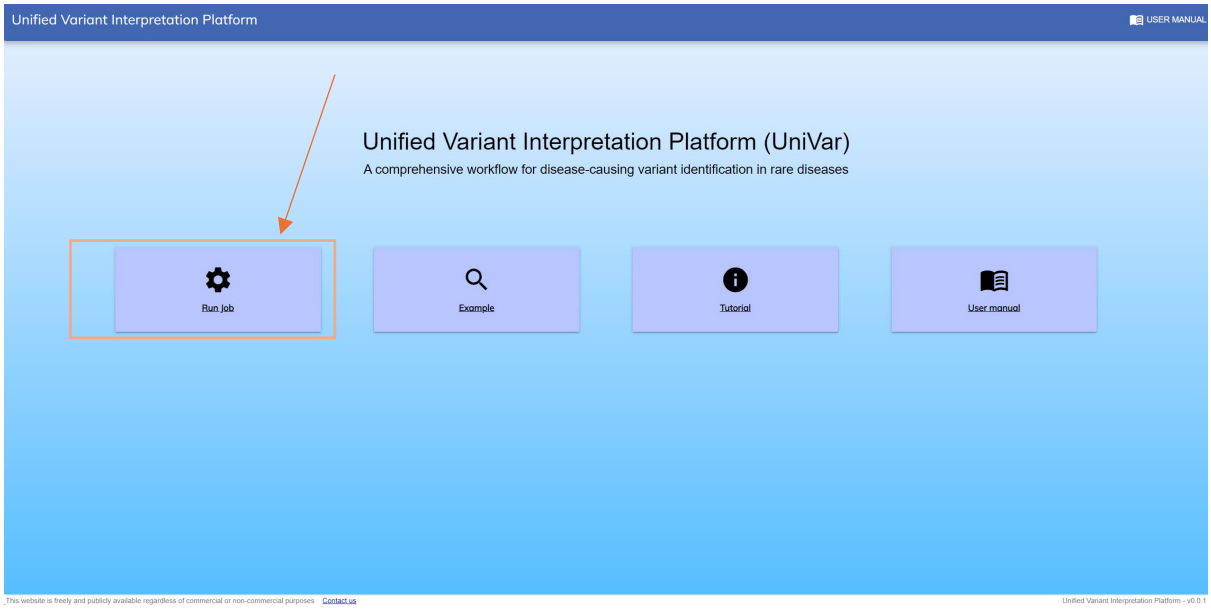
Unified Variant Interpretation Platform

Tutorial

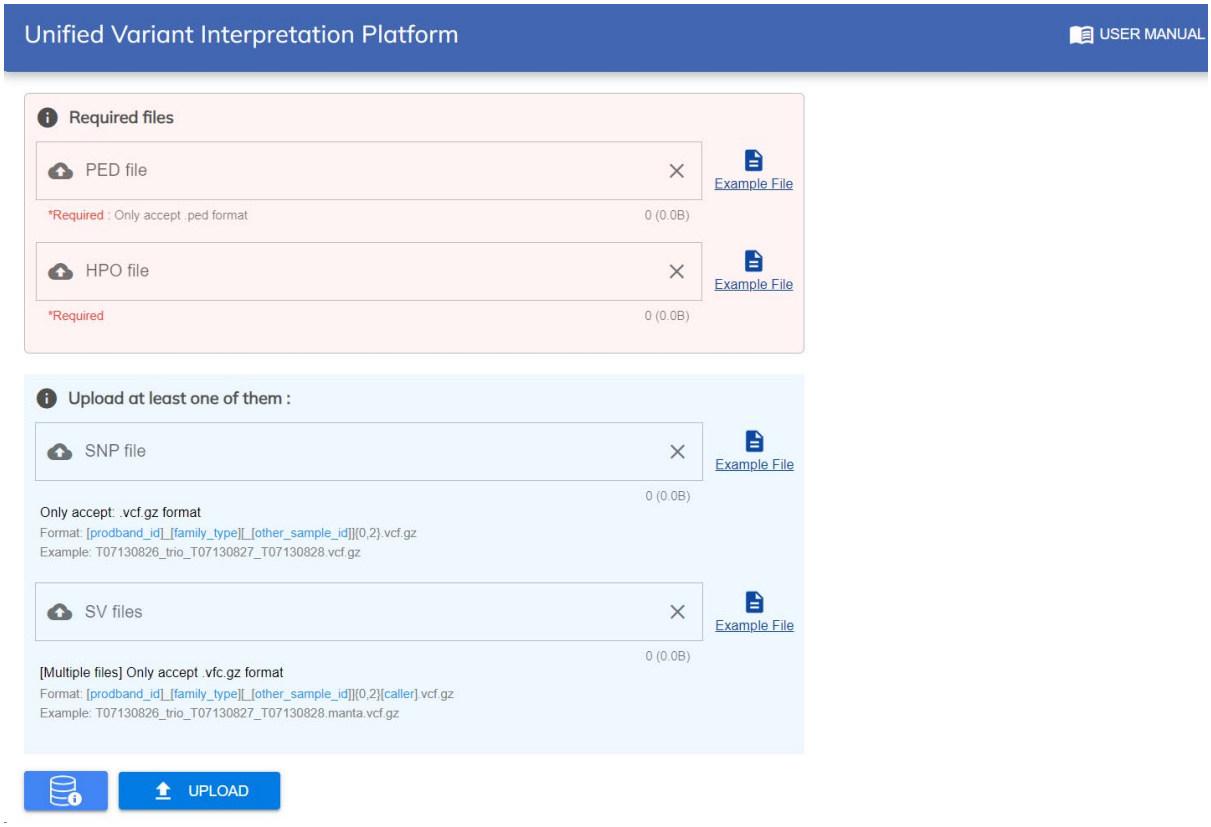
Version: 1.0

Table of Contents

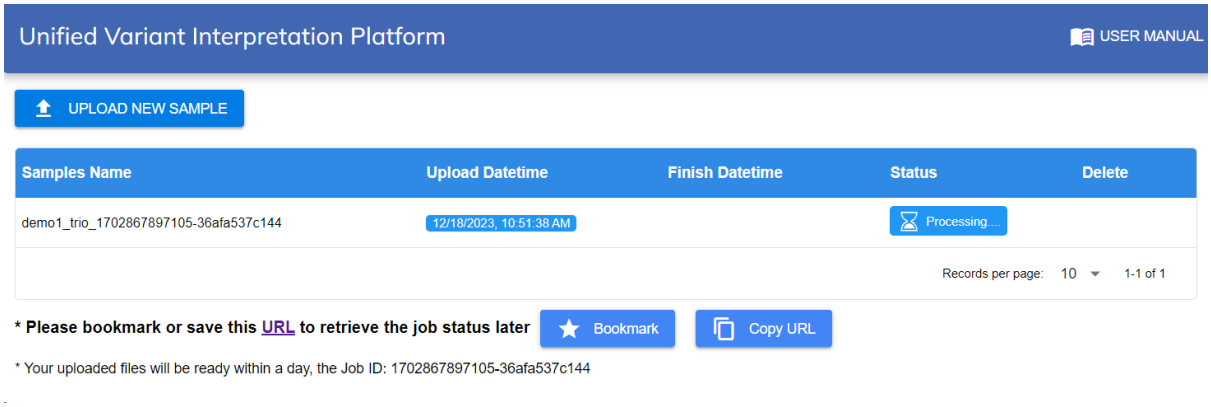
How to submit sample data?



1. On the Landing Page, click the “Run Job” button

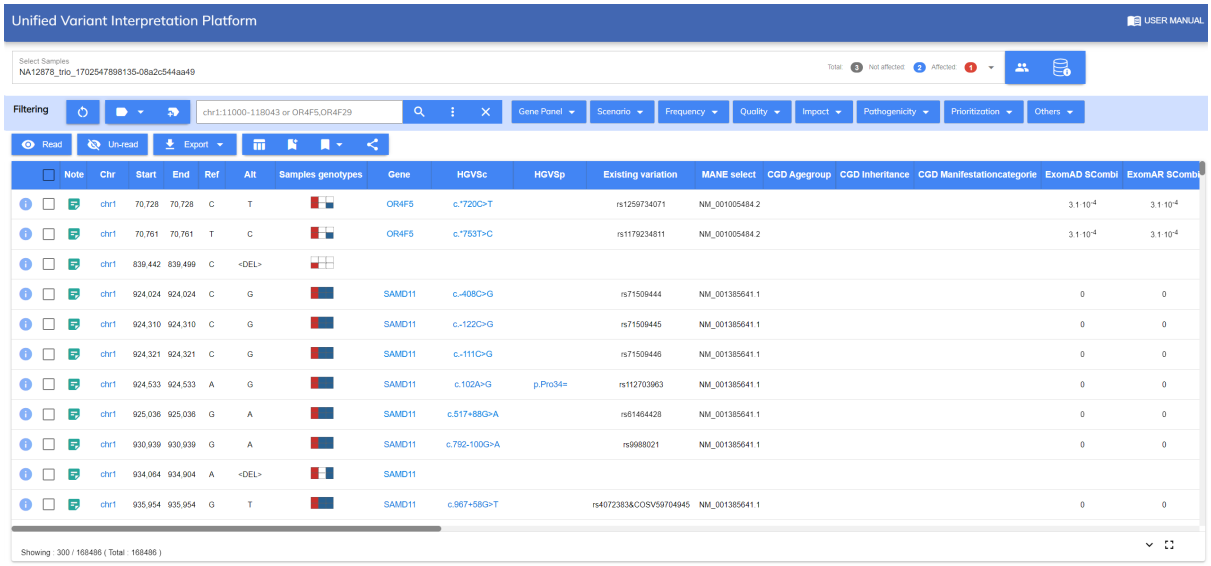


2. On the Sample Upload Page, user is required to upload one PED file, one HPO file and at least one VCF file of small variants or structural variants. Example file of each type can be downloaded through the hyperlink next to each file selection box. VCF files need to follow the predefined filename format as stated below the file selection box.

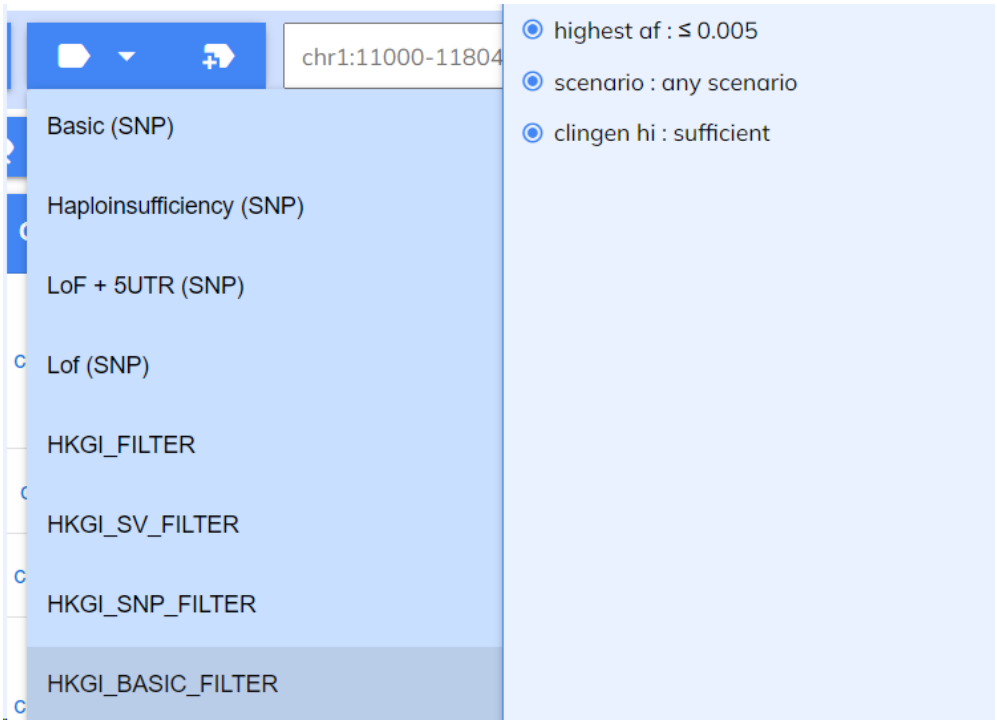


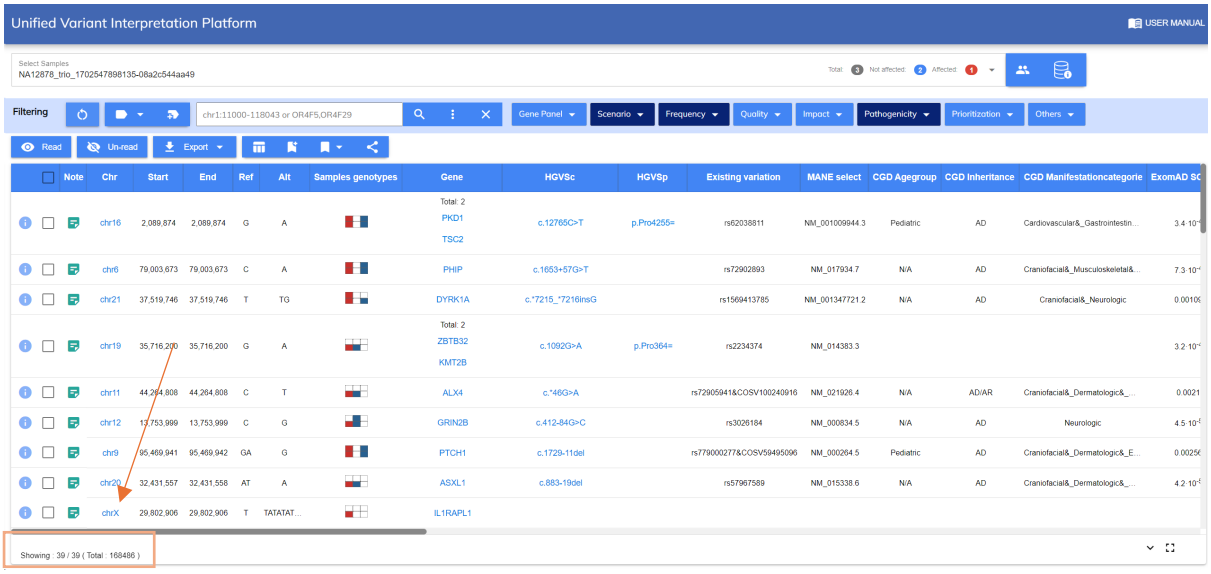
3. After uploading sample data, user can view the job status on the job status dashboard. User is required to bookmark or save the provided URL to retrieve the job status later. If the job is finished, user can click the sample name to enter the variants table page to browser the annotated results.

How to interpret the annotated results?

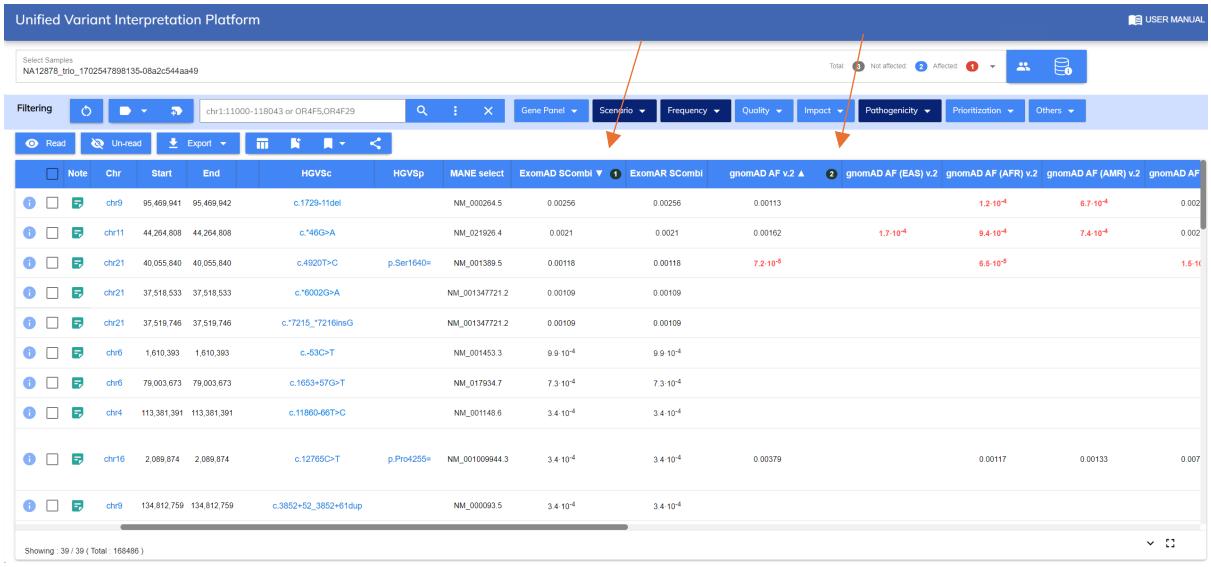


In the variants table page, variants are displayed as tabular form. Each row represents one variant, and each column represents different variant annotations. User can make use of the filtering options provided in the filtering panel to narrow down the scope of study. Some filtering presets are provided for filtering likely pathogenic variants. For example, the “HKGI_BASIC_FILTER” filters variants based on allele frequencies, mode of inheritance and Clingen haploinsufficiency scores.

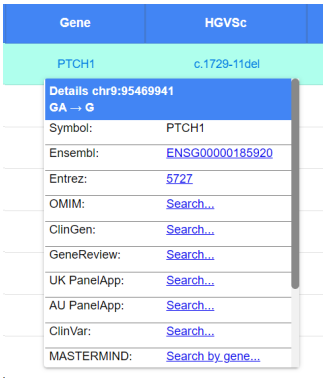




In the example dataset, after applying the “HKGI_BASIC_FILTER” preset, the total number of variants drops down to 39 from 168486. User can still adjust the applied filtering options after applying the preset.

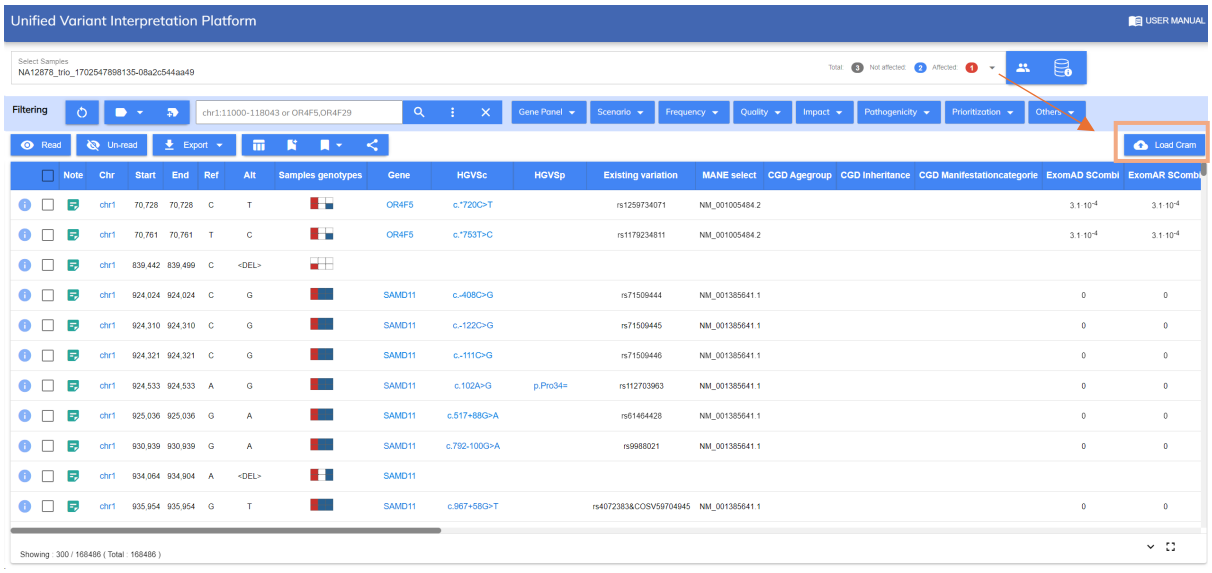


Besides, user can click the column header to sort the variants list. The arrow next to the column name indicates the sorting direction, which can be changed by clicking. Multi-column sorting is supported. The rightmost digit in the column header represents the sorting priority. So in the above example, variants are sorted by Exomiser combined AD scores in descending order and then sorted by gnomAD v.2 AF in ascending order. To cancel column sorting, click the digit of the column header.

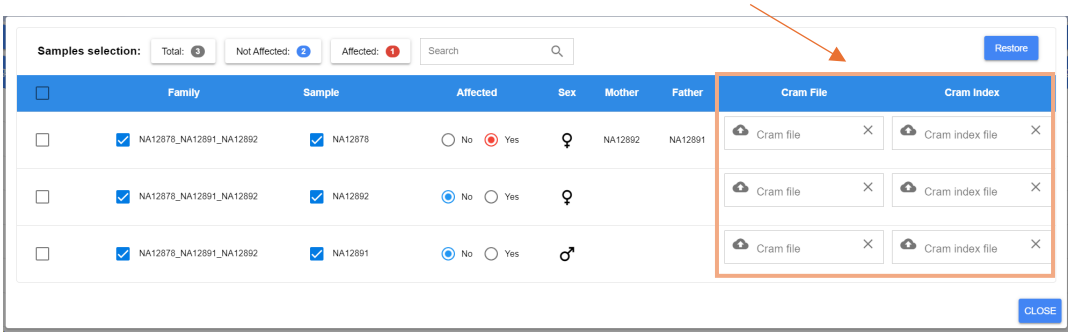


Upon identifying the interesting variants, user can click the hyperlinks (in blue colour) like gene symbol, chromosome, HGVSc or HGVSp on each row to navigate to external databases for cross-checking.

To validate the variants visually, user can view reads alignment of variants through Integrative Genomics Viewer (IGV). To use this feature, user first needs to click the "Load Cram" button on the top right corner of the variants table.



Then user can specify the local storage location of the cram files and the cram index files in the pop-up panel.



After that, user can view reads alignment of a variant by double clicking a row in the variants panel. An IGV will be opened with one track per sample, centred at the selected variant's position.


IGV
hg38
chr16
chr16:683,395-683,452
54 bp
Cursor Guide
Center Line
Track Labels
ROI Table
Save SVG
683,400 bp
683,410 bp
683,420 bp
683,430 bp
683,440 bp
683,450 bp
G C C A C T C G G T G A A G T T G T T G T C C C C G A A G A A G T A C A G G G T G T C T G C C A A C A G A
Sample 1
Sample 3
Sample 2
RefSeq Genes
CLOSE