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| -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 | Spacify the simulation coverage, the nubmer 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. |