**中央研究院 生物多樣性研究中心 新世代基因體定序核心實驗室**

**NGS Sample Submission Form　樣品明細表**

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Submission Date** | |  | | | | | **Case ID**  **(core only)** | |  | | | | |
| **Application Type** | |  | | | | |
| 1. Please refer to **NGS Sample Requirement** for the labeling and packing, and ensure the quantity and quality of your samples fulfill all the requirements. 2. Please attach **Gel Image (required)** or **BioAnalyzer Traces (optional)** at the end of the NGS Sample Submission Form. 3. **Sample Name** must be **the same as** the labeling on the tube cap. | | | | | | | | | | | | | |
| **Organism or**  **Species** | |  | | | | | **Sample Type:**  □ genomic DNA □ amplicon □ total RNA  □ ChIP DNA □ cDNA □ Ready-to-seq Library  □ plasmid DNA □ mRNA □ | | | | | | |
| **Genome Size or**  **DNA Length** | |  | | | | |
| **Purification**  **Method** | |  | | | | | **Enzyme Treatment & Usage:**  □ DNase □ RNase □ RNase Inhibiter | | | | | **Dissolved in:**  □ H2O  □ EB  □ | |
|  | | | | |
| **Sample Name**  **(tube labeling)** | | | **(optional)** | **Nano** | **Vol.** | **Amt.** | **OD**  **260/280** | **OD**  **260/230** | **(optional)** | **(optional)** | **Notes** | | **Sample ID**  **(core only)** |
| **Qubit** | **Drop** | **rRNA** | **RIN** |
| (ng/ul) | (ng/ul) | (**µ**l) | **(µg)** | **Ratio** |
| **1** | (English, numbers, & simple symbols) | |  |  |  |  |  |  |  |  | (Free text) | |  |
| **2** |  | |  |  |  |  |  |  |  |  |  | |  |
| **3** |  | |  |  |  |  |  |  |  |  |  | |  |
| **4** |  | |  |  |  |  |  |  |  |  |  | |  |
| **5** |  | |  |  |  |  |  |  |  |  |  | |  |
| **6** |  | |  |  |  |  |  |  |  |  |  | |  |
| **7** |  | |  |  |  |  |  |  |  |  |  | |  |
| **8** |  | |  |  |  |  |  |  |  |  |  | |  |
| **9** |  | |  |  |  |  |  |  |  |  |  | |  |
| **10** |  | |  |  |  |  |  |  |  |  |  | |  |
| **11** |  | |  |  |  |  |  |  |  |  |  | |  |
| **12** |  | |  |  |  |  |  |  |  |  |  | |  |
| **13** |  | |  |  |  |  |  |  |  |  |  | |  |
| **14** |  | |  |  |  |  |  |  |  |  |  | |  |
| **15** |  | |  |  |  |  |  |  |  |  |  | |  |
| **16** |  | |  |  |  |  |  |  |  |  |  | |  |
| **17** |  | |  |  |  |  |  |  |  |  |  | |  |
| **18** |  | |  |  |  |  |  |  |  |  |  | |  |
| **19** |  | |  |  |  |  |  |  |  |  |  | |  |
| **20** |  | |  |  |  |  |  |  |  |  |  | |  |

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**Supplemental Information of NGS Samples**

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| **Gel Image (required)**   1. **Post-run staining** only. 2. Please indicate **sample no.** & **major marker sizes** (ladder should cover at least 0.1-10kb). |
| 1. Gel percentage: % of □ TAE or □ TBE agarose gel 2. Run condition: voltage for min 3. Loading amount: ng of sample per lane; ng of ladder per lane   **【Please print this section into a PDF file for uploading to LIMS as “Supplementary File”】**  Kindly check the following contents where applicable (but not limited to):   1. □ Sample profiles: Gel images or FA traces, or tissue photo 2. □ Sample pooling ratios: “Equal pooling”, or “Specify desired pooling ratios” if unequal) 3. □ “Ready-seq” with demux: library barcode IDs and sequences (custom-designed or commercial source) 4. □ Illustration of “Ready-Seq” library architecture, if not prepared using a popular commercial kit 5. □ DNA/RNA extraction protocol 6. □ Reference genome database link 7. □ Reference paper (DOI or URL) 8. □ Any information helpful for project communication |

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| **BioAnalyzer Electropherogram (optional)**   1. Please arrange images of BioA traces according to the sample number on the sample submission form. 2. **BioA DNA** □ High Sensitive □ 1000 □ 7500 □ 12000; or **BioA RNA 6000** □ Nano □ Pico | |
| Sample # 1 | Sample # 2 |
|  |  |
| Sample # 3 | Sample # 4 |
|  |  |
| Sample # 5 | Sample # 6 |
|  |  |
| Sample # 7 | Sample # 8 |
|  |  |