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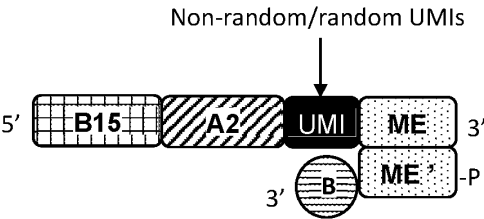


Fig. 1

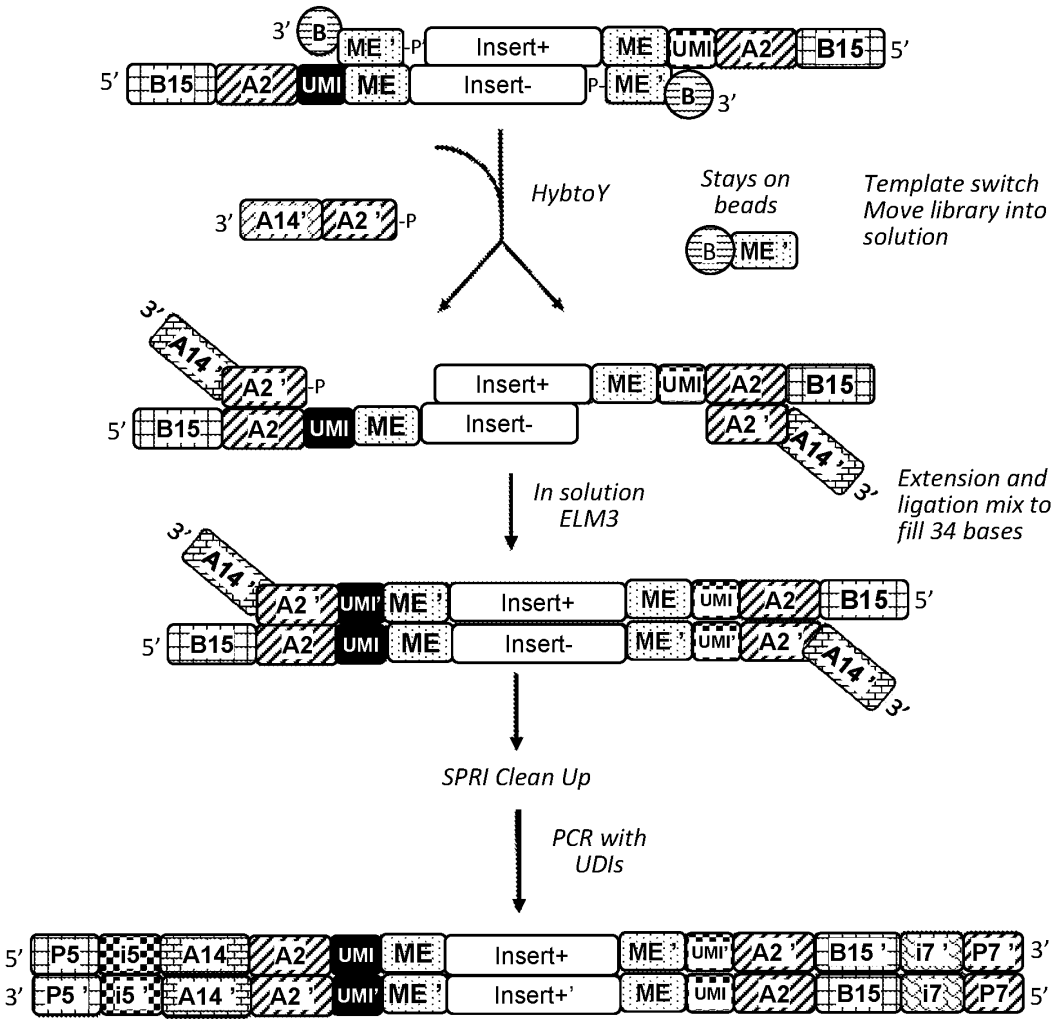


Fig. 2

Standard Nextera Sequencing:

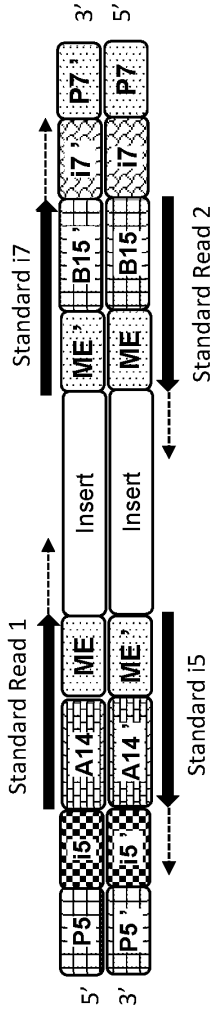


Fig. 3A

Duplex UMI Nextera Sequencing:

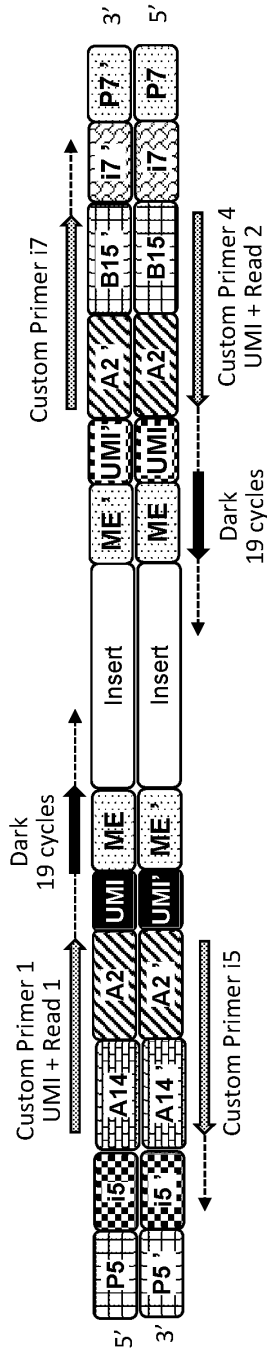


Fig. 3B

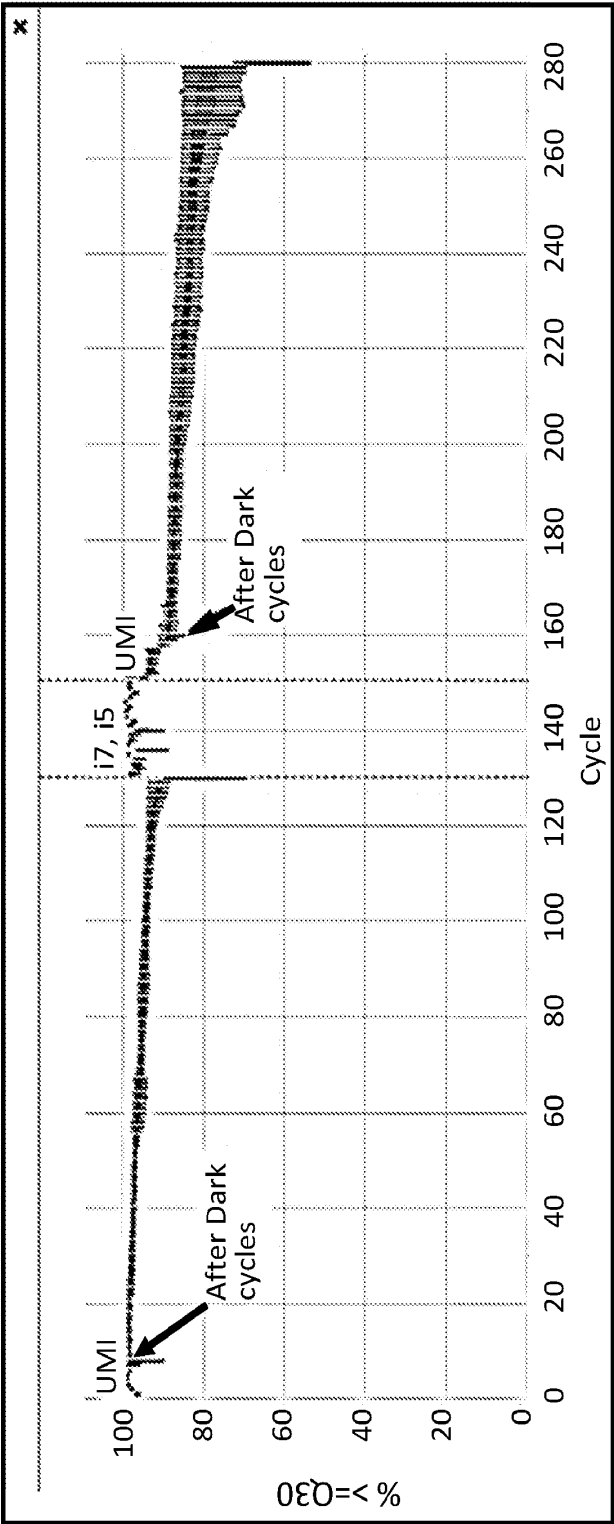


Fig. 3C

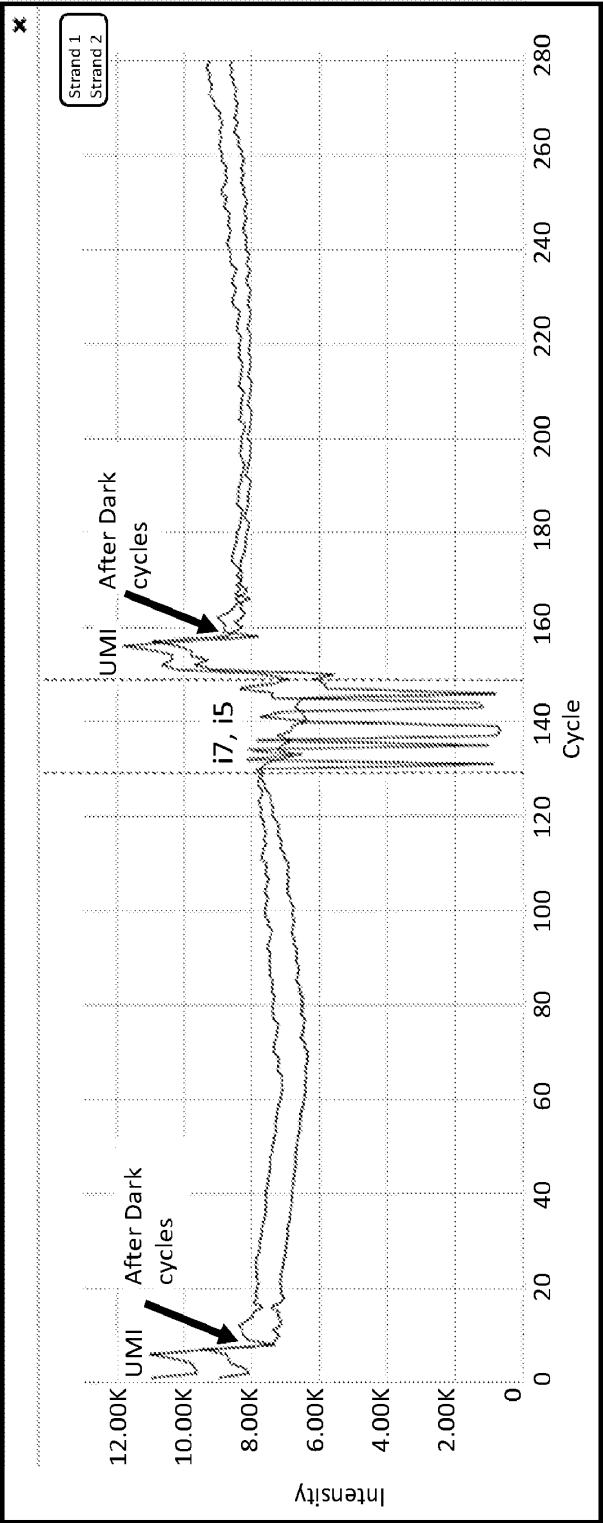


Fig. 3D

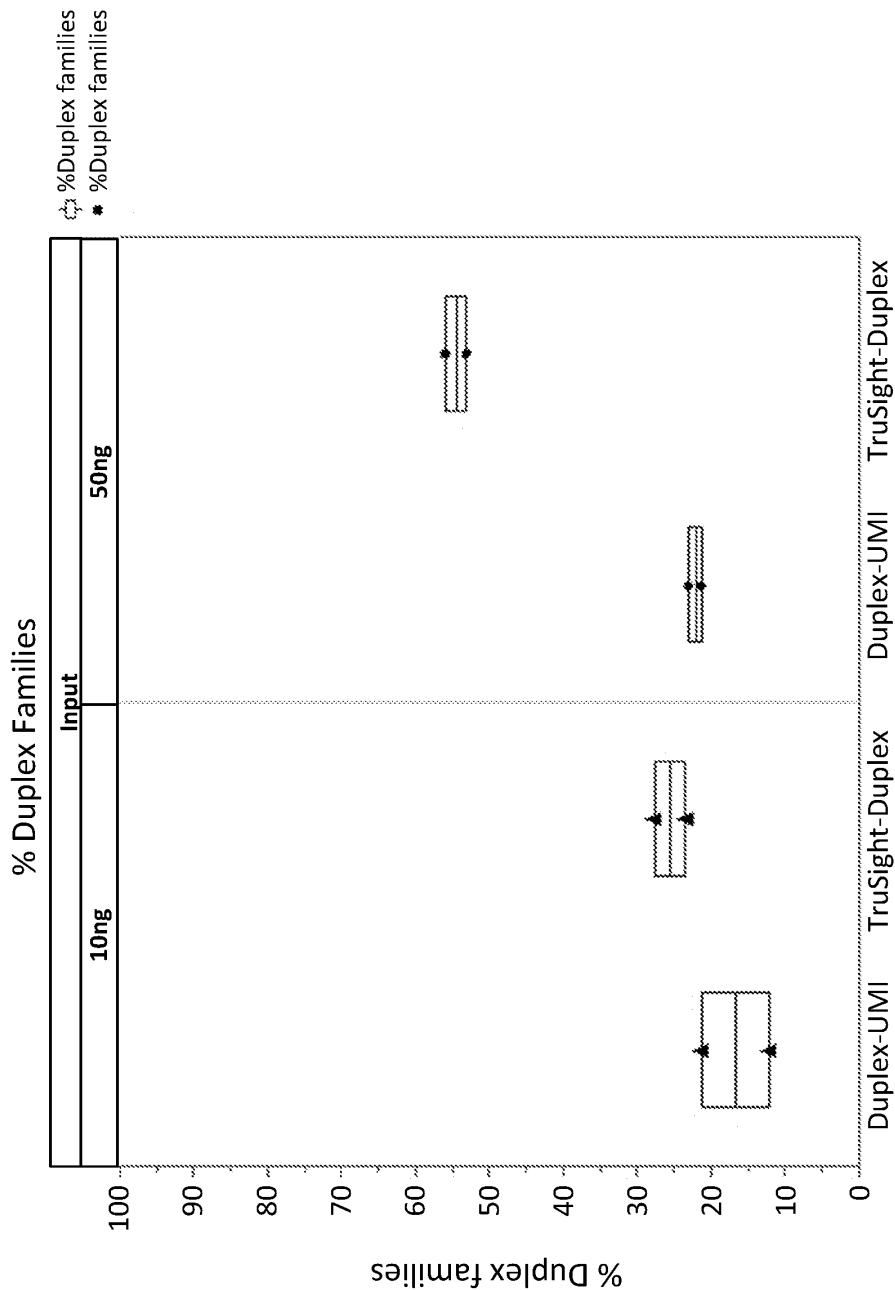


Fig. 3E

Duplex UMI Nextera Sequencing:
With no dark cycles

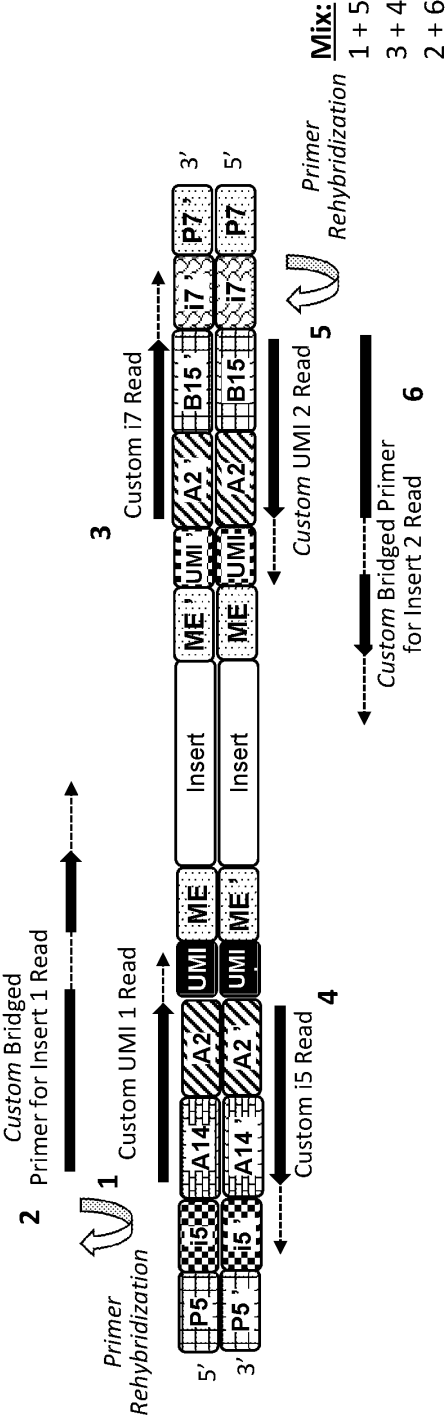


Fig. 4

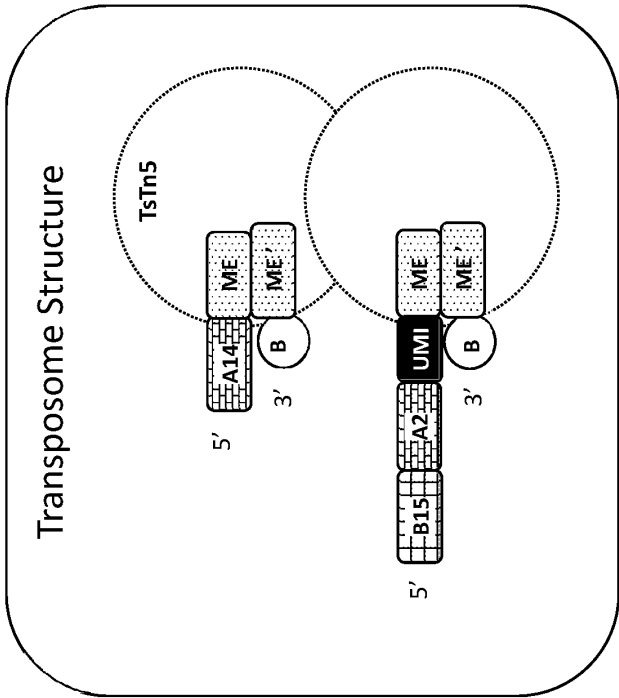


Fig. 5A

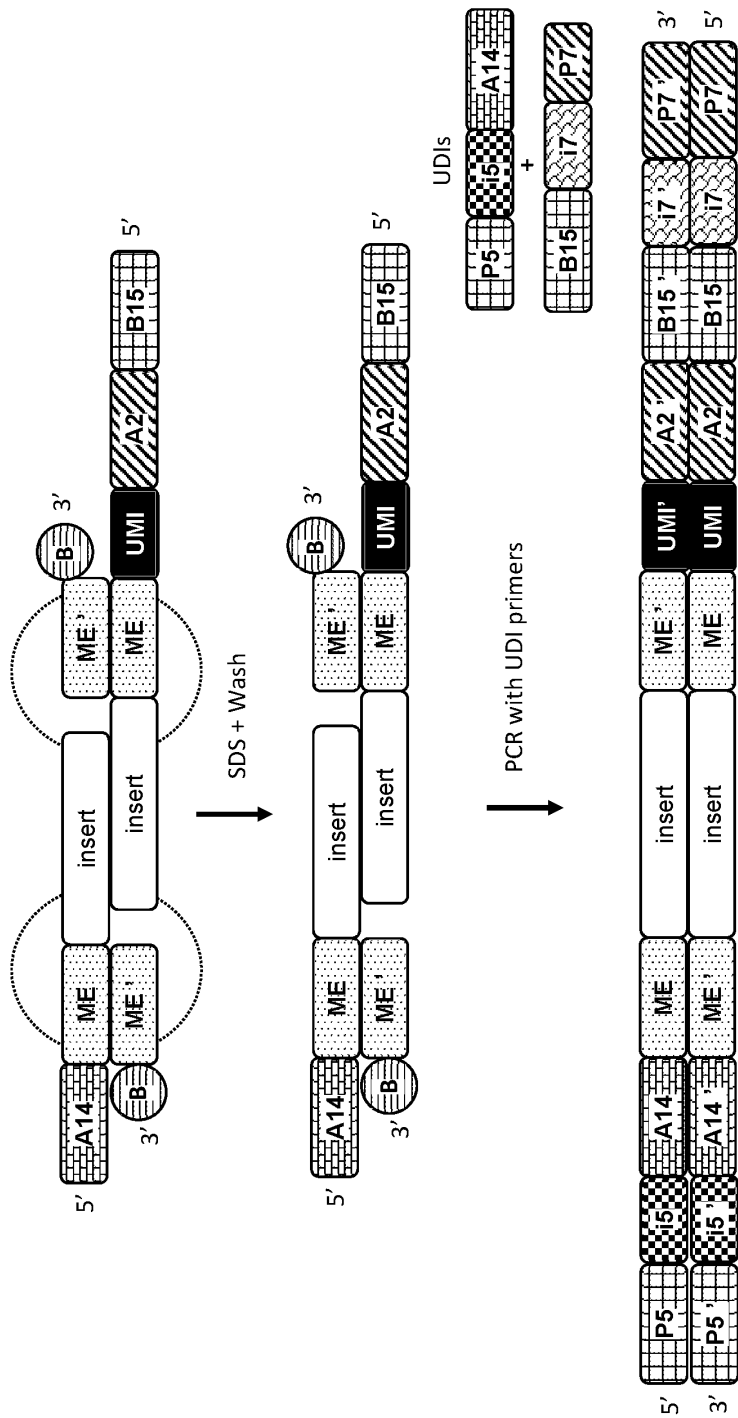


Fig. 5B

Fig. 6A

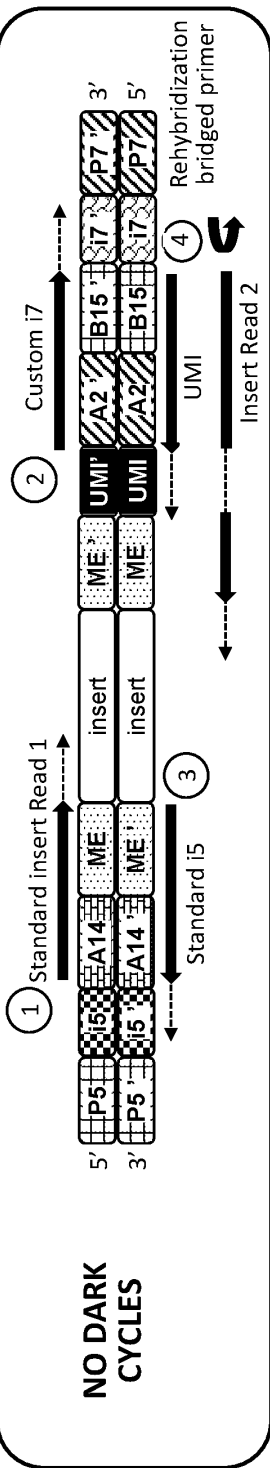
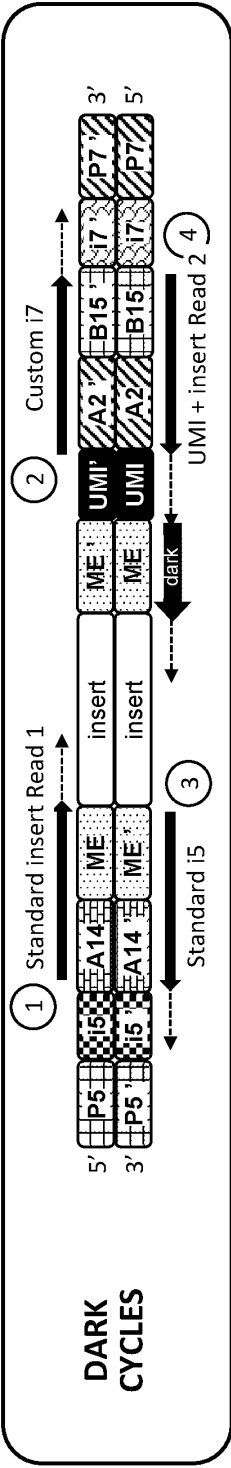


Fig. 6B

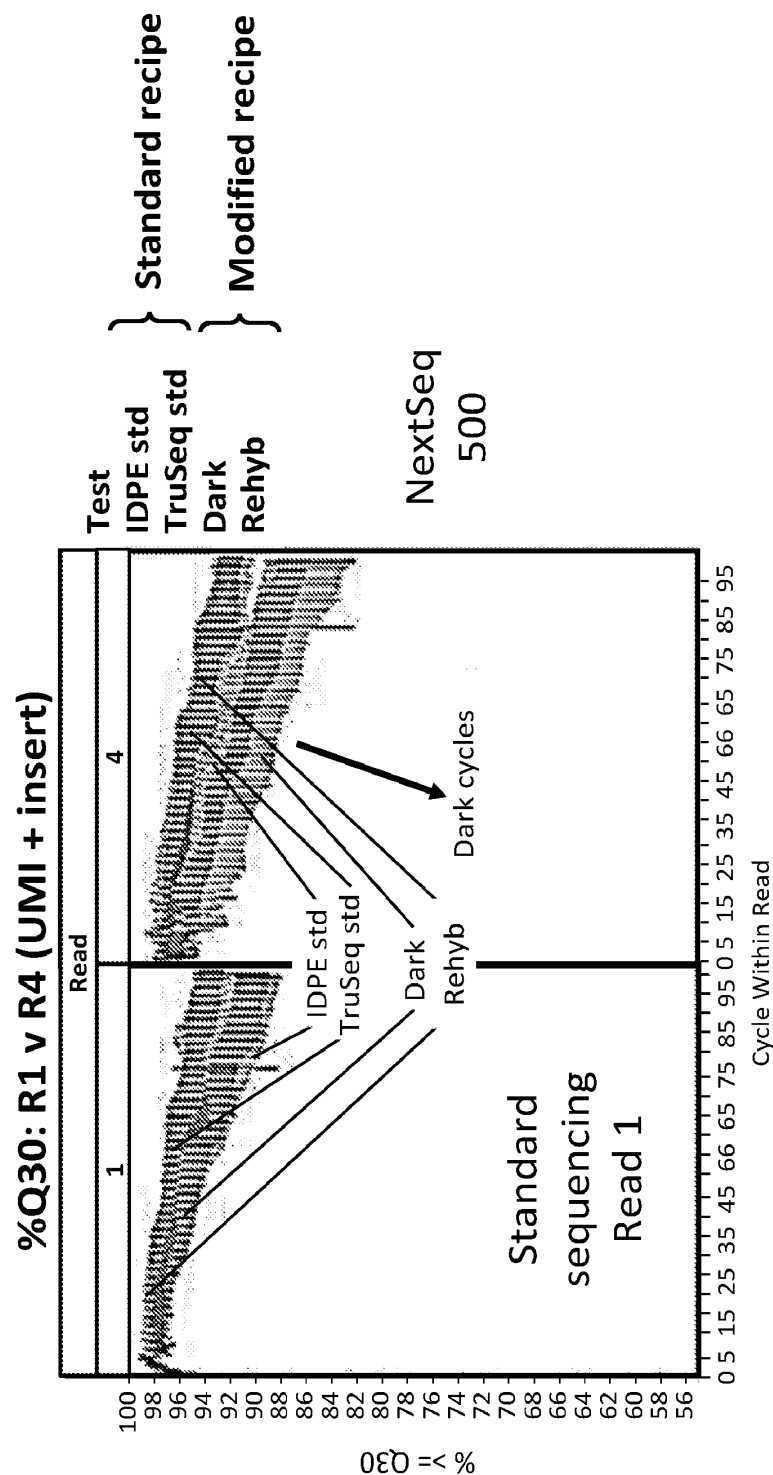


Fig. 7

TruSeq versus eBBN

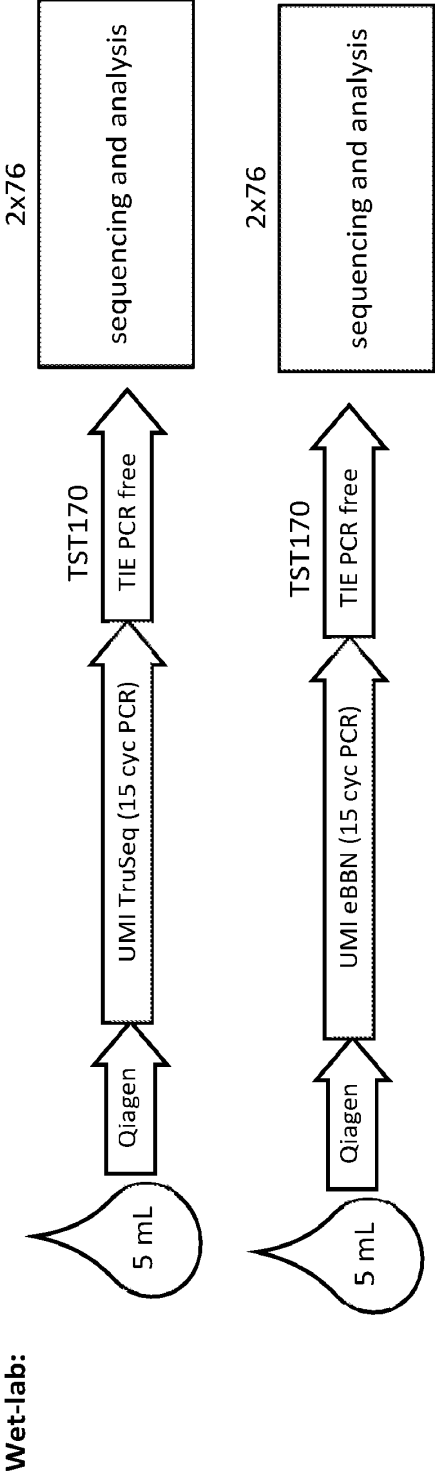


Fig. 8

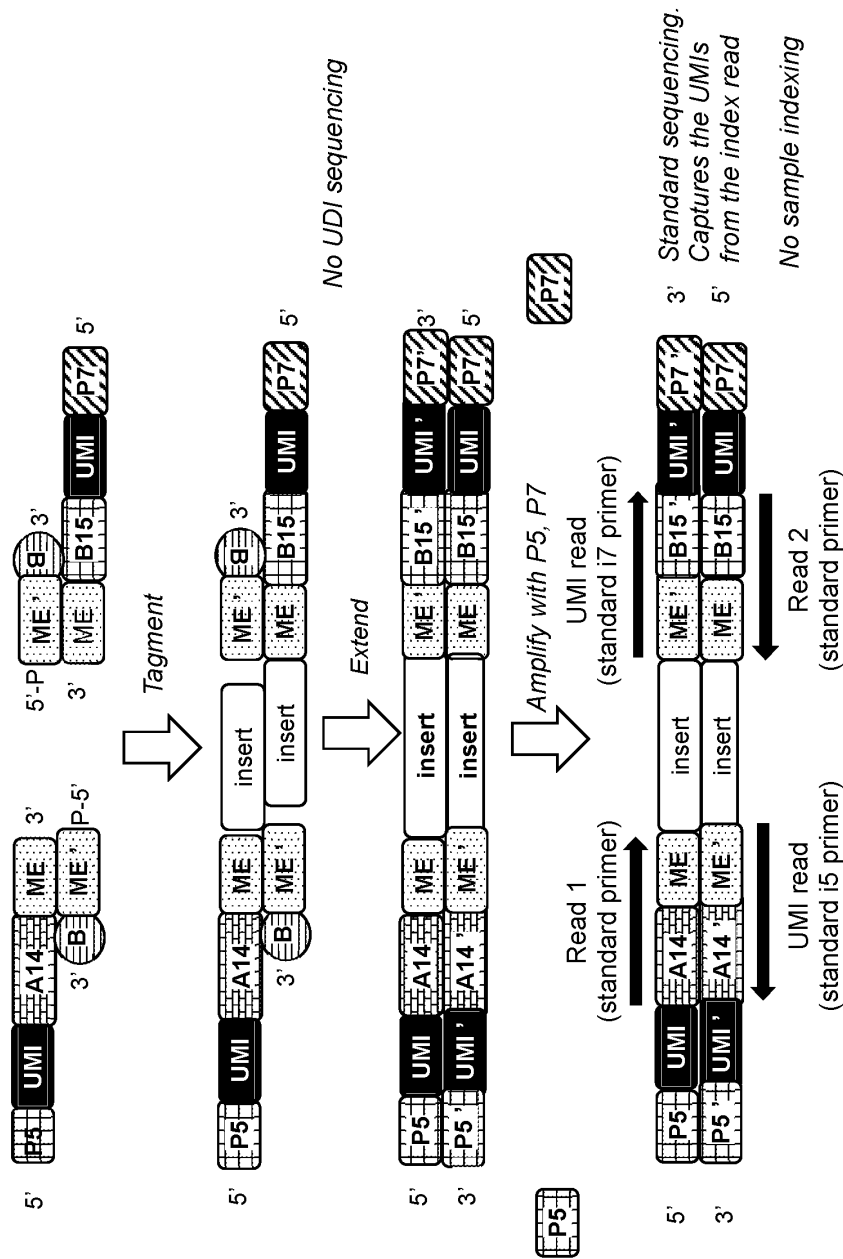


Fig. 9

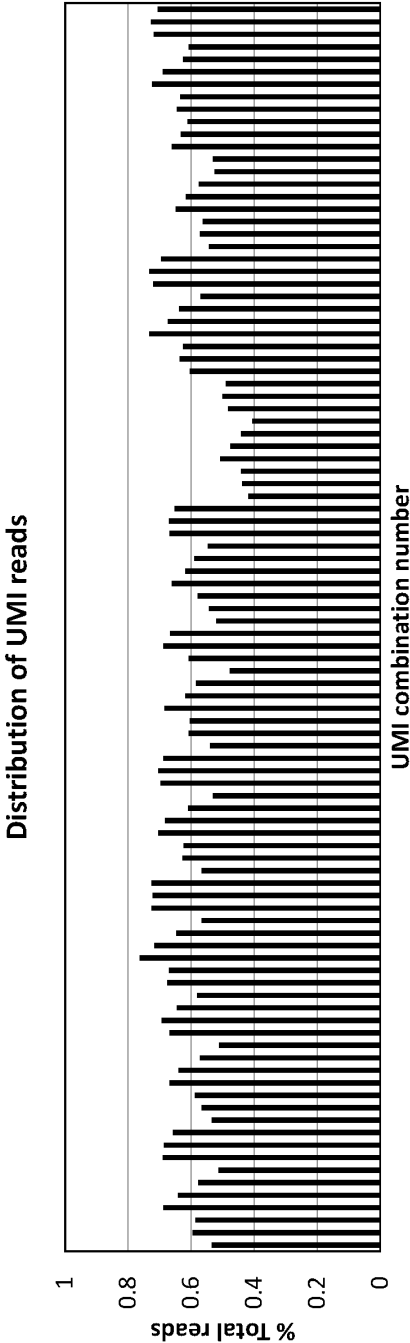


Fig. 10

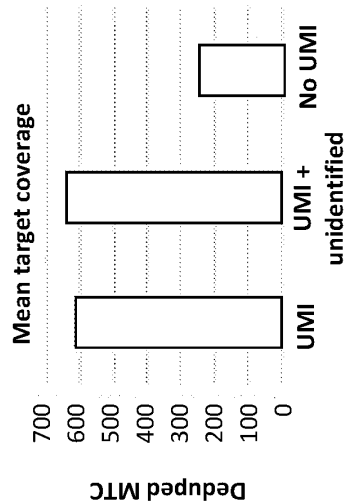


Fig. 11A

Results:

Library prep results					Enrichment results			
Library prep	Amount of cDNA in 5 mls	Genome equivalents	Amount of library	NestSeq Quant (number of reads)	% PRE with TST170	Deduped mean target coverage	Median fragment length	% Conversion
TruSeq (K2)	23.6 ng	6555	5.3 ng	31 million	76%	1128	169	17.2%
eBBN	21.2 ng	5888	5.8 ng	51 million	61%	1836	99	28%

Fig. 11B

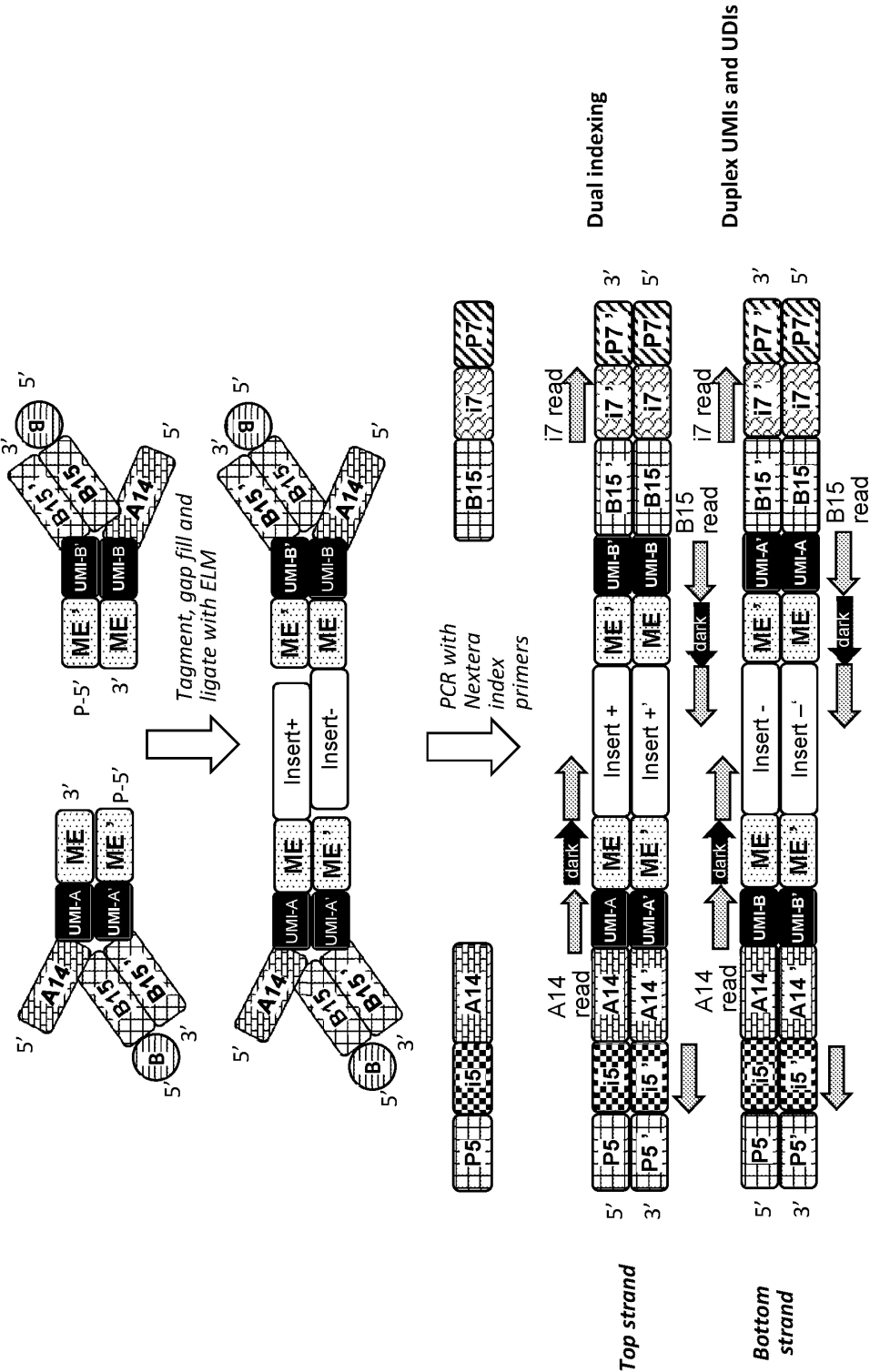


Fig. 12

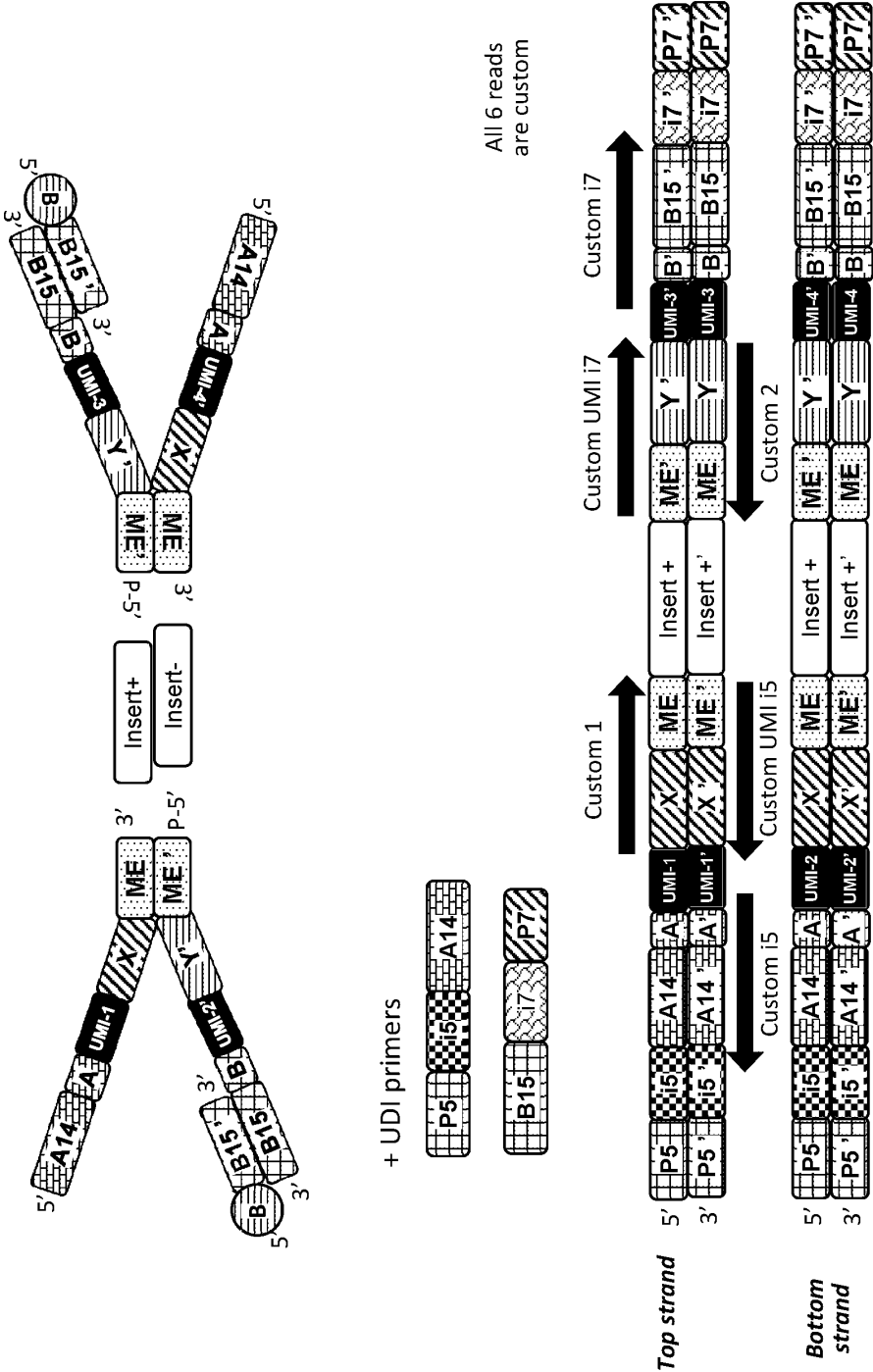
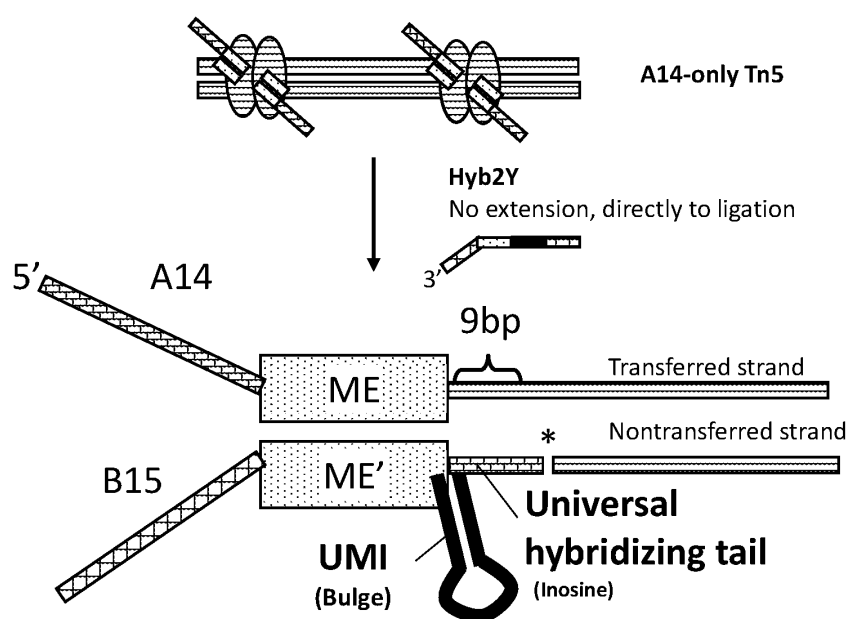
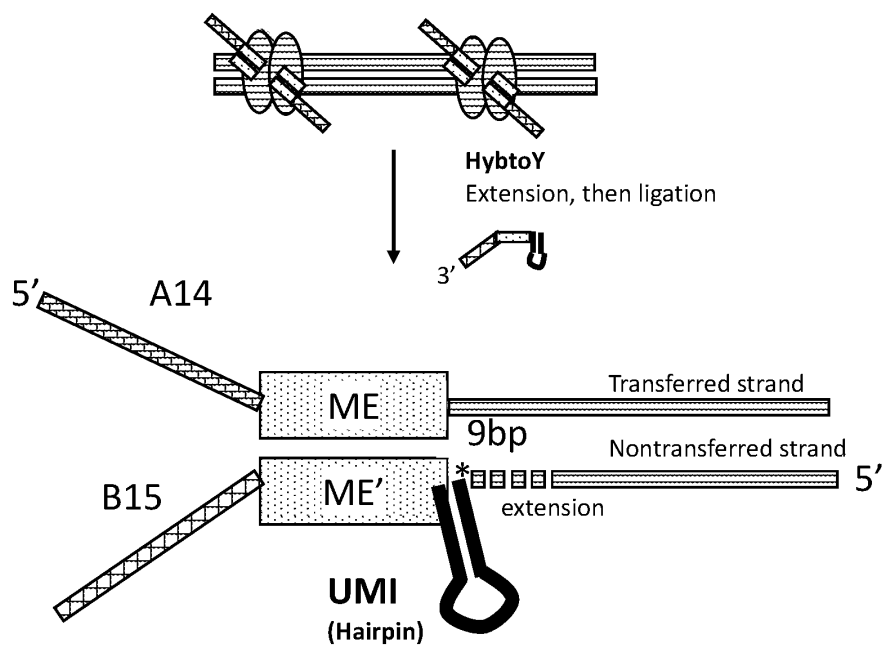


Fig. 13

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*Fig. 14*

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*Fig. 15*

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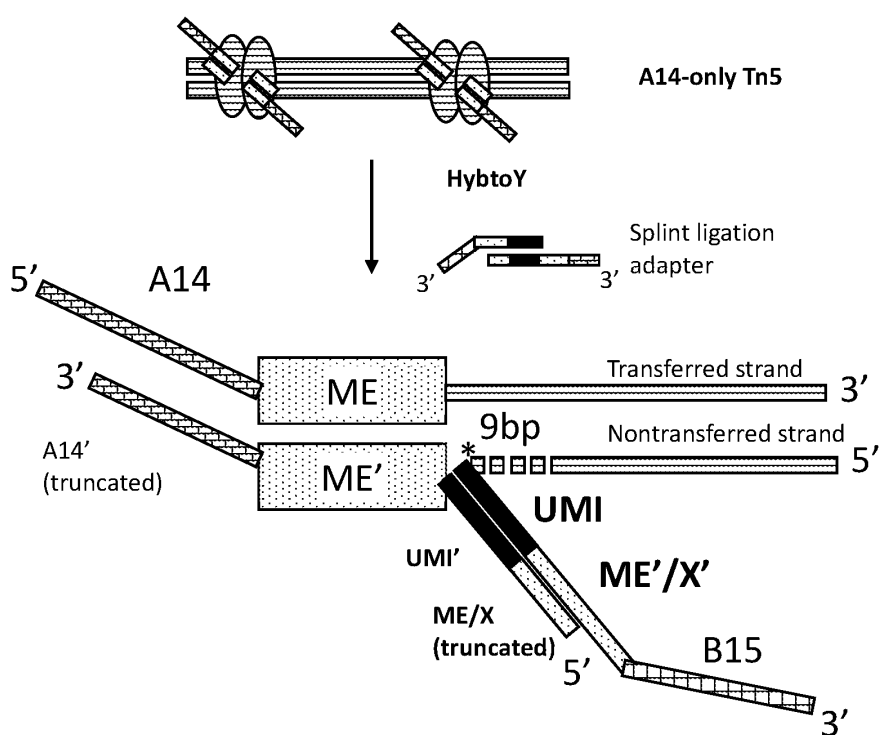


Fig. 16

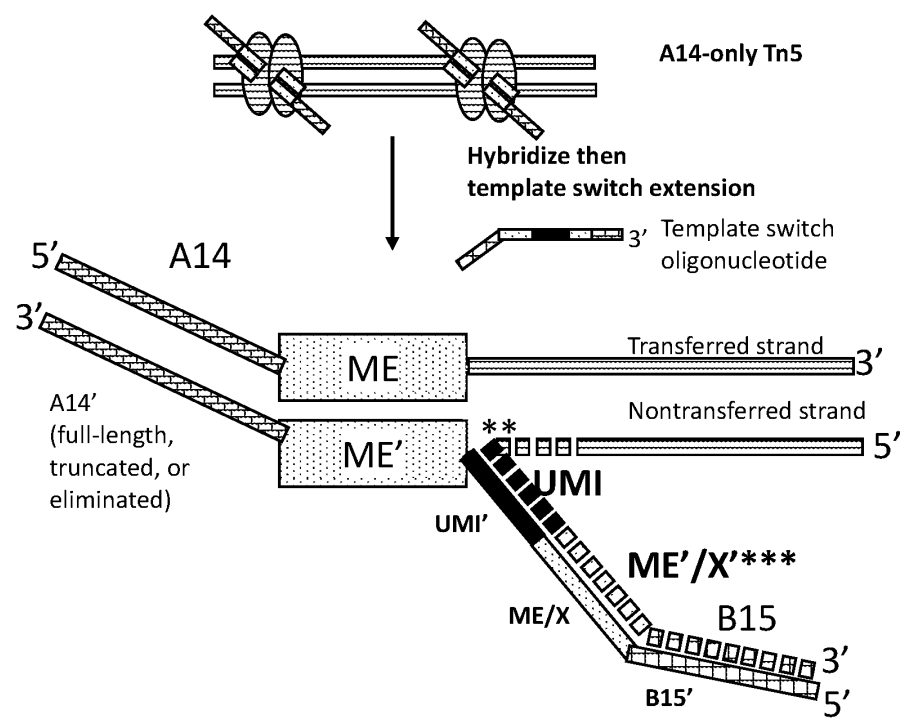


Fig. 17

Tagmentation with A14 Transposome (Tsm)

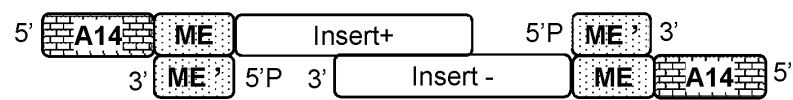


Fig. 18A

Hyb2Y to add adapter template

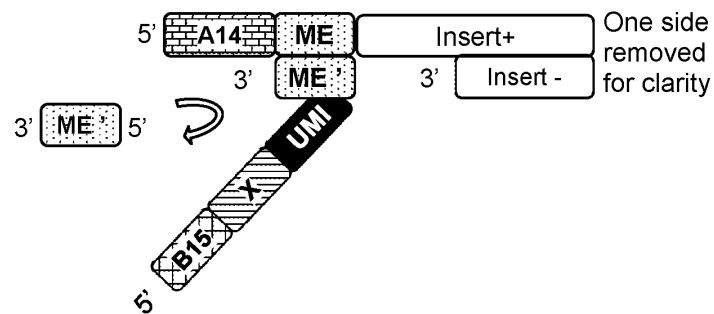


Fig. 18B

Polymerase extension across switched template

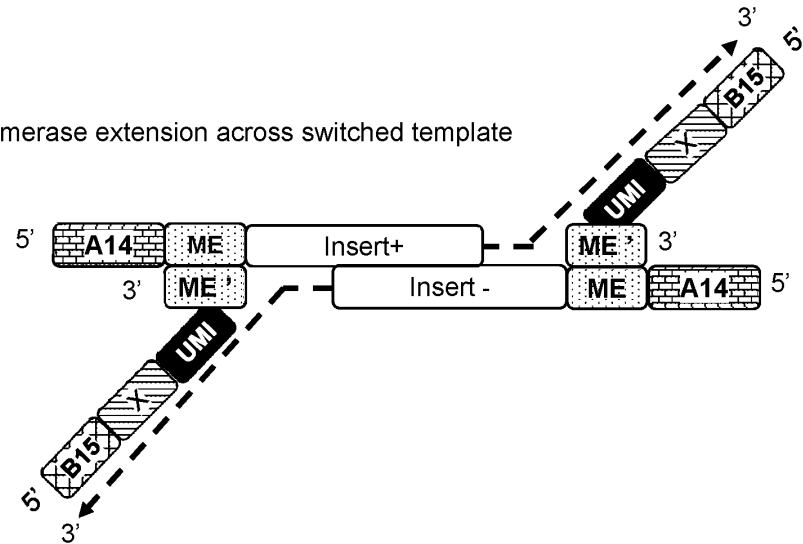


Fig. 18C

PCR to amplify library from A14 and B15 (adding sample indexes and flow cell primers)

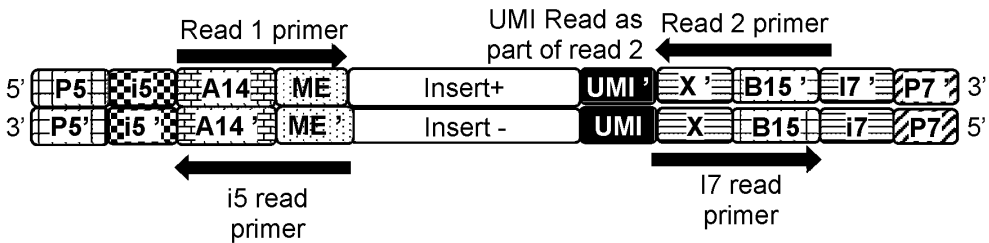


Fig. 18D

Tagmentation with A14 Transposome (Tsm)

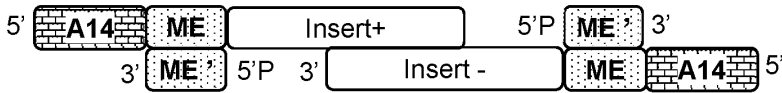


Fig. 19A

Hyb2Y to add adaptor template

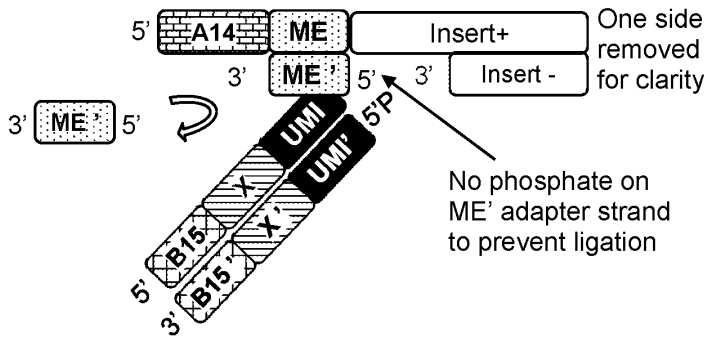


Fig. 19B

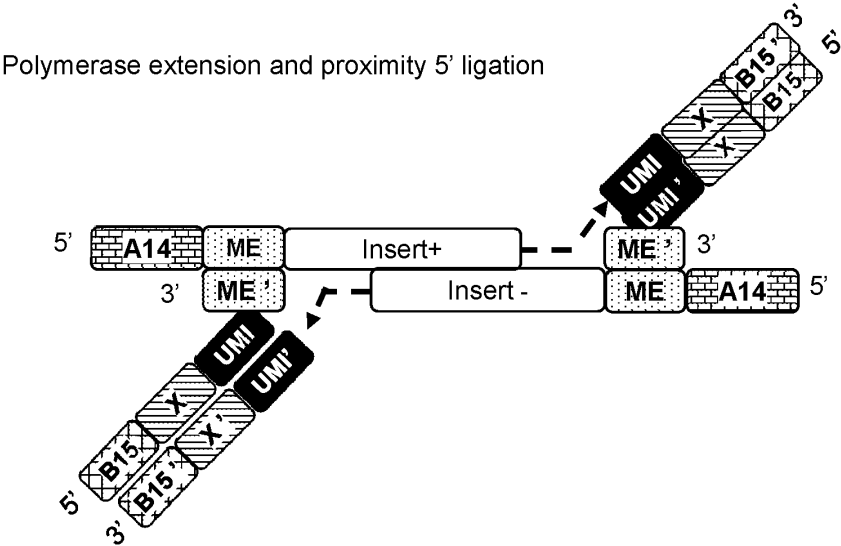


Fig. 19C

PCR to amplify library from A14 and B15 (adding sample indexes and flow cell primers)

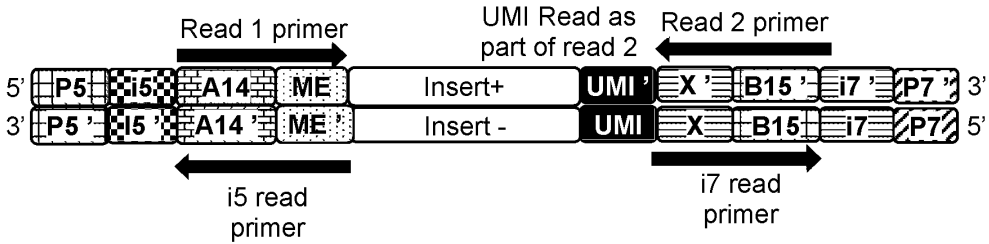


Fig. 19D

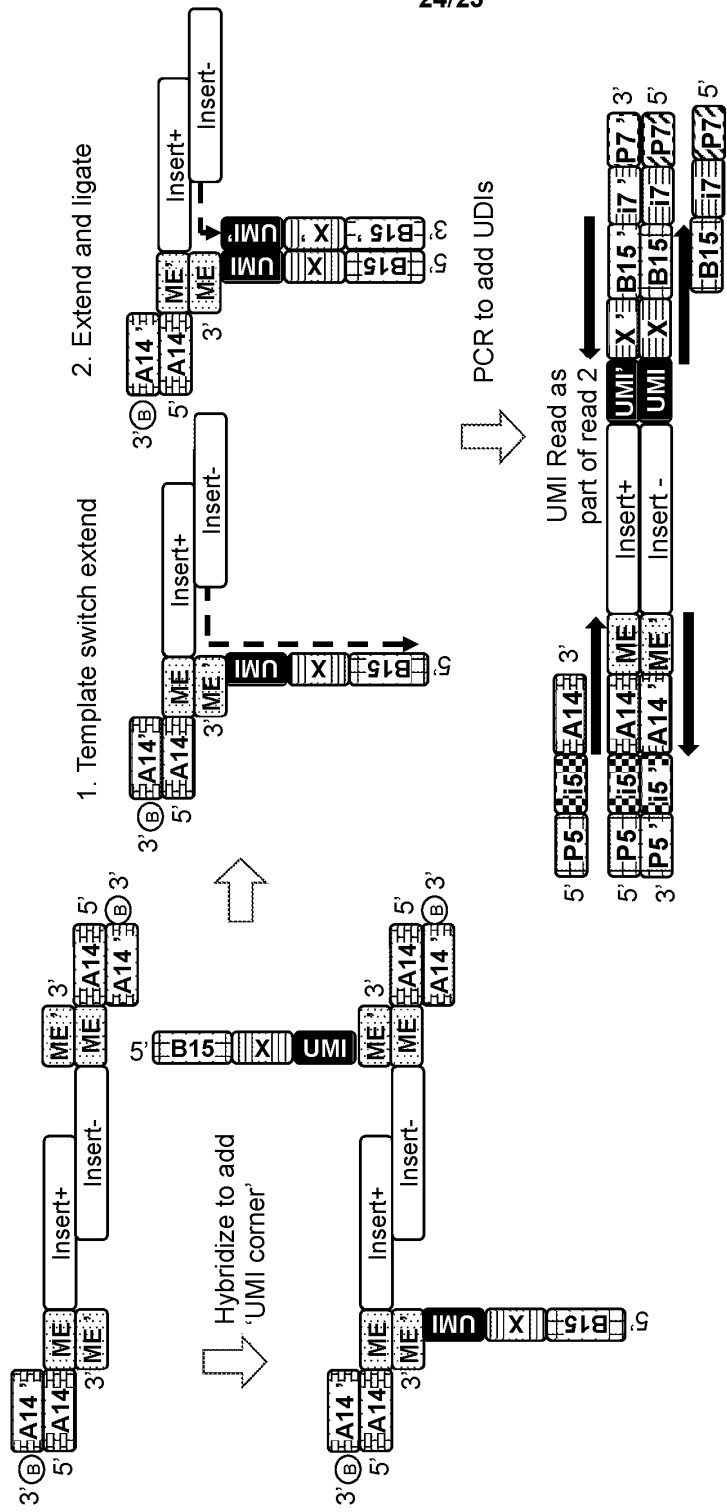


Fig. 20

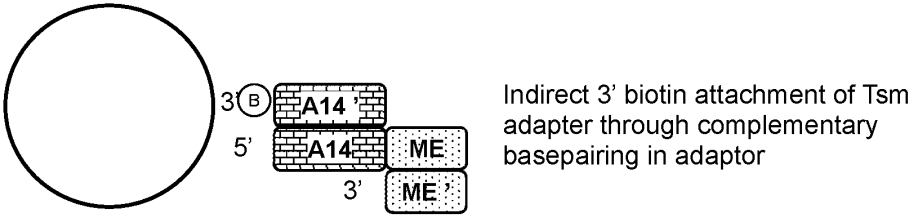


Fig. 21A

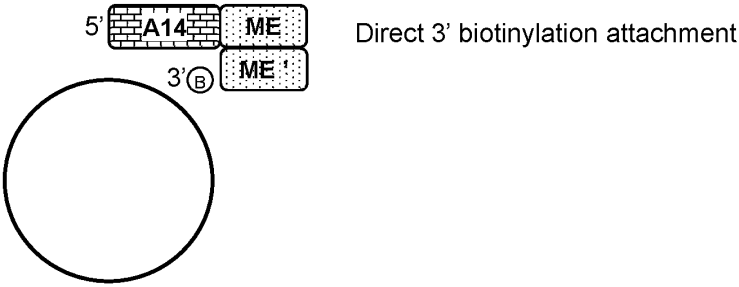


Fig. 21B

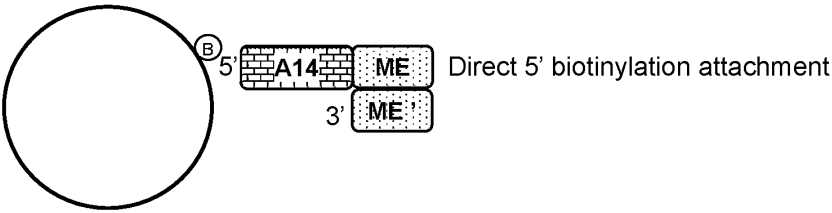


Fig. 21C