

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

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Manual author: Priit Paluoja

Contact information: priitpaluoja@gmail.com

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).

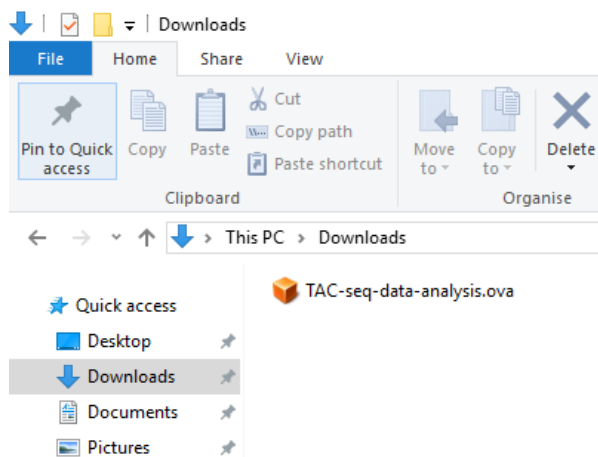


Figure 1 - The downloaded virtual appliance that needs to be imported to the Oracle VM VirtualBox.

4. Press 'import' (Figure 2).

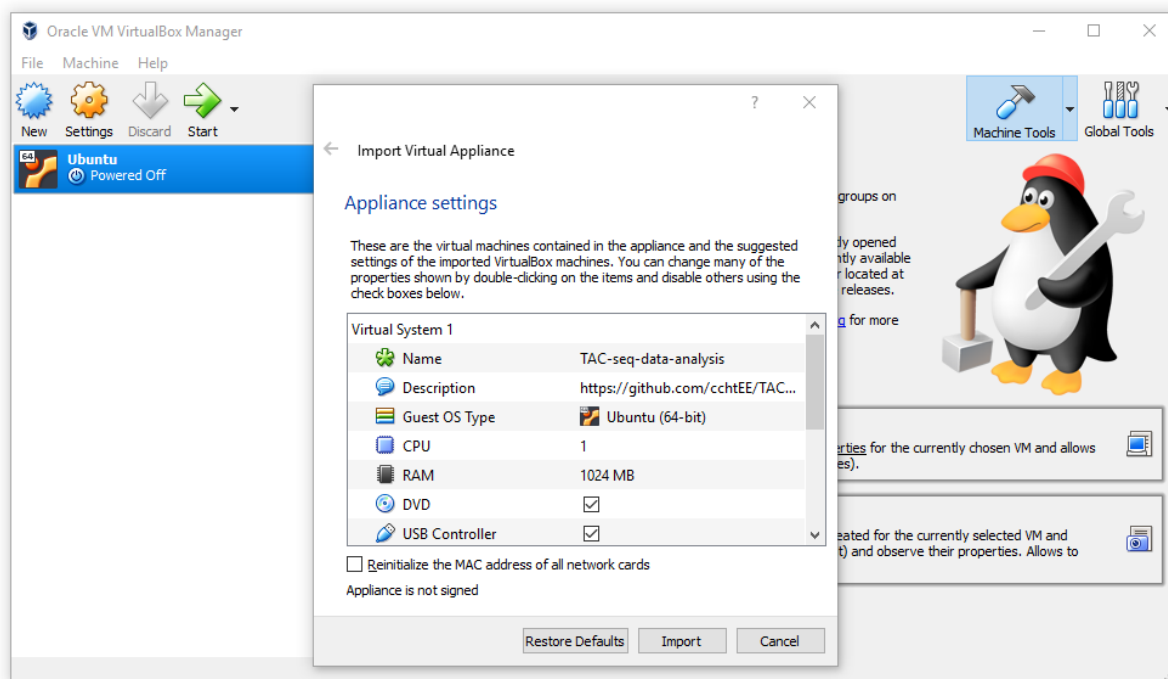


Figure 2 - To import virtual machine, click 'Import'.

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

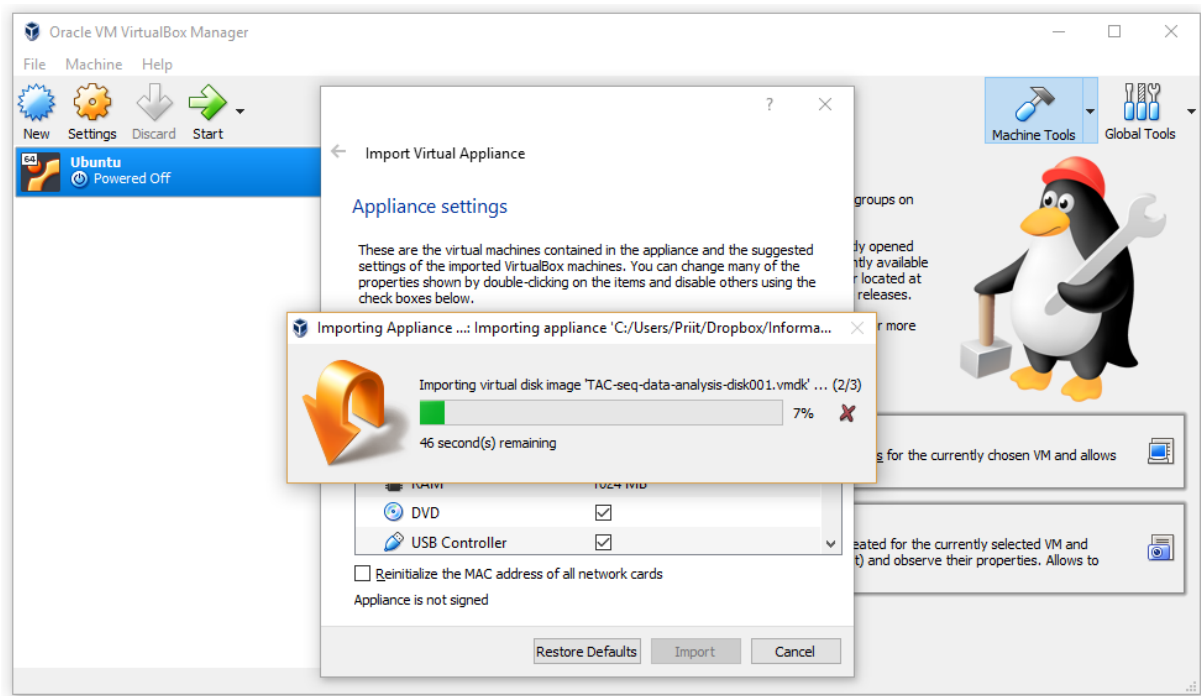


Figure 3 - The import procedure of the TAC-seq virtual machine.

Running the data analysis software

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

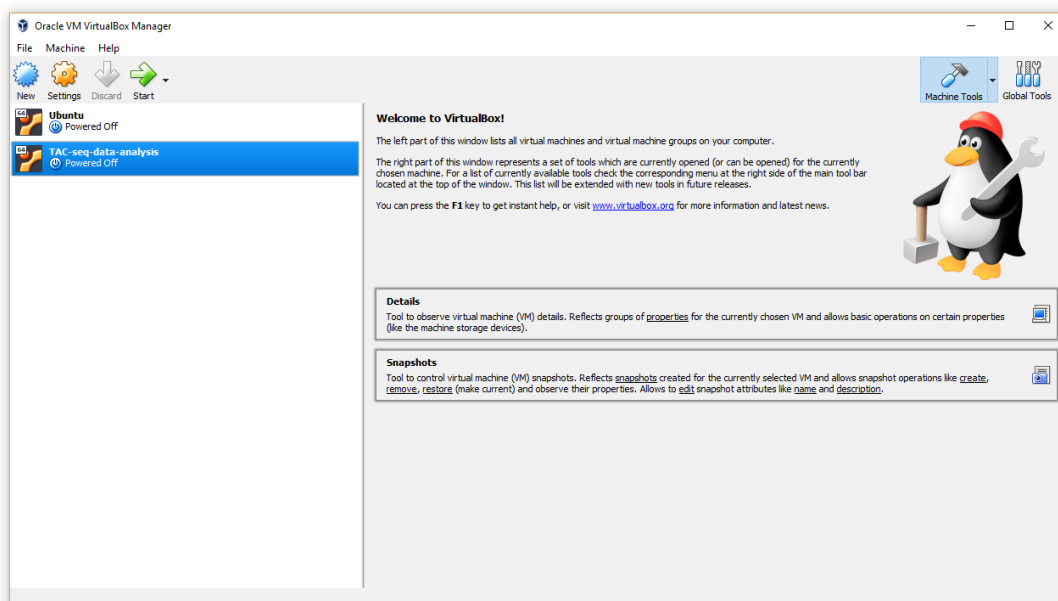


Figure 4 – To run the virtual machine, double click on the TAC-seq-data-analysis.

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

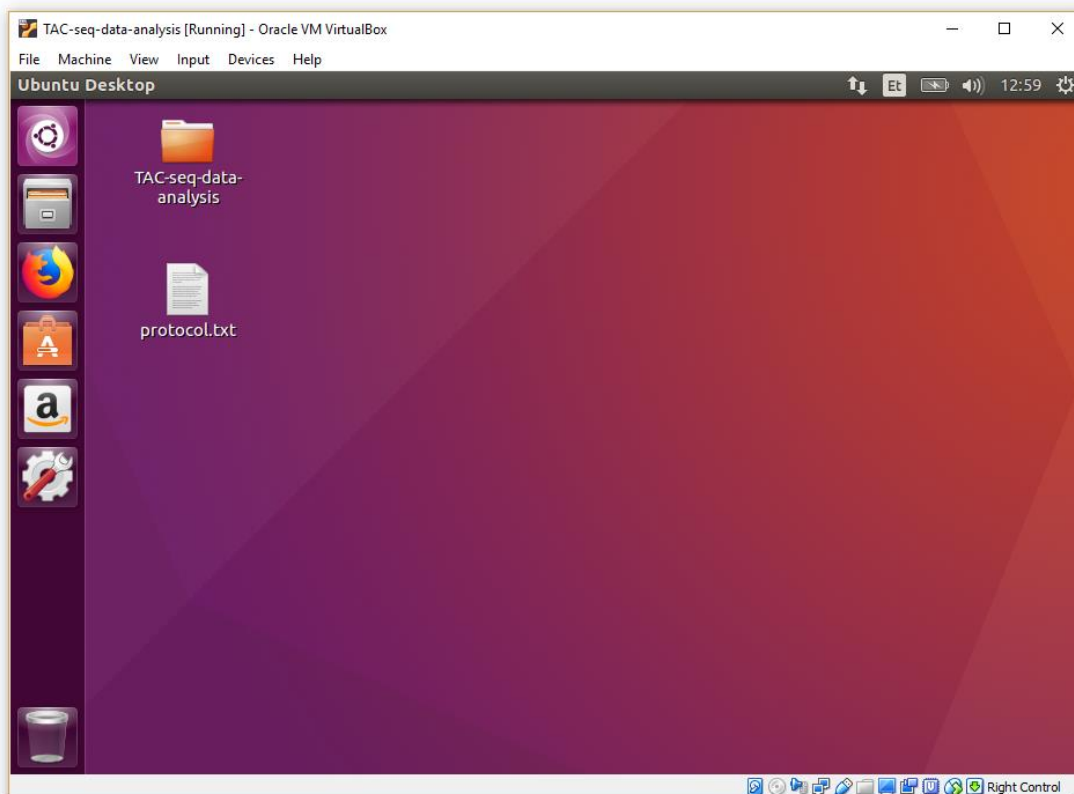


Figure 5 – Navigate to the folder ‘TAC-seq-data-analysis’.

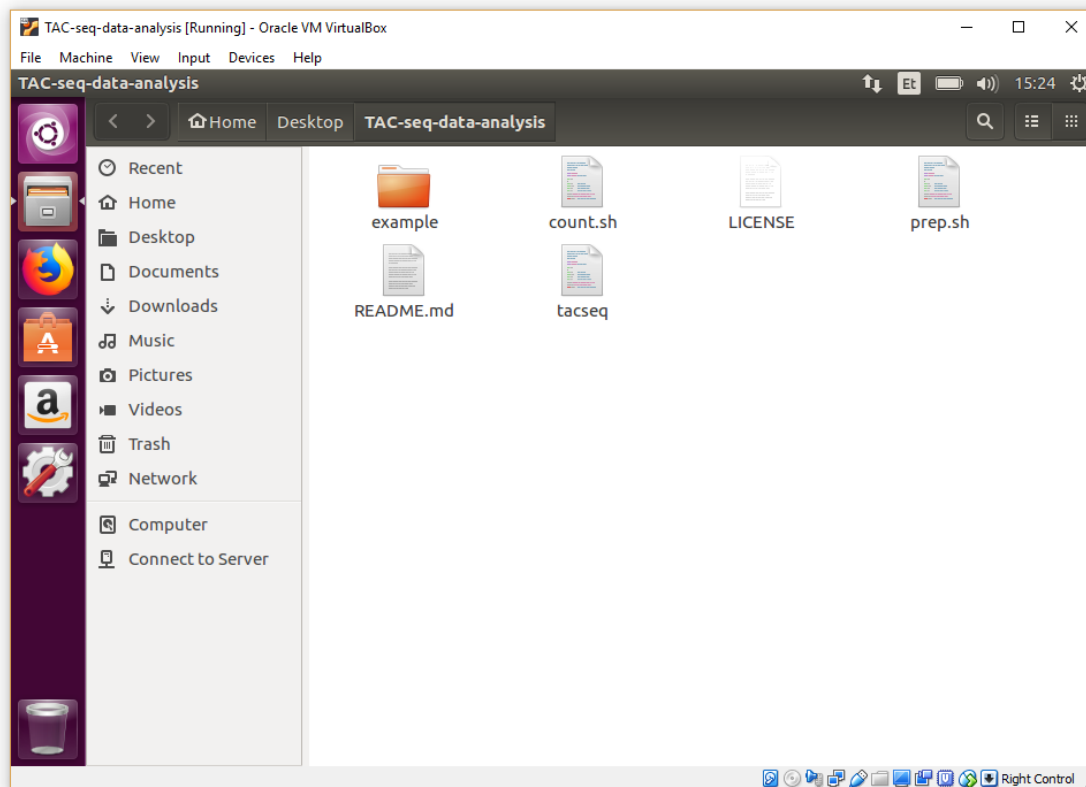


Figure 6 - Right click in the folder 'TAC-seq-data-analysis'.

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

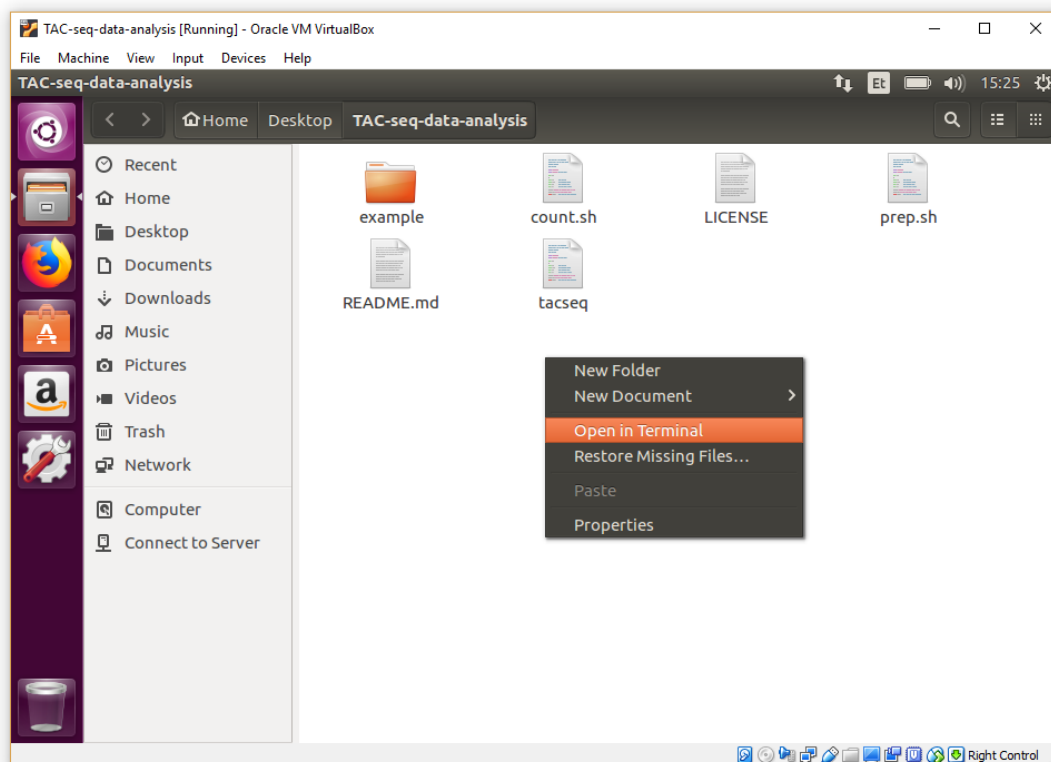


Figure 7 – Choose 'Open in Terminal'.

4. To prepare the samples, copy the command `./tacseq prep -i "example/*.fastq" -t example/targets.txt -o output/ -m 5` and press 'enter' (Figure 8, Figure 9).

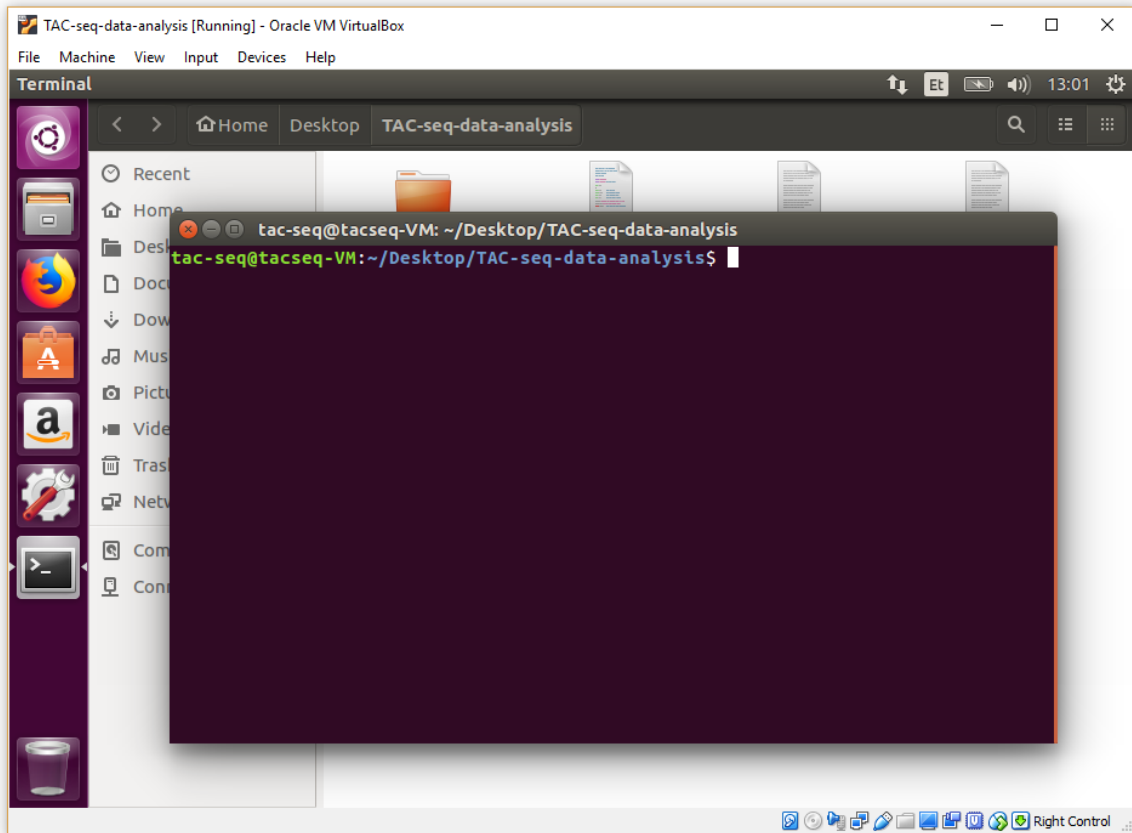


Figure 8 – Copy the command `./tacseq prep -i "example/*.fastq" -t example/targets.txt -o output/ -m 5` into the opened terminal.

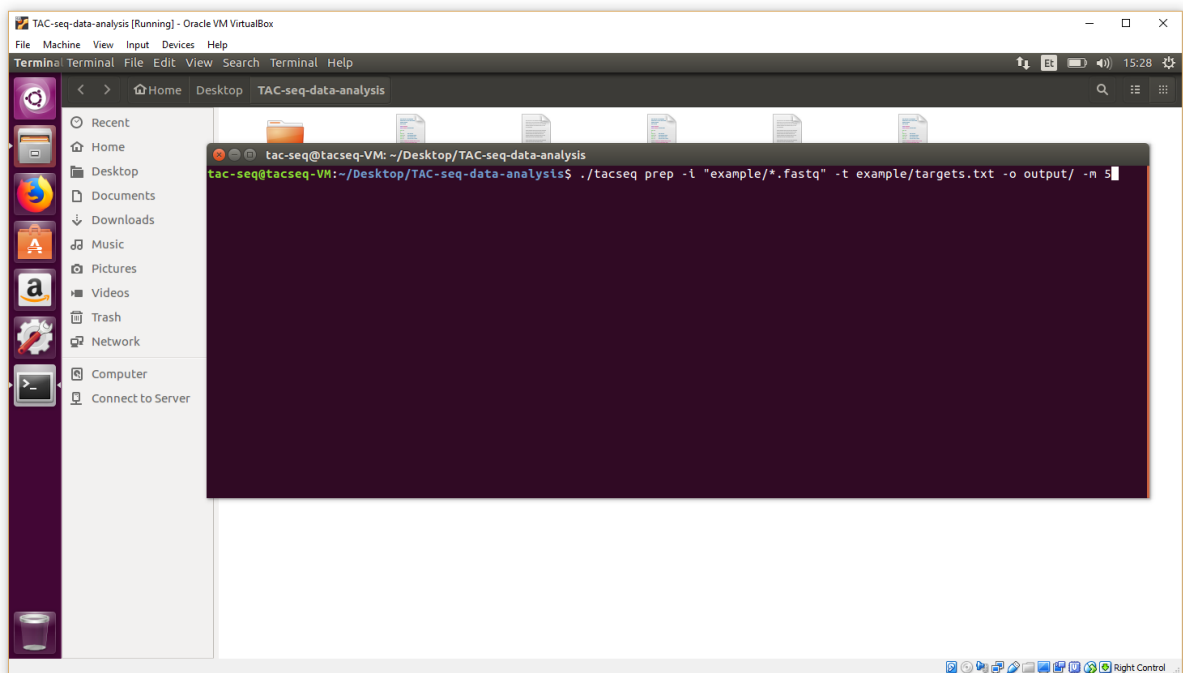


Figure 9 – Press 'enter' to prepare the samples.

5. To run the analysis, copy the command `./tacseq count -i output/ -u 2 > counts.tsv` into the terminal and press 'enter' (Figure 10).

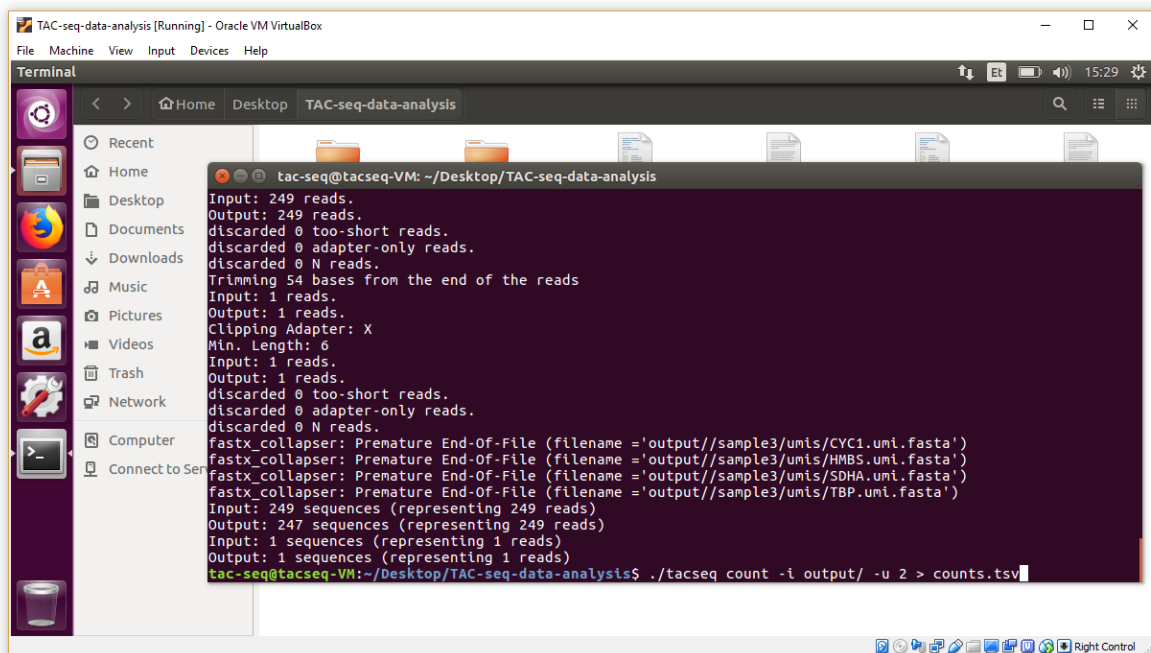


Figure 10 – To run the analyses, copy the command `./tacseq count -i output/ -u 2 > counts.tsv` and press 'enter'.

6. To see the results, open the file named 'counts.tsv' (Figure 11).

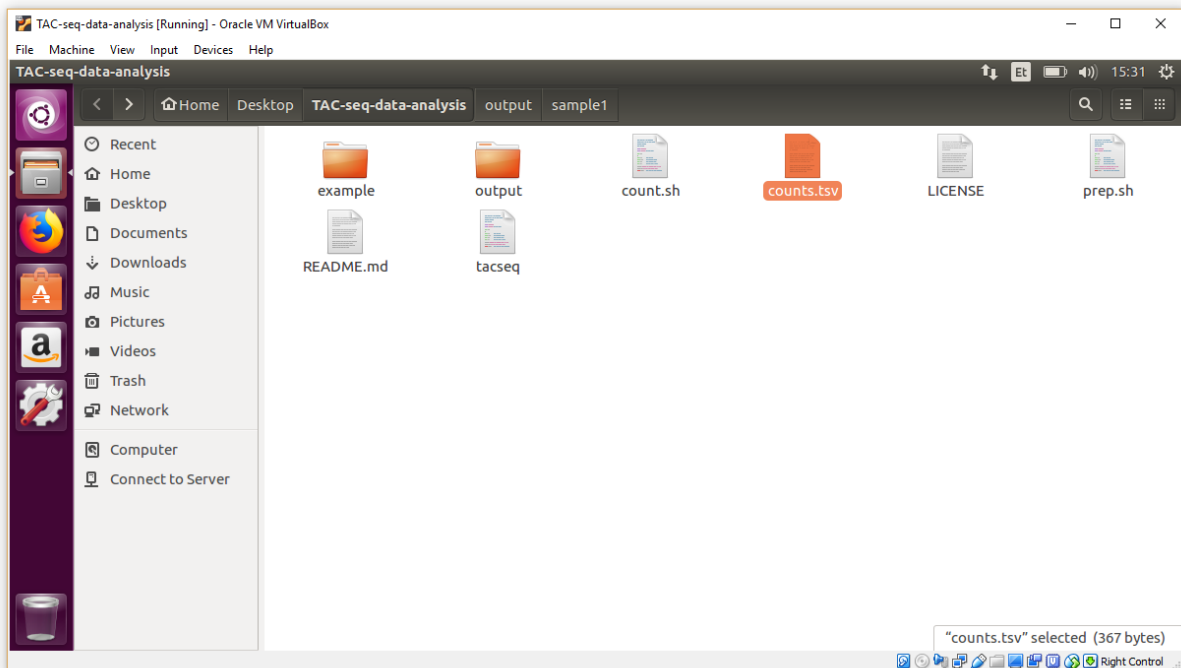


Figure 11 – Open file 'counts.tsv' to see the results.

Output

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

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