

miRBase for MiSeq Reporter v2.4+ to v20

Important Information About Updating Your Software

Follow these instructions to reanalyze small RNA data in MiSeq Reporter with miRBase v20 database (www.mirbase.org/). These instructions assume that you have MiSeq Reporter 2.4 or higher.

- 1 Back up the **HumanRNA** folder at **C:\Illumina\MiSeq Reporter\Genomes** by renaming it **HumanRNA.16**.
- 2 Back up the **HumanRNAMature** folder at **C:\Illumina\MiSeq Reporter\Genomes** by renaming it **HumanRNAMature.16**.
- 3 Download the compressed updater folder containing the **HumanRNA** and **HumanRNAMature** folders from the MiSeq Reporter Downloads.
- 4 Copy the downloaded folder to **C:\Illumina\MiSeq Reporter\Genomes**
- 5 Right-click on the folder and choose **Extract All**. This step decompresses the folder in the current directory **C:\Illumina\MiSeq Reporter\Genomes**
- 6 You now have **C:\Illumina\MiSeq Reporter\Genomes\HumanRNA** and **C:\Illumina\MiSeq Reporter\Genomes\HumanRNAMature** folders.
- 7 Perform the analysis in MiSeq Reporter as usual. This step assumes that the sample sheet was prepared in Illumina Experiment Manager following the MiSeq Reporter Small RNA Workflow Reference Guide.

These instructions use “hairpin.fa.gz” and “mature.fa.gz” files from miRBase. Modify these files to work with MiSeq Reporter Small RNA workflow. Contact Illumina Technical Support for questions.