Axiom Human Genotyping SARS-CoV-2 Research Array

Highly relevant research content covering cellular mechanisms in signaling pathways, underlying conditions, and immune response

This bulletin provides an overview of the content on the Applied Biosystems™ Axiom™ Human Genotyping (HG) SARS-CoV-2 Research Array. The array contains over 800,000 variants to conduct research into host genetics of SARS-CoV-2 infections and was designed in collaboration with several global organizations and biobank research communities.

There is currently an absence of a comprehensive solution that addresses the challenges in studying host genetics of SARS-CoV-2. Short-read sequencing and global generic screening arrays (GSAs) are unable to provide the resolution and comprehensive analysis for studies in genome-wide analysis (GWAS), cellular interactions in signaling pathways, pharmacogenetics, and immune response. The Axiom HG SARS-CoV-2 Research Array offers several advantages over GSAs by offering higher statistical power to help make scientific discoveries, and will help prevent false-positive identifications.

Key differentiators of the Axiom HG SARS-CoV-2 Research Array

- Array content contributions from key opinion leaders in the field, including relevant research content from pre-publications and peer-reviewed content
- Unique array design features that make it ideal for research into etiopathology of SARS-CoV-2 infections
- Dense coverage of various signaling pathways, such as the NF-kappa signaling pathway, involved in activating genes in immune response and inflammation; there are twice the number of markers on this array as on any other current GSA
- Rapid solution that converts samples to whole-genome data for multi-ethnic populations three times faster than whole-genome sequencing

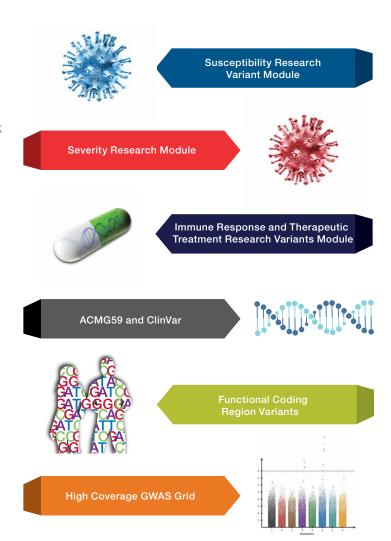


Figure 1. Key content modules on the Axiom HG SARS-CoV-2 Research Array.



- Relevant modules for SARS-CoV-2 research are as follows:
 - SARS-CoV-2 Susceptibility Research Variant Module
 - Includes structural variants for viral entry points and pathways that are associated with immunity and inflammation
 - Coverage of various signaling pathways to help decipher differences in underlying host genetics and individual responses to SARS-CoV-2
 - Dense coverage of the X chromosome for research into innate immunity

- SARS-CoV-2 Severity Research Module

- Includes variants involved in chronic underlying conditions that are implicated in research on the severity of the disease
- Blood group markers, including the ABO gene, and blood phenotypes that have been implicated in the severity of the disease

SARS-CoV-2 Immune Response and Therapeutic Treatment Research Variants Module

 Includes variants that cover regions involved in immune response, also important in vaccine development and pharmacogenomics for drug discovery and development

Table 1. Number of markers in each of the SARS-CoV-2 modules.

| Category | Number of markers* |
|---|--------------------|
| SARS-CoV-2 Susceptibility Research Variant Module | >180,000 |
| SARS-CoV-2 putative receptor variants | >1,200 |
| Signaling pathway variants | >122,000 |
| Variants on the X chromosome | >60,000 |
| SARS-CoV-2 Severity Research Module—underlying conditions implicated in severity of SARS-CoV-2 infections | >16,000 |
| Blood phenotypes and blood groups | >1,200 |
| Diabetes | >800 |
| Cardiovascular disease | >1,300 |
| Stroke | >50 |
| Lung function and COPD | >9,000 |
| BMI | >1,000 |
| CKD/RAAS | >450 |
| Asthma | >500 |
| SARS-CoV-2 Immune Response and Therapeutic Treatment Research Variants Module | >24,000 |
| ADME and protein markers for druggable targets | >6,000 |
| Immunoglobulin and miRNA markers for vaccine research | >5,800 |
| HLA/KIR markers for immune response research after vaccination | >13,500 |
| Multi-ethnic GWAS grid | >725,000 |
| ACMG 59 variants | >6,000 |
| Functional coding-region variants including eQTL and loss-of-function variants | >24,000 |

^{*} A marker may appear in more than one category.

Table 2. Full list of signaling pathways covered on the array.

| Signaling pathways, regulatory pathways, and cellular mechanisms* | Number of genes | Variants |
|---|-----------------|----------|
| NF-kappa signaling | 103 | >2,500 |
| AMPK signaling | 128 | >4,600 |
| B cell receptor signaling | 80 | >2,500 |
| TNF signaling | 112 | >2,300 |
| MAPK signaling | 289 | >10,500 |
| IFN signaling | 473 | >14,400 |
| TGF-beta signaling | 92 | >2,600 |
| FoxO signaling | 128 | >3,600 |
| Endoplasmic reticulum stress | 930 | >28,000 |
| Renin angiotensinogen | 23 | >1,763 |
| Notch signaling and ligands | 53 | >1,800 |
| NOD-like receptor pathway | 175 | >3,400 |
| Toll-like receptor signaling | 103 | >1,600 |
| Apoptosis | 4,038 | >100,000 |

^{*} An explanation of various pathways can be found in genome.jp/kegg/pathway.html.

Table 3. Markers classified into selected disease research categories.

| Details on sub-categories of markers | V ariants |
|--|------------------|
| Mental, behavioral, neurological, and neurodevelopmental risk variants | |
| Alzheimer's disease including ApOE markers | >170 |
| Parkinson's disease | >70 |
| Schizophrenia | >400 |
| Autoimmune and inflammatory disease risk variants | |
| Inflammatory bowel disease | >170 |
| Celiac disease | >60 |
| Crohn's disease | >300 |
| Graves' disease | >30 |
| Inherited eye disease | |
| Macular degeneration | >100 |
| Glaucoma | >70 |
| Blood phenotypes and blood groups | >1,200 |
| Asthma | >500 |
| Body mass index | >1,100 |
| Lung function phenotypes | >8,000 |
| Copy number variation | >3,000 |
| Markers from Applied Biosystems™ UK Biobank Axiom™ Array | >21,700 |
| Diabetes | >800 |
| Cardiovascular disease | >1,300 |
| Stroke | >50 |
| Lung function and COPD | >9,000 |
| Chronic kidney disease/RAAS | >450 |

Table 4. Number and accuracy of markers with $r^2 > 0.8$ covering the ancestral populations in phase 3 of the 1000 Genomes Project.

| | Imputation accuracy* | | Number of imputed markers with r² > 0.8 |
|---------------------------------------|----------------------|----------|---|
| Ancestral population covered on array | MAF > 1% | MAF > 5% | MAF > 1% |
| African (AFR) | 90% | 92% | 14.9M |
| Admixed American (AMR) | 92% | 94% | 10.2M |
| East Asian (EAS) | 87% | 92% | 7.3M |
| European (EUR) | 91% | 94% | 8.8M |
| South Asian (SAS) | 88% | 93% | 8.7M |

^{*} Accuracy is the mean r² calculated across autosomal SNPs from the highest-ranked markers.

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In summary, the various research modules create a powerful, scalable, and economical array for studies of host genetics involved in SARS-CoV-2 infections, population genomics, and vaccine and drug development research.

Acknowledgments

We are very grateful to the many scientists and research groups who provided markers for the Axiom HG SARS-CoV-2 Research Array: Ariel Precision Medicine, USA; Oswaldo Cruz Foundation (Fiocruz), Brazil; Universidade Federal do Pará, Brazil; Unidad de Genómica del ITER, Spain; University of Santiago de Compostela, Spain; IPATIMUP, Portugal; Dr. Helena Alves, INSA, Portugal; University of Oxford, UK; University of Pretoria, South Africa; CPGR and University of Stellenbosch, Cape Town, South Africa; the biobank research community, especially FinnGen (Finland), Million Veteran Program (USA), COVID-19 Host Genetics Initiative, UK Biobank (UK), and Spanish Biobank (Spain).

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Ordering information

| Product | Description | Cat. No. |
|---|---|----------|
| Axiom Human Genotyping SARS-CoV-2 Research Array | Includes one 96-array plate | 952401 |
| Axiom Human Genotyping SARS-CoV-2 Research Array Assay Kit | Includes one 96-array plate (Cat. No. 952401); Axiom 2.0 reagent kit (Cat. No. 901758); and GeneTitan MC consumables kit | 952402 |
| Axiom Human Genotyping SARS-CoV-2 Research Array Plus Assay Kit | Includes one 96-array plate (Cat. No. 952401); Axiom 2.0 Plus reagent kit (Cat. No. 951960); and GeneTitan MC consumables kit | 952403 |

