

NovaSeq 6000 Order Form

For libraries to be prepared by the BRF

**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 |

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

|  |  |
| --- | --- |
| Sample name(s): |  |
| Sample origin (species, tissue etc.): |  |
| Sample type (cells, RNA, DNA etc.) |  |
| Sample concentrations (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.