Glossary of terms

Job-related fields

1. **Brief Job Description**: Pertinent information about the sequencing job and experiment.
2. **Bioinformatics Analysis Desired**: Detailed list of analysis requested on the sequencing data. Example: Mapping to hg18 genome and SNP analysis.
3. **P.I.**: Principal Investigator for the project. If your PI is not in the drop-down menu, use "GSAF" if you are a UT user or "Outside User" otherwise, and enter your PI's name and email address in the "Brief Job Description" field.
4. **Grant/PO Number**: The Grant Number that should be billed for the sequencing job.
5. **Contact Name**: The contact person for the sequencing job.
6. **Contact email**: The contact email for the sequencing job. This email will be used for sending out all updates about the sequencing request and the sequencing job.
7. **DNA or RNA?**: The sample type—RNA or DNA.
8. **Requested Platform**: The sequencing platform requested for the job.
9. **Requested Run Type**: The type of sequencing run. If unsure, select undecided. Example - 50/35 bp paired end SOLiD run.
10. **Enter Job Samples**: The mode of entering sample information, either by filling out the information in the form manually or by attaching a file.
11. **Supplemental Data**: Any supplemental data files, such as completed QC reports, can be attached here.
12. **Organism(s)**: The organism(s) the samples pertain to.
13. **Sample Retention**: The policy for what to do with the samples after sequencing, either to retain them or discard them.
14. **Library Retention**: The policy for what to do with the libraries after sequencing, either to retain them or discard them.
15. **Number of Samples to Add**: Number of samples in the sequencing job. When adding sample information manually, a maximum of 30 samples can be submitted. For more than 30 samples, use 'Attachment' mode.
16. **Library Prep Required**: If requesting GSAF to do library prep for the samples, select Yes. If the libraries are ready and being submitted, select No. If there are some samples requiring library prep and some samples not requiring it, select both Yes and No.
17. **Job Number**: Once a sequencing request has been accepted and approved by the GSAF, it is given a job number. From then on, this identifier will be used to refer to the sequencing job in all further communications and to obtain updates and reports about the job.

Sample-related fields

1. **Request ID**: Autogenerated field with a unique identifier for the sequencing job request. If this field is changed by the user, it will be reverted back to the original value on submit.
2. **SampleName**: Unique identifier for each sample. No two samples can have the same SampleName.
3. **Concentration (ng/ul)**: Sample Concentration in ng/ul.
4. **Sample Volume (ul)**: Sample Volume in ul.
5. **Min Reads Required for Sample**: The minimum number of reads acceptable for the sample, in millions. This is the number of reads below which the sample will need to be resequenced. Example: 5.0
6. **Target Reads Required for Sample**: The number of reads targeted for the sample, in millions. Example: 7.0
7. **Library Prep Required**: If requesting GSAF to do library prep for the sample, select Yes. If the libraries are ready and being submitted, select No.
8. **Barcode (VxBC7yy)**: If custom barcodes have been used, provide the barcode information for each sample here.
9. **Bioanalyzer Required**: If requesting GSAF to run bioanalyzer on your sample, select Yes. If bioanalyzer is not required, select No.
10. **Sample Description**: Any information/instructions pertaining to specific sample that you would like GSAF to be aware of.