GenoBaits®

Rice 40K Panel

Molbreeding collaborated with Dr. Xu Jianlong's team (CAAS-CIMMYT), has developed a series of GBTS panels, including from 10K–40K (GenoBaits®). The GenoBaits® Rice 40K Panel obtained with 40,000 targeted sites based on 3,000 rice core germplasm resequencing data (average sequencing depth 14×). 90% of the genetic variety of rice is represented by these germplasm resources, which originate from 89 different nations and include both traditional and contemporary farmed types.

Application

- Genotype identification, Variety identification and Genetic diversity analysis of rice germplasm resources
- Genome-wide association analysis (GWAS) of agronomic traits
- Mapping and cloning of functional gene /QTL
- Marker-trait association
- Transgenic backcross background selection/Targeted improvement
- Molecular design breeding (Marker-assisted selection, Genome-wide selection, etc.)

Product Highlight

- **High representation and broad diversity information**
  The collection of 3,000 rice core germplasm resources from 89 countries represents 90% of the genetic diversity of rice, including indigenous, domesticated and modern cultivars.

- **Powerful functionality**
  The 14,226 developed functional markers covered a total of 2,747 cloned rice genes and comprised all the publicly available cloned gene-related markers. 504 functional markers encompassed 56 putative rice genes associated with crucial traits such as yield, heading stage, plant height, resistance to pests and diseases including blast, bacterial blight, rice planthopper, and quality attributes like processing and appearance, resilience against drought, salinity, temperature fluctuations, soil heavy metal toxicity as well as lodging-resistant property.

- **Various density designed for different applications**
  In rice 40K SNP panel, Molbreeding Biotech Co., Ltd designed a total of 151,743 multiple SNP sites (mSNPs). The Rice 20K panel has 70,674 mSNP sites and the 10K SNP has 33,579. Different application can select the appropriate marker density to minimize cost and analysis time.



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

The distribution of 40K markers across the genome

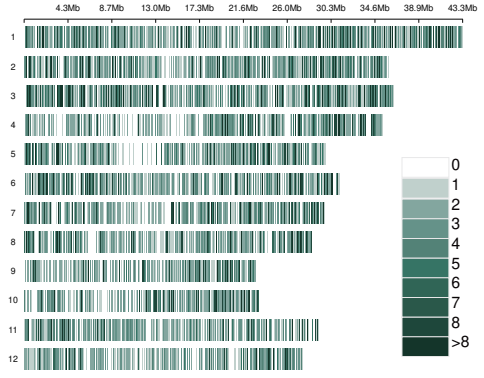


Figure 1 Distribution of Rice 40K SNP numbers on chromosomes

In Figure 1, 40,000 marker segments with 151,743 SNP markers, evenly distributed on 12 rice chromosome.

Definition of ruler: SNP numbers of each sliding window in genome (along a window size of 25,000bp)

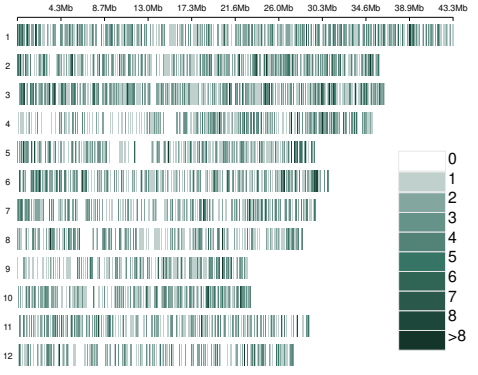


Figure 2 Distribution of Rice20K SNP numbers on chromosomes

In Figure 2, 20,845 marker segments with 70,674 SNP markers, evenly distributed on 12 rice chromosome.

Definition of ruler: SNP numbers of each sliding window in genome (along a window size of 25,000bp)

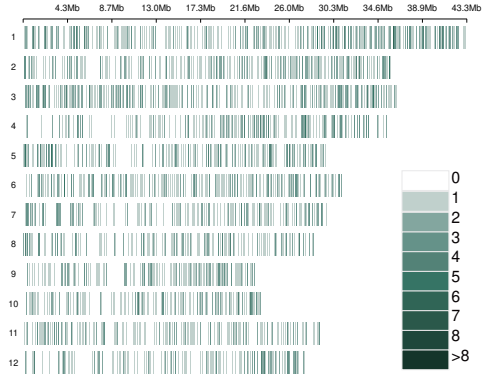


Figure 3 Distribution of Rice10K SNP numbers on chromosomes

In Figure 3, 10,325 marker segments with 33,579 SNP markers, evenly distributed on 12 rice chromosome.

Definition of ruler: SNP numbers of each sliding window in genome (along a window size of 25,000bp)

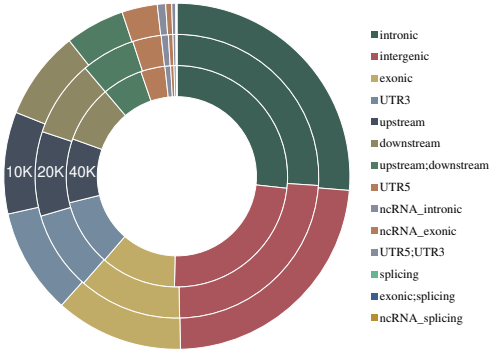


Figure 4 Annotated SNP information of Rice 40K, Rice 20K, Rice 10K

The markers present in Rice 20K and Rice 10K products, which are derived from the Rice 40K products, are uniformly distributed across chromosomes. They can be selected with high cost-effectiveness based on different breeding requirements and practical scientific research applications.

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.

According to customer requirements, customized bioinformatics analysis content can be confirmed in the project stage.