

# Axiom Equine Genotyping Array

Comprehensive high-density genotyping for equine genetics research



The Applied Biosystems™ Axiom™ Equine Genotyping Array was designed to provide optimal genomic coverage of known genetic diversity among domestic horse breeds [1], maximizing utility for research in equine genetics.

## Axiom Equine Genotyping Array features:

- **Relevant content**—designed through the Thermo Fisher Scientific Expert Design Program in collaboration with the University of Minnesota and members of the Equine Genetic Diversity Consortium
- **Robust marker selection**—marker selection based on screening more than 348 samples across 2 million SNPs that were derived from 166 whole-genome sequences representing 32 breeds; the 10 breeds genotyped on the SNP screening array represent each of the major clusters among modern horse breeds and were chosen based on their high genetic diversity, extent of haplotype sharing with other breeds, and census population sizes to maximize SNP informativeness—an emphasis was placed on breeds that are the subject of active and ongoing research
- **Maximum diversity and genomic coverage**—more than 670,000 reliable, well-annotated, and highly polymorphic markers that are uniformly distributed across the genome; these 670,000 markers were selected to maximize accuracy of imputation up to 1.8 million markers both within and across breeds
- **Cost-effective tool for multiple applications**—offers a low-cost-per-marker solution ideal for genome-wide association studies, high-resolution genetic mapping, Mendelian trait mapping, diversity analysis, and selection signature analysis

## Reference

1. Petersen J. L., Mickelson J. R., Cothran E. G., Rendahl A. K., Andersson L. S., Axelsson J., Bailey E., Bannasch D., Binns M. M., Borges A. S., Brama P., de Câmara Machado A., Distl O., Felicetti M., Fox-Clipsham L., Graves K. T., Guérin G., Haase B., Hasegawa T., Hemmann K., Hill E. W., Leeb T., Lindgren G., Lohi H., Lopes M. S., McGivney B. A., Mikko S., Orr N., Penedo M. C., Piercy R. J., Raekallio M., Rieder S., Røed K. H., Silvestrelli M., Swinburne J., Tozaki T., Vaudin M., Wade C. M., **McCue M. E.** Genetic diversity in the modern horse illustrated from genome-wide SNP data. *PLoS One* **8**(1):e54997 (2013). doi:10.1371/journal.pone.0054997

Find out more at [thermofisher.com/microarrays](http://thermofisher.com/microarrays)

**ThermoFisher**  
SCIENTIFIC