

-i	inputfile	The input file path.
-o	output_file	The output file for loading the raw sequences. 0: The default output path. Others: User specified output path.
-l	len_mean	The rough mean of the read length. It is recommended to set it 8000.
-n	seq_num	The number of output sequences. The default setting is 100.
-s	seed	The random seed, for reproducibility. The default setting is 0.
-c	coverage	Specify the simulation coverage, the number of read will be calculated. We use the larger one compared with seq_num. The default setting is 0.
-d	dis	Choose from the following distribution: 1: beta_distribution, 2: exponential_distribution, 3: mixed_gamma_dis. The default: 3. The default setting is 3.
-b	barcode	Choose barcode sequences. The default setting is Native Barcoding Expansion 96.
-e	ending	Choose whether to add barcode only in one segment: N: No. Y: Yes. The default setting is No.
-f	flanking	The path to the user-defined flanking sequence file.
-R	RLB12A	Choose barcode-RLB12A. 0: No. 1: Yes. The default setting is 0.
-dir	direction	Sequence direction, F: Forward. R: Reverse. The default setting is F.
-k	kit	Choose barcode library kit. 1: Native_Barcoding_Expansion. 2: Rapid_Barcoding_Kit. 3: PCR_Barcoding_Expansion. 4: PCR_Barcoding_Kit. 5: Rapid_PCR_Barcoding_Kit. 6: Barcoding_16S_Kit. 7: User_Custom_Kit. 8: No barcode.
-P	PCR	Choose PCR processing. -1: No. Others: Number of PCR. The default setting is -1.
-A	Poly_A	Choose how to add the A tail: -1: Default---Only one base is added. (The other is the length of adding A tail.)
-T	Poly_T	Choose how to add the T tail: -1: Default---Only one base is added. (The other is the length of adding T tail.)
-a	adapter	Choose an adapter. 1. 1D-adapter. Other: The fasta file path of User custom adapter. The default setting is 1.