**Genomics Core**

**Sample Submission Form**

*Ship or deliver samples to:*

*Genomics Core*

*c/o Graham Wiley*

*Oklahoma Medical Research Foundation*

*825 NE 13th Street, Research Tower Rm 2101*

*Oklahoma City, OK 73104*



**Sample Requirements**

**DNA:**

Whole genome- 100ng in 60uL H2O or 10mM tris

Exome- 700ng in 60uL H2O or 10mM Tris

**RNA:**

1ug in a wet ethanol pellet

**Shipping and Delivery Instructions**

*Please ensure there is sufficient refrigerating material with your samples. The Genomics Core is not responsible for samples which are compromised due to improper shipping.*

Ship all samples overnight for next day delivery on dry ice. Please email the tracking number to bebakm@omrf.org. If hand carried to the lab samples may be transported on ice.

*Please complete this form and submit it with your samples.* ***Your samples will not be processed until a completed form with a PO# is received.*** *You may send a copy of this form with the samples or email the form to bebakm@omrf.org*

|  |
| --- |
| **1. Contact Information** |
|   |  |  |  |       |  |  |  |
| Submitter Name |  |  | email |  |  |  |
|       |  |       |  |
| Phone |  |  | Fax |  |  |  |  |  |  |
| **2. Billing Information**  |
|       |  |  |  |  |       |  |  |
| PI Name |  |  |  |  | Phone |  |  |
|       |  |  |  |  |       |  |  |
| Institution |  |  |  |  | Fax |  |  |
|       |  |  |  |  |       |  |  |
| Address |  |  |  |  | email |  |  |
|       |  |  |       |  |       |  |       |  |  |
| City |  | State |  |  |  | Zip |  | PO# |  |  |
| **3. Sample Information** |
| Sample Type: | [ ] DNA | [ ]  RNA | [ ]  Amplicon | [ ]  FFPE DNA | [ ]  Library |
|  |  |  |  |  |  |  |  |
| Number of Samples: |       | Samples per Pool (Libraries): |       | Species: |       |
|  |  |  |  |  |  |  |
| Sample Format: | [ ]  Tube | [ ]  Plate | Plate Map(s) Included: | [ ]  With Shipment |
|  |  |  |  |  |  |  |  |  | [ ]  Via email |
| **4. Sample Preparation** |
| If you are providing ready to load libraries please indicate the kit used: |       |
| Please include a list of samples and indexes used. |  |  |  |  |
|  |  |  |  |  |  |  |  |
| If we are generating libraries for you please indicate your preferred kit, if known: |  |
|  |  |  |  |  |  |  |  |
| **5. Sequencing Information** |
| MiSeq: | [ ]  50v2 | [ ] 300v2 | [ ] 500v2 | [ ] 150v3 | [ ] 600v3 |  |  |
|  |  |  |  |  |  |
| NextSeq 500: | [ ]  HO 75 cyc | [ ]  150 cycle | [ ]  300 cycle | [ ]  High Output | [ ] Mid Output |
|  |  |  |  |  |  |
| HiSeq 3000: | [ ]  50 cycle | [ ]  150 cycle | [ ]  300 cycle | [ ]  PE | [ ]  SR |
|  |  |  |  |  |  |  |  |
| Number of Lanes: |  | Number of Flowcells: |  |  |  |
|  |  |  |  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |  |  |  |
| **6. Project Information- please be as detailed as possible**  |
| *Please attach a pedigree diagram if applicable.* |
| Project Name: |       |
| Sample Phenotype(s): |       |
| Sample Relationships: |       |
| Gene(s) of Interest: |       |
| Additional Information: |       |
|  |  |
|  |  |

For information on the Bioinformatics Support offered by the Genomics Core, please visit our [website](http://omrf.org/research-faculty/core-facilities/next-generation-sequencing/).