# Infinium<sup>™</sup> Wheat Barley 40K v1.0 BeadChip

An advanced genotyping solution for crop breeding and research applications

- Diverse wheat SNPs, representative of worldwide germplasm for research and breeding applications
- Accurate imputation from diverse backgrounds enables comparisons across global varieties
- High-throughput analysis of up to 96 wheat and barley samples in parallel on each BeadChip
- High-quality data with 99% average call rates and 99.9% reproducibility

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#### Introduction

Wheat is a vital food crop, ranking third in global crop production, and a key source of calories, fiber, and protein in human diets around the world. Barley is another important crop with uses in animal feed and beverage production, and is gaining popularity in human diets.<sup>2</sup> For these reasons, both wheat and barley are the subjects of substantial research and crop breeding improvement efforts. In support of these efforts, Illumina offers the Infinium Wheat Barley 40K v1.0 BeadChip (Figure 1).

The Wheat Barley 40K v1.0 BeadChip is powered by proven Infinium Assay technology, providing the highest call rates in the industry and flexible content design. With imputation power across global wheat and barley varieties, this BeadChip supports numerous applications including:

- Germplasm characterization of *H. vulgare*; hexaploid wheat, from bread to synthetic wheat; tetraploid wheat, from T. diccocum to T. durum
- Trait dissection, from genome-wide association studies (GWAS) to genetic mapping
- Marker-assisted selection
- Genomic prediction
- · Tracking of trait introgressions from related species

### Expertly selected SNP content enables broad utility across research and breeding

The Infinium Wheat Barley 40K v1.0 BeadChip was designed and created by researchers at Agriculture Victoria in Australia in collaboration with Intergrain, an Australian wheat, barley and oat breeding company. The high-density, genome-wide genotyping Wheat Barley BeadChip features a total of 35,052 informative single nucleotide polymorphism (SNP) probes that span the wheat and barley genomes for interrogation of genetic variation (Table 1).

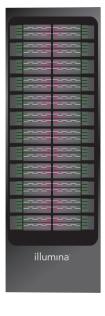




Figure 1: Infinium Wheat Barley BeadChip 40K v1.0 BeadChip—The multispecies Infinium Wheat Barley BeadChip is available in 24- and 96-sample formats and can analyze 22,163 wheat and/or 12,889 barley SNPs in parallel.

Table 1: Infinium Wheat Barley BeadChip key information

Description
Wheat and barley
Wheat: 22,163 Barley: 12,889 Total: 35,052°
99% average
99.9% average
Infinium HTS or XT
HTS format: 24 samples XT format: 96 samples
200 ng genomic DNA
iScan System
30 minutes
HTS: ~5760 samples/week XT: ~23,040 samples/week

a. 4,854 SNPs have been removed from the initial 40K assay in preparation for v1.1 which will include new content to further enhance and broaden the utility of the assay. The removed SNPs do not affect the described utility of the array.

b. Values are approximate. Scan times, and maximum throughput may vary depending on laboratory and system configurations.

Table 2: Average correlation and concordance between the Infinium Wheat Barley 40K v1.0 BeadChip and exomesequenced genotypes

	Including heterozygous calls		Excluding het	erozygous calls
	Correlation (%)	Concordance (%)	Correlation (%)	Concordance (%)
Wheat	95.7	98.1	98.1	99.5
Barley	97.2	99.2	99.2	99.8

This new Wheat Barley BeadChip incorporates recent research findings and newly available exome diversity sequencing data, which delivers new SNP targets. The SNP content was selected to enable robust imputation with high accuracy through tagging of LD blocks in globally diverse germplasm.

Trait-linked SNPs for wheat and barley are included to enhance utility in breeding and research. The Wheat Barley BeadChip also includes increased SNP assay density in regions with high recombination rates to facilitate quantitative trait loci (QTL) fine-mapping and trait-linked marker development. Both wheat and barley samples can be analyzed simultaneously from the same array position, doubling throughput and halving cost.

Wheat SNP content is based on published and unpublished data from 1300 exome-sequenced accessions. The content is selected to maximally capture genetic diversity among 6700 globally diverse accessions comprising landraces, released varieties, synthetic derivatives, novel trait donor, and historical breeding lines.<sup>3</sup>

Traits covered for wheat include metal ion tolerances, fungal and nematode resistances, frost tolerance, phenology, glutenin subunits, late maturity α-amylase (LMA), preharvest sprouting (PHS), grain end-use quality, plant height, and herbicide resistance.

Barley SNP content is based on 262 exome-sequenced H. vulgare landraces and H. spontenaeum accessions selected to capture geographical diversity, as well as 120 whole-genome sequences of historical breeding lines, and sequence capture data from 1000 globally diverse H. vulgare accessions.4-6

Traits covered for barley include metal ion tolerances, fungal and nematode resistances, frost tolerance, phenology, malting quality, grain characteristics, row number, and herbicide resistance.

#### Simple workflow

The Wheat Barley 40K v1.0 BeadChip is available in 24- or 96-sample formats (Figure 1). The BeadChip follows a user-friendly, PCR-free, single-tube preparation method that significantly reduces labor and potential sample-handling errors.<sup>7,8</sup> The multispecies design allows both Wheat and Barley samples to be run in parallel on each BeadChip.

#### High-quality data

Using the iScan™ System, integrated analysis software, and either the Infinium 24-sample high-throughput screening (HTS) or 96-sample XT assay, the Infinium Wheat Barley BeadChip provides exceptionally high call rates, allows for flexible content deployment, and enables the detection and measurement of copy number variation. Genotype call rates per sample show high concordance between called and true genotype (Table 2).

#### Ordering information

Contact your local sales representative to order the Infinium Wheat Barley 40K v1.0 BeadChip.

Product	Description				
Infinium HTS iSelect-24 Kit <sup>a</sup>					
Infinium HTS iSelect Custom BeadChip (48 samples)	Each package contains 2 BeadChips, along with reagents for amplifying, fragmenting, hybridizing, labeling, and detecting 48 DNA samples				
Infinium HTS iSelect Custom BeadChip (288 samples)	Each package contains 12 BeadChips, along with reagents for amplifying, fragmenting, hybridizing, labeling, and detecting 288 DNA samples				
Infinium HTS iSelect Custom BeadChip (1152 samples)	Each package contains 48 BeadChips, along with reagents for amplifying, fragmenting, hybridizing, labeling, and detecting 1152 DNA samples				
Infinium XT iSelect-96 Kitb					
Infinium XT iSelect Custom BeadChip (1152 samples)	Each package contains 12 BeadChips, along with reagents for amplifying, fragmenting, hybridizing, labeling, and detecting 1152 DNA samples				
Infinium XT iSelect Custom BeadChip (4608 samples)	Each package contains 48 BeadChips, along with reagents for amplifying, fragmenting, hybridizing, labeling, and detecting 4608 DNA samples				
Infinium XT iSelect Custom BeadChip (23,040 samples)	Each package contains 240 BeadChips, along with reagents for amplifying, fragmenting, hybridizing, labeling, and detecting 23,040 DNA samples				

Each BeadChip can be used to process 24 samples. Minimum order size is 288 samples

#### Summary

Advancing crop research requires up-to-date and comprehensive genetic information. The multispecies Infinium Wheat Barley 40K v1.0 BeadChip and the iScan System provide an ideal solution for economic, high-throughput genetic analysis across global wheat and barley varieties. Contact your local Illuminal sales representative to find our more about this powerful tool for crop breetiing and research applications.

#### References

- 1. Shewry PR, Hey SJ. The contribution of wheat to human diet and health. Food Energy Secur. 2015;4(3):178-202.
- 2. Newman RK, Newman CW. Barley for Food and Health: Science, Technology, and Products. John Wiley & Sons, Inc.; 2008.

- 3. He F, Pasam R, Shi F, et al. Exome sequencing highlights the role of wild-relative introgression in shaping the adaptive landscape of the wheat genome [published correction appears in Nat Genet. 2019 Jul;51(7):1194]. Nat Genet. 2019;51(5):896-904.
- 4. Russell J, Mascher M, Dawson IK, et al. Exome sequencing of geographically diverse barley landraces and wild relatives gives insights into environmental adaptation. Nat Genet. 2016;48(9):1024-1030.
- 5. Milner SG, Jost M, Taketa S, et al. Genebank genomics highlights the diversity of a global barley collection. Nat Genet. 2019;51(2):319-326.
- 6. Hill CB, Angessa TT, McFawn LA, et al. Hybridisation-based target enrichment of phenology genes to dissect the genetic basis of yield and adaptation in barley. Plant Biotechnol J. 2019;17(5):932-944.
- 7. Gunderson KL, Steemers FJ, Lee G, Mendoza LG, Chee MS. A genome-wide scalable SNP genotyping assay using microarray technology. Nat Genet. 2005;37(5):549-554.
- 8. Steemers FJ, Chang W, Lee G, Barker DL, Shen R, Gunderson KL. Whole-genome genotyping with the single-base extension assay. Nat Methods. 2006;3(1):31-33.

b, Each BeadChip can be used to process 96 samples. Minimum order size is 50,000 samples

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