

A read length exceeding 70 bases does not guarantee accurate interpretation; judgments should be made based on available sequence information and sequencing contour plots. A bimodal pattern in the sequencing results may indicate impure templates or multiple copies of the template genome. A posterior bimodality suggests mutations in the template genome. Second, seq-format data can be opened as a text file and represents the sequenced readable base sequence. The normal Ab1 peak profile is shown below:

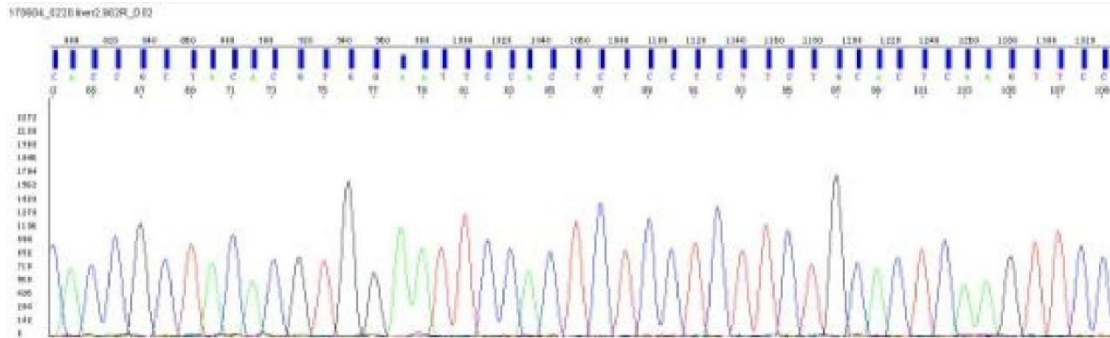


Figure 1 Sequencing peak profile

2.3 Electrophoretic band pattern of PCR products

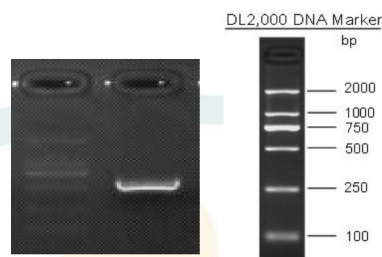


Figure 2: PCR electrophoresis band pattern of the samples

3. Project Summary

3.1 Technical information

One original sequencing color image, one sequence report, and one alignment analysis result; one electrophoretic band pattern of the PCR product.

3.2 Company Sealing

One copy of the technical documentation

3.3 Statement

Upon receiving our company's identification results, if the client has any inquiries regarding the sequencing results, they must undergo sequencing verification of the received samples within one month from the date of signature by the issuer and contact our company. After one month, our company will destroy and seal all related materials and will no longer accept any further appeals from the user.