illumına®

BovineLD v2.0 Genotyping BeadChip

Extend genomic selection to the entire herd with scalable content at an economical price.

Highlights

- **Cost-Effective Genotyping of Herd Animals**
  High data quality, robust imputation tool to estimate genomic breeding value accurately

- **High Imputation Accuracy**
  High call rates, with demonstrated imputation efficiency of > 98%

- **Superior, Scalable Content**
  Expertly selected content can be enhanced with up to 80,000 custom markers

- **High-Throughput Format**
  Up to 24 samples can be interrogated in parallel
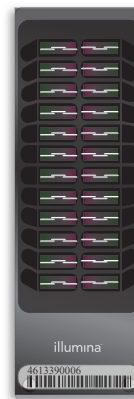
Introduction

Delivering superior, scalable content at an economical price, the Infinium® BovineLD v2.0 BeadChip (Figure 1) is a robust imputation tool for global dairy breeds, extending genomic selection to the entire herd. The BovineLD v2.0 BeadChip, together with the Infinium BovineSNP50 v2, Infinium BovineHD, and iSelect® BeadChips, creates a broad genotyping portfolio that breeders can rely on to characterize genetic variation and accurately estimate genomic breeding value.

Illumina developed the BovineLD BeadChip as part of a BovineLD Consortium in collaboration with global bovine agricultural thought leaders, including the Department of Primary Industries (DPIViC); French National Institute for Agricultural Research (INRA); National Association of Livestock and Artificial Insemination Cooperatives (UNCEIA); and U.S. Department of Agriculture, Agricultural Research Service (USDA-ARS). The strategically selected SNPs on the BeadChip possess demonstrated reliability, high average minor allele frequency (MAF), uniform distribution across the bovine genome, and excellent imputation performance for a range of global dairy breeds.

While the BovineHD and BovineSNP50 BeadChips provide superior power to interrogate genetic variation in high-value animals and support genome-wide studies, the BovineLD BeadChip enables the cost-effective genotyping of lower-value animals. Featuring 7931 SNPs, the BovineLD v2.0 BeadChip provides a robust solution for high-accuracy imputation to the BovineSNP50 BeadChip. The BovineLD BeadChip enables accurate genotyping to understand the impact of genetics on milk production, reproduction, health, and more. For ultimate design flexibility, Infinium BovineLD v2.0 BeadChips can be customized with additional add-on content of up to 80,000 custom markers.

The Infinium Assay powers this multi-sample genotyping panel, delivering the highest call rates and reproducibility in the industry. The assay features PCR-free, single-tube sample preparation, which significantly reduces labor and potential sample handling errors.[1,2] A multi-sample format further reduces experimental variability and overall project cost by allowing breeders to interrogate up to 24 samples in parallel.

Figure 1: BovineLD v2.0 BeadChip—The BovineLD v2.0 BeadChip features nearly 8000 evenly spaced SNPs across the entire bovine genome with higher density at chromosomal ends for increased imputation efficiency.

BovineLD v2.0 BeadChip Content

Illumina scientists and collaborators referenced historical data generated with the BovineSNP50 BeadChip to identify the best SNP content for imputation efficiency among global dairy breeds. *In silico* testing determined that the highest imputation efficiency could be achieved by optimizing MAF among targeted breeds and evenly spacing SNPs across the entire bovine genome with higher marker densities at the chromosomal ends. Content includes coverage of all chromosomes, including X, known Y haplotypes, and mitochondrial DNA (Table 1). Uniform genomic coverage provides an average gap size of 383 kb and a median gap size of 347 kb (Figure 2). To ensure backward compatibility with the GoldenGate® 3K Bovine array, the BovineLD Consortium retained 2162 overlapping markers in the BovineLD v2.0 BeadChip content. The BovineLD v2.0 BeadChip also contains all 200 SNPs on the International Society for Animal Genetics (ISAG) panel for bovine parentage (100 core SNPs and 100 additional SNPs).

High-Quality Data

The 7931 SNPs on the BovineLD v2.0 BeadChip were subjected to rigorous functional testing on multiple breeds to ensure strong performance. High call rates and accurate genotype calls are important for successful, accurate imputation to the BovineSNP50 BeadChip content. Illumina ensures that every BovineLD BeadChip offers > 99% average call rate across common dairy and beef cattle breeds. Table 2 shows results from internal validation testing of the BovineLD v2.0 BeadChip content using samples provided by collaborators and the Bovine HapMap Consortium.[3] The performance and content validation results clearly demonstrate the high data quality delivered by the product. In addition, analysis of overlapping content for BovineLD v2.0 and BovineSNP50 BeadChips shows > 99.99% concordance for all breeds evaluated.

The BovineLD BeadChip shows high call rates by breed (Table 3), high estimated percent of polymorphic loci by breed (Table 4), and demonstrated imputation efficiency of greater than 98% (Figure 3). These features provide the dairy community with the same high accuracy and reliability for interrogating bovine genotypes in *Bos taurus taurus* as provided by the BovineSNP50 and BovineHD BeadChips. Based on *in silico* estimates of imputation efficiency on Angus (93%, N=232)[4], the BovineLD BeadChip could be expected to perform well for many *Bos taurus taurus* beef breeds.
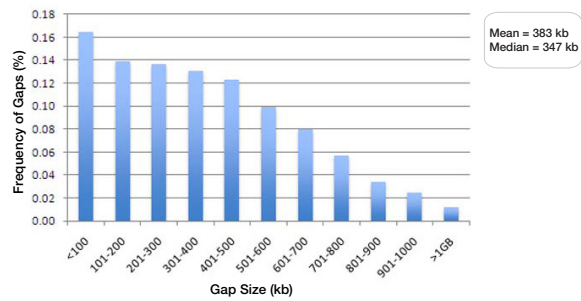

Mean = 383 kb
Median = 347 kb

Figure 2: BovineLD v2.0 BeadChip Probe Spacing (Chromosomes 1–29, X)—The BovineLD v2.0 BeadChip provides uniform coverage across the entire bovine genome.

Table 1: BovineLD v2.0 BeadChip Content

Parameter	Number of SNPs
BovineSNP50 v2	
Parentage	121
Chromosomal Ends	433
Breed Identification (JER, HOL, BSW)	98
Other Autosomal	6000
X Chromosome	219
BovineHD	
X Chromosome	18
Y Chromosome	9
Mitochondrial	13
Additional Content on BovineLD v2.0 BeadChip	
Parentage SNPs, SNPs for imputation to microsatellite alleles, causative mutations, and milk protein polymorphisms	1020
Total	7931

Table 2: Product Performance and Specifications

Parameter	Total Population[a]	Product Specifications
Average Call Rate	99.90%	> 99%
Reproducibility	100%	> 99.9%
Mendelian Inconsistencies	0.01%	< 0.1%

a. Based on 164 samples.

Table 3: BovineLD Call Rate by Breed

Breed	Number of DNA Samples	Average Call Rates (%)[a]
Angus	10	99.98
Ayrshire	10	99.97
Beefmaster	10	99.85
Blonde d'Aquitaine	10	99.97
Brahman	10	99.50
Brown Swiss	10	100
Charolais	10	99.99
Fleckvieh	20	99.98
Fresian	17	99.93
Gelbvieh	5	99.97
Guernsey	10	99.86
Hereford	10	99.97
Holstein	14	99.96
Jersey (US)	19	99.96
Jersey (Denmark)	10	99.91
Limousin	10	99.97
Montbeliard	10	100
N'Dama	10	99.85
Normande	10	99.98
Norwegian Red	11	99.88
Red Angus	10	99.99
Red Dairy (Angier)	10	99.98
Red Danish (Denmark)	10	99.92
Red Danish (Finland)	10	99.93
Red Danish (Sweden)	10	99.92
Santa Gertrudis	10	99.84
Total	286	99.93

a. Call rate estimates based on unrelated individuals.

Illumina Solutions for Genotyping

The BovineLD v2.0 BeadChip is compatible with the iScan® and HiScan® Systems. These cutting-edge array scanners feature high-performance lasers and powerful optical systems that enable rapid scan times and precise assay detection.

The convenient modular design enables researchers to build out the system easily for evolving research needs. An optional Laboratory Information Management System (LIMS) is available to track samples accurately and efficiently. Robotic automation capabilities can be added to improve throughput for labs processing large numbers of samples. With the Infinium Assay workflow, data are processed directly into GenomeStudio® software to provide streamlined genotype calling, analysis, and reporting. Customers can also choose to use the convenient Illumina FastTrack™ genotyping service to have samples genotyped and data delivered in a format suitable for GWAS or QTL analysis.
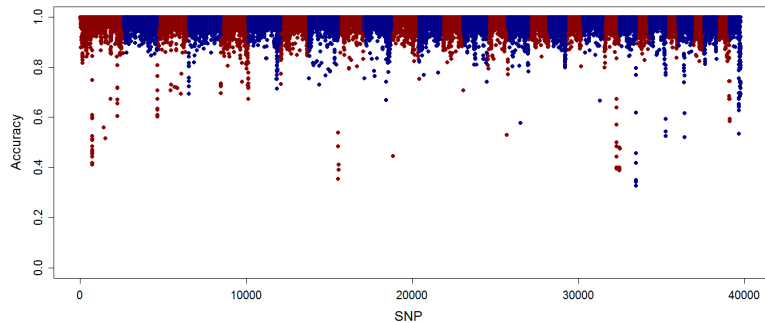
SNPs	Accuracy[a]
BovineLD sire in reference	97.4%
BovineLD no sire in reference	95.6%
GoldenGate3K sire in reference	93.2%
GoldenGate3K no sire in reference	89.8%

a. Imputation analysis based on N = 2257 Holstein animals.

Figure 3: Imputation Accuracy by SNP and Chromosome in Holstein—The BovineLD BeadChip provides a robust solution for high-accuracy imputation with the BovineSNP50 BeadChip for cost-effective, accurate genotyping of all herd animals.[4]

Table 4: BovineLD BeadChip Estimates of MAF and Percent Polymorphic Loci by Breed

Breed	Region	Number of DNA Samples[a]	Average MAF Combined	Median MAF Combined	Estimated Percent Polymorphic Loci (%)[b]
Ayrshire	North America	434	0.31	0.33	96.7
Angus	USA	6400	0.33	0.35	98.3
Angus	Australia	282	0.31	0.33	97.4
Brahman	Australia	80	0.21	0.18	89.7
Brown Swiss	North America/Europe	2039	0.31	0.34	96.2
Fleckvieh	North America	800	0.37	0.39	99.5
Holstein	Australia	2257	0.36	0.38	98.7
Holstein	North America	72,824	0.35	0.37	98.5
Holstein	Europe	16,000	0.36	0.38	98.9
Jersey	Australia	545	0.30	0.32	95.6
Jersey	North America	5958	0.29	0.31	94.0
Limousin	Europe	90	0.35	0.37	98.4
Montbeliard	Europe	1500	0.34	0.36	98.7
Normande	Europe	1200	0.34	0.36	98.4

a. DNA samples used to determine MAFs were from historical BovineSNP50 data.
b. Polymorphic loci with MAF ≥ 0.05.

Summary

Developed through a collaboration between Illumina scientists and leading global bovine thought leaders, the BovineLD v2.0 BeadChip features 7931 evenly spaced SNPs across the bovine genome. This BeadChip provides a robust imputation tool for characterizing genetic variation and accurately estimating genomic breeding value. This 24-sample BeadChip, along with the proven Infinium Assay, presents a powerful high-throughput solution for genomic selection in any breed of cattle.

References

1. Gunderson KL, Steemers FJ, Lee G, Mendoza LG, Chee MS. A genome-wide scalable SNP genotyping assay using microarray technology. *Nat Genet.* 2005;37:549-554.
2. Steemers FJ, Chang W, Lee G, Barker DL,Shen R, et al. Whole-genome genotyping with the single-base extension assay. *Nat Methods.* 2006;3:31-33.
3. Van Tassell CP, Smith TPL, Matukumalli LK, et al. Simultaneous SNP discovery and allele frequency estimation by high-throughput sequencing of reduced representation libraries. *Nat Methods.* 2008;5:247-252.
4. Boichard D, Chung H, Dassonneville R, et al. Design of a bovine low-density SNP array optimized for imputation. *PLoS One.* 2012;7:e34130.

Ordering Information

Product	Description	Catalog No.
BovineLD v2.0 Whole-Genome Genotyping Kit (48 samples)	Each package contains 2 BeadChips, along with reagents for amplifying, fragmenting, hybridizing, labeling, and detecting 48 DNA samples.	WG-451-2001
BovineLD v2.0 Whole-Genome Genotyping Kit (288 samples)	Each package contains 12 BeadChips, along with reagents for amplifying, fragmenting, hybridizing, labeling, and detecting 288 DNA samples.	WG-451-2002
BovineLD v2.0 Whole-Genome Genotyping Kit (1152 samples)	Each package contains 48 BeadChips, along with reagents for amplifying, fragmenting, hybridizing, labeling, and detecting 1152 DNA samples.	WG-451-2003
BovineLD v2.0+ Whole-Genome Genotyping Kit (48 samples)	Each package contains 2 BeadChips and allows researchers to include up to 25,000 additional custom probes per sample for targeted studies.	WG-451-2011
BovineLD v2.0+ Whole-Genome Genotyping Kit (288 samples)	Each package contains 12 BeadChips and allows researchers to include up to 25,000 additional custom probes per sample for targeted studies.	WG-451-2012
BovineLD v2.0+ Whole-Genome Genotyping Kit (1152 samples)	Each package contains 48 BeadChips and allows researchers to include up to 25,000 additional custom probes per sample for targeted studies.	WG-451-2013

Each BovineLD v2.0 DNA Analysis BeadChip can process 24 samples and analyze 7931 loci.

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