The NovaSeq 6000 System

The HTSF is proud to announce the addition of the NovaSeq 6000 sequencing system, an investment in the future of sequencing. The NovaSeq 6000 delivers a bold vision for the next decade of genomics by allowing access to the highest levels of throughput with flexible performance to complete projects more quickly and efficiently. Whether you are part of a large or small-scale project, the NovaSeq will empower you with innovative opportunities to meet your varying data needs.

Overview

The NovaSeq 6000 is currently the most powerful Illumina sequencing platform. This system provides users with the speed and flexibility to complete projects faster and with greater output than previous HiSeq systems. By releasing this system at a more economical price point, the NovaSeq makes high throughput sequencing more widely available for researchers from different scientific backgrounds.

Many projects will benefit from the faster turnaround time, flexible performance, and improved yield (i.e. reads per flow cell). By providing multiple flow cell types and read lengths, the NovaSeq can accommodate a variety of sequencing methods, project scales, and data needs. Through powerful cutting-edge technology, the NovaSeq offers new opportunities at a throughput that can fit individual project's research goals.

Solutions to Current Problems

Turn Around Time

The NovaSeq 6000 system offers higher throughput at faster turnaround times when compared to the HiSeq platforms. Run times range from ½ day for the paired end 50 cycle run on the S1 flow cell to 2 days for a paired end 150 cycle run on the S4 flow cell (Table 1). Compared to the 4-day sequencing time of the HiSeq 4000 paired end 150 cycle, the NovaSeq can sequence the same read length on the latest S4 flow cell in half the time

Table 1: Run Time Per Flow Cell

Run Time	SP§	S1	S2	S4
2 × 50 bp	~13 hr	~13 hr	~16 hr	N/A
2 × 100 bp	N/A	~19 hr	~25 hr	~36 hr
2 × 150 bp	~25 hr	~25 hr	~36 hr	~45 hr

§ The SP cell will be available in Fall of 2019

Yield and Requirements

Currently, the NovaSeq provides more data when compared to previous HiSeq systems. In previous systems, the HiSeq 4000 could provide a maximum of 2.5 billion reads per flow cell. The increased quantity of data from S4 flow cells will allow larger-scale projects to pursue higher output applications. Smaller format flow cells, e.g. S1 and SP, maintain the system's flexibility for smaller-scale projects. To get ensure that you get the most reads possible out of your NovaSeq submission, there are requirements to follow. Table 2 in the Appendix elaborates on the minimum volume and molarity required to sequence on both standard and XP versions of the NovaSeq. The number of clusters per lane and reads per lane are also included. When designing your experiment to best fit the NovaSeq, it is also fundamental to consider the number of samples to include in your pool. Table 3 in the appendix provides the recommended number of samples per pool for specific library preparation methods. If the HTSF is not using a type of library preparation for the sequencing format you are interested in, please be sure to contact the HTSF.

Summary

The NovaSeq 6000 system is the most powerful high-throughput sequencing system available today. This system creates new sequencing possibilities and makes these possibilities more widely available for researchers from all backgrounds. This innovative concept for the next decade of sequencing provides a more flexible alternative to the HiSeq systems while providing improved turnaround time with the capability of providing an unprecedented amount of data.