

Sample specification

Materials to be provided:

### **1. Sequencing service of quantified library**

-Quantified Library

The library (or pool of libraries) should be provided at a concentration of 2nM, and minimum volume of 25ul

Please also include: Bioanalyzer and Q-RT-PCR outputs

For first time users, we can provide quantified controls of RNA-seq and ATAC-seq libraries for reference to calculate loading concentration

- Loading concentration
- Sample spreadsheet (with barcodes for demultiplexing)
- A ftp/sftp-accessible folder with a good network connection where to transfer the output demultiplexed fastq files

### **2. Quantification and Sequencing service**

-Library

The library (or pool of libraries) should be provided at a minimum volume of 25ul

- Sample spreadsheet (with barcodes for demultiplexing)
- A ftp/sftp-accessible folder with a good network connection where to transfer the output demultiplexed fastq files

Output:

-Demultiplexed fastq files at the provided ftp/sftp-accessible folder. We can also upload the samples to BaseSpace or provide a Globus endpoint as an alternative.

Notes:

The optimal output for one run of Nextseq 500 is 800 million paired end (PE) reads in high output (HO) mode and 260M PE reads in mid-output (MO) mode.

If performing sequencing service of a quantified library, we cannot guarantee that such output will be achieved, as it is strongly dependent on the loading concentration and calculating the loading concentration may be challenging, depending on the type of library. We will repeat the run only if Illumina tech support acknowledges an instrument failure and issues a refund to us.

If we are provided with a quantified library and loading concentration, we will generally run a sample within 2-weeks of receiving it. More specific run times will be provided on a project-to-project basis.

We reserve the right to refuse loading of a library that does not pass our QC because of its fragment size distribution (presence of high concentration of adapter dimers), if not enough material is provided or if the library is too diluted.