

## An overview of PN40024 genomics resources

A new annotation (v5.1) has been released (Nov 2024) on the most recent T2T.v5 genome assembly. To promote its use, we have provided gene id equivalences between all annotations by transferring previous annotations to the T2T genome and working out overlap metrics using the Aegis genomics package. Obtain the equivalences file in the downloads section or access the gene cards app for a more interactive approach. In addition, we have updated the grapevine reference gene catalogue to match the new annotation and incorporate previous submissions, taking the number of genes from 2,000 to over 3,000.

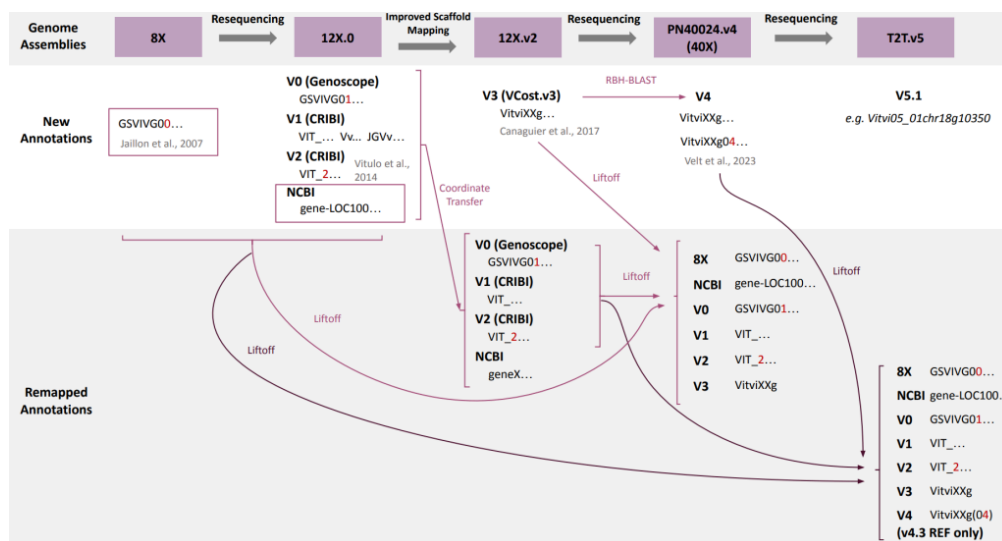
[PN40024 Downloads](#)

[GeneCards](#)

[Gene Catalogue](#)

The **PN40024 downloads** section above, centralises access to files and clarifies their nature.

The five different genome assemblies of PN40024 are shown below, together with their *de novo* annotations. Transfers from previous annotations to newer assemblies are also shown, as these transferred annotation files are commonly used in the community. It also becomes relevant to understand to which genomes these annotations belong to. Scroll down for further descriptions of the different grapevine genomes and their available resources.



## PN40024.T2T (v5)

[JBrowse 2](#)

[JBrowse 1](#)

[BLAST](#)

[Genome, Annotation and Feature Files](#)

The Genome browser contains reference and alternative (heterozygous, ALT) chromosomal regions of the T2T assembly, plus a chr00 with all unanchored contigs. It also contains accurate mapping of all previous gene annotations (using Liftoff on copies mode), together with mapped long-read (Iso-seq) and short-read (Illumina) sequencing data, which was generated from vegetative and reproductive organs of PN40024 at different developmental stages. This RNA-seq data was kindly provided by Daniela Holtgräwe (Bielefeld University · CeBiTec), Camille Rustenholz (University of Strasbourg · INRAE Colmar) and Doreen Ware (Cold Spring Harbour Laboratory). The most recent annotation on the T2T is the 5.1 version, which includes both protein coding genes and long non-coding RNAs and has been obtained with the TITAN (The Intense Transcript ANnotator) pipeline.

[Click for more details on the assembly.](#)

[Click for more details on the annotation.](#)



Please cite:

**The complete reference genome for grapevine (*Vitis vinifera* L.) genetics and breeding**

Xiaoya Shi, Shuo Cao, Xu Wang, Siyang Huang, Yue Wang, Zhongjie Liu, Wenwen Liu, Xiangpeng Leng, Yanling Peng, Nan Wang, Yiwen Wang, Zhiyao Ma, Xiaodong Xu, Fan Zhang, Hui Xue, Haixia Zhong, Yi Wang, Kekun Zhang, Amandine Velt, Komlan Avia, Daniela Holtgräwe, Jérôme Grimplet, José Tomás Matus, Doreen Ware, Xinyu Wu, Haibo Wang, Chonghui Liu, Yuling Fang, Camille Rustenholz, Zongming Cheng, Hua Xiao, Yongfeng Zhou

Horticulture Research, Volume 10, Issue 5, May 2023, uhad061, <https://doi.org/10.1093/hr/uhad061>

**PN40024.v4 (40X)**

Genome Browser

BLAST

Genome, Annotation and Feature Files

Apollo (Manual Curation of Gene Models)

Please cite:

**An improved reference of the grapevine genome reasserts the origin of the PN40024 highly homozygous genotype**

Amandine Velt, Bianca Frommer, Sophie Blanc, Daniela Holtgräwe, Éric Duchêne, Vincent Dumas, Jérôme Grimplet, Philippe Hugueney, Catherine Kim, Marie Lahaye, José Tomás Matus, David Navarro-Payá, Luis Orduña, Marcela K Tello-Ruiz, Nicola Vitulo, Doreen Ware, Camille Rustenholz,

G3 Genes|Genomes|Genetics, 2023, jkad067, <https://doi.org/10.1093/g3journal/jkad067>

**Apollo for manual curation of gene models:** request an account by email to Amandine Velt and/or Camille Rustenholz | [camille.rustenholz \(at\) inrae.fr](mailto:camille.rustenholz@inrae.fr) | [amandine.velt \(at\) inrae.fr](mailto:amandine.velt@inrae.fr)

**Assembly:** The PN40024.v4 assembly is based on the Sanger scaffolds of the 12Xv2 version that were corrected, extended and completed using 30X PacBio data. The heterozygous regions are better identified (**Velt et al. 2023**).

**European Nucleotide Archive:** The genome assembly can be also accessed at **ENA**.

**Annotation:** The PN40024.v4 annotation is based on a mixed approach, derived from *de novo* annotation and matching with the previous structural annotation version. In an effort to preserve VCOST.v3 gene IDs where possible (e.g. in cases where chromosome numbers are unchanged) a reciprocal best-hits strategy between VCOST.v3 and **PN40024.v4.1** annotations was carried out. This allowed the transfer of 67% of VCOST.v3 gene IDs. In general, the new *de novo* annotation performed better than the previous annotation in terms of BUSCO stats.

The current version is v4.3, released after Integrage **Annot'Training School** for gene model manual curation.

To indicate possible matches between the current annotation and previous versions (see overview above), a feature-overlap strategy was carried out to work out id correspondences between all annotation versions associated to PN40024.v4 (40X) which includes previous annotations (8x, NCBI, v0, v1, v2, v3) remapped using Liftoff and the most up to date v4.3 annotation.

**PN40024 12X.2 Assembly (URGI)**

Blast (Hosted by Grapegenomics)

Catalogue and Gene Cards

Genome, Annotation and Feature Files

**Assembly:** The 12Xv2 chromosome assembly is based on the scaffolds of the grapevine reference genome build (FN594950-FN597014, EMBL release 102; *Vitis vinifera* cv. PN40024).

Further information about the 12Xv2 can be found at **URGI** (as well as original **genome** and **annotation** files).

The most up to date VCost.v3 annotation file shared in **Grapedia** also includes the reference gene catalogue (v2) symbols in the "Name=" field. Please access the **catalogue and gene cards** section to submit gene names to the catalogue (a recording of the online workshop is available) or to explore the expression of your genes of interest in VitViz.

The PN40024 reference assembly (12Xv2) is also hosted at **Grapegenomics** and is equipped with a blast server. The site is actively maintained by the **CantuLab** at the University of California, Davis.

## Other wine grape cultivar and *Vitis* species assemblies/annotations

Additional genomes of different cultivars, subspecies and species of the *Vitis* genus are also hosted at **Grapegenomics**, and include several chromosome-scale phased assemblies.

### Provider

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