

Axiom® Equine Genotyping Array

Novel equine genotyping array for whole-genome, high-density genotyping of 20 diverse worldwide breeds

Axiom® Equine Genotyping Array is a novel array, and the only array that can be used for genotyping 20 different breeds. This array offers maximum utility for research in equine genetics. It features 670,796 markers that were selected through a screening of 2 million markers for optimal genomic coverage of known genetic diversity among domestic horse breeds.¹ This unique single-nucleotide polymorphism (SNP) array offers the capability to perform imputation up to 2 million markers and is the only solution for genotyping 20 different breeds with >95% 2 million imputation rate.

Axiom Equine Genotyping Array was designed through the Expert Design Program at Affymetrix in collaboration with the University of Minnesota and members of the Equine Genetic Diversity Consortium.* The array is available in 96 format and supports a wide range of genotyping applications for equine research.



Highlights

Content

Axiom Equine Genotyping Array includes a total of 670,796 markers:

- Approximately 400,000 markers between population tag SNPs
- Approximately 200,000 markers within population tag SNPs
- Approximately 70,000 SNPs from legacy arrays
- Additional SNP density within the equine major histocompatibility complex (MHC)

Diversity

Axiom Equine Genotyping Array includes markers that were selected to maximize accuracy of imputation up to 1.8 million markers both within and across 20 breeds (Table 1). An emphasis was placed on breeds with high commercial relevance.

Applications

Complex trait research

- Genome-wide analysis and fine mapping
- Diversity analyses
- Genomic prediction of disease risk

Molecular breeding

- Association mapping
- Improved efficiency of breeding programs
- Selection signature analyses

Table 1. Breeds and number of samples screened on the Axiom® equine screening array.

Breed	No. samples
Arabian	21
Belgian	21
Black Forest	3
Duelmener	3
Edelblut-Haflinger	3
French Trotter	11
Haflinger	3
Hanoverian	6
Icelandic	18
Lusitano	21
Marremanno	22
Mongolian	2
Morgan	43
Old-Oldenburger	1
Quarter Horse	77
Sorraia	2
Standardbred	22
SueddeutschesKaltblut	4
Thoroughbred	24
Welsh	40

*The Equine Genetic Diversity Consortium (EGDC) led by the University of Minnesota represents a collaborative international community of equine researchers who are working to build a comprehensive understanding of genetic diversity among equine populations across the world. (<http://www.cvm.umn.edu/equinegenetics/egdc/>)

SNP discovery

SNP selection for Axiom Equine Genotyping Array required an initial candidate set of 5 million SNPs. These 5 million markers were derived from 166 whole-genome sequences representing 32 breeds. The markers were filtered based on even genome distribution (37 SNPs per 50 kb window), variant calling group distribution, and linkage disequilibrium. Markers within the pony and draft groups were given priority as they have been under-represented in the legacy 50K and 70K equine arrays. From this first round of filtering, 2 million SNPs were chosen as candidate SNPs. A total of 74,000 SNPs from legacy equine arrays were included in the design to enable backwards compatibility. Backwards compatibility allows comparison to earlier studies and provides continuity for existing projects. These markers were automatically included in both forward and reverse strand. The remaining SNPs were grouped into 50 kb windows. Additionally, all SNPs within the equine MHC regions were included. Taking these criteria into consideration, 2,076,397 high-quality probe sets representing 2,001,829 SNPs were chosen and submitted to Affymetrix for manufacturing on the Axiom® equine screening array.

Results

DNA isolated from the blood and hair of 347 horses from 20 breeds was genotyped on the Axiom equine screening array, which contained the 2 million markers identified in the SNP discovery process. The breeds genotyped on the Axiom screening array represented 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. The genotyping data from the screening array was analyzed as per the *Best Practice Supplement to Axiom® Genotyping Solution Data Analysis Users Guide* (P/N 703083). SNPs that failed QC metrics developed by Affymetrix were dropped. Tagging SNPs were identified in both inter- and intra-breed scenarios. Table 2 shows the results from the 347 samples processed on the array.² The average call rate of the markers in the PolyHighResolution category was 99.69%. A total of 670,796 best-performing markers from the screening array were selected for Axiom Equine Genotyping Array. Axiom Equine Genotyping Array can be used to genotype the 20 different breeds and have >95% 2 million imputation rate. The data from Axiom Equine Genotyping Array is analyzed using Axiom™ Analysis Suite software. SNP filtering is performed as per the *Best Practice Supplement to Axiom® Genotyping Solution Data Analysis Users Guide* (P/N 703083).

Table 2: Results from processing 347 samples across 670,776 markers on the equine screen assigned into six different categories. The 670,776 markers were transferred to Axiom® Equine Genotyping Array.

SNP classification	No. markers	Percentage (%)
All markers	670,776	100
Recommended markers		
PolyHighResolution	498,639	74.3
NoMinorHomozygous	105,250	15.7
MonoHighResolution	21,695	3.2
OffTargetVariant	2,469	0.4
CallRateBelowThreshold (<97%)	18,273	2.7
Other	24,450	3.6

References

- 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).
- Schaefer R., Schubert, M., Orlando L., Mickelson J. R., McCue M. E. Selection of tagging SNPs and imputation efficiency of the 670K commercial SNP chip, Plant & Animal Genome XXIII Conference, Abstract #P0318 (2015).

Ordering information

Part number	Description	Details
550583	Axiom® Equine Genotyping Array	Contains one plate with 96 arrays
901606	Axiom® GeneTitan® Consumables Kit	Contains all GeneTitan® Instrument consumables to process one 96-format array plate
901758	Axiom® 2.0 Reagent Kit	Includes all reagents (except isopropanol) to process one Axiom® 96-format array plate

Affymetrix, Inc: (US) +1-888-362-2447, +1-408-731-5000 ■ (EU) +44-(0)1628-552550 ■ (JP) +81-(0)3-6430-4020 ■ (CN) +86-21-63915511

eBioscience Products: (US) +1-888-999-1371, +1-858-642-2058 ■ (EU) +43 1 796 40 40 305 ■ (JP) +81-(0)3-6430-4020

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P/N GGNO05917 Rev. 1

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