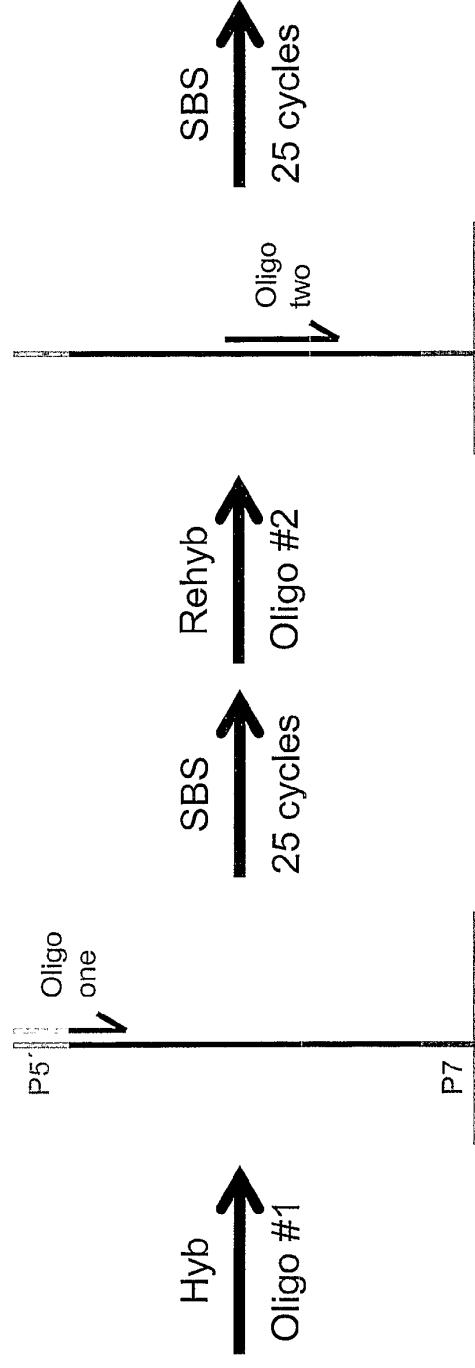


Paired-end read POP:



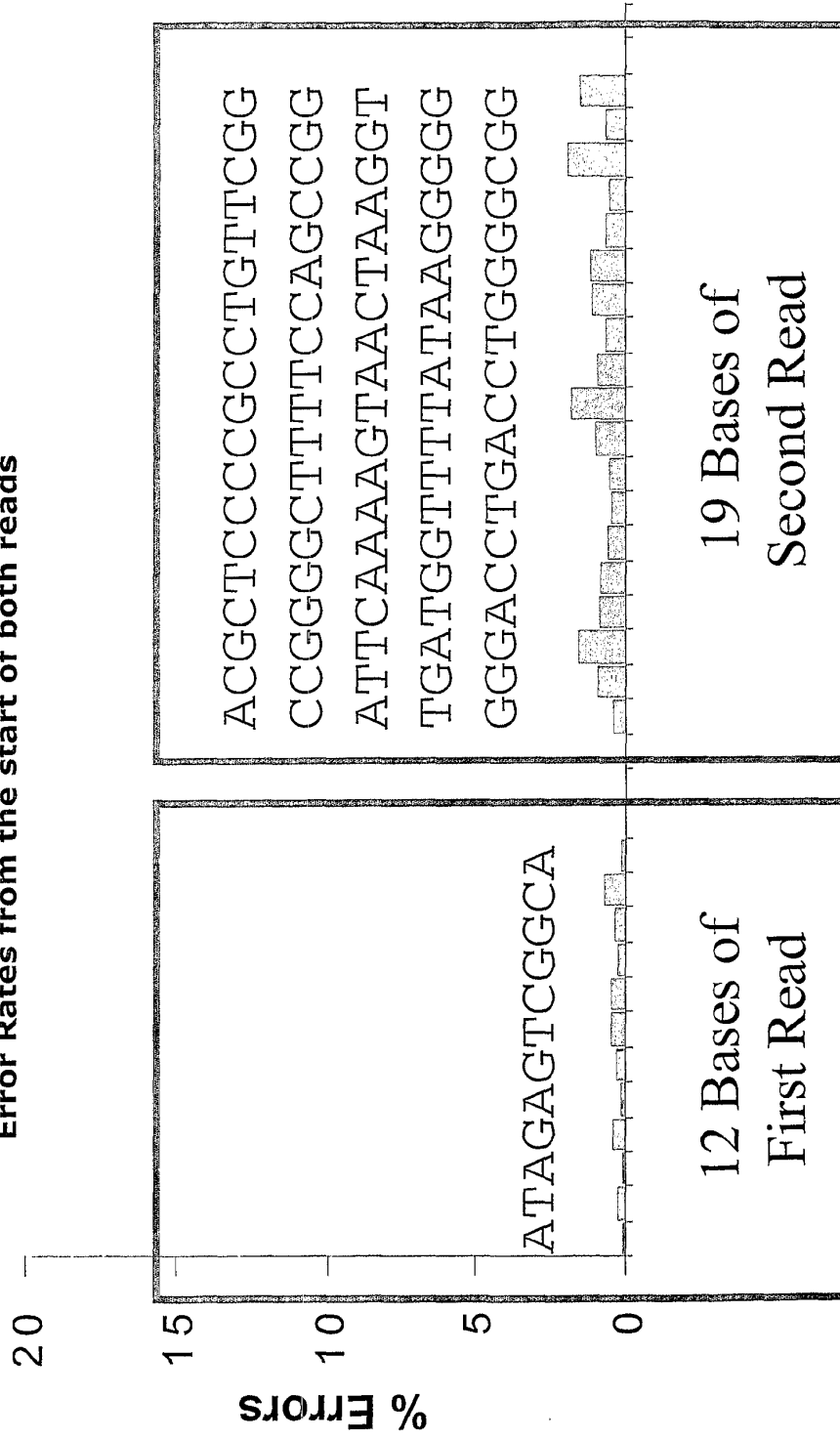
Procedure

- Hybridise oligo 1 and perform sequencing run 1
- Strip extended primer with the chip on the sequencing instrument.
- Hybridise primer 2 on instrument.
- Perform sequencing run 2
- Result is two sets of sequences obtained from different positions within the same clusters.

Fig. 1

Paired End Reads

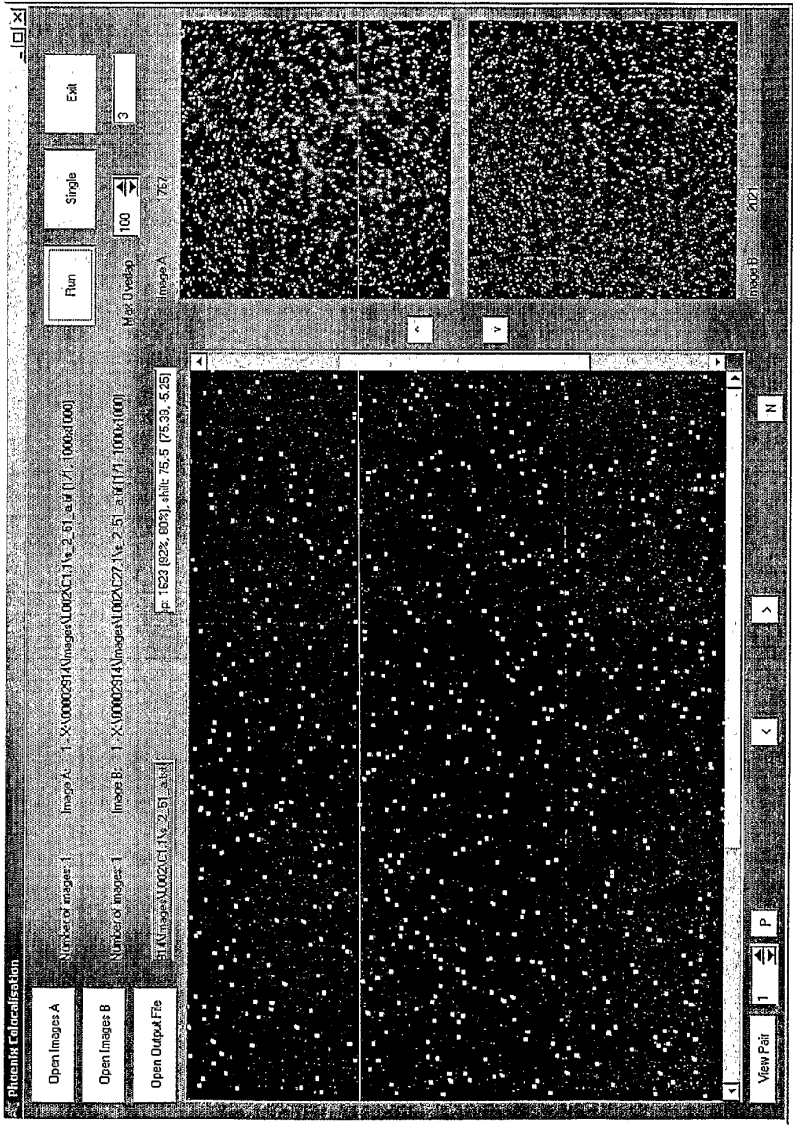
Error Rates from the start of both reads



First Cycle Intensities of Both Reads are Similar

Fig. 2

The same clusters are sequenced in each read



Phoenix co-localisation of the same tile at C1 of the two reads
Both A incorporations hence A images used
92% of Run 1 clusters align with Run 2.
7.5% of R2 do not due align with run 2 due to image shift
Therefore >99% are detected in Run 2.

Fig. 3

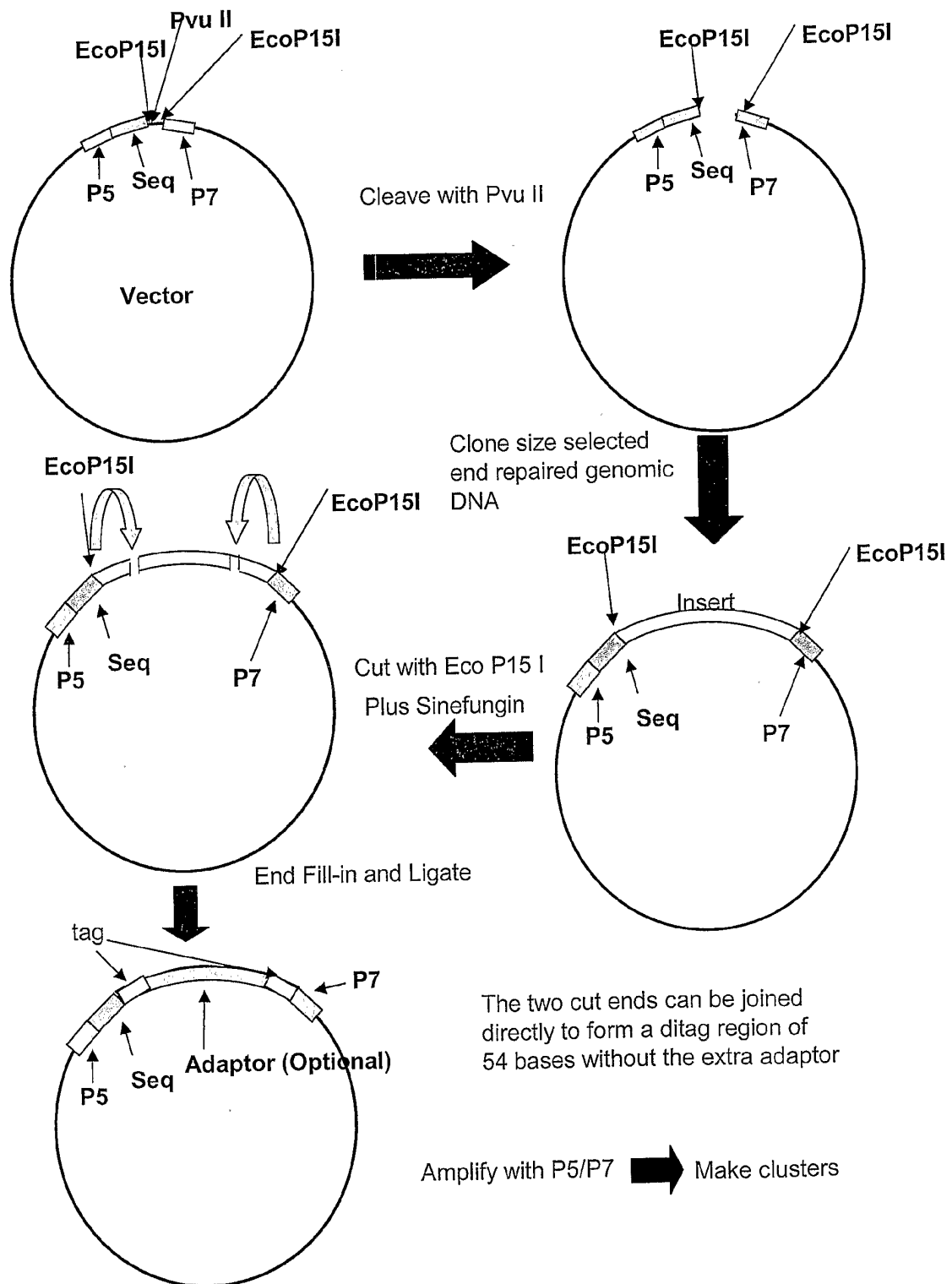


Fig. 4

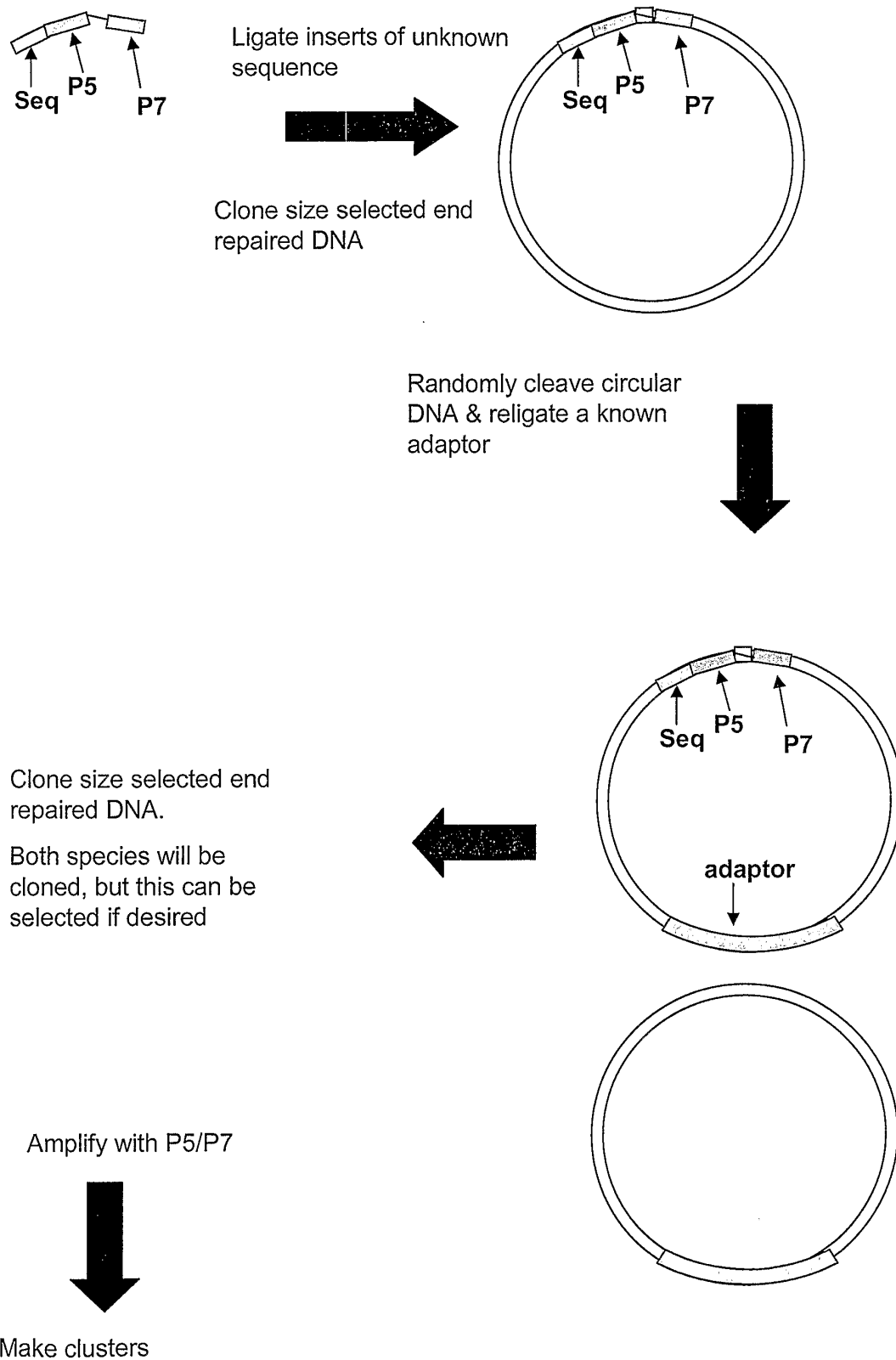


Fig. 5

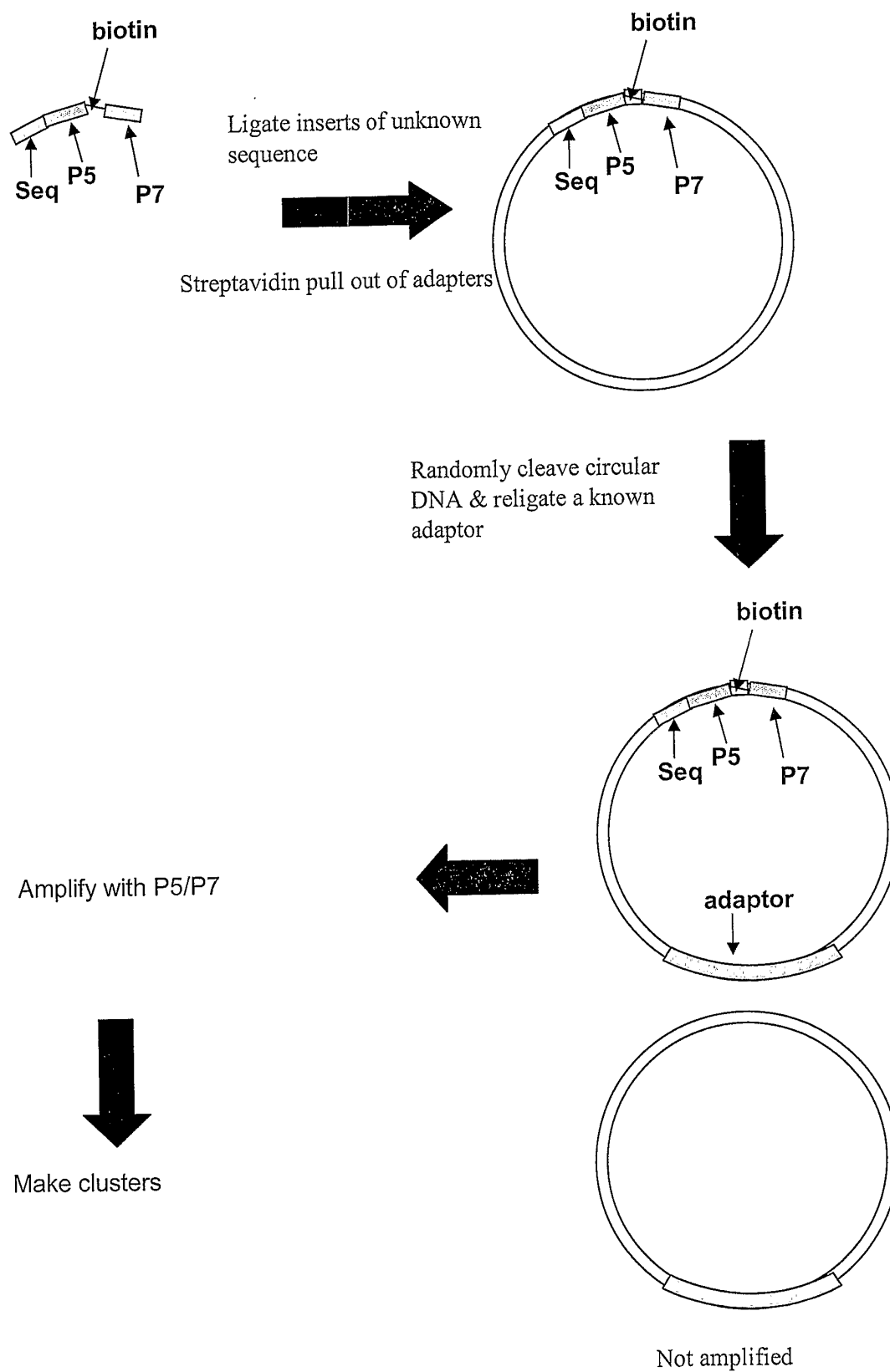


Fig. 6

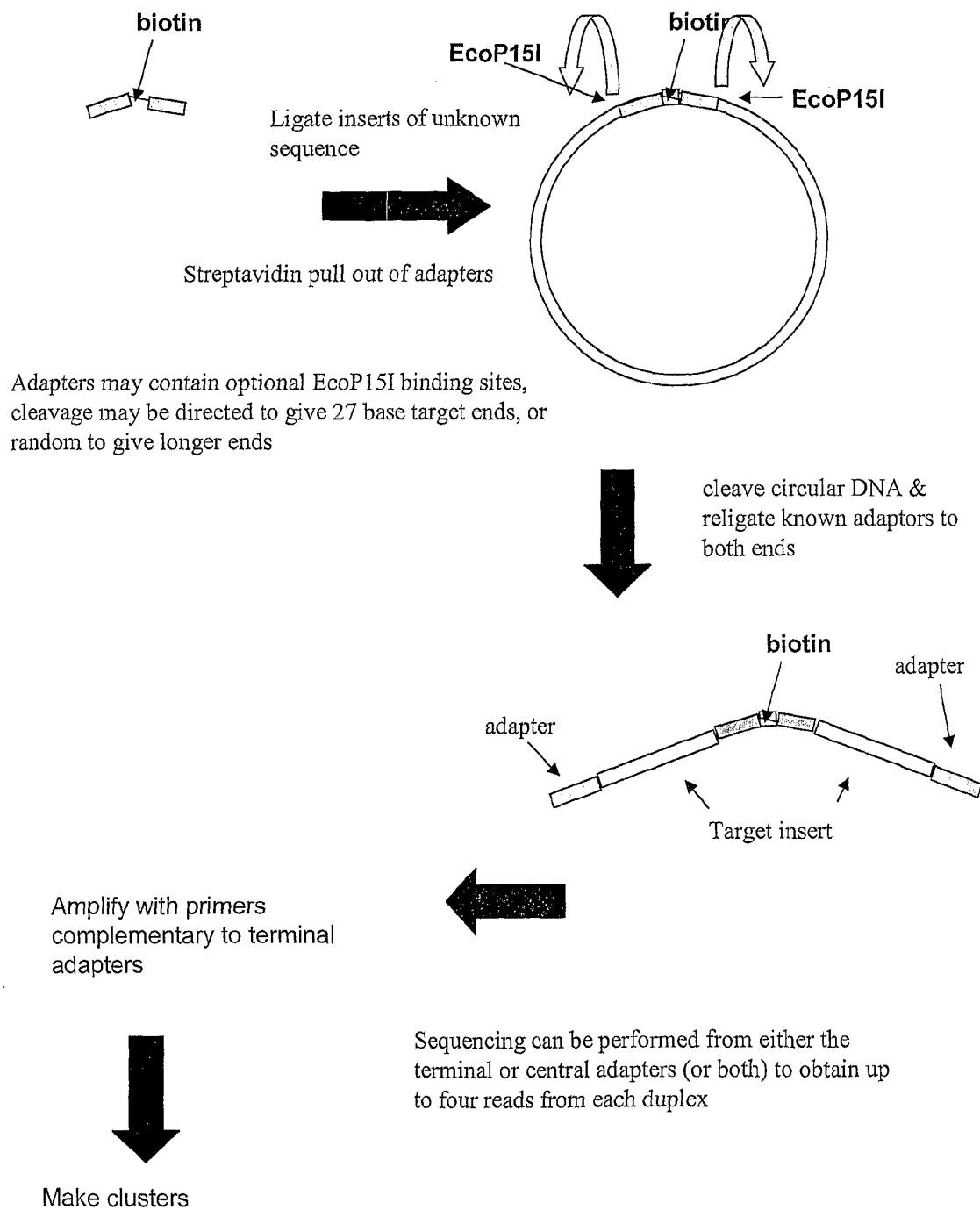
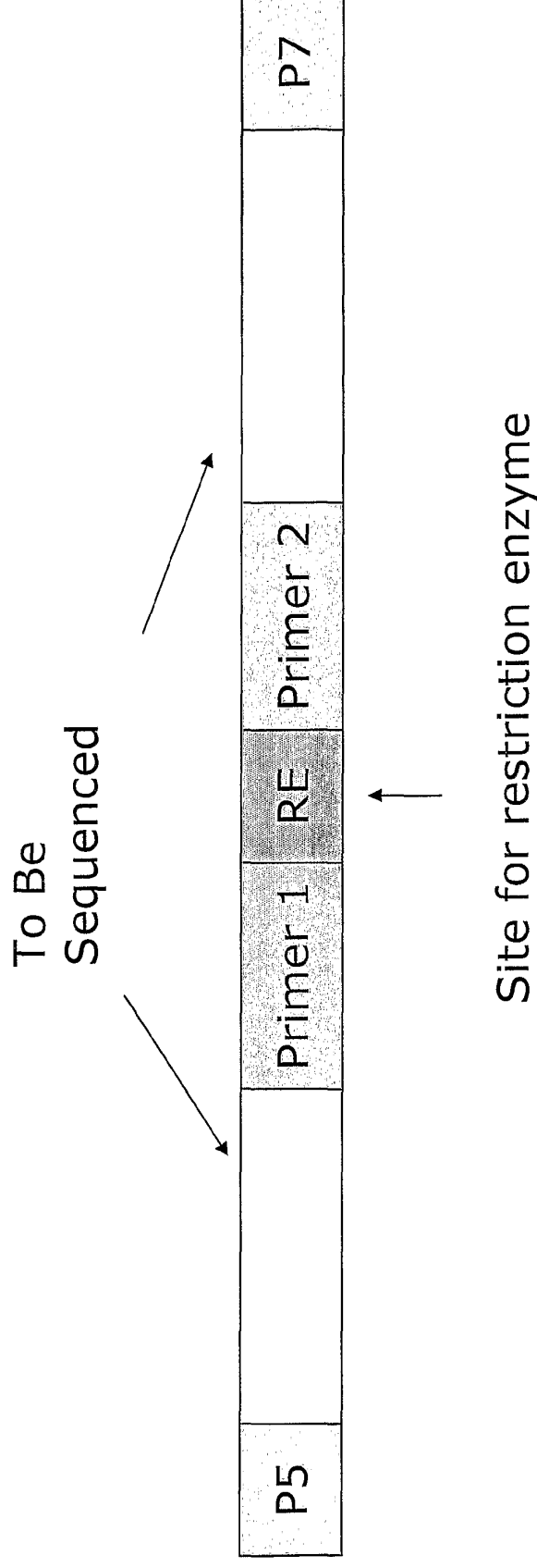


Fig. 7

Construct with Central Restriction site



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Clusters cut with restriction enzyme can be sequenced twice using two different sequencing primers

Fig. 8

Method for making PE genomic libraries with large insert sizes

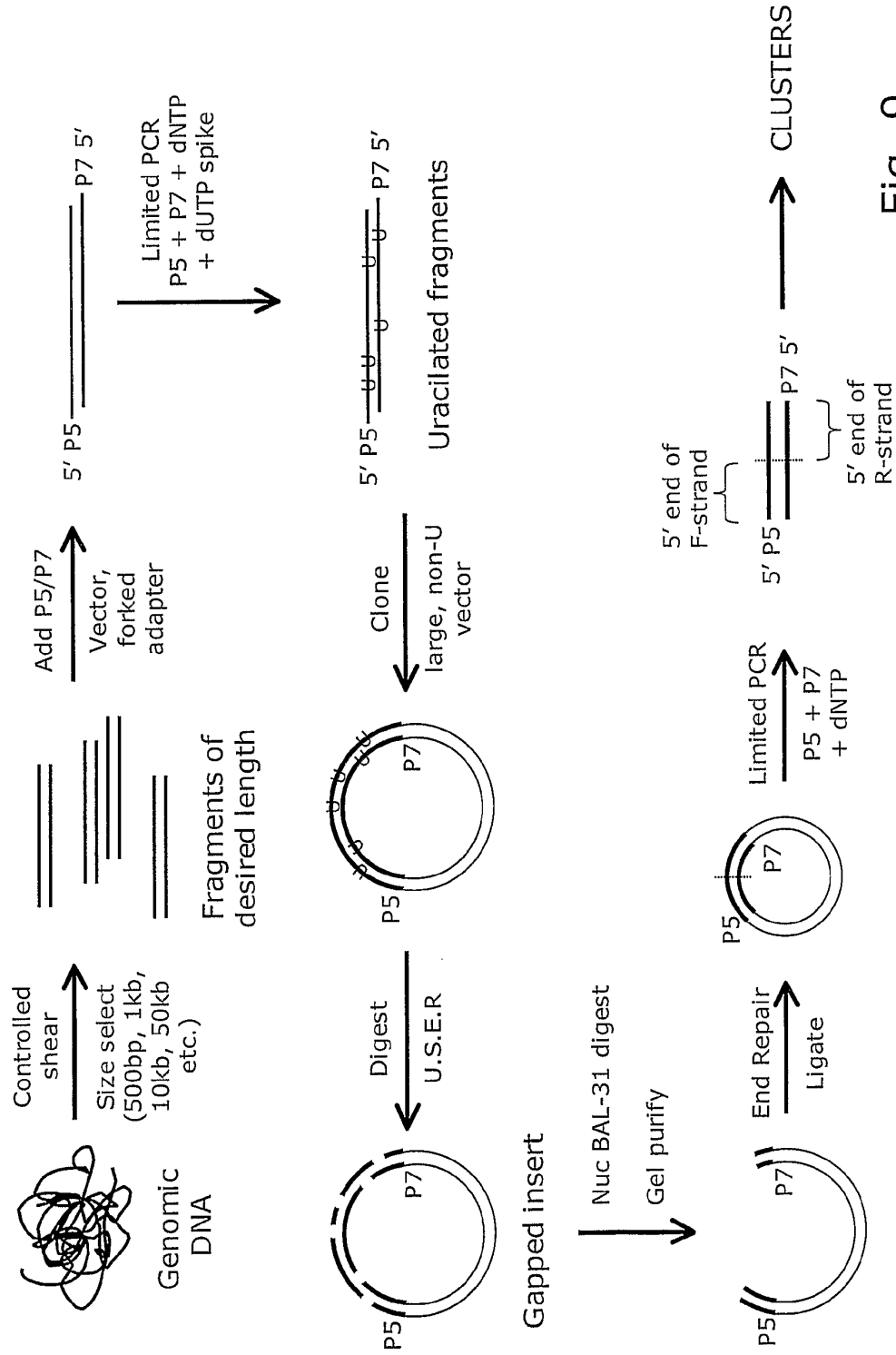


Fig. 9

Method for making PE genomic libraries with large insert sizes

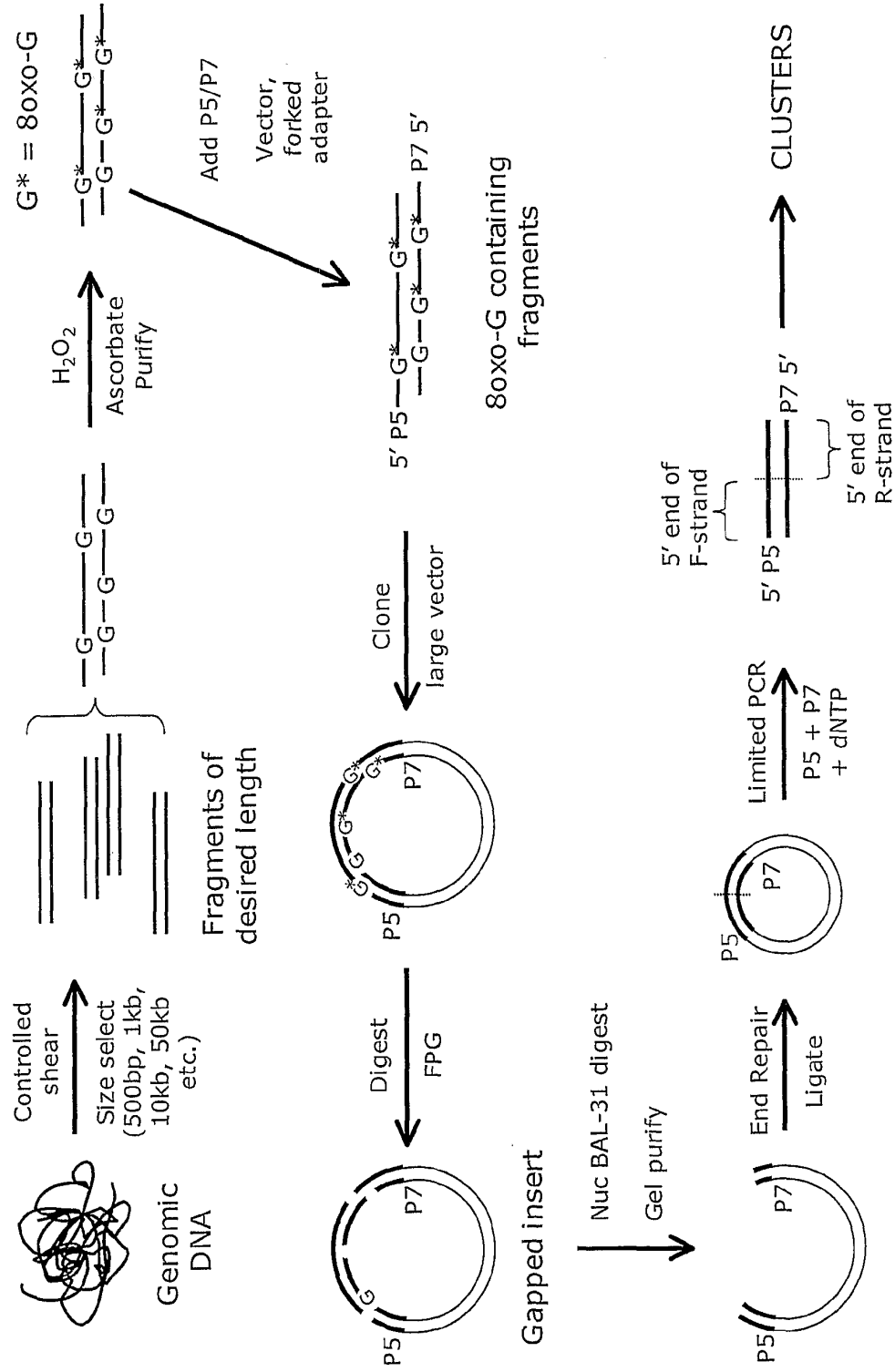


Fig. 10

Method for making PE genomic libraries with large insert sizes

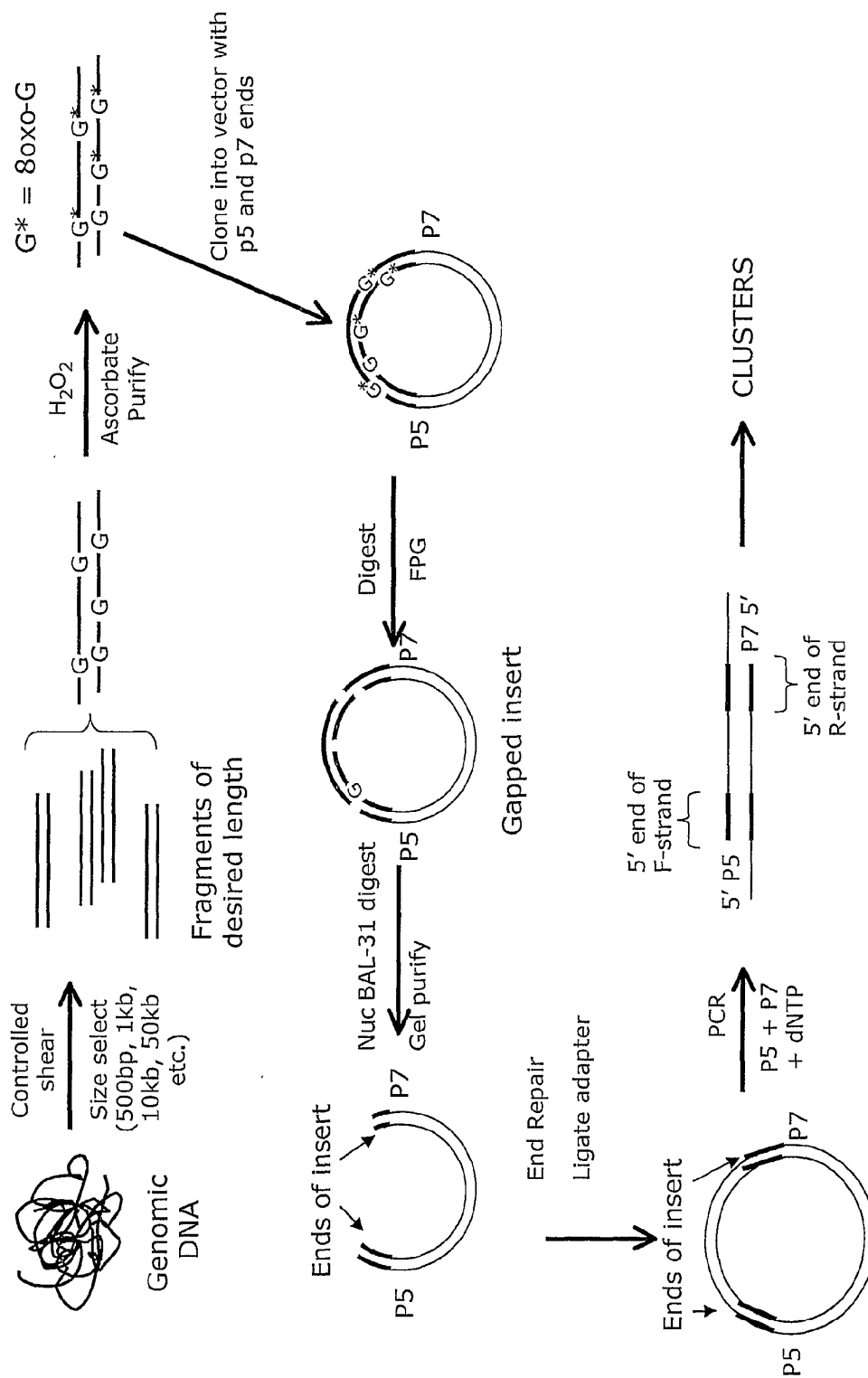
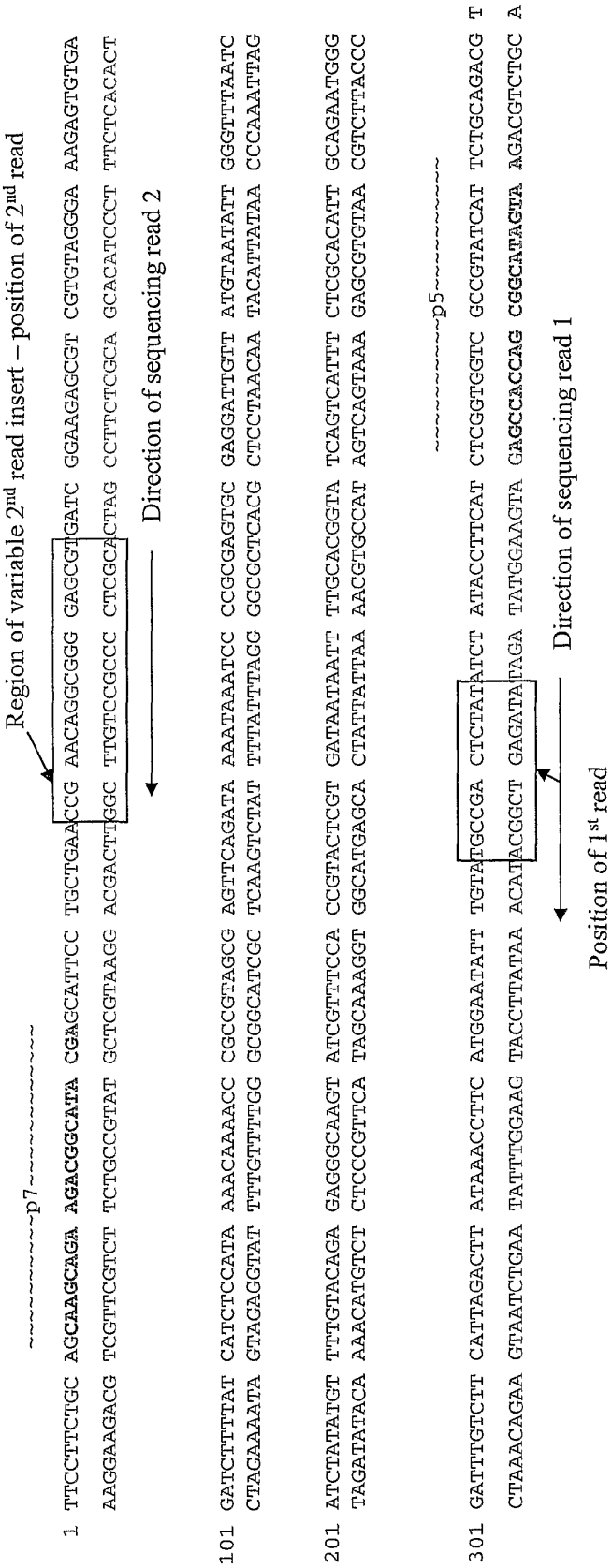


Fig. 11

One of the Five Monotemplate Sequences



Seq primer for first read: 5' AATGATACGGCGACCACCGAGATGAAGGTATAGAT
Seq primer for second read: 5' ACACTCTTTCCCTACACGACGCTCTTCCGATC

Fig. 12