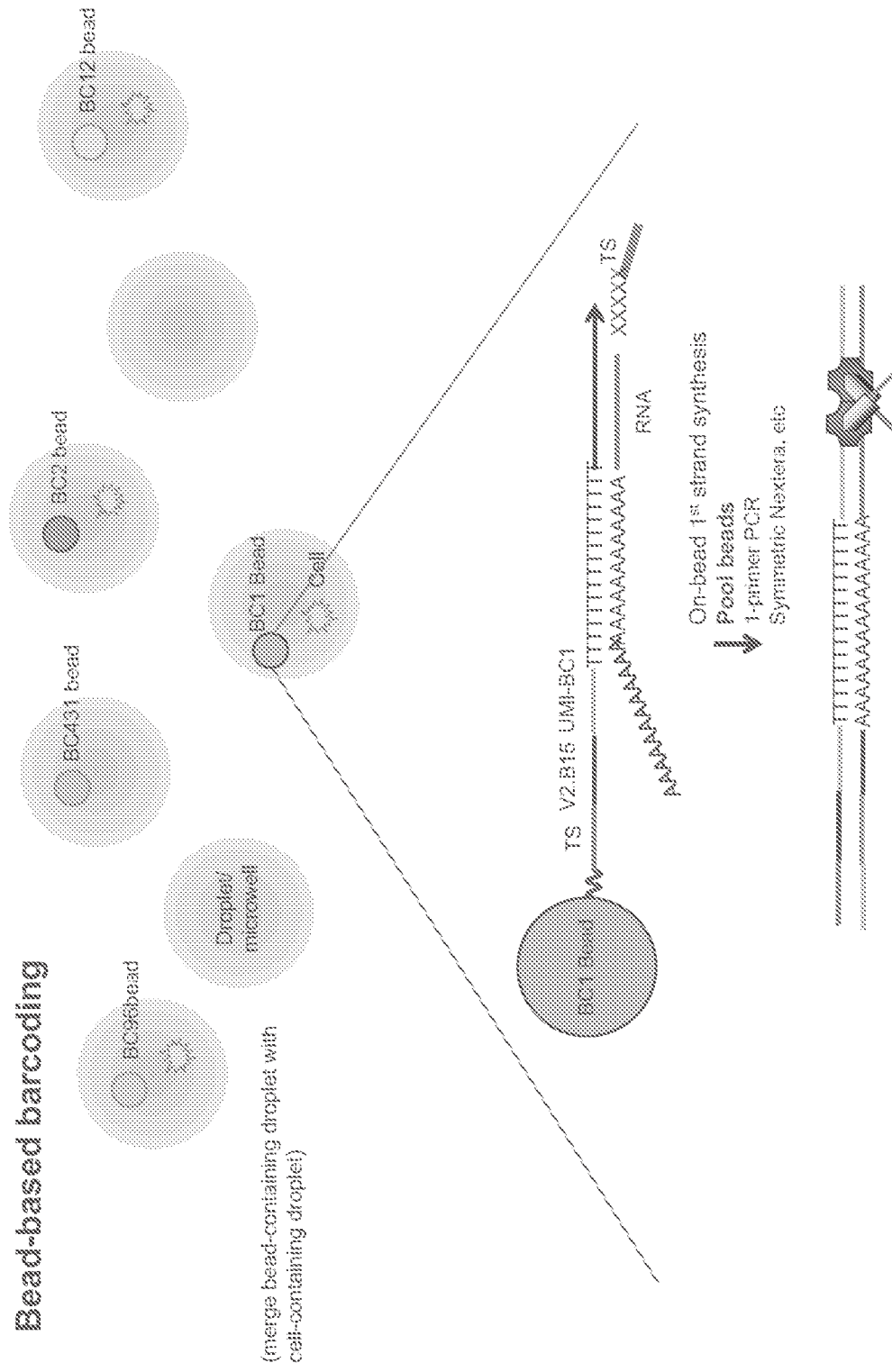


Fig. 11

Bead-based barcoding



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