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DATA SHEET

Infinium™ Bovine Methylation Array

Dedicated array for cattle epigenetics research

Includes high-impact content designed by experts from the RUMIGEN consortium

Reveals cattle epigenetic variation influencing economically important traits

Maximizes sample processing efficiency using the 24-sample Infinium HTS methylation array

Introduction

With the expansion of cattle epigenetics, new bovine-specific methylation tools are needed to streamline biomarker discovery and support precision livestock management. Illumina has developed the first designated methylation array for bovine epigenetics. Designed by RUMIGEN and powered by Illumina microarray technology, the Infinium Bovine Methylation Array delivers high-resolution detection of DNA methylation marks that influence key performance, health, and welfare traits in cattle.

The Infinium Bovine Methylation Array (Figure 1) is an innovative addition to the established Illumina methylation array portfolio, giving researchers the ability to profile more than 40,000 CpG sites across the bovine genome (Table 1, Table 2). The assay is compatible with blood and semen samples and can be run as a manual, or semiautomated workflow.

Table 1: Infinium Bovine Methylation Array specifications

Feature	Description
Species	Bovine
Markers	~42,000
No. of samples per BeadChip	24
Minimum order size	48 samples
Recommended DNA input	250 ng
Assay chemistry	Infinium HTS methylation
Instrument support	iScan System
Liquid handling automation	Infinium Automated Pipetting System with Illumina Automation Control

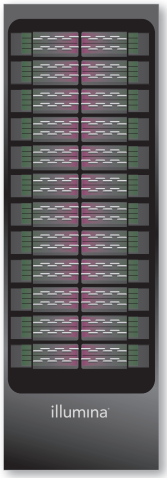

Figure 1: Infinium Bovine Methylation Array BeadChip

BeadChips with probes for analyzing > 40K CpG sites are available in a 24-sample format for high-volume studies.

Why study bovine epigenetics

Epigenetic analysis provides a deeper understanding of how regulatory mechanisms influence key traits related to productivity, health, and welfare in cattle. By mapping methylation signatures associated with fertility, growth efficiency, and developmental regulation, epigenetic profiling can support more informed breeding decisions and reveal biomarkers linked to long-term performance.[1-3] Epigenetic assessments of stress-responsive pathways, particularly those activated during thermal load, provide insight into molecular adaptations to heat stress and improve the identification of animals with superior thermotolerance.[4] Environmental exposures such as nutrition, season, and management practices also leave measurable methylation footprints that can be used to evaluate how environmental conditions shape physiological outcomes and resilience.[5] Additionally, epigenetic markers tied to immune regulation, chronic stress, and inflammatory responses offer a promising approach for animal welfare monitoring, enabling earlier detection of subclinical strain and more precise management interventions.[6]

Expertly selected content

The Bovine Methylation Array features content sourced from various experts in the field of agriculture and bovine genomic research. Content was designed by RUMIGEN, a European research consortium that is focused on improving ruminant breeding through genomic and epigenomic approaches. RUMIGEN combines large-scale phenotypic, genomic, and epigenomic data to refine genomic selection equations, address climate challenges, and deliver actionable insights for precision livestock management. The Bovine Methylation Array probes target markers from bisulfite sequencing studies across the bovine genome (Table 2, Table 3), including markers from known and novel associations to phenotype, to enable epigenetic biomarker discovery in cattle.

Table 2: Marker coverage by genomic mapping features

Feature	No. covered	% covered	Avg no. of loci per feature
CpG island	3901	10%	0.15
North shelf	2958	8%	0.11
North shore	2192	6%	0.07
South shelf	3056	8%	0.11
South shore	2279	6%	0.08

Table 3: Coverage of bovine genomic regions

Feature type	No. covered	% covered	Avg probe count
Intronic	14,921	40%	0.37
Exonic	8312	2%	0.03
First exon	2765	6%	0.08
TSS200	2812	6%	0.07
TSS1500	13,479	31%	0.35
5′ UTR	1121	5%	0.05
3′ UTR	676	3%	0.04

Accurate bovine methylation data

Infinium array chemistry employs many bead replicates for each CpG site queried, each bead with thousands of probes attached, to provide highly precise methylation measurements. Technical validation studies performed by RUMIGEN show > 99% reproducibility between technical replicates in bovine blood and semen samples (Figure 2).

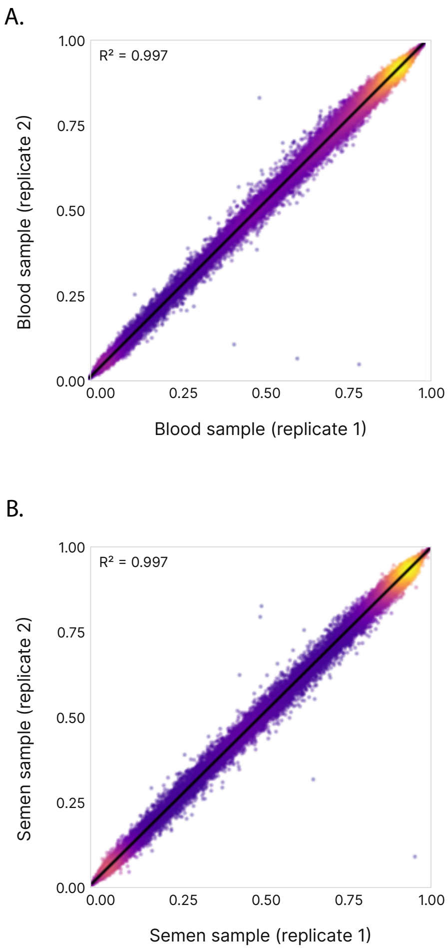

Figure 2: Infinium Bovine Methylation Array generates highly reproducible methylation data

Comparison of beta values from technical replicates for bovine (A) blood and (B) semen samples on the Infinium Bovine Methylation Array show an R^2 value > 99%. Data were analyzed using SeSAMe.

Streamlined high-throughput workflow

The Infinium Bovine Methylation Array uses the proven Infinium HTS 24-sample BeadChip format to enable laboratories to scale efficiently. The three-day workflow features rapid bisulfite conversion, automated BeadChip processing steps, high-throughput scanning on the iScan™ System, making this array an ideal solution for high-volume studies and applications.

Simplified data analysis

User-friendly Bioconductor tools can be used for downstream methylation analysis of data generated using the Infinium Bovine Methylation Array. For example, SeSAMe offers signal preprocessing, detection calling, quality control, interpretation of bisulfite conversion, differential methylation modeling, visualization, and inference for bovine methylation analysis.

To learn more about best practices and protocols for the Bovine Methylation Array, contact your Illumina sales representative.

Summary

The Infinium Bovine Methylation Array is a scalable, innovative solution for advanced bovine epigenetics research and livestock management. This array, designed by the RUMIGEN consortium, combines expertly selected content from the field of bovine agricultural research with trusted Infinium HTS workflows to enable accurate epigenetic analysis in bovine species.

Learn more

Infinium methylation assays

RUMIGEN consortium

Unlocking epigenetic insights in livestock webinar

Ordering information

Contact your Illumina sales representative to order the Infinium Bovine Methylation Array.

References

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