

GRAPEGENOMICS DATA SUBMISSION GUIDELINES

VISIBILITY

Grapegenomics offers 3 visibility levels:

- Fully private: tools and data are not available to the public, only available to you and the people you grant access to.
- Public services/Private data: the genome has a public page, and the tools are available to the public. The data are not available to anyone but can be accessed through a private page with the appropriate credentials.
- Fully public: Usually post publication status. Genome tools and data are fully available to the public.

Please let us know which option fits your needs.

DATA REQUIREMENTS

The following items are used to generate the genome page. Not all the fields are required.

For the genome page information:

- Species name
- Accession name
- Clone name
- Assembly version
- Previous assembly version (if already hosted or posting more than one version)
- Assembly type: contigs without phasing, contigs with primary/haplotigs phasing, pseudomolecules (chromosome-scale), graphical format (pangenome)
- Representative picture of the genotype
- Picture credits
- References: Please indicate the appropriate references. DOIs pointing to a Zenodo repository, pre-print or published article are accepted. Multiple references can be added.

Regarding the files (Uncompressed and gzip-compressed files are accepted):

- Genome sequences (FASTA): The genome file can be provided as a single file or split per haplotype if more convenient.
- Feature sequences (FASTA): mRNA, CDS, and protein files
- Structural annotations (GFF): gene and repeat annotations
- Functional annotations (TXT): gene functional annotation