

UPLOAD METADATA

Any files associated with an experiment (excluding sequencing files, references, and annotations) can be uploaded through the **METADATA** (Fig.) tab. During upload, the metadata files should always be associated with an organism and tagged appropriately, as explained in Table below.

Data Type	Tag Name	Format	Details
List of genes	Gene List	Tab, CSV, TXT	Ensembl Gene IDs only
Target markers	Hotspots	BED, VCF	SNPs, MNPs, INDELS
Amplicon ranges	Amplicon Range	BED, VCF	Target region with start and ends
Variants/genotypes	Genotypes	BED, VCF	Called variants

Table. Metadata file formats and associated upload tags.

Similar to Sequence and reference file uploads, the following actions are performed on the uploaded metadata files:

- Uncompression of the files
- Validation of the format and integrity of the file and its compatibility to the reference genome.
- Registration into the **METADATA**
- Status notification through email

Uploader

SEQUENCE DATA REFERENCES ANNOTATIONS **METADATA**

Type

Select File

Successfully uploaded metadata files are stored in **METADATA** and can be accessed while executing the pipelines.

Revision #3

Created 26 January 2022 11:42:37 by Kshama

Updated 2 March 2022 17:31:01 by Kshama