

# SEQUENCHER®

## Installing RNA-Seq Tools for Sequencher

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## Introduction

Now that RNA-Seq analysis using Next-Generation Sequencing is a widely available technology, the **Cufflinks** suite for RNA-Seq and **Samtools** have been integrated into **Sequencher** to enable you to analyze your RNA-Seq data for Differential Expression on your own desktop computer. This suite joins the **BWA-MEM**, **GSNAP**, **Maq**, **Velvet**, **Clustal**, and **MUSCLE** algorithms that are already accessible in **Sequencher**. The **Cufflinks** suite of tools was written to run on Unix-based systems. Mac OS X is a Unix-based operating system. We have built native binaries for Windows, so that there is no longer any need to have Cygwin, a Unix emulation environment, installed in order to run the **Cufflinks** suite.

The instructions which follow show you how to use the all-in-one installers which will place almost everything you need to run this suite of tools on your computer. **THESE TOOLS ARE SUPPORTED AND INSTALLABLE ON 64-BIT SYSTEMS ONLY.**

## Quick and Easy Set Up for the Cufflinks Suite

### INSTALLING RNA-SEQ TOOLS ON WINDOWS

The Windows installer will place the RNA-Seq suite of tools (**Cufflinks**, **Cuffmerge**, **Cuffdiff**, **Cuffnorm**, **Cuffquant**, etc. and **Samtools**) and their related files where they need to be. That location is Programs Files (x86)/Gene Codes/Sequencher External Tools.

1. Download the RNA-Seq Tools Installer zip archive from the Gene Codes website at [www.genecodes.com/download](http://www.genecodes.com/download).
2. Extract/unzip the archive and open the installer folder. It will contain `RNA-SeqToolsInstaller.exe`, and a `src` folder, and a `liense.txt` file.
3. Double-click on `RNA-SeqToolsInstaller.exe`. Accept the installation defaults including the license agreement terms.
4. A new window appears which shows the progress of the installer. When the installation is complete, the **Cufflinks** suite is ready for use in **Sequencher**.

### INSTALLING RNA-SEQ TOOLS ON MAC OS X

You must be an Administrator or have an administrator's password in order to install the RNA-Seq tools on Mac. The Mac OS X installer will place the RNA-Seq suite of tools (**Cufflinks**, **Cuffmerge**, **Cuffdiff**, **Cuffnorm**, **Cuffquant**, etc. and **Samtools**) and their related files where they need to be. That location is `/usr/local/bin`.

1. Download the RNA-Seq Tools installer disk image file (.dmg) from the Gene Codes website at [www.genecodes.com/download](http://www.genecodes.com/download).
2. Double-click on the downloaded dmg file.
3. To begin installation, double-click on the RNA-Seq Tools Installer package or right-click on the package and select Open.

4. Accept installation defaults including the license agreement.
5. The installer starts. You will see various status messages as the files are written to your system. Finally, a screen appears telling you that everything was installed successfully. Click on the **Close** button. The **Cufflinks** suite of tools, **Samtools**, **Cufflinks**, **Cuffmerge**, **Cuffdiff**, **Cuffnorm**, **Cuffquant**, etc., are now ready for use in **Sequencher**.
6. If you opened the dmg instead of saving it, eject the installer disk image.

## **MORE INFORMATION**

If you would like more information on using the RNA-Seq tools, refer to the NGS for DNA and RNA-Seq chapter of the Sequencher User Manual. You will find this manual in the **Sequencher** installation folder. You can also find additional information in the "RNA-Seq" tutorial in the Tutorials folder in the **Sequencher** installation folder or on our website at [www.genecodes.com/training/tutorials](http://www.genecodes.com/training/tutorials).