

Data Analysis for NEXTFLEX® Combo-Seq™ mRNA/miRNA Kit

We recommend the exceRpt pipeline (<https://hub.docker.com/r/rkitchen/excerpt>) for analyzing fastq files generated using the NEXTFLEX® Combo-Seq™ mRNA/miRNA Kit. The exceRpt pipeline is deployed as a docker container and can be run using the following arguments:

```
docker run -v <input_dir>:/exceRptInput \  
-v <output_dir>:/exceRptOutput \  
-v <db_dir>:/exceRpt_DB/<db> \  
-t rkitchen/excerpt \  
INPUT_FILE_PATH=/exceRptInput/<sample> \  
MAIN_ORGANISM_GENOME_ID=<db> \  
ADAPTER_SEQ=AAAAAAAAA \  
MIN_READ_LENGTH=15 \  
STAR_outFilterMatchNmin=15 \  
RANDOM_BARCODE_LENGTH=4 \  
RANDOM_BARCODE_LOCATION='-5p'
```

Alternatively, the exceRpt pipeline may be run with singularity using the following arguments:

```
singularity run -B <input_dir>:/exceRptInput \  
-B <output_dir>:/exceRptOutput \  
-B <db_dir>:/exceRpt_DB/<db> \  
excerpt_latest.sif \  
INPUT_FILE_PATH=/exceRptInput/<sample> \  
MAIN_ORGANISM_GENOME_ID=<db> \  
ADAPTER_SEQ=AAAAAAAAA \  
MIN_READ_LENGTH=15 \  
STAR_outFilterMatchNmin=15 \  
RANDOM_BARCODE_LENGTH=4 \  
RANDOM_BARCODE_LOCATION='-5p'
```

As an example:

```
<input_dir> = ~/my_sequencing_run/input  
<output_dir> = ~/my_sequencing_run/output  
<db_dir> = ~/exceRpt/hg38  
<db> = hg38  
<sample> = control01.fastq.gz
```

Revision History

Version	Date	Description
V0.0	June 2019	Initial release
V01	April 2020	Changed ADAPTER_SEQ from 10 A's to 8 A's; added arguments for singularity