GenoBaits®

Barley 40K panel

The Genobaits® Barley 40K Liquid Chip is jointly developed by Dr. Song Weining/Nei Xiaojun's team from the Northwest A&F University and Molbreeding Biotechnology Co.,Ltd. Screening of SNP from resequencing data (10×) of barley materials from 155 different ecological regions worldwide, along with 200 drought resistance-related and grain-related functional markers, a total of 40,000 SNP markers were designed to form the Barley 40K liquid chip using the GenoBaits® technology.

Product Highlight

- **High representativeness and rich diversity information**
  The marker information is derived from barley materials obtained from 155 different ecological regions worldwide, including 43 wild barley materials, 54 landrace varieties, 27 cultivated barley varieties, and 31 Tibetan barley materials.

- **200 functional markers**
  200 drought resistance-related and grain-related functional markers were included.

- **Different density products cater to different application scenarios**
  In addition to meeting the detection of 40K marker loci, this product has also derived series products with 20K and 10K markers, which are suitable for different application scenarios.

Application

Genetic diversity analysis

Genetic map construction
Genetic diversity analysis
QTL analysivs
Genome-wide association study
Functional gene mapping and cloning

Breeding selection and screening

Varietiy authentication
Germplasm resources assessment and conservation
Molecular marker assisted selection
Genome-wide selective breeding



Service process

Submit sample for DNA QC

Library construction and sequence capture

High-throughput sequencing

Data quality control and sequence trimming

Automatic Bioinformatics analysis on cloud

Report visualization

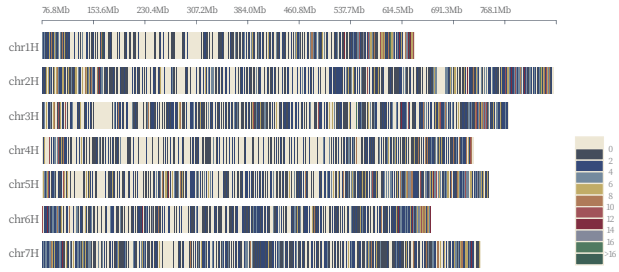


Figure 1 Distribution of SNP numbers on chromosomes

In Figure 1, 40,000 marker segments are evenly distributed on the 7 Barley chromosomes.
Definition of ruler: SNP numbers of each sliding window in genome (along a window size of 200,000bp)

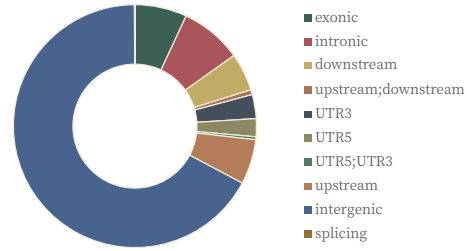


Figure 2 Annotation of SNP

In Figure 2, 32.83% of the markers in the Genobaits® Barley 40K panel were located in the coding region, while approximately 6.92% of the markers were located in the exon region.

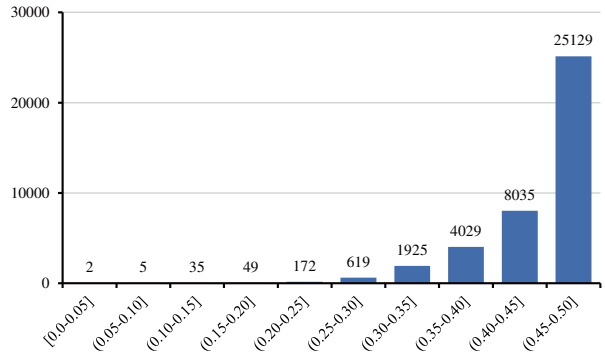


Figure 3

As shown in the figure 3, the MAF average of 40,000 target SNP markers in GenoBaits®Barley 40K Panel is 0.45.

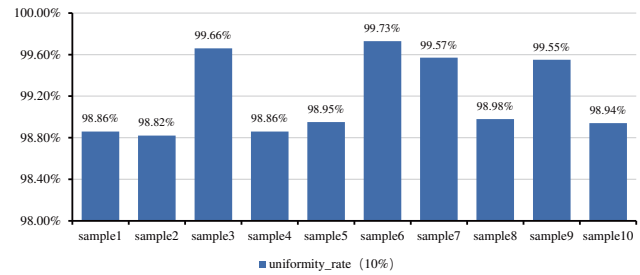


Figure 4 Uniformity_rate10 of test samples by using GenoBaits® Barley 40K Panel.

As shown in the figure 4, the uniformity_rate10 of test samples were 98.82%-99.73%.

Bioinformatics analysis

GBTS Basic analysis

QC and reference sequence comparison: sequencing data QC, reference sequence comparative analysis, sequencing depth and coverage statistics;
Detection and Annotation of the variation loci include SNP, indel, STR/SSR.

Advanced analysis

Phenotypic analysis;
Population genetic study;
Species identification, Species fingerprint construction;
Genome-wide selection;
Genome-wide association study;
Genetic map construction and QTL mapping;
BSA mixed pool sequencing analysis.