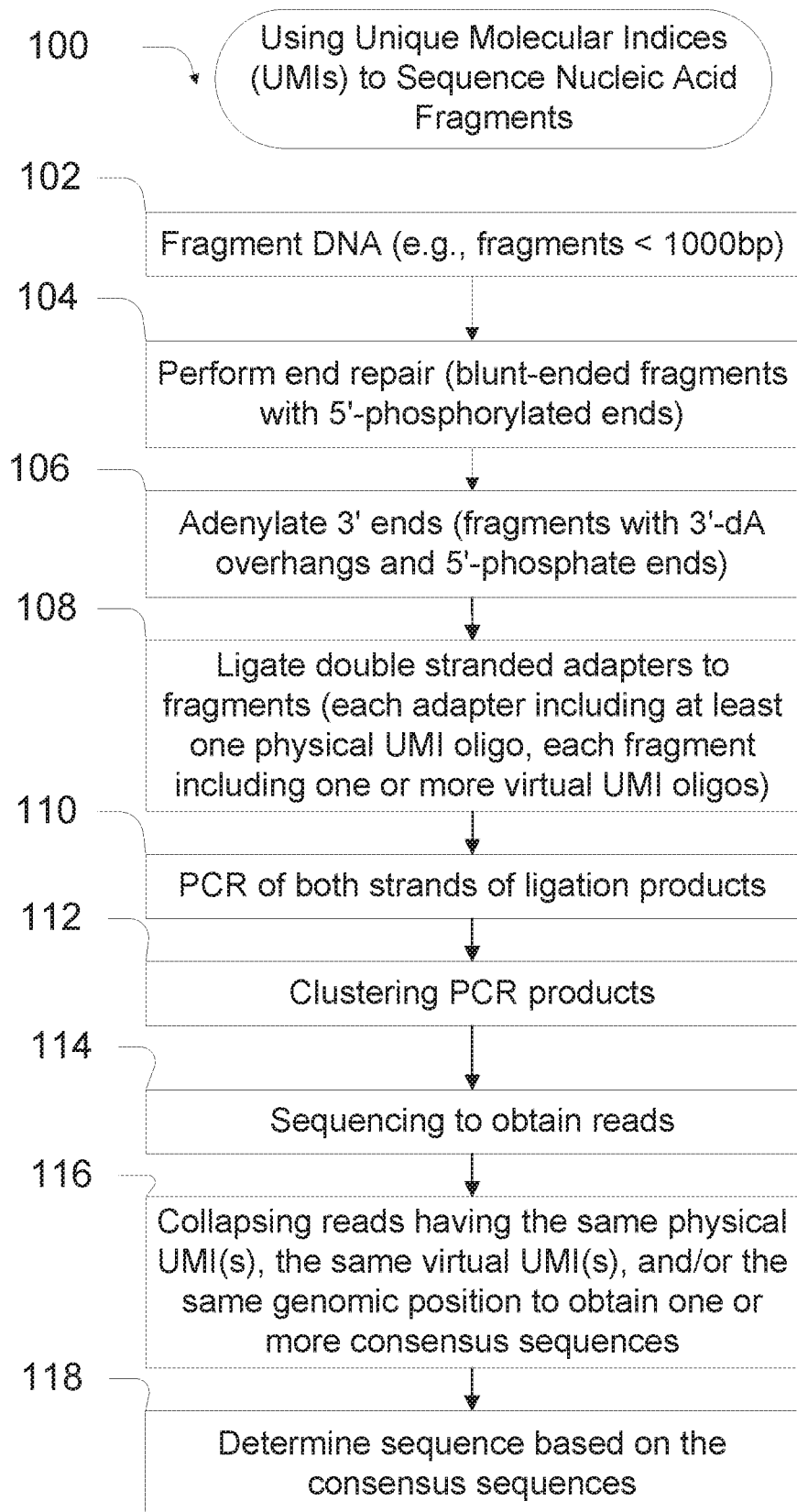


**Figure 1A**

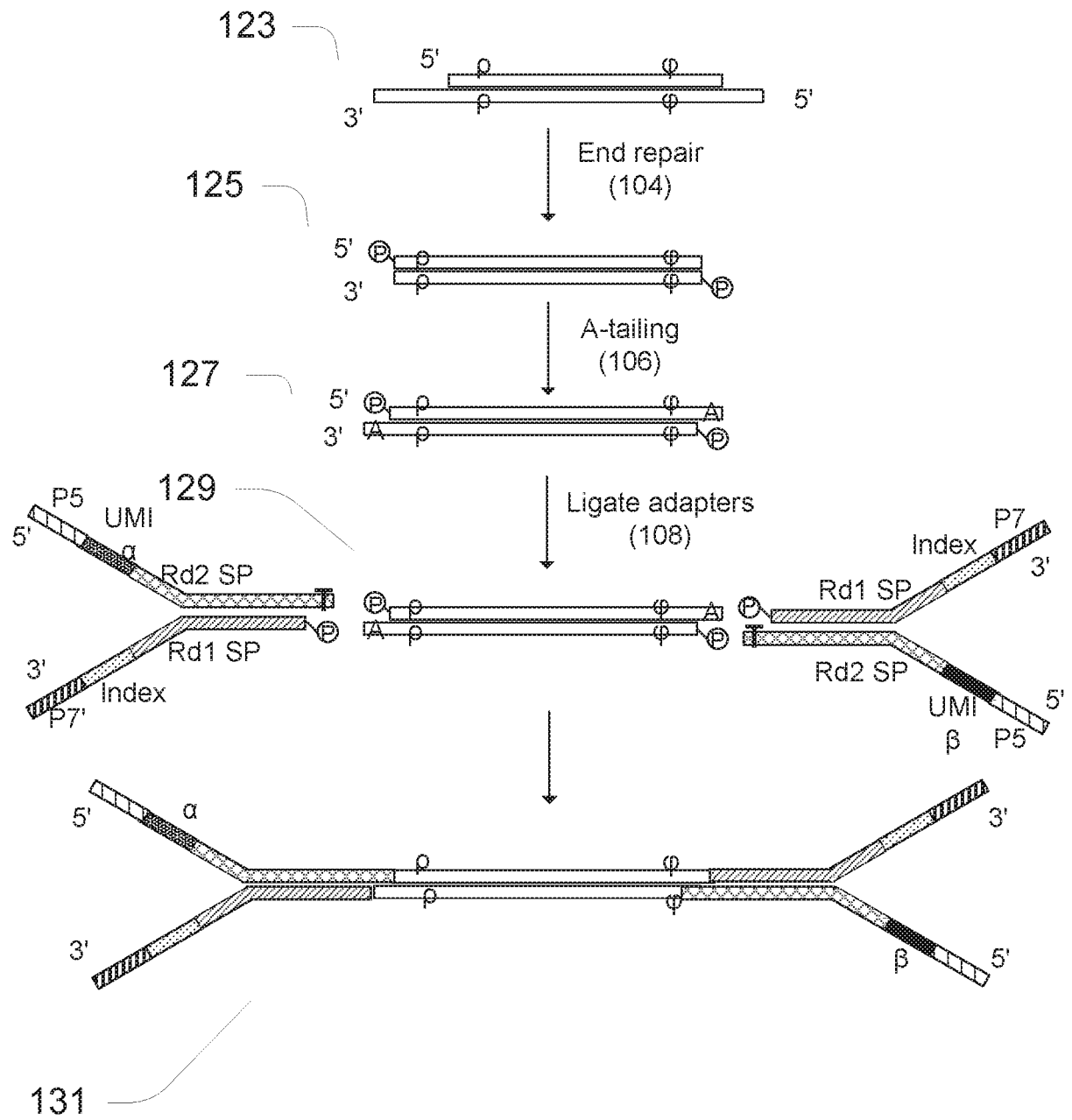
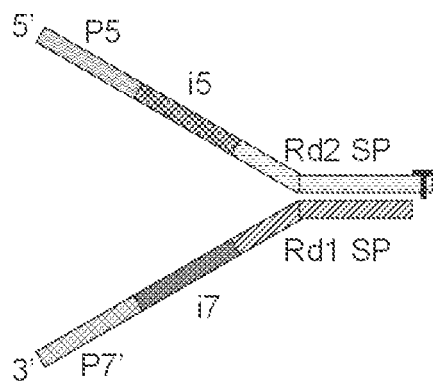
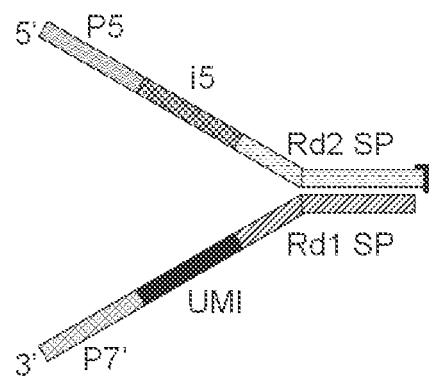


Figure 1B

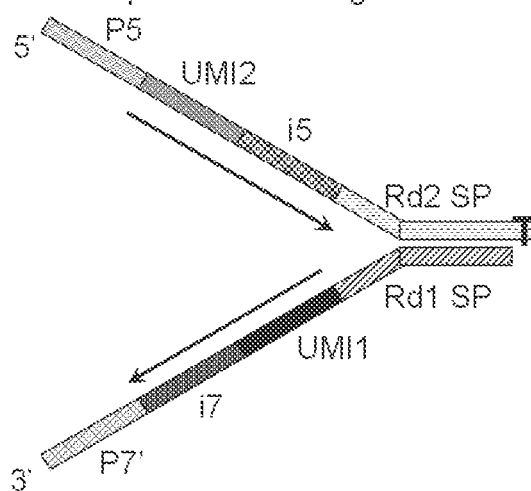
(i) Standard dual index TruSeq adapter



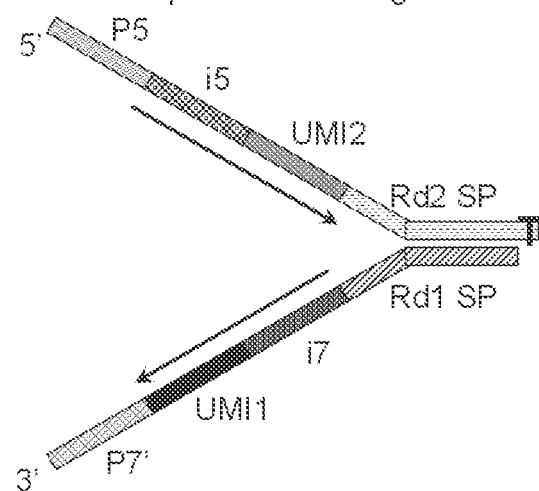
(ii) UMI replacing sample index 1 position



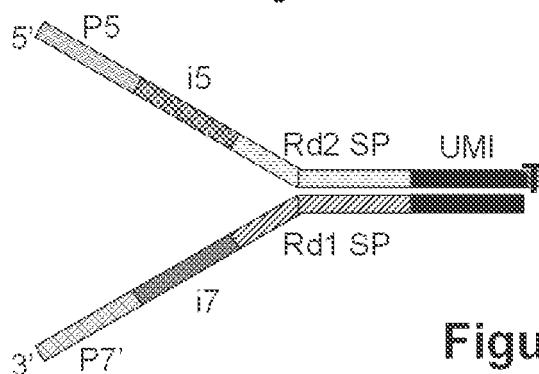
(iii) UMIs in both P5 and P7 arms, prior to sample index reading



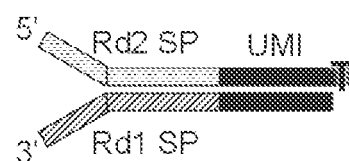
(iv) UMIs in both P5 and P7 arms, behind sample index reading



(v) Dual index adapter with a UMI in the double-stranded region



(vi) Short adapter with a UMI in the double-stranded region

**Figure 2A**

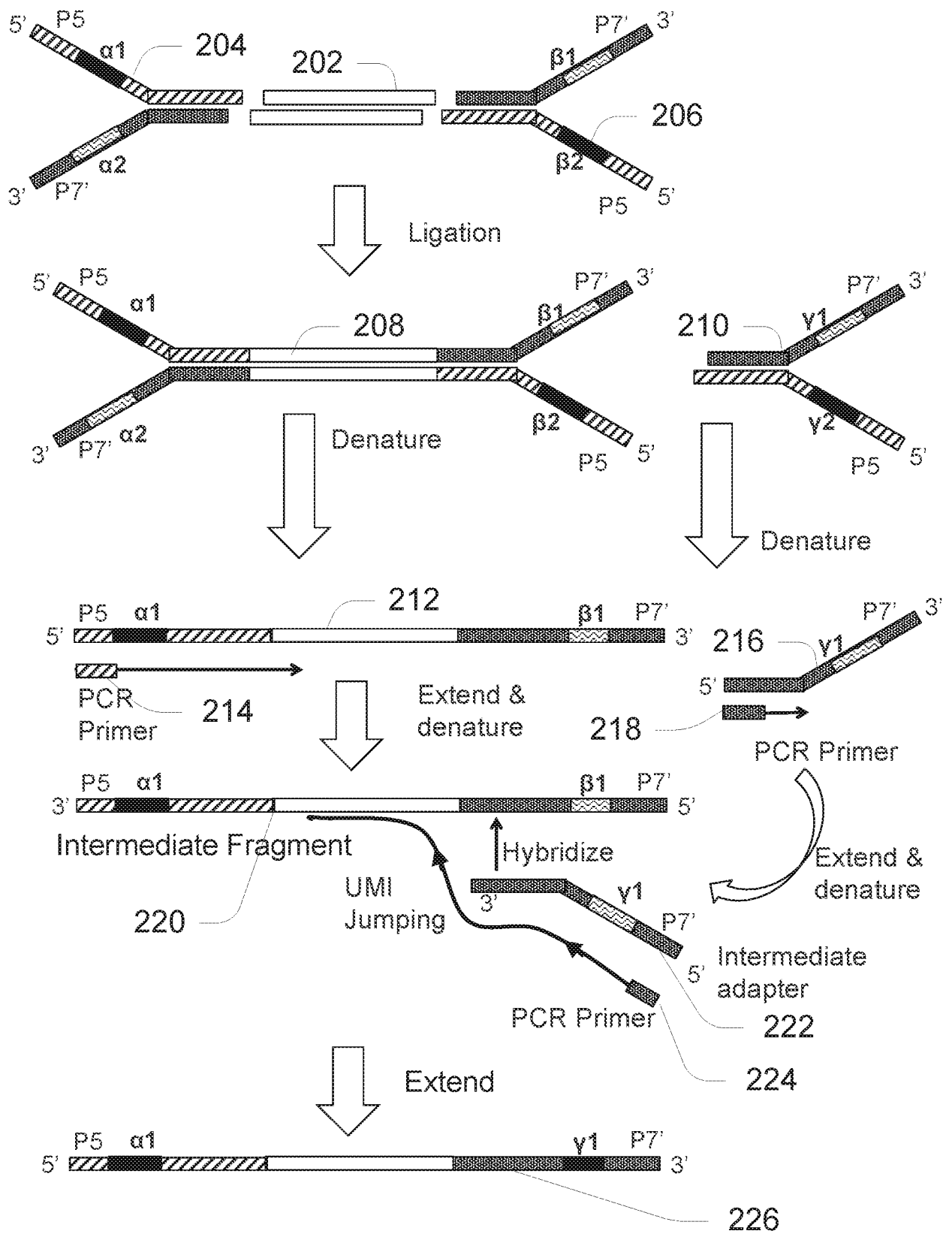


Figure 2B

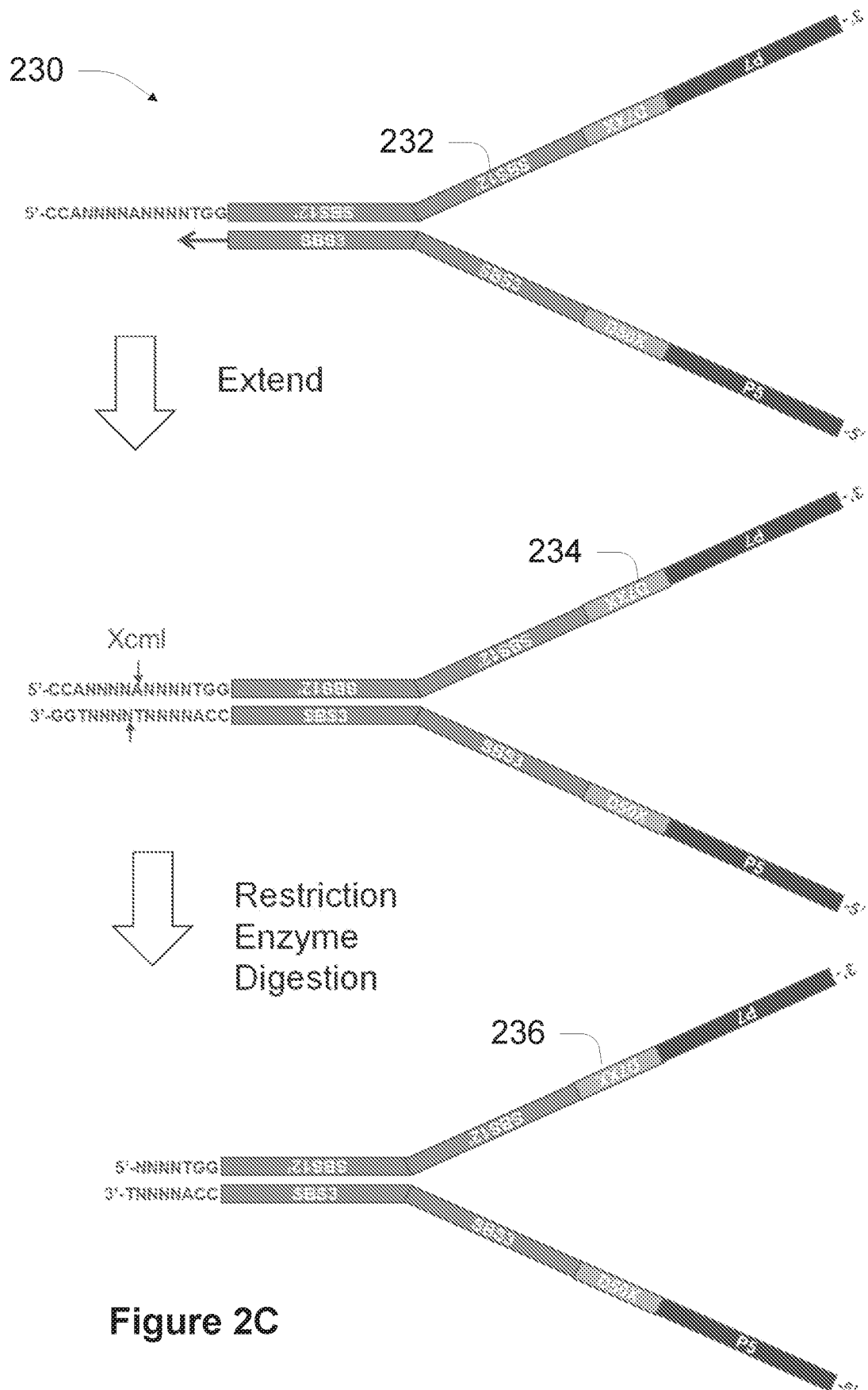


Figure 2C

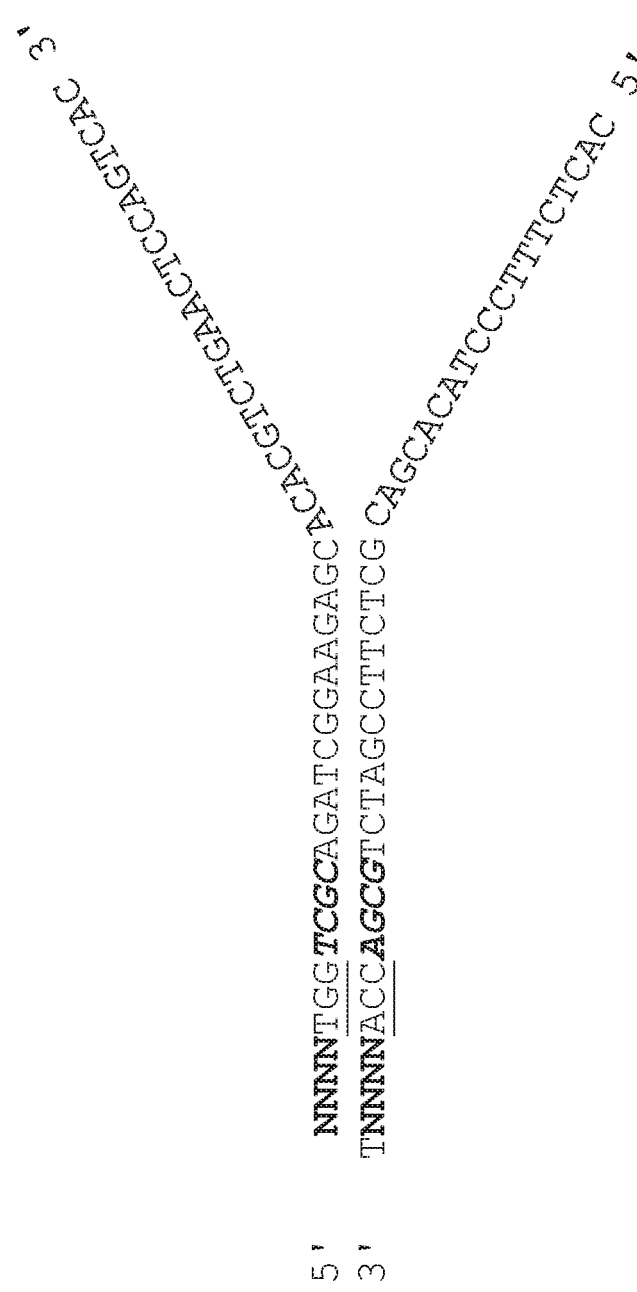


Figure 2D

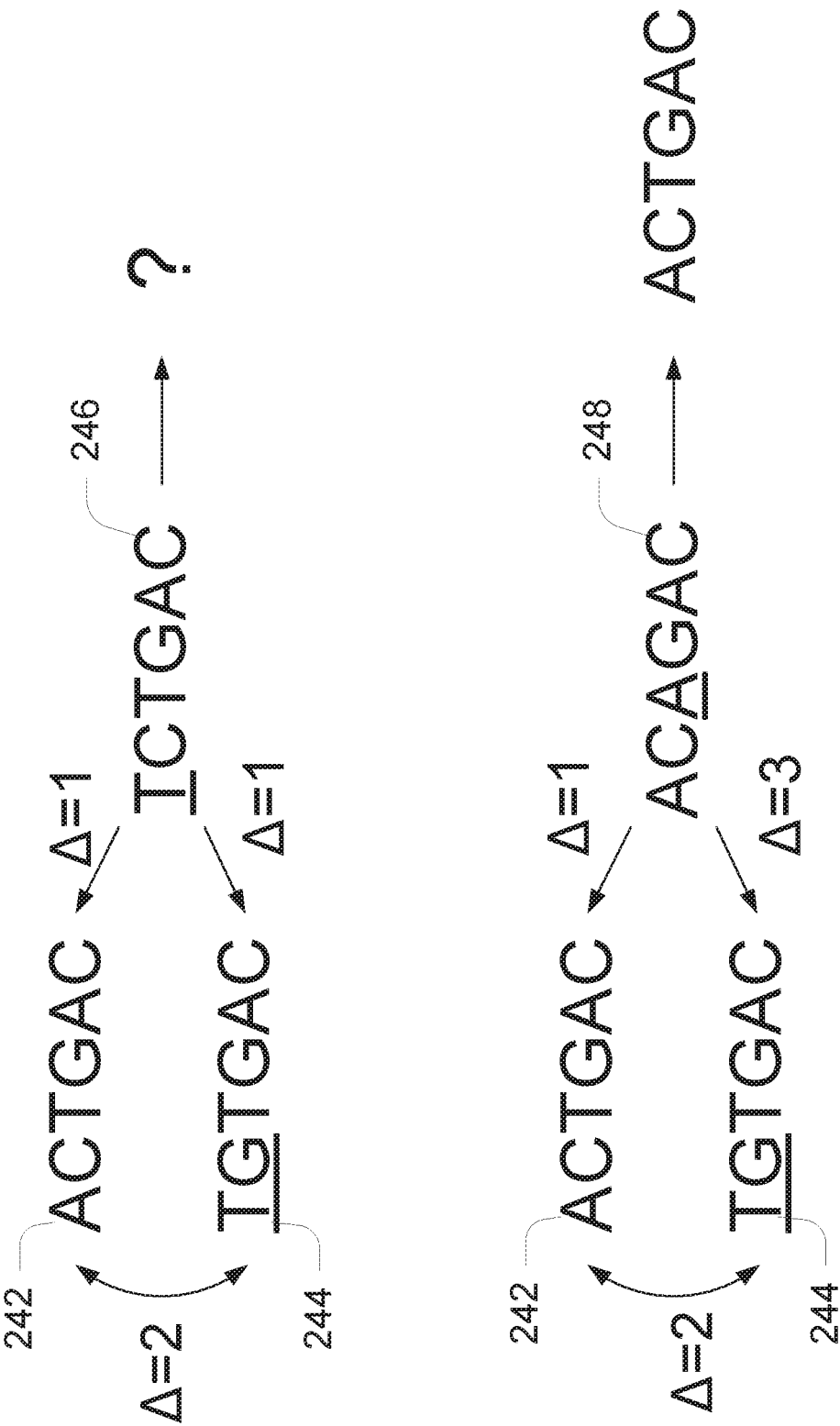


Figure 2E

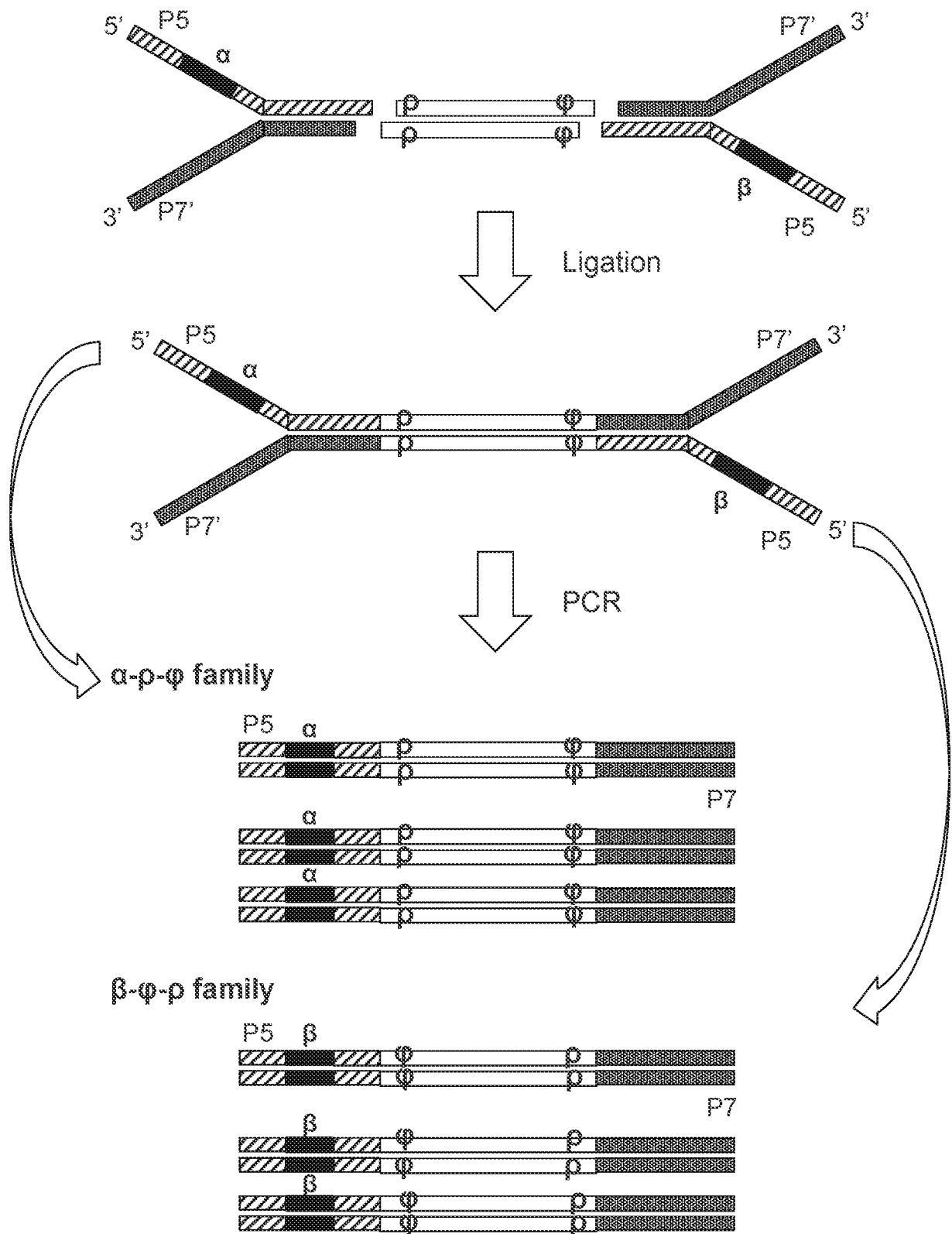


Figure 3A

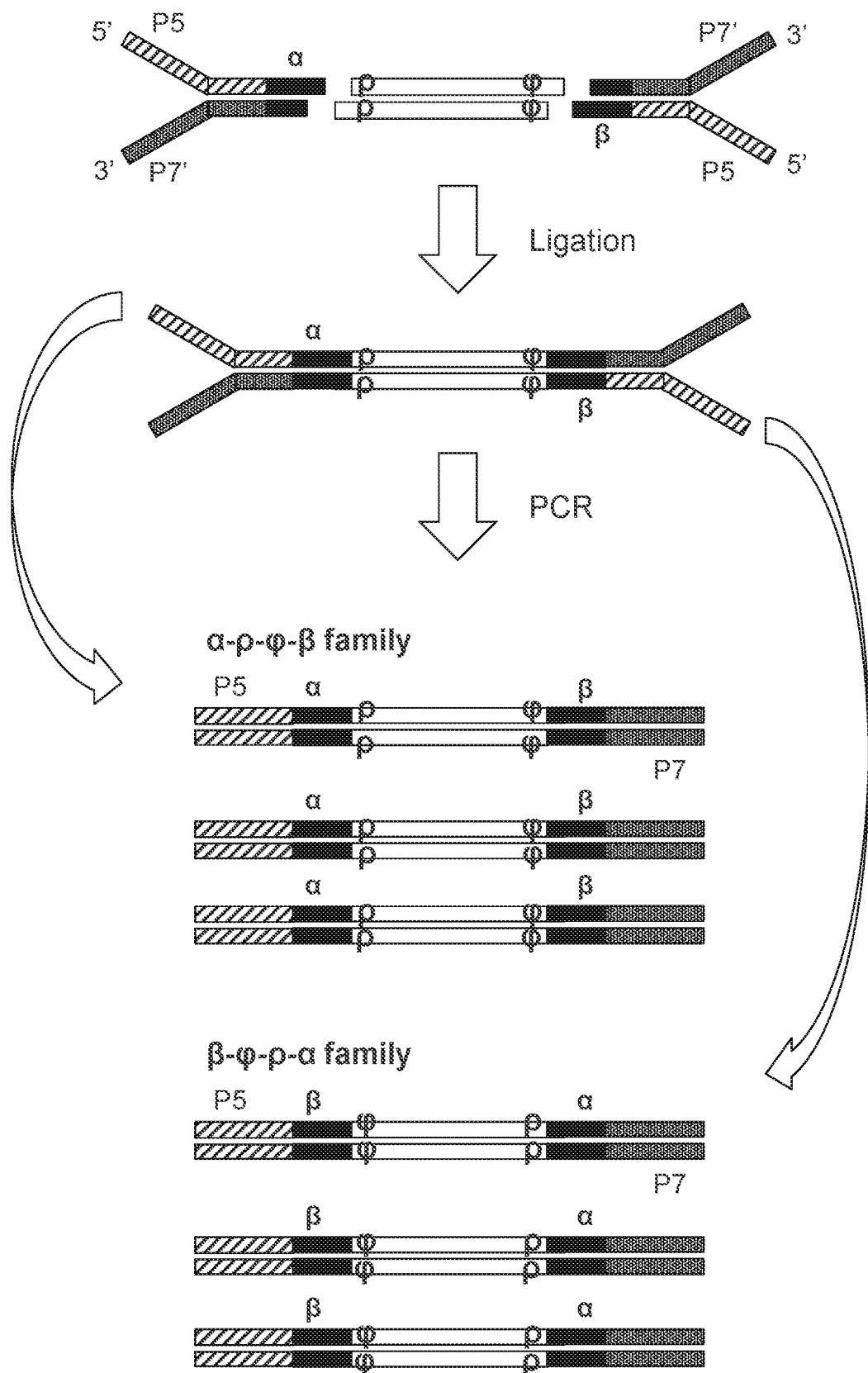


Figure 3B

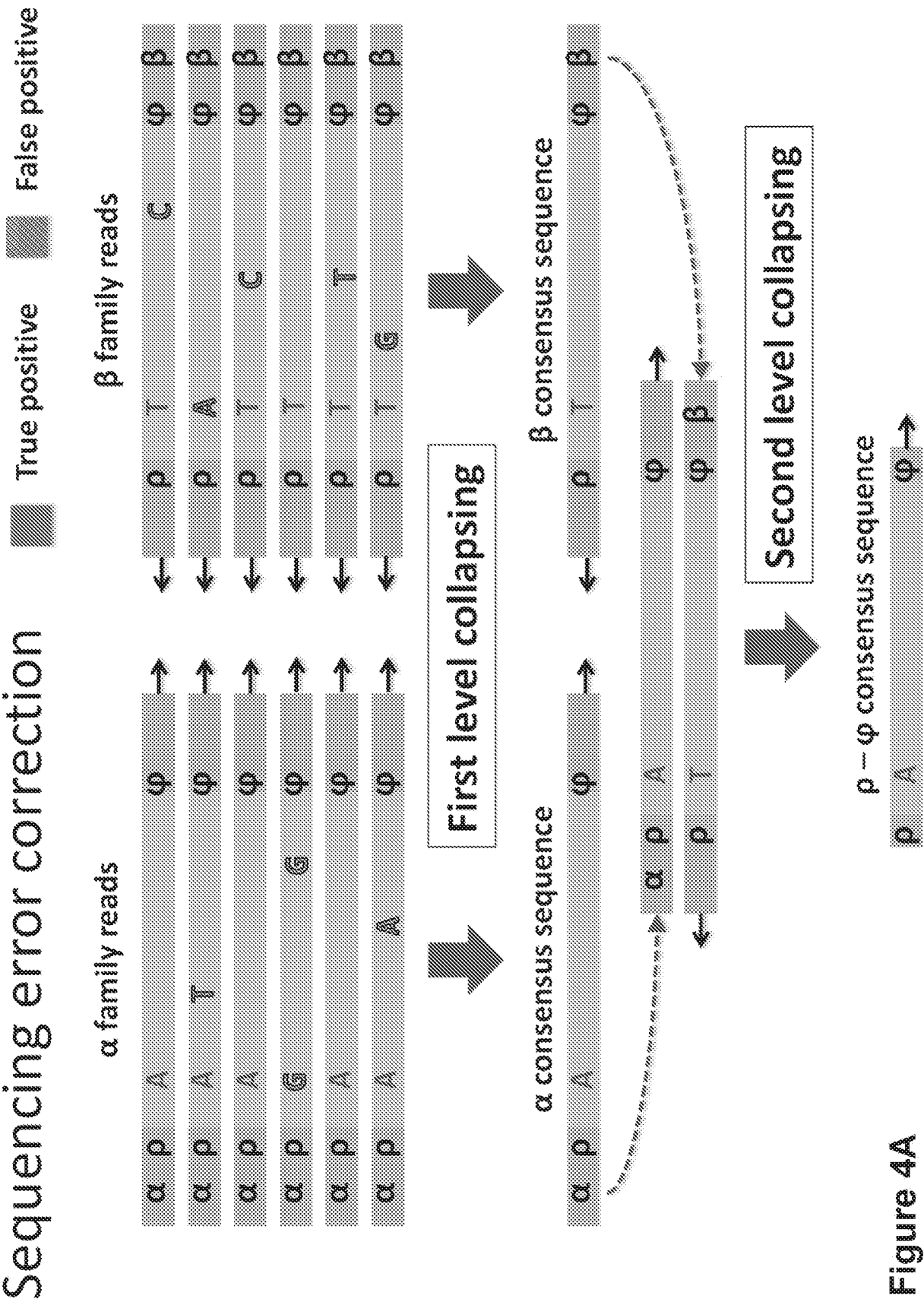


Figure 4A

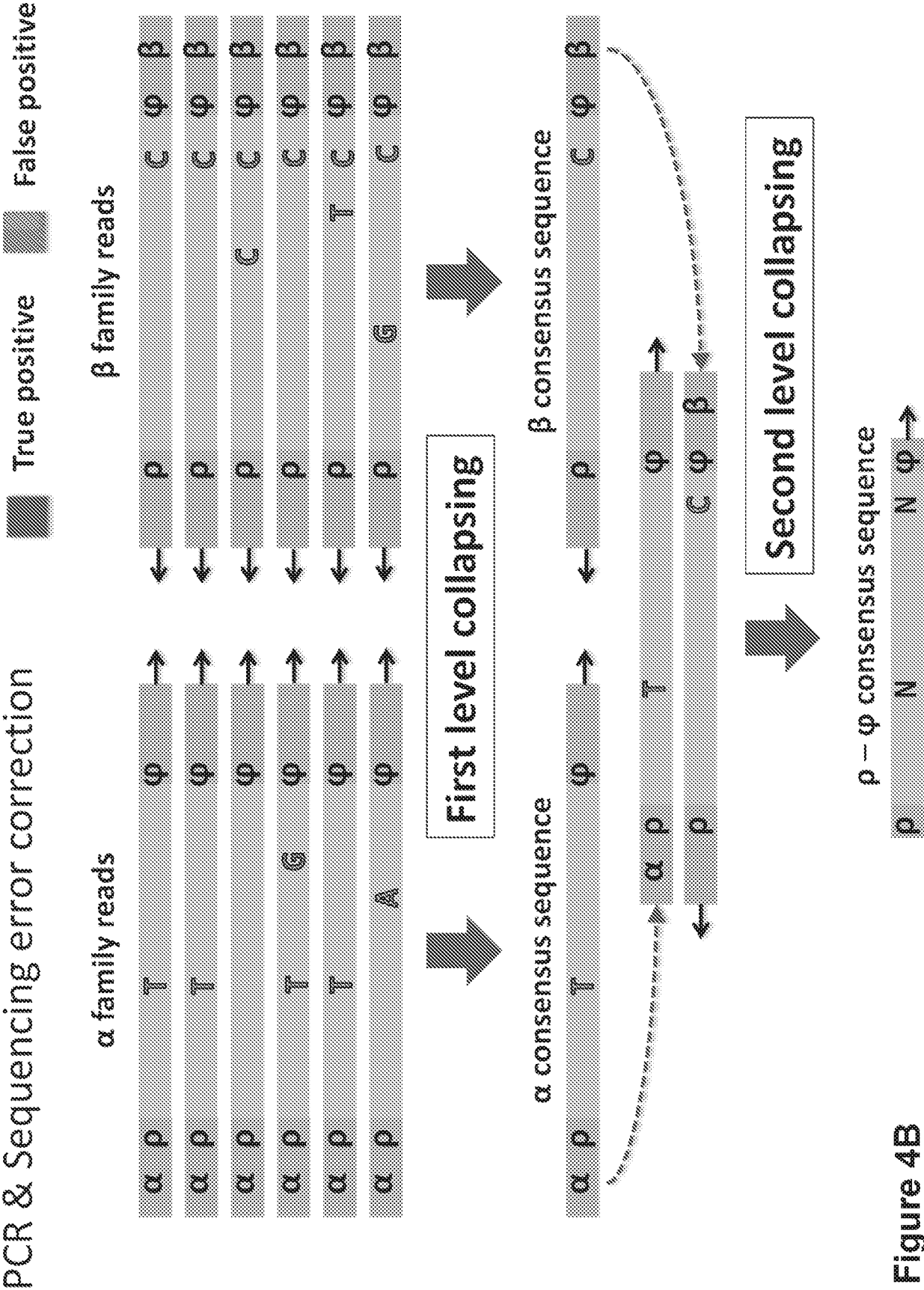


Figure 4B

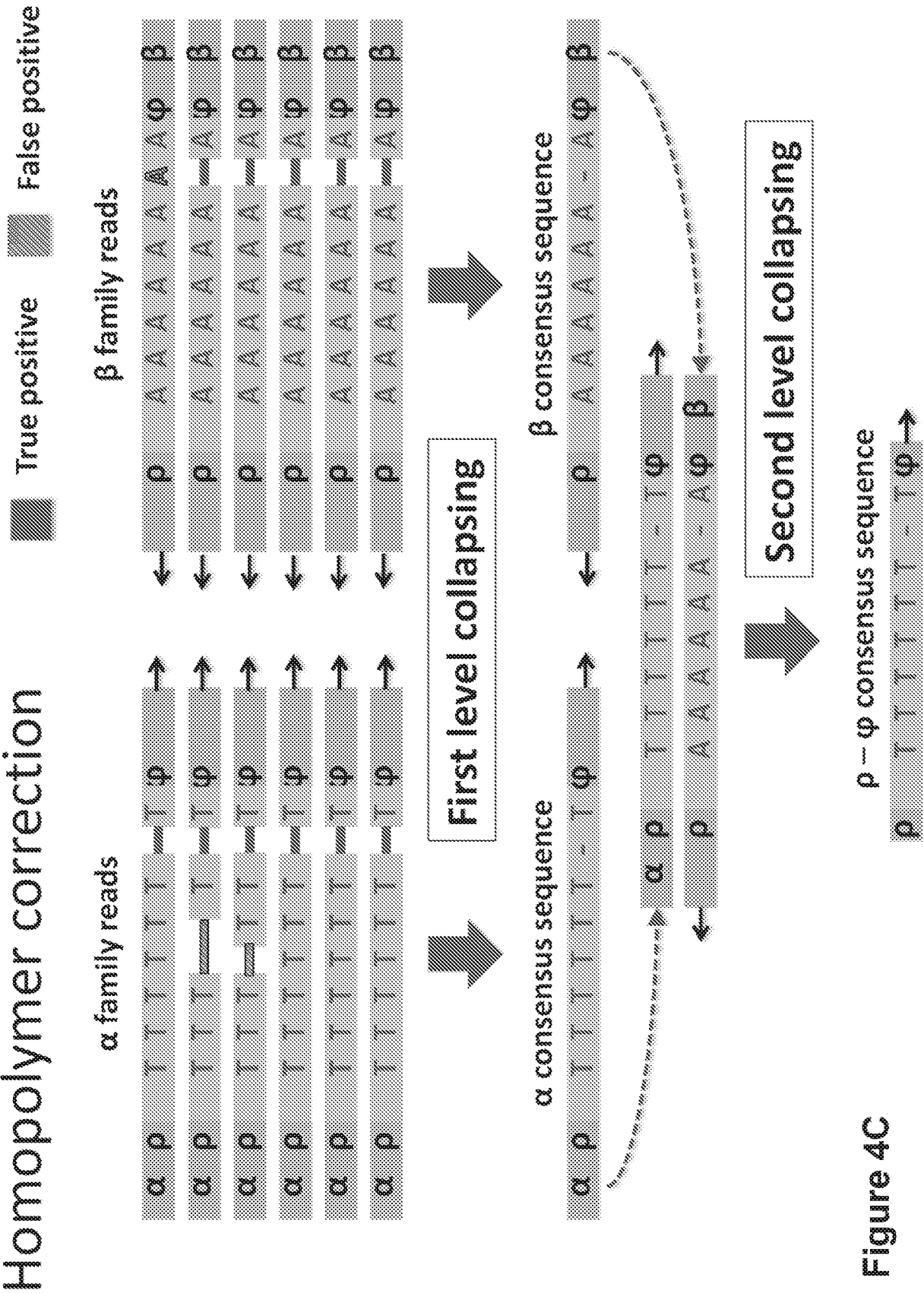


Figure 4C

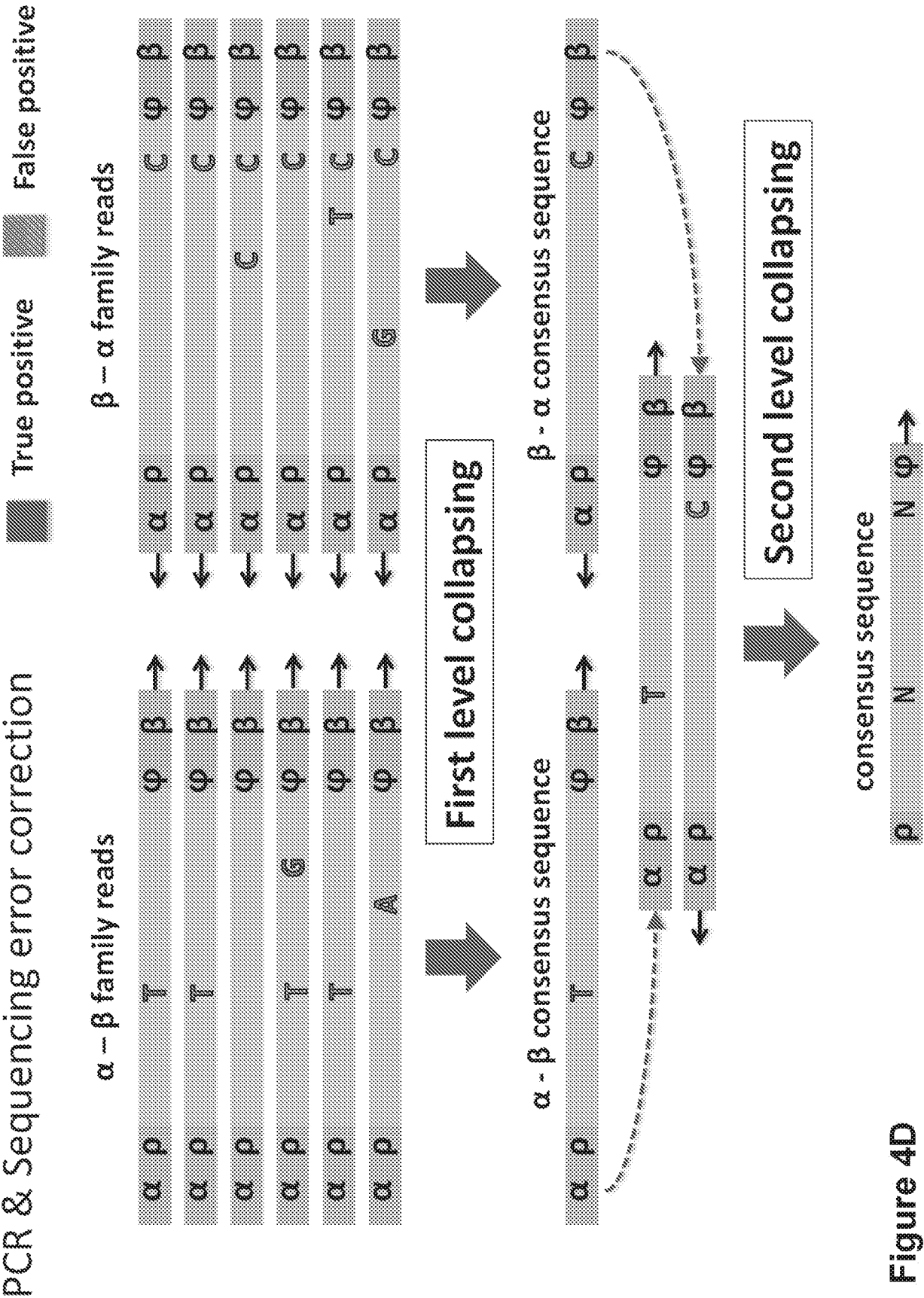


Figure 4D

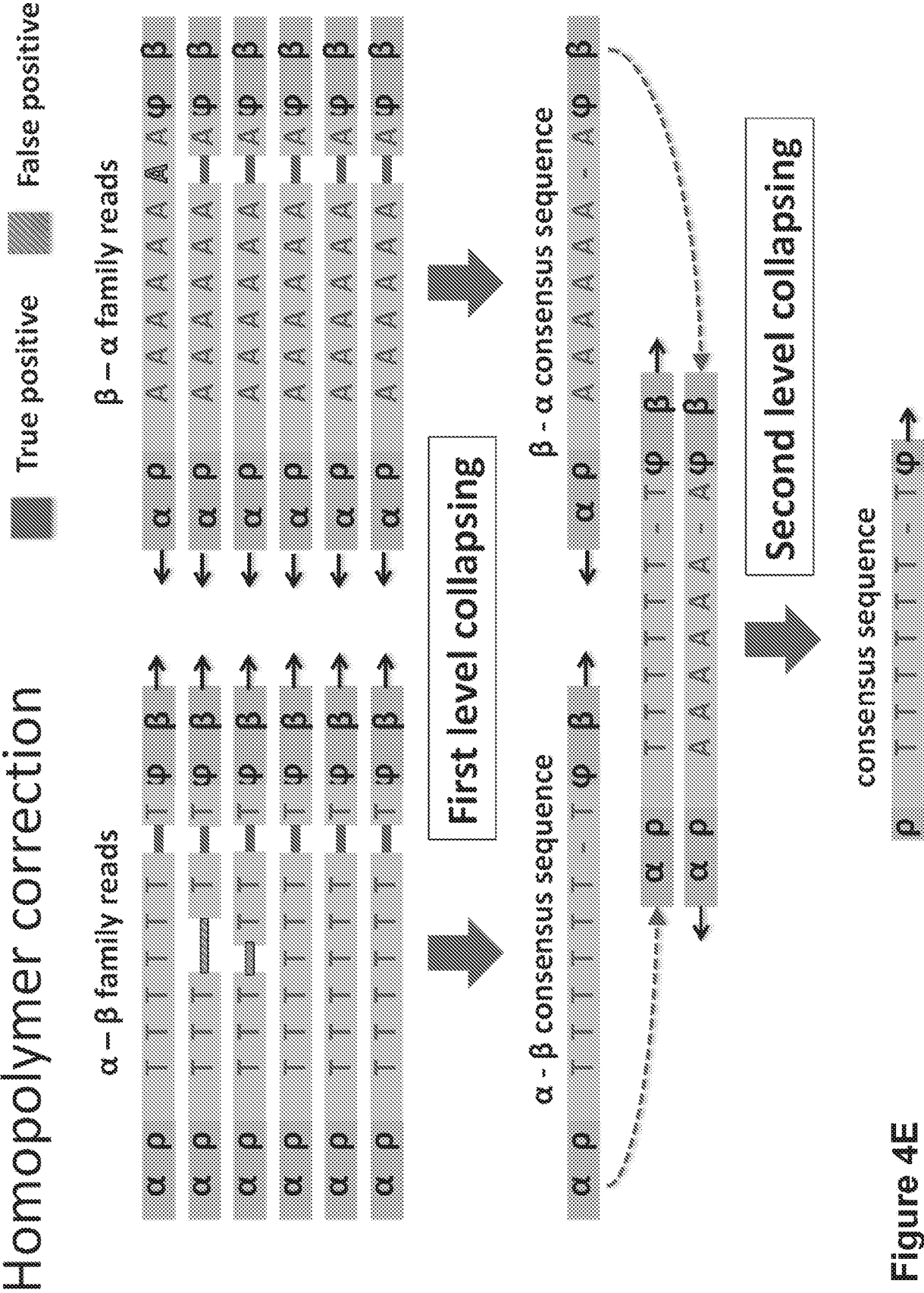


Figure 4E

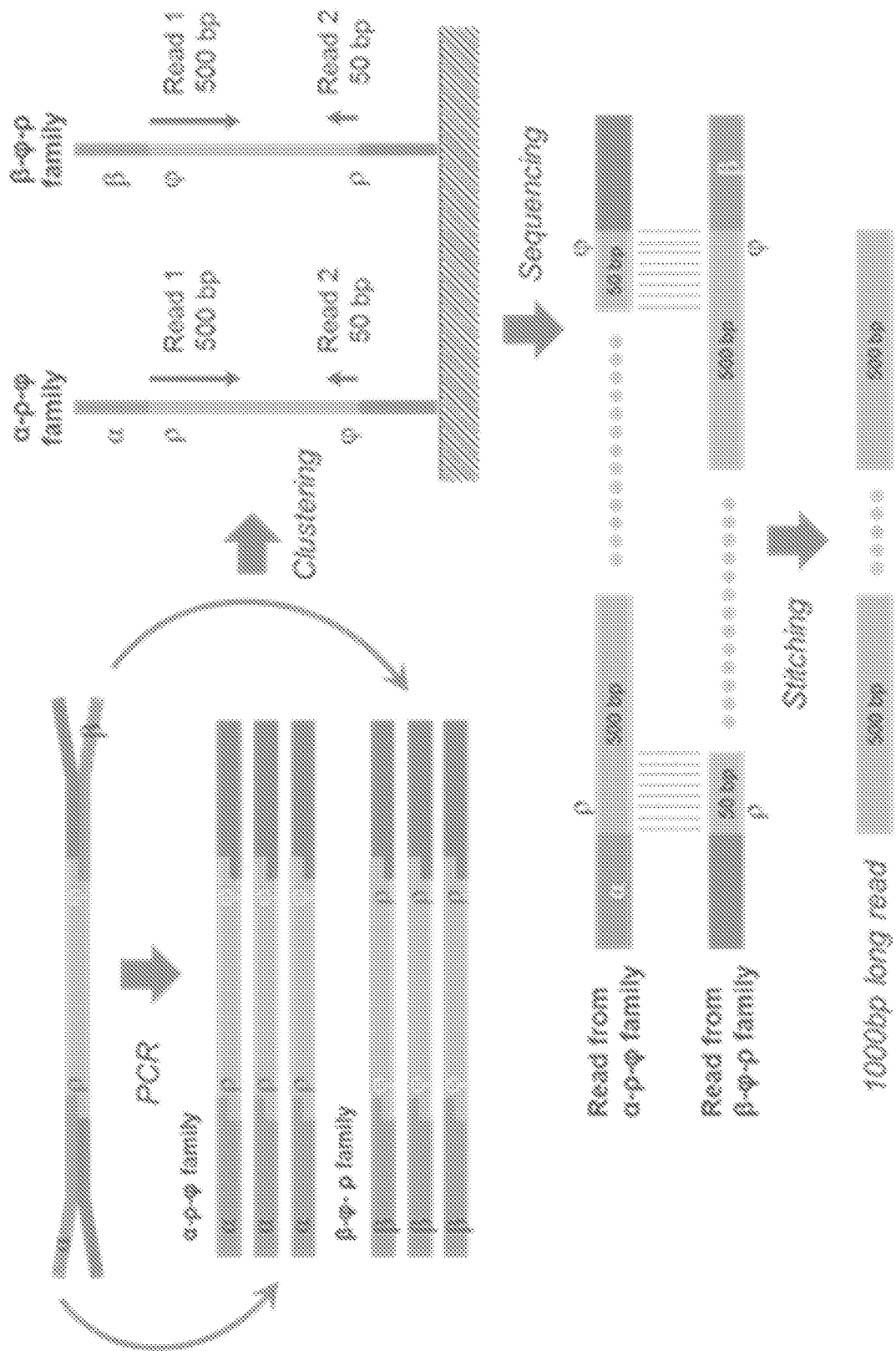


Figure 5

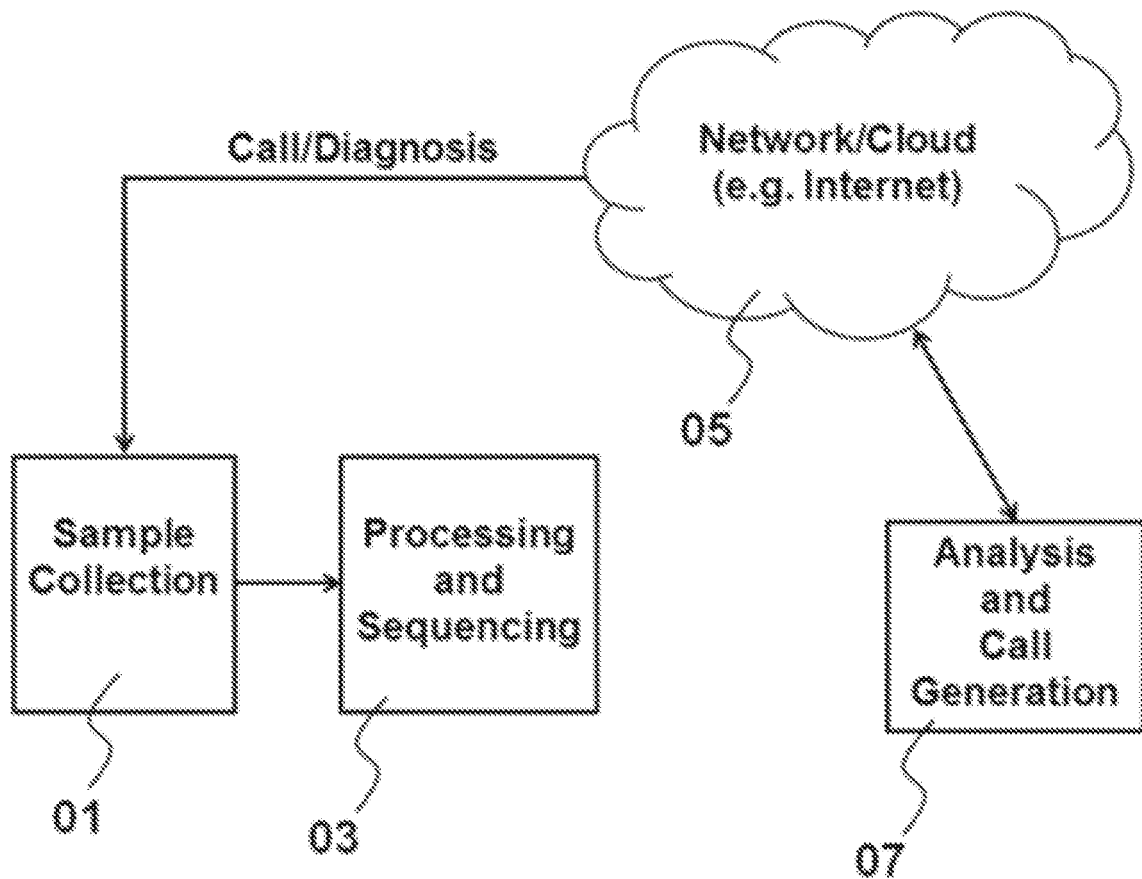
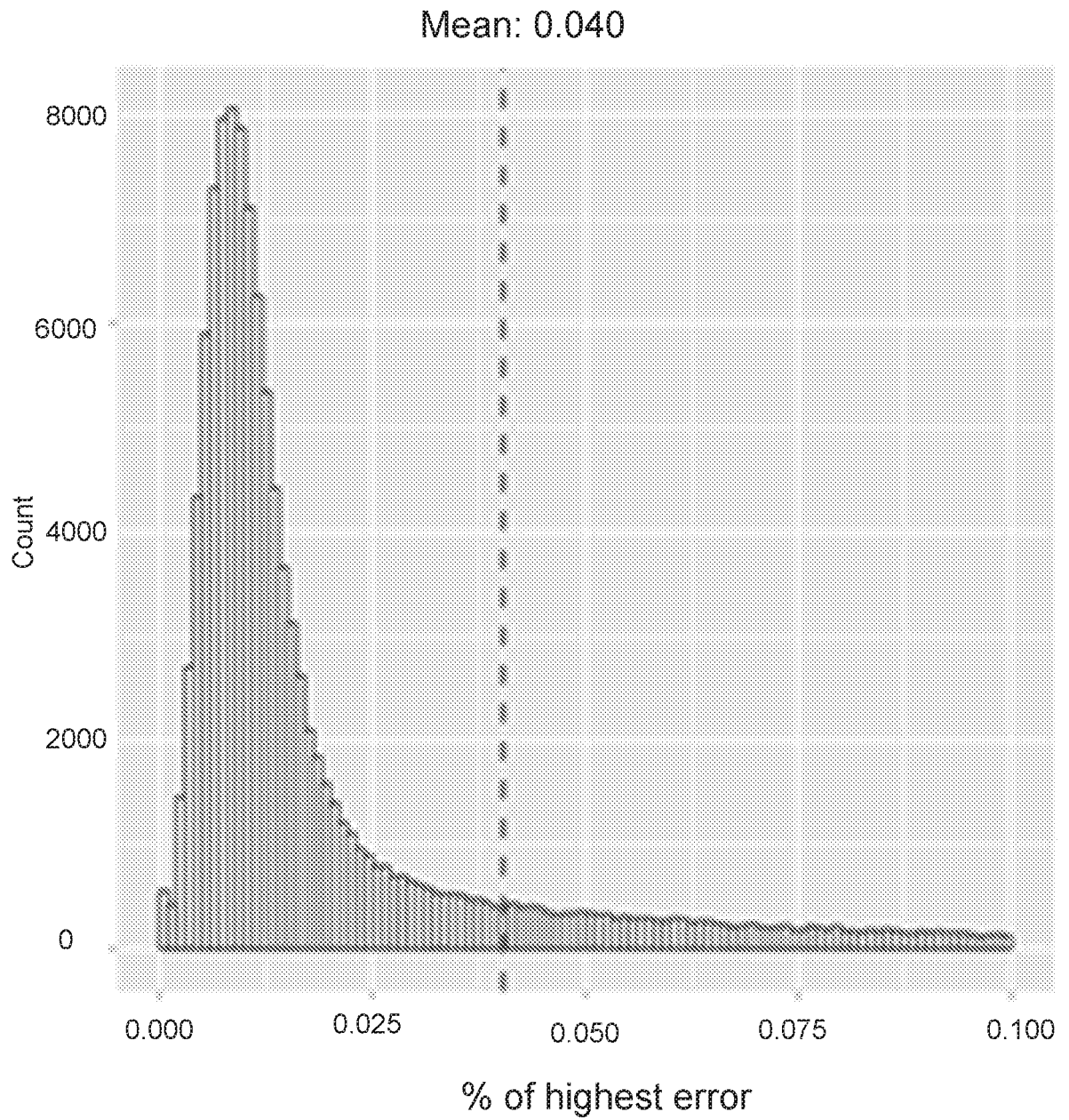
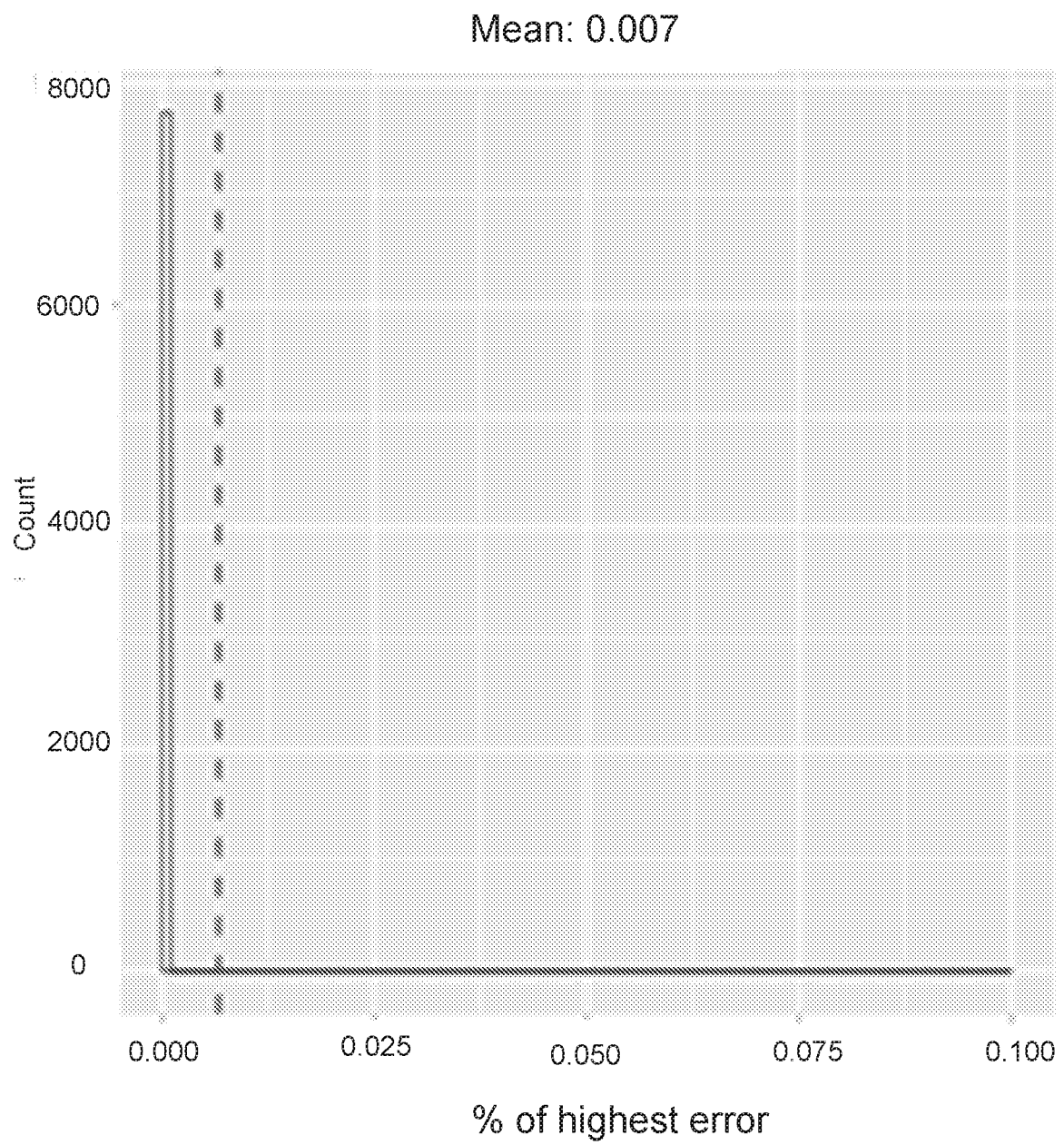
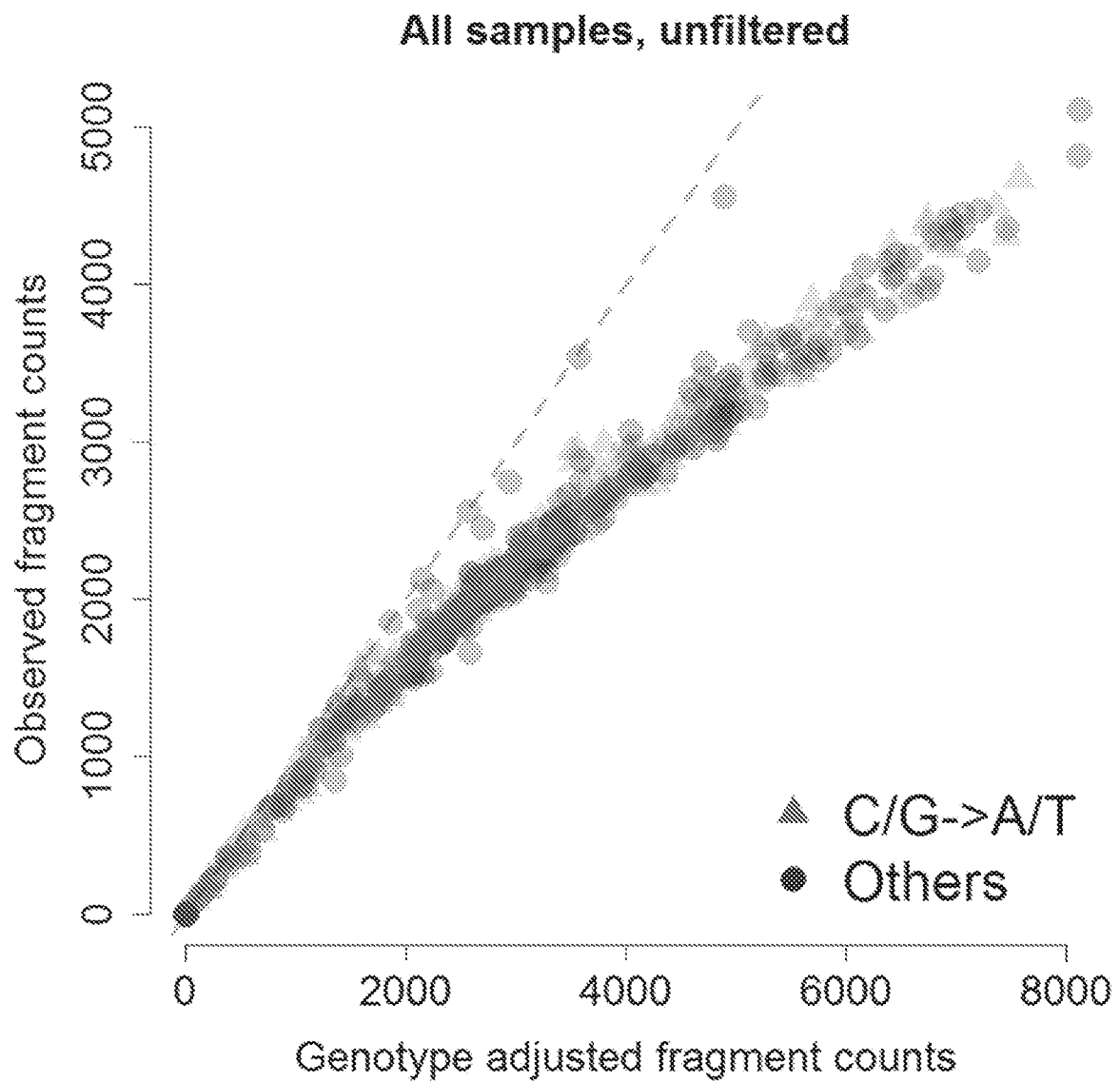


Figure 6

**Figure 7A**

**Figure 7B**

**Figure 8**

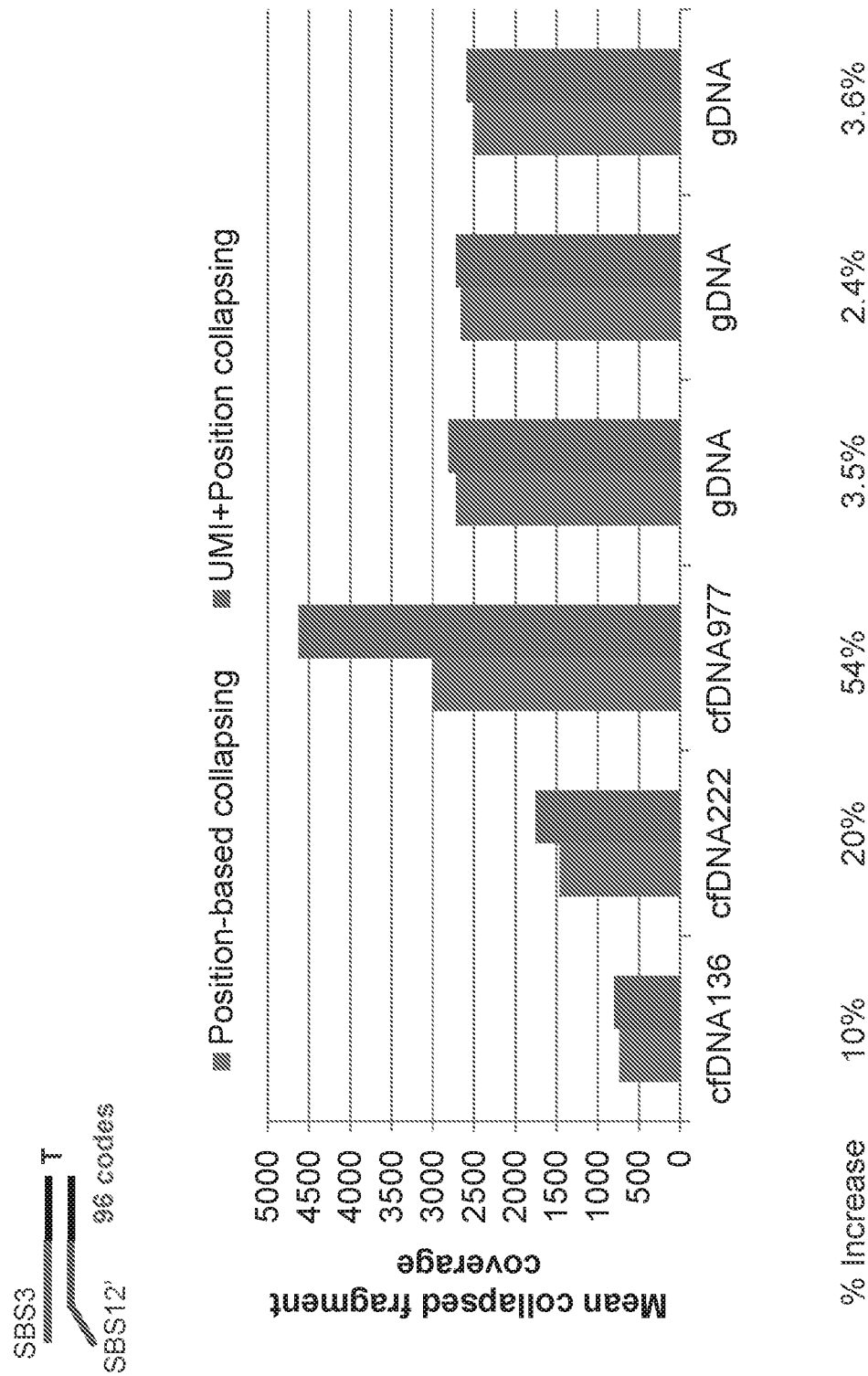


Figure 9

	0 errors	1 error, recoverable	1 error, non-recoverable	2+ errors/1+ indels
NA18506-0-4-UMI-a	98.03%	0.81%	0.33%	0.82%
NA18506-0-4-UMI-b	97.21%	1%	0.25%	1.53%
NA18506-0-4-UMI-c	97.51%	1.31%	0.26%	0.91%
Overall	97.58%	1.07%	0.28%	1.09%

>98.65% of total UMIs are usable

Many of these could still be usable based on the context

Figure 10

Results: Sheared gDNA (sensitivity and specificity)

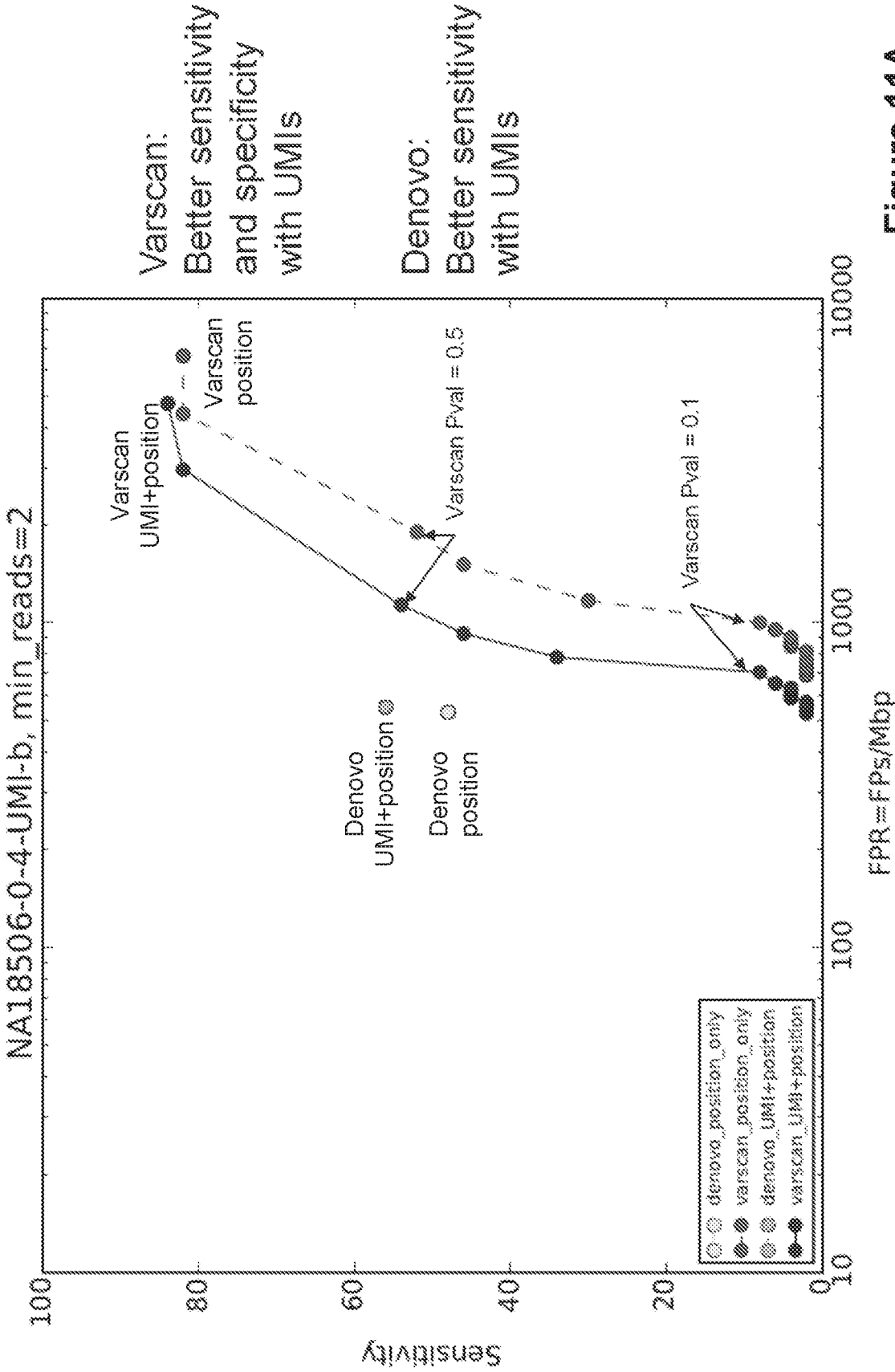


Figure 11A

Results: cfDNA136 (Specificity only)

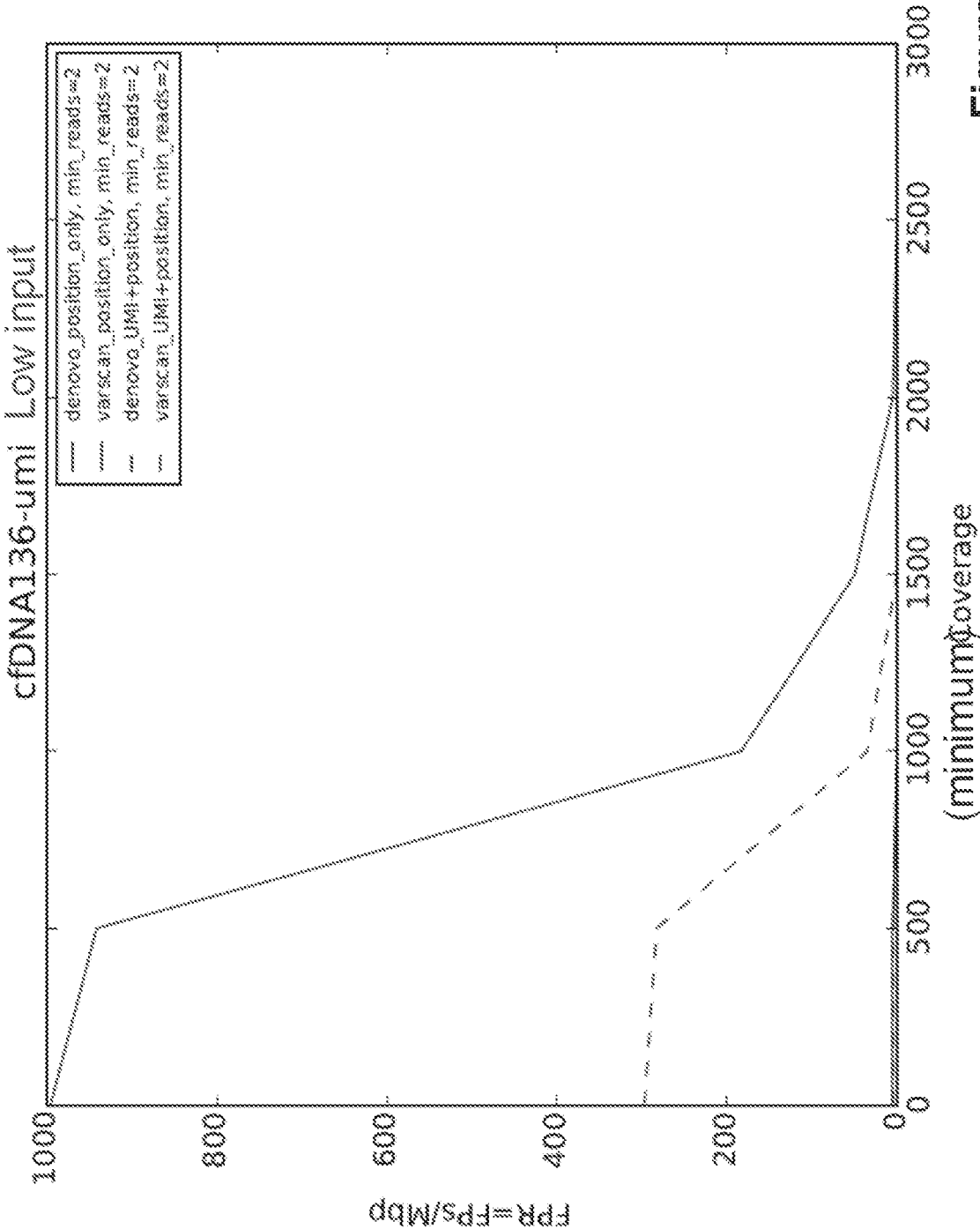


Figure 11B

Results: cfDNA222 (Specificity only)

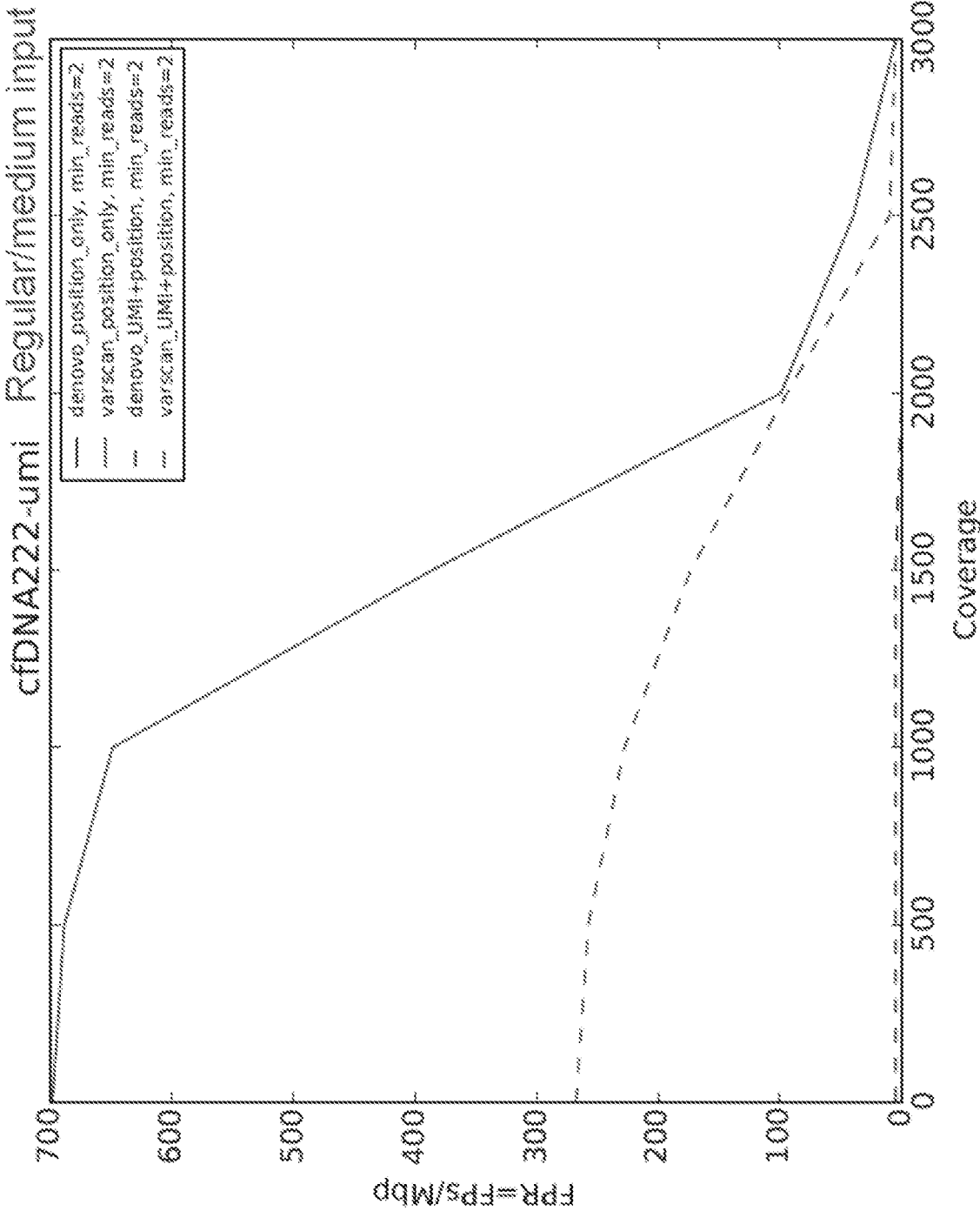


Figure 11C

Results: cfDNA977 (Specificity only)

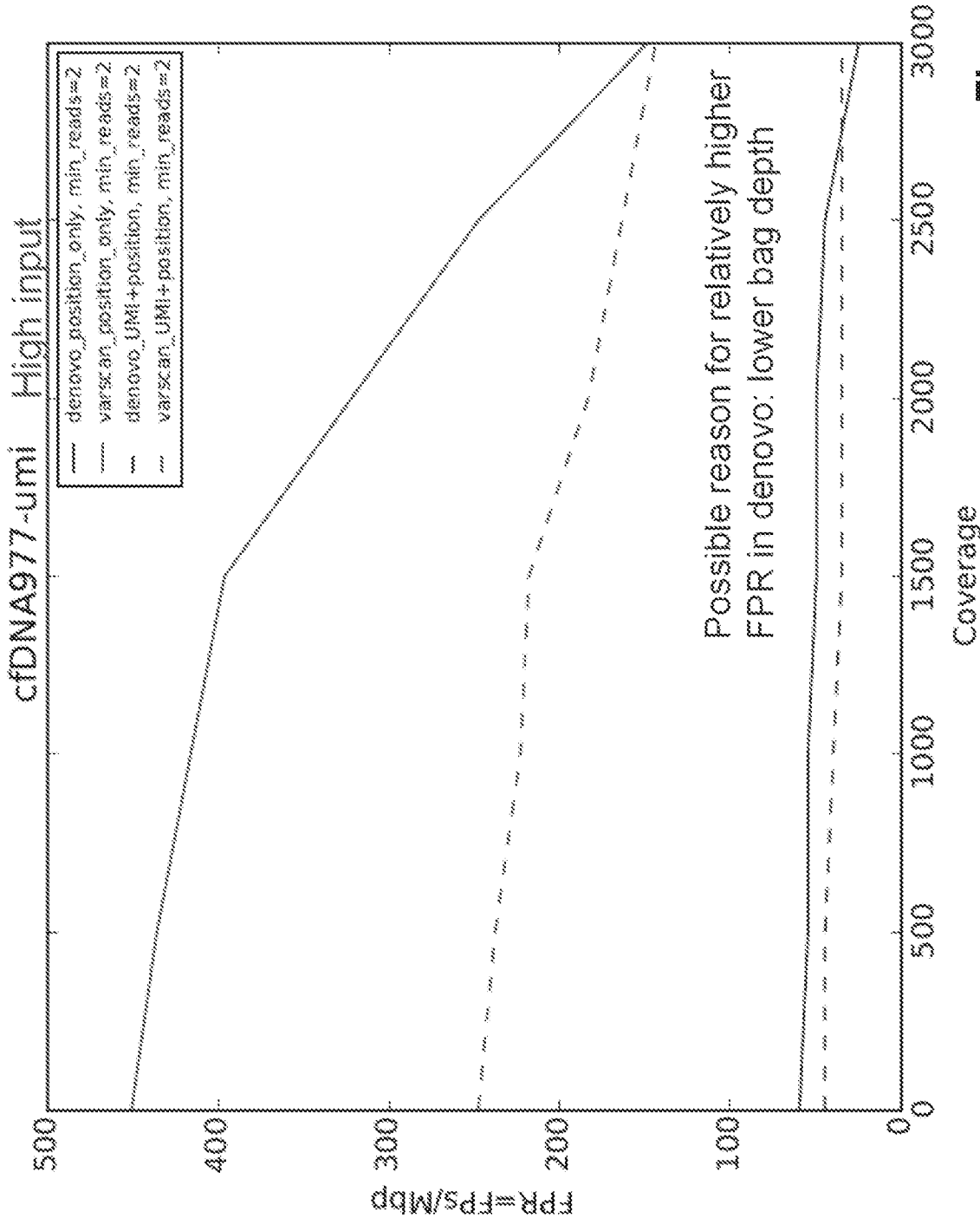


Figure 11D