FAQS

1. **What organisms are supported?**

Currently the Simple tool can map genes for the following species: Arabidopsis\_thaliana, Oryza\_sativa\_Japonica, Zea\_mays, Solanum\_lycopersicum, Drosophila\_melanogaster, caenorhabditis\_elegans and danio\_rerio. However, it is very easy to enable Simple to map mutants of other species; see question 2.

1. **What if my organism is not included?**

You can simply add it; open the file data\_base.txt with a text editor. You want to add another new row with information about your organism in a way Simple can read it (each row in data\_base.txt stores information for a single organism). In the first column write your organism name (no special characters besides \_ (underscore)), in the second column paste the link to the gz (compressed) genome fasta file. Many are hosted on Ensembl. You can look at the other species rows to figure out how to find this link. In the third column you will need the compressed, gz link to the known variants gz file. You can find it the same way you found the link for the compressed fasta file. If your species doesn’t have this file, copy the following string to your knownsnps column: <https://raw.githubusercontent.com/wacguy/test/master/empty.vcf.gz>. The fourth column information should be taken from the snpEff\_database.txt file inside the folder scripts. Find your organism name (column #1 in the snpEff\_database.txt file) and copy it; if your genome has more than one entry we recommend to use the highest number (genome annotation). Paste it to the fourth column of your newly added species in the data\_base.txt file. Save the file and close it.

1. **How much time will it take the program to run?**

We experienced time ranging from a few hours to ~48 hours depending on your machine, the size of your fastq files (which actually reflects the size of your genome and depth of coverage).

1. **How do I know that the program finished running?**

The terminal will show a beautiful “Simple is done” red-yellow-blue text.

1. **What if I have no genes in my EMS.candidates list?**

Don’t Panic! We have mapped several genes even though the EMS.candidates.txt file was empty. There can be four possible reasons for that:

* It is possible that as a result of sampling error or a modifying locus, a few wt or heterozygous individuals were in your mutant bulk, meaning that your causal mutation was not recognized as homozygous in the mutant bulk. Open the file EMS.allSNPs.txt. Now you are looking for a record (row/SNP) that has a low number in the mut.ref column #10 a much higher number in mut.alt column #11 and wt.ref/wt.alt ratio should be ~2:1. Additionally, you might prefer SNPs that have a significant impact on the coding region (column #9) and ones with C>T or G>A changes (column #8) which are the majority of changes induced by EMS. Obviously you can use some advanced functionality of your spreadsheet editor like sorting.
* Simple uses reference FASTA and VCF files downloaded from the internet but we noticed that some releases have mistakes in them. For example, in the FASTA file of Arabidopsis thaliana, release 31, the chromosomes are organized incorrectly; the VCF file of release 32 of the same species is missing most of the known SNPs in chromosome 1. These errors lead to incorrect execution of commands in the pipeline. We have already checked that the listed species links to the FASTA are correct but if you are working with a different species and had a problem with the pipeline, you might want to check these files in the refs folder (you will most likely have to open them with the Terminal since they are too large for applications such as Word or Excel).
* Simple will only report indels up to a certain size; large genomic deletions that are rare but possible in EMS like screens are not likely to be detected. However, such deletions are genetically linked to other SNPs. You can sort your data and find the SNPs with values that might qualify them as causal mutations (see first point in this section (5) and then look for your data using IGV.
* There is a very low chance that your mutation originated from a non-reference nucleotide. These SNPs are reported in the EMS.cands\_alt4.txt (since this is a very unlikely event, this file will usually be empty). This file is in the archive folder.

1. **How much disk space do I need?**

Quite a lot, the output folder will fill up with ~50-100 gb, depending on the size of the input files (determined by the number of reads) and species (large genome size requires more reads) but essentially, only the three pdf, EMS.candidates.txt, EMS.allSNPs.txt and EMS.cands\_alt4.txt are necessary; the rest of the files are not necessary for final analysis. You might want to keep them for further analysis e.g., visualizing the data with tools like the IGV browser. These additional files will be in a the archive folder.

1. **I have data from two different runs, can I use SIMPLE?**

Most likely, yes. If you just concatenated two lanes that were separated by your sequencing facility, that shouldn’t be a problem. If the two runs were sequenced at two different time points, it is possible that the fastq files have different quality scores encoding; the pipeline should be able to deal with this issue. However, if a single bulk was generated by concatenating fasq files with different encodings, the program might

spit an error message. In such case, you should try and fix this. Here are some tools that can help you deal with this kind of problem: <https://en.wikipedia.org/wiki/FASTQ_format#cite_note-7>

1. **What if my mutation is dominant?**

First, refer to the README file for instructions on how to set the mutation to dominant in the simple\_variables.sh file. Mapping dominant mutations applies the same principles as recessive mutations. The only difference is that the wt bulk is expected to be homozygous for the reference allele, and the mutant bulk is expected to be segregating for heterozygous and mutant individuals in a 2:1 ratio, respectively, meaning that the alternate allele: reference allele ration should be 2:1.