Nanopore Project Submission Form

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| Date of Submission: |       |
| Contact Name: |       |
| Contact Email: |       |
| Contact Phone #: |       |
| PI Name: |       |
| Billing Address: |       |
| PI Email: |       |
| PI Phone #: |       |
| Chart Field String # (UNC-CH only) or PO# (all others): |       |

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| **Sample Name:** |       |
| **Source Organism:** |       |

**Submission Criteria**

* Please submit at least 1.5 µg high molecular weight DNA as measured by Qubit.
* Purity as measured using Nanodrop - OD 260/280 of 1.8 and OD 260/230 of 2.0-2.2
* Average fragment size, as measured by pulse-field, or low percentage agarose gel analysis >30 kb. Please provide a copy of your QC gel to ensure it is high quality, high molecular weight DNA.
* No detergents or surfactants in the buffer

NOTE – It is important that you check your input DNA for quality before submitting to HTSF. Low molecular weight, incorrectly quantified and/or contaminated DNA (e.g. salt, EDTA, protein, organic solvents) can have a significant impact on downstream processes and ultimately, your sequencing runs.

WARNING – Purely spectrophotometric-based methods are more variable and overestimate concentration, sometimes by as much as 10-fold if RNA and other contaminates are present, and are not recommended for determining concentration.

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| Submitted DNA (ng/µL): |       |
| Total Volume (µL): |       |
| Method: |  [ ]  Qubit® [ ]  PicoGreen® [ ]  qPCR |
| A260/A280 ratio :  |  |
| A260/A230 ratio: |  |
| Sample Buffer: |  |

(Optional: Fill in if you have specific assembly or coverage needs. Please contact HTSF staff with any questions.)

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| Approx. Genome/DNA Size |  |
| Approx. Coverage Needed |  |
| Estimated number of Flow Cells |  |
| Additional Comments |       |

Bioinformatics and Data Delivery:

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|[ ]  FASTQ files |
|[ ]  Bioinformatics Consulting Analysis (Assembly, Custom Solutions, etc. – may be subject to extra costs) |

Data Delivery Notification email address if different from Contact Email:

END