|  |
| --- |
| **Genomics Requisition Form/REQUISITION FORM** |
| **PROJECT INFORMATION** |
| Project Name |  | Project code |  |
| **Study sample size** |  |

|  |  |
| --- | --- |
| Project Description |  |
| Service Requested (check all that applies) |  [ ]  Automated DNA Extraction |  [ ] qPCR Based Genotyping |  [ ] Exome Sequencing |  [ ] Whole Genome Sequencing |  [ ] SBS Sequencing for submitted Library |  [ ] Bioinformatics |
| Result format |  |
| Preferred mode of communicating results |  |
| Additional Contacts to share results with | Name | institute | Contact info  |
|  |  |  |
|  |  |  |
|  |  |  |
| **PRINCIPLE INVESTIGATOR/PROVIDER** |
| Name: Email:Phone: | Clinic/Hospital/Institution name:Department:Address: |
| **Billing Information** |
| Billing Code:  |  |

|  |
| --- |
| **SAMPLE INFORMATION\*** |
| **For Biological Samples** |
| Sample type | **Sample volume / size for that type** | No. of samples for that type | **Sample collection date for that type** |
|  |  |  |  |
|  |  |  |  |
|  |  |  |  |
|  |  |  |  |
| \*Only blood in purple/lavender EDTA tubes, please use the attached form for submitting multiple blood samples. A minimum volume of 1mL is required. |
| **For DNA samples\*** |
| Number of samples |  | Date of extraction and storage method |  |
| Sample Source |  | Method of Extraction |  |
| **For prepared libraries (\*\*)** |
| Number of samples |  | Date of extraction and storage method |  |
| Sample Source |  | Method of Extraction |  |
| NGS application  |  | Fluorometric Quantitation method |  |
| Library Prep Method |  | Fragment analysis and Size confirmation method |  |
|  |  |  |  |
| \*DNA quality will be assessed in the facility after sample reception and in case of samples not meeting QC resubmission may be requested.It is recommended that the DNA samples be purified by column/magnetic bead methods.It is highly recommended that Total blood samples are submitted, if not applicable, a total volume of high purity 200 ng gDNA is required for Exome SeqIt is highly recommended that Total blood samples are submitted, if not applicable, a total volume of high purity 200 ul of 40 ng/ul gDNA, 20 ng/ul gDNA is required for WGS Seq for a 550 bp / 350 bp insert size.\*\* Additional QC step (quantitation and size selection) will be performed to ensure proper Library pooling, if library does not meet standards set for set library type, resubmission might be requested |

|  |
| --- |
| **Total Request Information** |
| Total number of samples Requested for Automated DNA Extraction |  |
| Total number of Samples Requested for Sequencing  |  |
| Number of Samples requested for Exome Seq |  |
| Number of samples requested for Whole Genome Seq |  |
| Total Number of Samples submitted for SBS sequencing (prepared libraries) |  |
| Total number of bioinformatics analysis requests |  |