

NovaSeq X Plus Order Form

For sequencing-ready libraries

**Contact Information**

|  |  |
| --- | --- |
| Date: |  |
| Customer name: |  |
| Customer address: |  |
| Phone (lab): |  |
| Phone (mobile): |  |
| Email address: |  |
| PI (or lab head) name: |  |
| PI (or lab head) email: |  |
| PI (or lab head) signature\*: |  |

\*By signing, you acknowledge and accept BRF charges, terms and conditions.

**Billing Information**

|  |  |
| --- | --- |
| ANU account code (ANU customers): |  |
| Non-ANU customers email address\*\*: |  |

\*\*A tax invoice will be emailed to the PI/lab head, unless alternative billing information is provided.

Phone: +61 2 6125 4326

Email: brf@anu.edu.au

Website: https://jcsmr.anu.edu.au/research/facilities/brf

The Australian National University

131 Garran Road (Level 2), Acton ACT 2601, Australia

**Data Output (please select your desired option)**

|  |  |
| --- | --- |
| ❑ | Analysis by the ABC (contact abc@anu.edu.au or 6125 1128 for a consultation) |
| ❑ | Purchase a 2 TB hard drive from the BRF ($210.00 per hard drive) |
| ❑ | Supply your own hard drive\* |
| ❑ | BaseSpace Sequence Hub |

\*The amount of storage space required on the hard drive varies based on the flow cell used in the sequencing run. If supplying your own hard drive, please bring this hard drive to the BRF at the same time you submit your sample(s). It is your responsibility to keep a backup of your data even if it is being analysed by the ABC. All data must be checked by the customer within 2 weeks of receiving it. Any problems must be reported to the BRF within this time.

**Libraries and Sequencing Parameters**

The table below details flow cell types (1.5B, 10B and 25B) and their output in gigabases (Gb) or terabases (Tb) and single-end reads in billions (B) for a given read length.

|  |  |  |  |
| --- | --- | --- | --- |
|  | **1.5B** | **10B** | **25B** |
| **2 × 50 bp**  **(100 cycles)** | ~165 Gb | 1.6 B | ~1 Tb | 10 B | N/A |
| **2 × 100 bp**  **(200 cycles)** | ~330 Gb | 1.6 B | ~ 2 Tb | 10 B | N/A |
| **2 × 150 bp**  **(300 cycles)** | ~500 Gb | 1.6 B | ~3 Tb | 10 B | ~8 Tb |

Please choose your desired reagent kit and sequencing parameters below.

|  |  |
| --- | --- |
| Reagent kit: | e.g. 10B flow cell, 300 cycles |
| Sequencing parameters: | e.g. 150 bp paired-end, or 300 bp single-end |

Please describe the nature of your sample(s) below.

|  |  |  |
| --- | --- | --- |
| **Illumina Method** | | **Non-Illumina Method** |
| Library kit used: | e.g. Illumina DNA Prep | Please supply the library preparation protocol you used. Custom adapter and primer sequences also need to be included. |
| Part number: | e.g. 20060060 |
| Lot number: |  |
| Sample 1 | e.g. mouse liver genomic DNA | |
| Sample 2 | e.g. mouse genomic DNA exon capture | |
| Sample(s) concentration | nM, ng/µL | |

Where possible, we require a fragment analysis report for your samples, quantified on instruments such as the Agilent Bioanalyser or TapeStation (or similar). Please email a copy of your quantification results to the BRF email address, as well as a digital copy of this completed form.

After filling in this form, please print a copy and submit it to the BRF office with your sample(s) and hard drive if you are supplying one.

If your library requires custom primers for sequencing, these will need to be supplied with the samples to perform the sequencing run. The custom primers must be brought in individual tubes. Do not combine any of the custom Read 1, Read 2, Index 1 or Index 2 primers into single tubes.

**Sample Sheet**

If you want your data as demultiplexed .fastq files, you will need to email a sample sheet to the BRF for your libraries as a .csv file. The NovaSeq X Plus uses a reverse-complement workflow, however, we require your sample sheet to have the i5 indexes in their true, forward-strand sequences. This is because the software on the instrument will automatically reverse-complement the i5 indexes during demultiplexing. If you give us a sample sheet with the i5 indexes already reverse-complemented, then the instrument will undo this, and the demultiplexing will have to be re-queued.

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| Sample sheet file name: |  |