

NGS CORE - RESEARCH SAMPLE PREPARATION



Please adhere to the following guidelines when submitting your samples for submission.

Post-PCR1 submissions:

Normalize your samples, which is crucial for good library prep and sequencing.

- Concentration: 20ng/ul (For higher concentration samples, normalize to 50ng/ul, but all samples need to be one concentration or the other, not a combination).
- Volume: 20ul-50ul
- Product Stage: Post PCR1-bead cleaned sample and quantified.
- Quantification: Picogreen or nanodrop or TapeStation or BioAnalyzer quantified.
- Plates: Hardshell plates (Biorad 96-well Cat# HSP9601) with clear bottoms not opaque (NOT Eppendorf tubes/strip tubes)
- Seals: Biorad B-seal (Cat # MSB1001).

Pools for Sequencing:

Pooled libraries need to be qPCR'd and perform the trace analysis using a BioAnalyzer, TapeStation, or Fragment Analyzer.

- Concentration: at least 10ng/ul.
- Volume: Minimum 20ul.
- Quantification: qPCR and Trace Analysis (BioAnalyzer, TapeStation, or Fragment Analyzer).
- Tubes: Submit pool/s in 1.5ml Eppendorf tubes and label the tube with the Project name.

Label your Samples

Please clearly label plates with project name, submission date, and initials. Please ensure that each of your projects uses never-used, unique IDs.