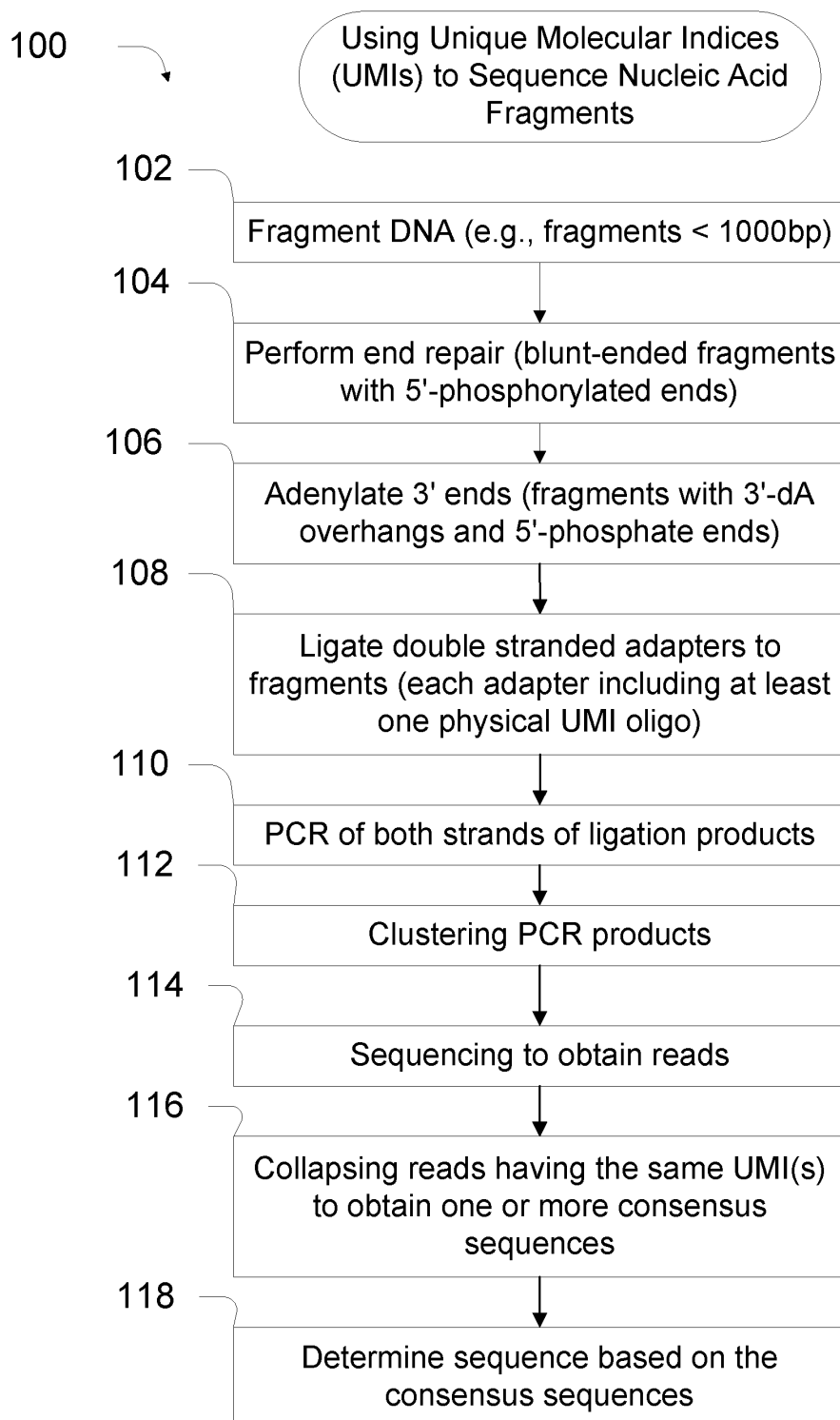


**Figure 1A**

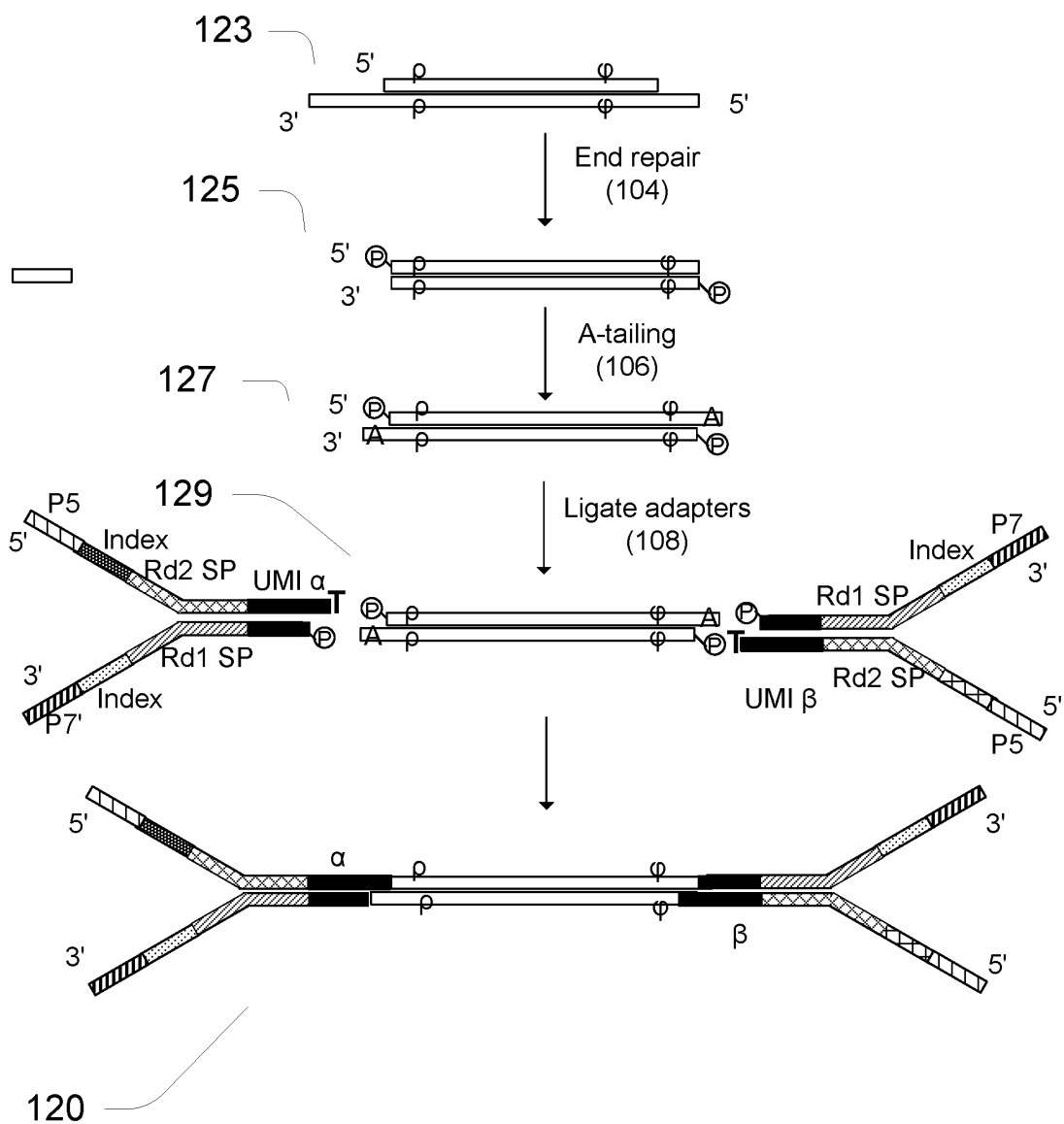
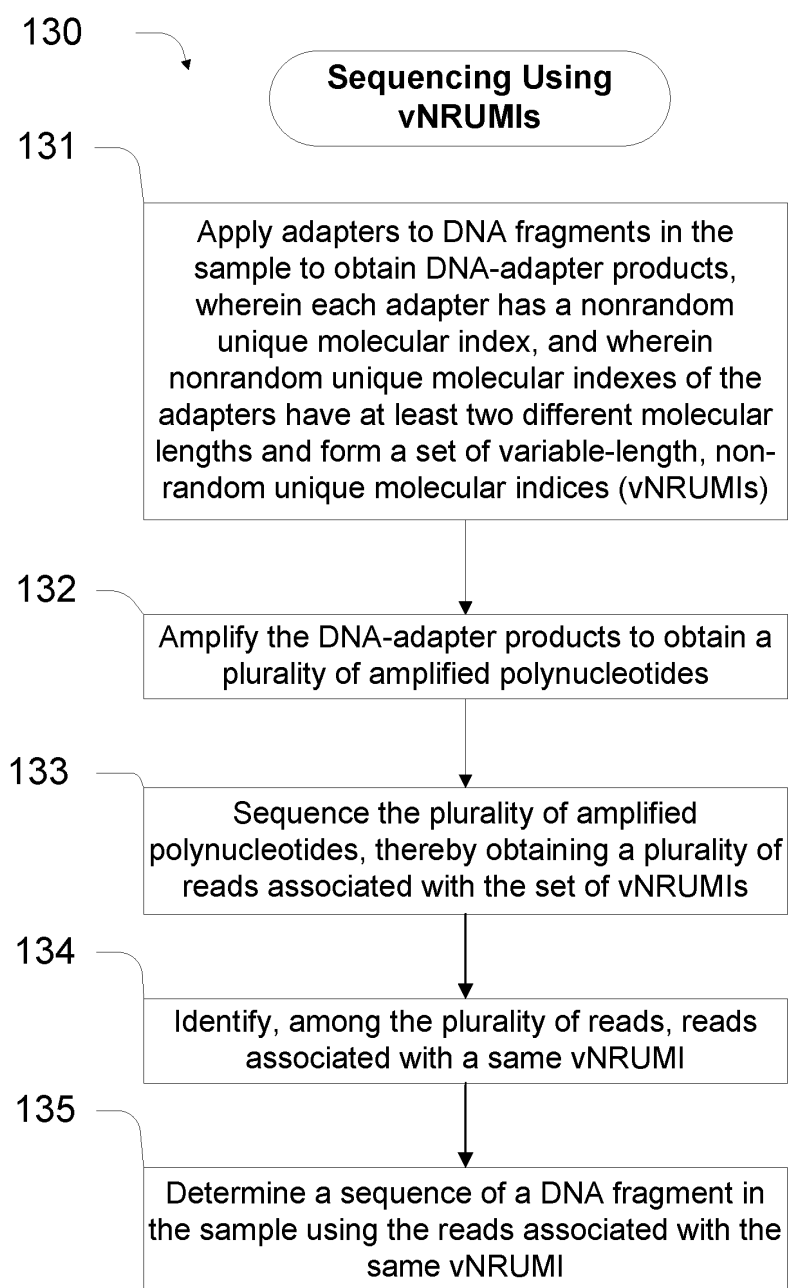
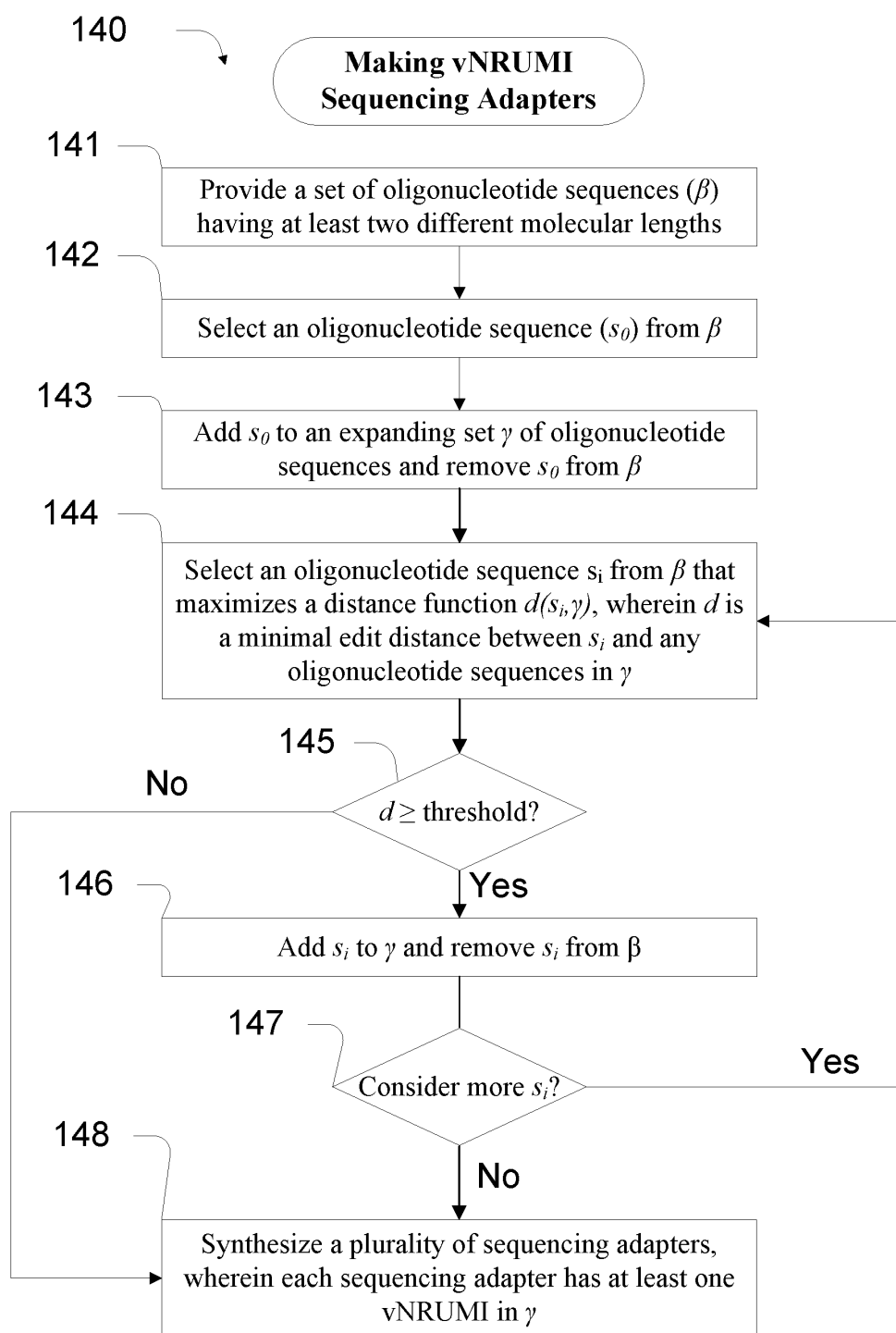


Figure 1B

**Figure 1C**

**Figure 1D**

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150

|           | <i>Q</i> | G  | T  | C  | T  | T  | C  | G  |
|-----------|----------|----|----|----|----|----|----|----|
| <i>S1</i> | 0        | -1 | -2 | -3 | -4 | -5 | -6 | -7 |
| A         | -1       | -1 | -2 | -3 | -4 | -5 | -6 | -7 |
| A         | -2       | -2 | -2 | -3 | -4 | -5 | -6 | -7 |
| C         | -3       | -3 | -3 | -1 | -2 | -3 | -4 | -5 |
| T         | -4       | -4 | -2 | -2 | 0  | -1 | -2 | -3 |
| T         | -5       | -5 | -3 | -3 | -1 | 1  | 0  | -1 |
| C         | -6       | -6 | -4 | -2 | -2 | 0  | 2  | 1  |

Q: GTCTTC  
S1: AACTTC } Levenshtein Distance (# addition + # deletion + # substitution) = 2

Q: GTCTTC  
S1: AACTTC } Glocal alignment score (# match – Levenshtein Distance) = 2

Levenshtein Distance = 2

152

|           | <i>Q</i> | G  | T  | C  | T  | T  | C  | G  |
|-----------|----------|----|----|----|----|----|----|----|
| <i>S2</i> | 0        | -1 | -2 | -3 | -4 | -5 | -6 | -7 |
| C         | -1       | -1 | -2 | -3 | -4 | -5 | -6 | -7 |
| G         | -2       | 0  | -1 | -2 | -2 | -3 | -4 | -3 |
| C         | -3       | -1 | -1 | 0  | -1 | -2 | -2 | -3 |
| T         | -4       | -2 | 0  | -1 | 1  | 0  | -1 | -2 |
| T         | -5       | -3 | -1 | -1 | 0  | 2  | 1  | 0  |
| C         | -6       | -4 | -2 | 0  | -1 | 1  | 3  | 2  |
| G         | -7       | -5 | -3 | -1 | -1 | 0  | 2  | 4  |

Q: GTCTTCG  
S2: CGCTTCG } Levenshtein distance = 2

Q: GTCTTCG  
S2: CGCTTCG } Glocal alignment score = 4

Figure 1E

160

|                | Q  | T  | T  | G  | G  | C  | A  | T  |
|----------------|----|----|----|----|----|----|----|----|
| S <sub>1</sub> | 0  | -1 | -2 | -3 | -4 | -5 | -6 | -7 |
| T              | -1 | 1  | 0  | -1 | -2 | -3 | -4 | -5 |
| T              | -2 | 0  | 2  | 1  | 0  | -1 | -2 | -3 |
| G              | -3 | -1 | 1  | 3  | 2  | 1  | 0  | -1 |
| T              | -4 | -2 | 0  | 2  | 2  | 1  | 0  | 1  |
| G              | -5 | -3 | -1 | 1  | 3  | 2  | 1  | 0  |
| A              | -6 | -4 | -2 | 0  | 2  | 2  | 3  | 2  |
| C              | -7 | -5 | -3 | -1 | 1  | 3  | 2  | 2  |

Q: TTGGCAT

S<sub>1</sub>: TTGTGAC

Global alignment score = 2

Glocal alignment score = 3

162

161

163

|                | Q  | T  | T  | G  | G  | C  | A  | T  |
|----------------|----|----|----|----|----|----|----|----|
| S <sub>2</sub> | 0  | -1 | -2 | -3 | -4 | -5 | -6 | -7 |
| G              | -1 | -1 | -2 | -1 | -2 | -3 | -4 | -5 |
| G              | -2 | -2 | -2 | -1 | 0  | -1 | -2 | -3 |
| C              | -3 | -3 | -3 | -2 | -1 | 1  | 0  | -1 |
| C              | -4 | -4 | -4 | -3 | -2 | 0  | 0  | -1 |
| A              | -5 | -5 | -5 | -4 | -3 | -1 | 1  | 0  |
| T              | -6 | -4 | -4 | -5 | -4 | -2 | 0  | 2  |

Q: TTGGCAT

S<sub>2</sub>: GGCCAT

Global alignment score = 2

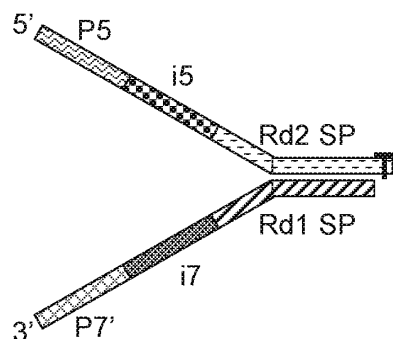
Glocal alignment score = 2

164

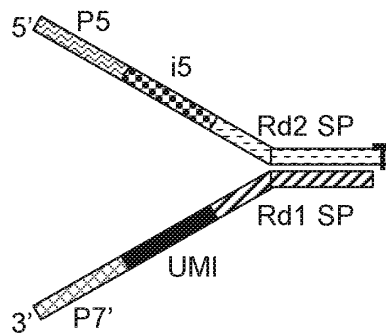
Figure 1F

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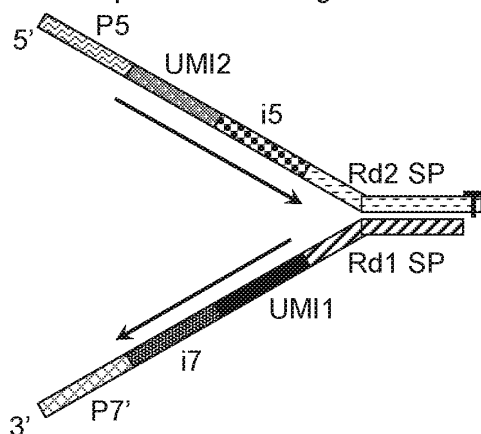
(i) Standard dual index TruSeq adapter



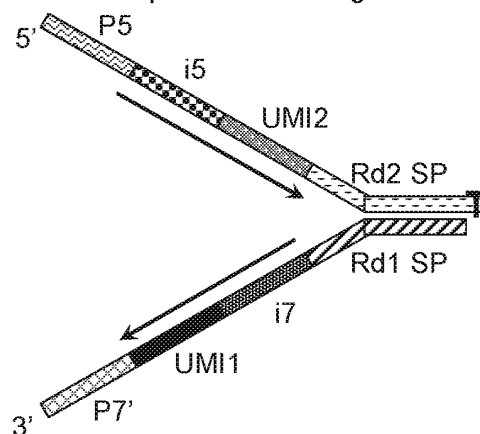
(ii) UMI replacing sample index 1 position



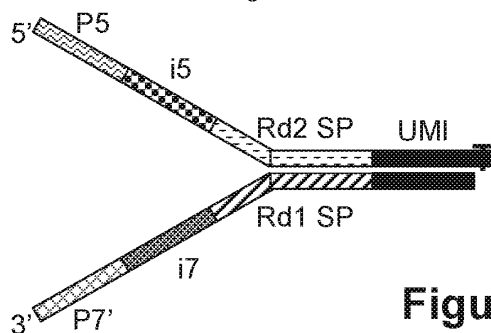
(iii) UMIs in both P5 and P7 arms, prior to sample index reading



(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

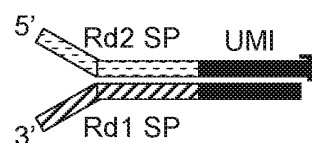


Figure 2A

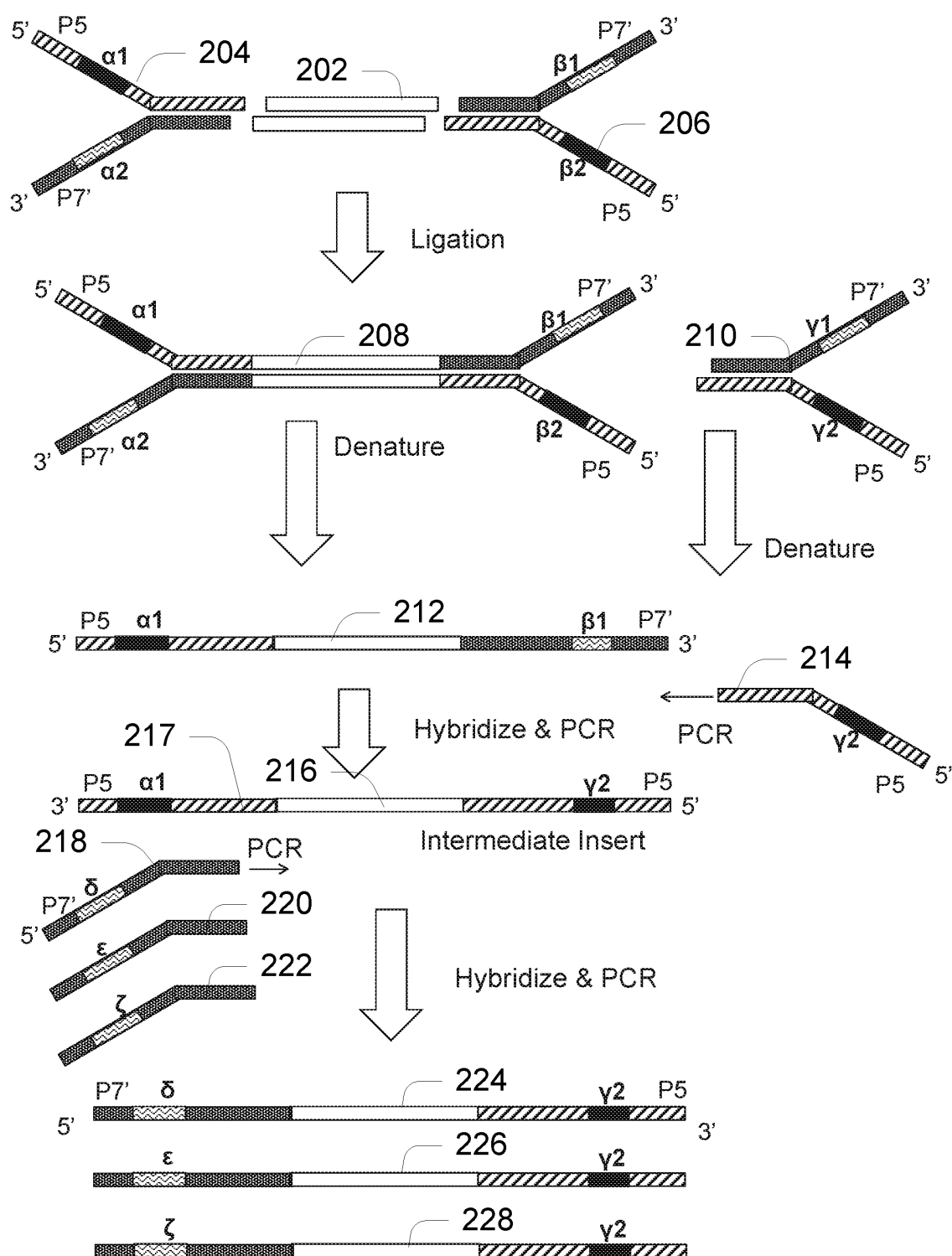


Figure 2B

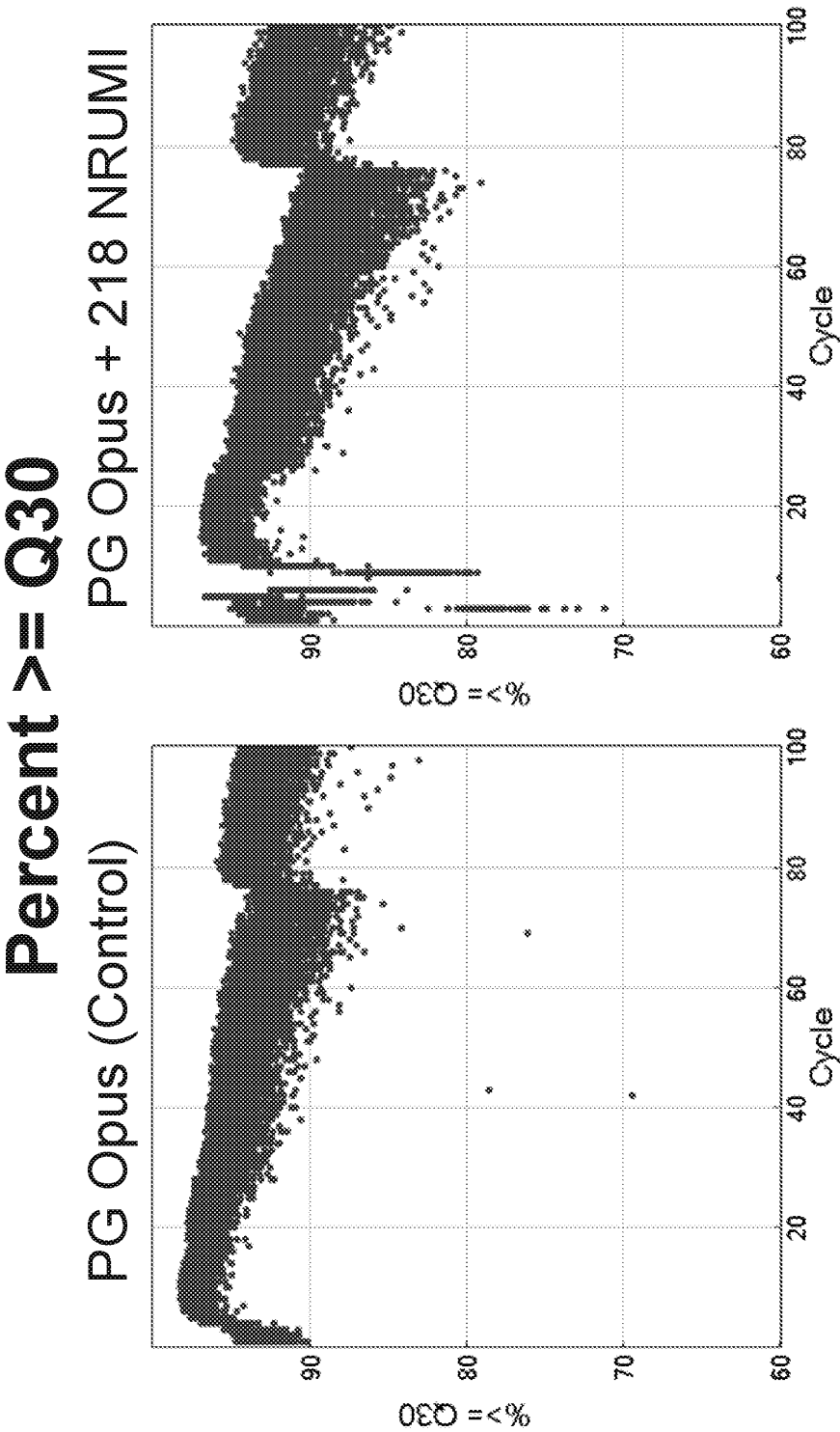


Figure 2C

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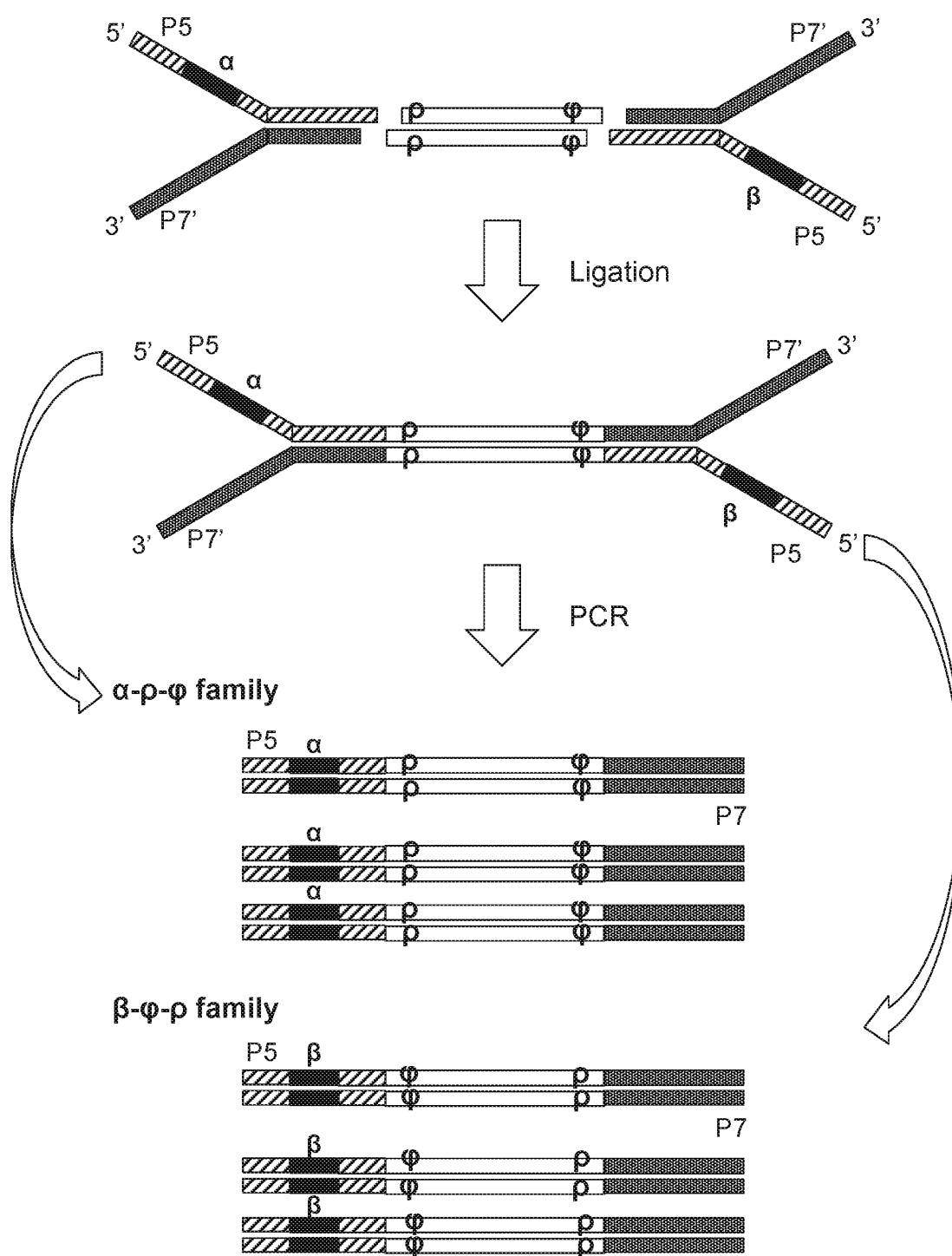


Figure 3A

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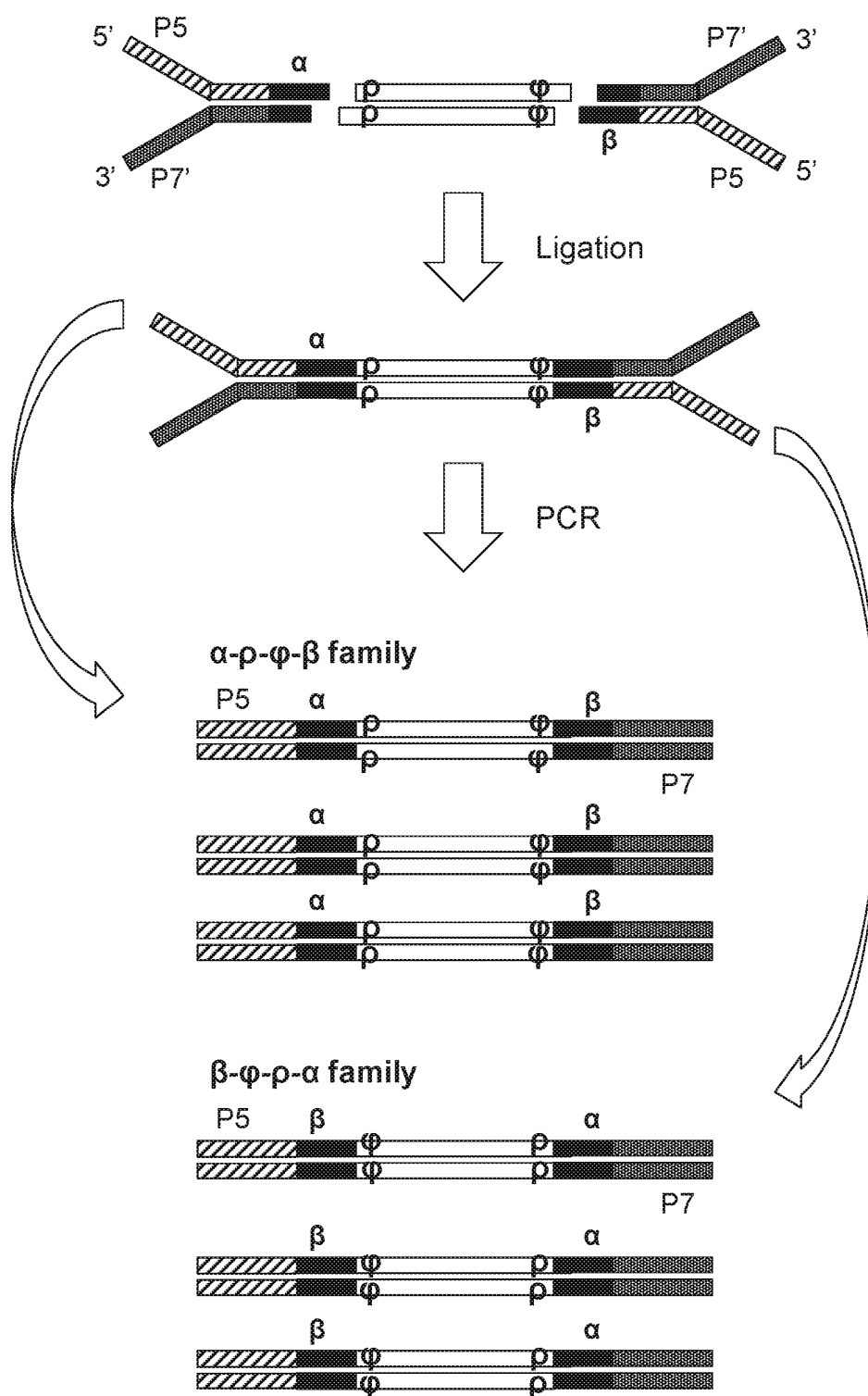


Figure 3B

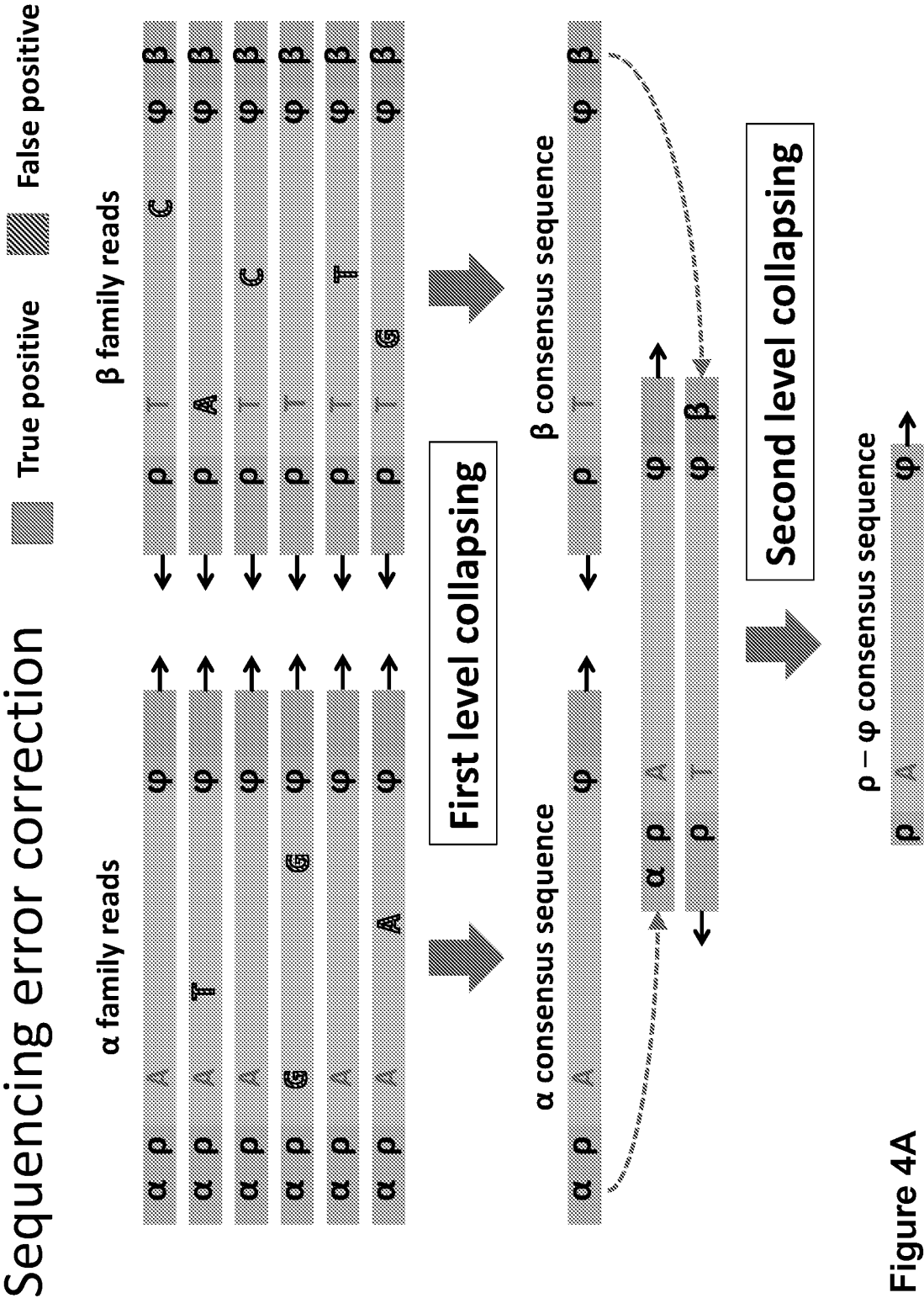


Figure 4A

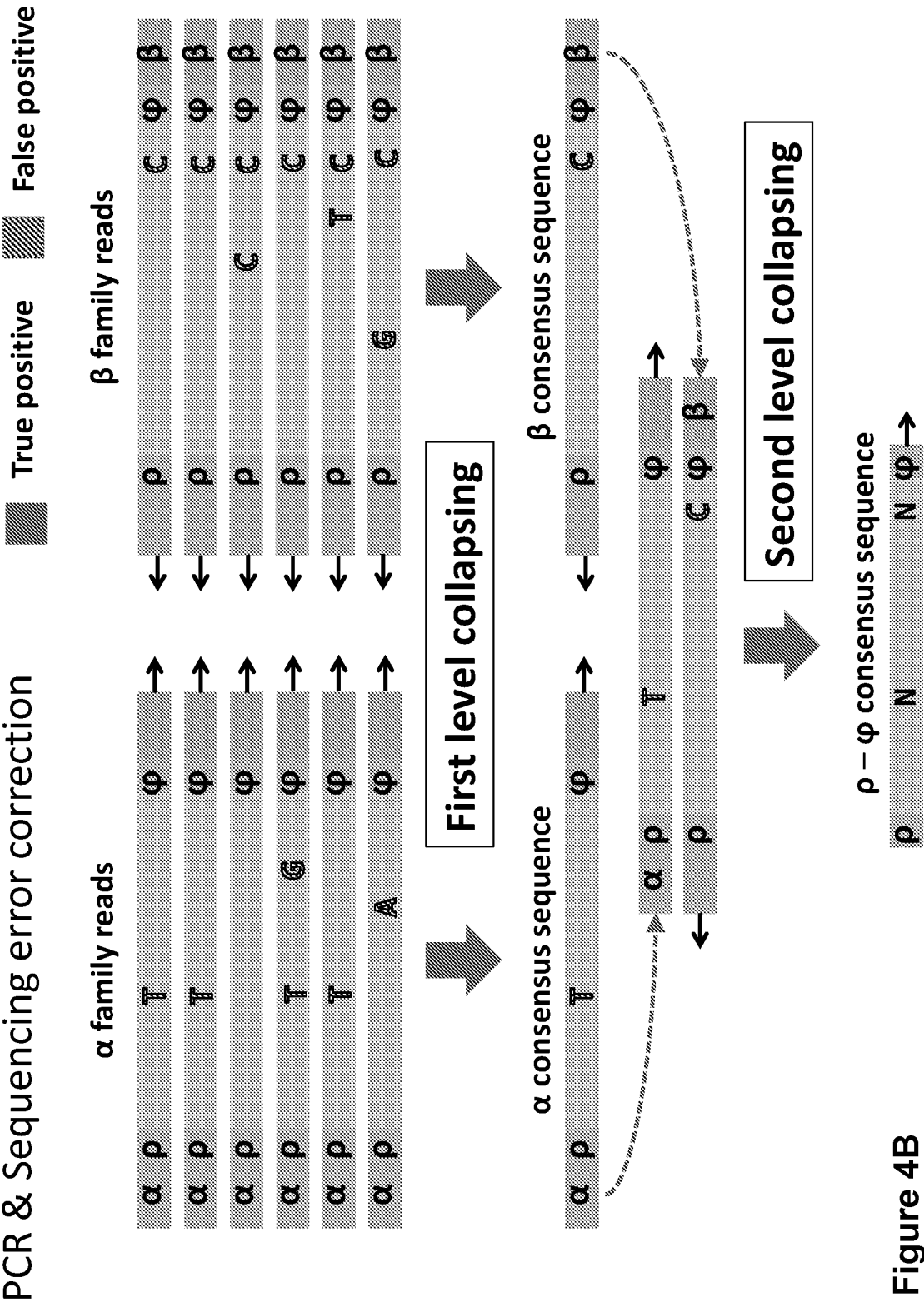


Figure 4B

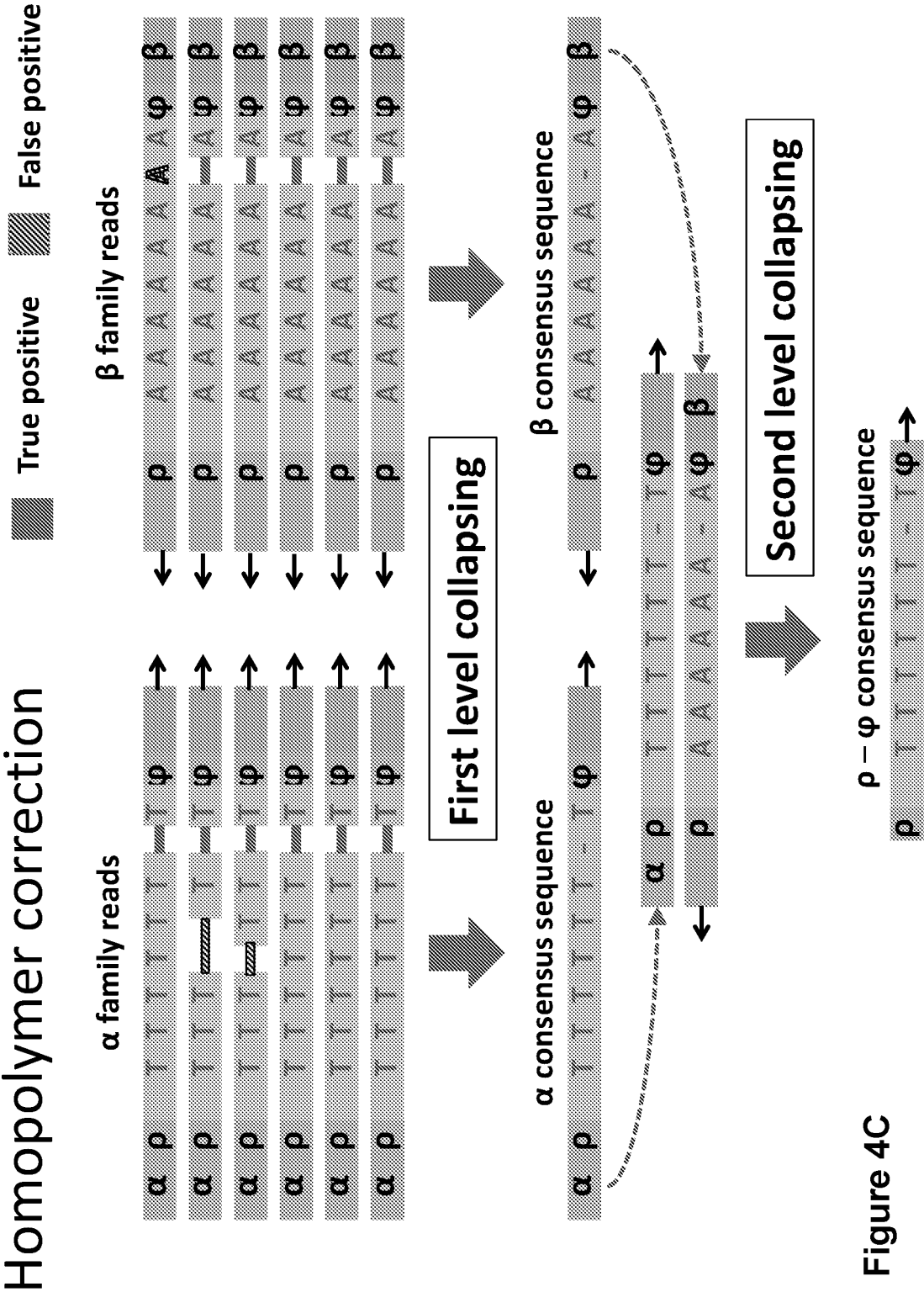


Figure 4C

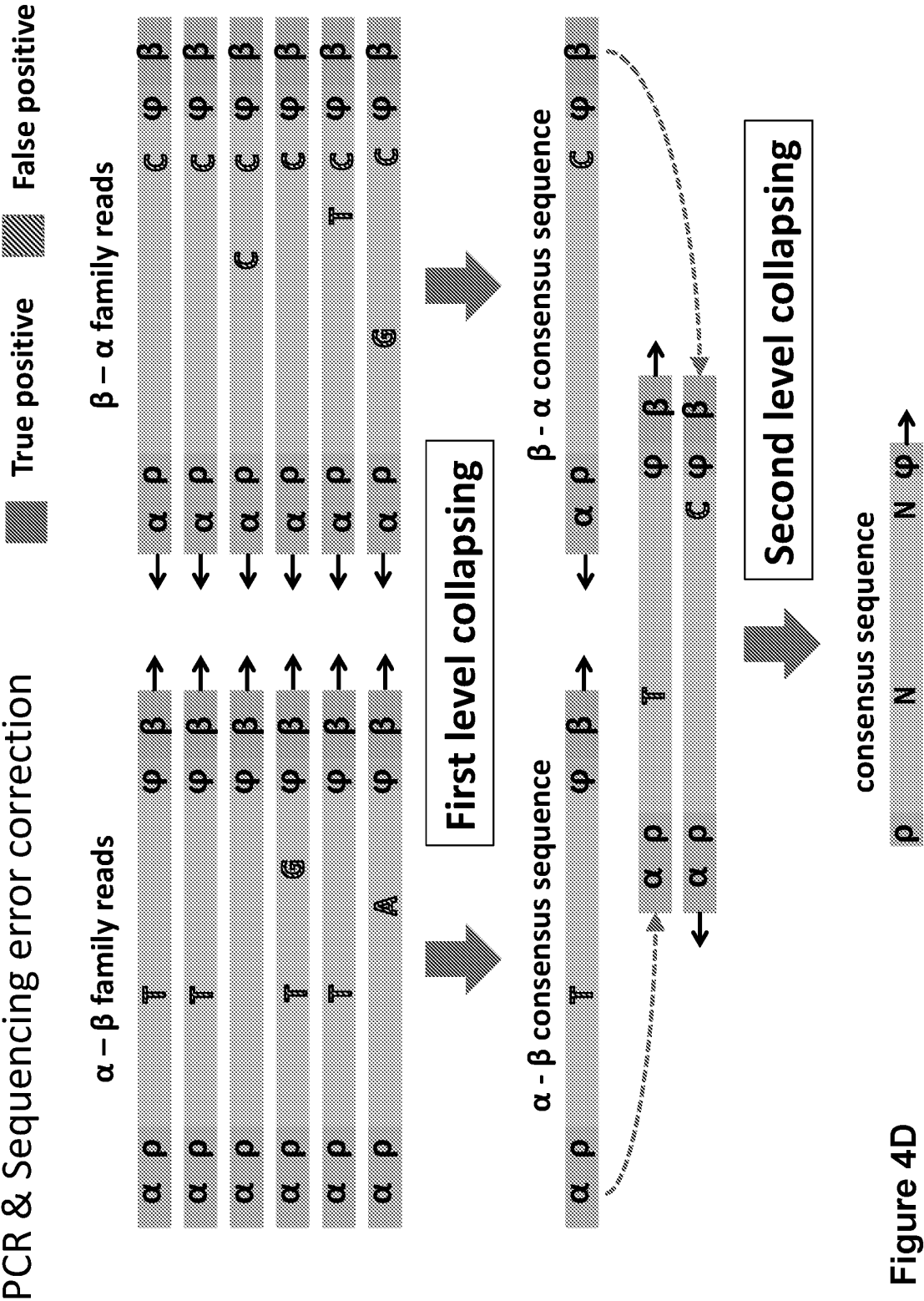


Figure 4D

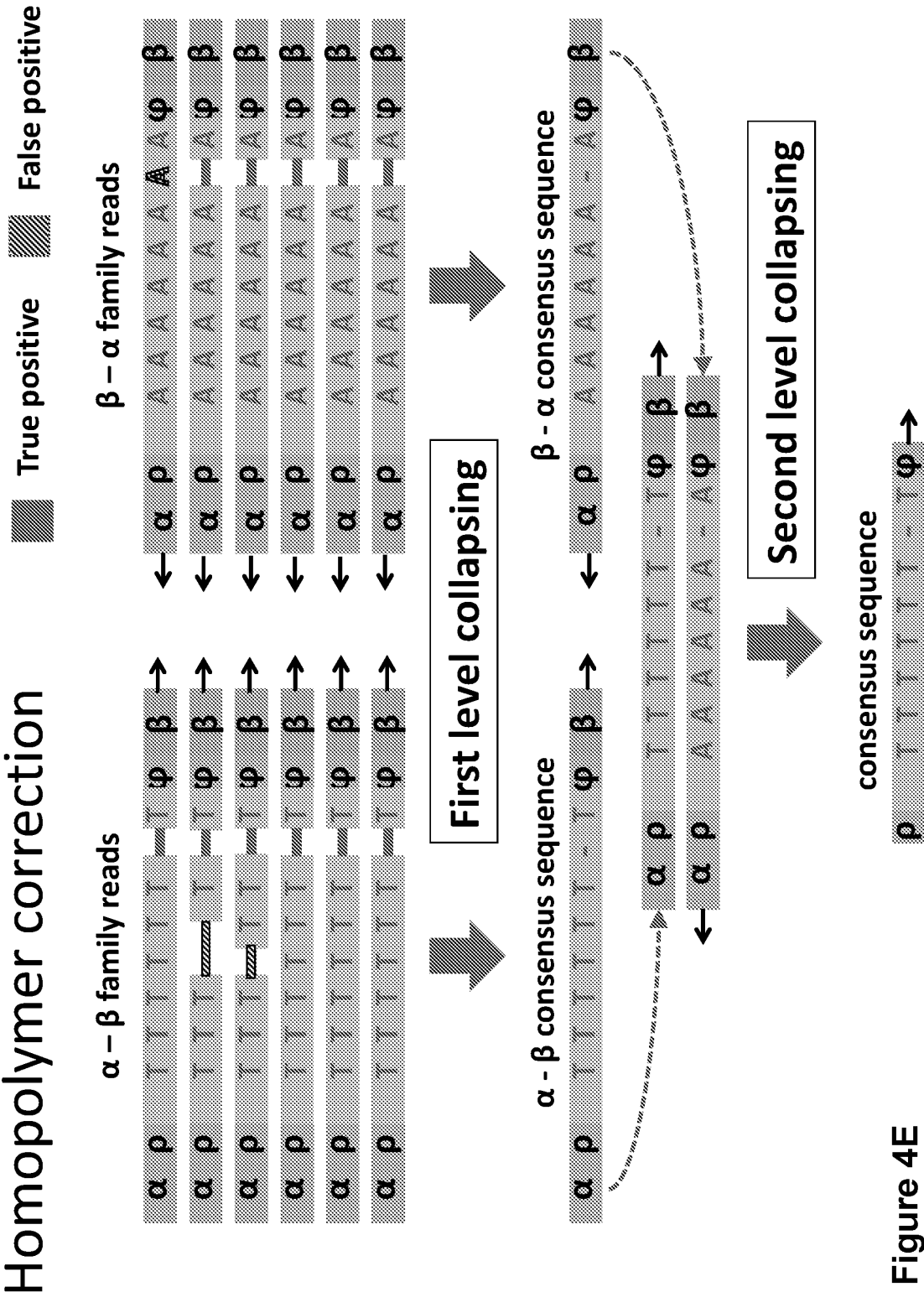


Figure 4E

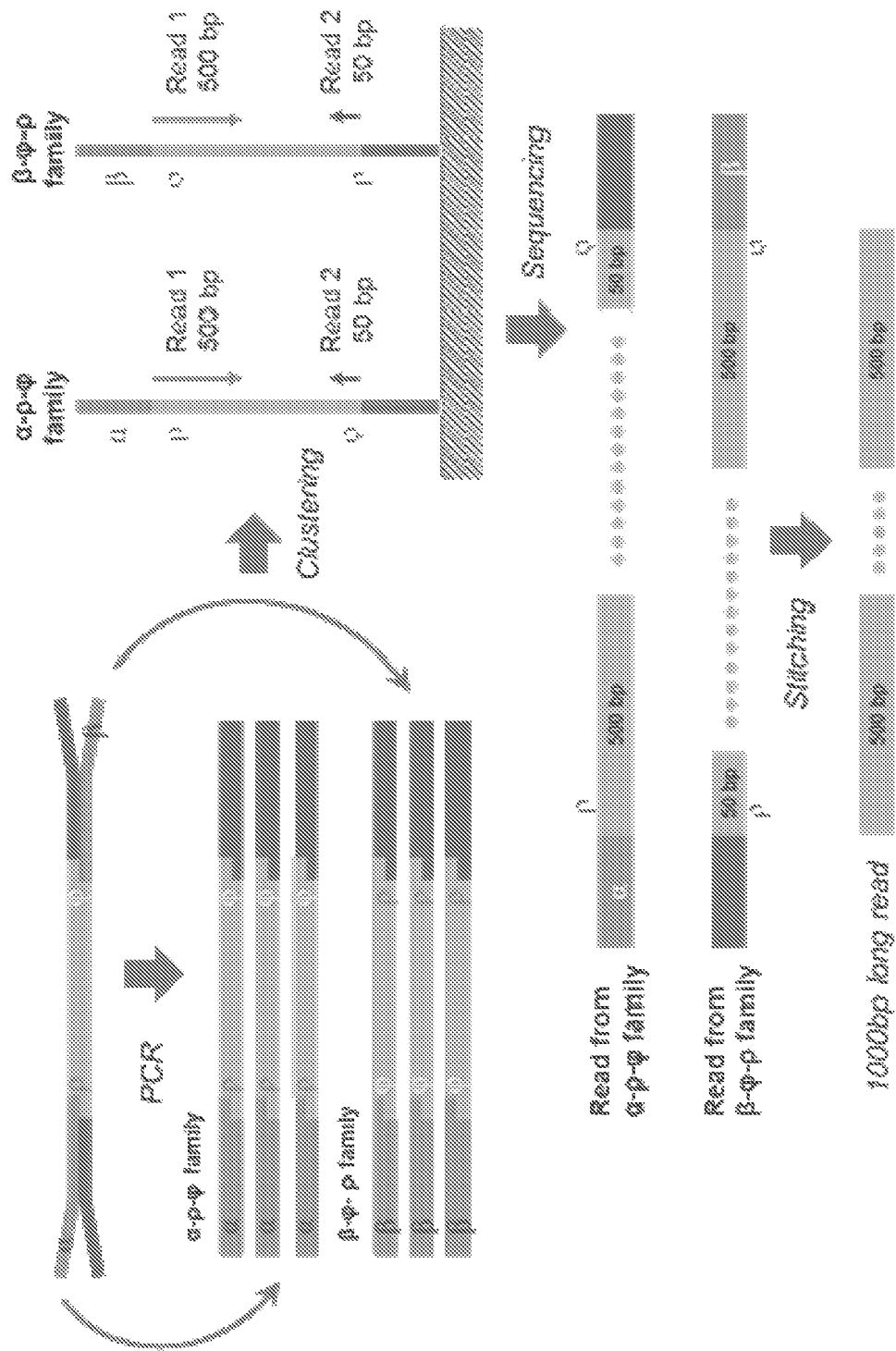


Figure 5

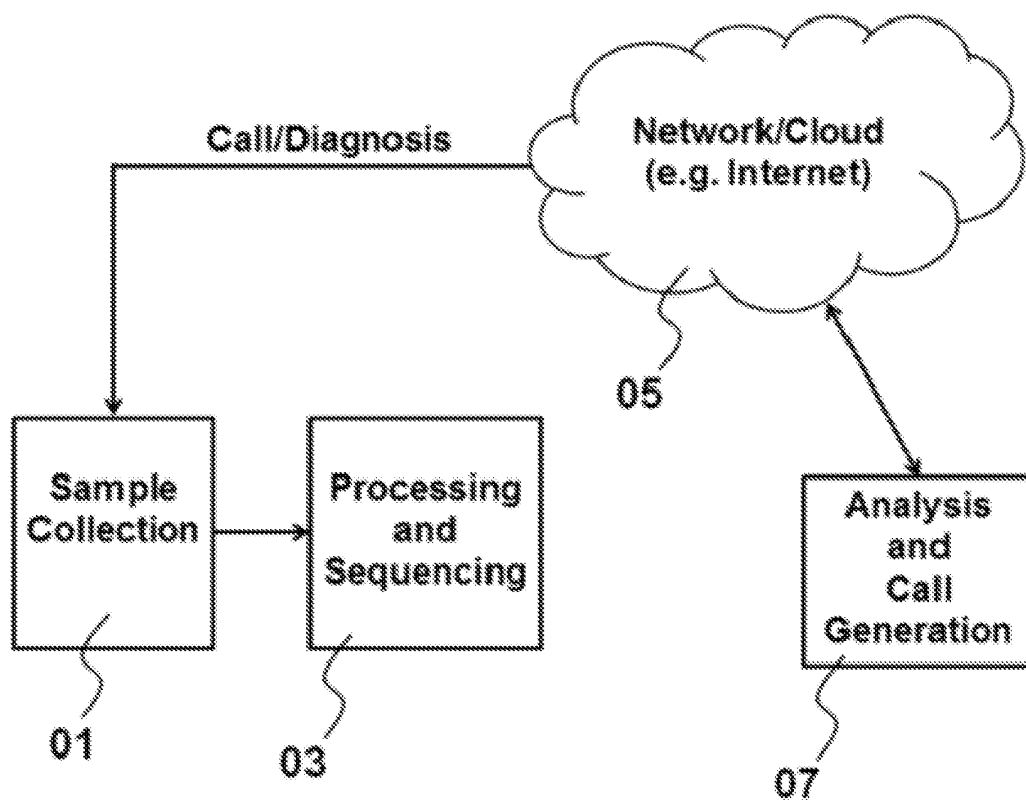
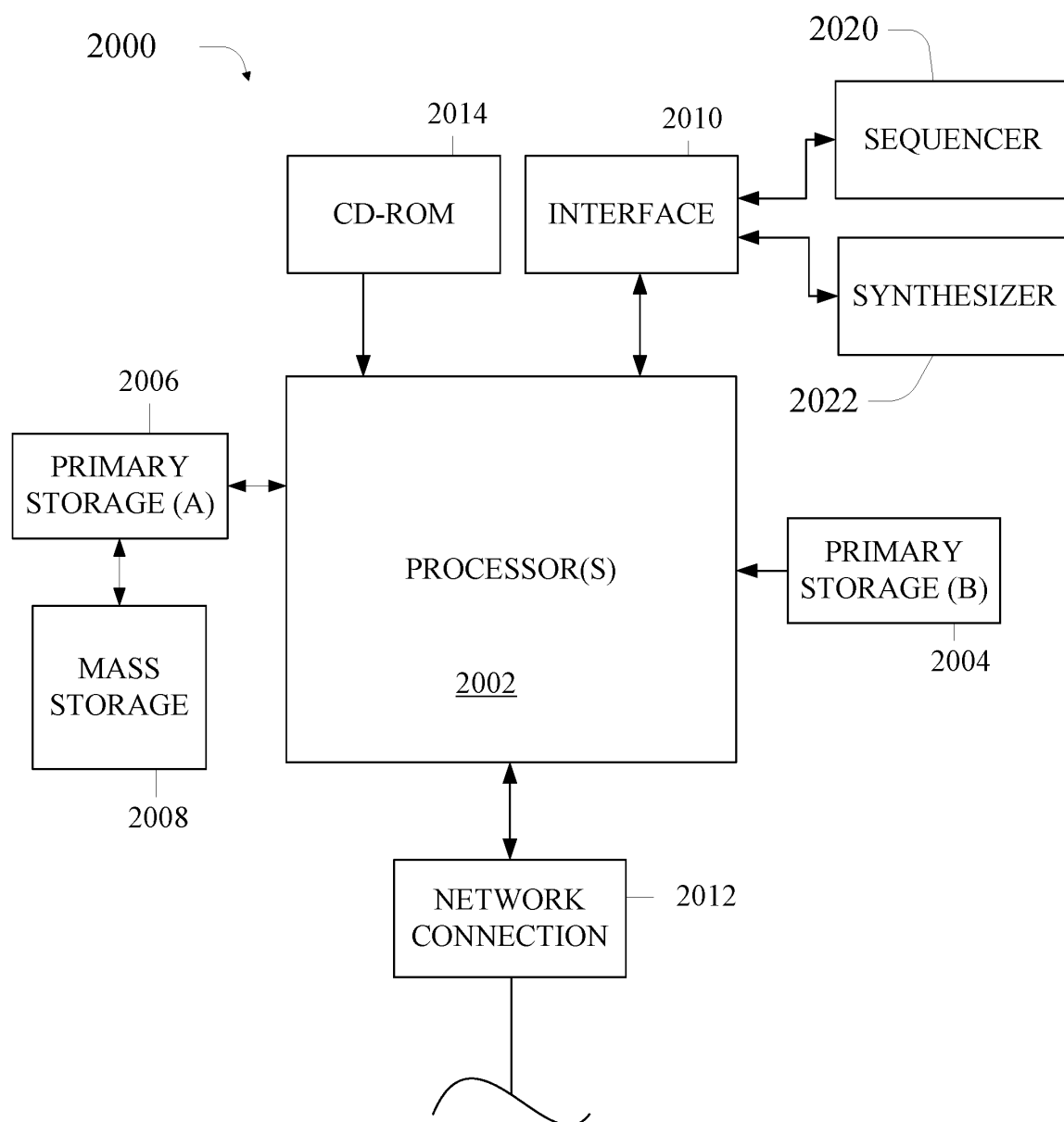


Figure 6

**Figure 7**