Bionano Saphyr Project Submission Form

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

**Note:** Please read the Project Submission Instructions before filing out this form (please contact HTSF staff with any questions)

**Sample information (please submit separate forms for different organisms or types of samples):**

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| --- | --- | --- |
| **Type of Sample :** | ☐ Fresh cells | **Source Organism:** |
| ☐ Frozen cells |        |
| ☐ Fresh blood |
| ☐ Frozen blood |
| **Sample(s) Name:** | **Volume (µl)** | **Concentration (cells or WBC/µl)** |
| 1.         |        |            |

**Experimental Design:**

|  |  |
| --- | --- |
| **Approx. Genome/DNA Size (Gbp)** |       |
| **Reference genome to be used** (please also deliver fasta file with reference if submitting non-human sample for the first time) |       |
| **Number of flowcells** |       |
| **Heterogeneous cell population** (different genome expected in population as in mixed cancer sample) | [ ]   |
| **Additional Comments:** |       |

**Bioinformatics and Data Delivery:**

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|[x]  De Novo Assembly (assembly files, vcf) |
|[ ]  Primary Analysis Output Files (molecule files) |
|[ ]  Variant Annotation Pipeline - human only (container files, vcf) – please specify below which samples should be compared in this pipeline |
| VAP | 1.
 |
|[ ]  Bioinformatics Consulting Analysis (May be subject to extra costs) |

Data Delivery Notification email address if different from Contact Email: