**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**

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| **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** |  |  |  |  |  |  |  |  |  |  |  |
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| **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 |
|  |  |