NUSeq Sequencer Selection Guide

February 2024

Please refer to the NUSeq Sequencing Technologies page for the current list of sequencers and their capabilities. Familiarity with the sequencers' capabilities will help make informed decisions with consideration of the following key factors.

Key deciding factors:

1. How many reads do I need?

2. What read length do I need?

3. Between cost effectiveness and turnaround time, which one is more important to me?

4. Do I need to be consistent with previous sequencing runs?

1. Number of Reads Needed: Depending on how many reads you need, you might find only one sequencer meets your needs. This is especially true if you need to sequence a large number of samples, and/or each sample requires a large number of reads like in the cases of whole genome sequencing, single-cell sequencing, and high-resolution spatial transcriptomics. In these cases, the Illumina NovaSeq X Plus is often the choice. If the number of reads needed falls within the range of intermediate or low throughput sequencers, you might find that more than one sequence can suit your needs. In this case, the other questions may help you narrow down your choices.

For projects that do not need a lot of reads, 100 or multiples of 100 million reads can be ordered. For users who used to order 300 million SE50 reads on the HiSeq 4000, you can continue to order 300 million SE50 reads using "General SE50 Sequencing" with no change in cost.

2. Read Length Needed: As shown on the NUSeq Sequencing Technologies page, different sequencers offer different read lengths. If you need long reads (e.g., over 10 kb), a long-read sequencer from Oxford Nanopore or PacBio is required. If short read length (50-400 bases) is sufficient, short read sequencers from Complete Genomics, Element Biosciences and Illumina offer a variety of read lengths to choose from. Because these

technology providers price their technologies differently, shorter read length does not necessarily mean lower cost. Sometimes you may find longer reads are more cost effective if turnaround time is less important (see below).

3. Balance between Cost Effectiveness and Turnaround Time: In the Iron Triangle of Quality – Speed – Cost, a choice has to be made as it is impossible to attain all three goals at the same time. Fortunately, all the core's sequencers produce high quality data. The choice is between speed and cost. With some advance planning, you can achieve cost efficiency without affecting your project progress. Best cost efficiency is typically achieved through pooling multiple users' projects together. For time sensitive situations, we have sequencers that provide a quick turnaround time, which is achieved by setting up dedicated runs.

4. Consistency: If you need to be consistent with previous sequencing runs, the simplest approach is to utilize the same sequencer that was used before and maintain the same setup. It should be noted that some of the earlier generations of Illumina sequencers may be retired due to technology upgrades. As Illumina sequencers are backward compatible and use the same basic sequencing chemistry, newer Illumina sequencers can be used. Batch effects can be removed bioinformatically.