BovineHD Genotyping BeadChip

More than 777,000 SNPs that deliver the densest coverage available for the bovine genome.

Highlights

- **Comprehensive and Uniform Coverage**
  Evenly distributed polymorphic SNPs with a median < 3 kb gap spacing
- **Unrivaled Call Rates and Accuracy**
  > 99% average call rates and > 99.9% reproducibility
- **Simple Workflow**
  PCR- and ligation-free protocol
- **High-Throughput Format**
  Up to 8 samples can be interrogated in parallel

Introduction

The BovineHD BeadChip (Figure 1) is the most comprehensive genome-wide genotyping array, providing superior power to interrogate genetic variation across any breed of beef and dairy cattle. Illumina has developed this product in collaboration with major bovine agricultural thought leaders, including USDA-ARS, UNCEIA-INRA, Pfizer Animal Genetics, and the University of Missouri. Featuring more than 777,000 SNPs that uniformly span the entire bovine genome, the BovineHD BeadChip enables a broad range of applications such as genome-wide selection, identification of quantitative trait loci, evaluation of genetic merit, cross-breed mapping, linkage disequilibrium studies, comparative genetic studies, and breed characterization for evaluating biodiversity.

This multi-sample genotyping panel is powered by the Infinium® HD Assay, delivering the industry's highest call rates and reproducibility, along with precise detection and measurement of copy number variation (CNV) (Table 1). The assay's PCR-free single-tube sample preparation significantly reduces labor and potential sample handling errors.[1,2] A multi-sample format further reduces experimental variability and overall project cost by allowing researchers to interrogate up to 8 samples in parallel.

The combination of proprietary Illumina assay technology, unconstrained locus selection, and high-throughput format presents the most comprehensive solution for whole-genome studies in beef and dairy cattle.

BovineHD BeadChip Content

Illumina scientists and collaborators strategically selected informative markers across the bovine genome. The BovineHD BeadChip covers SNPs validated in economically important beef and dairy cattle, encompassing temperate and tropically adapted species *Bos taurus taurus (Btt), Bos taurus indicus (Bti),* and several *Bti* × *Btt* breeds. The average minor allele frequency (MAF) across all loci is 0.25 for *Btt* and 0.17 for *Bti*. More than 749,000 SNPs were validated across all breeds with a MAF > 0.05 (Table 2, "polymorphic loci"). Over 99% of the markers are mapped to the UMD3 bovine genome assembly,[3] which include coverage of autosomal, mitochondrial, and sex-linked (X/Y) SNPs. Uniform genomic coverage, with an average gap size of 3.43 kb and a median gap size of 2.68 kb, provides excellent SNP density to power robust genome-association studies and CNV detection in cattle (Figure 2).[4] The BovineHD BeadChip is the most comprehensive tool in the Illumina portfolio of bovine products.

More than 93% of SNPs featured on the BovineHD BeadChip target novel SNP loci that were discovered by sequencing > 20 individual breeds of economically important beef and dairy cattle (Table 3). Using Illumina next-generation paired-end sequencing technology, > 90% of the included SNPs were identified from over 180× coverage of the mappable *Btt* genome. Prioritization for SNP selection included the following parameters: 1) breed-specific expected MAF, 2) Infinium HD design score, 3) unmapped contig coverage, 4) breed weighting, 5) breed-specific spacing, and 6) and position based on region of genome (ie, exon, repetitive, segmental duplication/CNV).

High-Quality Data

The 777,962 SNPs on the BovineHD BeadChip were subjected to rigorous functional testing on multiple breeds to ensure strong performance using the Infinium HD Assay. High call rates and accurate genotype calls are important for successful whole-genome association studies. Because complex traits often have relatively small gene effects, potential associations can be missed if the assayed SNP in linkage disequilibrium with the SNP of interest has a low call rate or incorrect genotype call. Illumina ensures that every BovineHD BeadChip offers > 99% average call rate across common beef and dairy cattle breeds.

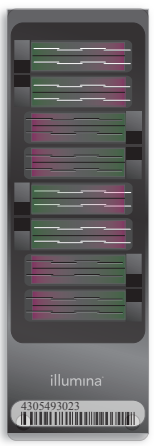

Figure 1: BovineHD BeadChip—The BovineHD BeadChip features more than 777,000 evenly spaced SNPs across the entire bovine genome.

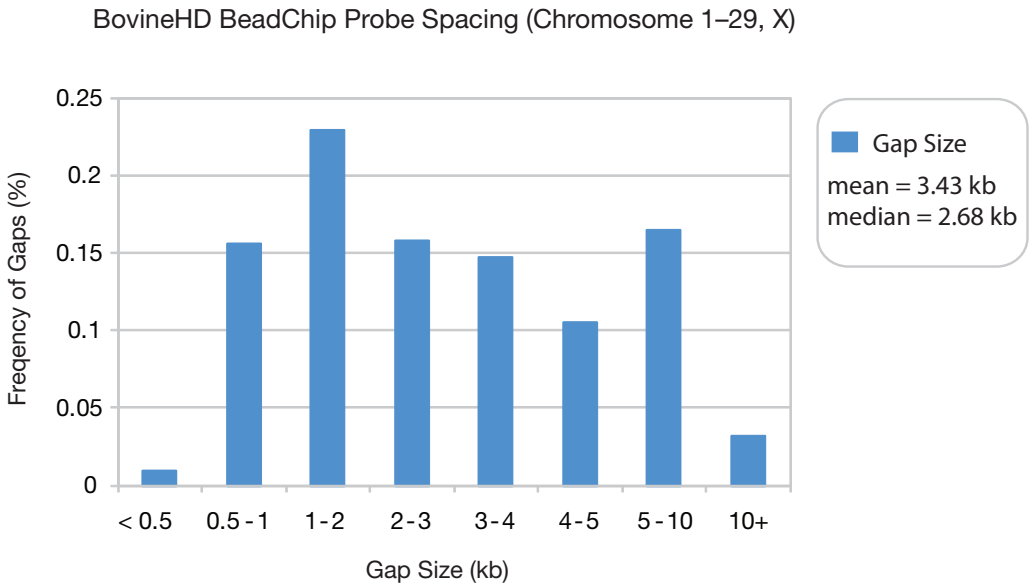

Figure 2: BovineHD BeadChip Probe Spacing—The BovineHD BeadChip provides uniform coverage across the entire UMD3 genome.

Table 1 shows the results from internal validation testing of the BovineHD BeadChip content using samples provided by collaborators and the Bovine HapMap Consortium.[5] Illumina scientists and collaborators identified and retained 29,968 loci that appear to have an adjacent polymorphism or deletion among the breeds sampled. Although these loci yielded lower call rates when compared to most loci on the panel, they were retained because they might provide biologically relevant information, especially between breed groups (*Bti* vs *Btt*), for traits of interest and future improvements in the genome build. These performance and content validation results clearly demonstrate the high data quality delivered by the product.

With such high data quality, the BovineHD BeadChip provides the highest accuracy and reliability for interrogating bovine genotypes in *Bos taurus taurus* and *Bos taurus indicus* breeds.

Illumina Solutions for Genotyping

The BovineHD 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 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 Illumina GenomeStudio® software to provide streamlined genotype calling, analysis, and reporting. Researchers can also choose to use the 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 bovine thought leaders, the BovineHD BeadChip features more than 777,000 evenly spaced SNPs that provide comprehensive coverage of the bovine genome, enabling a diverse range of genetic research applications. This 8-sample BeadChip, along with the proven Infinium HD Assay, presents a powerful, high-throughput solution for whole-genome studies in any breed of beef and dairy cattle.

Table 1: Product Performance and Specifications

Parameter	*Bos taurus taurus (Btt)*[a]	*Bos taurus indicus (Bti)*[b]	Hybrid *Btt* × *Bti*[c]	Total Population[d]	Product Specification
Average call rate	99.8%	99.6%	99.8%	99.8%	> 99%
Reproducibility	100%	100%	N/A	100%	> 99.9%
Mendelian inconsistencies	0.05%	0.12%	0.13%	0.08%	< 0.1%

a. Based on 503 samples, 20 breeds, 21 replicates, 22 trios, 8 pairs
b. Based on 114 samples, 3 breeds, 1 replicate, 7 trios, 1 pair
c. Based on 90 samples, 4 breeds, 5 trios, 2 pairs
d. Based on 707 samples, 27 breeds, 22 replicates, 34 trios, 11 pairs

Table 2: BeadChip Content Validation

Species	Breed	Samples	Polymorphic Loci[a]	Mean MAF	Median MAF
Bos taurus taurus	Angus	42	573,437	0.21	0.21
Bos taurus taurus	Blonde d'Aquitaine	5	556,296	0.20	0.20
Bos taurus taurus	Brown Swiss	22	531,212	0.19	0.18
Bos taurus taurus	Charolais	37	627,800	0.23	0.24
Bos taurus taurus	Guernsey	21	533,297	0.20	0.19
Bos taurus taurus	Hereford	35	632,414	0.25	0.27
Bos taurus taurus	Holstein	60	594,290	0.22	0.23
Bos taurus taurus	Jersey	38	587,081	0.21	0.20
Bos taurus taurus	Lagunaire	5	378,480	0.13	0.00
Bos taurus taurus	Limousin	50	610,524	0.23	0.23
Bos taurus taurus	Montbeliard	5	533,869	0.19	0.20
Bos taurus taurus	N'Dama	23	444,452	0.16	0.11
Bos taurus taurus	Normande	5	533,325	0.19	0.20
Bos taurus taurus	Norwegian Red	17	592,815	0.22	0.21
Bos taurus taurus	Piedmontese	21	603,865	0.23	0.24
Bos taurus taurus	Red Angus	10	589,836	0.21	0.20
Bos taurus taurus	Romagnola	21	580,950	0.21	0.21
Bos taurus taurus	Senepol	12	580,001	0.21	0.21
Bos taurus taurus	Simmental	10	624,820	0.22	0.20
Bos taurus taurus	Wagyu	13	527,210	0.19	0.15
Bos taurus taurus	**All**	**452**	**651,994**	**0.25**	**0.27**
Bos taurus indicus	Brahman	46	561,834	0.18	0.14
Bos taurus indicus	Gir	27	472,928	0.15	0.09
Bos taurus indicus	Nelore	31	453,361	0.15	0.10
Bos taurus indicus	**All**	**104**	**538,517**	**0.17**	**0.13**
Hybrid *Btt* × *Bti*	Beefmaster	23	704,057	0.27	0.28
Hybrid *Btt* × *Bti*	Brangus	12	655,334	0.24	0.25
Hybrid *Btt* × *Bti*	Santa Gertrudis	32	683,588	0.25	0.25
Hybrid *Btt* × *Bti*	Sheko	16	617,445	0.22	0.22
Hybrid *Btt* × *Bti*	**All**	**83**	**730,448**	**0.27**	**0.28**
All	**All**	**639**	**749,577**	**0.28**	**0.28**
Outgroup[b]	Outgroup[b]	10	167,215	0.06	0.00

a. MAF > 0.05

b. Includes water buffalo, yak, and guar

Table 3: BeadChip Content Sources

Source	BovineHD Probes
Novel content derived > 180× coverage of > 20 breeds (*Btt* and *Bti*)	727,252
Holstein BAC sequence data	1,229
iBMAC RRL sequencing project[5]	22,379
Parentage[a]	116
Whole-genome shotgun reads[b]	5,435
SNPs from Baylor genome build Btau2.0	8,703
Bovine Hapmap data set[c]	11,723
Other	1,125
Total	**777,962**

a. Highly curated parentage markers that include 30 duplicates.
b. Reads derived from 6 cows/breeds (Norwegian Red, Holstein, Brahman, Angus, Jersey, and Limousin) compared against Btau2.0.
c. Includes common SNPs validated by the Institute for Food and Agricultural Sciences Alberta and INRA, the French International Institute of Agriculture.

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.
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3. Zimin AV, Delcher AL, Florea L, et al. A whole-genome assembly of domestic cow, *Bos taurus*. *Genome Biol.* 2009;10:R42.
4. Khatkar MS, Zenger KR, Hobbs M, et al. A primary assembly of a bovine haplotype block map based on a 15,036-single-nucleotide polymorphism panel genotyped in Holstein-Friesian cattle. *Genetics.* 2007;176:763-772.
5. Van Tassell CP, Smith TPL, Matukumalli LK, et al. SNP discovery and allele frequency estimation by deep sequencing of reduced representation libraries. *Nat Methods.* 2008;5:247-252.

Ordering Information

Catalog No.	Product	Description
WG-450-1002	BovineHD Whole-Genome Genotyping Kit (48 samples)	Each package contains 6 BeadChips, along with reagents for amplifying, fragmenting, hybridizing, labeling, and detecting 48 DNA samples
WG-450-1003	BovineHD Whole-Genome Genotyping Kit (96 samples)	Each package contains 12 BeadChips, along with reagents for amplifying, fragmenting, hybridizing, labeling, and detecting 96 DNA samples
WG-450-1004	BovineHD Whole-Genome Genotyping Kit (384 samples)	Each package contains 48 BeadChips, along with reagents for amplifying, fragmenting, hybridizing, labeling, and detecting 384 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 BovineHD DNA Analysis BeadChip can process 8 samples and analyze 777,962 loci.

Illumina • 1.800.809.4566 toll-free (US) • +1.858.202.4566 tel • techsupport@illumina.com • www.illumina.com

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