

Manual for setting up TAC-seq-data-analysis virtual machine

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Prerequisites

1. Operating system that supports Oracle VM VirtualBox¹.
2. Minimum of 2048 MB of RAM.
3. 10 GB of free space.

¹ <https://www.virtualbox.org/>

Setting up virtual machine for TAC-seq

1. Download and install Oracle VM VirtualBox.
2. Download TAC-seq-data-analysis.ova.
3. Open the TAC-seq-data-analysis.ova with Oracle VM VirtualBox (Figure 1).

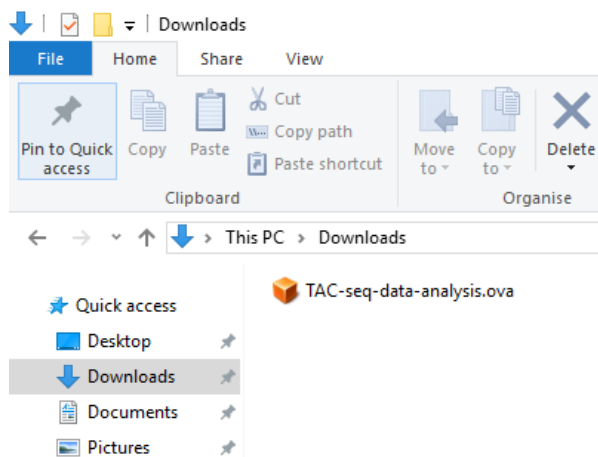


Figure 1 - The downloaded virtual appliance that needs to be imported to the Oracle VM VirtualBox.

4. Press 'import' (Figure 2).

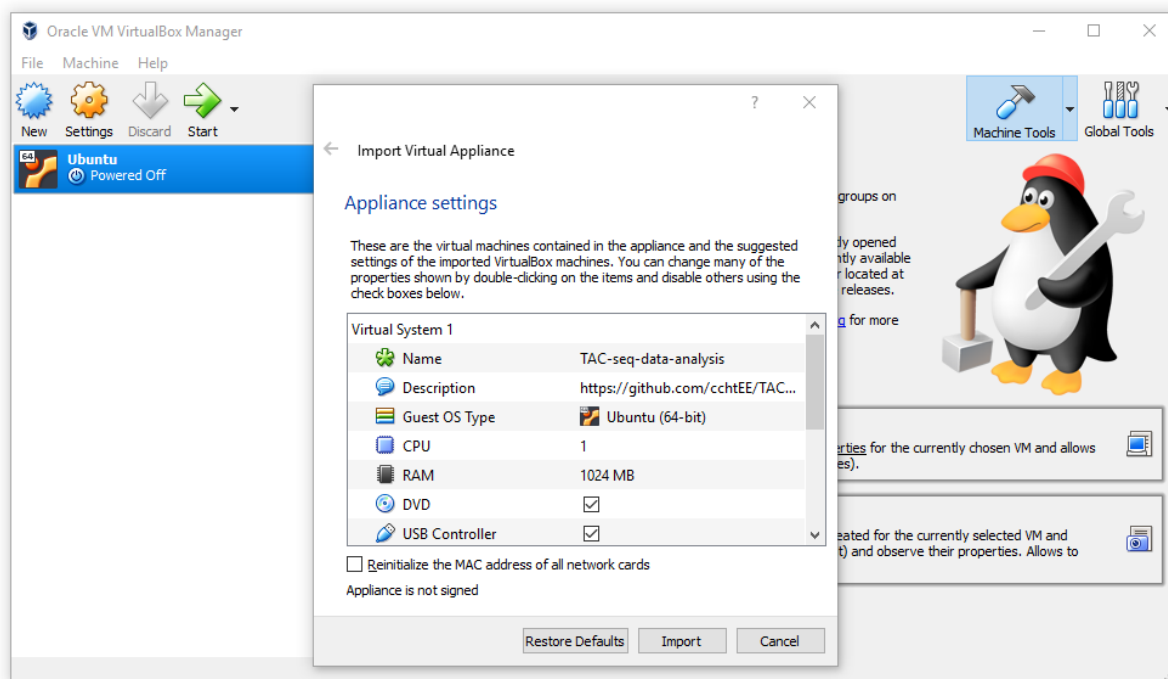


Figure 2 - To import virtual machine, click 'Import'.

5. Wait while the virtual machine is being imported (Figure 3).

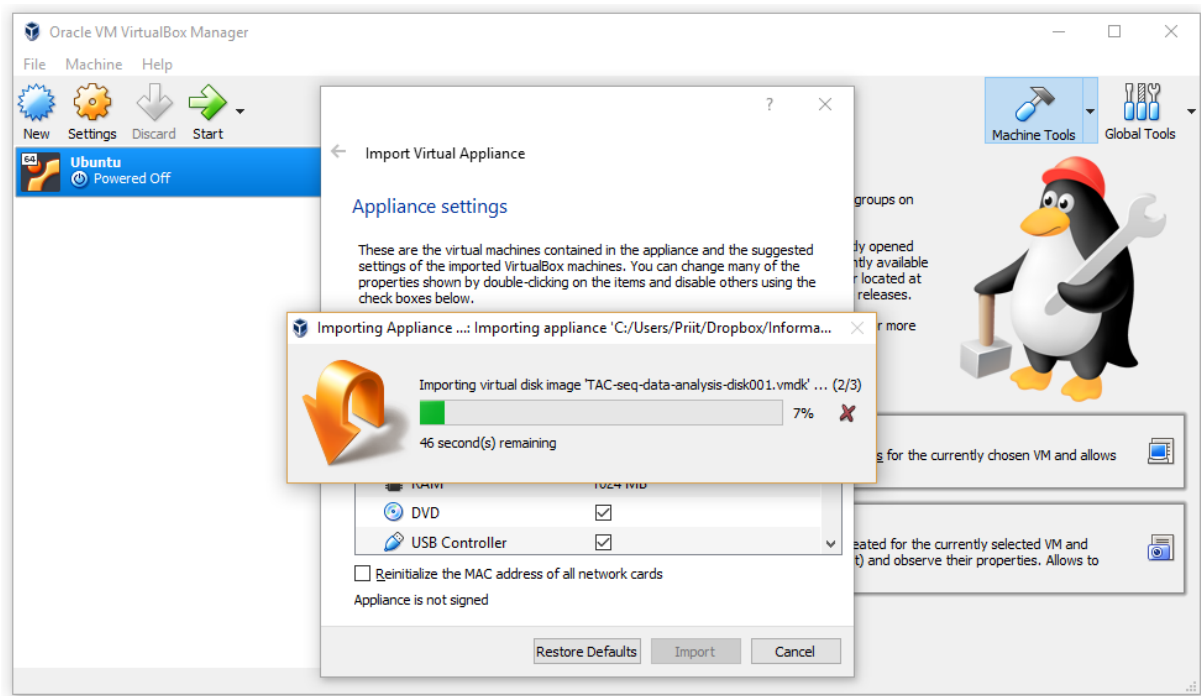


Figure 3 - The import procedure of the TAC-seq virtual machine.

Running the data analysis software

1. To run the virtual machine, double click on the TAC-seq-data-analysis (Figure 4).

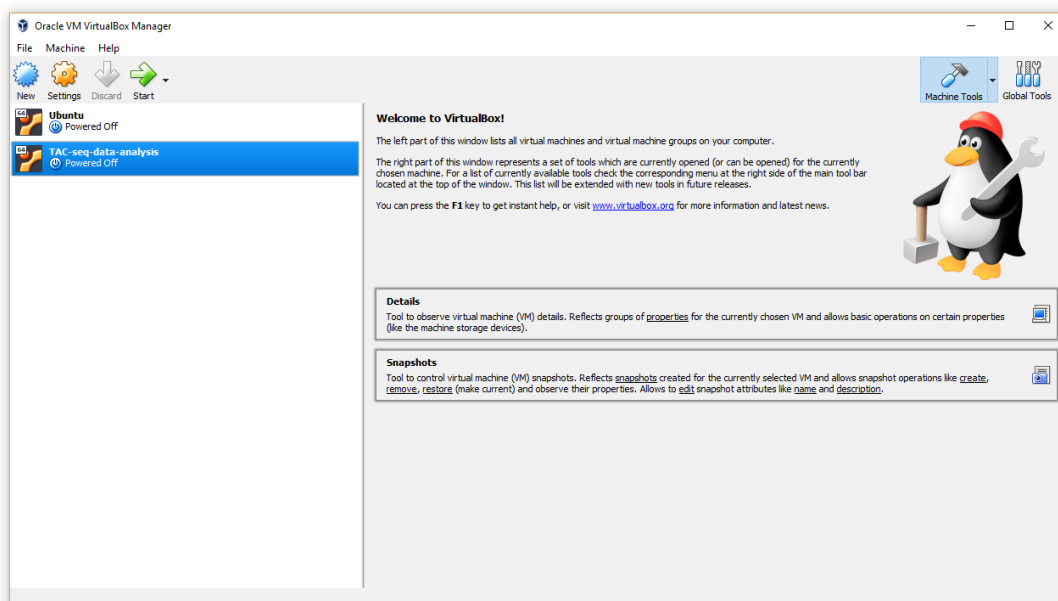


Figure 4 – To run the virtual machine, double click on the TAC-seq-data-analysis.

2. On the desktop of the virtual machine, navigate to the folder ‘TAC-seq-data-analysis’ (Figure 5, Figure 6).

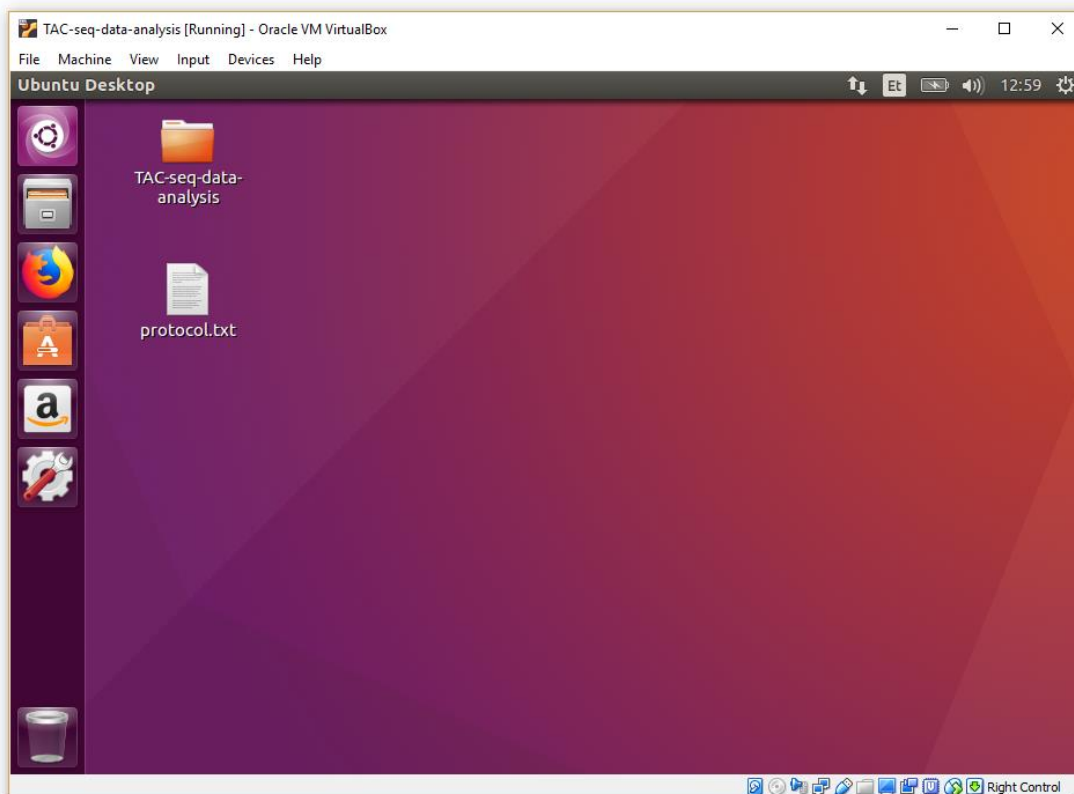


Figure 5 – Navigate to the folder ‘TAC-seq-data-analysis’.

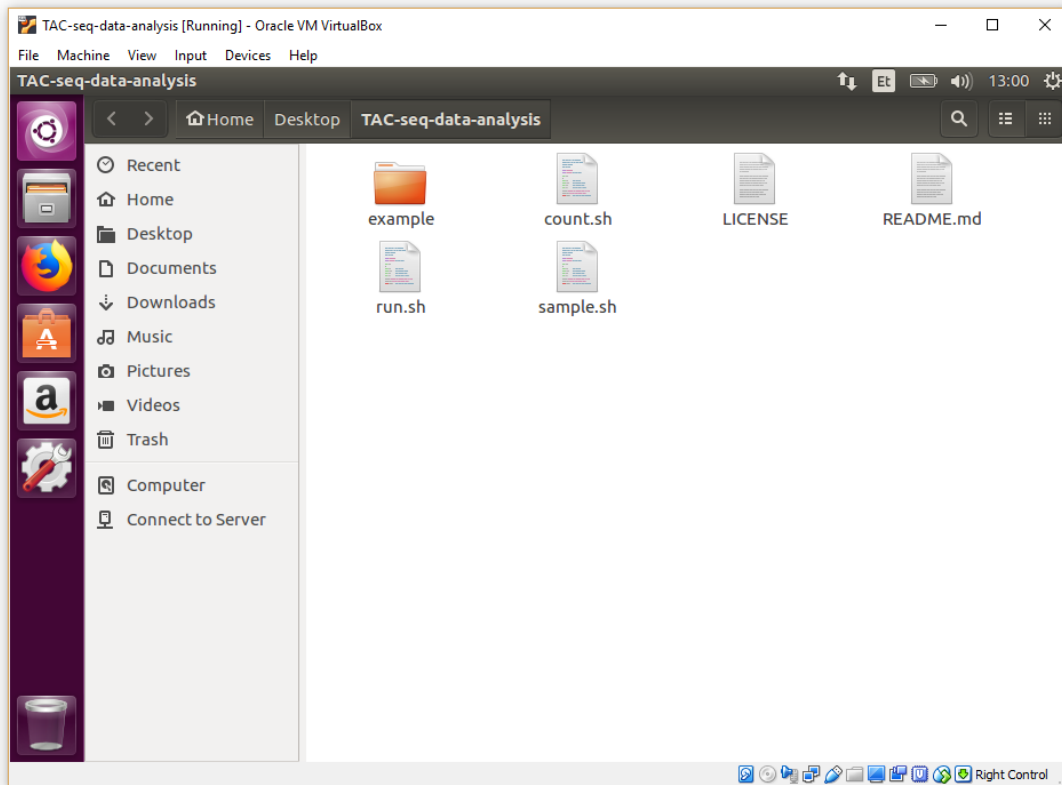


Figure 6 - Right click in the folder 'TAC-seq-data-analysis'.

3. Press right click in the folder and choose 'Open in Terminal' (Figure 7).

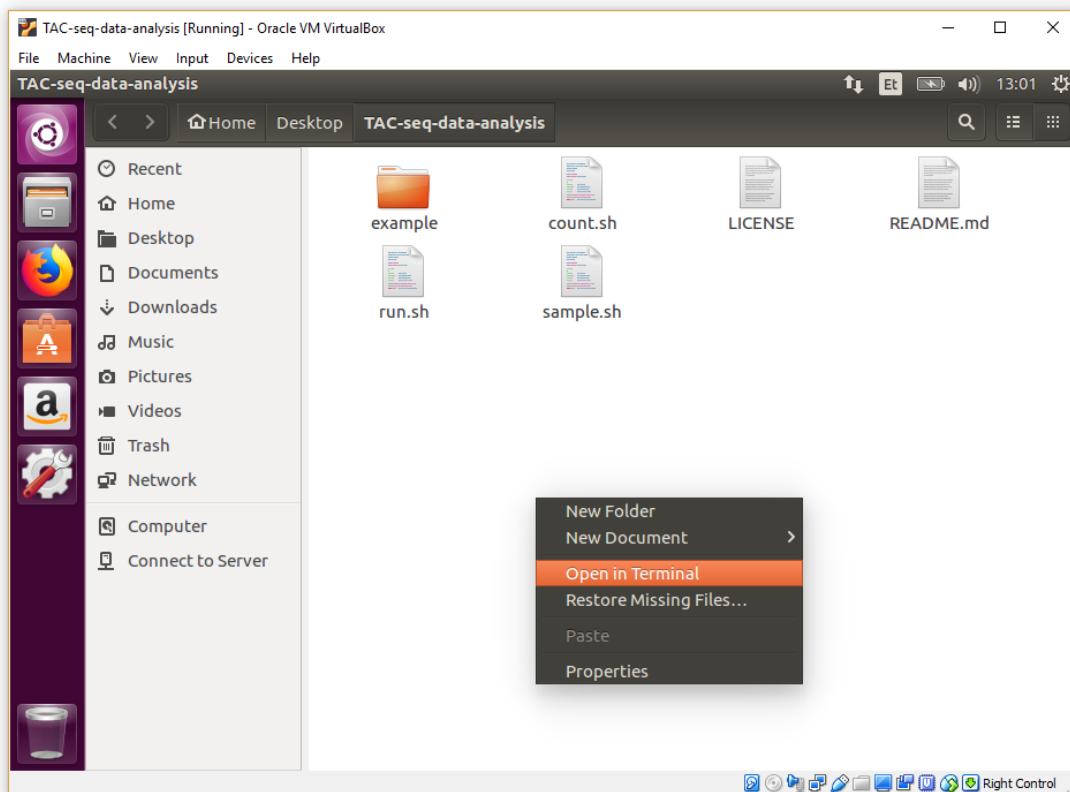


Figure 7 – Choose 'Open in Terminal'.

4. To run the analysis, copy the command `./run.sh 'example/*.fastq' example/targets.txt output/ 5 2` and press 'enter' (Figure 8, Figure 9, Figure 10).

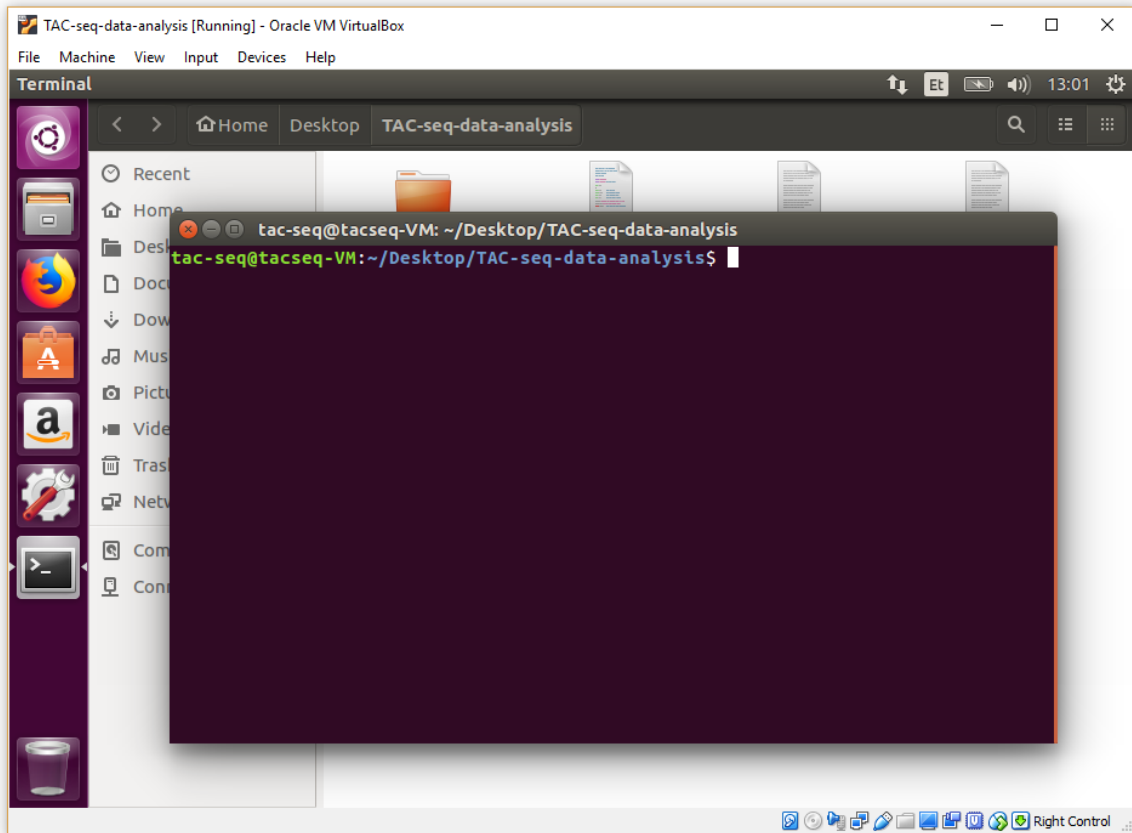


Figure 8 – Copy the command `./run.sh 'example/.fastq' example/targets.txt output/ 5 2` to the terminal.*

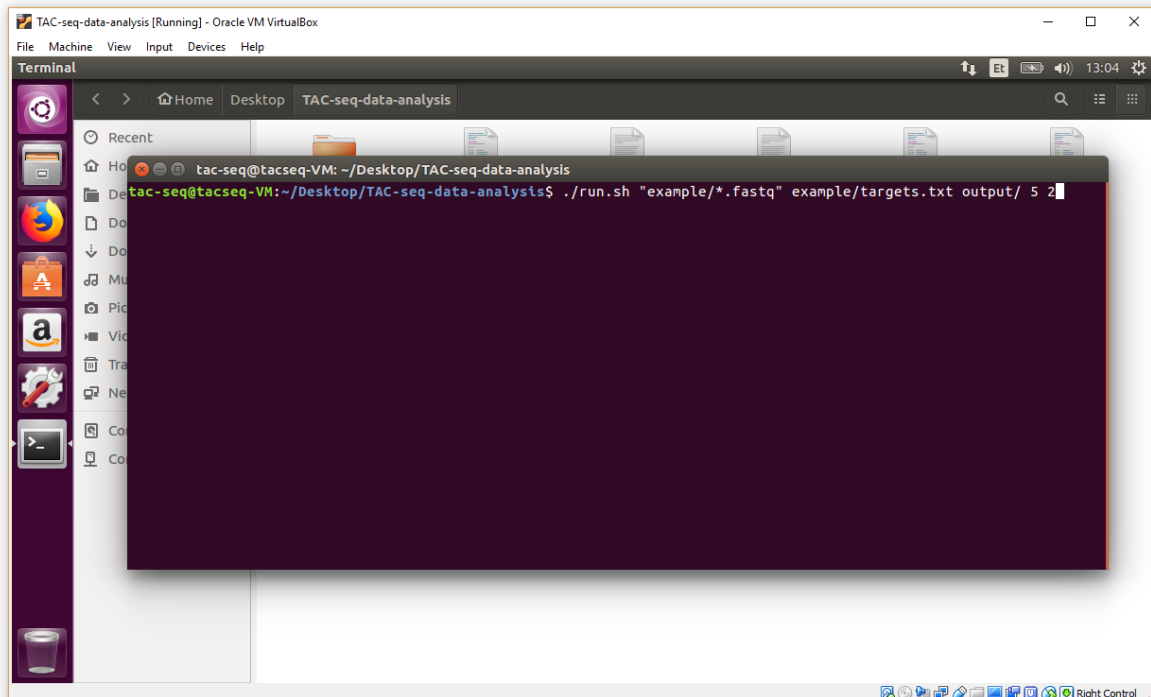


Figure 9 – Press 'enter' to run the TAC-seq data analysis.

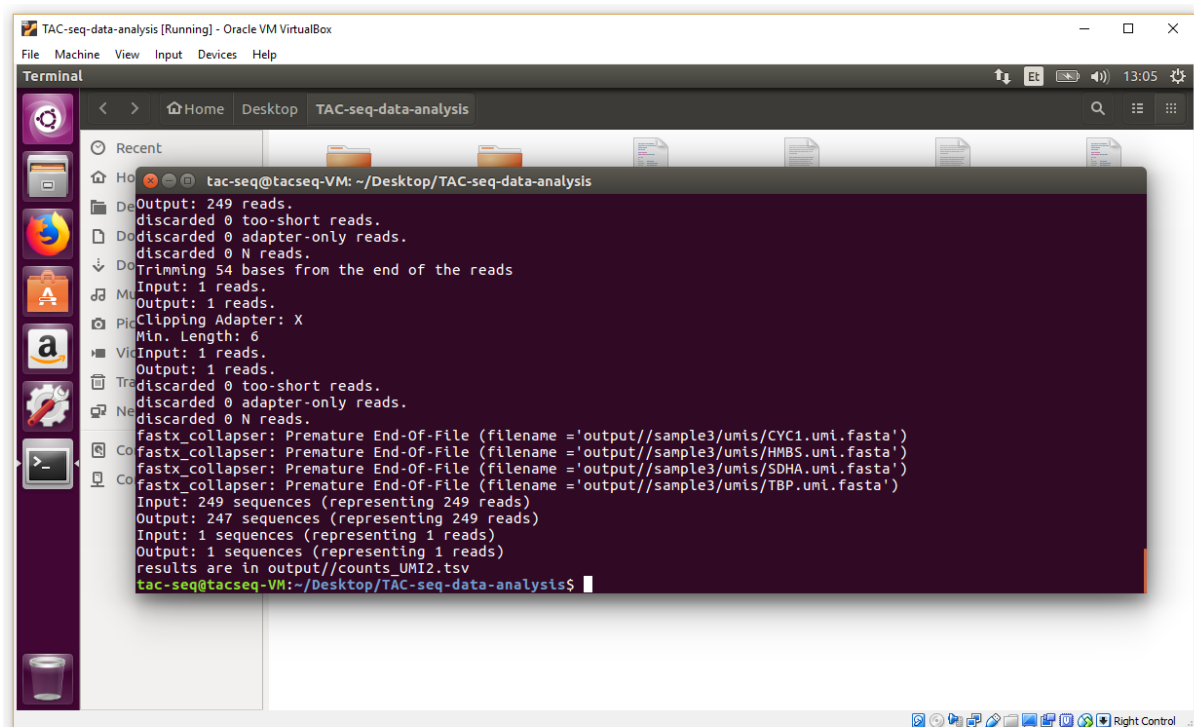


Figure 10 – After end of the analysis close the terminal.

5. To see the results, navigate to folder 'output' (Figure 11) and open 'count_UMI2.tsv' (Figure 12)

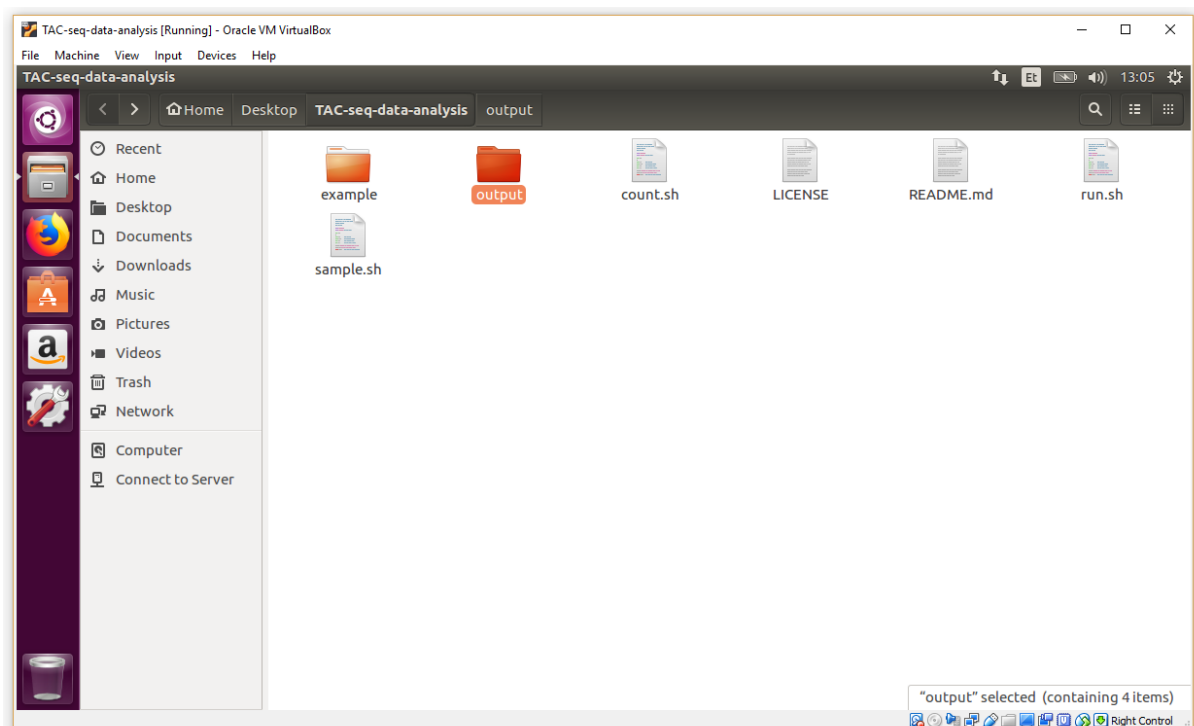


Figure 11 – Navigate to folder 'output'.

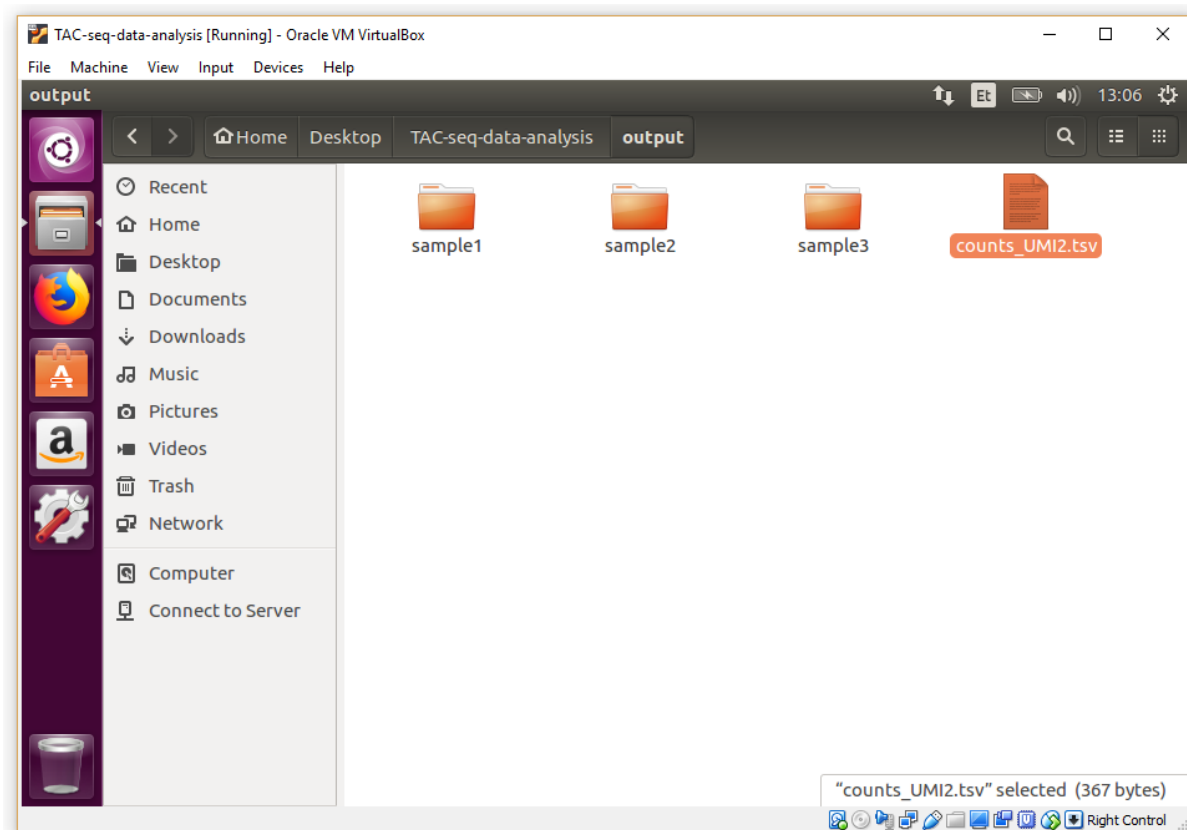


Figure 12 – Open count_UMI2.tsv to see the results.

Output

When analyses finish, output folder with intermediate files and results have been created.

Results are in counts_UMI2.tsv file with read and molecule counts per sample and locus.