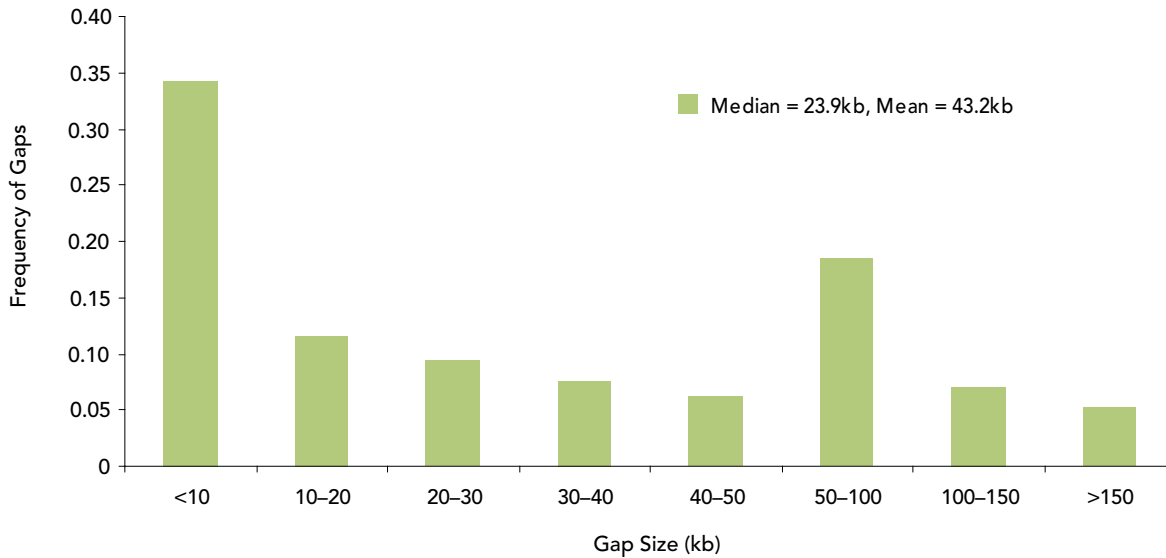


Figure 2: EquineSNP50 BeadChip Marker Spacer



The EquineSNP50 BeadChip offers more than sufficient marker density for confident identification and mapping of quantitative trait loci in modern horse breeds.

Analysis Simplified

Illumina's BeadStudio analysis software is a powerful and user-friendly tool for analyzing data generated by the EquineSNP50 Genotyping BeadChip. The Genotyping Module provides automated genotype calling and sample clustering. Powerful visualization tools and quality-control features enable graphical output of data and reports on reproducibility and Mendelian consistency.

As with all of Illumina's standard products, an optional Laboratory Information Management System (LIMS) and robotic automation are available to accurately and efficiently track samples throughout analysis.

Researchers can genotype their samples using the Illumina high-throughput iScan™ System, submit samples to Illumina's FastTrack Genotyping Service, or assess Illumina's genotyping products through the Illumina Customer Sample Evaluation (CSE) program.

Infinium Genotyping Solutions

The combination of Illumina proprietary assay technologies and flexible content deployment provides the most comprehensive solution available for genome-wide genotyping. Like all Infinium products, the EquineSNP50 BeadChip delivers the industry's highest data quality, allowing researchers to confidently pursue the fastest path to discovery.

References

1. <http://www.uky.edu/Ag/Horsemap/>
2. www.morrisanimalfoundation.org/equine
3. Gunderson KL, Steemers FJ, Lee G, Mendoza LG, Chee MS (2005) A genome-wide scalable SNP genotyping assay using microarray technology. Nat Genet 37(5): 549-554.
4. Steemers FJ, Weihua Chang W, Lee G, Barker DL, Shen R, et al. (2006) Whole-genome genotyping with the single-base extension assay. Nat Methods 3(1): 31-33.
5. <http://www.broad.mit.edu/mammals/horse/>

Table 1: EquineSNP50 BeadChip Performance Data and Specifications

Parameter	results*	Product Specification
Average Call Rate†	99.54%	> 99%
Reproducibility	100%	> 99%
Mendelian Inconsistencies	0.01%	< 0.1%

*Results based on 372 DNA samples including 8 replicates and 15 trios from fifteen breeds. See Table 2 for the list of breeds tested.

†Excludes Hokkaido samples. Average call rate including Hokkaido samples is 99.41%.

