To solve Exercise III, you will need a genome browser. The Analyze Genomes platform offers a ready-to-use genome browser with several predefined, aligned genomic files which have been already processed for variant calling. You will be provided with a Task ID for the exercise. This manual guides you through the steps necessary to successfully complete this assignment.

Step 1. Logon into the Analyze Genomes Platform

In order to log on the Analyze Genomes Platform, please use the ▶ Launch exercise tool button available on the course exercise page. It will automatically log you on the platform using your openHPI credentials.

Step 2. Choose alignment task

After login, you will be provided with a list of alignment tasks, as displayed below (Fig. 1). Simply click on the one indicated on the exercise description.

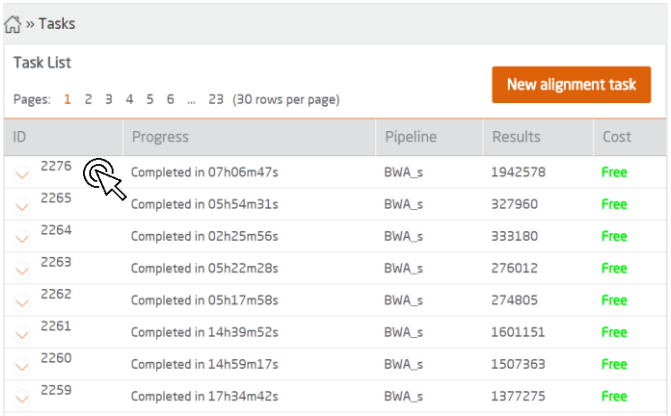

Figure 1. Task list

Step 3. Choose variant

Once you click on a given task, a list of genetic variants is displayed, according to the specific location it appears on the genetic code (Fig 2.). The last column on the left identifies the affected gene. Locate on the list the gene provided on the exercise and click on it to open the genome browser. **Important tip:** note that a click on any of the column headers (Chr, Pos, Ref, etc.) will sort the list alphabetically (A-Z, Z-A). That is helpful if you want to identify all variants related to a disease or gene. You can also access a given position changing the URL directly (see below).

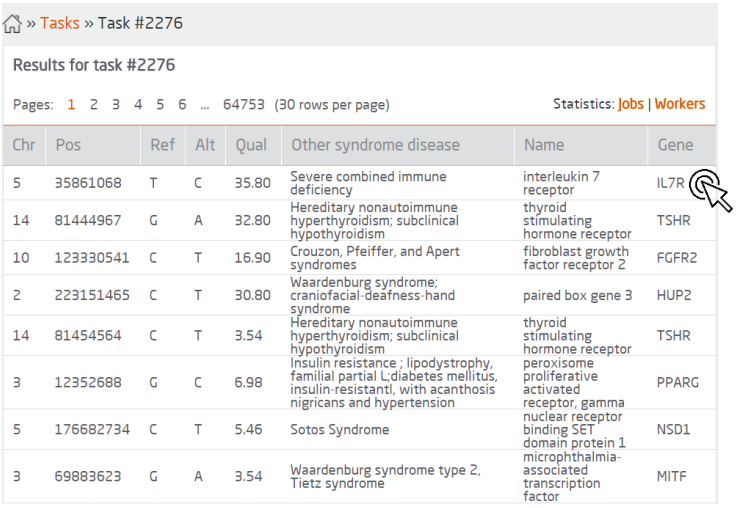

Figure 2. List of genetic variants

Step 4. Explore the genome browser

The questions asked on the exercise are based on the information provided on the genome browser. An example is shown on Fig. 3. The relevant genetic sequence is displayed, alongside with the respective translated aminoacids in both 5'-3' and 3'-5' direction. Note that the start codon (ATG), which codes for Methionine (M), is marked in dark grey. Similarly, end codons (i.e. TGA) are marked in red.

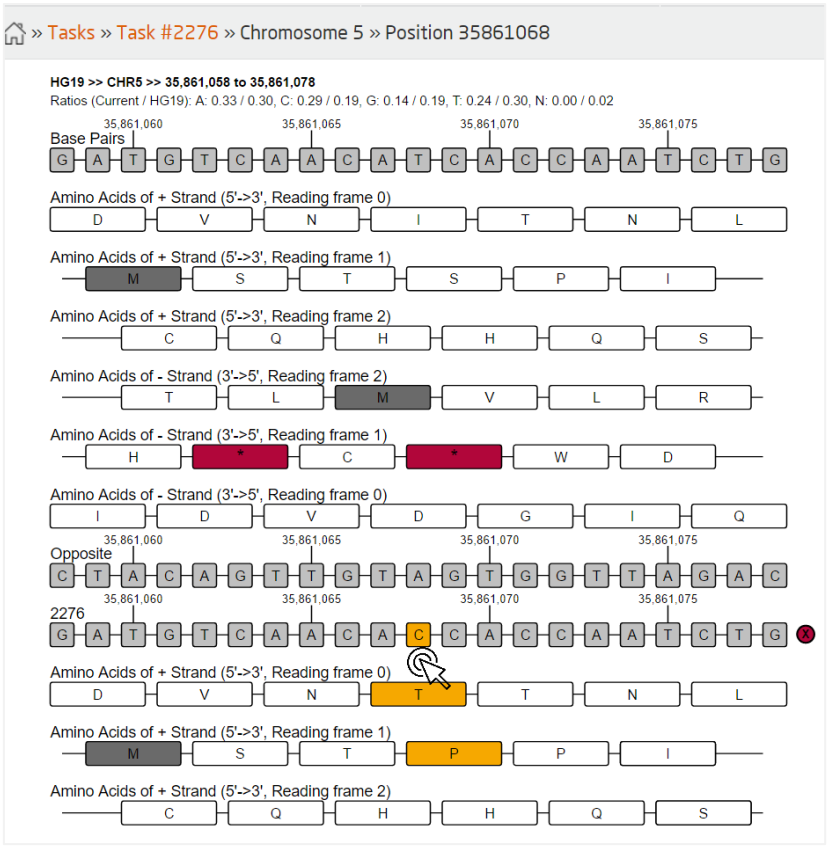

Figure 3. Genome browser

Step 5. Retrieve information from literature

With properly annotated genomic files, specific variants can be traced back to the studies that originally identified them for the first time and further references to it in available research. Click on the respective variant (cf. Fig. 3) to display more information. An infobox will be displayed on the right (Fig. 4). At this point, you're good to go! Just refer back to the genome browser to answer the questions. ☺

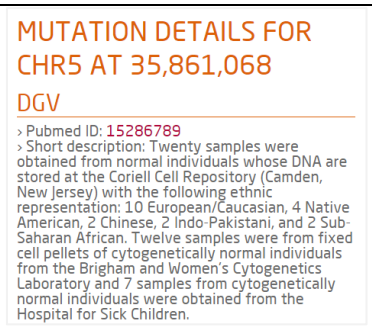

Figure 4. Literature information on genetic variant

Quickly finding a given position within the Genome Browser

If you have trouble finding a given position on the Genome Browser, you can quickly access it by changing the URL as follows:

`https://we.analyzegenomes.com/now/alignment/tasks/<<task id>>/<<chromosome number>>/<<position>>`

Just change `<<task id>>`, `<<chromosome number>>` and `<<position>>` accordingly.