

Fig. 1

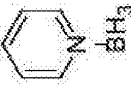
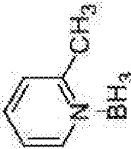
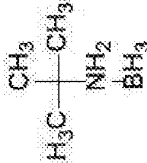
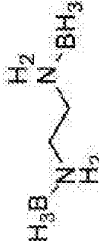
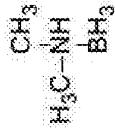
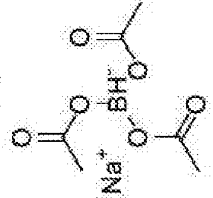
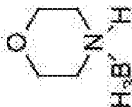
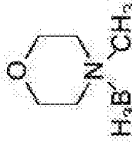
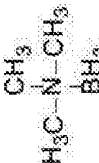
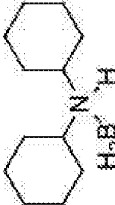
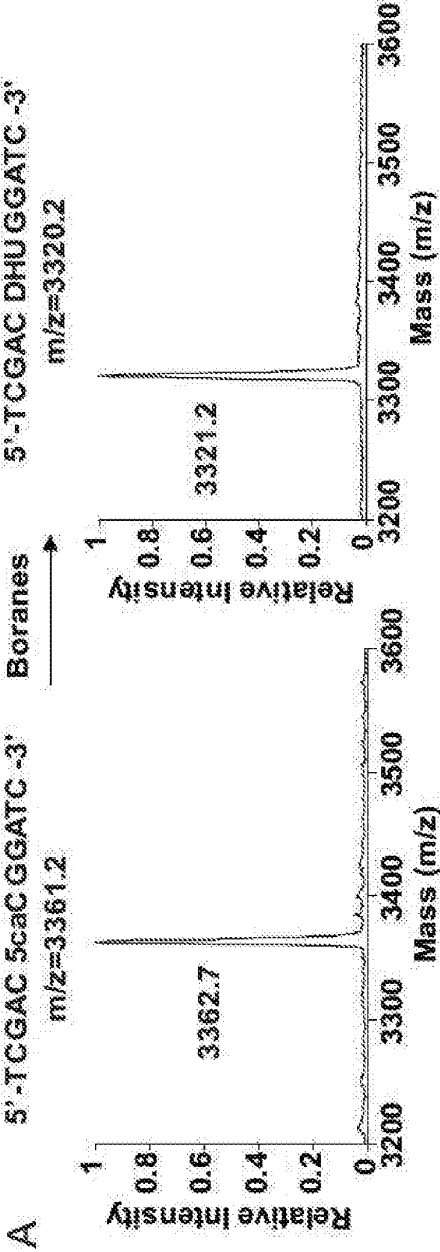
 pyridine borane 100%	 2-picoline borane 100%	 tert-butylamine borane 100%	NH_3BH_3 ammonia borane 100%
NaBH_4 sodium borohydride ~60%	 ethylenediamine borane ~30%	 dimethylamine borane ~30%	 sodium triacetoxymethylborohydride ~20%
 morpholine borane n.d.	 4-methylmorpholine borane n.d.	 trimethylamine borane n.d.	 dicyclohexylamine borane n.d.

Fig. 2



B

Cytosine modification in Oligo	Conversion to DHU
C	0%
5mC	0%
5hmC	0%
5fC	97.6±0.1%
5caC	98.1±0.6%

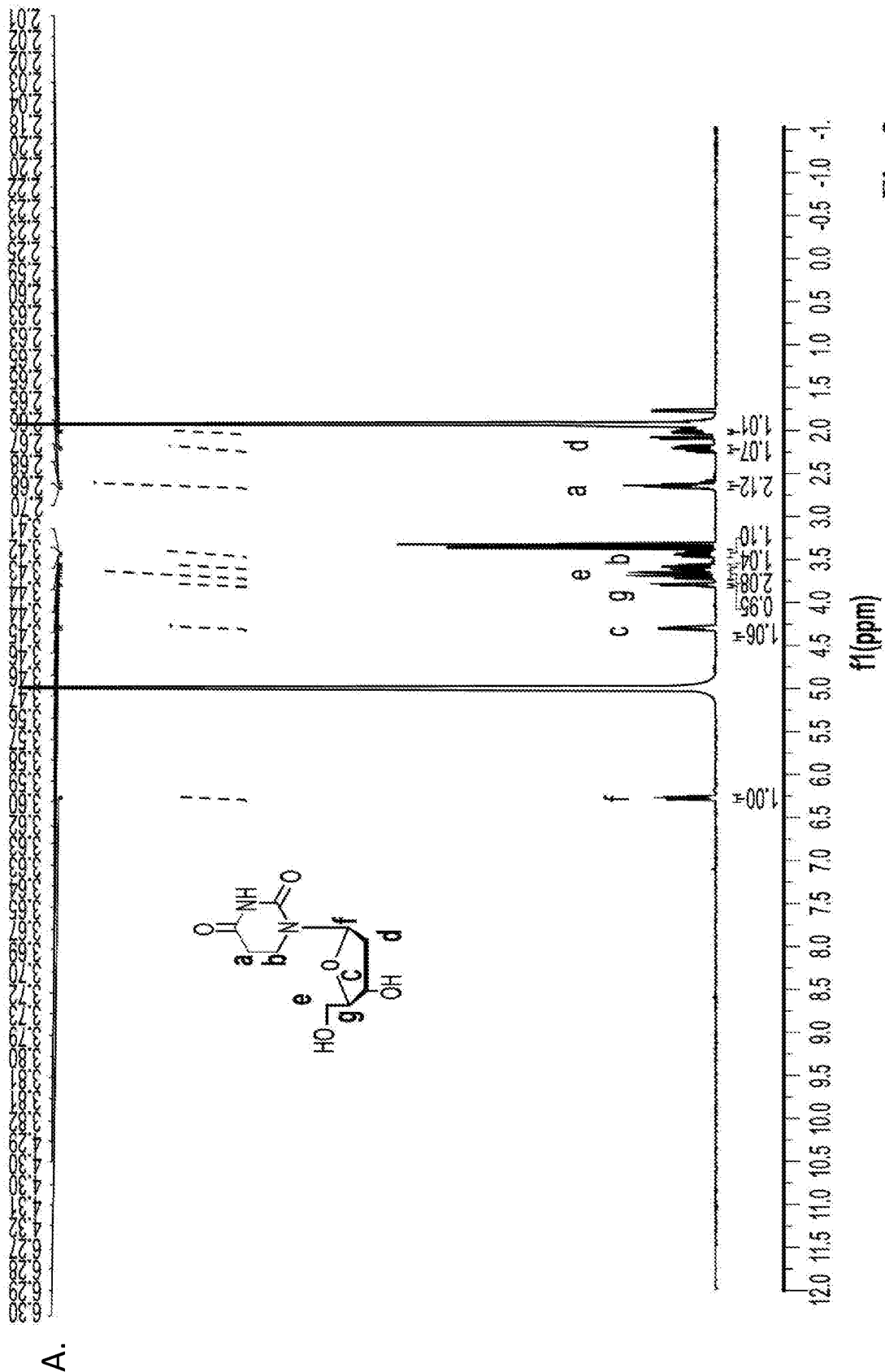
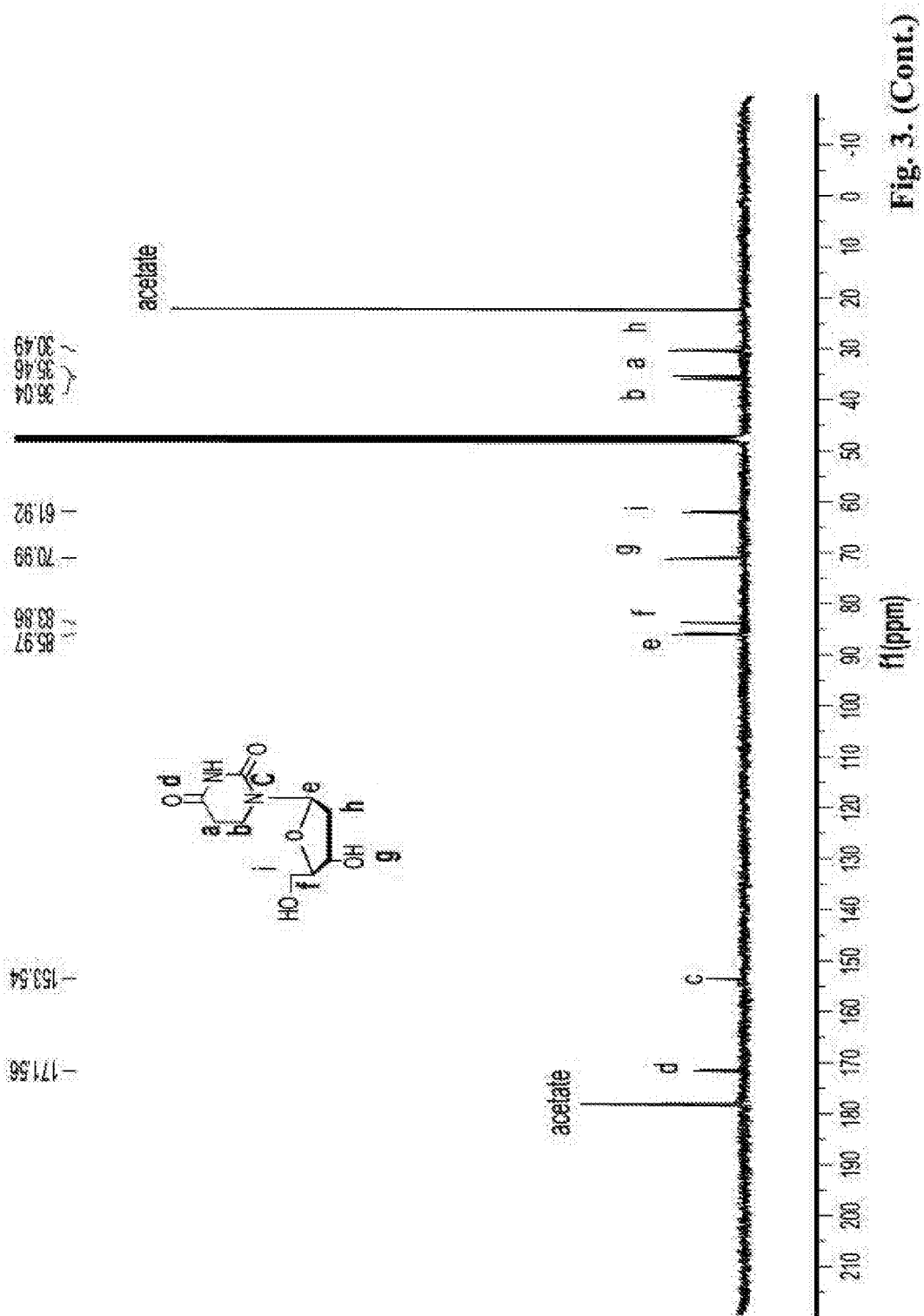


Fig. 3.



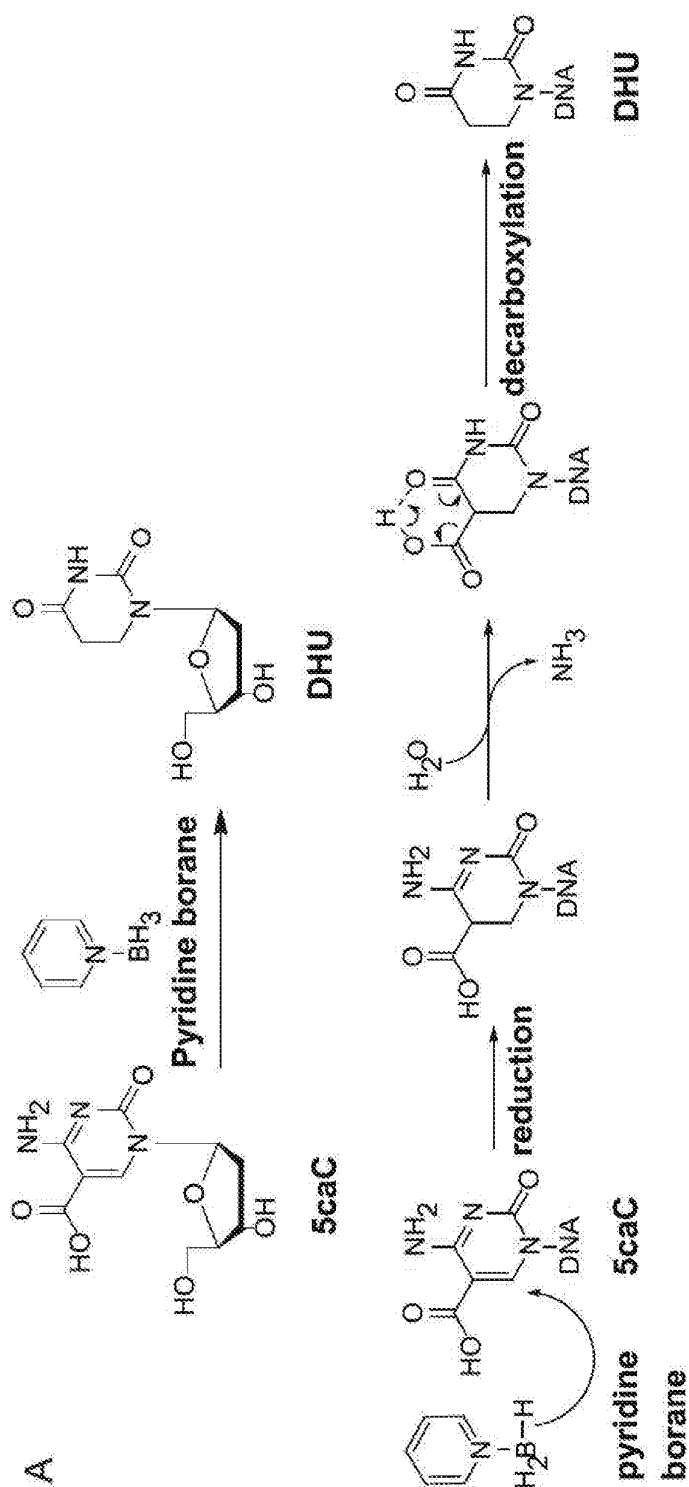


Fig. 4

B

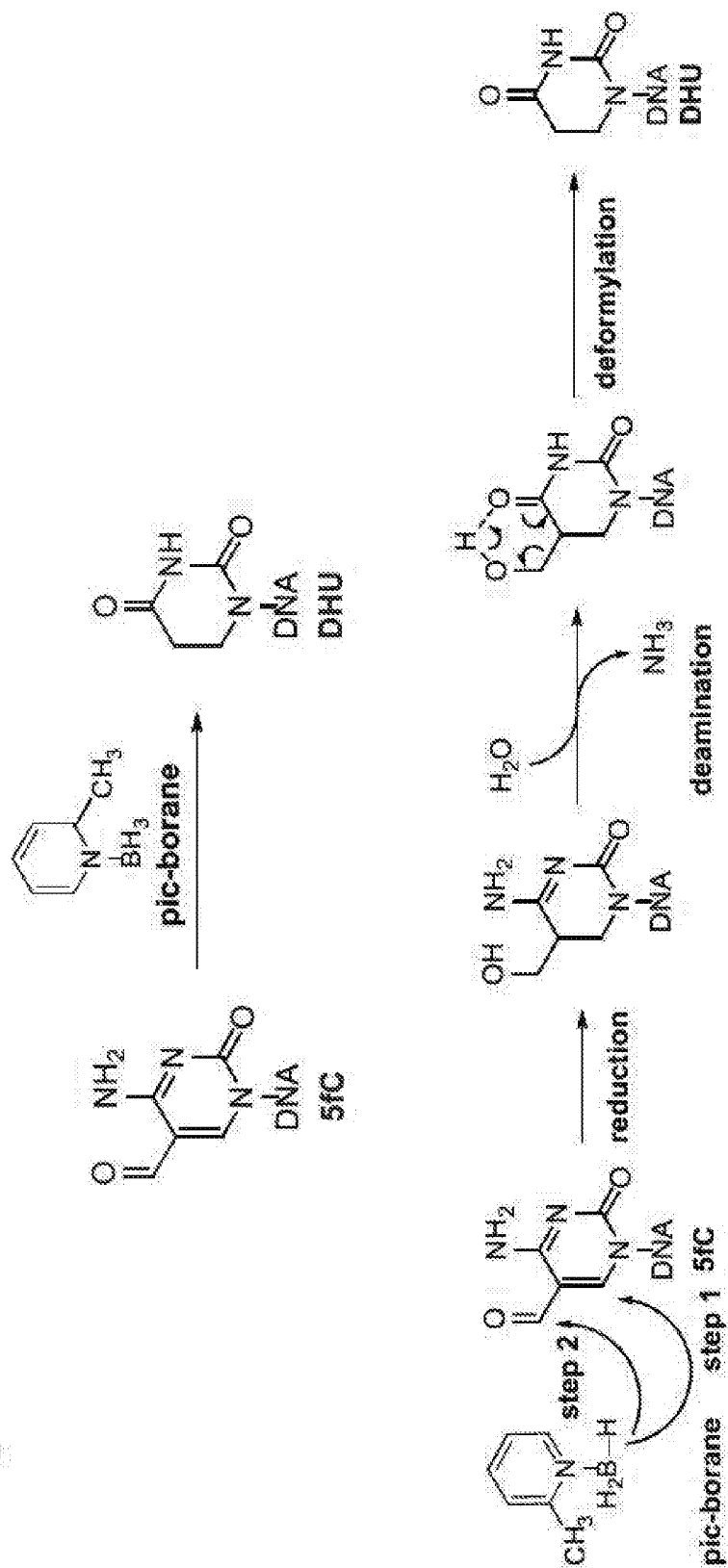
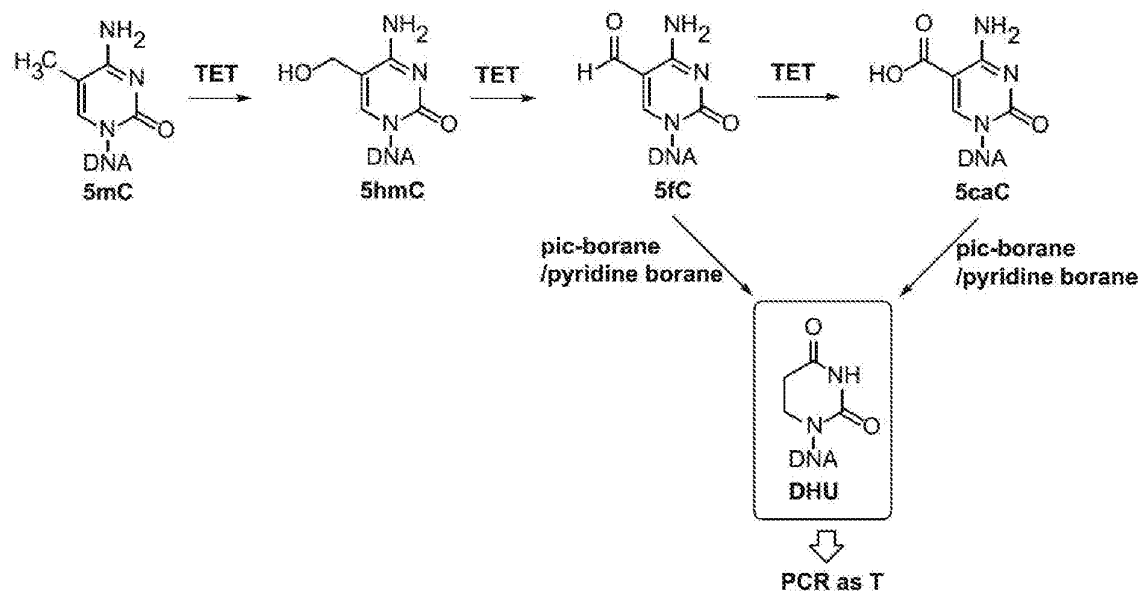
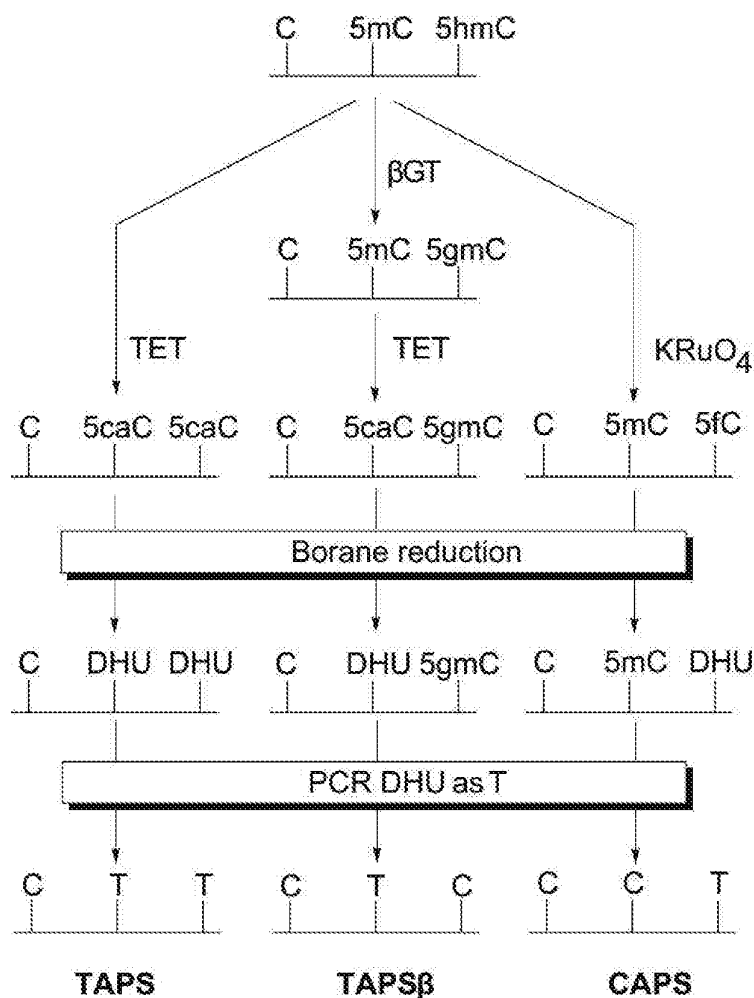


Fig. 4 (Cont.)

A.**B.****Fig. 5**

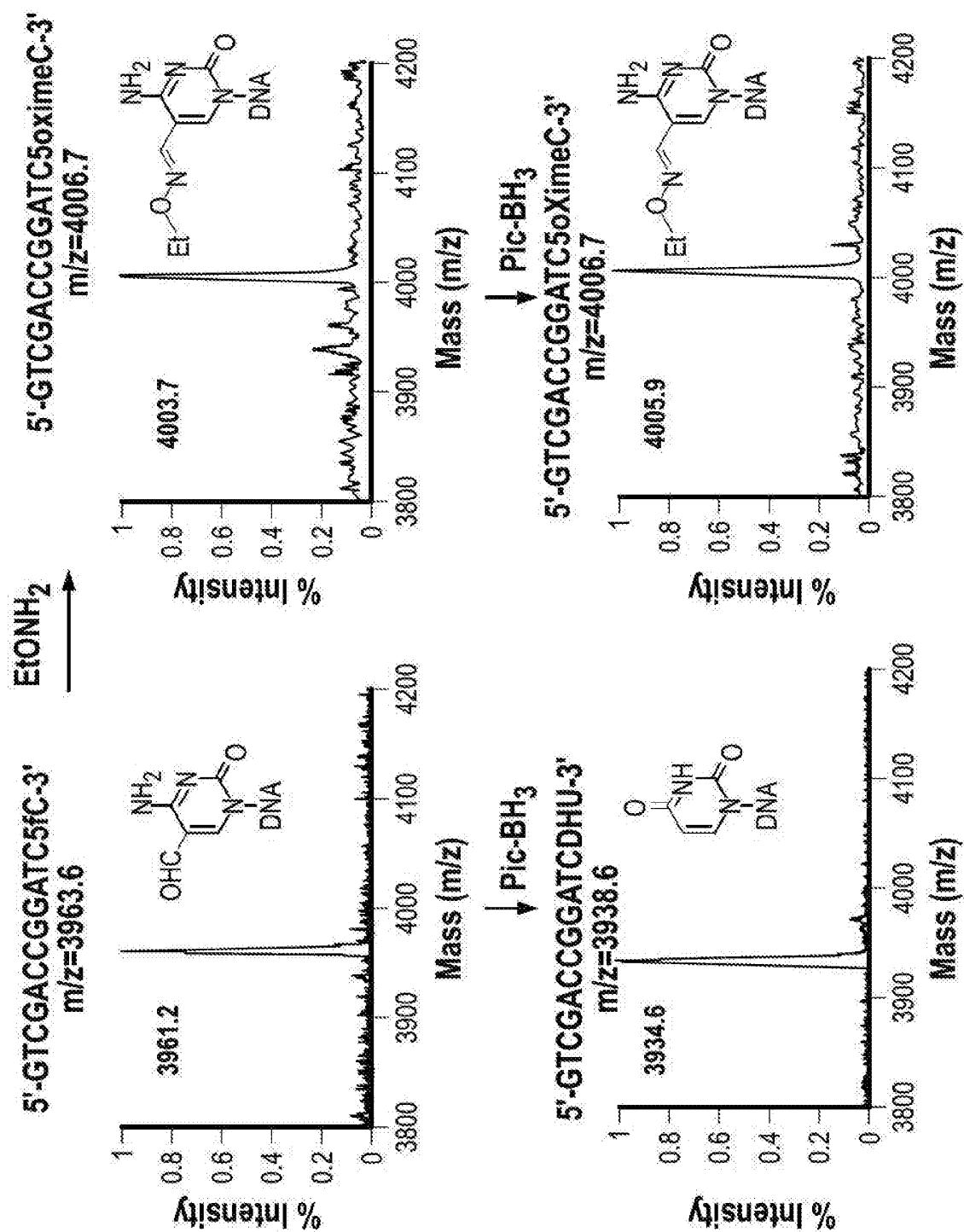


Fig. 6.

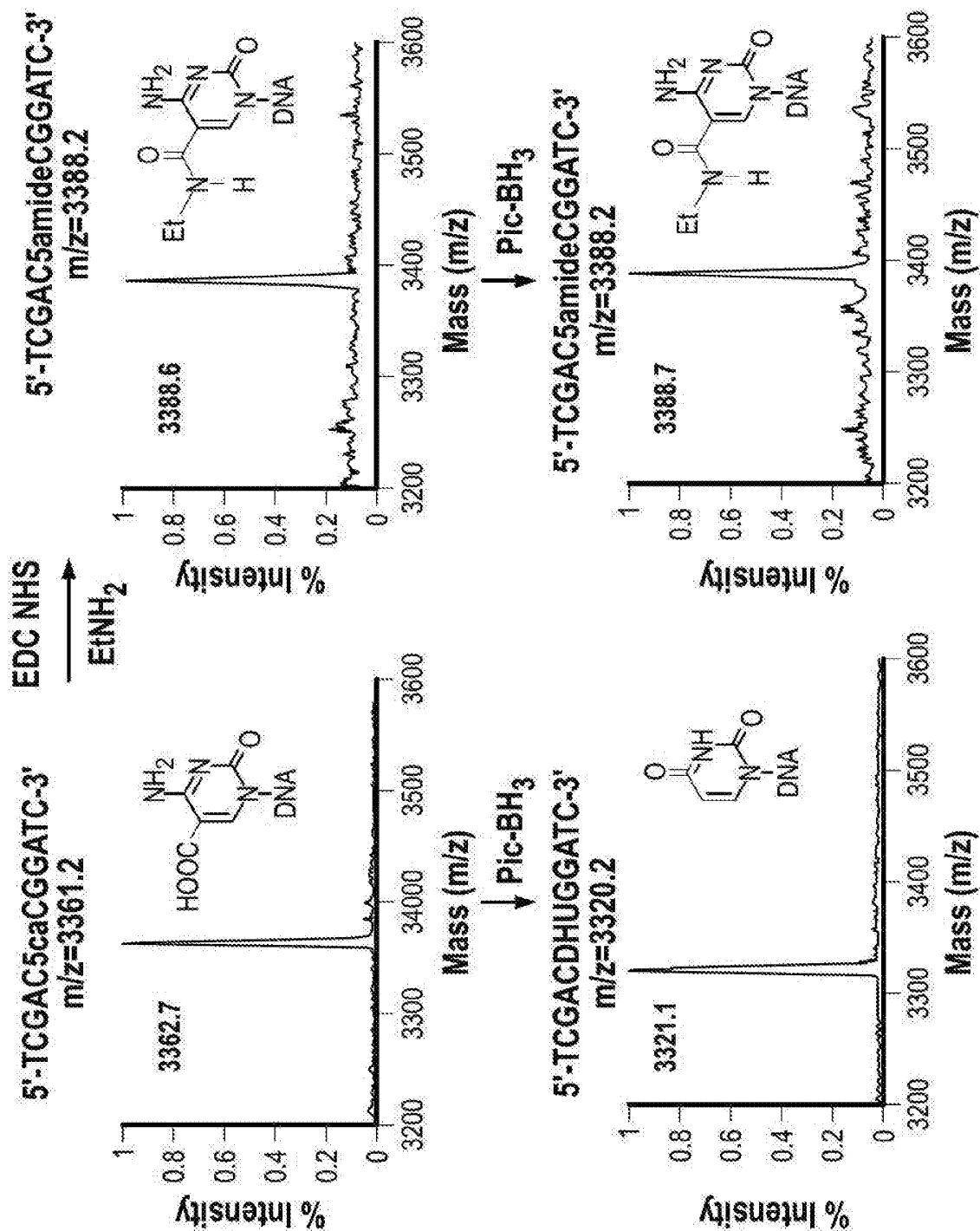


Fig. 6. (Cont.)

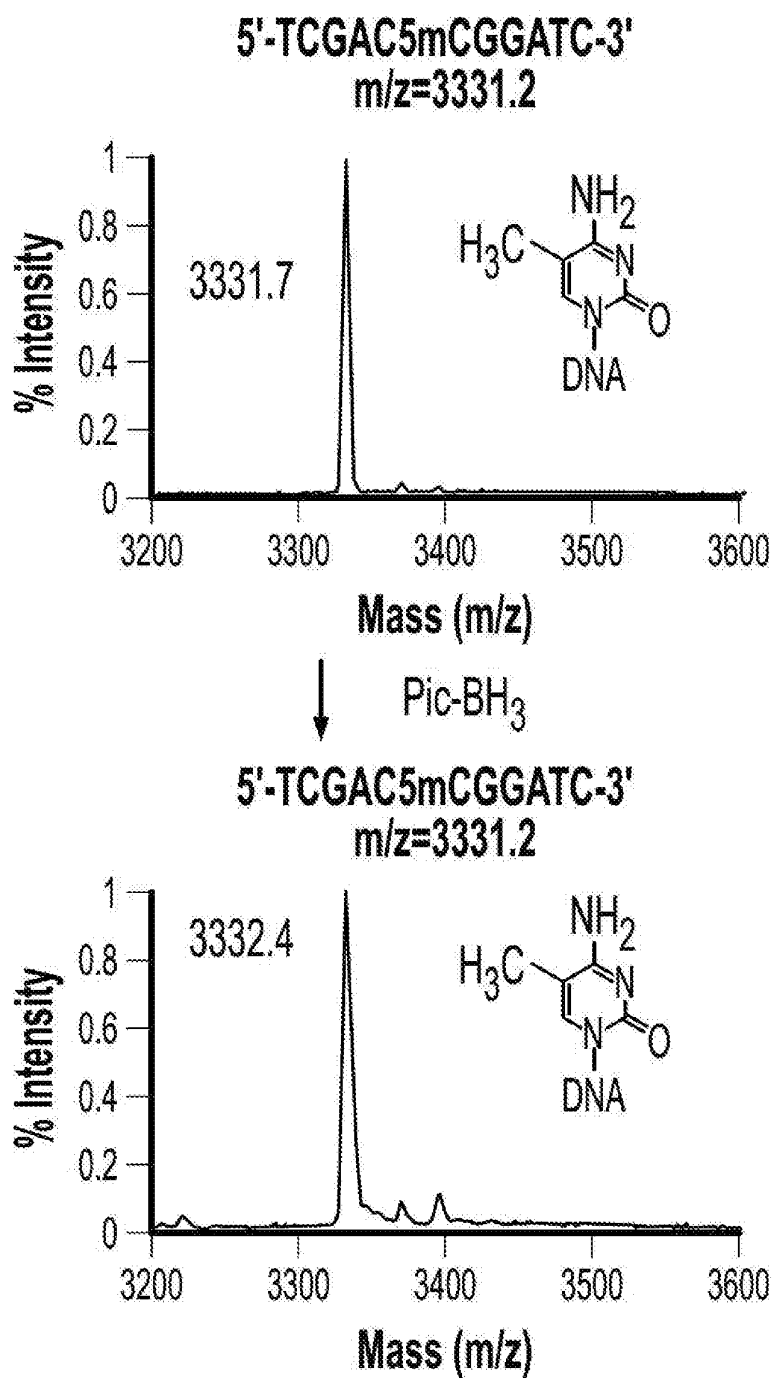


Fig. 7.

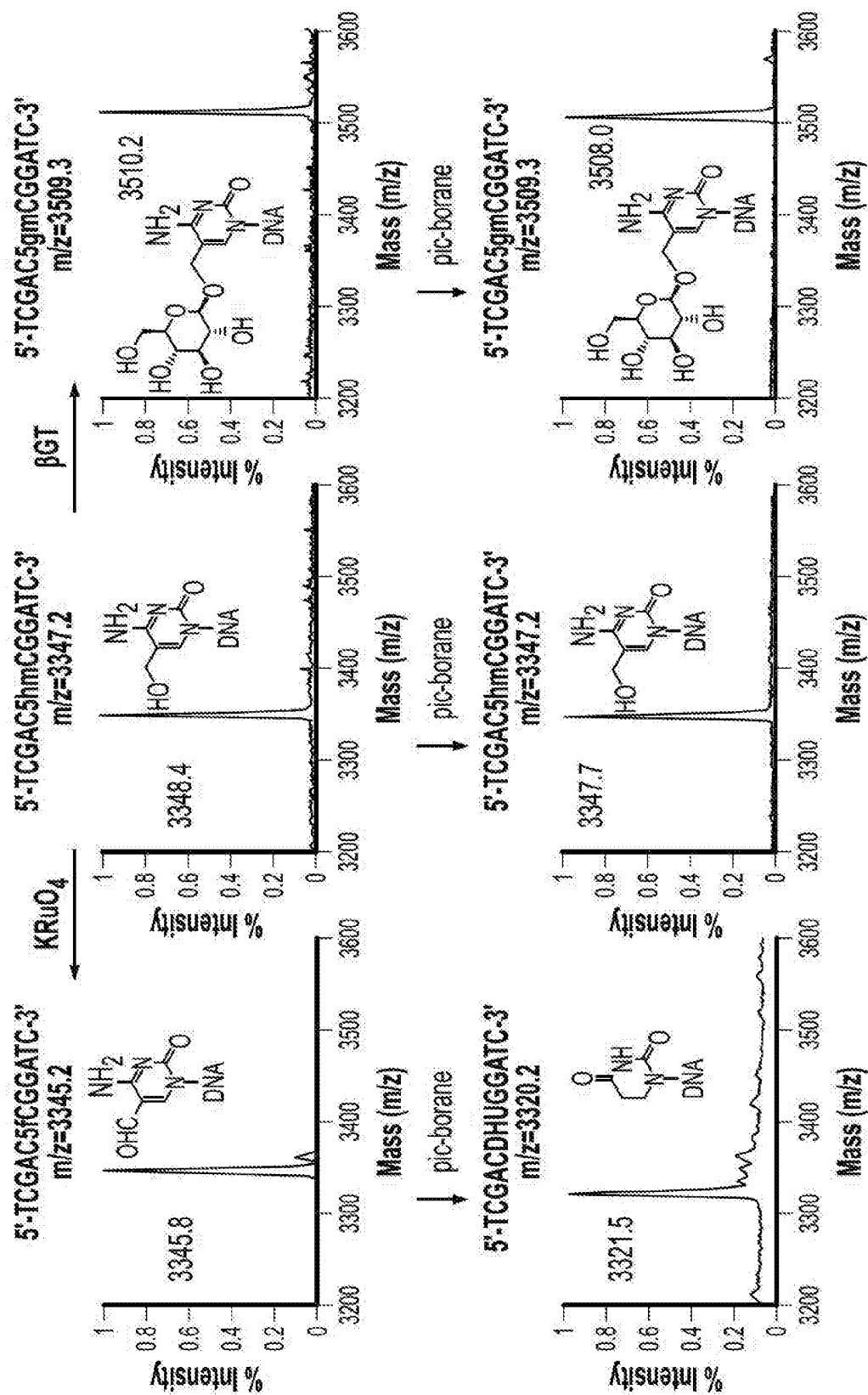
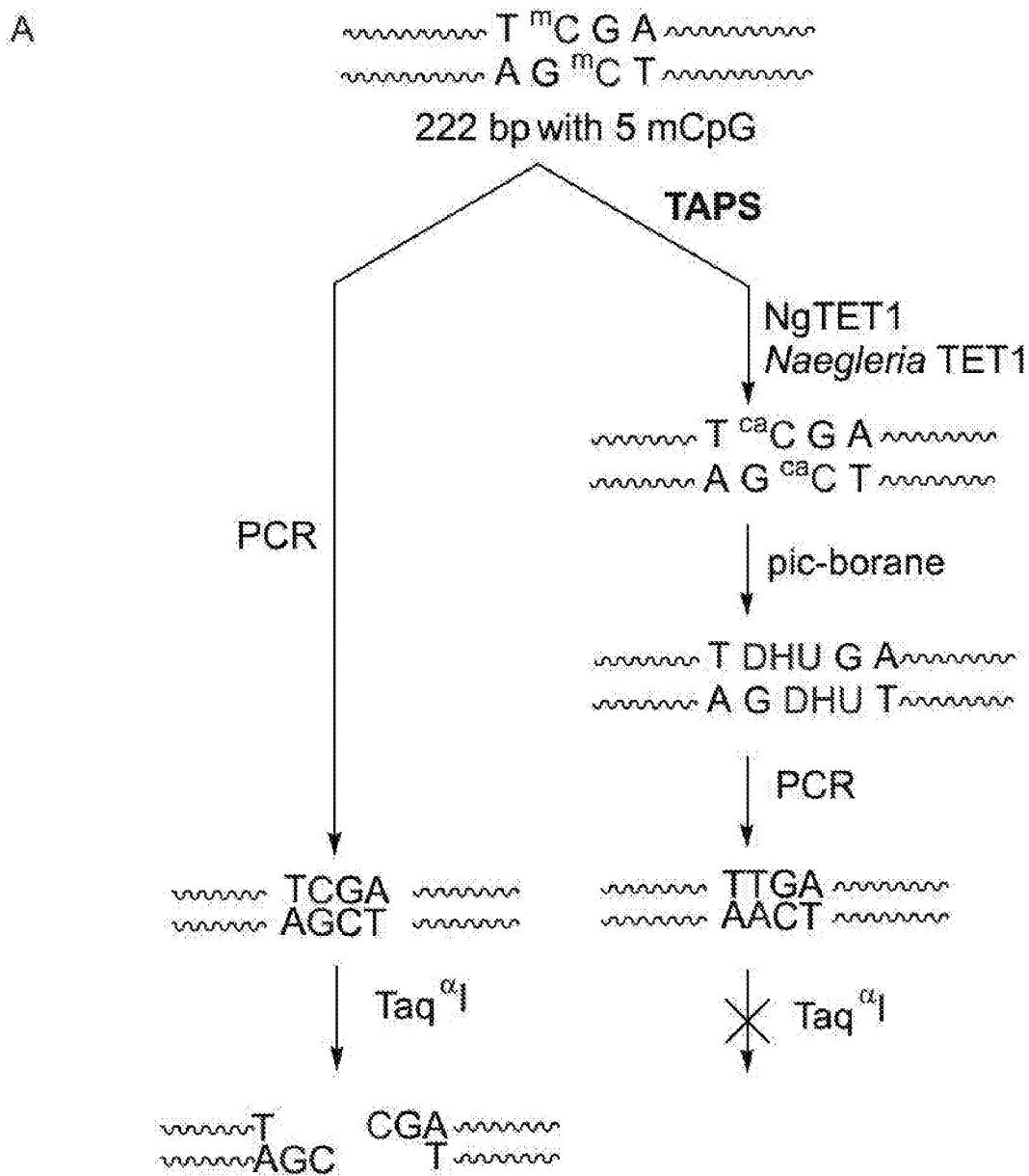


Fig. 7. (Cont.)



B

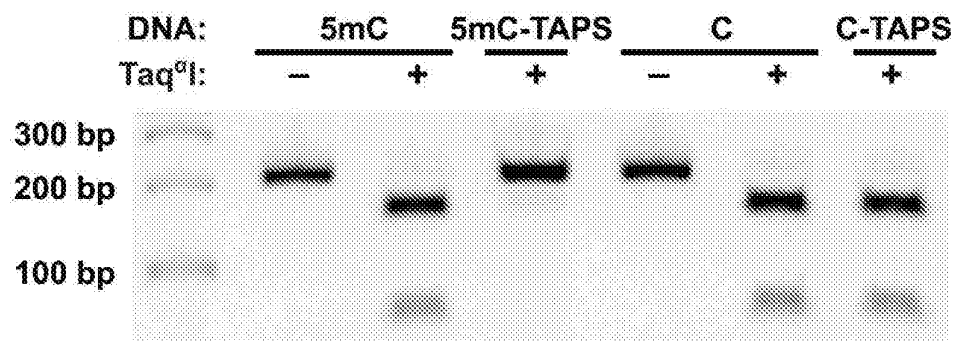
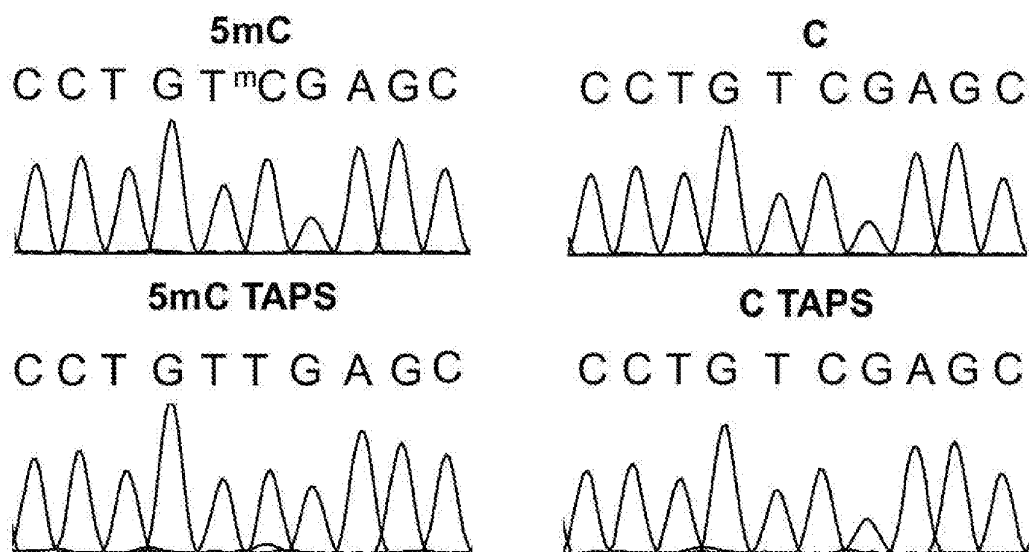
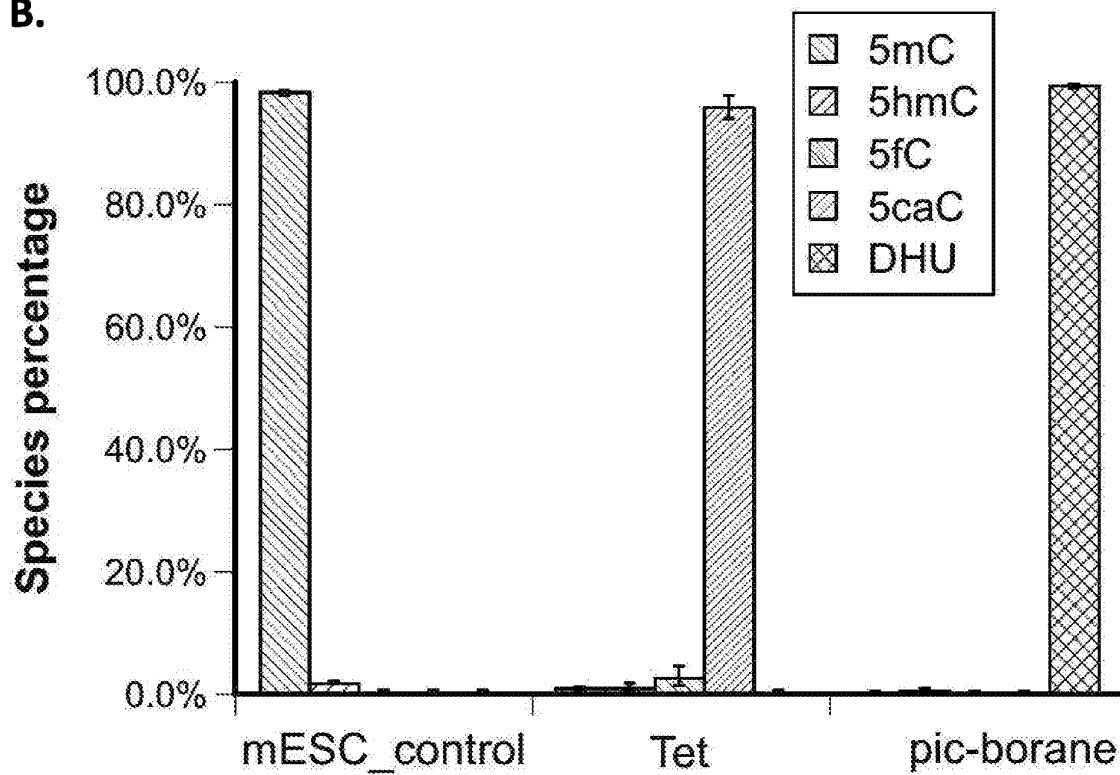


Fig. 8.

A.**B.****Fig. 9.**

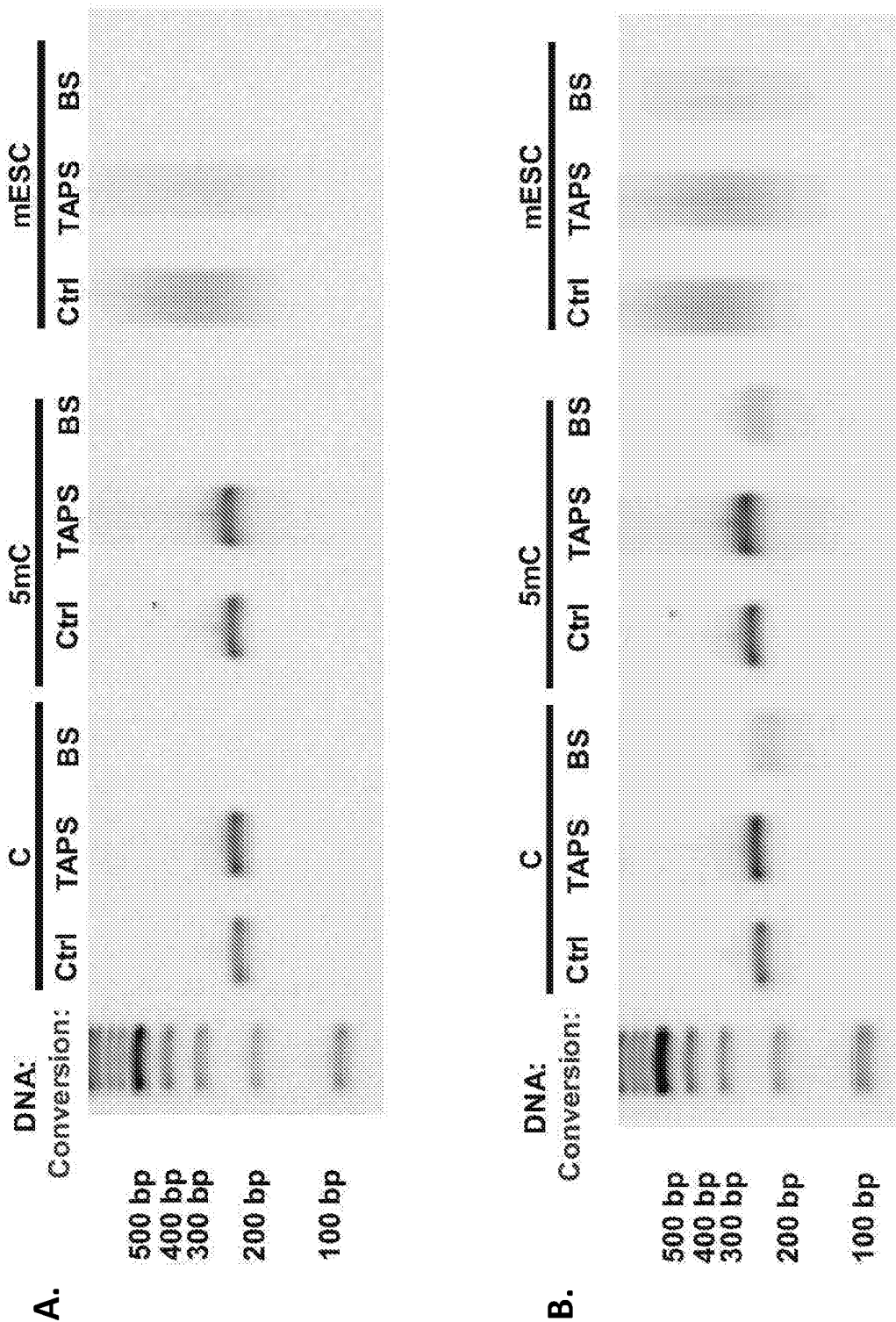


Fig. 10.

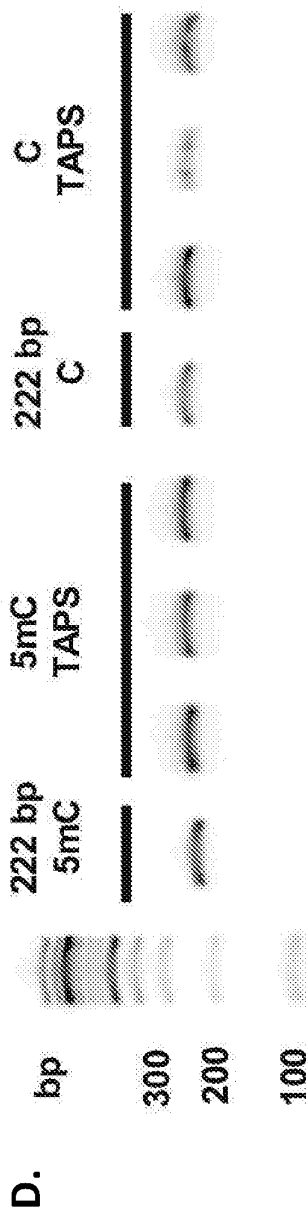
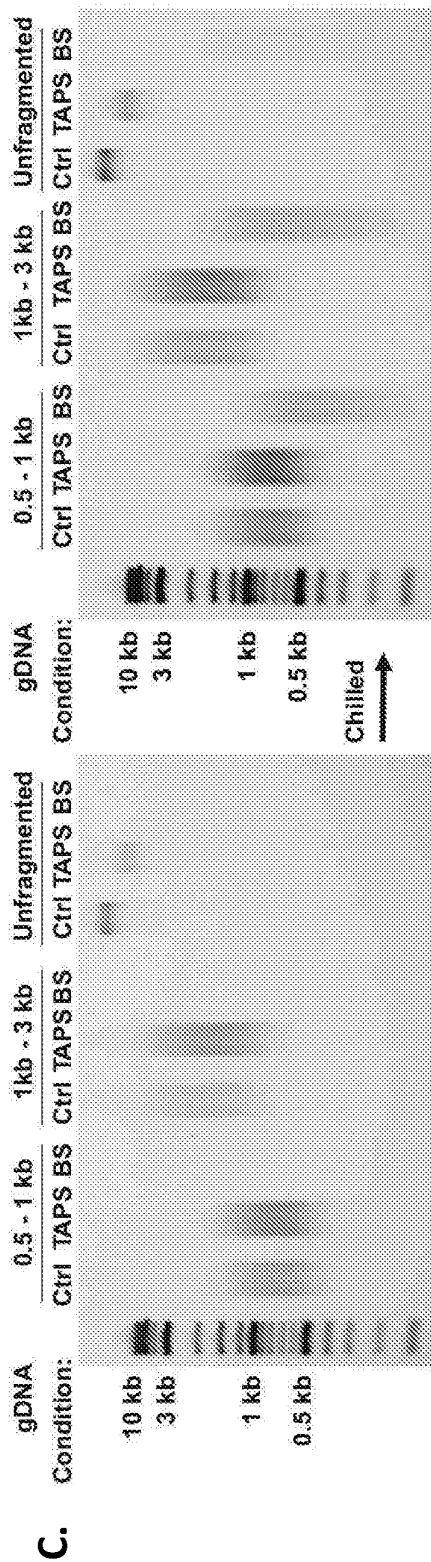


Fig. 10. (Cont.)

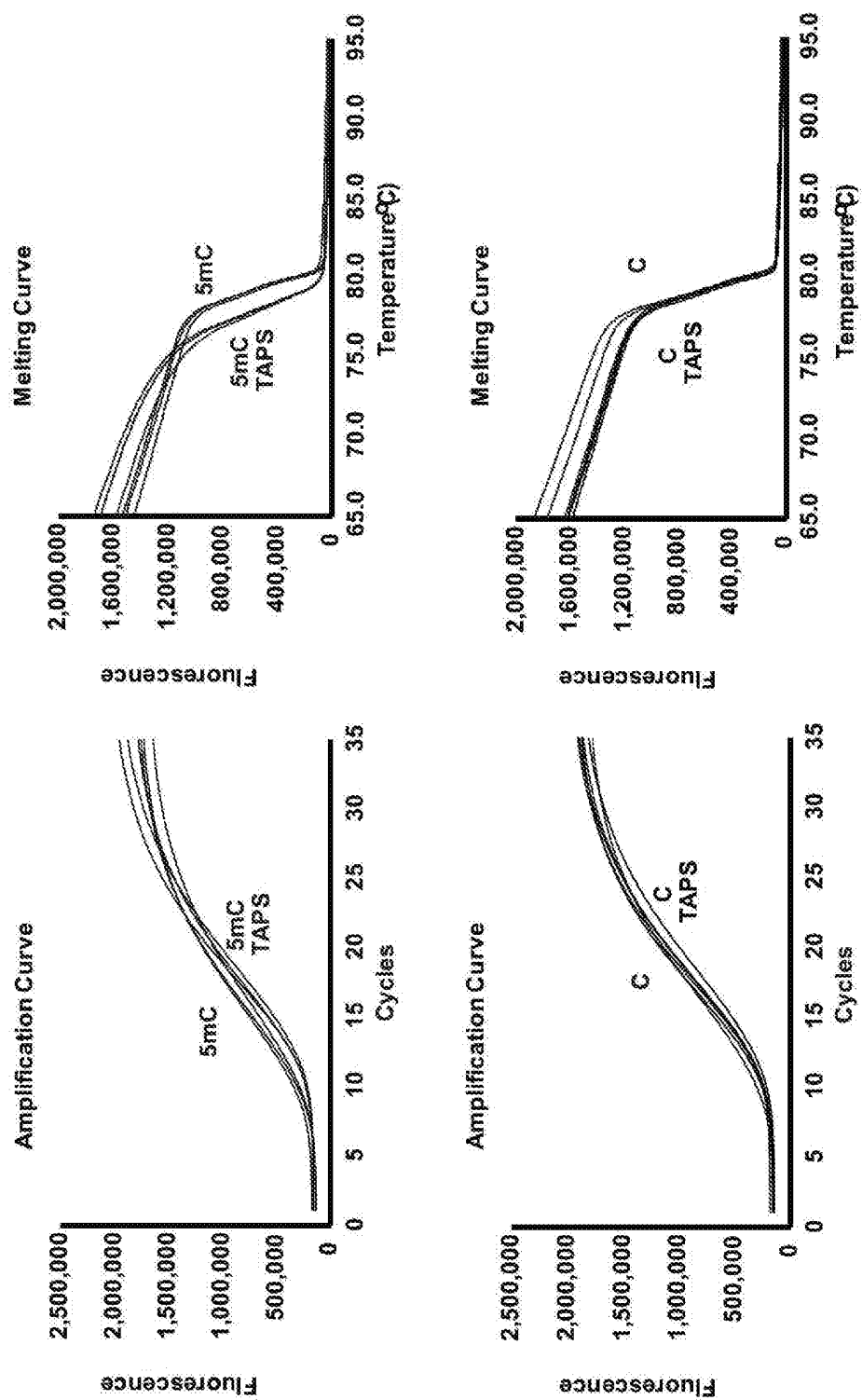


Fig. 11.

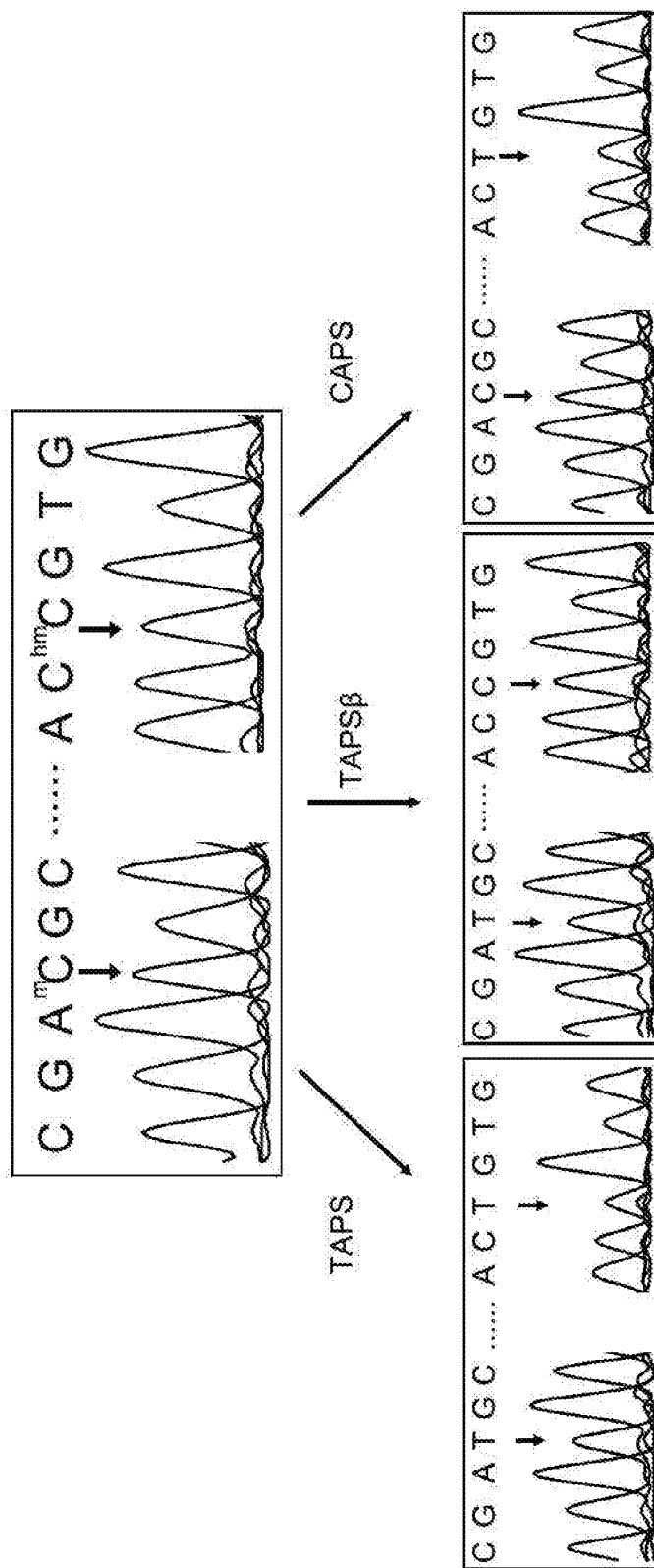


Fig. 12.

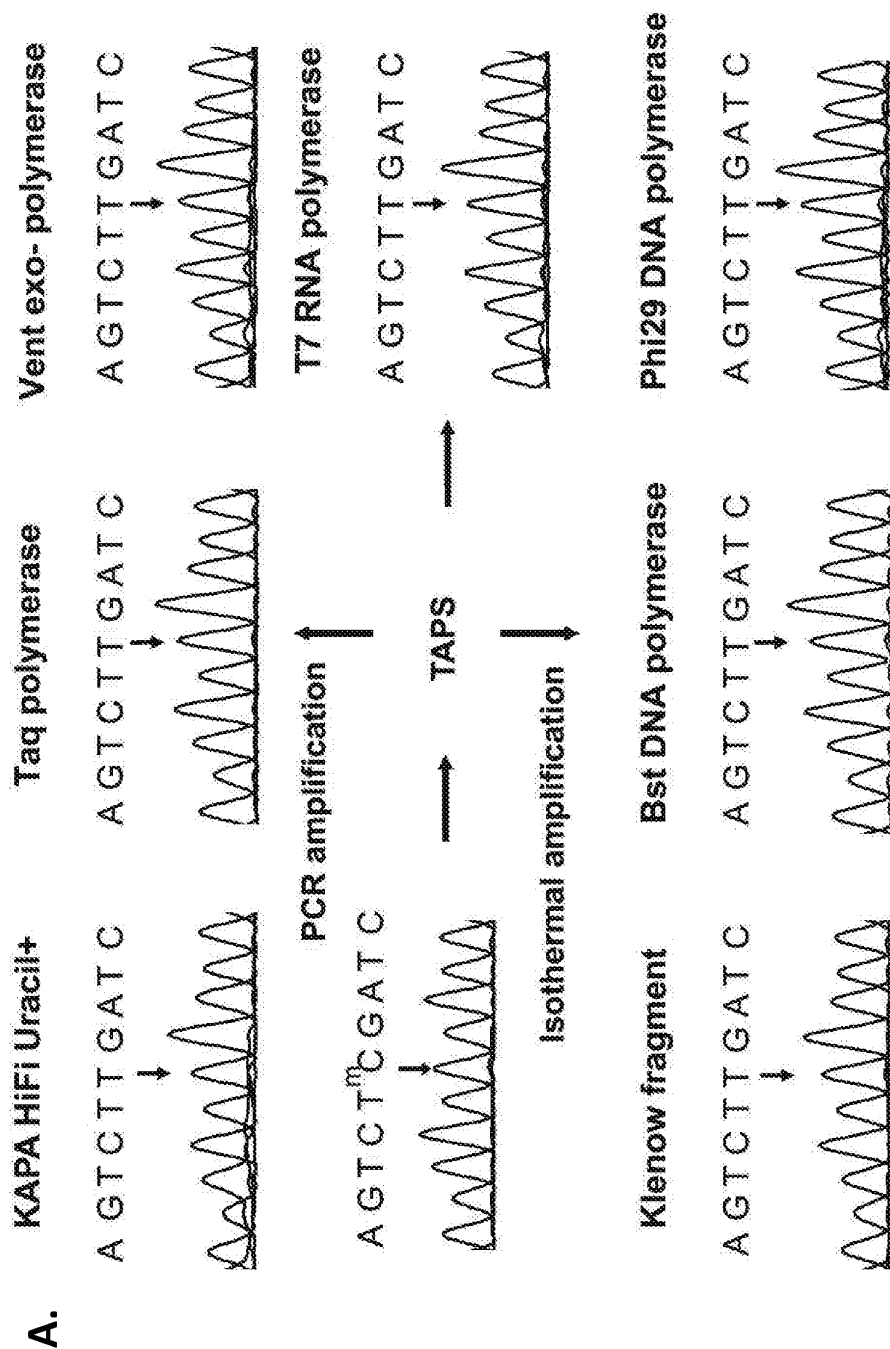


Fig. 13.

B.

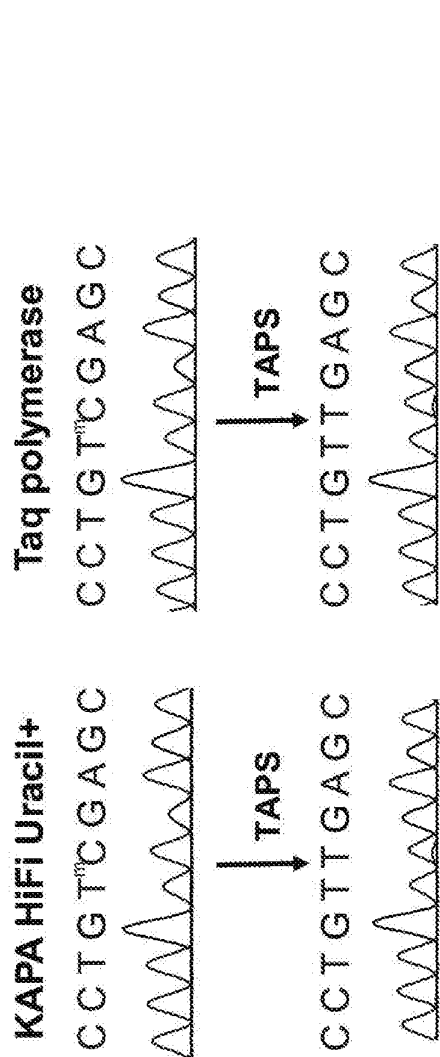
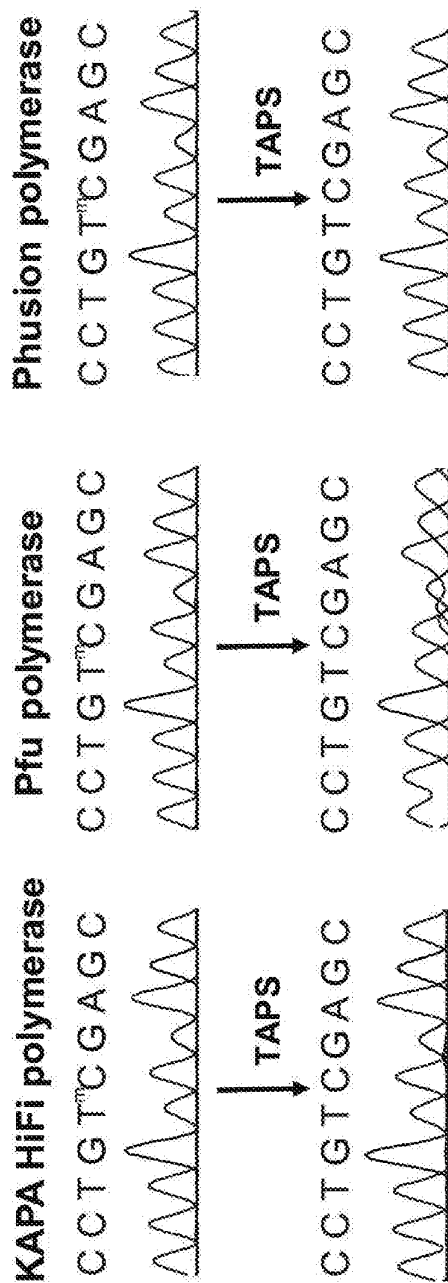
Complete
C-to-T transitionLow or no
C-to-T transition

Fig. 13. (Cont.)

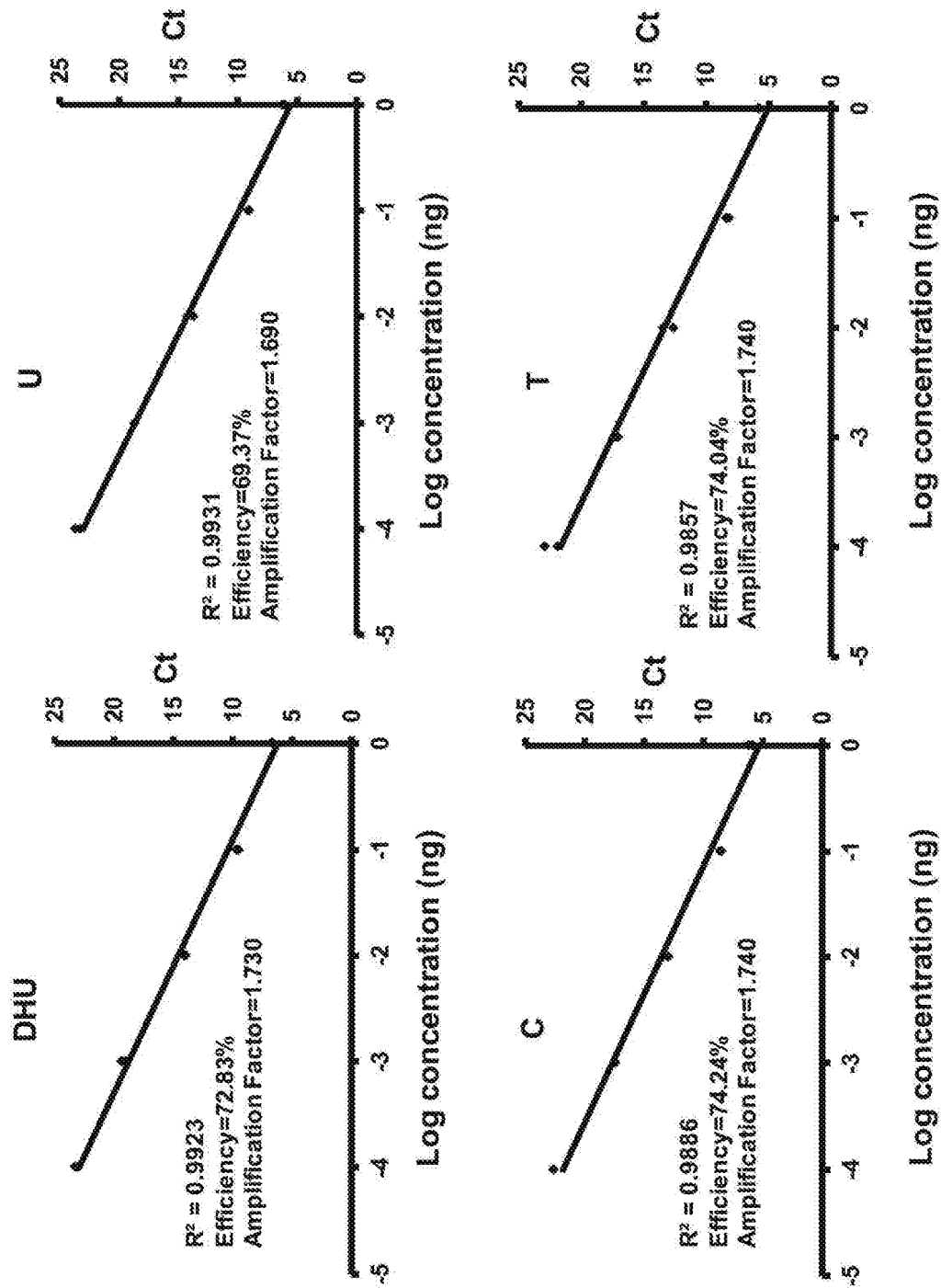
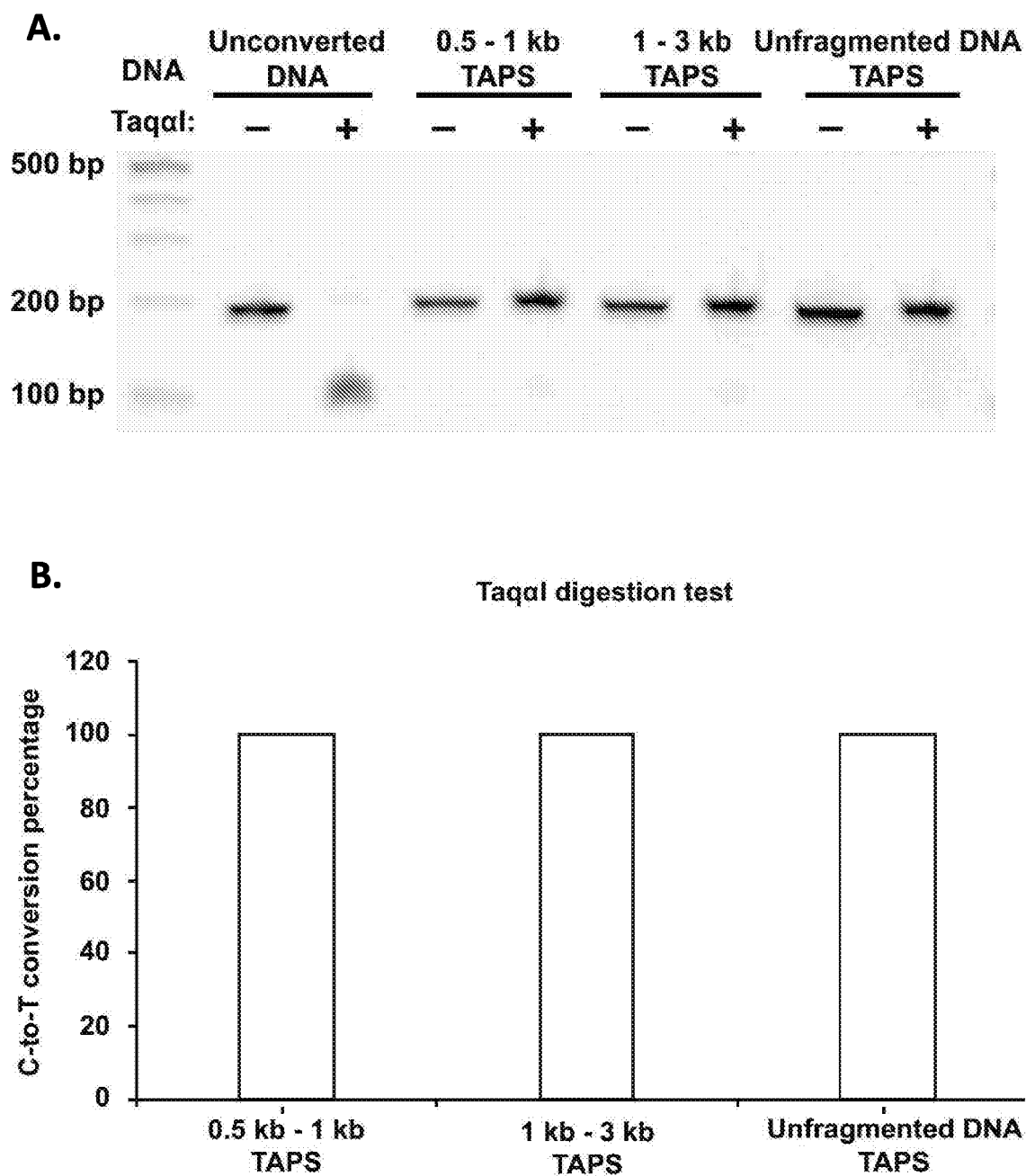
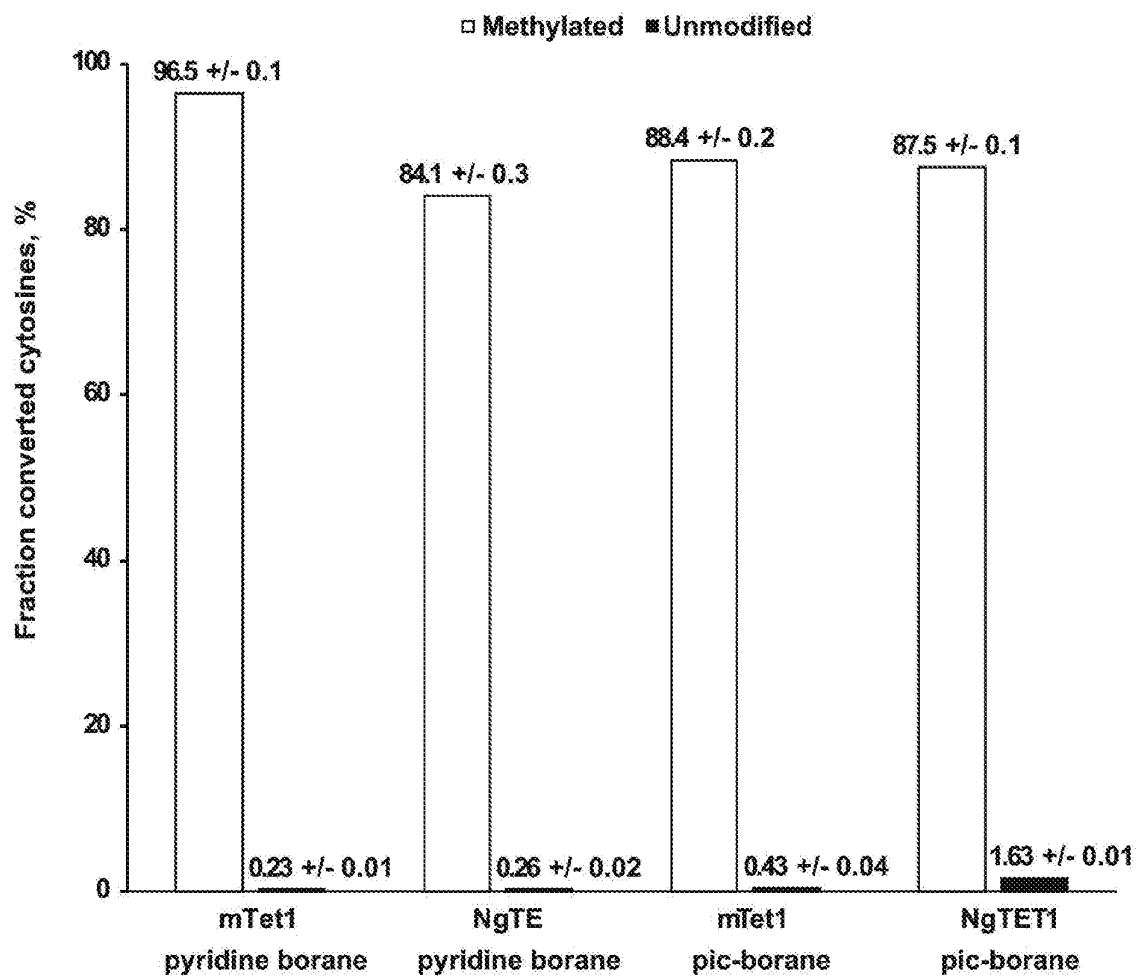


Fig. 14.

**Fig. 15.**

**Fig. 16.**

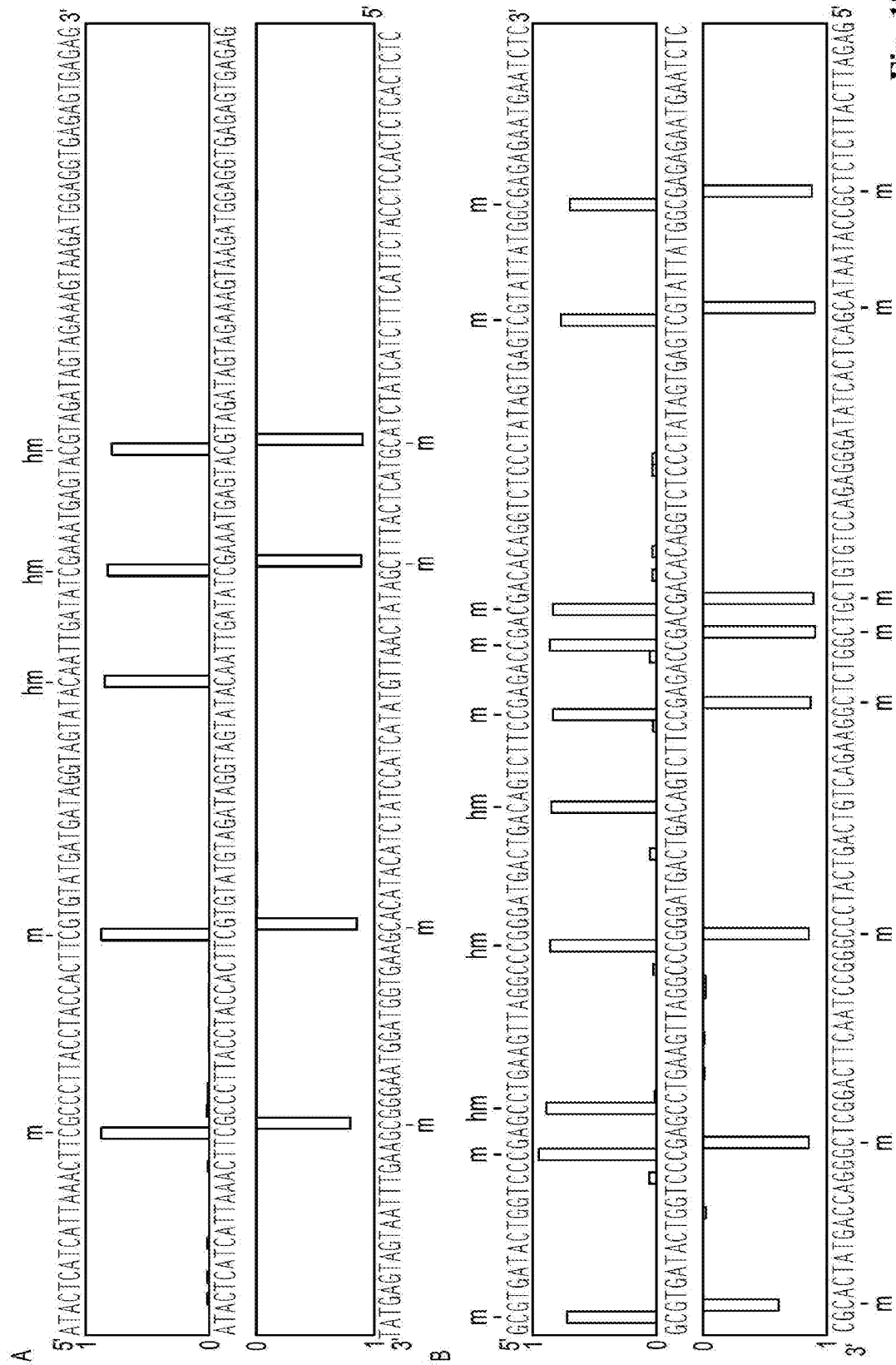
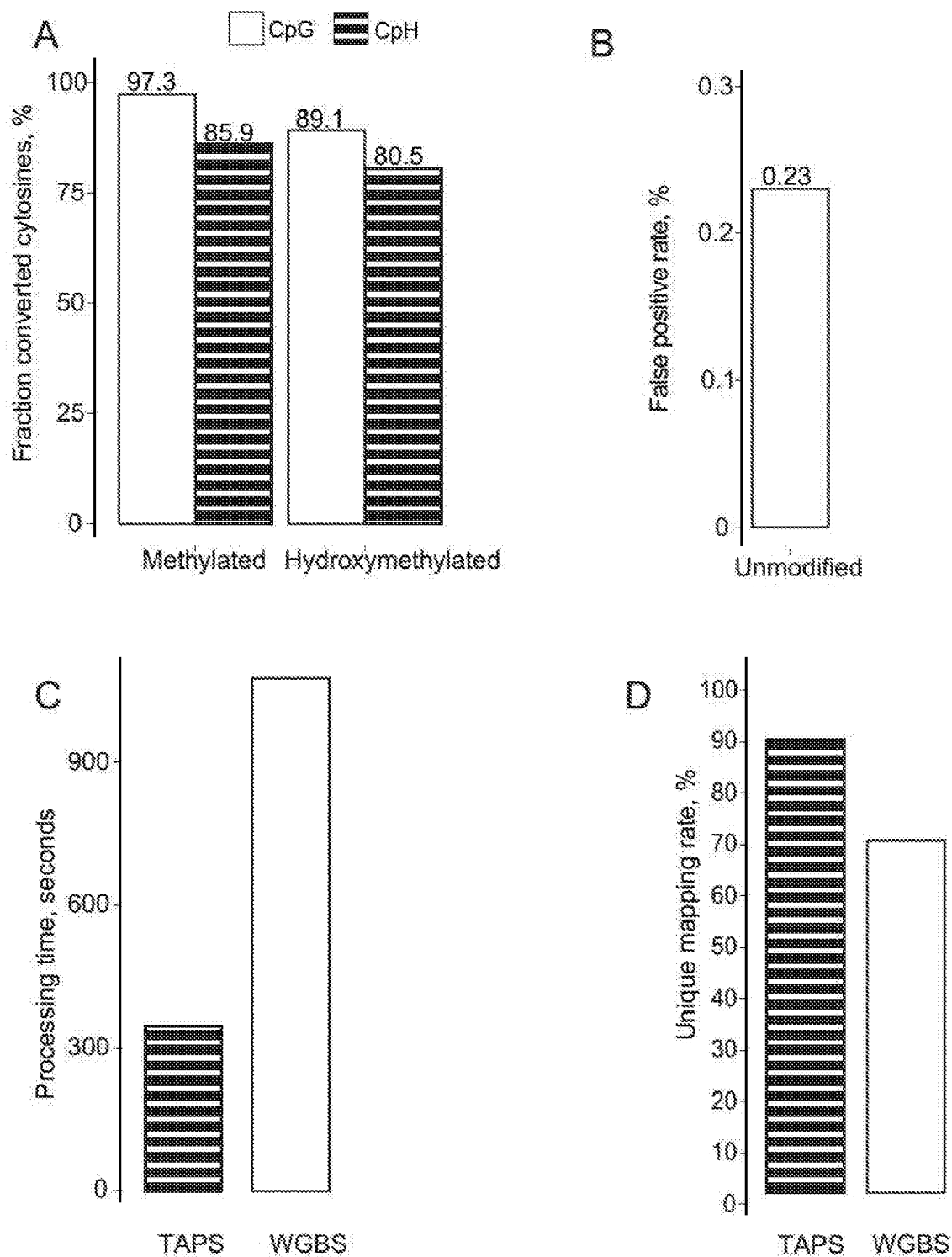
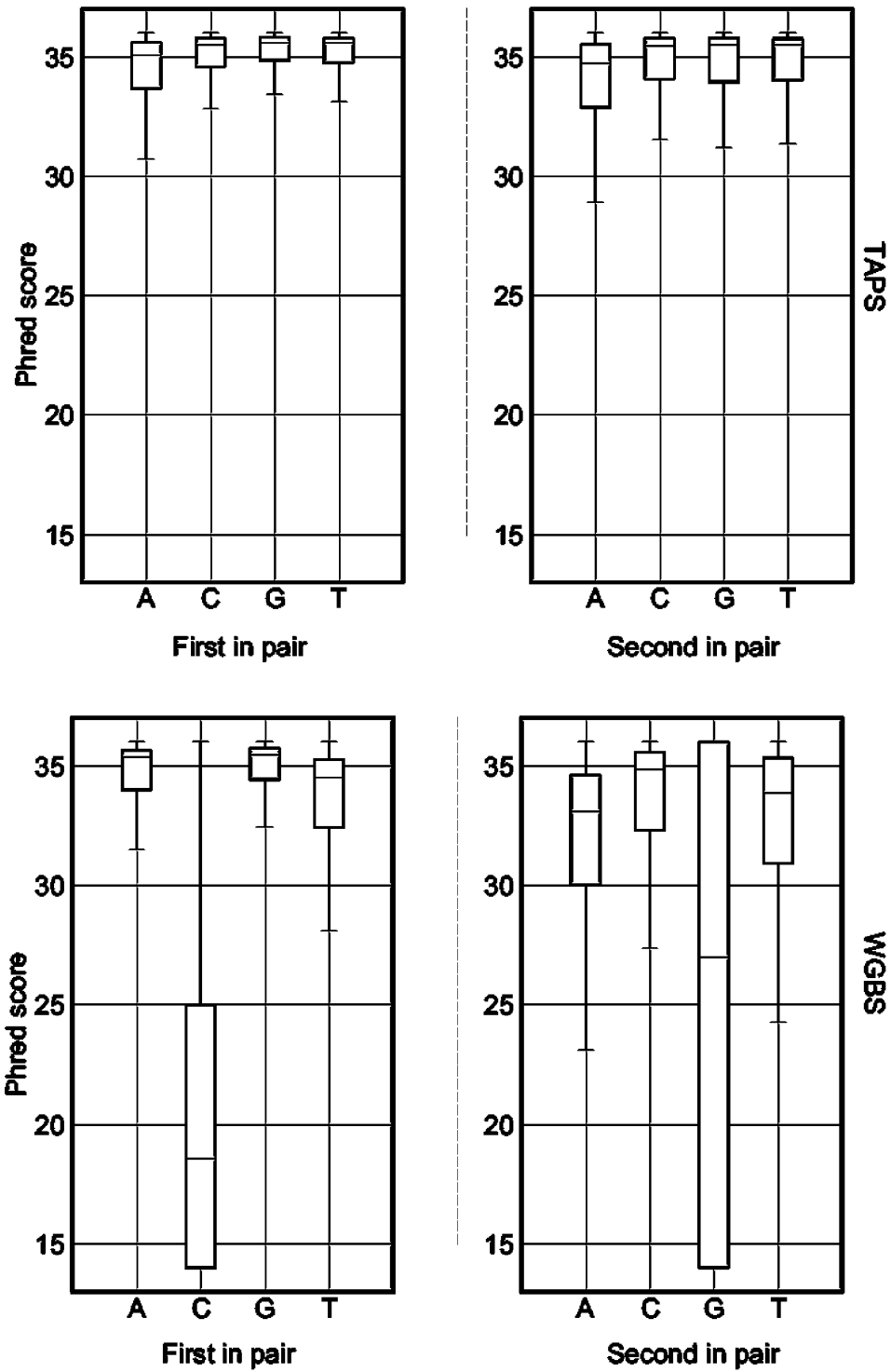


Fig. 17

**Fig. 18.**

E**Sequencing base quality****Fig. 18 (Cont.)**

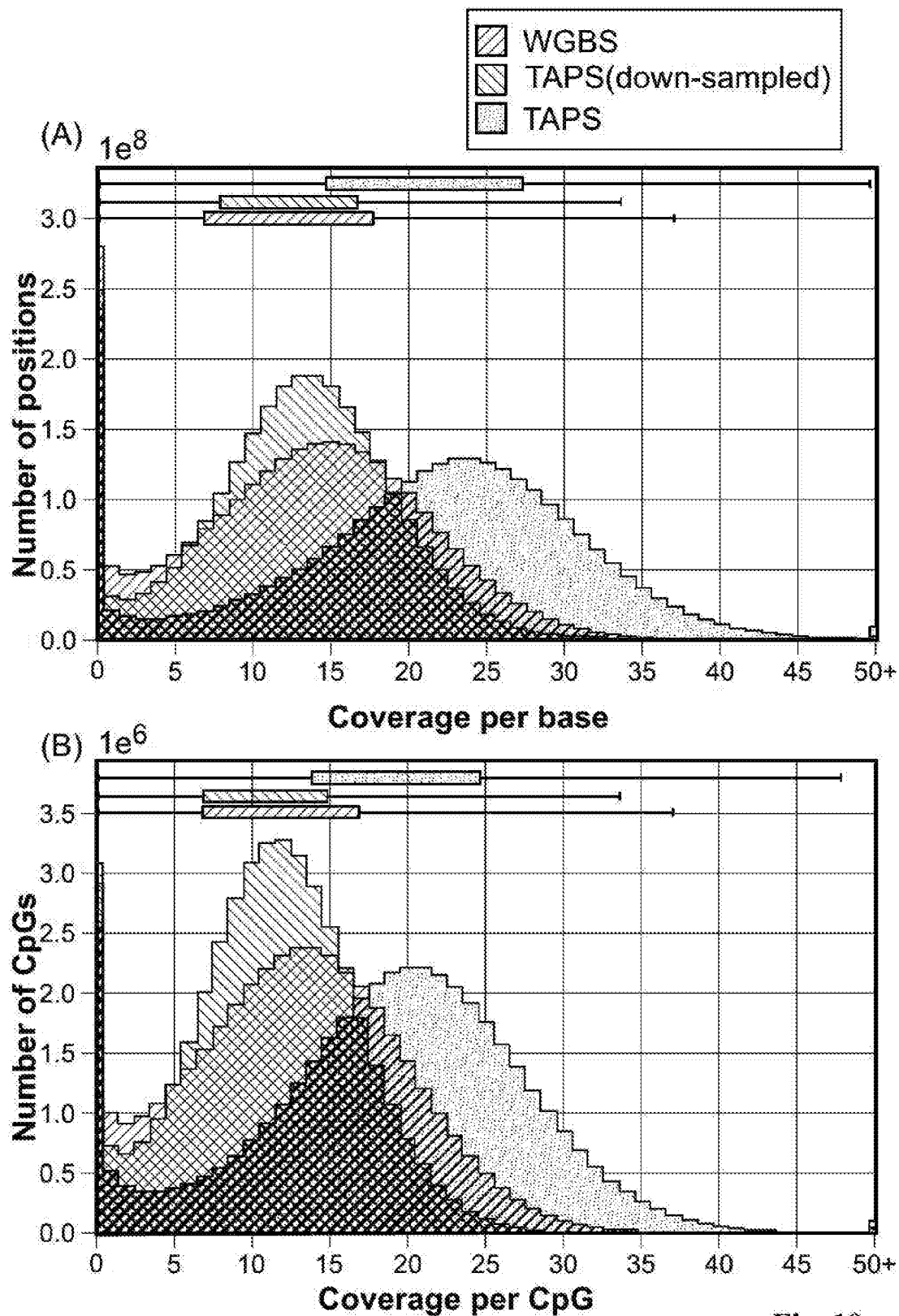


Fig. 19.

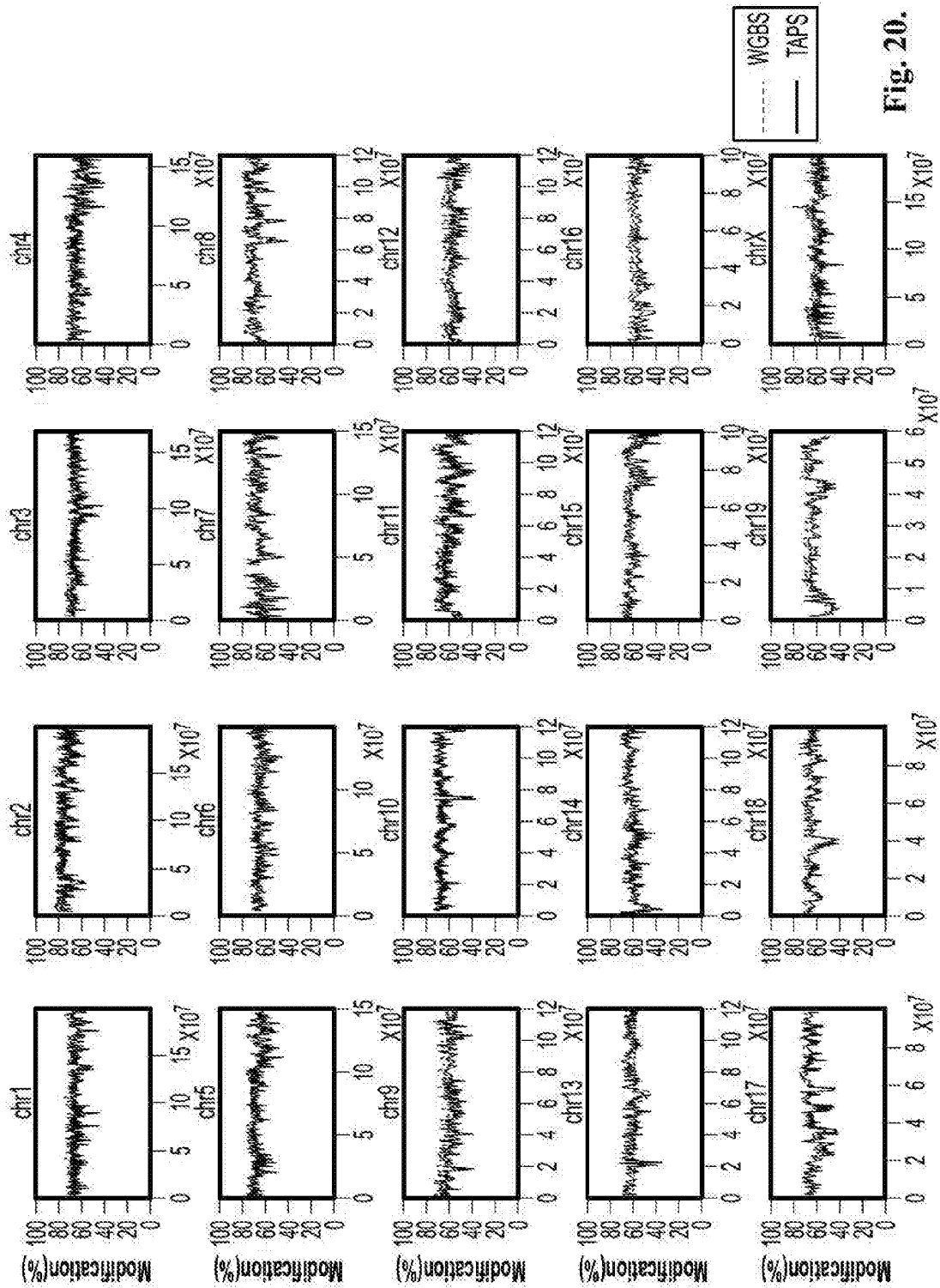
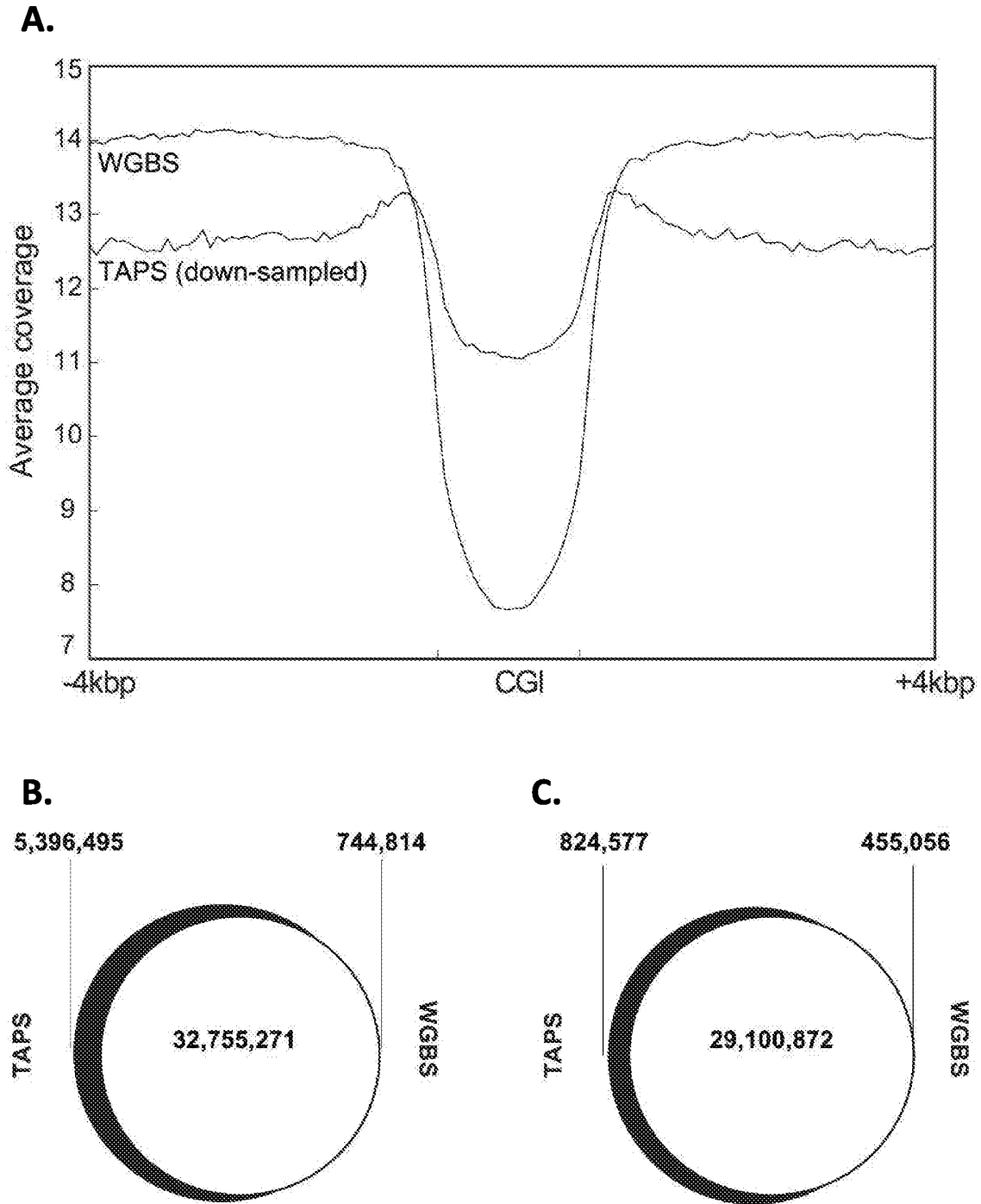


Fig. 20.

**Fig. 21.**

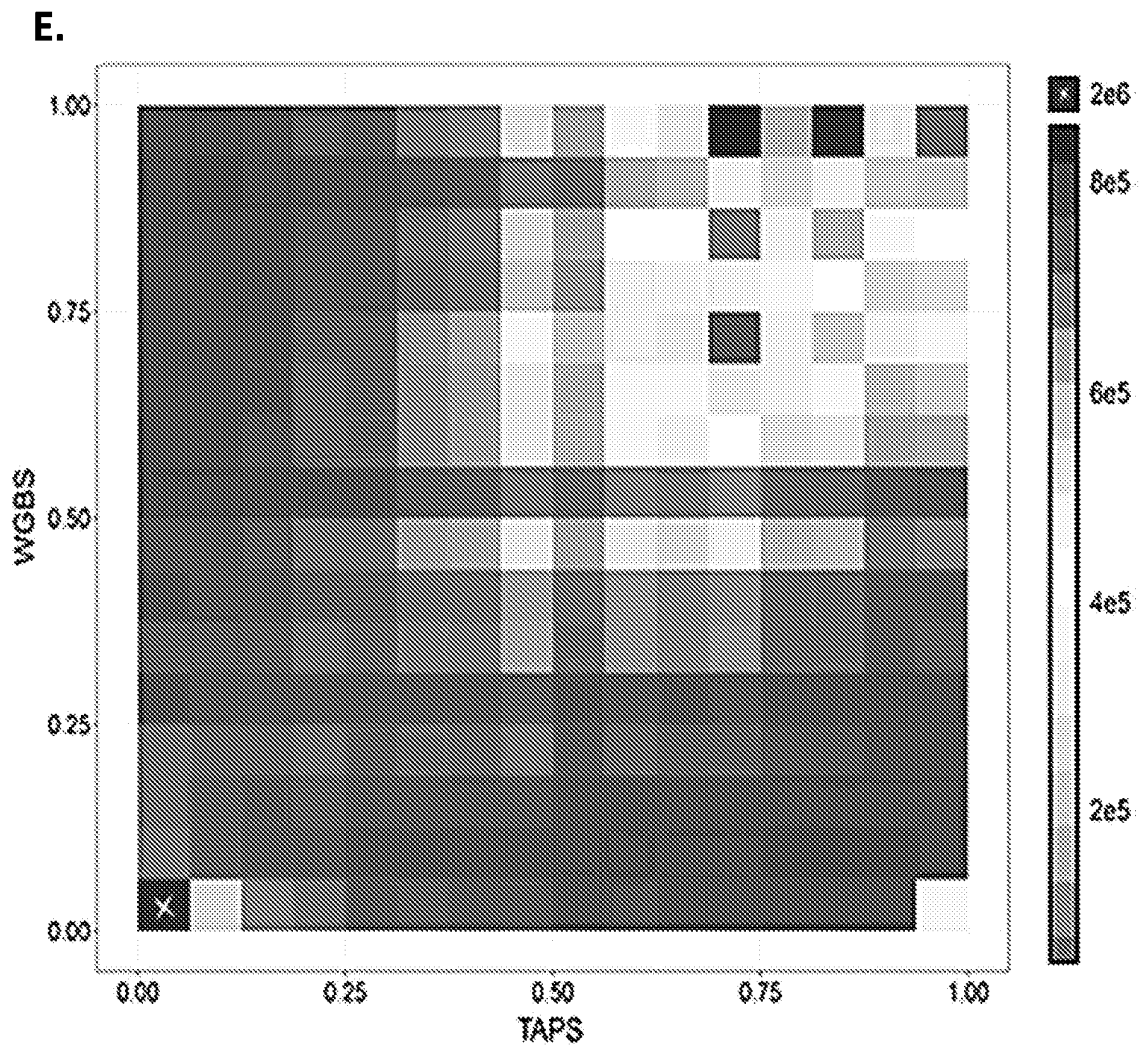
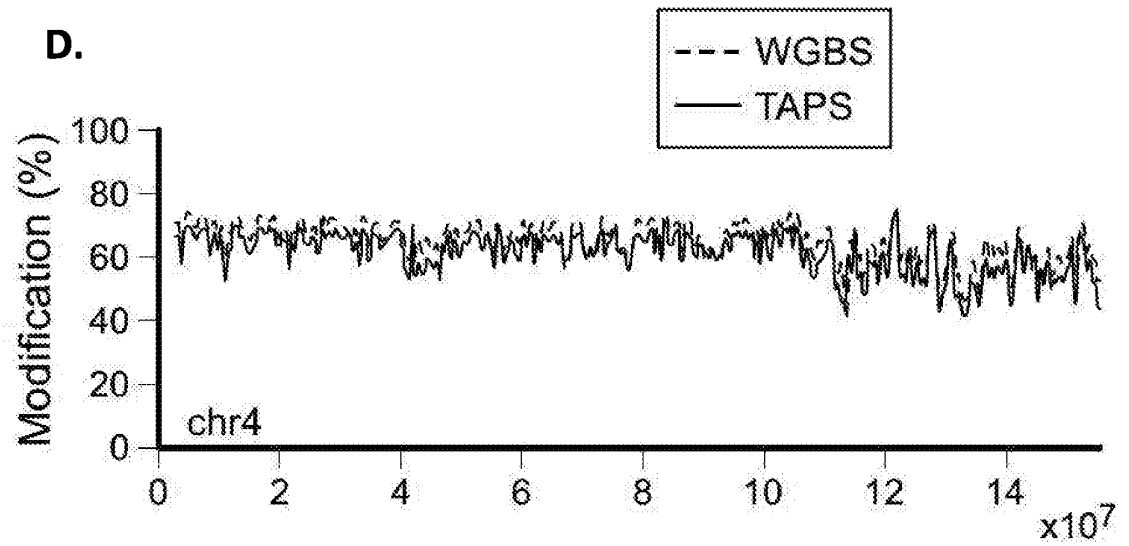
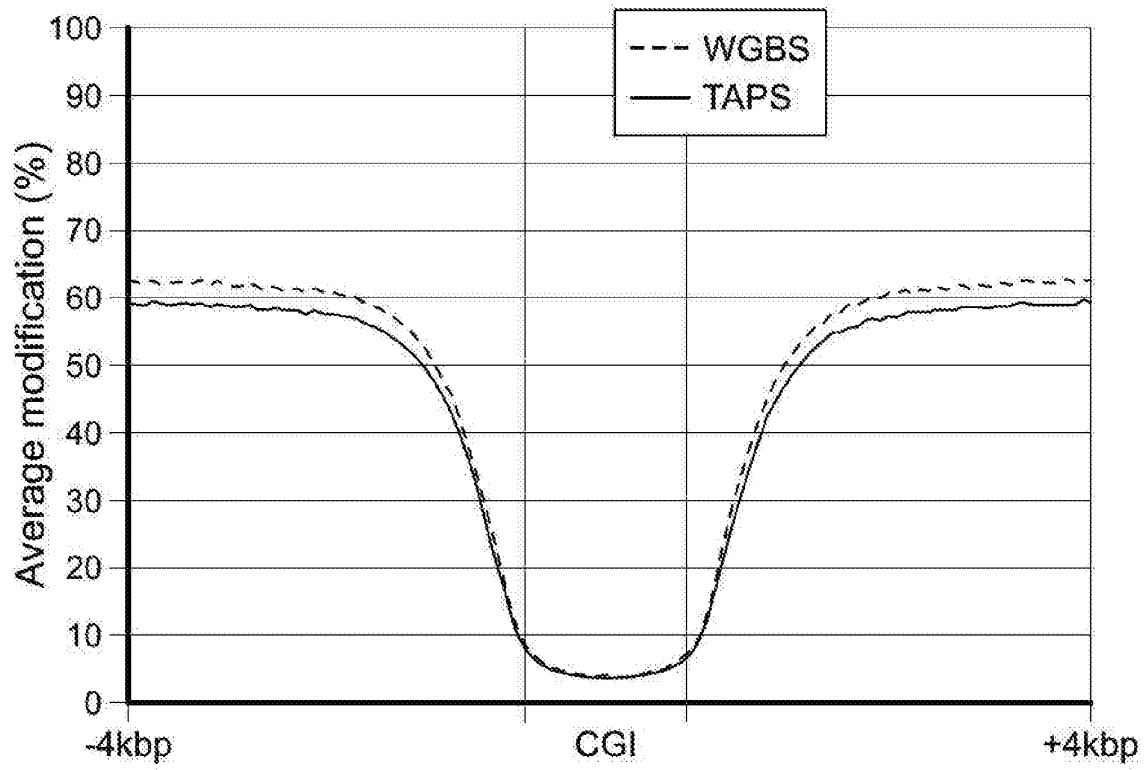
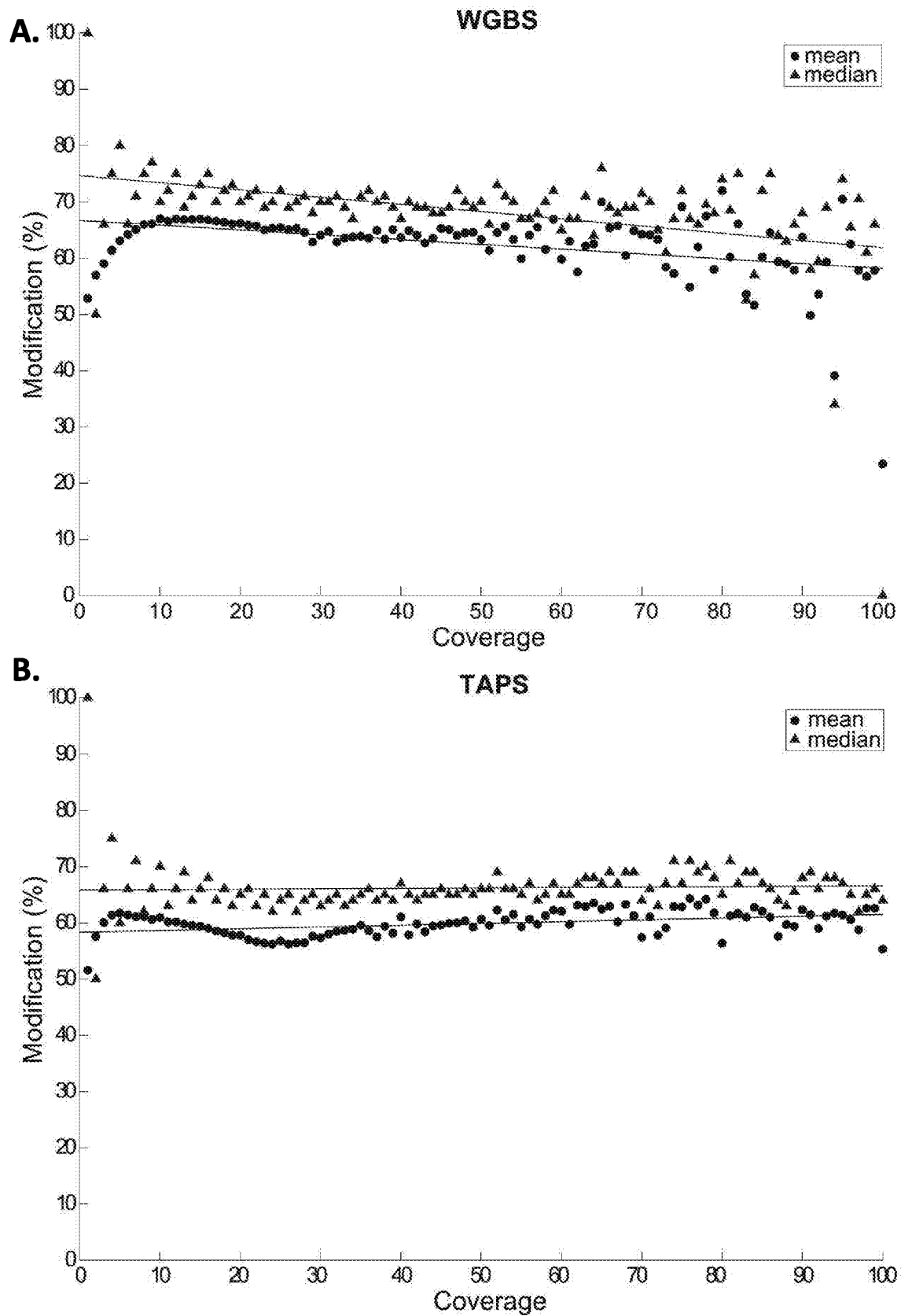


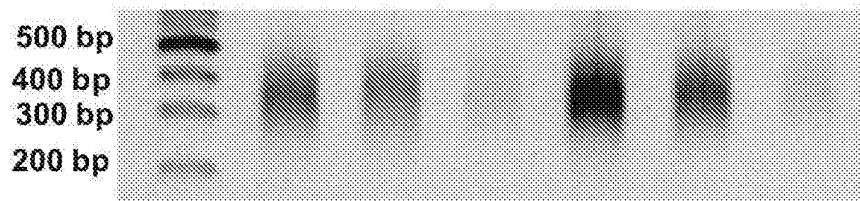
Fig. 21 (Cont.).

**Fig. 22.**

**Fig. 23.**

A**Library preparation kits for dsDNA**

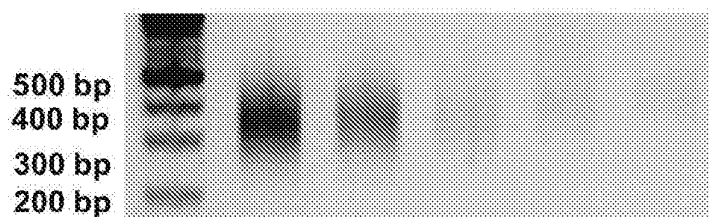
	<u>NEBNext Ultra II</u>			<u>KAPA HyperPlus</u>		
Input DNA (ng):	100	10	1	100	10	1



PCR cycles:	8	12	16	9	13	17
Library conc. in 10 μ L (nM):	68	43	15	120	75	15

B**Library preparation kit for ssDNA**

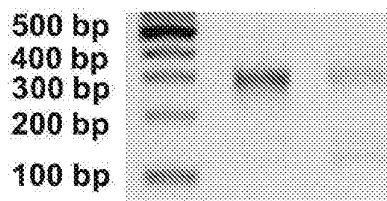
	<u>Accel-NGS Methyl-Seq</u>				
Input DNA (ng):	100	10	1	0.1	0.01



PCR cycles:	6	9	13	16	21
Library conc. in 10 μ L (nM):	42	22	6.9	6.1	4.9

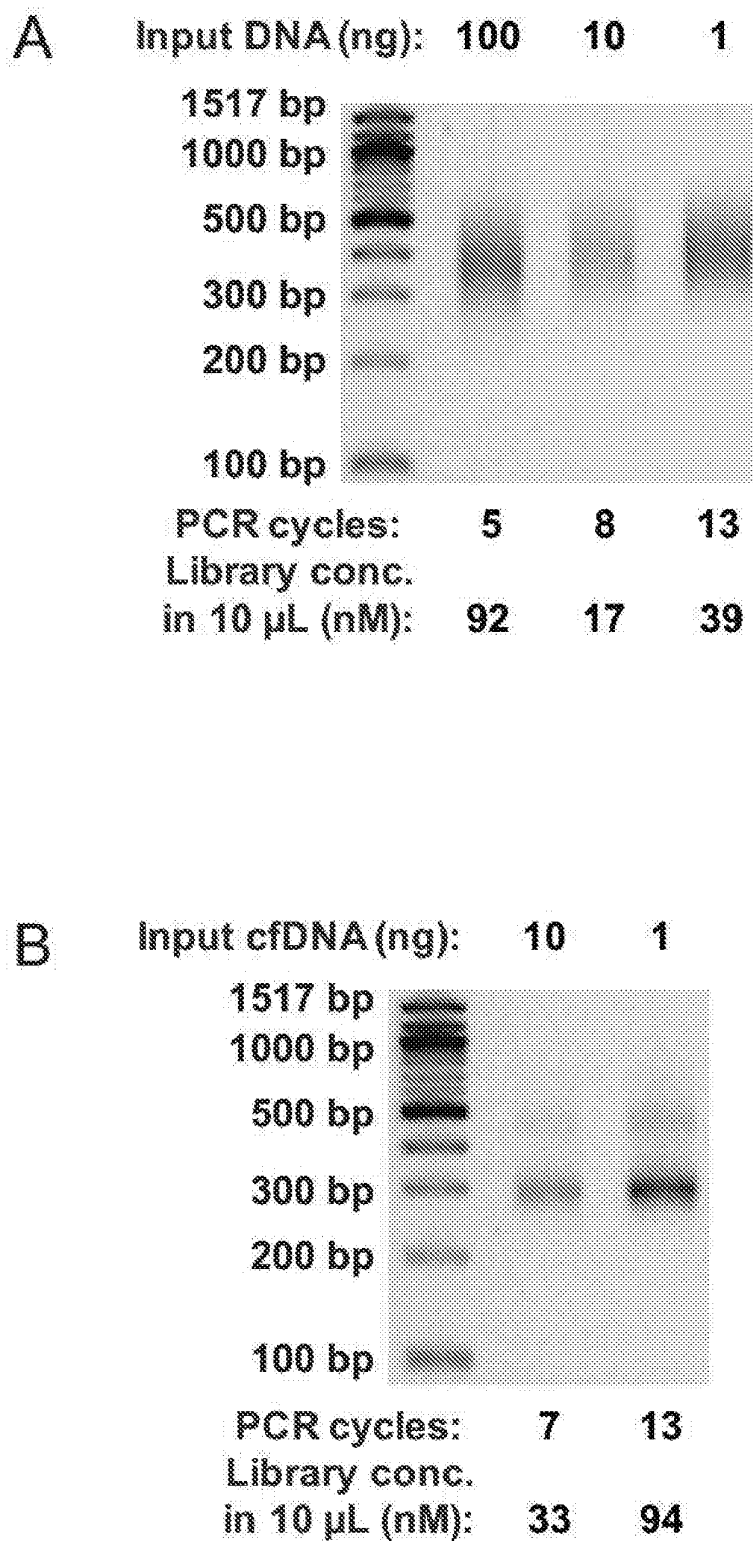
C

Input cfDNA (ng):	10	1
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PCR cycles:	9	13
Library conc. in 10 μ L (nM):	23	13

Fig. 24.

**Fig. 25.**

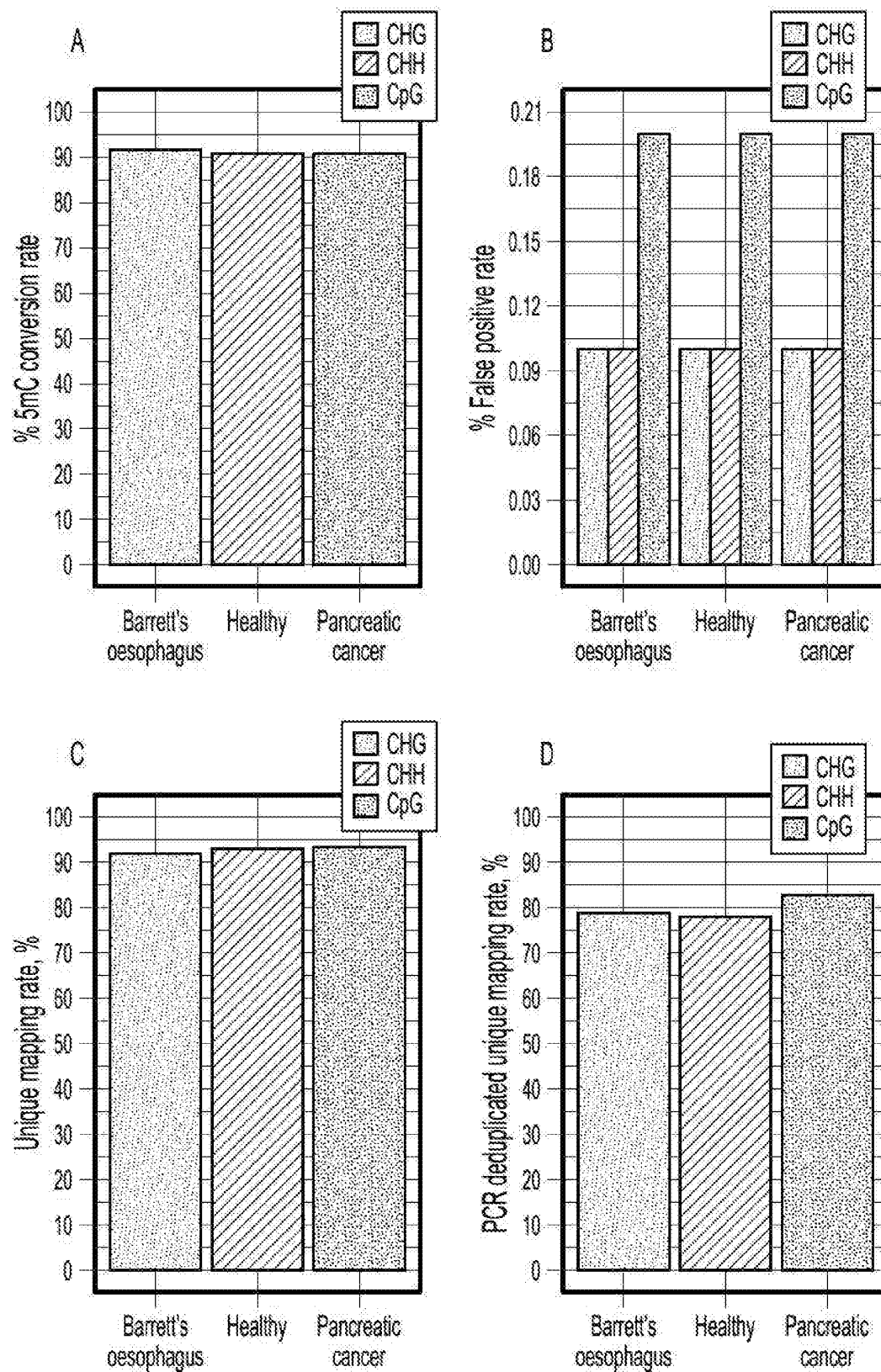


Fig. 26.

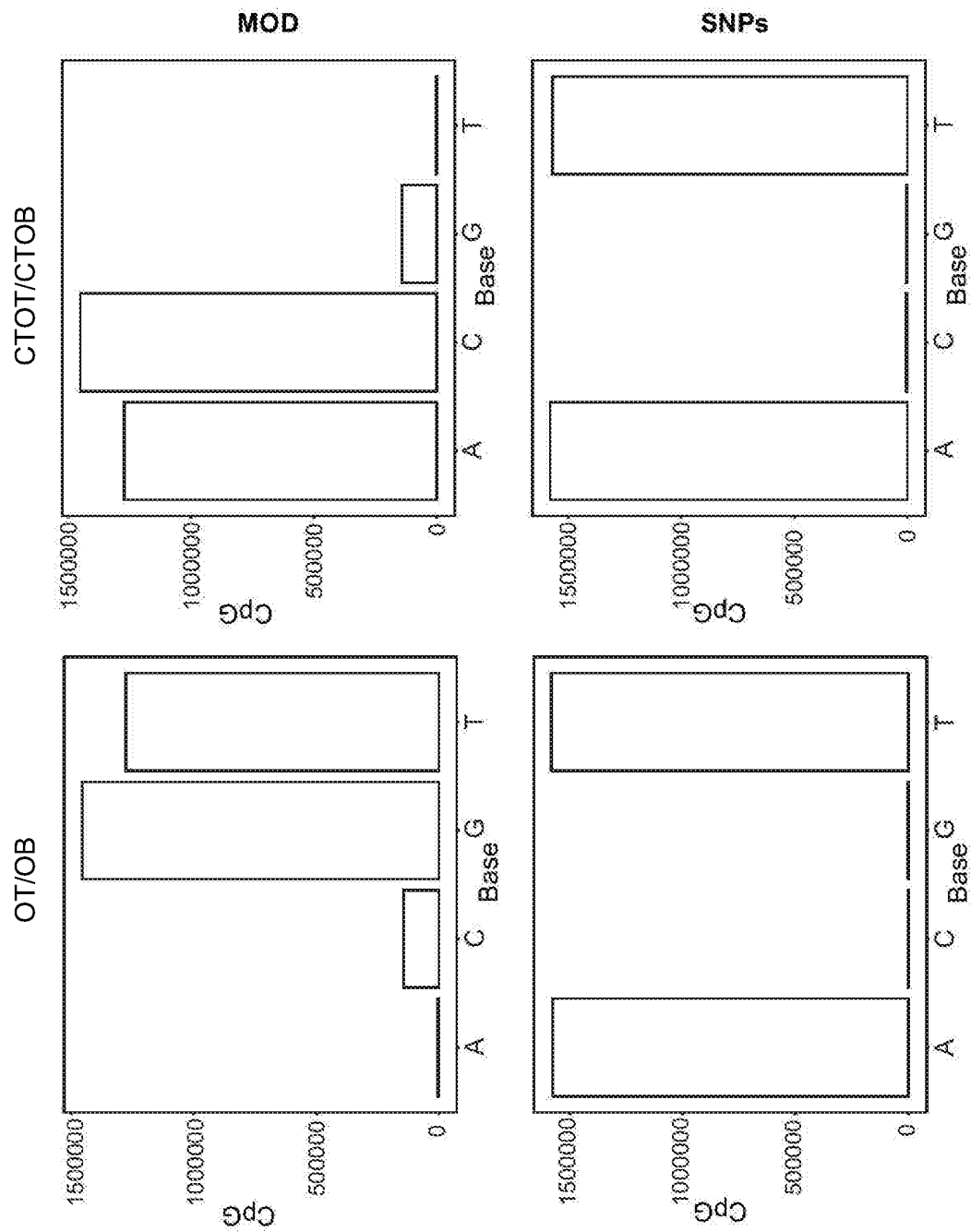


Fig. 27.