

NovaSeq 6000 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) |
| ❑ | Supply your own 2 TB hard drive\* |
| ❑ | BaseSpace Sequence Hub |

\*If supplying your own 2 TB 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 (SP, S1, S2 and S4) and their output in gigabases (Gb) and single-end reads in millions (M) or billions (B) for a given read length.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **SP** | **S1** | **S2** | **S4** |
| **1 × 35 bp**  **(35 cycles)** | N/A | N/A | N/A | 280-350 Gb | 8-10 B |
| **2 × 50 bp**  **(100 cycles)** | 65-80 Gb | 650-800 M | 134-167 Gb | 1.3-1.6 B | 333-417 Gb | 3.3-4.1 B | N/A |
| **2 × 100 bp**  **(200 cycles)** | 134-167 Gb | 650-800 M | 266-333 Gb | 1.3-1.6 B | 667-833 Gb | 3.3-4.1 B | 1600-2000 Gb | 8-10 B |
| **2 × 150 bp**  **(300 cycles)** | 200-250 Gb | 650-800 M | 400-500 Gb | 1.3-1.6 B | 1000-1250 Gb | 3.3-4.1 B | 2400-3000 Gb | 8-10 B |
| **2 × 250 bp**  **(500 cycles)** | 325-400 Gb | 650-800 M | N/A | N/A | N/A |

Please choose your desired reagent kit and sequencing parameters below.

|  |  |
| --- | --- |
| Reagent kit: | e.g. S1 flow cell, 300 cycles |
| Sequencing parameters: | e.g. 150 bp paired-end, or 300 bp single-end |

SP, S1 and S2 flow cells have two lanes. S4 flow cells have four lanes. If you plan to submit multiple library pools for a single sequencing run and these pools share barcode combinations with each other, these library pools will need to be submitted in separate tubes and they will be loaded onto separate flow cell lanes.

If all samples in the pool are uniquely barcoded, the pool will be loaded evenly across all lanes of the flow cell.

For SP and S1 flow cells, we require 200 µL of ~2.5 nM DNA.

For S2 flow cells, we require 300 µL of ~2.5 nM DNA.

For S4 flow cells, we require 600 µL of ~2.5 nM DNA.

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 6000 uses a reverse-complement workflow, meaning the instrument synthesises the complementary DNA strand before performing the i5 index read. For this reason, the i5 indexes will need to be written as the reverse-complement sequences in the sample sheet. If you are using the Illumina Experiment Manager software to generate the sample sheet, the i5 indexes will be reverse-complemented automatically when you indicate it is a NovaSeq 6000 sample sheet.

|  |  |
| --- | --- |
| Sample sheet file name: |  |