

User Manual

Version:1.0

Installation:

artMAP can be run on a local computer in four simple step.

- 1) First, install Docker on your computer (Linux/Windows/Mac. Docker can be installed from <https://docs.docker.com/install/>
- 2) Another requirement for running the artMAP is Docker-compose. For Mac and windows, docker-compose is a part of docker installation. However, for Linux, you need to install it from <https://docs.docker.com/compose/install/>.
- 3) Place the docker-compose.yml file (link) in the desired folder from where you want to run artMAP
- 4) Finally, to run artMAP open your command prompt and navigate to the folder where the docker-compose.yml file is placed. Next, type docker-compose up which will pull down the artMAP and run it on port 3000. Now open an internet browser like Chrome or Mozilla or Internet Explorer and type localhost:3000

Now you are ready to use artMAP for analyzing EMS-induced mutations in Arabidopsis.

Stepwise example how to run on windows:

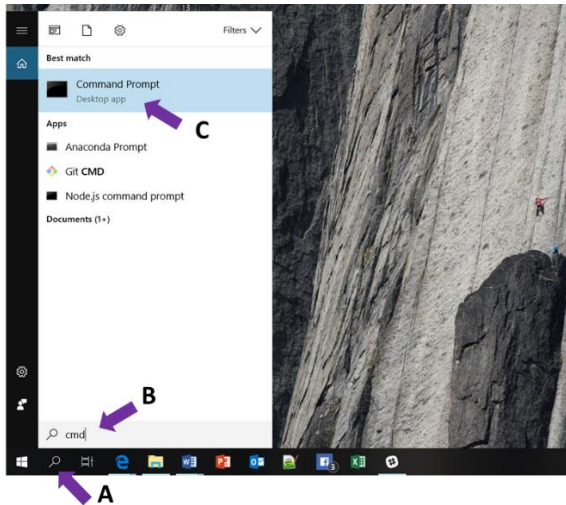
Pre-requisite: Installed docker and internet connection

For example purpose, I place the docker-compose.yml file on the partition disk E under the folder named "artMAP".

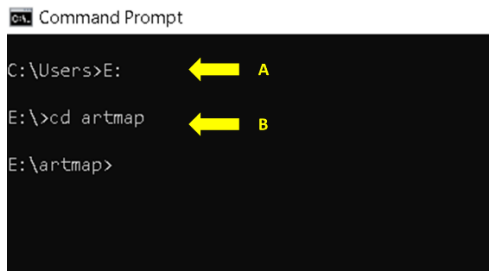
Steps:

- 1) **Open the command prompt.**

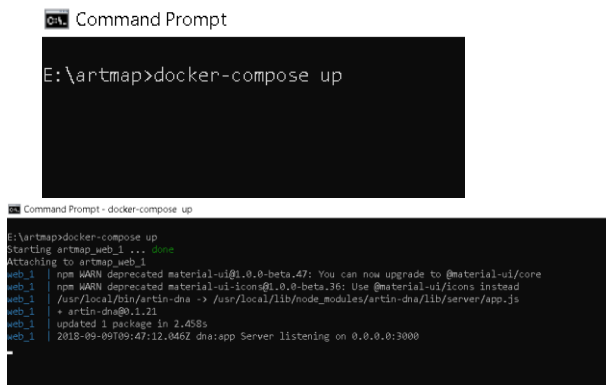
In Windows 10, command prompt can be open by clicking the search toolbar (A) and typing cmd in search toolbar (B) followed by clicking the command prompt button (C).



- 2) **Navigate to the desired folder.** Change the default command prompt directory to the desired one. In this example, I placed the docker-compose.yml file in disk E having a folder named “artMAP”. Therefore, I first change the disk C: to disk E: by typing E: and pressing enter (A) and then change to the directory artMAP by typing cd artMAP and pressing enter (B)



- 3) **Running the tool.** Next to run the tool, type “docker-compose up” in the terminal.

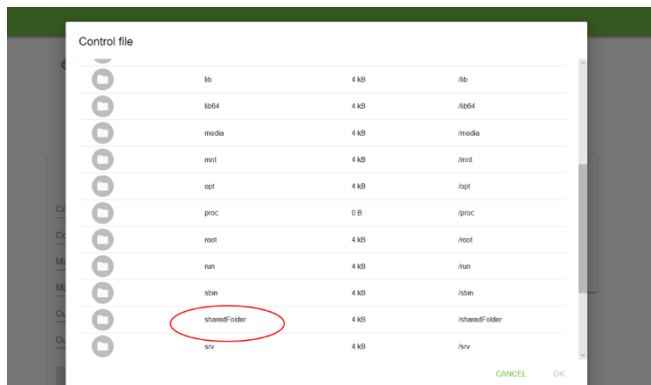


artMAP should start running on port 3000.

- 4) Final step: Open the internet browser (Mozilla, Firefox, Safari, Chrome etc) and type <http://localhost:3000/>
- 5) Here you go. artMAP is ready to do the analysis.

Important note:

The access to the directories of local host machine is defined in the volume section of the docker-compose.yml file. For example, “C:/:/sharedFolder” provide access to the C: drive and can be accessed from the shareFolder in artMAP (see the picture below).



User can change the access to the directory by editing the docker-compose.yml file. For example, if a user wants to input files present in the E: drive then s/he just have to replace C with E (E:/:/sharedFolder).

For Linux and Mac

Similar to windows, place the docker-compose.yml file in a folder and set the working directory of the mac or linux command terminal to the same. For example, user stored the docker-compose.yml file on the desktop. S/he can access the desktop by typing command

```
cd /home/nameofuser/Desktop
```

The typing docker-compose up will initialize the artMAP and user can open internet browser and access artMAP by typing <http://localhost:3000/>

User can access content of the computer by changing the volume section of the docker-compose.yml file from “C:/:/sharedFolder” to “/:/sharedFolder”.

Using artMAP:

artMAP require information about the input files before it can proceed to analyze NGS data.

- 1) artMAP ask the user about the format of the input files. Currently, artMAP can handle two file formats, BAM and FASTQ. A user can select any one of the file formats. To select click on the green button (**Figure S1**) saying either “ I HAVE DATA IN BAM FORMAT” or “ I HAVE DATA IN FASTQ FORMAT”

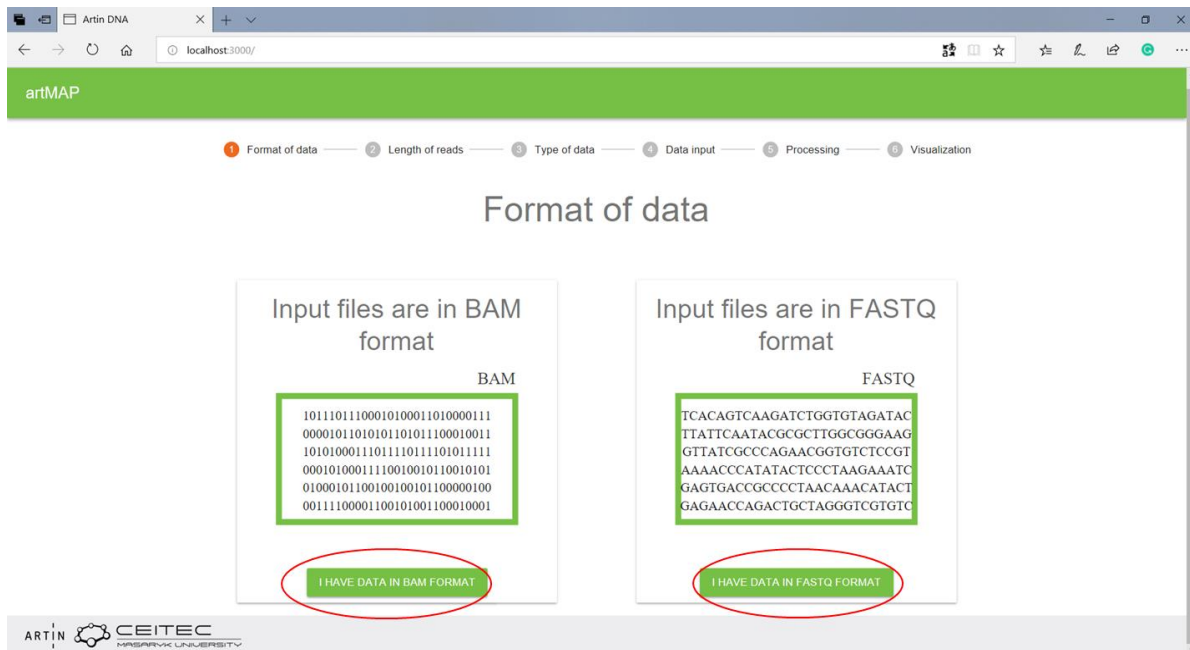


Figure S1: Screenshot of artMAP showing screen for selecting right format of the data.

2) Next, user has to select appropriate length of the sequencing reads. artMAP accepts two options short reads or long reads. Based on the read length, artMAP decide on the aligner. Reads greater than 100 bp are considered as long reads whereas less than or equal to 100 bp are considered as short reads. To select correct size of reads, click on green button (**Figure S2**) saying either “I HAVE DATA WITH BP>100” for long reads or “I HAVE DATA WITH BP ≤100” for short reads.

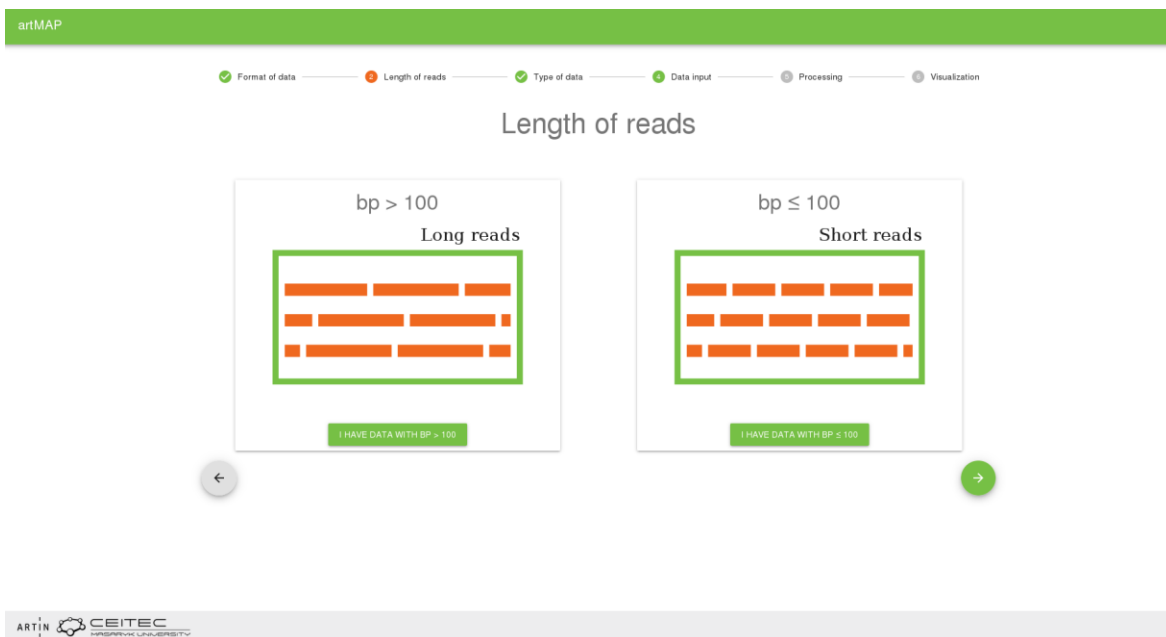


Figure S2: Screenshot of artMAP showing screen for selecting correct length of the sequencing reads.

- 3) Next, artMAP need to know whether sequencing reads are generated from single end or paired end. If your samples are sequenced from only one end of the read then please click on green button saying “I HAVE SINGLE END DATA”. If your samples are sequenced from both the end of the reads then please click button saying “ I HAVE PAIRED END DATA” (**Figure S3**).

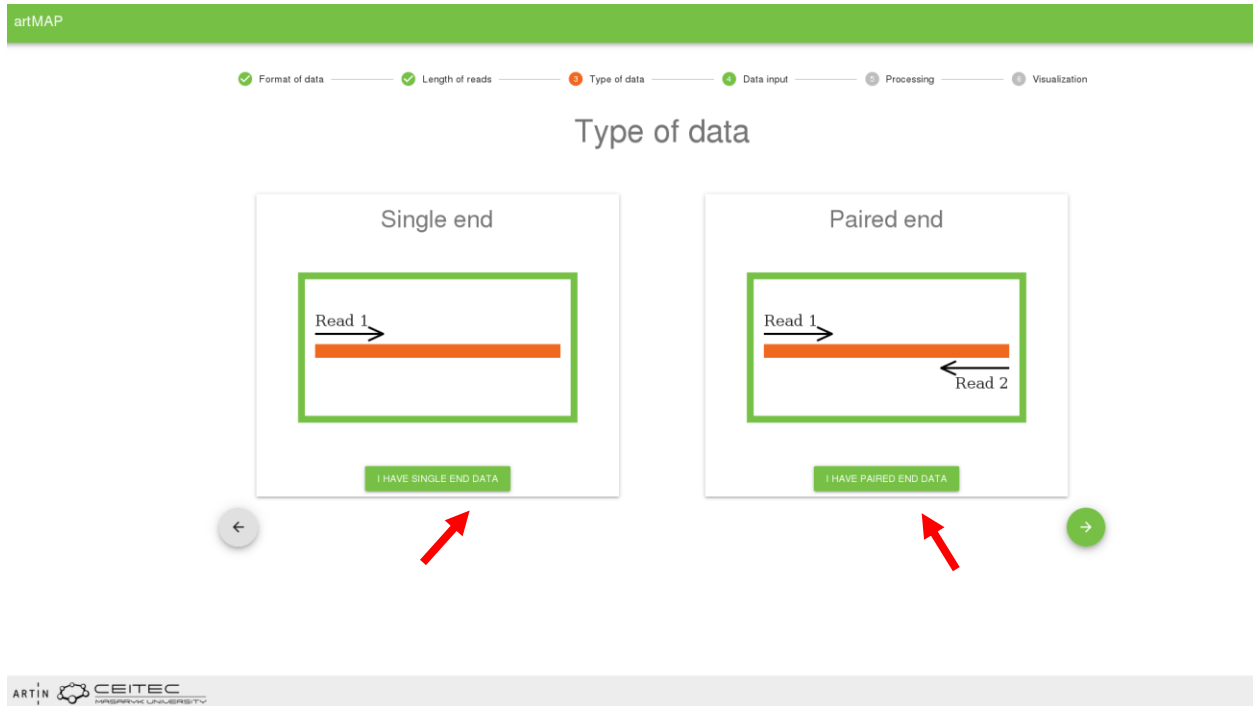


Figure S3: Screenshot of artMAP showing screen for selecting correct data type for sequencing reads.

- 4) If single end is selected at the previous stage then artMAP ask user to upload one input file each from control (green arrow) and mutant samples (red arrow). Sequencing reads generated from plants showing phenotype of interest after treatment with EMS is uploaded as mutant samples whereas non-treated reads from non-treated parent plants are taken as control sample. Also, artMAP ask user about the destination of folder for output as well name for the output file (Figure S4).

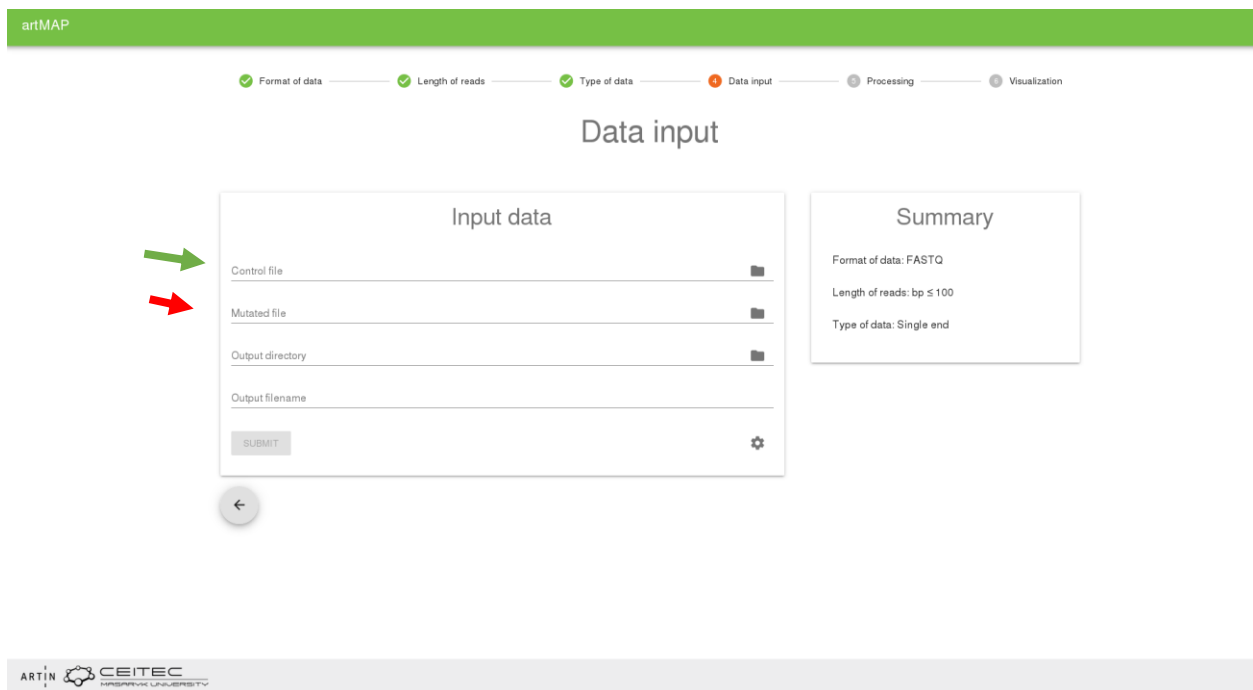


Figure S4: Screenshot of artMAP showing screen for uploading input files for single end sequencing data type.

If paired end option was selected at the previous step then artMAP ask user to upload 4 input files (**Figure S5**). Two files are coming from control and other two from mutant samples.

artMAP

Format of data Length of reads Type of data Data input Processing Visualization

Data input

Input data

Control file

Control file (second end)

Mutated file

Mutated file (second end)

Output directory

Output filename

SUBMIT

Summary

Format of data: FASTQ

Length of reads: bp ≤ 100

Type of data: Paired end

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Figure S5: Screenshot of artMAP showing screen for uploading input files for paired end sequencing data type.

- 5) artMAP also provide regulatory control to the user in advanced setting option which can be accessed by clicking the setting icon (red arrow, **Figure S6**). Advanced setting provide control over depth filter and frequency threshold. Also, it provide option to turn ON/OFF quality control as well as PCR duplicate removal step.

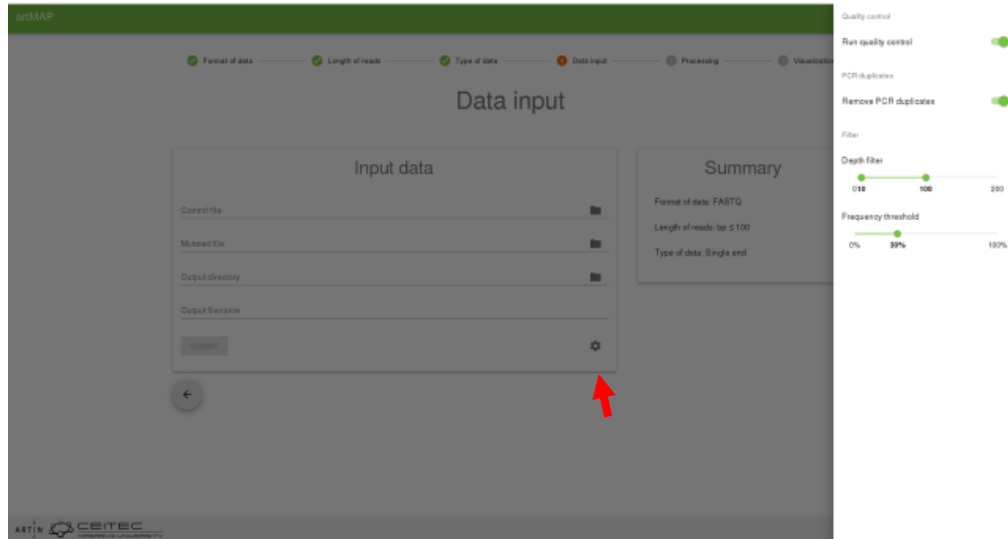


Figure S6: Screenshot of artMAP showing screen for accessing advanced options

- 6) After submitting all the information, user should click on submit button to run the artMAP. artMAP provide information about each and every step of the pipeline on the screen (**Figure S7**).

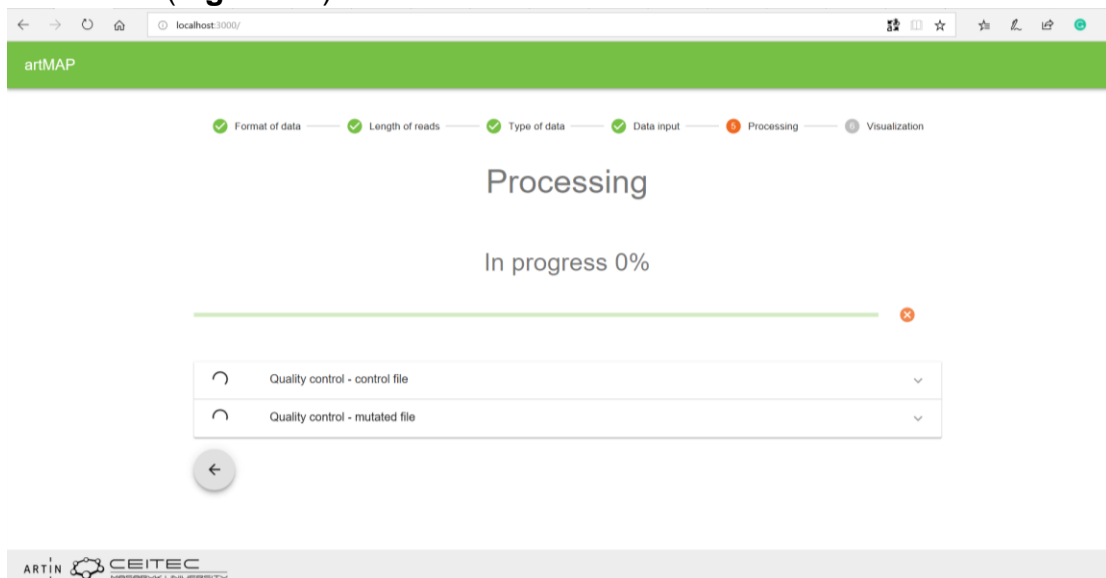


Figure S7: Screenshot of artMAP showing an example run in progress.

- 7) After analysis is completed, artMAP shows result in the form of the graph (**Figure S8**). These graph can be zoomed in or out using mouse. Hovering the mouse over each point will show annotation details for individual mutations (**Figure S9**).

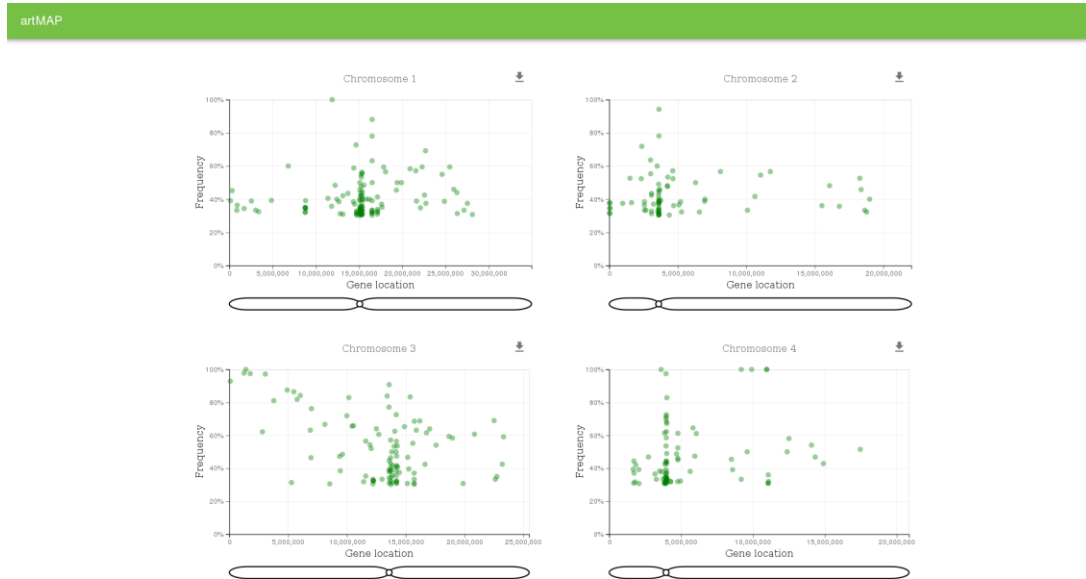


Figure S8: Screenshot of artMAP screen showing result an example run on graph. Each mutation is plotted as a function of frequency (Y-axis) vs location on chromosome (X-axis).