# 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

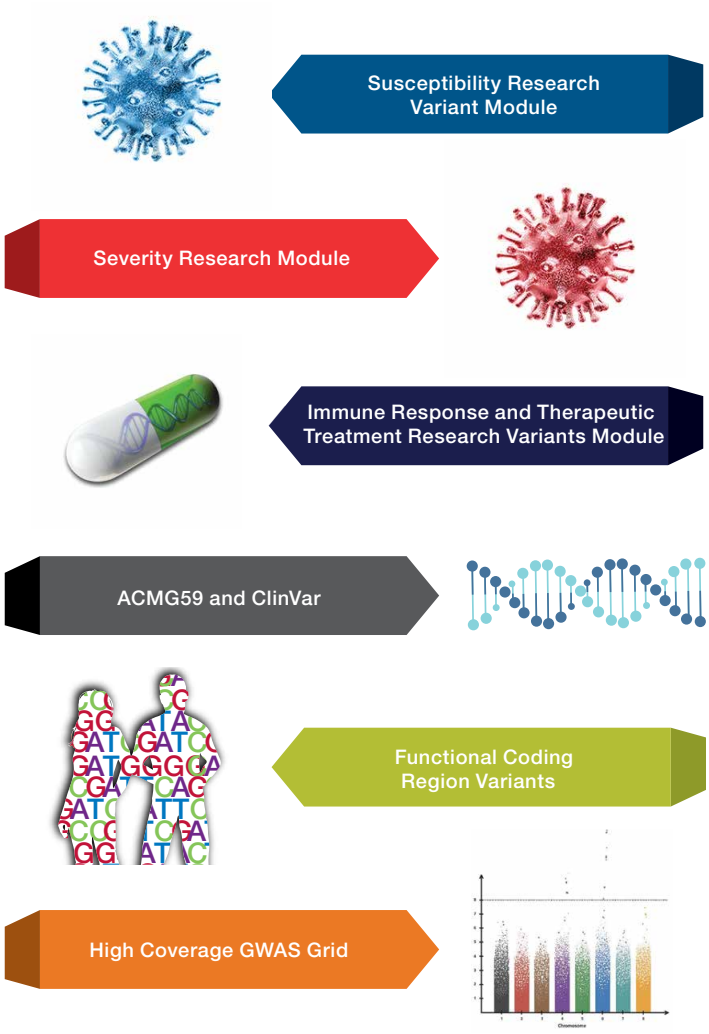


**Figure 1. Key content modules on the Axiom HG SARS-CoV-2 Research Array.**

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- 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 | Variants |
|---|---|
| **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 $r^2 > 0.8$ |
|---|---|---|---|
| **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 $r^2$ 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.


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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 |

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