**Prepared Library Submission Information**

Investigator Name:

Investigator Institution:

Contact Name and Phone #:

Quote Number:

Submission Date:

|  |  |
| --- | --- |
| **Sample Information: Please fill out as much of this form as possible. Ask if you have any questions.** | |
| Pool/Project ID(s): |  |
| Number of Samples: |  |
| Single samples or pre-pooled? |  |
| Sample or Pool Concentrations in nM (Min= 5nM): |  |
| QC needed (Qubit, BioAnalyzer)? |  |
| PhiX Spike % (for low base diversity samples): |  |
| Sequencing Platform (HiSeq (4000 or X), MiSeq, NextSeq (HO or MO), NovaSeq (S2 or S4): |  |
| Sequencing Read Length (ex. PE25, PE75, PE100): |  |
| Sequencing Depth (# of lanes needed): |  |
| Index Length (ex: +6, +8, +8+8): |  |
| Index Sequences (for demultiplexing): |  |
| Primer Sequence (TruSEQ Standard, Nextera, other): |  |
| Sample Type (genome, exome, RNA, other): |  |
| Sample Source: |  |
| Data Delivery Type (FASTQ is standard, inquire for other): |  |

\*Please include any Bioanalyzer traces, MiSeq data (if available), and sample barcode list with sample submission.

\*\*Email form to [nwgcseq@uw.edu](mailto:nwgcseq@uw.edu) when complete

\*\*\*Data will be removed from our server after 1 month

Notes:\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_