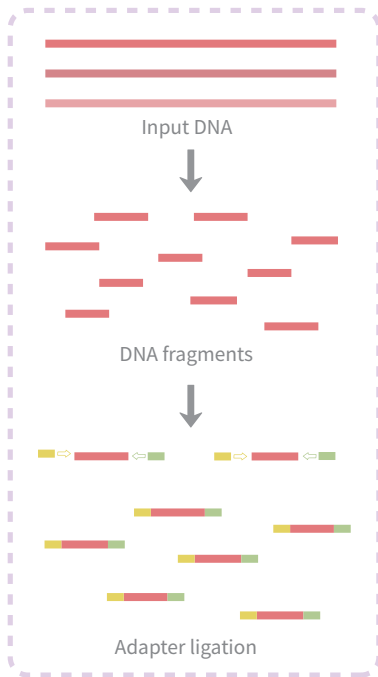


Next-generation sequencing (NGS) technologies have progressive advantages in terms of cost-effectiveness, unprecedented sequencing speed, high resolution and accuracy in genomic analyses, thus are playing an increasing important role in fields of oncology and immunology.

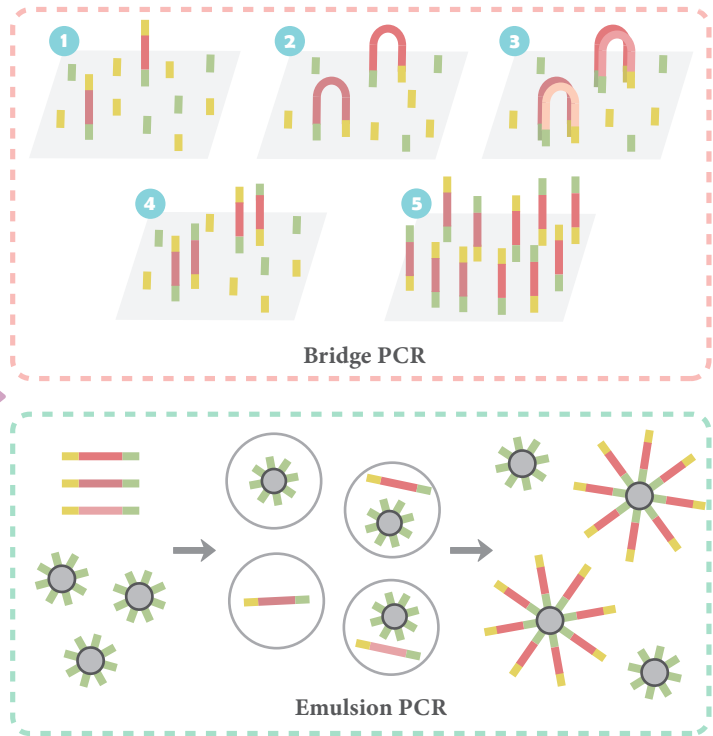
The sequencing principles of common sequencing instruments on the market: (1) first, construct a DNA template library. Obtain DNA library fragments (tens to hundreds of bases in length) by randomly breaking genomic DNA, or construct paired-end fragments that control the distance distribution. Adapter sequences were ligated to both ends of the DNA fragment and then denatured to obtain a single-stranded template library and immobilized on a solid surface. (2) Second, amplify the clones, which performed by one of several methods, such as bridge PCR and emulsion PCR. (3) Then, forming DNA clusters or amplifying microspheres of DNA cluster arrays on a chip, performing a series of cyclic reaction operations using a polymerase or ligase, and monitoring the optical events generated in each cycle biochemical reaction by a microscopic detection system. Time series analysis of the resulting array images is performed to obtain sequences of DNA fragments. These fragments are then assembled into longer contigs according to certain computer algorithms.

Creative Biolabs uses the advanced SuPrecision™ platform to support researchers all over the world with their sequencing needs for cancer.

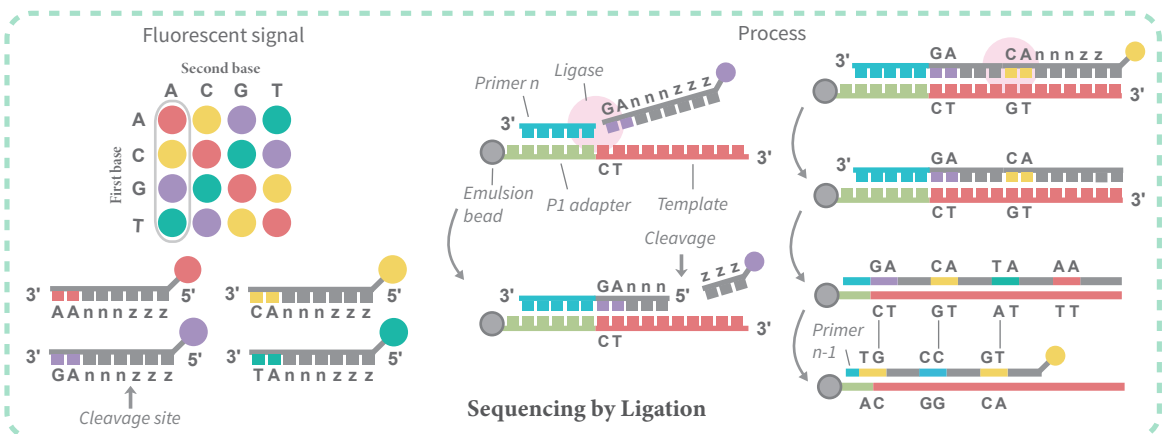
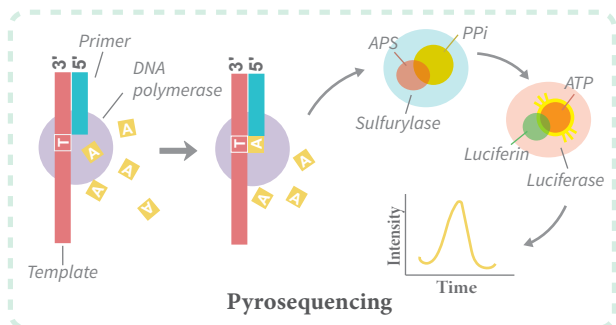
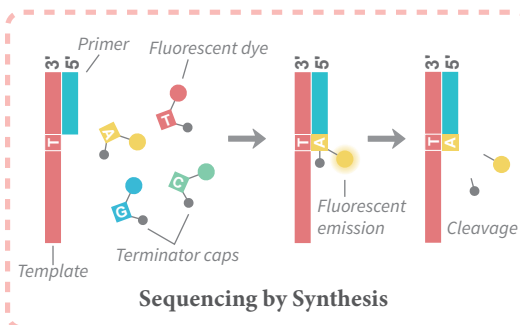
1 DNA Library Preparation



2 Clonal Amplification



3 Cyclic Array Sequencing



WHAT WE DO:

- **Whole Genome Sequencing (WGS) Service for Cancer**
- **Whole Exome Sequencing (WES) Service for Cancer**
- **Targeted Sequencing Service for Cancer**

- **Whole Transcriptome Sequencing (WTS) Service for Cancer**
- **Immune Repertoire Sequencing (Rep-seq) Service for Cancer**
- **Bioinformatics Analysis Service**