GoldenGate® Bovine3K Genotyping BeadChip

Featuring 2,900 SNPs that provide high capacity for prediction of the genetic merit of cattle.

Highlights

- **Uniform Coverage**
  Evenly distributed polymorphic SNPs across the bovine genome
- **Unrivaled Call Rates and Accuracy**
  > 99% average call rates and > 99.9% reproducibility
- **High-Throughput Format**
  Up to 32 samples interrogated in parallel

Introduction

DNA analysis microarrays are revolutionizing the cattle industry, providing a powerful, cost-effective approach for trait selection and breed characterization. Traditional progeny testing of bulls to select desired traits is a slow and expensive process, requiring multiple years per animal to complete. With the release of the Illumina BovineSNP50 Genotyping BeadChip in late 2007, this process has been dramatically improved. Now breeders can obtain whole-genome genotyping information that enables a greater capacity to predict the genetic merit of an animal at birth with a high degree of confidence.

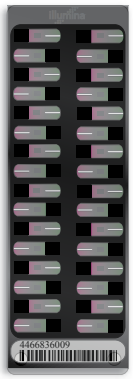
To improve the accessibility of this technology, Illumina has released the Bovine3K Genotyping BeadChip (Figure 1), a low-complexity DNA analysis tool that provides 2,900 SNPs spanning the bovine genome. Content on the Bovine3K was developed in collaboration with the Agriculture Research Service (ARS), the in-house research arm of the US Department of Agriculture (USDA). The panel features strategically selected makers from the bovine genome intended to provide a comparable level of information to the BovineSNP50 BeadChip.

Each Bovine3K BeadChip can analyze 32 samples, providing a high-throughput, economical genotyping solution for a range of applications that includes large-scale screening of bulls/dams for mating and potential genetic improvements, determination of genetic merit for valuable traits, parentage verification, and cattle traceability.

Accurate Genotype Imputation

Using the SNP content available on the Bovine3K panel, researchers can impute the genotypes to the approximately 50,000 SNPs available on the BovineSNP50 BeadChip. Imputation takes advantage of linkage disequilibrium, the phenomenon that groups of alleles (haplotypes) are inherited in blocks along the chromosome. Because alleles within each haplotype block are tightly associated to one another, identifying just a fraction of the alleles from a block allows others to be predicted with a high degree of certainty. Since the 2,900 markers in the Bovine3K panel provide a comprehensive representation of the bovine genome, the remaining markers from the BovineSNP50 BeadChip can be accurately imputed. Several groups have already actively created models to impute this data[1].

Figure 1: Bovine3K BeadChip



The Bovine3K BeadChip features 2,900 SNPs that span the entire bovine genome.

To demonstrate the high imputation accuracy achievable with the Bovine3K BeadChip, the accuracy of phenotype predictions was calculated for three bovine traits and evaluated using the BovineSNP50 BeadChip (Figure 2). *In silico* modeling showed that through imputation, the Bovine3K generated a 80–90% prediction accuracy relative to the BovineSNP50 BeadChip in Jersey cattle[2]. This illustrates that the Bovine3K BeadChip can be used to effectively impute a comparable level of genotypic information as the BovineSNP50 BeadChip.

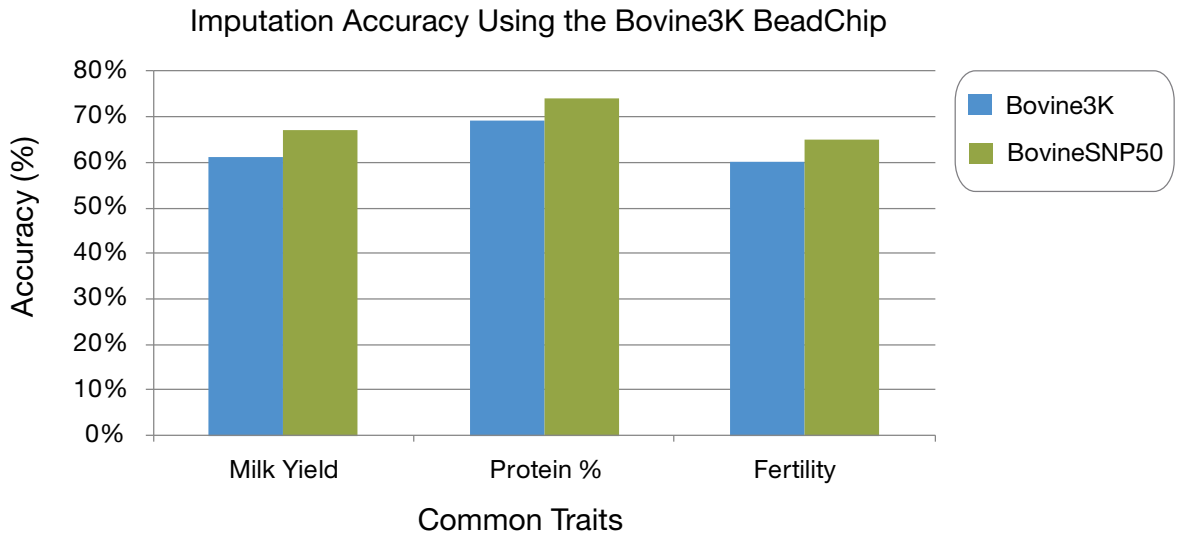
BeadChip Content

The 2,900 SNPs on the Bovine3K BeadChip were selected based on their position in the cattle genome, ensuring even spacing and proper minor allele frequency (MAF). Each SNP was validated *in silico* by the vast genotyping databases of leading bovine research institutions, including the University of Wisconsin and dairy breed associations worldwide. Content on the chip includes > 100 parentage SNPs, 154 X-linked markers, and 14 Y-chromosome markers for gender determination.

Proven Assay, High Data Quality

The Bovine3K panel is powered by the GoldenGate Assay, a highly successful genotyping technology proven in labs worldwide, as demonstrated by a vast publication record. With the industry's highest call rates and best reproducibility, this assay delivers the accuracy and reliability to effectively interrogate genetic merit.

Figure 2: Bovine3K BeadChip Imputation Accuracy



Phenotypes were predicted based upon genotypes using SNP content from the Bovine3K and BovineSNP50 BeadChips The accuracy of those predictions is shown for each BeadChip. Relative to the BovineSNP50, the Bovine3K generated 80–90% prediction accuracy, demonstrating its effectiveness for evaluating of genetic merit.

High call rates and accurate genotype calls are important for successful imputation studies. Illumina ensures that every Bovine3K BeadChip offers > 99% average call rate across common beef and dairy cattle breeds (Table 1).

Assay Workflow

GoldenGate technology uses illumiCodes, unique 23-bp single-stranded DNA oligos, to correctly identify each DNA sample as well as the loci being interrogated[3] (Figure 3). During sample preparation, primers containing illumiCodes and universal primer sites are hybridized directly to the genomic DNA. Since the IllumiCodes are discreet within the well, each allele can be independently examined during downstream analysis. Unbound genomic DNA is removed and only hybridized DNA is amplified and labeled with fluorescent dyes.

The resulting fluorescently labeled PCR products are hybridized to a Universal BeadChip. The BeadChip contains randomly assembled universal beads, each displaying an illumiCode corresponding to a specific locus. DNA will bind to the bead containing the complementary illumiCode. Unbound DNA is removed and the bound DNA with fluorescence signal provides the individual SNP genotype readout.

Table 1: Bovine3K BeadChip Performance and Specifications

Parameter	Results	Product Specification
Average Call Rate*	99.8%	> 99%
Reproducibility	100%	> 99.9%
Mendelian Inconsistencies	< 0.1%	< 0.1%

* Based on genotype results from HapMap samples.

This information is then analyzed for automated genotype clustering and calling. The entire assay can be completed in only three days with convenient stop times incorporated into the process.

Illumina Solutions for Genotyping

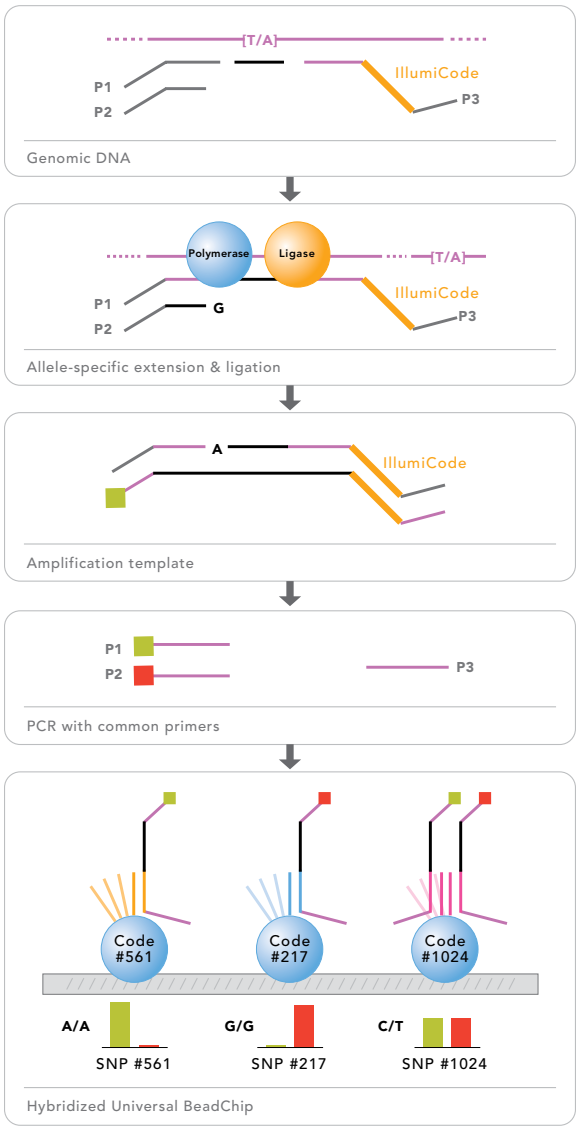
The Bovine3K BeadChip is compatible with the BeadArray™ Reader, iScan, and HiScan™SQ systems. These cutting-edge array scanners feature high-performance lasers and powerful optical systems that enable rapid scan times and precise assay detection. The HiScanSQ system can also perform Illumina sequencing by synthesis chemistry, the world's most widely adopted next-generation sequencing platform.

Illumina's 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 GoldenGate assay workflow, data are processed directly by Illumina's GenomeStudio® software to provide streamlined genotype calling, analysis, and reporting. Researchers can also choose to use Illumina's expert FastTrack Genotyping service to have samples genotyped and data delivered in a format suitable for downstream analysis.

Product Summary

Developed through a collaboration between Illumina and USDA-ARS, the Bovine3K BeadChip features 2,900 strategically selected SNPs that span the bovine genome, providing a high capacity to predict genetic merit for a number of important traits. This 32-sample BeadChip, along with the proven GoldenGate assay, presents a cost-effective, high-throughput solution for accurate genetic analysis in many breeds of beef and dairy cattle.

Figure 3: GoldenGate Assay Workflow



Streamlined GoldenGate Genotyping Assay Workflow

Online Imputation Resources

Resource	Web Address
BEAGLE	http://www.stat.auckland.ac.nz/~bbrowning/beagle/beagle.html
IMPUTE	http://mathgen.stats.ox.ac.uk/impute/impute.html
MACH	http://www.sph.umich.edu/csg/abecasis/mach
snpMatrix	http://www.bioconductor.org/packages/bioc/html/snpMatrix.html
PLINK	http://pngu.mgh.harvard.edu/purcell/plink

References

1. Druet T, Georges M. (2010) A Hidden Markov Model Combining Linkage and Linkage Disequilibrium Information for Haplotype Reconstruction and Quantitative Trait Locus Fine Mapping. Genetics, 184: 789-798
2. VanRaden PM, Van Tassell CP, Wiggans GR, Sonstegard TS, Schnabel RD, et al. (2009) Reliability of genomic predictions for North American Holstein bulls J. Dairy Sci. 93: 2229–2238
3. http://www.illumina.com/Documents/products/workflows/workflow_goldengate_assay.pdf

Ordering Information

Catalog No.	Product	Description
GT-450-1001	Bovine3K BeadChip 96 sample kit	The kit includes the OPA, arrays, and reagents necessary to assay 96 samples of the Bovine3K BeadChip
GT-450-1002	Bovine3K BeadChip 96 sample kit	The kit includes the OPA, arrays, and reagents necessary to assay 576 samples of the Bovine3K BeadChip

Each Bovine3K DNA Analysis Panel can process 32 samples and analyze 2,900 loci per sample.

Illumina, Inc. • 9885 Towne Centre Drive, San Diego, CA 92121 USA • 1.800.809.4566 toll-free • 1.858.202.4566 tel • techsupport@illumina.com • illumina.com

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AGAATGATAACAGTAACACACTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTCTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAAC
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