

Guidelines for submitting samples for Next Generation Sequencing

Please consult with the Director of the Genomics of the Core Facility *before* you start you NGS sample preparation.

Contact information:

Christoph_Schorl@brown.edu

Telephone: 401-863-2875

Please provide your samples in H₂O or in ≤ 10 mM Tris. Submit 8-10 ul of your samples at a concentration of 2-4 ng/ul in 1.5 ml low attachment tubes, labeled with date, three initials and a consecutive number. For example Joe A. Smith sample 1 would be JAS0001 etc.

Please ensure that the tubes are tightly closed to prevent evaporation and hence changes in sample concentration.

Any excess sample not used in a sequencing experiment will be stored or can be returned.

The NextSeq550 system has one sample injection port per flow cell and therefore one 'lane' is equal to one experiment. You can submit samples as single samples or as a pool. Make sure that the barcodes of all samples run in a single experiment are not redundant and compatible with each other.

If you use custom primers please provide these in clearly labeled tubes together with your samples and include information on their concentration on the sample submission form.

Please download the 'library prep template' CSV file which you should be able to find on your library manufacturer's website and submit the completed form electronically.

Please submit the sample submission form, both by email to Christoph_Schorl@brown.edu and as a hard copy when you submit your samples.

Please see Christoph Schorl when you submit your samples or leave your samples in the -20 C freezer at the entrance of the Genomics Core, LMM room 109, in the box labeled 'Incoming NGS samples'.

For quality control purposes the Genomic Core will include Phix control library at a low concentration (1%) in each run.