

# Barley SNP Databases and GVT

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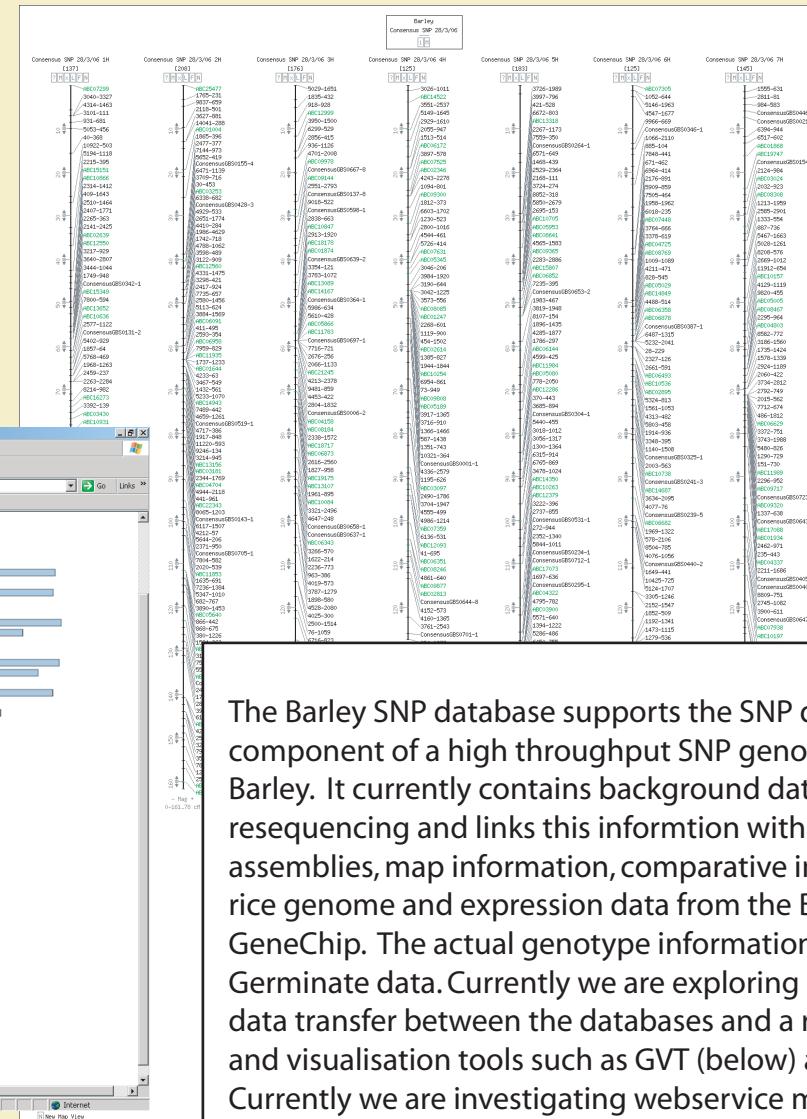


## SCRI Barley SNP Database

[http://bioinf.scri.sari.ac.uk/barley\\_snpdb/](http://bioinf.scri.sari.ac.uk/barley_snpdb/)

The screenshot shows the SCRI Barley SNP Database interface. It includes:

- DNA Sequence of ABC00076:** Displays the sequence from position 1 to 661.
- BLASTN hits for ABC00076:** Limited to the top ten hits against various species.
- Schematic of mutation locations within contig assembly:** A bar chart showing mutation locations across contigs.
- Polymorphic base positions:** A grid showing polymorphic sites with red arrows indicating mapped SNPs.
- SNPs detected by primers:** A table showing primer details and SNP positions.



The Barley SNP database supports the SNP development component of a high throughput SNP genotyping project in Barley. It currently contains background data on SNP assays and resequencing and links this information with Barley EST assemblies, map information, comparative information from the rice genome and expression data from the Barley1 Affymetrix GeneChip. The actual genotype information will be stored in the Germinate data. Currently we are exploring a variety of modes of data transfer between the databases and a range of analytical and visualisation tools such as GVT (below) and TASSEL. Currently we are investigating web-service methodologies.

## The Genotype Visualisation Tool (GVT)

The Genotype Visualisation Tool (GVT) is a Java application designed for the visualisation and analysis of plant genotype data in the form of graphical genotypes. It has been designed to support a range of genotyping technologies, including SSRs, SNPs, AFLPs and RBIPS. We anticipate that it should be extendable to other technologies.

The screenshot shows the Genotype Visualisation Tool (GVT) interface. It includes:

- Data Board:** Shows a tree view of datasets, including "map", "Data", and "All Chromosome".
- Pedigree View:** A pedigree chart showing relationships between individuals across multiple generations.
- Chromosome Map:** A map of chromosomes showing genotypes for various loci.

Data can be loaded into the GVT platform through the GERMINATE database or similar GDPC enabled databases or from a local Excel spreadsheet based on a supplied template. GVT is a Java 1.5 application and currently we are working to develop additional analysis tools as well as the visualisation of genotypes in both pedigree and clustering contexts into the GVT framework.