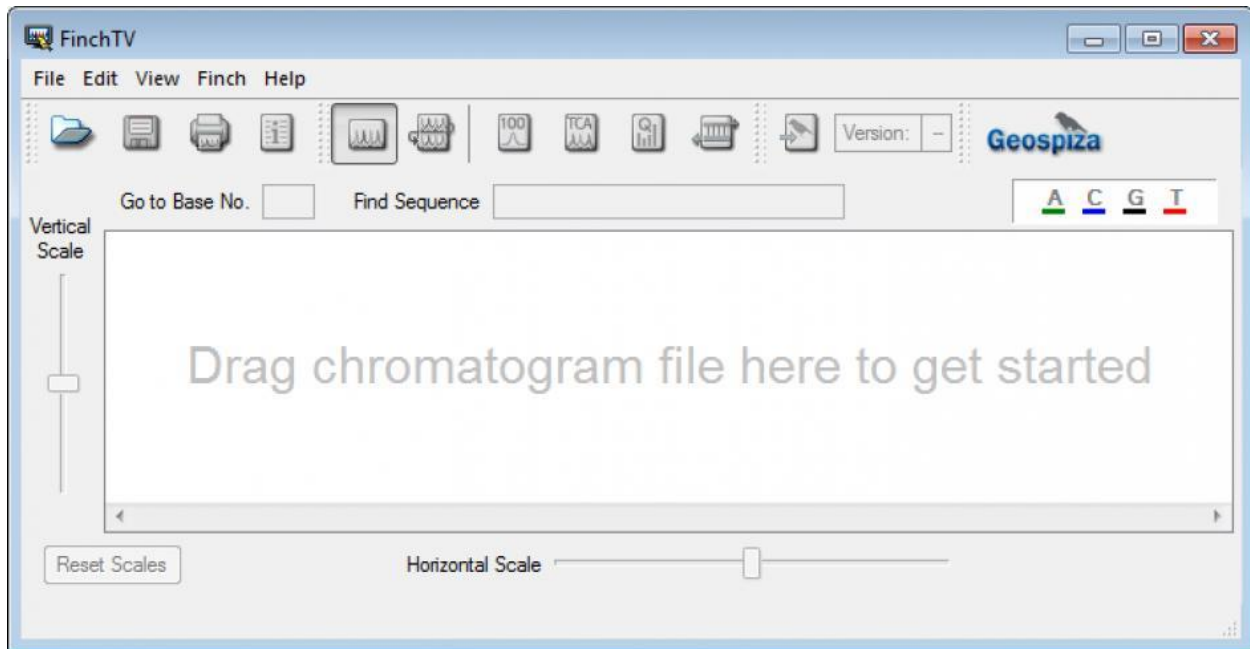
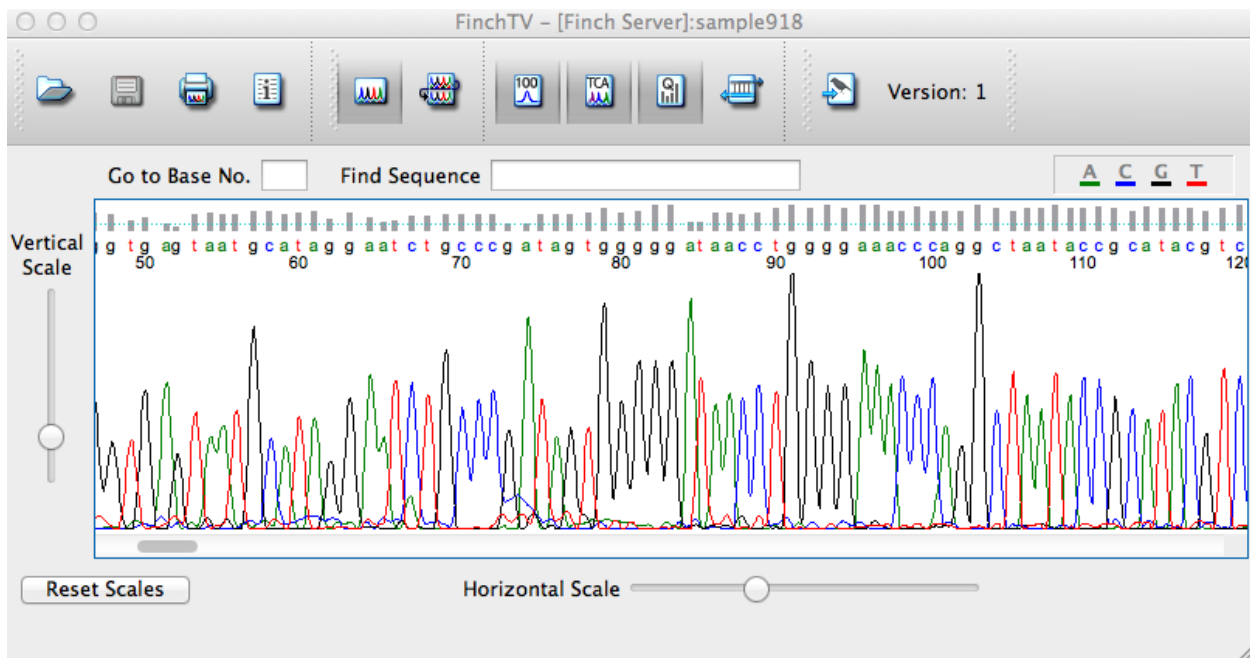


DNA Sequence – Data Quality Assessment

1. Go to “<https://digitalworldbiology.com/FinchTV>”
2. Download and install the FinchTV DNA analysis software.
3. Run the software



4. Drag and drop your sequence file (.abi) onto the software interface



5. In a new tab, visit the NCBI page for **Standard Nucleotide BLAST**:
https://blast.ncbi.nlm.nih.gov/Blast.cgi?PAGE_TYPE=BlastSearch
 (Hint: this should be the first Google hit for “blastn”)
6. Copy your sequence from the DNA analysis software (Copy regions with reasonable clean sequencing; you can use the Phred scores as a guide for this.)
7. Paste onto the NCBI interface as seen below:
 - Select “nr/nt” (non-redundant/nucleotide)
 - Select “Somewhat similar sequence”
 - Click BLAST (Basic Local Alignment Search Tool)

The screenshot shows the NCBI Standard Nucleotide BLAST interface. Red arrows point to the following elements:

- The query sequence input field containing:


```
CCTTCGTTTCCTGGTGAATTTGGGATGTAGTGAAGAGGCGG
AGGTTGGCTTGGTTTGCAATCATC
```
- The "Database" dropdown menu set to "Nucleotide collection (nr/nt)".
- The "Program Selection" section where "Somewhat similar sequences (blastn)" is selected.
- The "BLAST" button at the bottom of the form.

8. Confirm if the search result corresponds with your marker e.g. 23S, Scar 3, Scar 4 and Scar 5.
9. Complete the form assigned to you by your TA.