GenoBaits®
Wheat 16K Panel

The GenoBaits® Wheat 16K Panel was a collaborative effort between the Molbreeding R&D team and the research teams led by Prof. Kang Zhensheng from China Northwest A&M University. The SNPs were selected from 20 sequenced pan-genomes and 1,520 germplasm data collected worldwide. Through validation and optimization, Molbreeding designed 14,868 mSNP (multiple single-nucleotide-polymorphism cluster) capture regions (total 37,669 SNPs markers) into one liquid chip. This 16K panel can be used for germplasm evaluation and linkage map construction.

Product Highlight

1.Enriched polymorphism selection and a broad spectrum of variation
The 16K markers were selected from resequencing data and validated through a wide varieties of wheat accessions (wild, land race or cultivated) in all regions of the globe (spring and winter wheat regions).

2.Marker even distribution on all chromosomes
After several round of optimization, the current 16K panel contains ~ 1800 SNP markers evenly distributed on each chromosome.

3.Higher density and lower cost
This 16K panel provides more than 37K SNP marker genotypes, which greatly enhance the prediction accuracy and lower cost while comparing to other similar product.

Application

1. Genetic diversity analysis

Genetic map construction
QTL analysis
Genome-wide association study

2.Breeding selection and screening

Germplasm characterization
Variety protection, Varietiy authentication

Application example

200 Yaco 'S'/Mingxian 169 RIL7 family materials were detected and genotyped by GenoBaits® Wheat 16K Panel, and a total of 14,868 markers were obtained, and 4,883 markers with differences between parents were selected to construct genetic maps, using QTL lciMapping 4.2, combined with the phenotypic traits and genetic map information from the four environments, two stable QTLs were mapped on 2BS and 3BS, respectively.

ALL Traits

Qyr.nwafu-2BS.2

ALL Traits

Qyr.nwafu-3BS.2

Service process

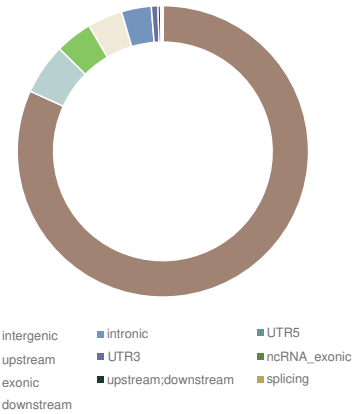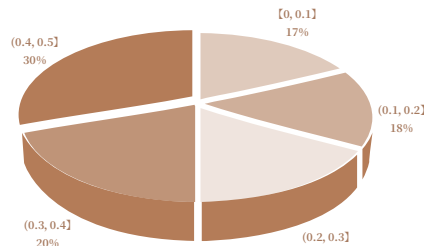| Submit sample for DNA QC	Library construction and sequence capture	High-throughput sequencing	Data quality control and sequence trimming	Automatic Bioinformatics analysis on cloud
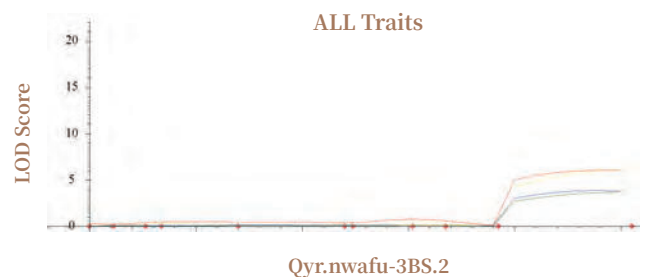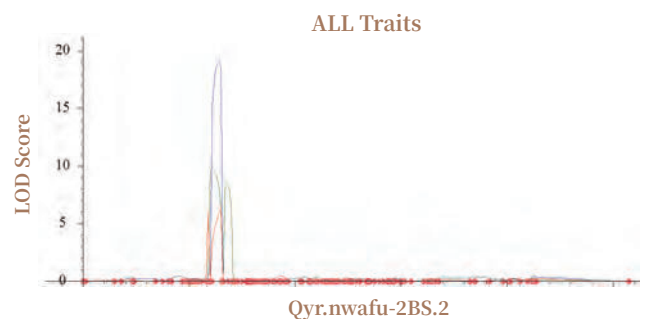
Report visualization

Figure 1 Distribution of SNP numbers on all wheat chromosomes

Figure 2 MAF Distribution of target SNP sites

Figure 3 Annotation statistics of target SNP sites

In Figure 1, the 14,868 mSNP marker regions (37,669 SNP markers) evenly distributed on wheat chromosome.
Definition of ruler: Core SNP numbers of each sliding window in genome (along a window size of 1M)

In Figure 2, the MAF average of target SNP sites in 14,868 mSNP regions is 0.28.
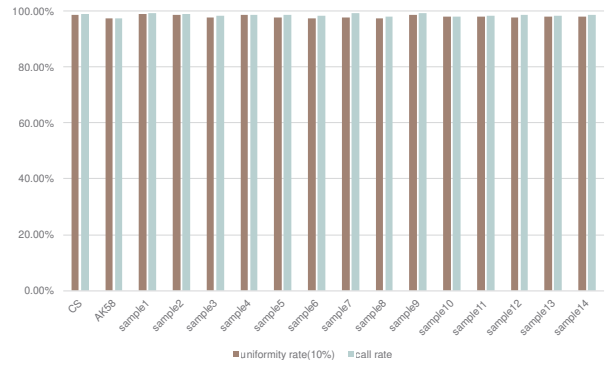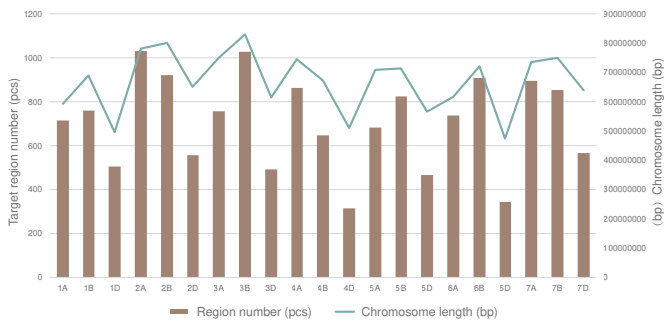

Figure 4 Statistics of mSNP regions numbers on all wheat chromosomes

Figure 5 Uniformity rate and calling rate of target SNP sites

Wheat Capture Kit ordering information

Product Name	Target SNP Sites	Marker Type
GenoBaits®Wheat Breeding Panel	128	SNP
GenoBaits® Wheat Exome Panel	CDS	gene
GenoBaits® Wheat SNP40K	40017	mSNP
GenoBaits® Wheat 16K Panel	14868	mSNP
GenoBaits® Wheat 2K Panel	3035	mSNP

References

[1]Juliana, P. et al. 2019. Improving grain yield, stress resilience and quality of bread wheat using large-scale genomics. Nature Genetics, 51(10):1530-1539.

[2]Cheng, H. et al. 2019. Frequent intra- and inter-species introgression shapes the landscape of genetic variation in bread wheat. Genome Biol 20, 136.

[3]Wu, J. et al. 2020. Association Analysis Identifies New Loci for Resistance to Chinese Yr26-Virulent Races of the Stripe Rust Pathogen in a Diverse Panel of Wheat Germplasm. Plant Dis 104, 1751-1762.

[4]Wu, J. et al. 2021. A large-scale genomic association analysis identifies the candidate causal genes conferring stripe rust resistance under multiple field environments. Plant Biotechnol J 19, 177-191.

[5]Juliana, P. et al. 2019. Improving grain yield, stress resilience and quality of bread wheat using large-scale genomics. Nature Genetics, 51(10):1530-1539.