Axiom myDesign custom genotyping arrays for human research applications

Cost-effective customization made fast and easy

Overview

Applied Biosystems™ Axiom™ myDesign™ custom genotyping arrays for human research applications are a cost-effective way to modify an existing array or create an entirely new design.

- Adding, replacing, and removing markers on your array is a simple process
- For as few as 480 samples, we can optimize your array to a target population, trait, or application
- Arrays can be updated as new genomic information becomes available
- Working closely with you, our bioinformatics specialists finalize your array design quickly and efficiently (Figure 1)
- No markers are lost during manufacturing, so important variants always appear on every array
- Your new custom arrays will typically be delivered 6 weeks after the final design review

Optimize your array to your population

For the most powerful research genotyping studies, how the array markers are selected is more important than how many. Intelligent SNP selection enables better genomic coverage of the millions of variants in your target population.

There are two ways to achieve the best genomic coverage in your population with Axiom myDesign custom arrays:

- Add one of our convenient, predefined population "booster" panels (Table 1) to an existing GWAS design, such as the Applied Biosystems™ Axiom™ Biobank Genotyping Array
- Work with us to design a novel GWAS panel using your own population reference data

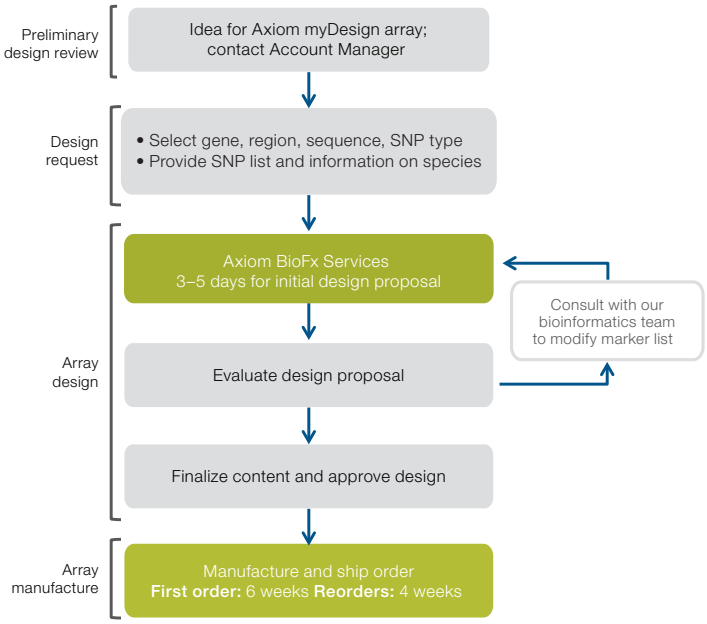

Figure 1. The Axiom myDesign custom array design process.

Table 1. Population booster panels are available for the following 1000 Genomes Project populations.

CHB	GBR	ACB	STU
JPT	IBS	MXL	ITU
CHS	YRI	PUR	AFR
CDX	LWK	CLM	AMR
KHV	GWD	PEL	ASN
CEU	MSL	GIH	EUR
TSI	ESN	PJL	SAN
FIN	ASW	BEB	

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Sources of genomic markers for Axiom myDesign arrays

Variants for Axiom myDesign arrays may be selected from several sources, including but not limited to the following:

- dbSNP
- Markers identified by sequencing
- The Applied Biosystems™ Axiom™ Genomic Database
- Markers personally chosen by you

Axiom Genomic Database

- Enables fast and easy selection of public domain SNPs and indels for Axiom myDesign arrays
- Marker annotation collated from 14 different data sources helps save hours of data mining to define SNP lists
- Contains 9.4 million wet lab–tested markers that have been verified via genotyping in HapMap 270 samples
- Choose from markers in the Axiom Genomic Database that, directly or through pairwise tagging ($r^2 \geq 0.8$), cover 25.8 million of the 39.5 million 1000 Genomes Project variants in at least one of the reference populations
- Figure 2 is a Venn diagram detailing the content of the Axiom Genomic Database compared to the 1000 Genomes Project Database (1KG), March 2012 release
- For markers not found in the Axiom Genomic Database, novel probe design and performance prediction algorithms will be deployed

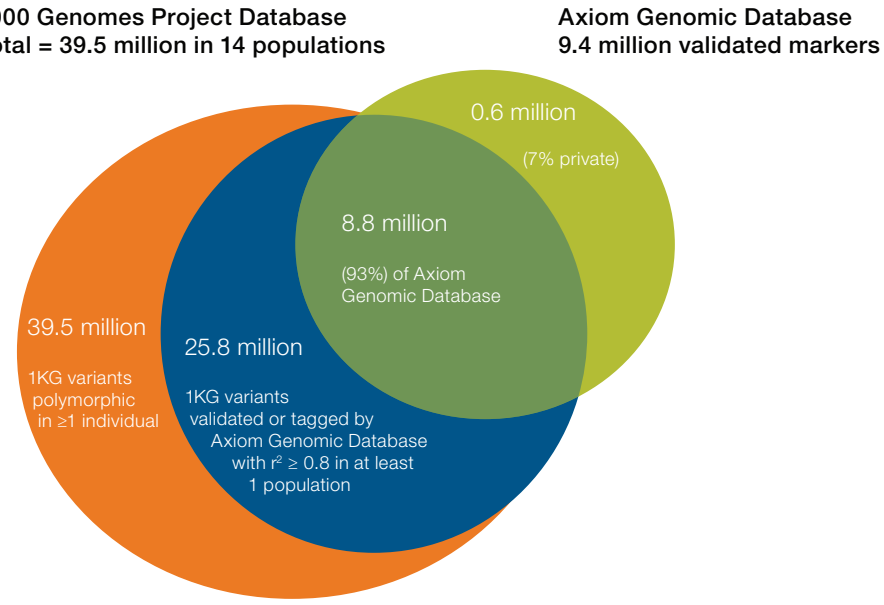

Figure 2. Venn diagram detailing the content of the Axiom Genomic Database compared to the 1000 Genomes Project Database (1KG), March 2012 release

Specific information regarding submission of a marker list to to create an Axiom myDesign custom genotyping array can be found in the technical note, Axiom myDesign Custom Array design guide for human genotyping applications (Pub. No. COL21654).

Find out more at **thermofisher.com/microarrays**

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