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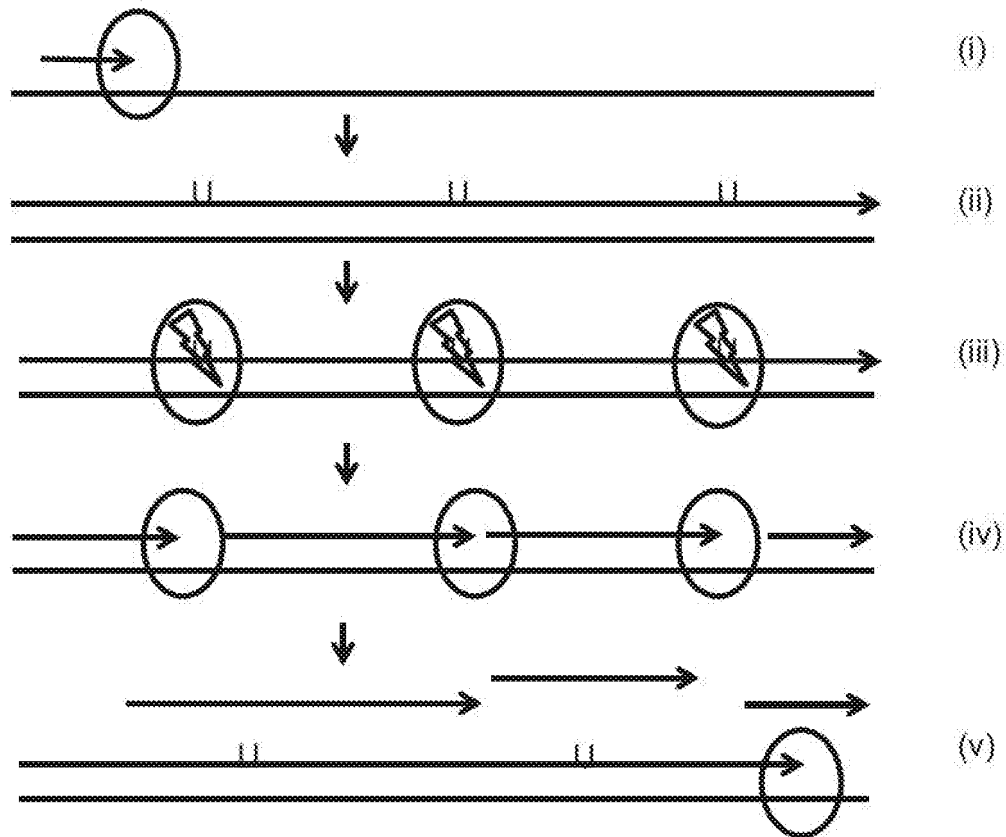


Fig. 1

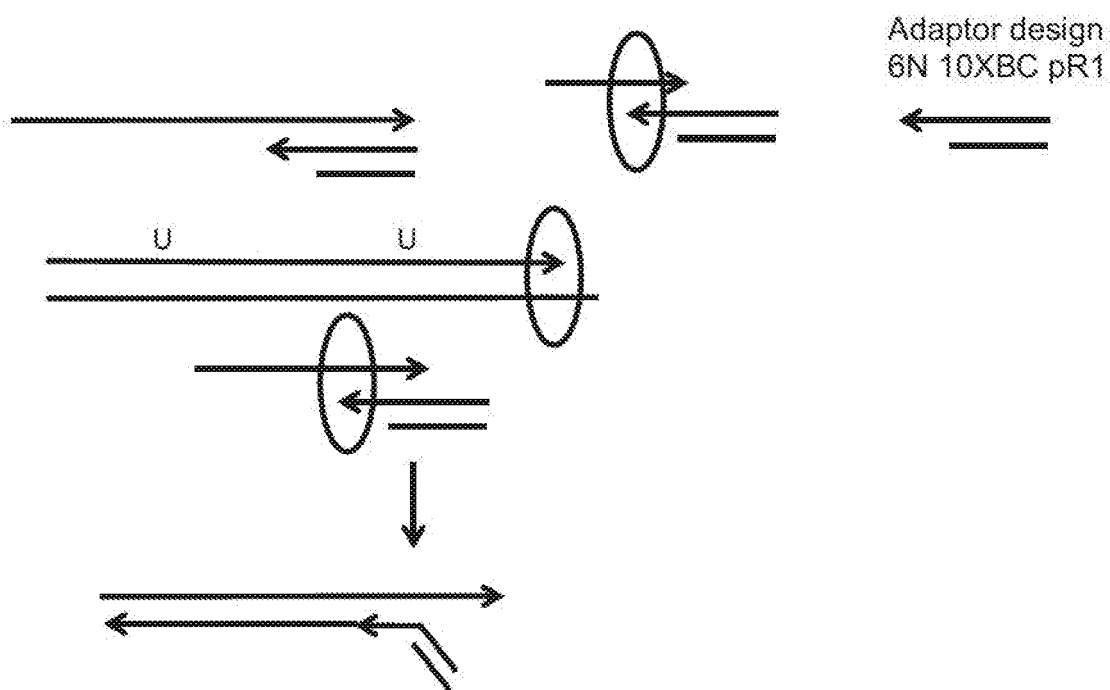


Fig. 2A

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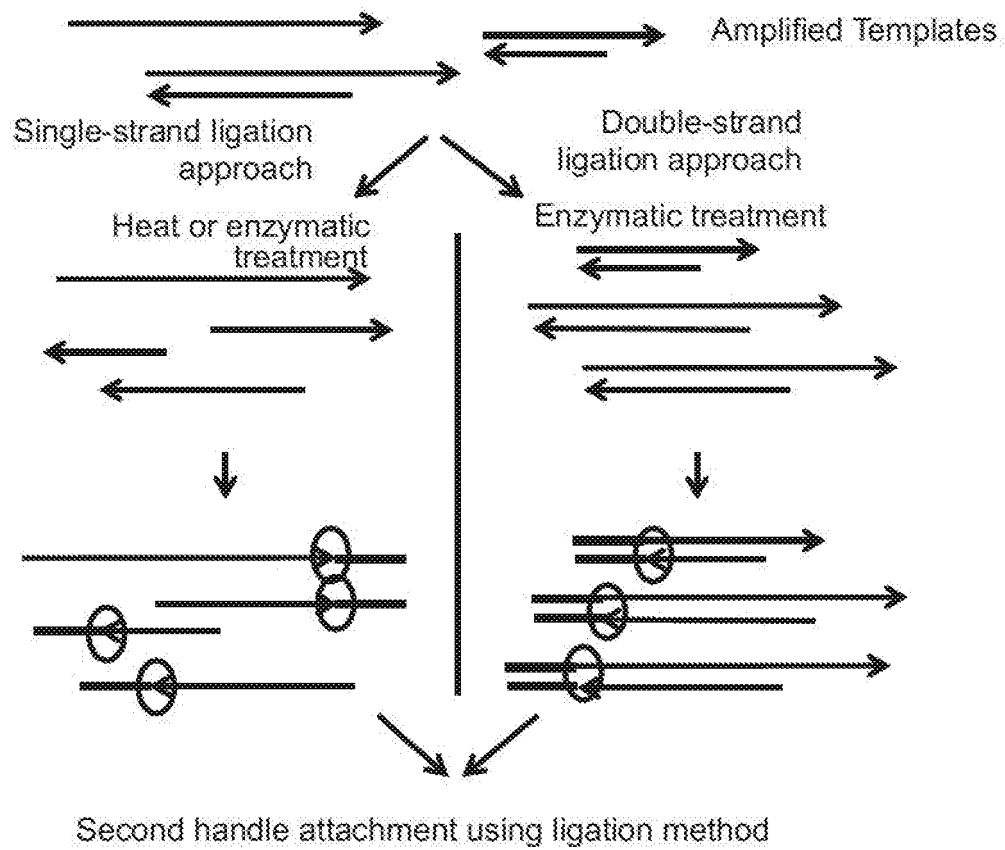


Fig. 2B

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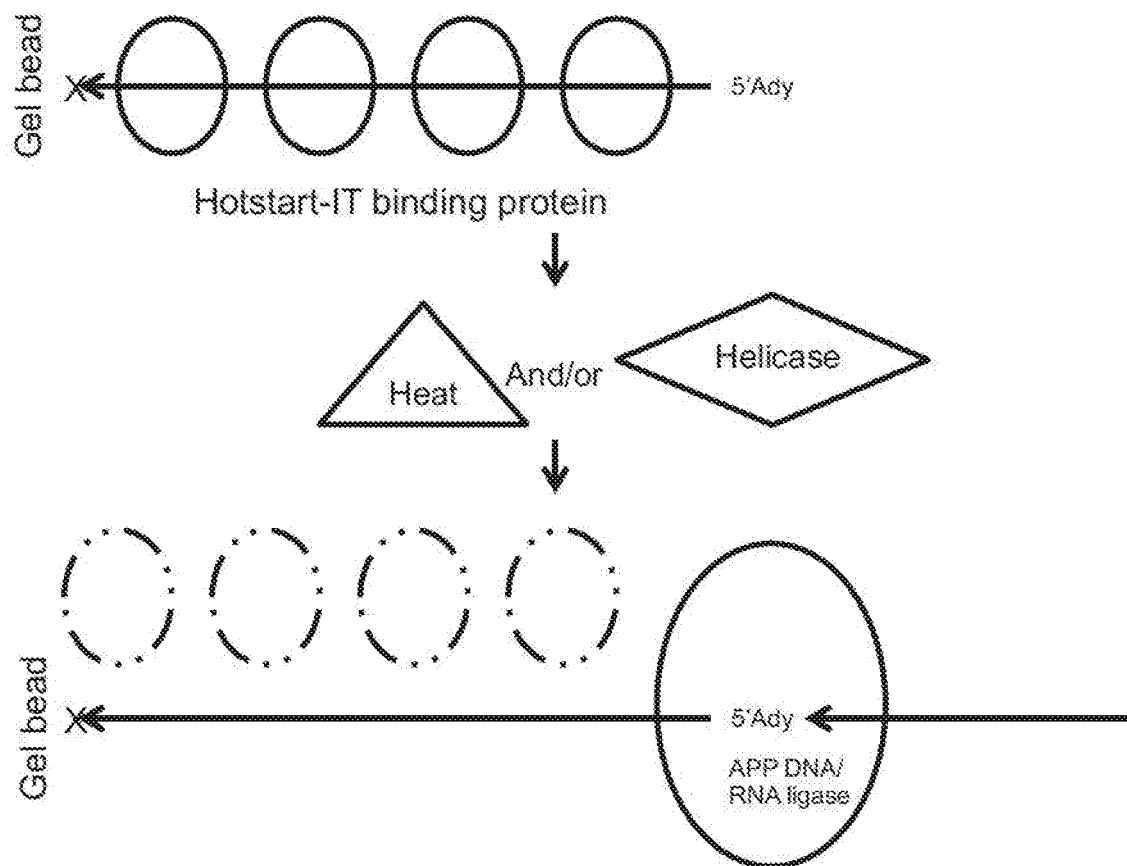


Fig. 2C

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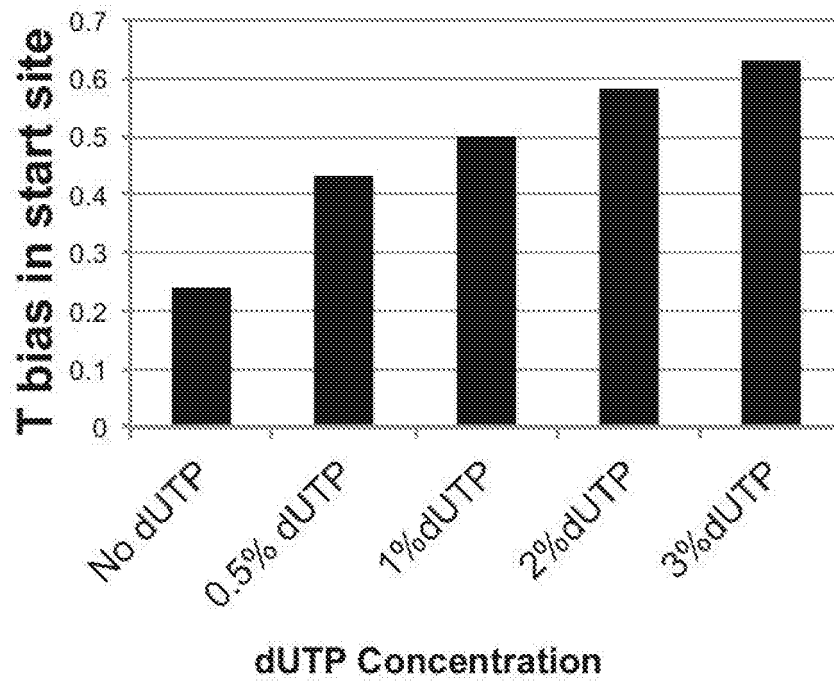


Fig. 3

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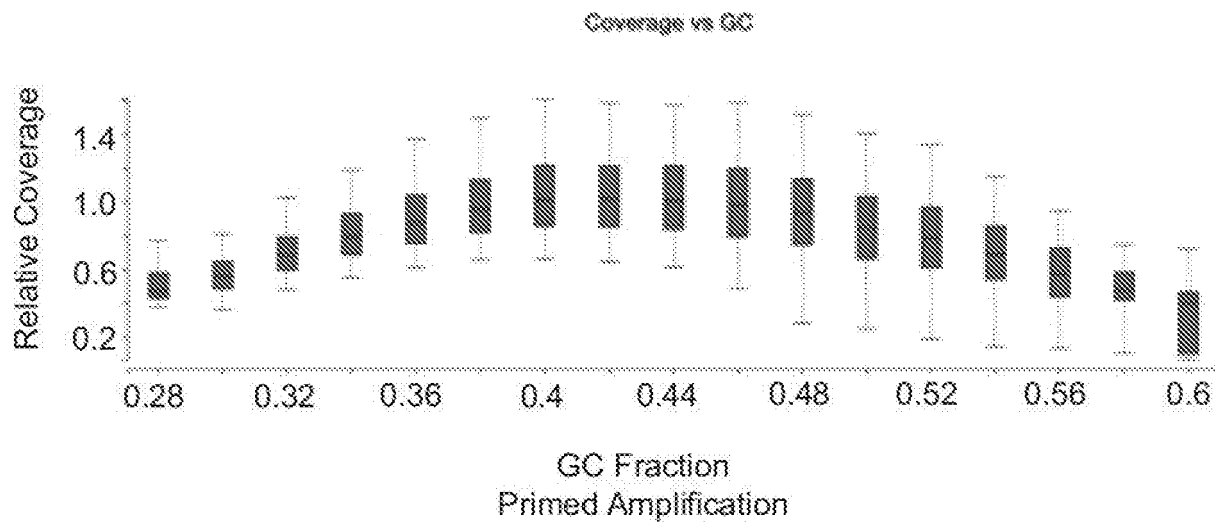


Fig. 4A

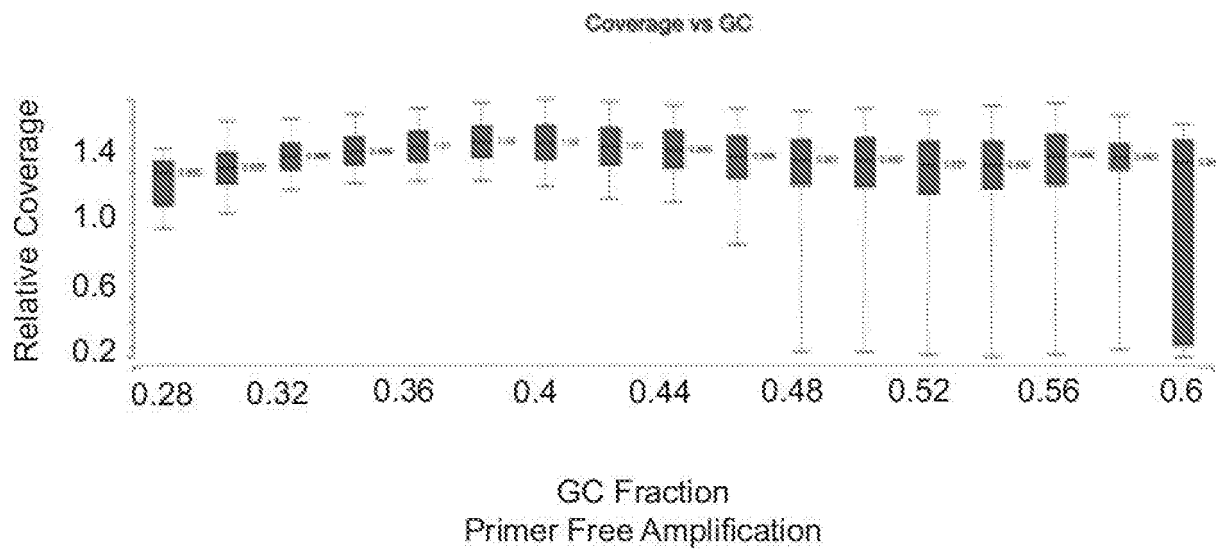
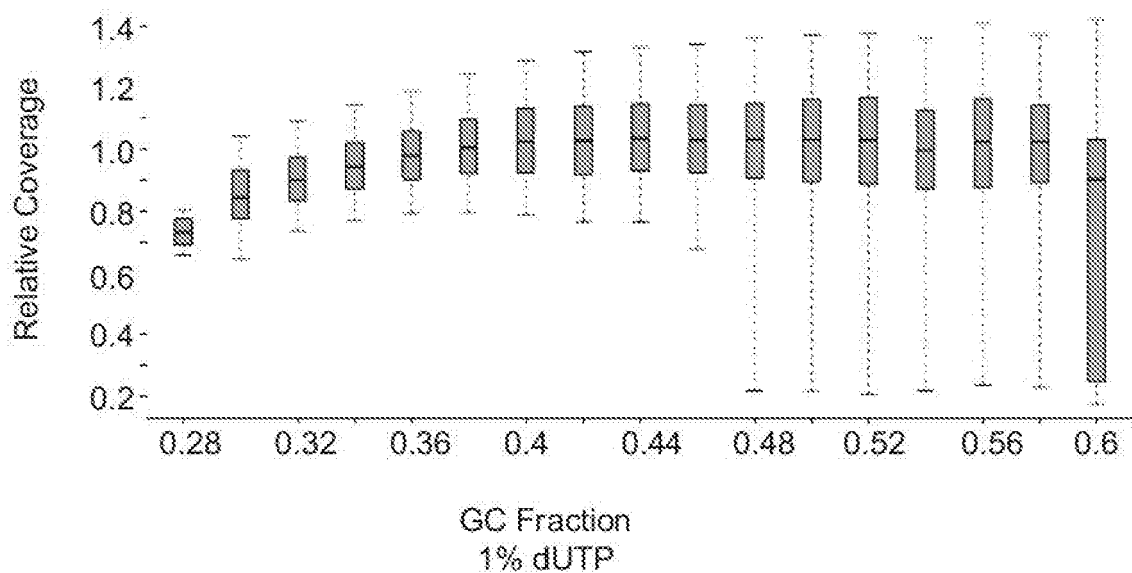
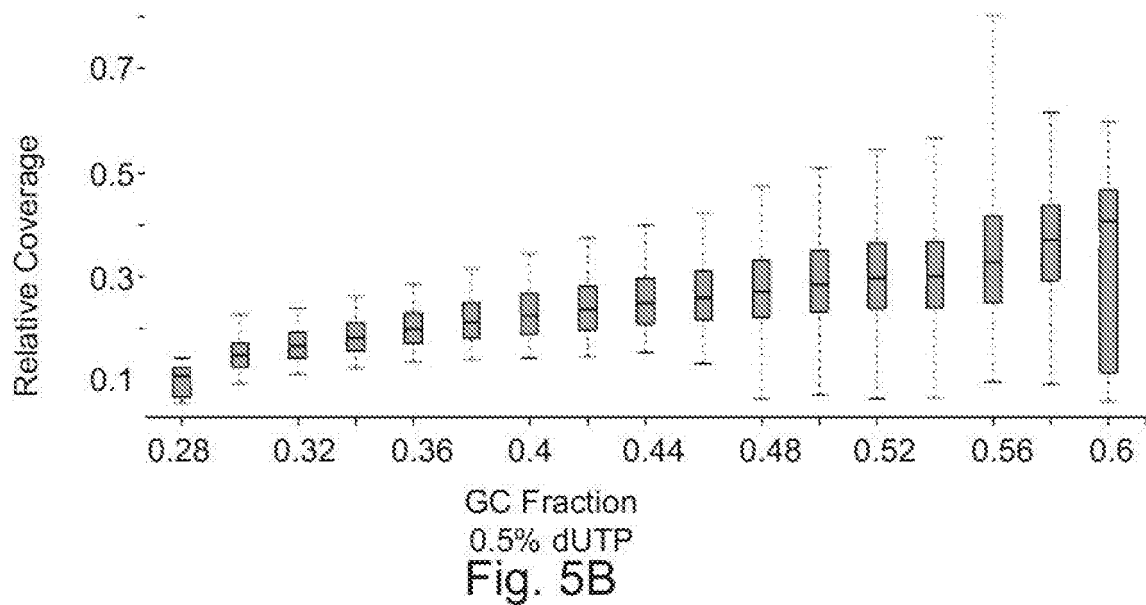
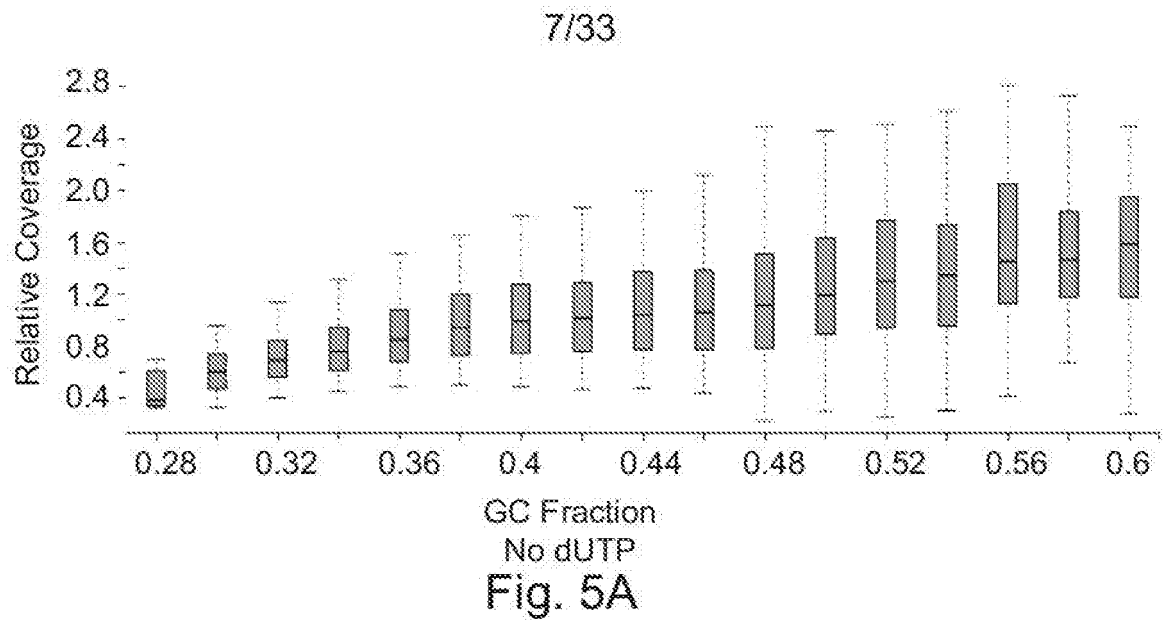
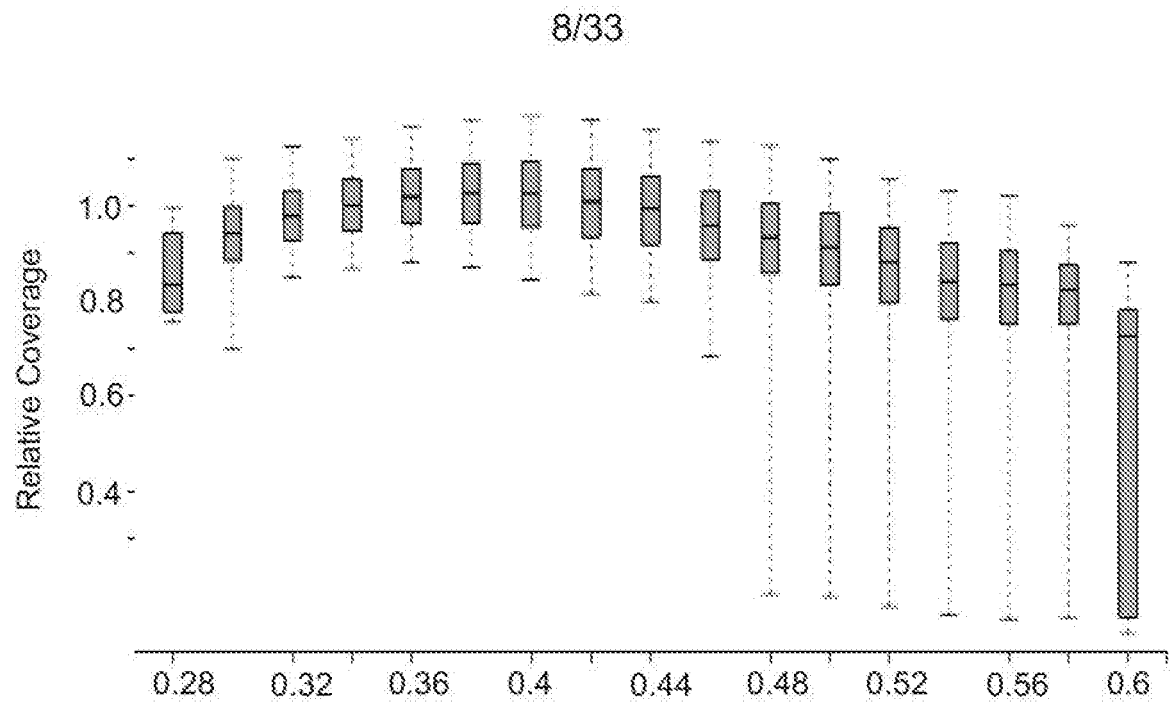


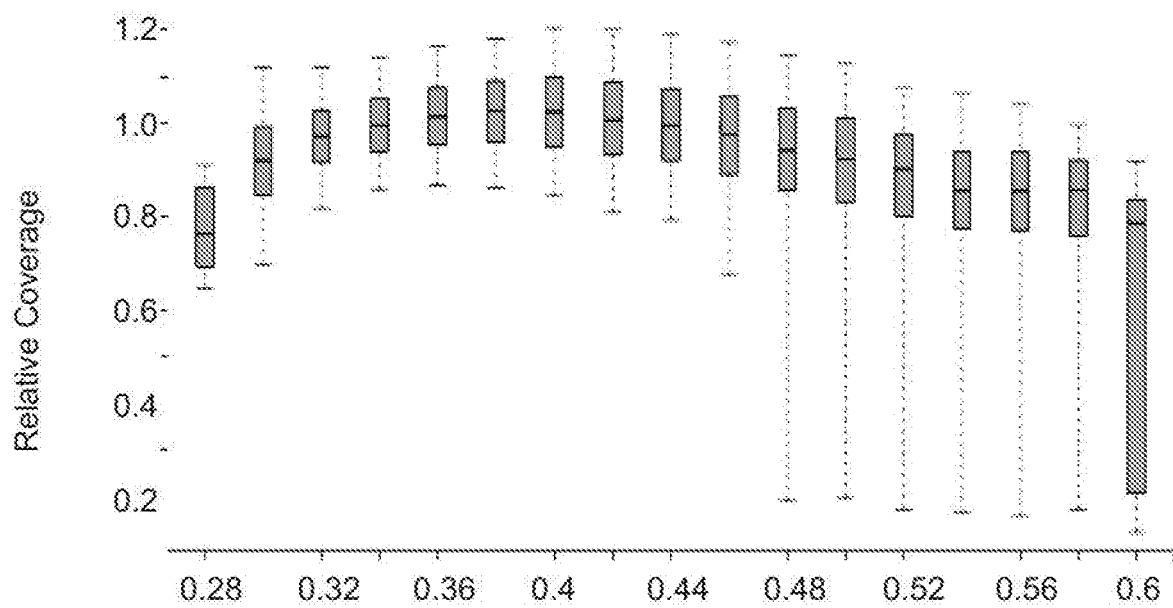
Fig. 4B





GC Fraction
2% dUTP

Fig. 5D



GC Fraction
3% dUTP

Fig. 5E

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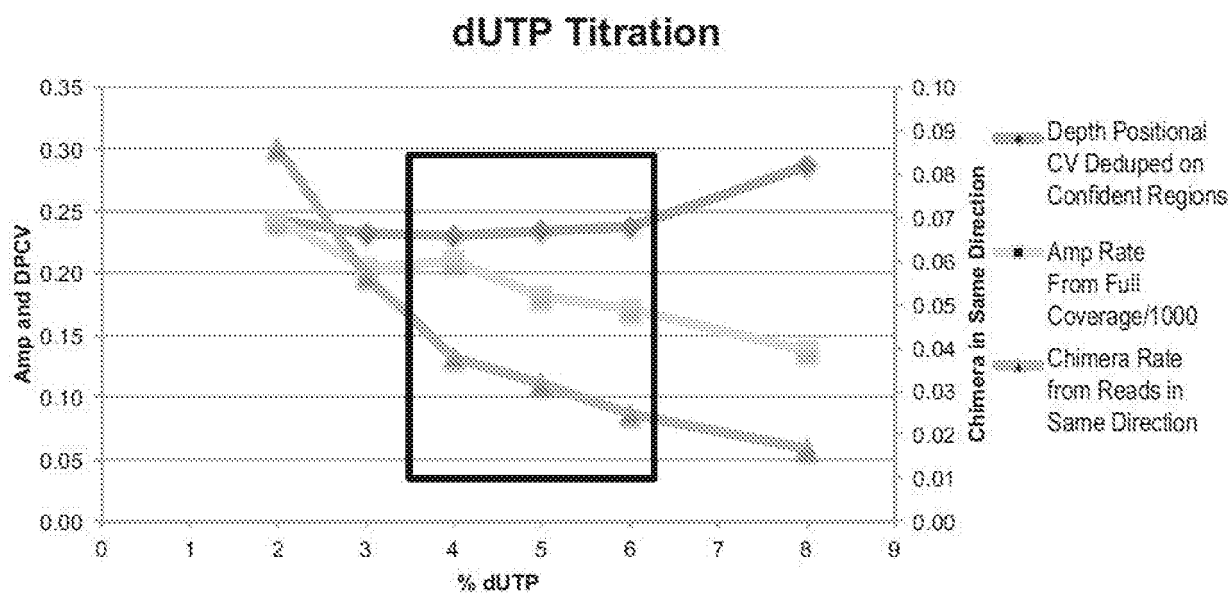


Fig. 6

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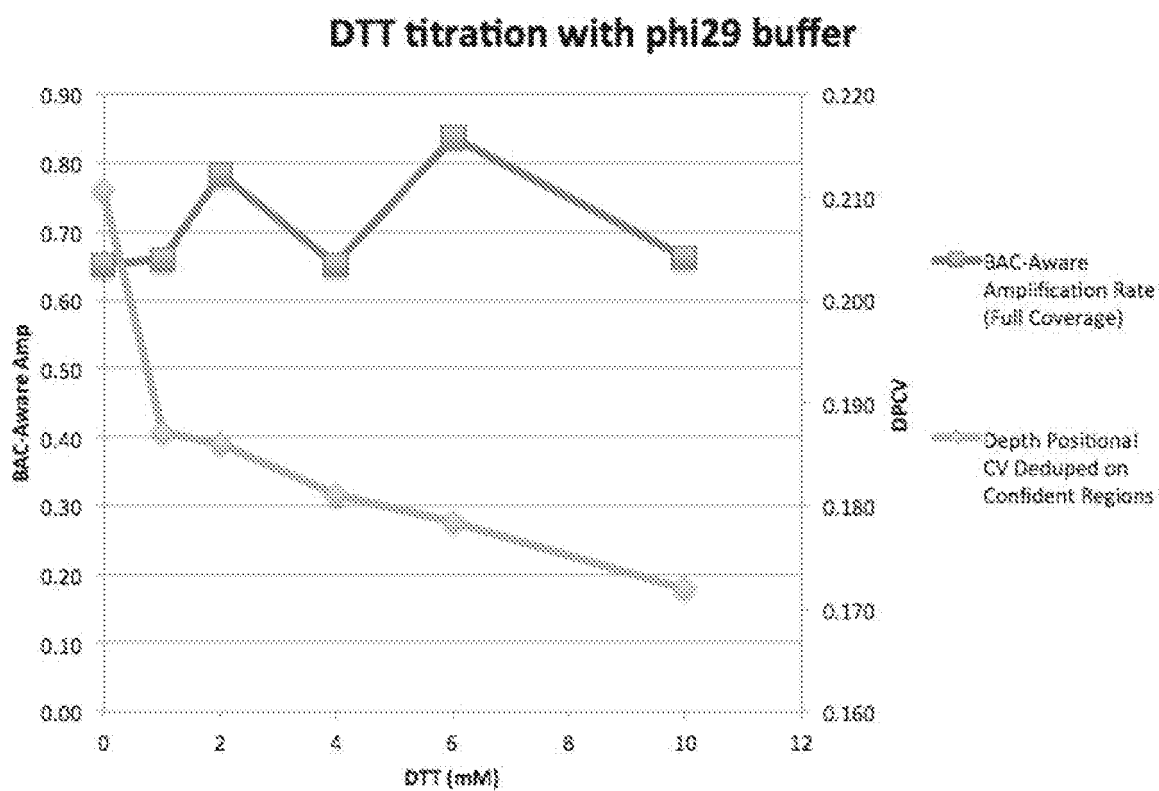


Fig. 7

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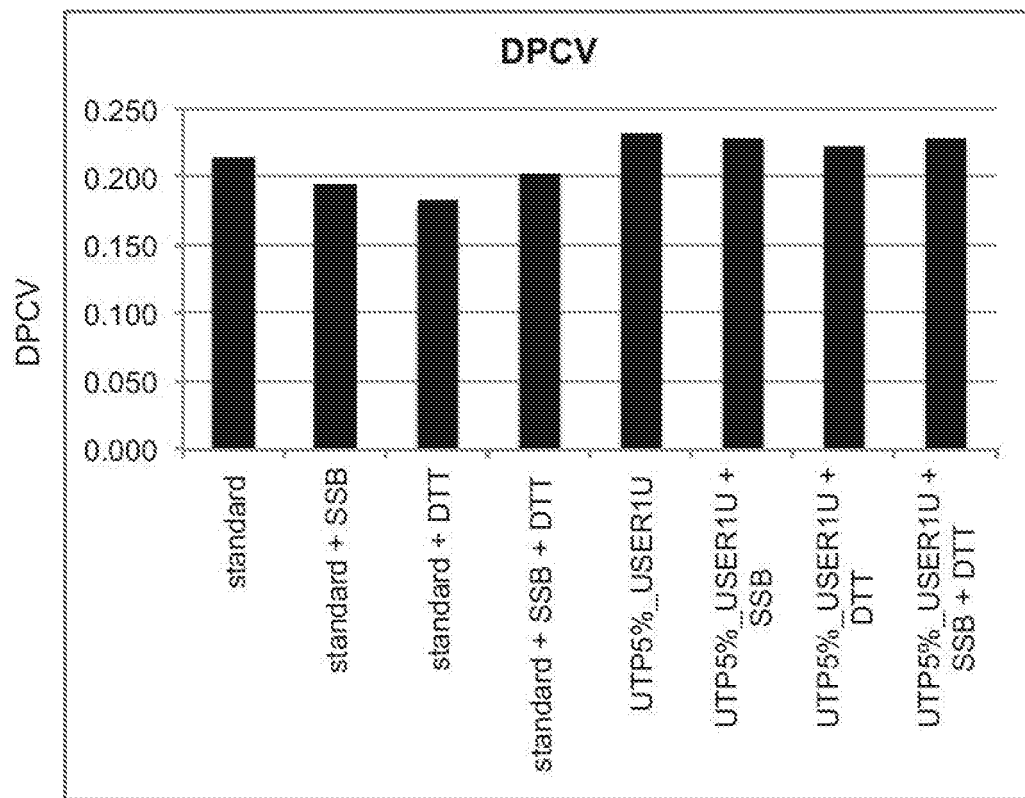


Fig. 8A

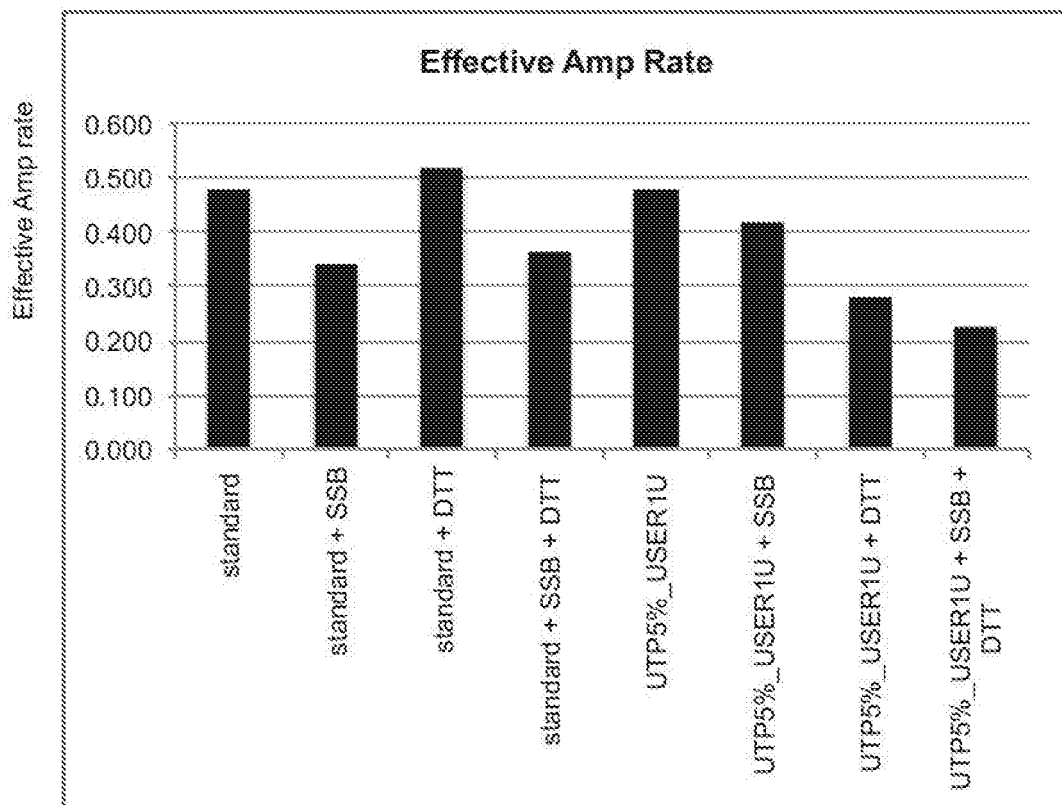


Fig. 8B

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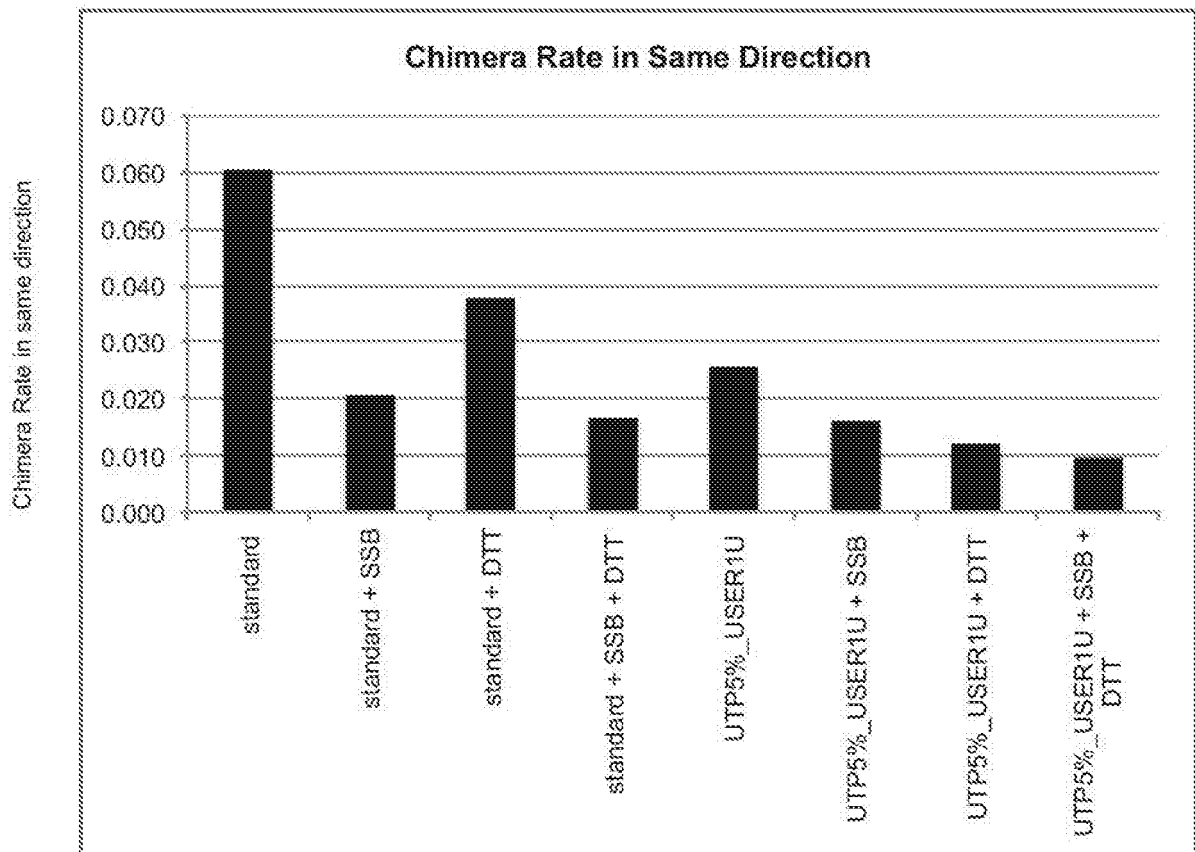


Fig. 8C

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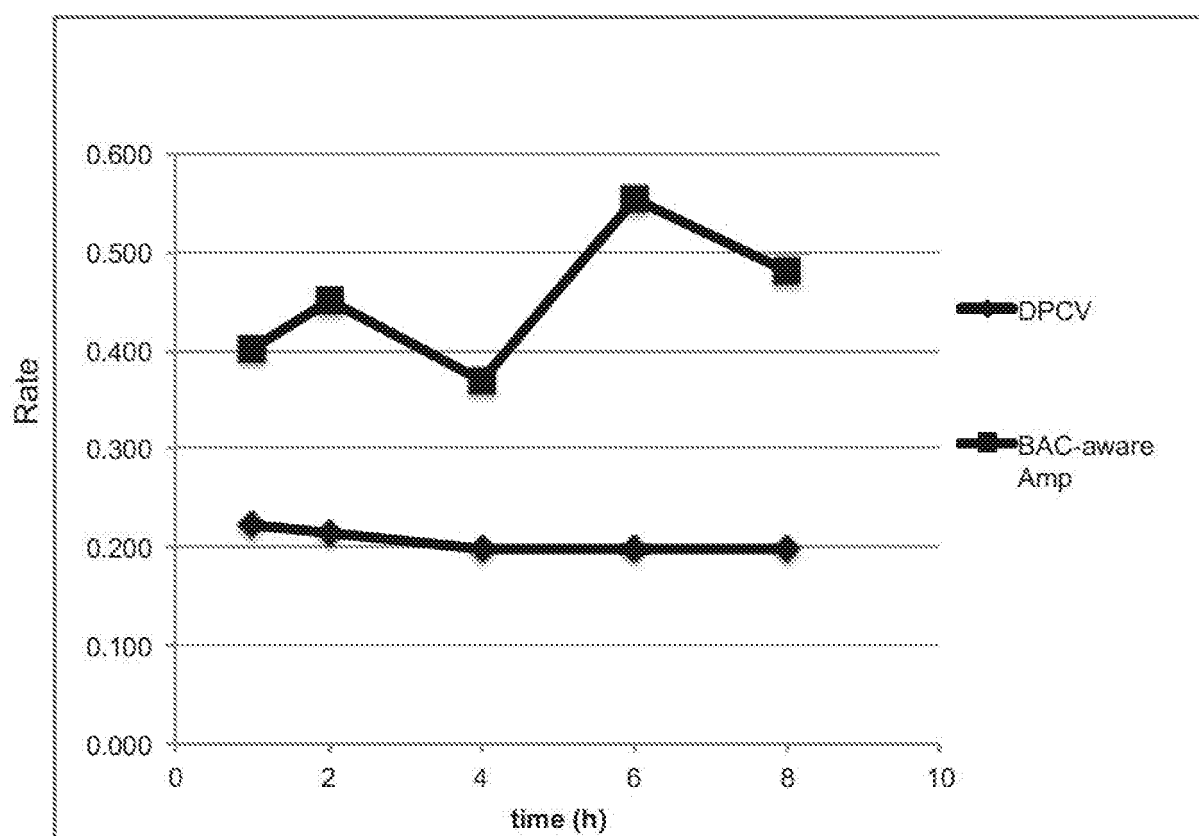


Fig. 9

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Sample Description	Sample ID	Mean Depth Deduped	DPCV Deduped on Confident Regions	BAC Aware Amplification Rate (Full Coverage)
GEM_No heat #1	9929	90.1	0.201	0.271
GEM_No heat #2	9930	95.7	0.191	0.332
GEM_NaOH denature #1	9931	128.8	0.236	0.683
GEM_NaOH denature #2	9932	150.1	0.241	0.669
GEM_heat #1	9933	149.7	0.218	0.842
GEM_heat #2	9934	196.5	0.219	0.916

Fig. 10

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Sample Description	Sample ID	Mean Depth Deduped	Mean Dup Rate (0.25X ign BC)	DPCV Deduped on Conf Reg
All Human Non-Targeted				< 0.7
500nM adapt-12	10723	10.5	1.000180	0.29
400nM adapt-12	10724	9.9	1.000188	0.29
320nM adapt-12	10725	13.8	1.000371	0.29
256nM adapt-12	10726	10.6	1.000183	0.29
205nM adapt-12	10727	12.1	1.000184	0.28
164nM adapt-12	10728	12.3	1.000186	0.28
131nM adapt-12	10729	11.7	1.000188	0.28
105nM adapt-12	10730	9.8	1.000187	0.28
84nM adapt-12	10731	11.6	1.000182	0.27
67nM adapt-12	10732	12.1	1.000376	0.27
54nM adapt-12	10733	14.1	1.000182	0.27
LL-ctrl	10734	5.8	1.000178	0.17

Fig. 11

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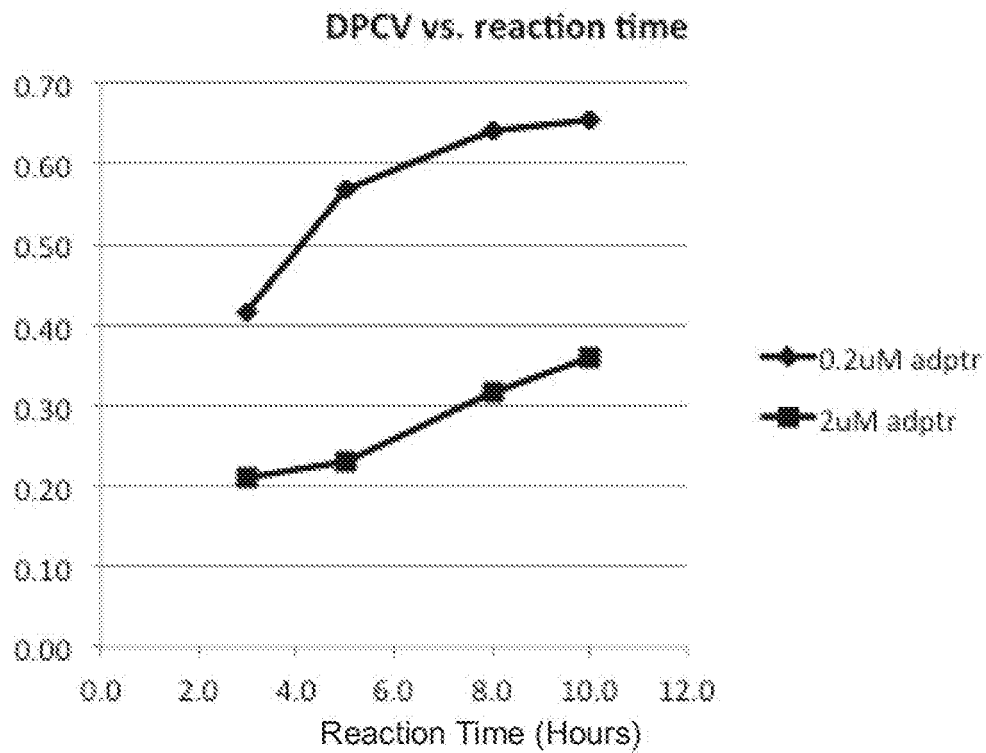


Fig. 12A

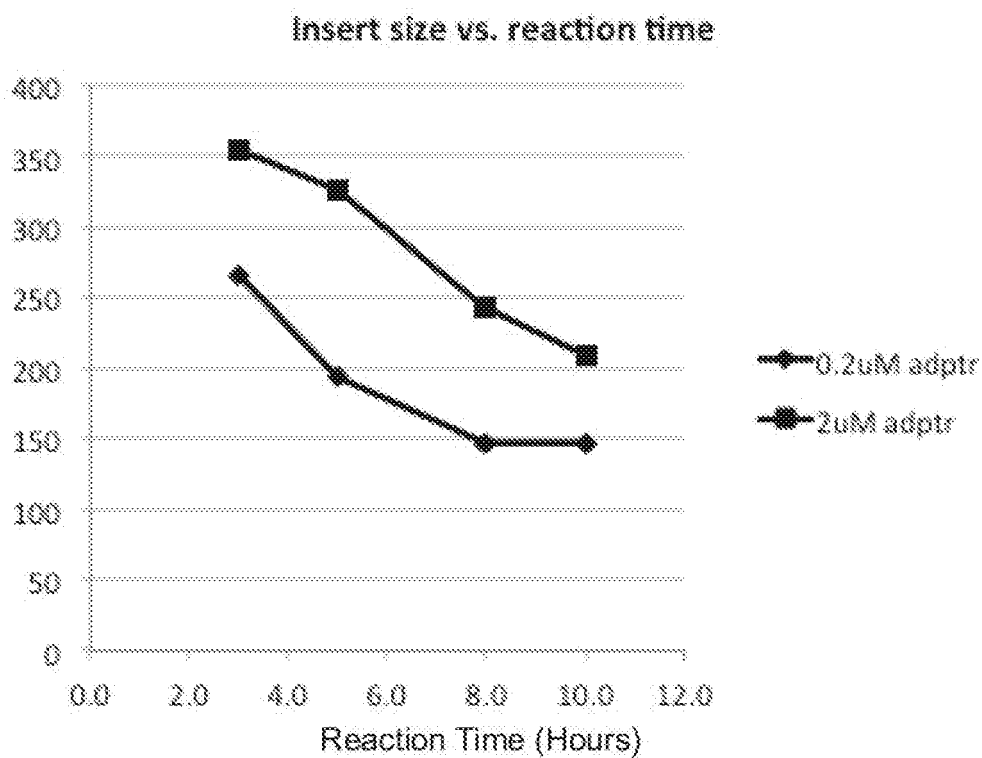


Fig. 12B

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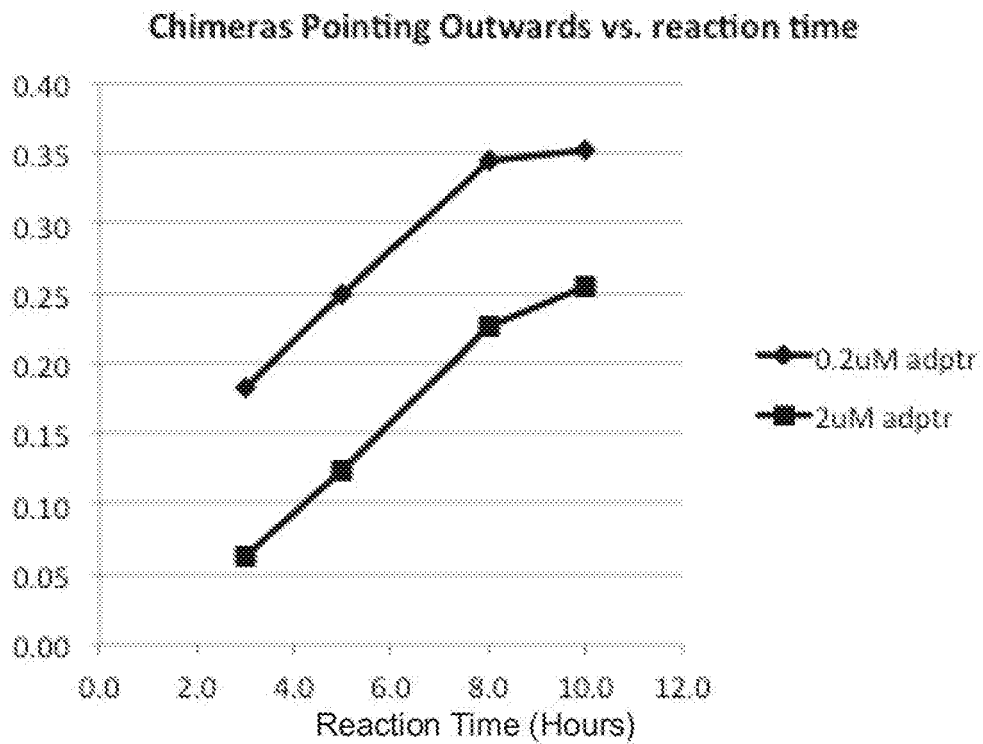


Fig. 12C

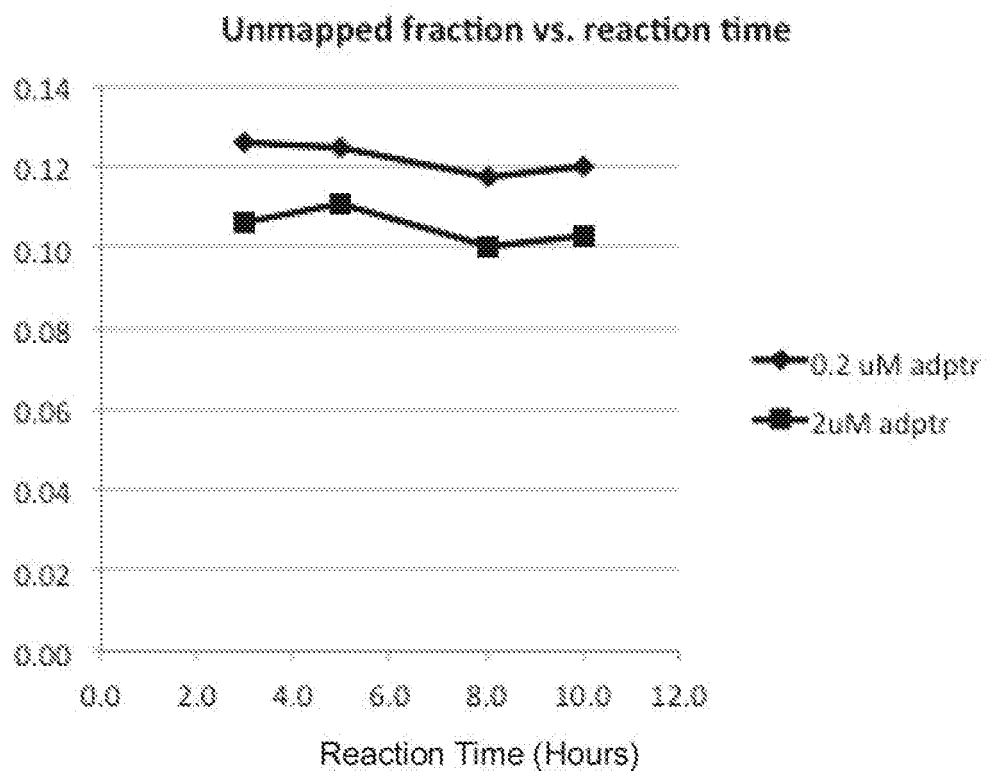


Fig. 12D

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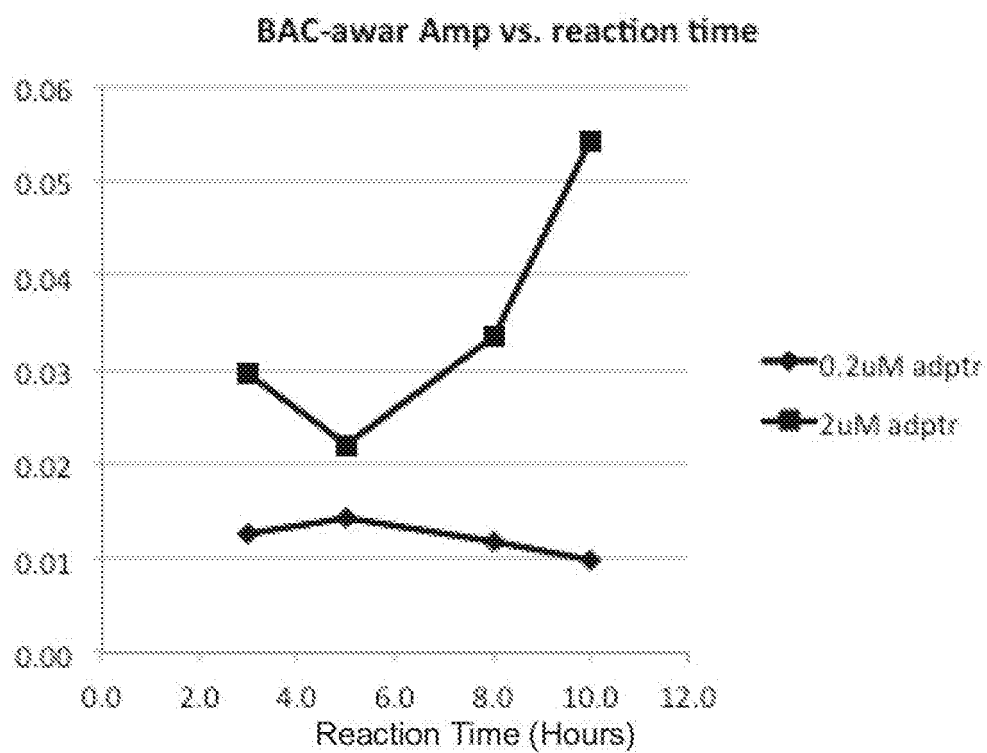


Fig. 12E

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Ligase	Template kind	Adaptor	Adap conc	P5/P7 quant
No ligase	NTC	Phos degenerate	0.2	0.17
No ligase	NTC	Phos inline	0.2	0.52
No ligase	NTC	No Phos inline	0.2	0.9
No ligase	NTC	No Phos degenerate	2	0.38
No ligase	NTC	Phos inline	2	0.78
No ligase	NTC	No Phos inline	2	1.8
No ligase	BACS	No adap	0	0.25
No ligase	BACS	Phos degenerate	0.2	0.47
No ligase	BACS	Phos inline	0.2	0.67
No ligase	BACS	No Phos inline	0.2	0.97
No ligase	BACS	No Phos degenerate	2	0.36
No ligase	BACS	Phos inline	2	1.03
No ligase	BACS	No Phos inline	2	2.74
+ ligase	NTC	Phos degenerate	0.2	0.66
+ ligase	NTC	Phos inline	0.2	1.01
+ ligase	NTC	No Phos inline	0.2	1.42
+ ligase	NTC	No Phos degenerate	2	0.5
+ ligase	NTC	Phos inline	2	2.28
+ ligase	NTC	No Phos inline	2	2.99
+ ligase	BACS	No adap	0	2.37
+ ligase	BACS	No Phos inline	0.2	43.55
+ ligase	BACS	Phos degenerate	0.2	53.39
+ ligase	BACS	Phos inline	0.2	104.2
+ ligase	BACS	No Phos degenerate	2	10.78
+ ligase	BACS	No Phos inline	2	85.99
+ ligase	BACS	Phos inline	2	106.56

Fig. 13

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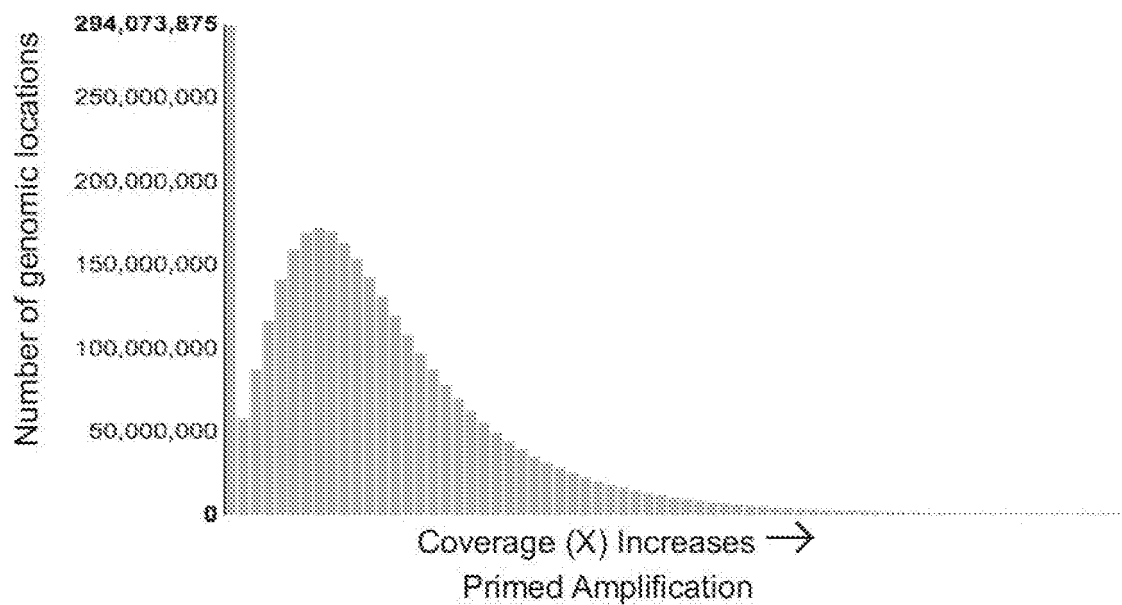


Fig. 14A

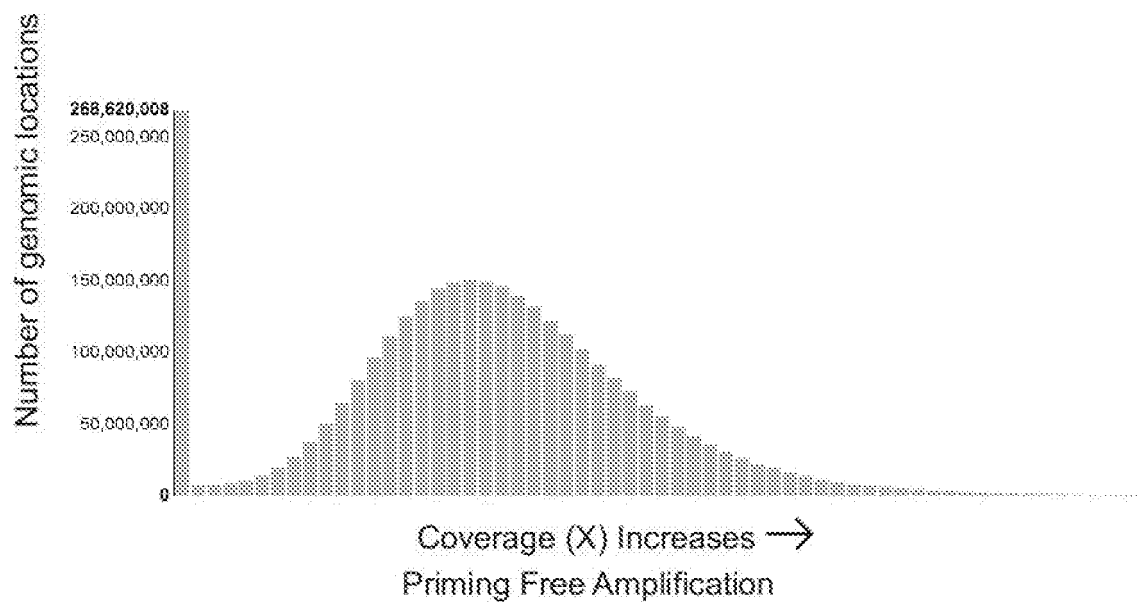


Fig. 14B

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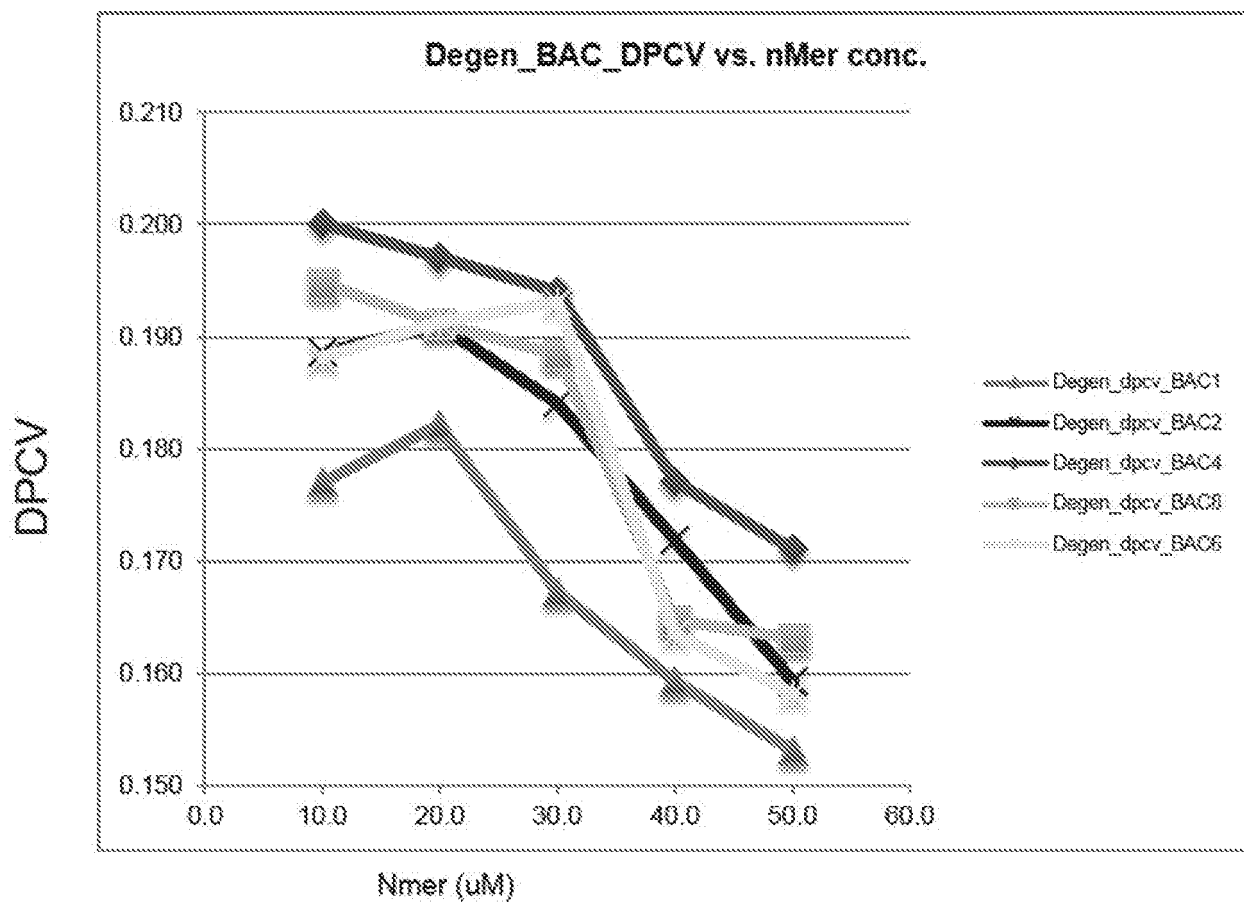


Fig. 15

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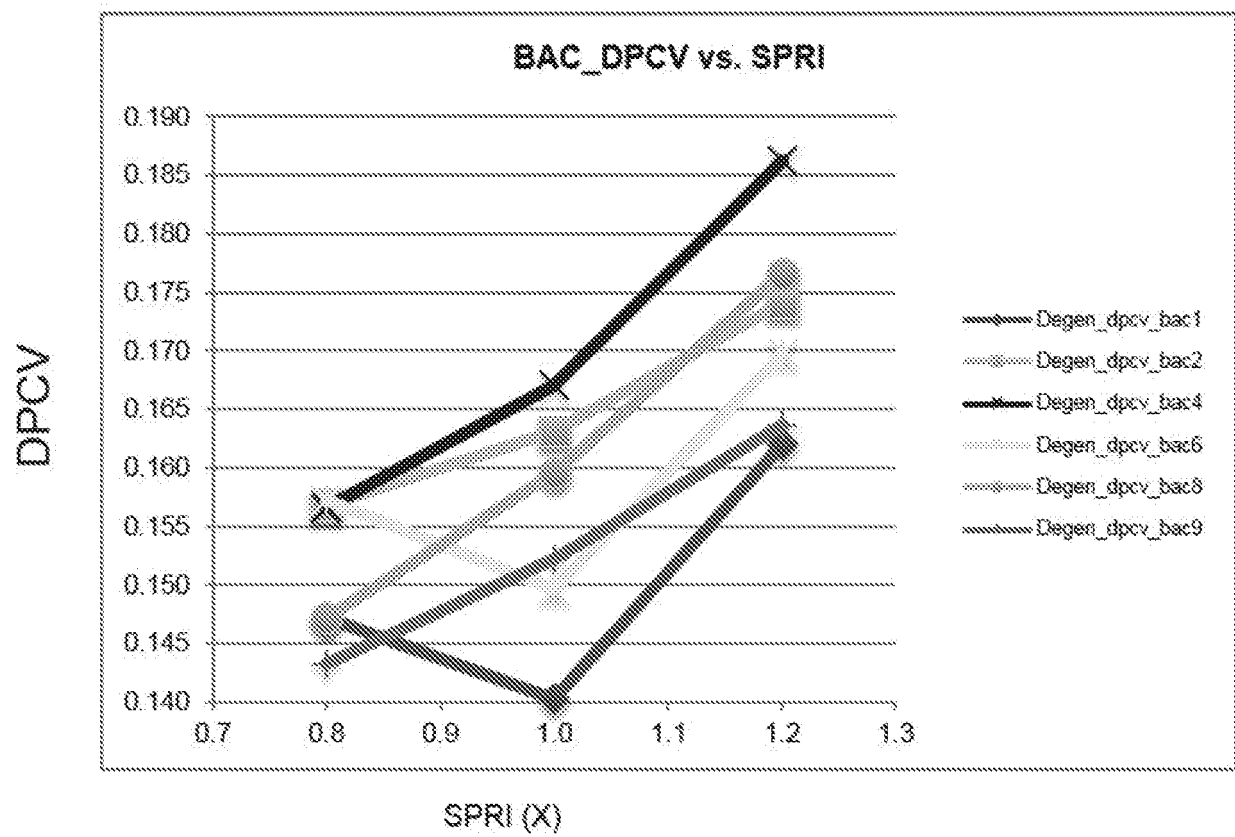


Fig. 16

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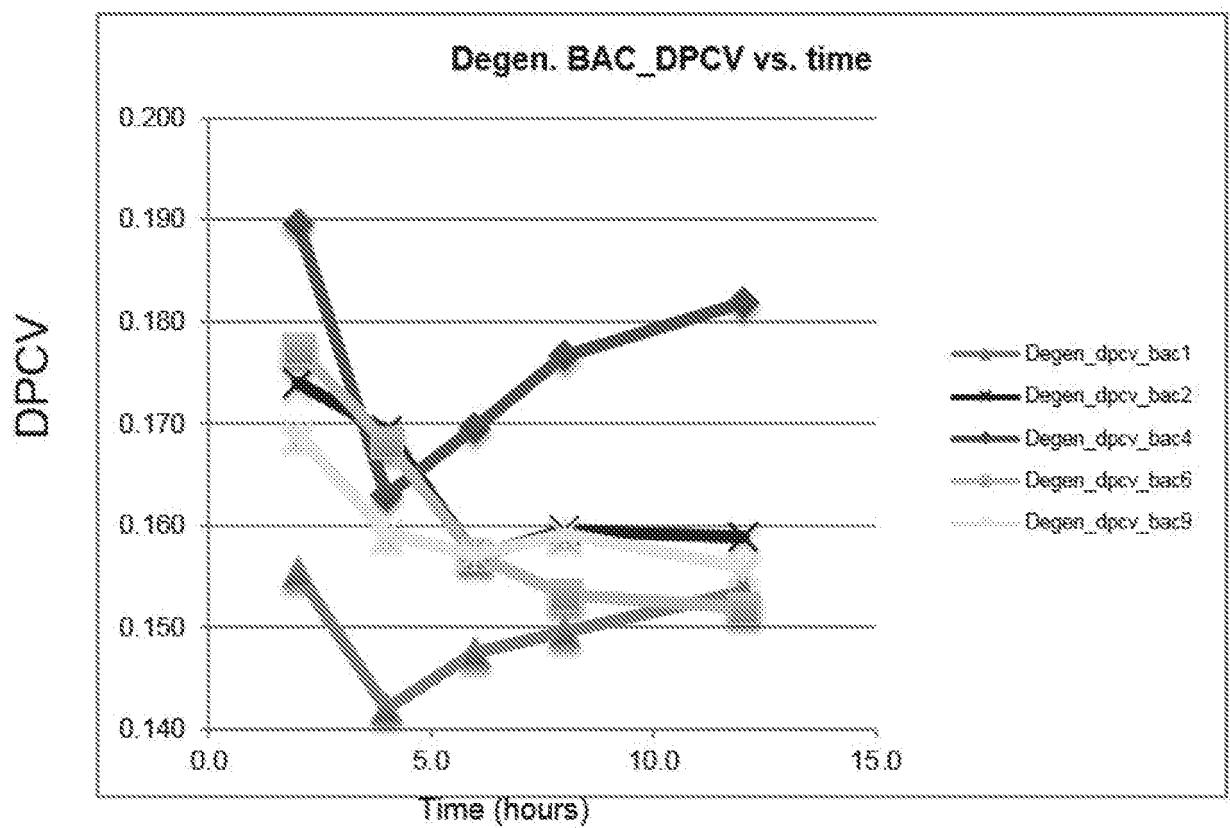


Fig. 17

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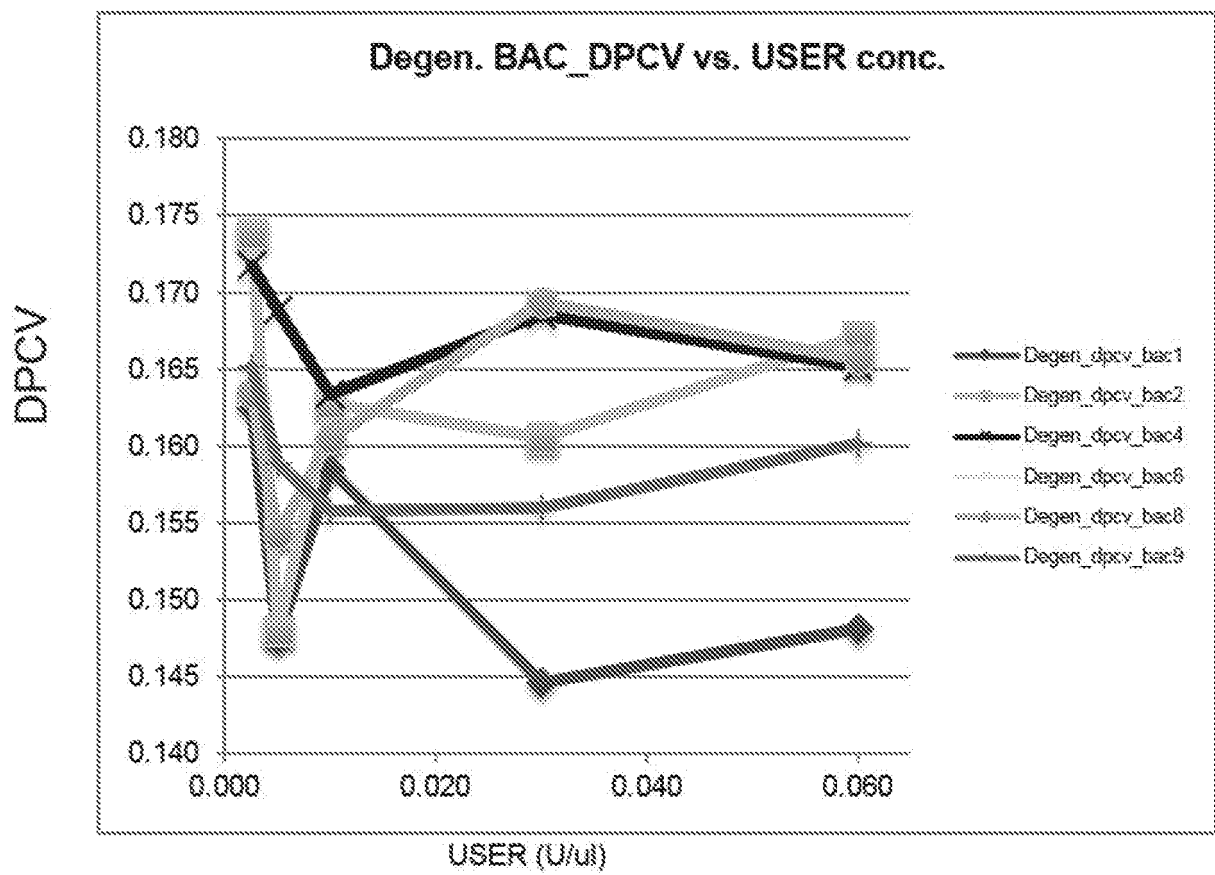


Fig. 18

Fig. 19A

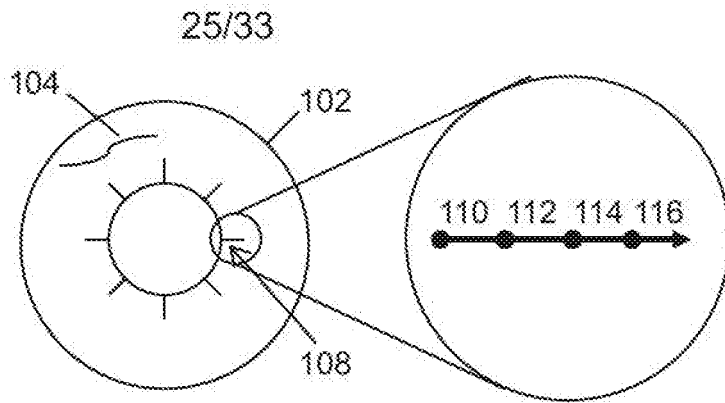


Fig. 19B

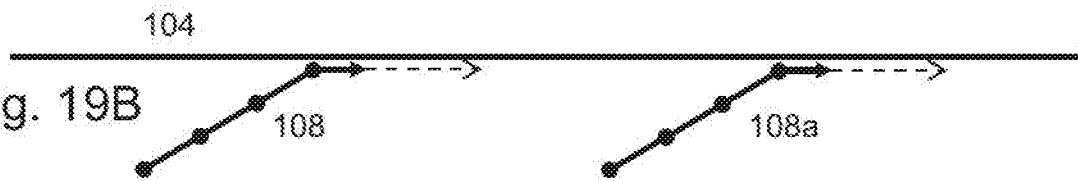


Fig. 19C

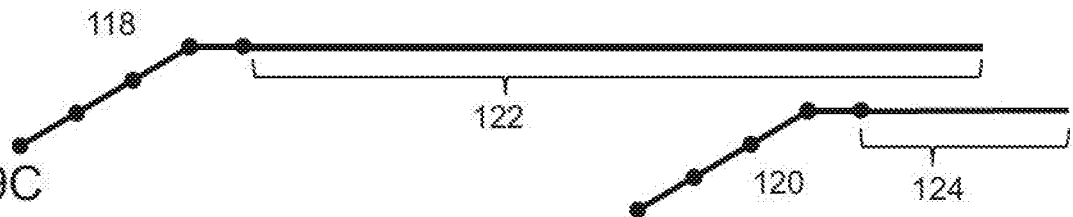


Fig. 19D

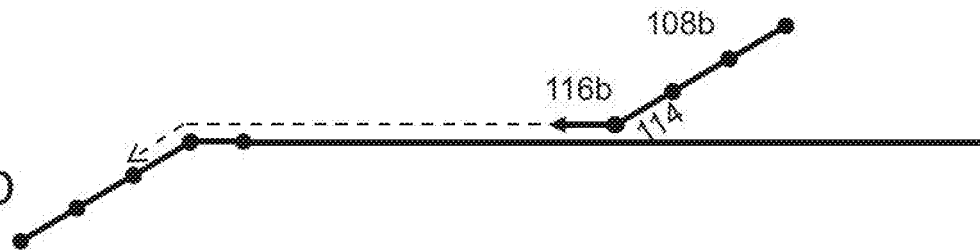
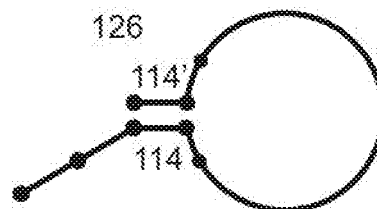
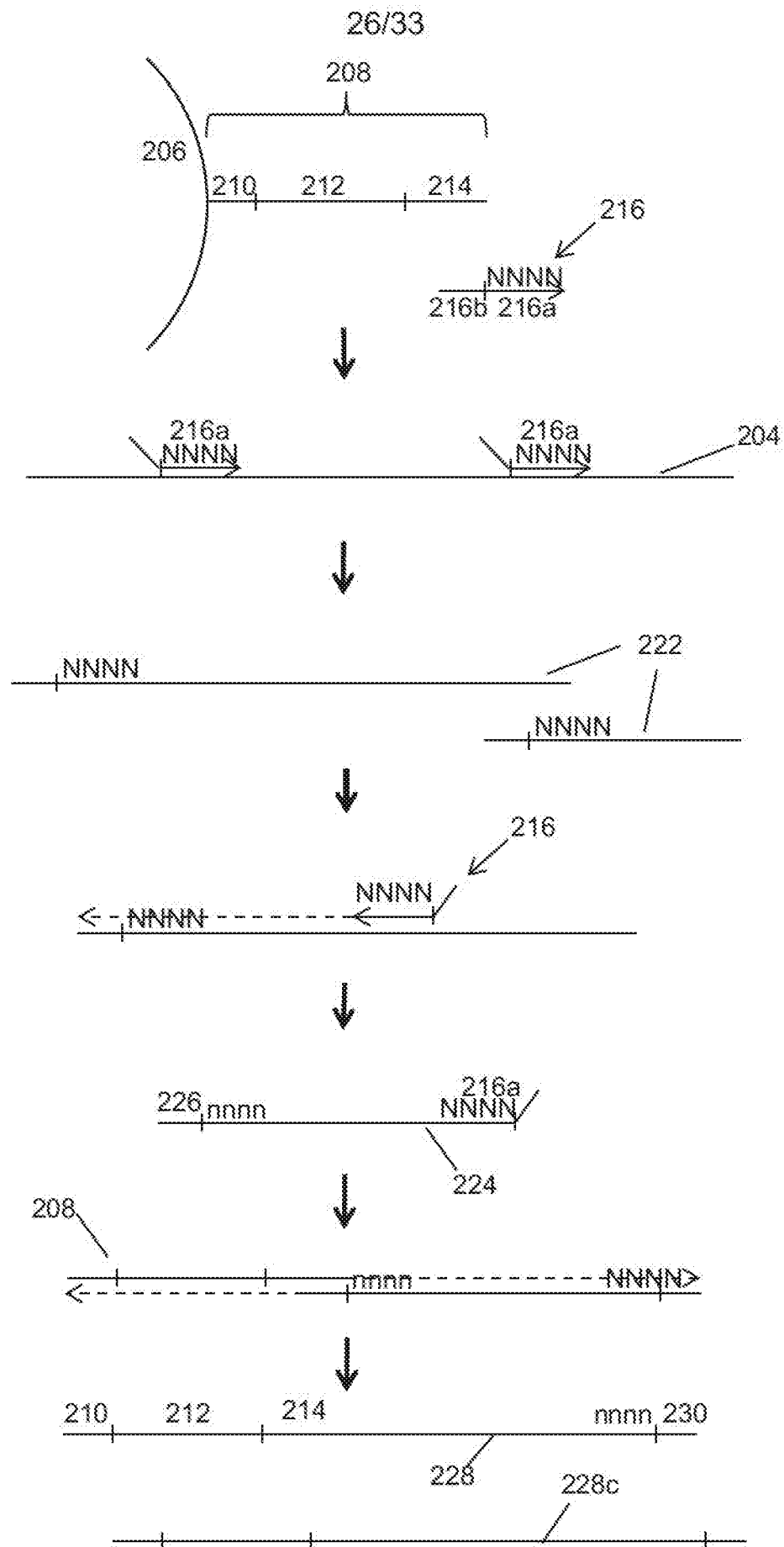


Fig. 19E

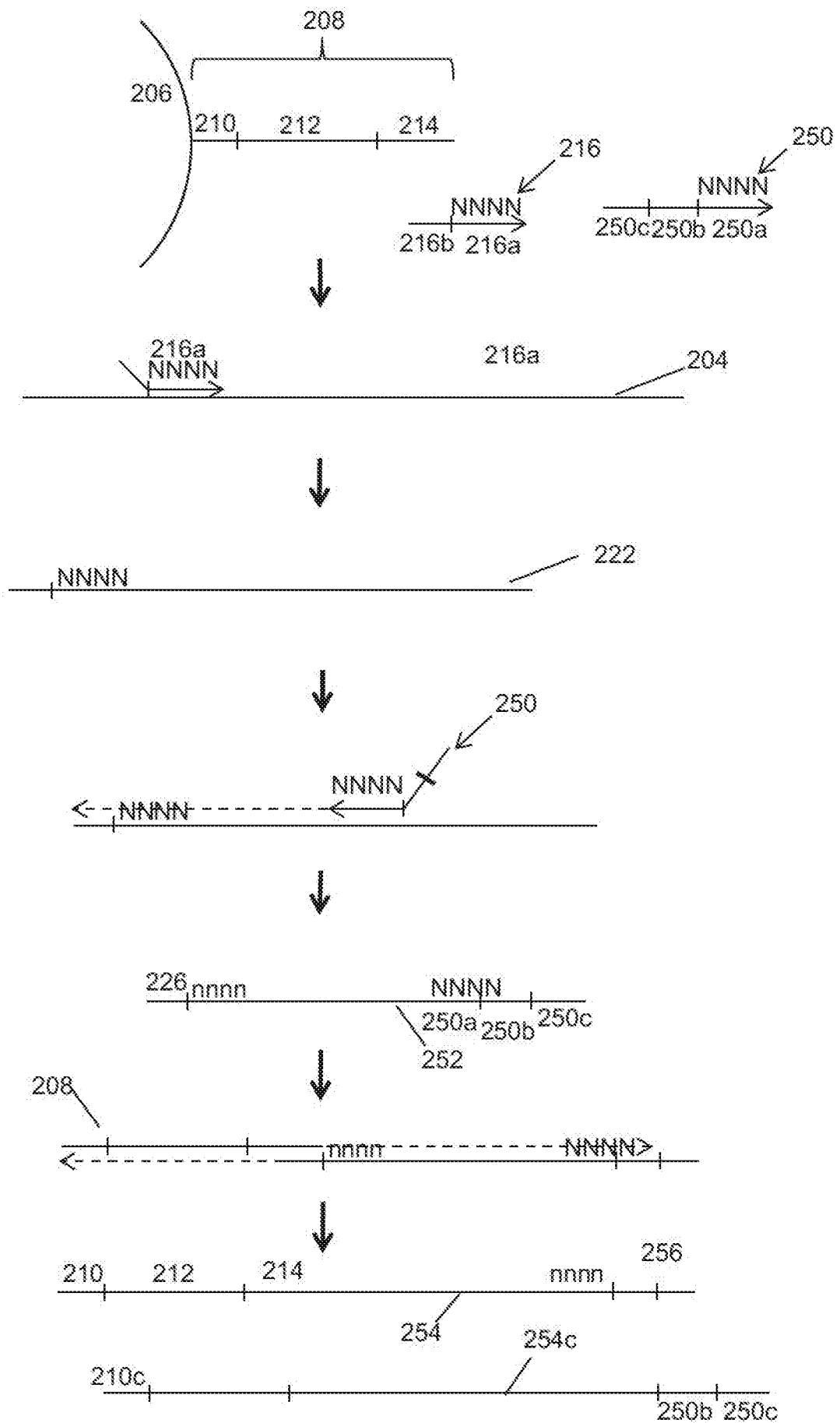


Fig. 19F

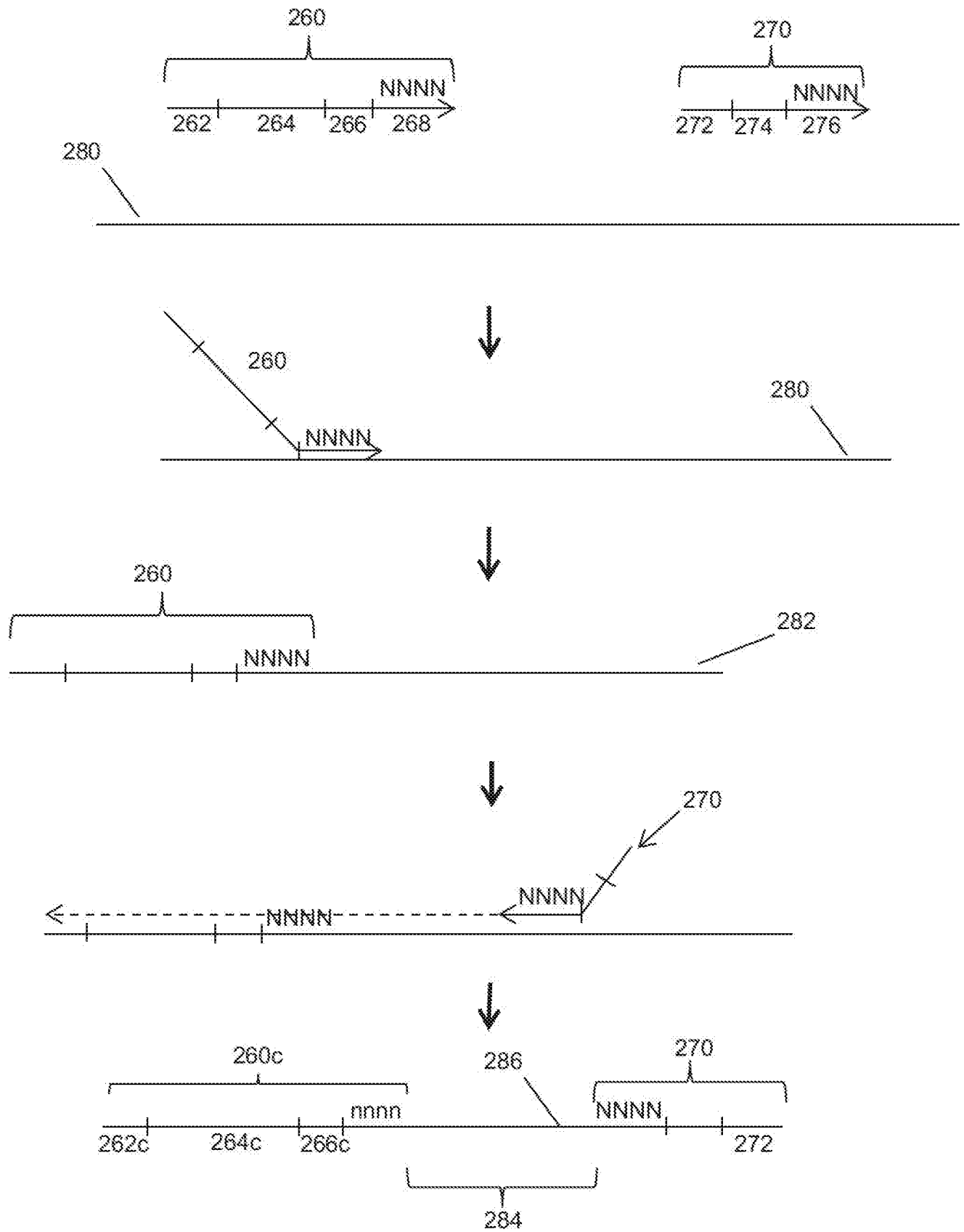




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Chimera Rate from Distant Reads vs. Q35 or Greater Error Rate

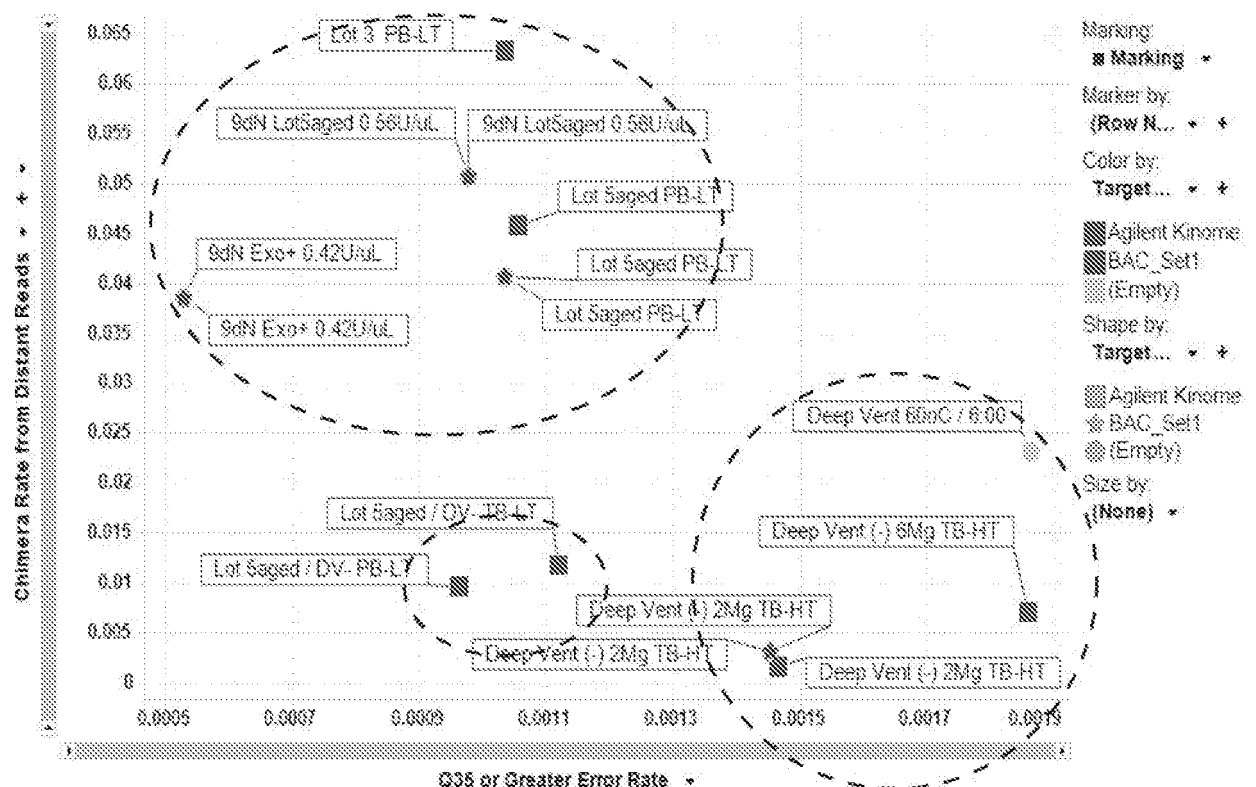


Fig. 21

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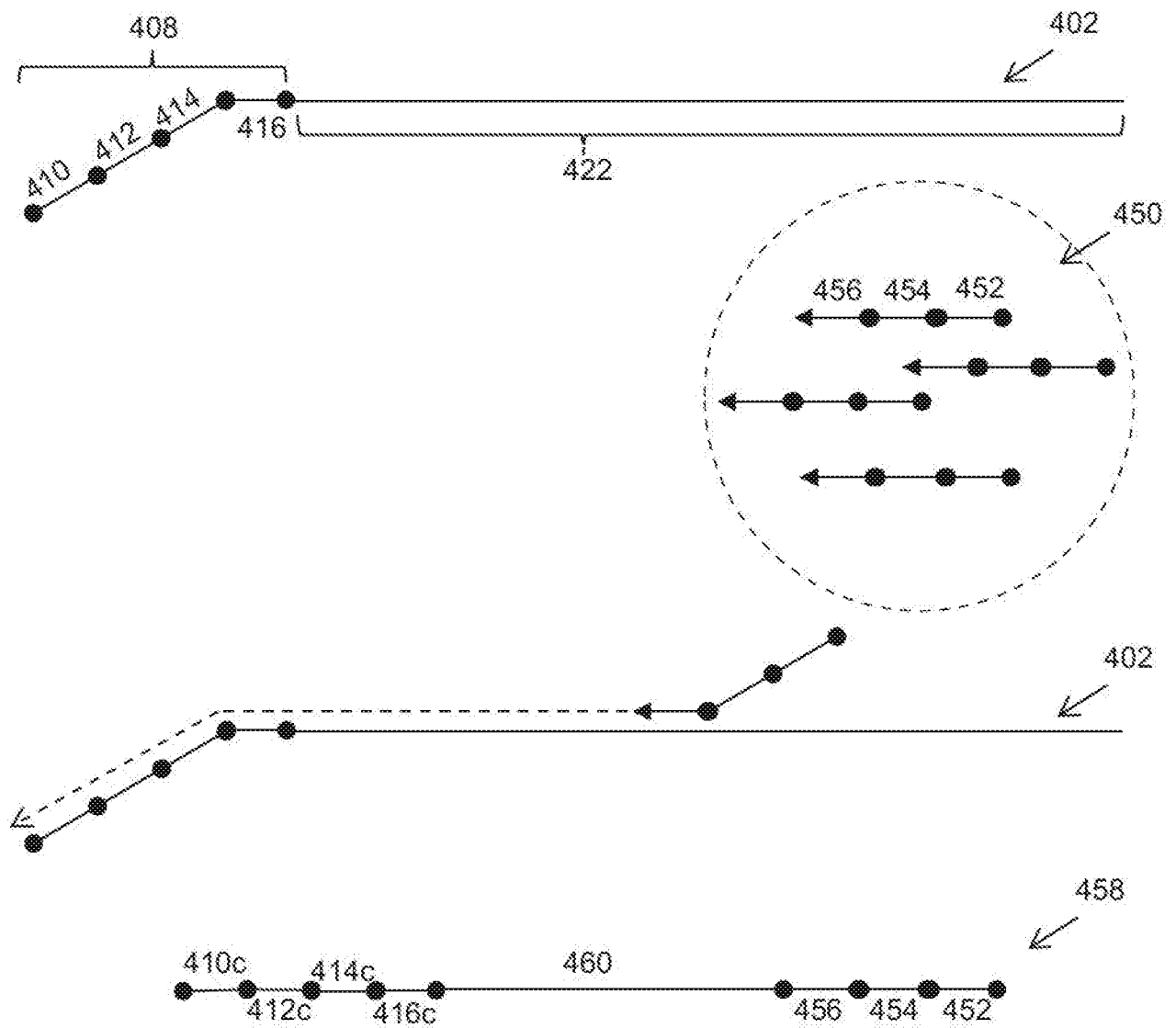


Fig. 22

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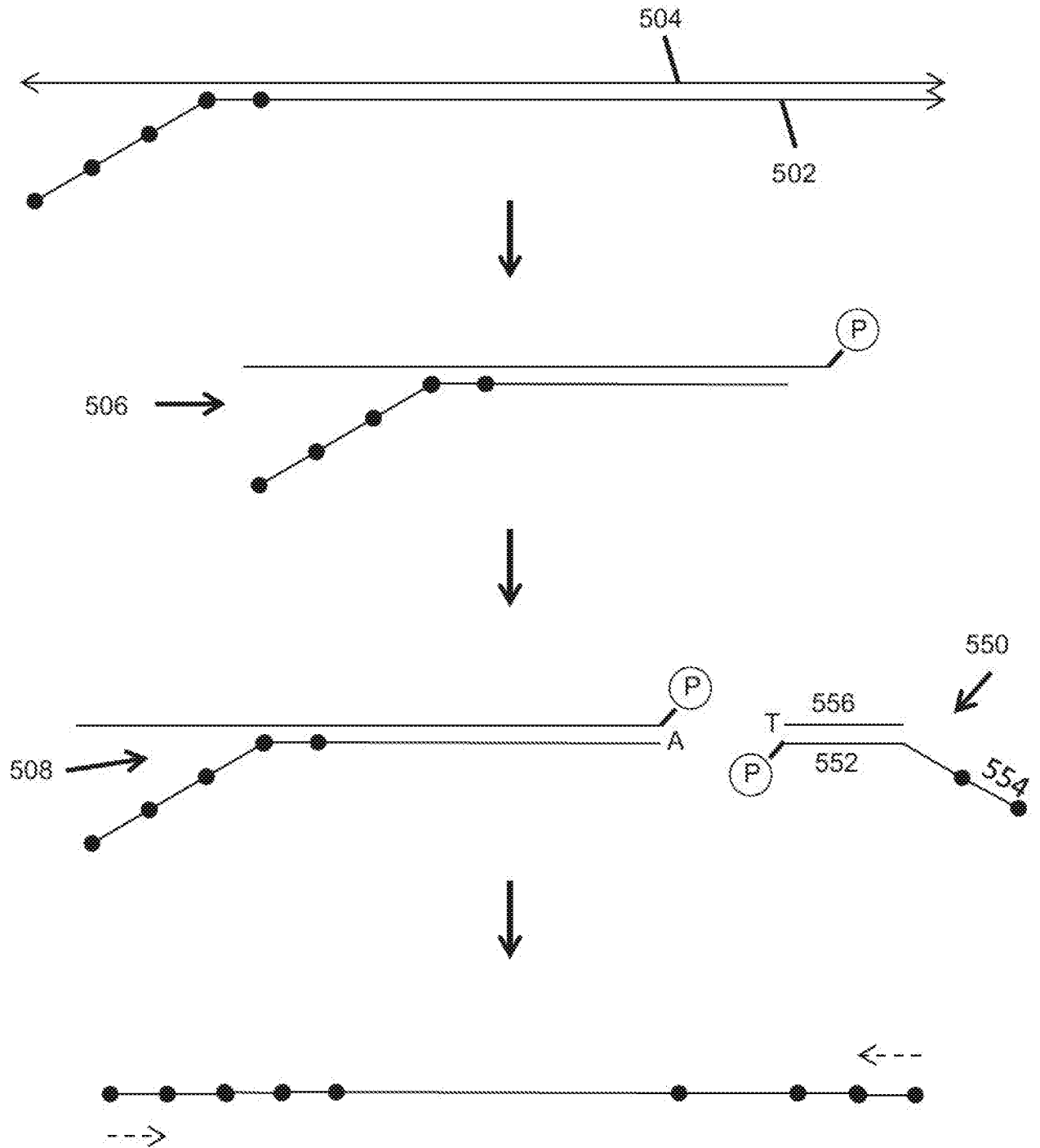


Fig. 23

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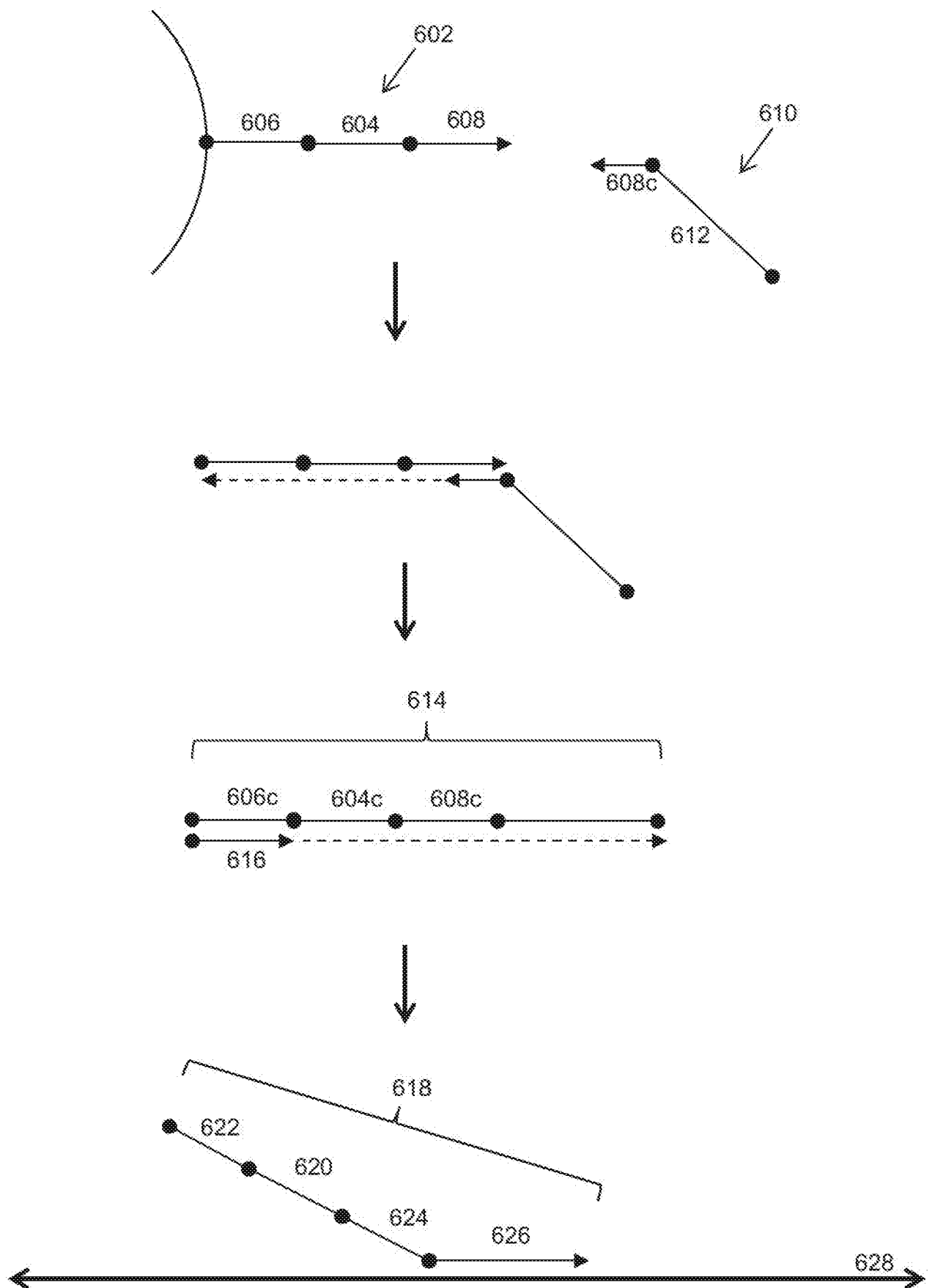


Fig. 24

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