BovineLD 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 accurately estimate genomic breeding value.
- **High Imputation Accuracy**
  High call rates, with demonstrated imputation efficiency of > 98%.
- **Superior, Scalable Content**
  World expert–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

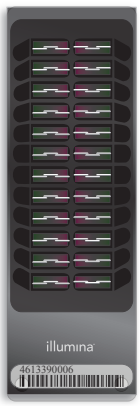
Delivering superior, scalable content at an economical price, the Infinium® BovineLD BeadChip (Figure 1) is a robust imputation tool for global dairy breeds, extending genomic selection to the entire herd. The BovineLD BeadChip, together with the Infinium BovineSNP50, Infinium BovineHD and iSelect® BeadChips, 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 & Artificial Insemination Cooperatives (UNCEIA); and U.S. Department of Agriculture, Agricultural Research Service (USDA-ARS). The BeadChip's strategically selected SNPs 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 6,909 SNPs, the BovineLD BeadChip provides a robust solution for high accuracy imputation to the BovineSNP50 BeadChip, the world's most widely adopted genotyping array. The BovineLD BeadChip enables accurate genotyping to understand the impact of genetics on milk production, reproduction, health, and more. For ultimate design flexibility, Infinium BeadChips can be customized with additional add-on content of up to to 80,000 custom markers.

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

Figure 1: BovineLD BeadChip



The BovineLD BeadChip features nearly 7,000 evenly spaced SNPs across the entire bovine genome with higher density at chromosomal ends for increased imputation efficiency.

BovineLD 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 2,162 overlapping markers in the BovineLD BeadChip content.

High-Quality Data

The 6,909 SNPs on the BovineLD 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 BeadChip content using samples provided by collaborators and the Bovine HapMap Consortium[3]. These performance and content validation results clearly demonstrate the robust data quality delivered by the product. In addition, analysis of overlapping content for BovineLD and BovineSNP50 BeadChips shows >99.99% concordance for all breeds evaluated.

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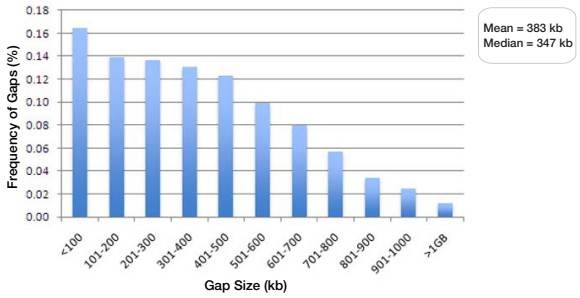
The BovineLD BeadChip shows high call rates by breed (Table 3), high estimated percent of polymorphic loci by breed (Table 4), and demonstrated imputation efficiency of greater than 98% (Figure 3) providing the dairy community with the same high accuracy and reliability for interrogating bovine genotypes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

Figure 2: BovineLD BeadChip Probe Spacing (Chromosome 1-29, X)



The BovineLD BeadChip provides uniform coverage across the entire bovine genome.

Table 1: BovineLD BeadChip Content

	Number of SNPs
BovineSNP50v2	
Parentage	121
Chromosomal Ends	433
Breed Identification (JER, HOL, BSW)	93
Other Autosomal	6,004
X Chromosome	219
BovineHD	
X Chromosome	17
Y Chromosome	9
Mitochondrial	13
Total	6,909

Table 2: Product Performance and Specifications

Parameter	Total Population*	Product Specifications
Average Call Rate	99.93%	> 99%
Reproducibility	100%	> 99.9%
Mendelian Inconsistencies	0.01%	< 0.1%

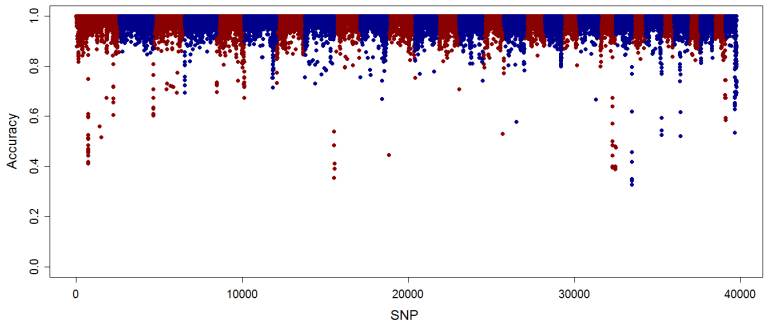
*Based on 290 samples, 22 breeds, 2 replicates, and 2 trios.

Table 3: BovineLD Call Rate by Breed

Breed	Number of DNA Samples	Average Call Rates (%)*
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

*Call rate estimates based on unrelated individuals.

Figure 3: Imputation Accuracy by SNP and Chromosome in Holstein



SNPs	Accuracy*
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%

*Imputation analysis based on N = 2,257Holstein animals.

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*	Average MAF Combined	Median MAF Combined	Estimated Percent Polymorphic Loci (%)**
Ayrshire	North America	434	0.31	0.33	96.7
Angus	USA	6,400	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	2,039	0.31	0.34	96.2
Fleckvieh	North America	800	0.37	0.39	99.5
Holstein	Australia	2,257	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	5,958	0.29	0.31	94.0
Limousin	Europe	90	0.35	0.37	98.4
Montbeliard	Europe	1,500	0.34	0.36	98.7
Normande	Europe	1,200	0.34	0.36	98.4

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

AAAGAATGATAACAGTAACACACTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTCTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAA
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Illumina Solutions for Genotyping

The BovineLD BeadChip is compatible with the iScan and HiScanSQ™ systems. These cutting-edge array scanners feature high-performance lasers and powerful optical systems that enable rapid scan times and precise assay detection. The HiScanSQ system can also perform Illumina sequencing by synthesis chemistry, the world's most widely adopted next-generation sequencing platform.

The convenient modular design enables researchers to easily build out the system for evolving research needs. An optional Laboratory Information Management System (LIMS) is available to accurately and efficiently track samples. 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 Illumina's convenient FastTrack Genotyping service to have samples genotyped and data delivered in a format suitable for GWAS or QTL analysis.

Summary

Developed through a collaboration between Illumina scientists and leading global bovine thought leaders, the BovineLD BeadChip features 6,909 evenly spaced SNPs across the bovine genome, providing 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 (2005) A genome-wide scalable SNP genotyping assay using microarray technology. Genet 37: 549–554.
2. Steemers FJ, Chang W, Lee G, Barker DL,Shen R, et al. (2006) Whole-genome genotyping with the single-base extension assay. Nat Methods 3: 31–33.
3. Van Tassell CP, Smith TPL, Matukumalli LK, Taylor JF, Schnabel RD, et al. (2008). Simultaneous SNP discovery and allele frequency estimation by high-throughput sequencing of reduced representation libraries. Nature Methods 5: 247–252.
4. Hayes, Ben (2011). Unpublished data.

Ordering Information

Catalog No.	Product	Description
WG-450-1007	BovineLD 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-450-1008	BovineLD 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-450-1009	BovineLD Whole-Genome Genotyping Kit (1,152 samples)	Each package contains 48 BeadChips, along with reagents for amplifying, fragmenting, hybridizing, labeling, and detecting 1,152 DNA samples
FT-310-1206	FastTrack Genotyping Services	Illumina scientists provide personalized service, industry-leading data quality, and guaranteed turnaround time for bovine genotyping studies

Each BovineLD DNA Analysis BeadChip can process 24 samples and analyze 6,909 loci.

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