SNAPSHOOT
ENGINEERED FOR A SAFER TOMORROW

# 현장을 이해하고, 필요한 솔루션을 연결합니다.

산업안전 · 추락방지 시스템
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제품 제안부터 공급·시공·설치·교육까지




COMPANY INFORMATION

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TECHNICAL DOCUMENTS

## 인증서 · 데이터시트 · 기술자료

제품의 규격과 성능, 인증 및 적용 조건을 확인하기 위한 자료입니다.

ABOUT SNAPSHOOT

### 제품 공급을 넘어, 현장에 맞는 해결책으로

스냅슛은 산업현장의 작업 환경과 요구 조건을 바탕으로
적합한 제품과 시스템을 제안합니다. 현장 실사를 통해 설치 조건을 확인하고,
공급부터 시공·설치 및 사용 교육까지 필요한 과정을 함께합니다.

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본 페이지는 스냅슛의 자료 제공 안내용 표지입니다. 첨부된 인증서 및 기술자료의 발행 주체, 인증 대상과 적용 범위는 해당 원문을 기준으로 확인해 주세요.

DataSheet

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Biology for a better world

# 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.

**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 |

### 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

*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


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).
2. 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 |


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