

Sample Submission Guideline

Instructions

Fill out the Sample Submission Form excel sheet:

Make sure that upon labeling your samples, the name on the excel sheet matches the name printed on the vial of your sample. Send completed sheet along with the samples.

Prepare samples:

For each sample, prepare a vial of $5-7 \times 10^6$ drug-treated or vehicle-treated cells (~70-80% confluency at time of collection), collected right after drug treatment in 1 mL of complete media + 10% DMSO into cryovials and frozen to -80°C with isopropyl alcohol. Treatment of cells with Caspase inhibitor alongside of drug treatment to decrease apoptotic cell fraction will increase sensitivity to label and retrieve drug-related DNA breaks. Submission of biological replicate samples of each condition and of vehicle-treated negative controls are highly recommended.

Customers will receive a 1.5 mL Eppendorf tube of purified DNA break fragments in 50 μL TE (retrieval) and a 1.5 mL Eppendorf tube of genomic DNA in 100 μL TE (input) from each processed sample. Turnaround time is typically 7 business days after BreakSight receives the samples.

If customers choose to follow up on their own with NGS, sonication of BrITL samples to an appropriate fragment size and library preparation is necessary. Please inform BreakSight if sonication after BrITL processing is requested.

Send samples:

Please ship samples overnight on dry ice to:

BreakSight, Inc
ATTN: Nishita Shastri
7540 Windsor Drive
Suite 210
Allentown, PA 18106

Include printed excel sheet listing samples and services requested.

**Samples may be shipped Mon-Thurs for overnight delivery.*

If NGS is requested on BrITL samples (BrITL-Seq):

BreakSight will ship customer's BrITL-processed samples (retrievals and inputs will henceforth be considered as separate samples) to MedGenome, Inc directly from our facilities. MedGenome will perform sample QCs, library preparation, and 100 bp paired-end sequencing to generate ~60 million read pairs per sample.

If Bioinformatics is requested on BrITL-Seq samples:

BreakSight will perform bioinformatics on customer's NGS-generated FASTQ files to call statistically significant peaks through its stringent analysis pipeline. A data report with quality checks and analysis results will be sent to customers.

For best interpretive results, retrieval and input FASTQ data from two biological replicates per condition are recommended, including from two biological replicates of vehicle-treated samples (negative control).