

4.5 - Sequencing

Parameters

| Parameter Name | Default Value | Description |
|----------------|---------------|--|
| LIB_FILE_NAME | | input file that contains the set of fragments from which reads are sampled |
| SEQ_FILE_NAME | | output file where genomic positions of sequenced reads are stored to |
| READ_NUMBER | 5,000,000 | number of reads sequenced |
| READ_LENGTH | 36 | length of the reads |
| PAIRED_END | false | switch on/off paired-end reads |

Overview

During the "Final Library Preparation" step of the Flux Simulator pipeline the cDNA fragments are optionally filtered by gel segregation, and also optionally amplified by a PCR (i.e., polymerase chain reaction).

Details

[4.5.1 - The Sequencing Process](#)

[4.5.2 - Read Identifiers](#)

[4.5.3 - Output Read Sequences](#)

[4.5.4 - Error Models](#)

[4.5.5 - Uniformity Measurements](#)