**Instruction for F13A1 result analysis**

Your sequencing result will be available on the course website.

The file name will be: “Initial\_F13A1.dna”

1. Download Install “Snapgene Viewer” from the link (<https://www.snapgene.com/snapgene-viewer/>). This is a free software.
2. Download the sequenceing result and open the result file using Snapgene Viewer. You will see windows below.



1. Go to “Sequence” tab.
2. Search (CTRL+f) “AAAG” which is the sequence of the short tandem repeat we are looking for.



1. You may see multiple “AAAG” in the sequencing results. We need to count the consecutive repeat of “AAAG” as highlighted below.

