

## Wheat Exome Capture Kit

Wheat (*Triticum aestivum* L.) is a globally important crop, accounting for 20% of the calories consumed by mankind. Whole genome sequence analysis of wheat, especially the CDS region, can speed up gene mapping, trait discovery and cloning of wheat functional genes, and facilitate wheat breeding and crop protection.

The GenoBaits® Wheat Exome Capture Kit is based on the newest wheat reference genome: IWGSC RefSeq V2.1. Total 1.7M probes were designed to fit into this exome capture kit, which cover 132.83 Mbps wheat CDS regions.

### Product Highlight

- Reference genome:**  
 The latest reference genome of wheat (IWGSC RefSeq v2.1) and annotation information (IWGSC Annotation v2.1) were used in this exome capture design to improve the accuracy of probe capture.
- High CDS coverage and uniform probe sequence capture:**  
 When sequencing 10G per wheat sample, the average capture probe sequence depth is ~32x, uniformity of target region is 98% (>10%). More than 97% of the CDS regions are captured. The high coverage and deep read depth are essential for the genotyping analysis of polyploidy species, such as wheat.
- Validation in a wide variety of cultivars:**  
 More than dozens of wheat cultivars were validated with this kit. In addition to SNPs, Indel and CNVs can also be detected in hexaploid and tetraploid wheat varieties.
- Modular design:**  
 Additional modular components can be added into this kit. We have subdivide the following packages: the promoter panel, the enhancer panel, and the intron panel. Any of these modular panel can be used independently or combined with the exome kit.

### Cost-effective and high-throughput:

Due to the high coverage and capture efficient design, Molbreeding can provide the most cost effective wheat exome capture service with high uniformity of samples.

### Product Information

| Product name                                   | GenoBaits® Wheat Exome Capture Kit |
|------------------------------------------------|------------------------------------|
| Reference genome                               | IWGSC RefSeq v2.1                  |
| Target capture area                            | High confidence gene CDS region    |
| Number of high-confidence genes (CDS)          | 106,913                            |
| High confidence gene CDS length                | 132.83Mb                           |
| Proportion of captured CDS area                | >97%                               |
| The amount of data recommended for each sample | 10Gb                               |
| Average coverage depth of target area          | ≥32x                               |

### Product application

1. Construction of mutagenesis population mutant libraries;
2. Genome-wide association studies of large population;
3. BSA or linkage analysis of segregating populations.



### 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

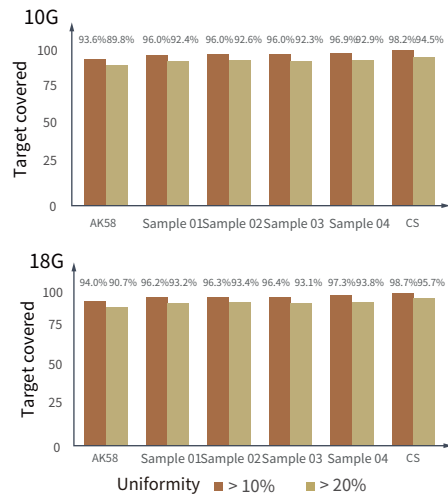


Fig. 1 Uniformity of performance in different wheat varieties

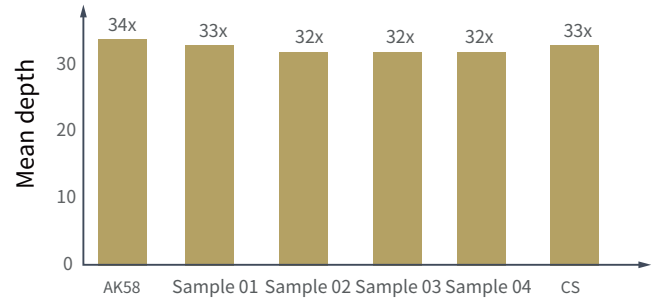


Fig. 2 Average sequencing depth when sequencing 10Gb per sample

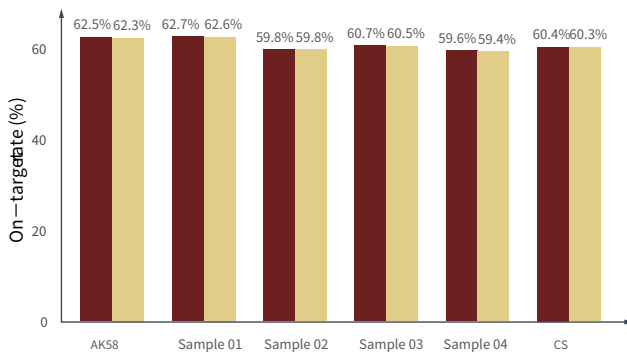


Fig. 3 The wheat exome kit capture on-target rate

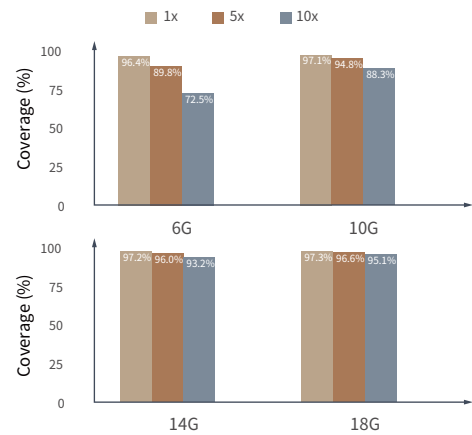


Fig. 4 CDS coverage under different sequencing volume

## Wheat Capture Kit ordering information

| Catlog             | Product Name                   | Target SNP Sites | Marker Type |
|--------------------|--------------------------------|------------------|-------------|
| PHD0117_Ta_V2.0    | GenoBaits®Wheat Breeding Panel | 128              | SNP         |
| PHR0106_TaWES_V1.0 | GenoBaits® Wheat Exome Panel   | CDS              | gene        |
| PHR0048_Ta40K_V1.0 | GenoBaits® Wheat SNP40K        | 40017            | mSNP        |
| PHD0039_Ta16K_V2.0 | GenoBaits® Wheat 16K Panel     | 14868            | mSNP        |
| PHD0100_Ta2K_V1.0  | GenoBaits® Wheat 2K Panel      | 3035             | mSNP        |

## References

- [1] Zhu, T., Wang, L., Rimbart, H., Rodriguez, J.C., Deal, K.R., De Oliveira, R., Choulet, F., Keeble-Gagnère, G., Tibbits, J., Rogers, J., Eversole, K., Appels, R., Gu, Y.Q., Mascher, M., Dvorak, J., Luo, M.C. (2021). Optical maps refine the bread wheat *Triticum aestivum* cv. Chinese Spring genome assembly. *Plant J.* 107, 303-314. <https://doi.org/10.1111/tpj.15289>.
- [2] Guo, Z., Yang, Q., Huang, F., Zheng, H., Sang, Z., Zhang, C., Wu, K., Tao, J., Prasanna, B.M., Olsen, M.S., Wang, Y., Zhang, J., and Xu, Y. (2021). Development of high-resolution multiple-SNP arrays for genetic analyses and molecular breeding through genotyping by target sequencing and liquid chip. *Plant Comm.* 2, 100230.