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