

# Genome-Wide Association Study of Immune Response to Twelve Common Pathogens

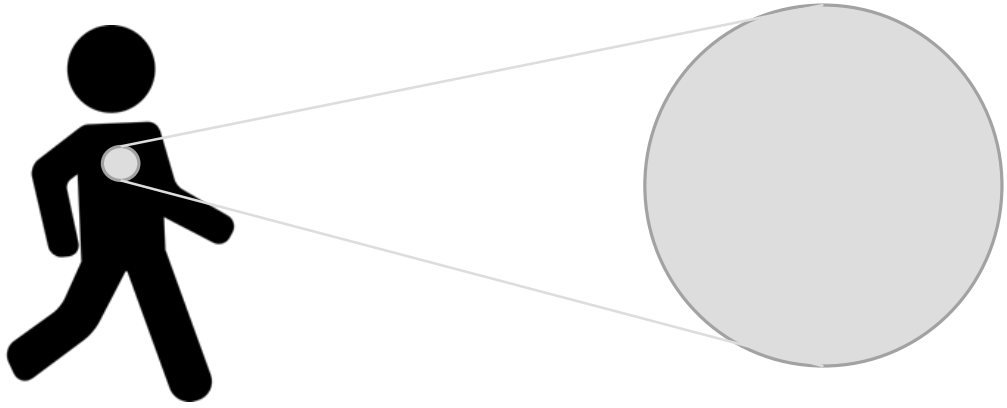
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Maïke Morrison, Dr. Linda Kachuri, Dr. Sara Rashkin, Dr. John Witte

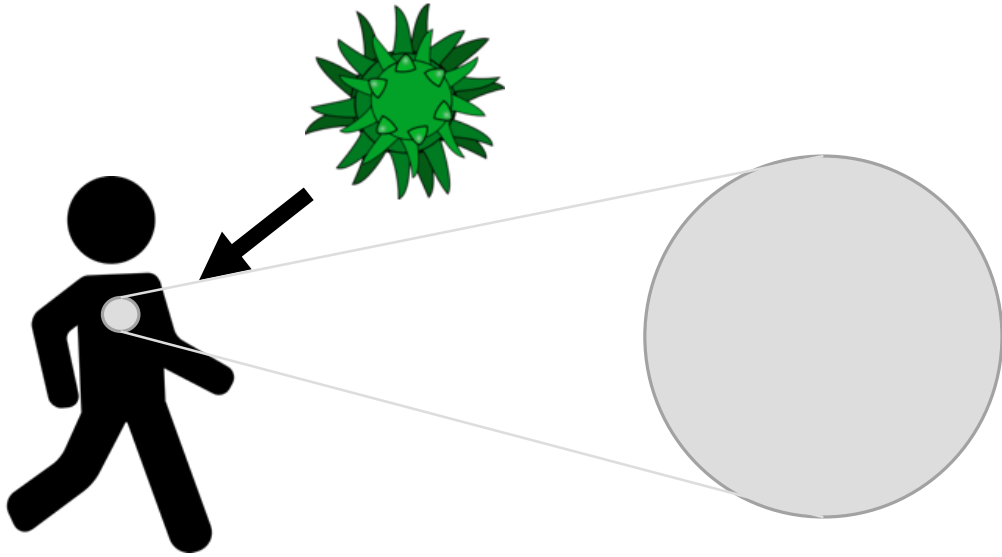
Department of Biostatistics and Epidemiology, University of California San Francisco

Summer Research Training Program 2019

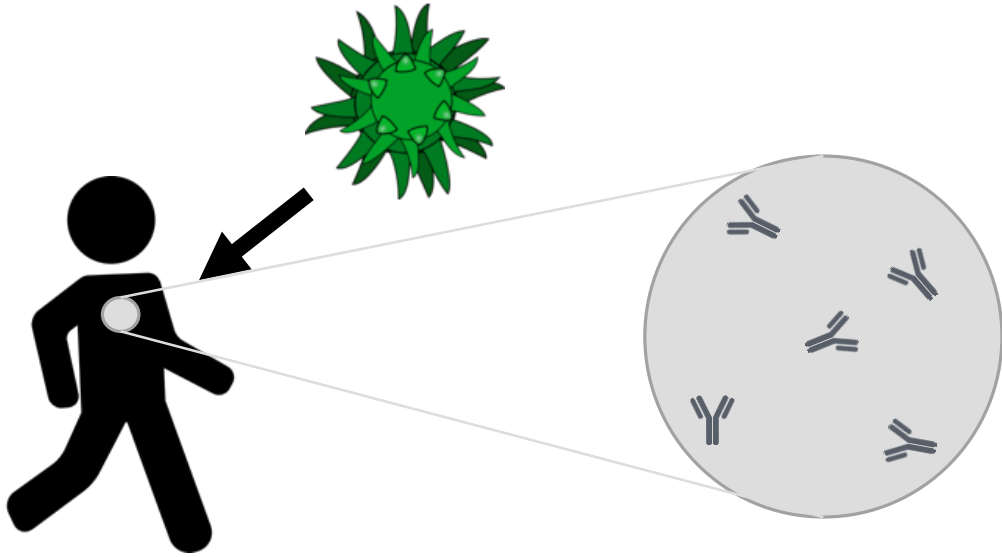




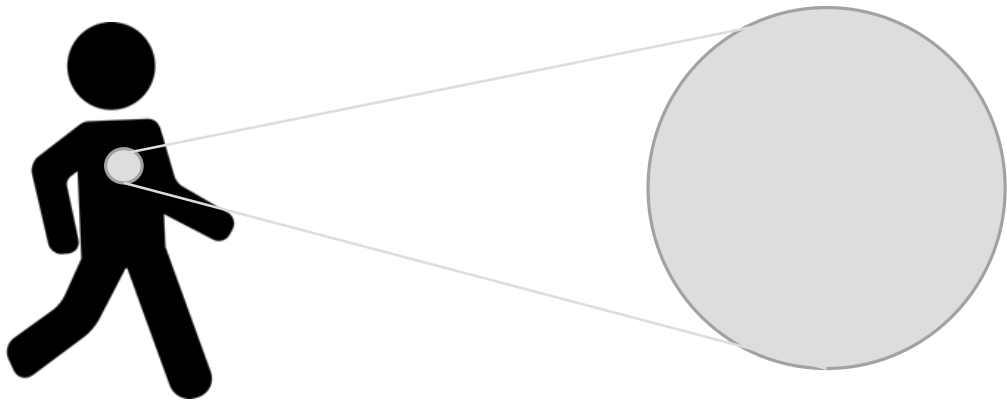
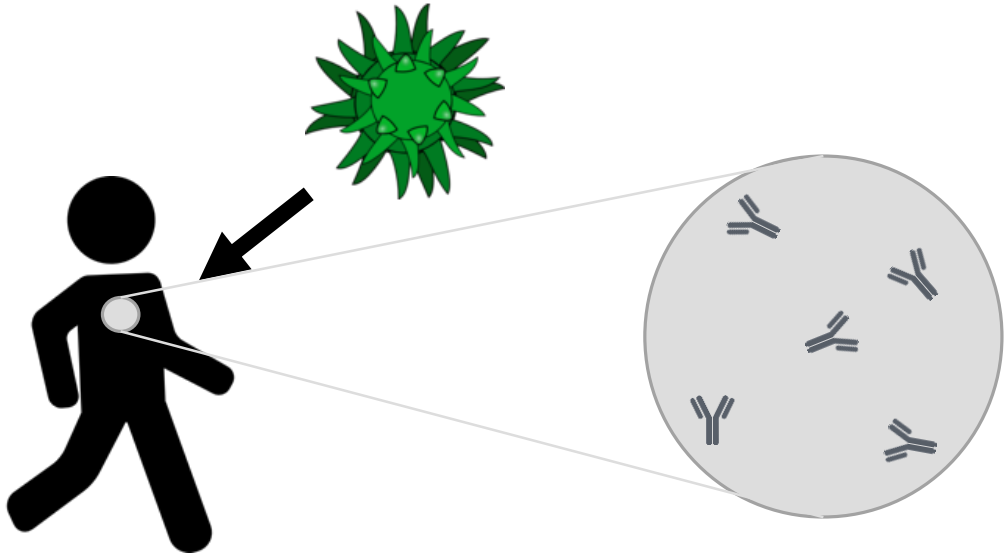
Immune response varies between individuals.



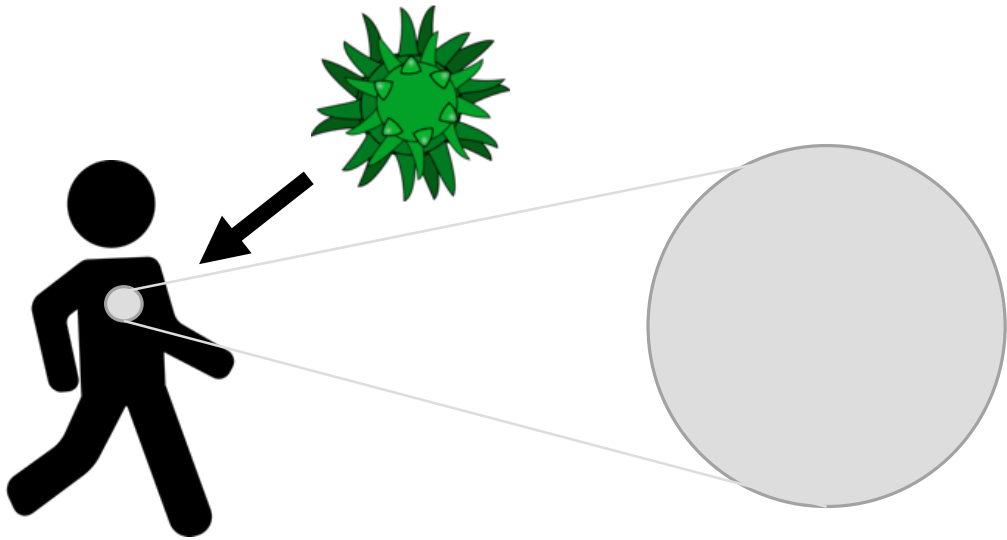
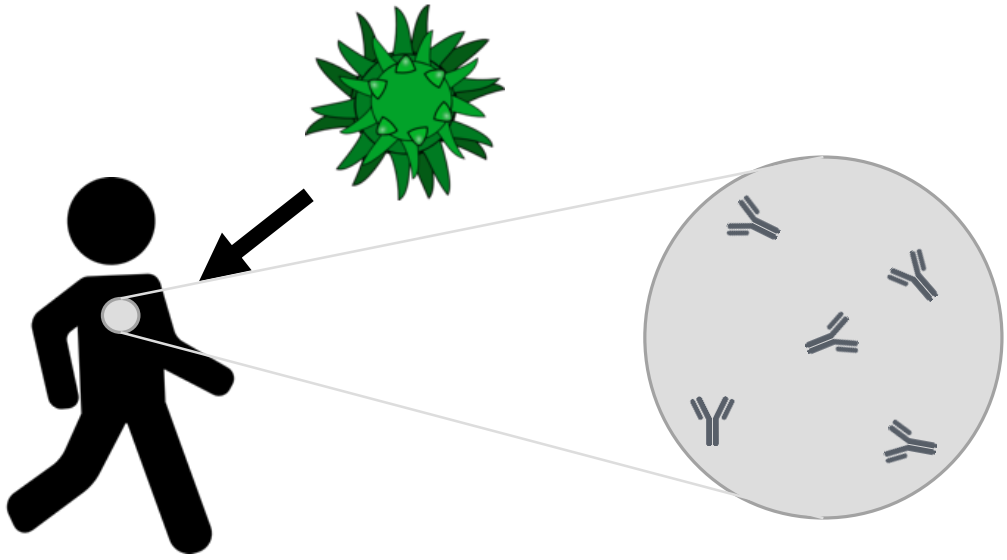
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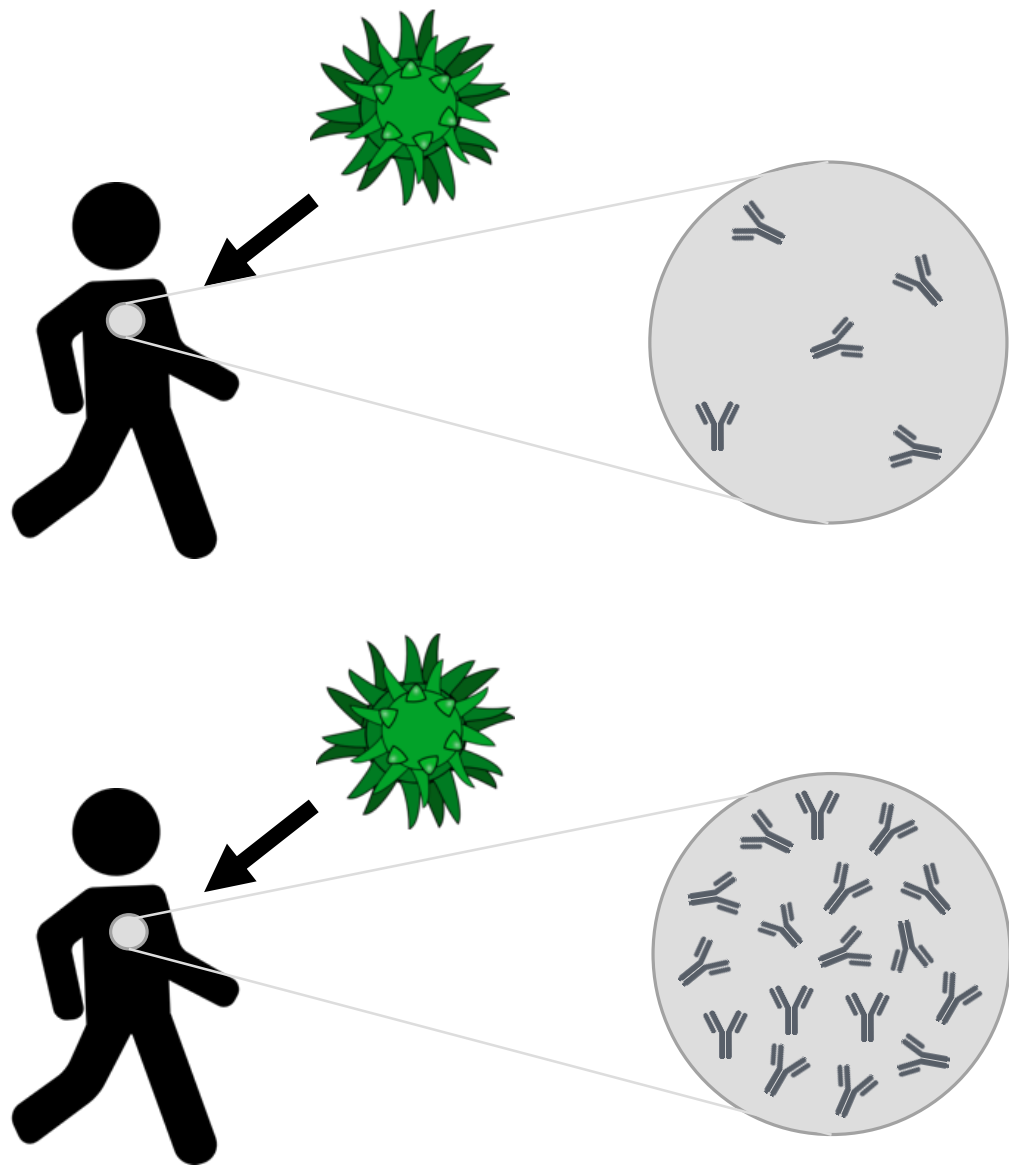
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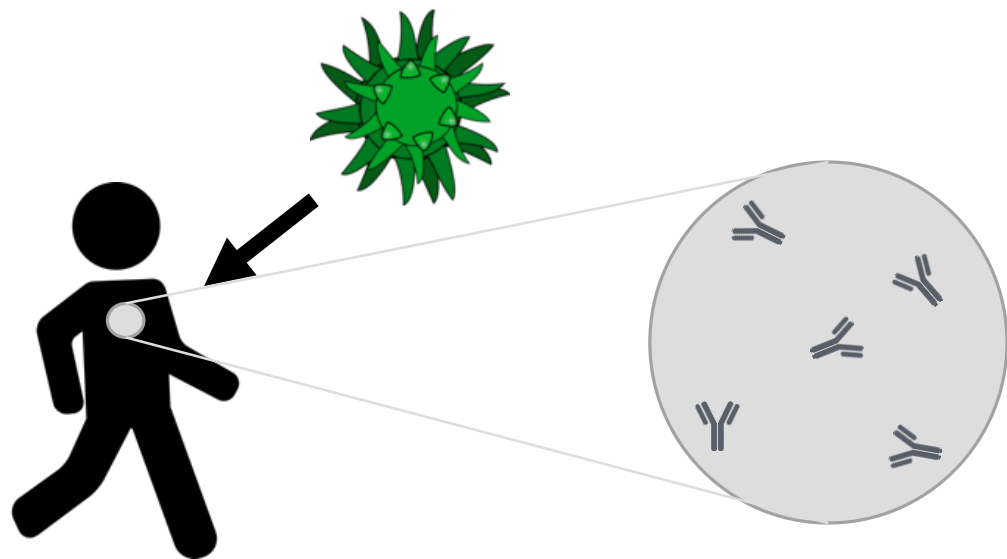
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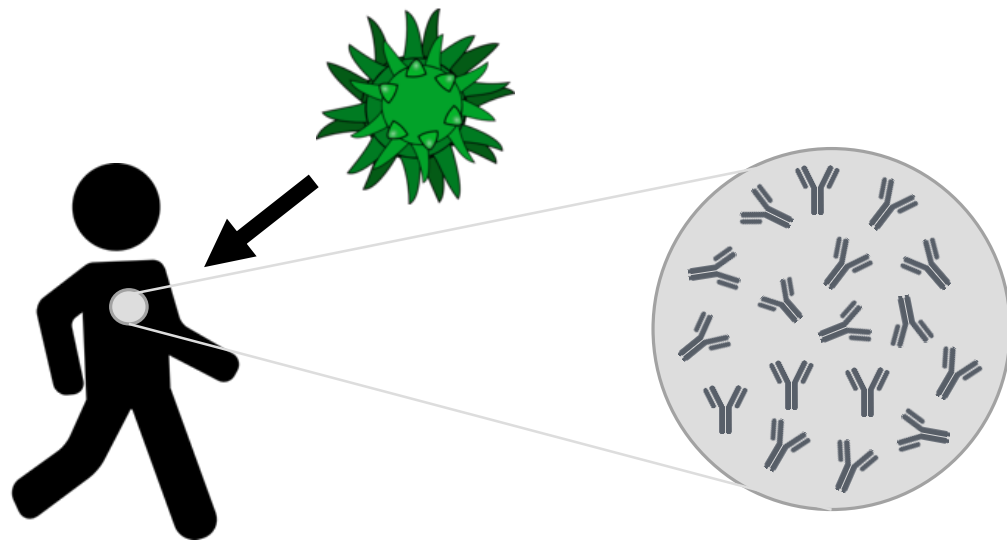
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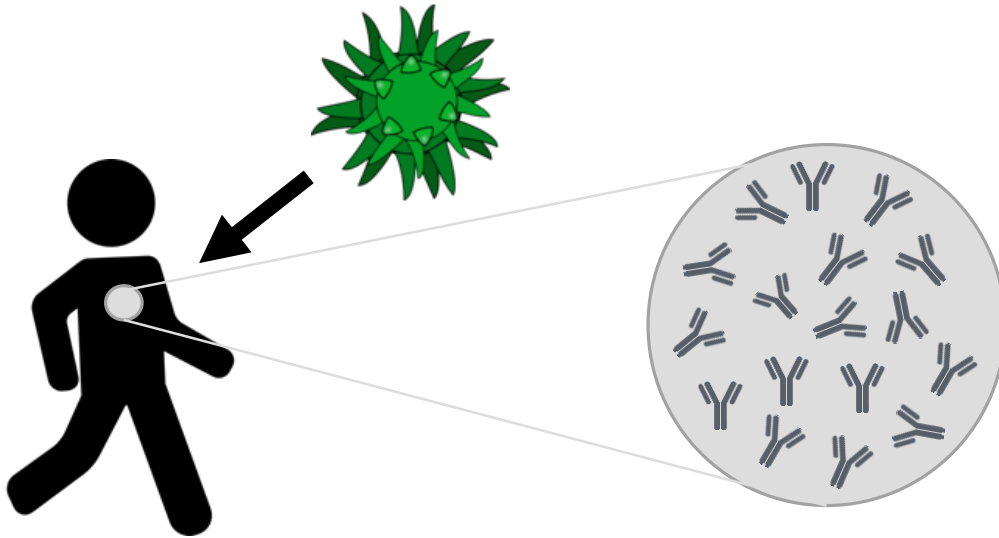
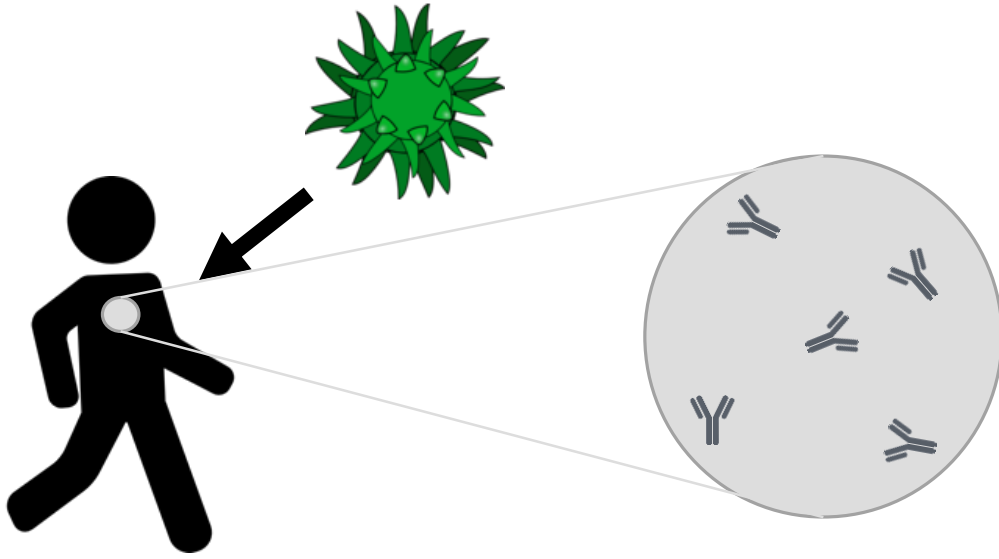


**“Strength of  
Immune Response”**



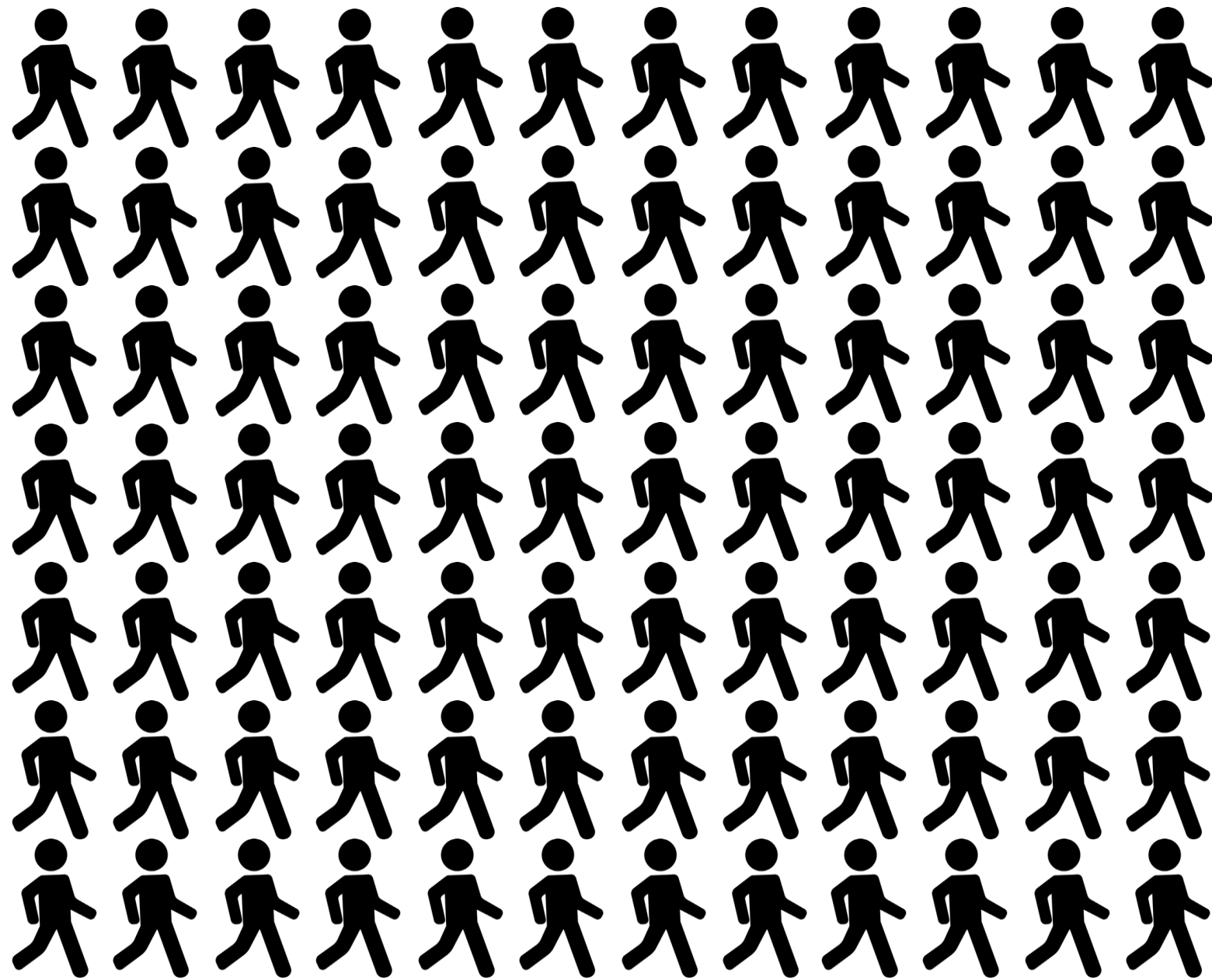
**Immune response varies between individuals.**





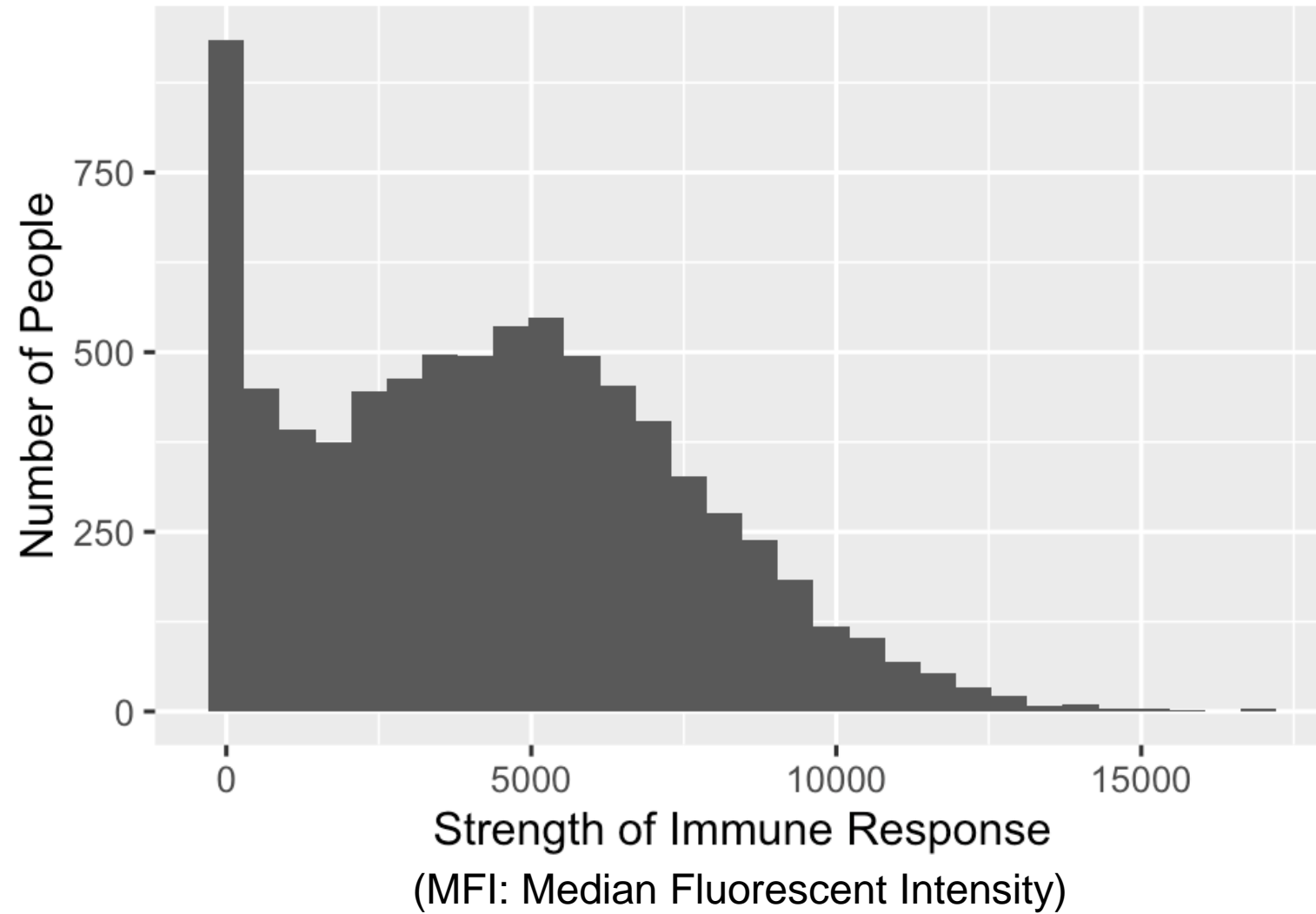
- Vaccine efficacy
- Pathogen-induced disease etiology
- Biological mechanisms of immune response
- Potential drug targets
- Immune-related cancer therapies

Immune response varies between individuals.



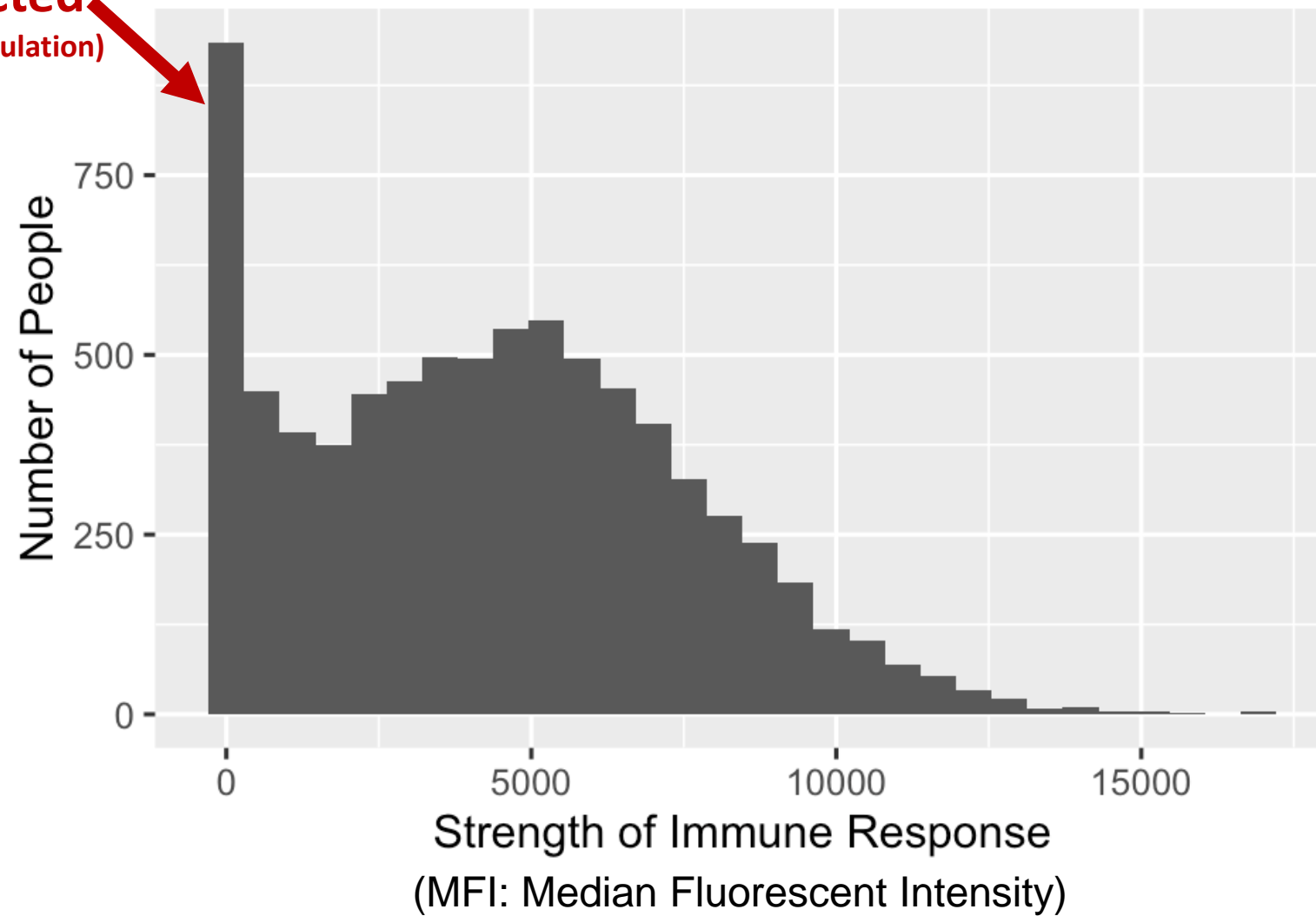
$N \approx 8,000$

# EBNA-1 antigen for Epstein-Barr Virus



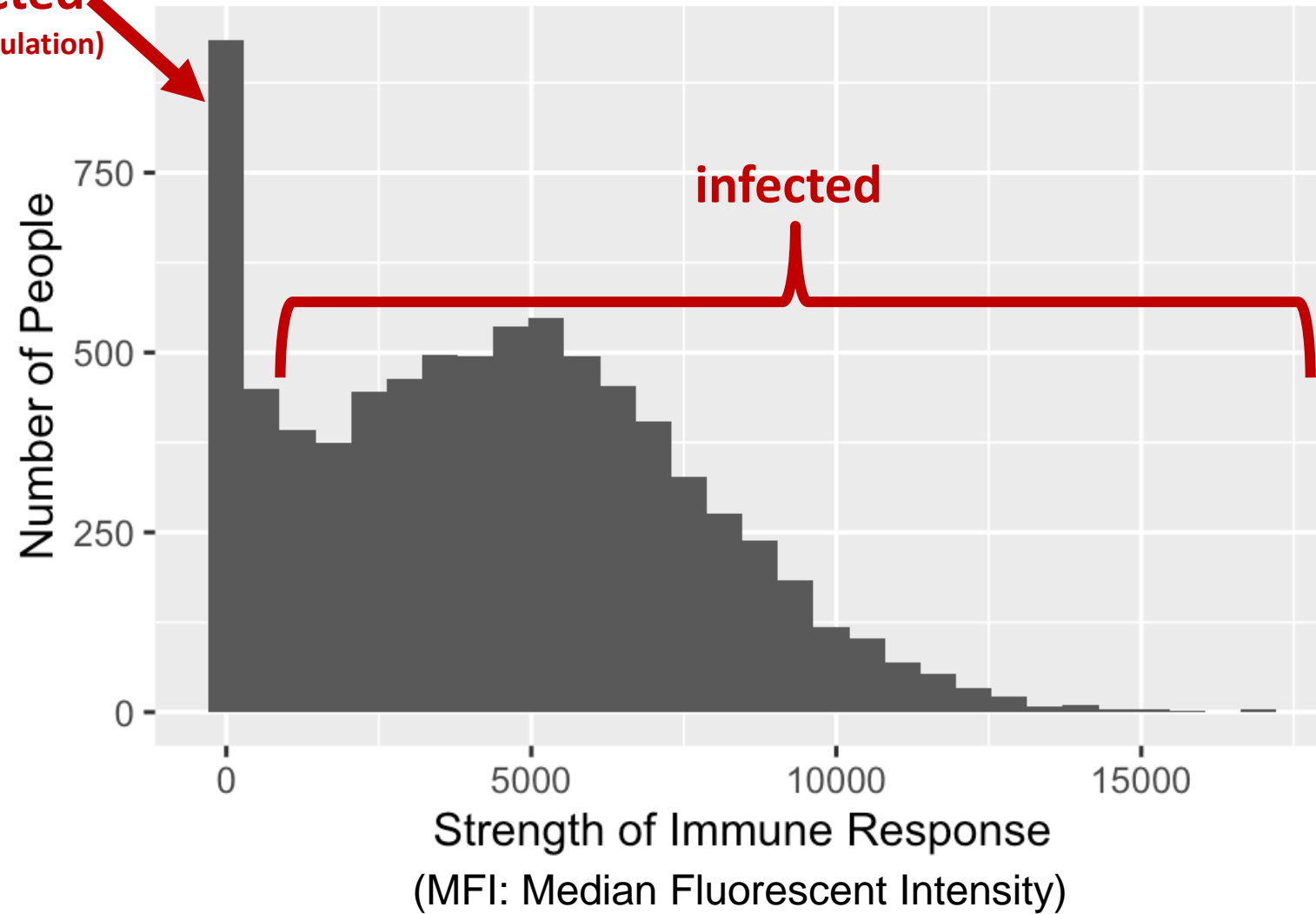
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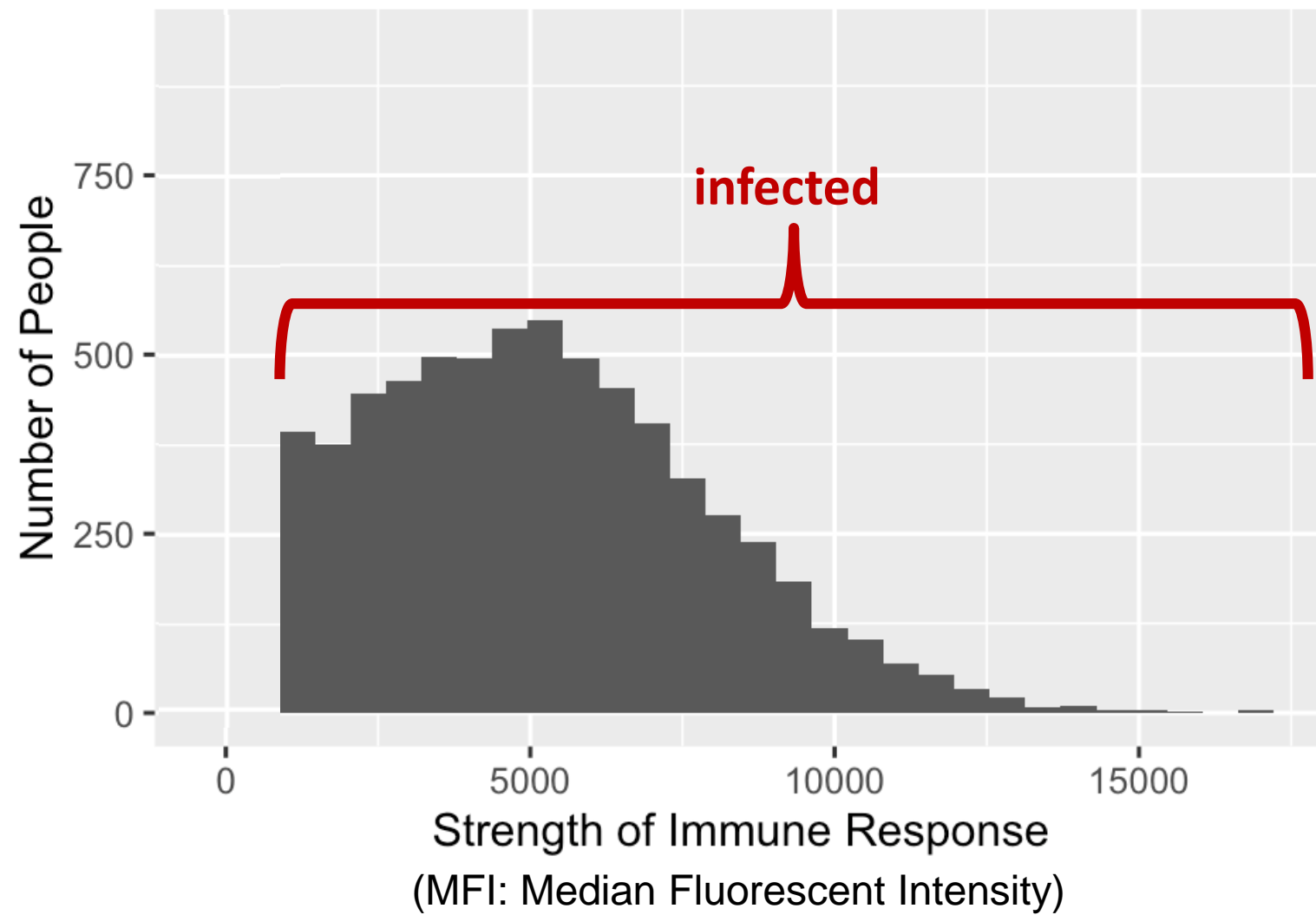
**uninfected**  
(11% of population)

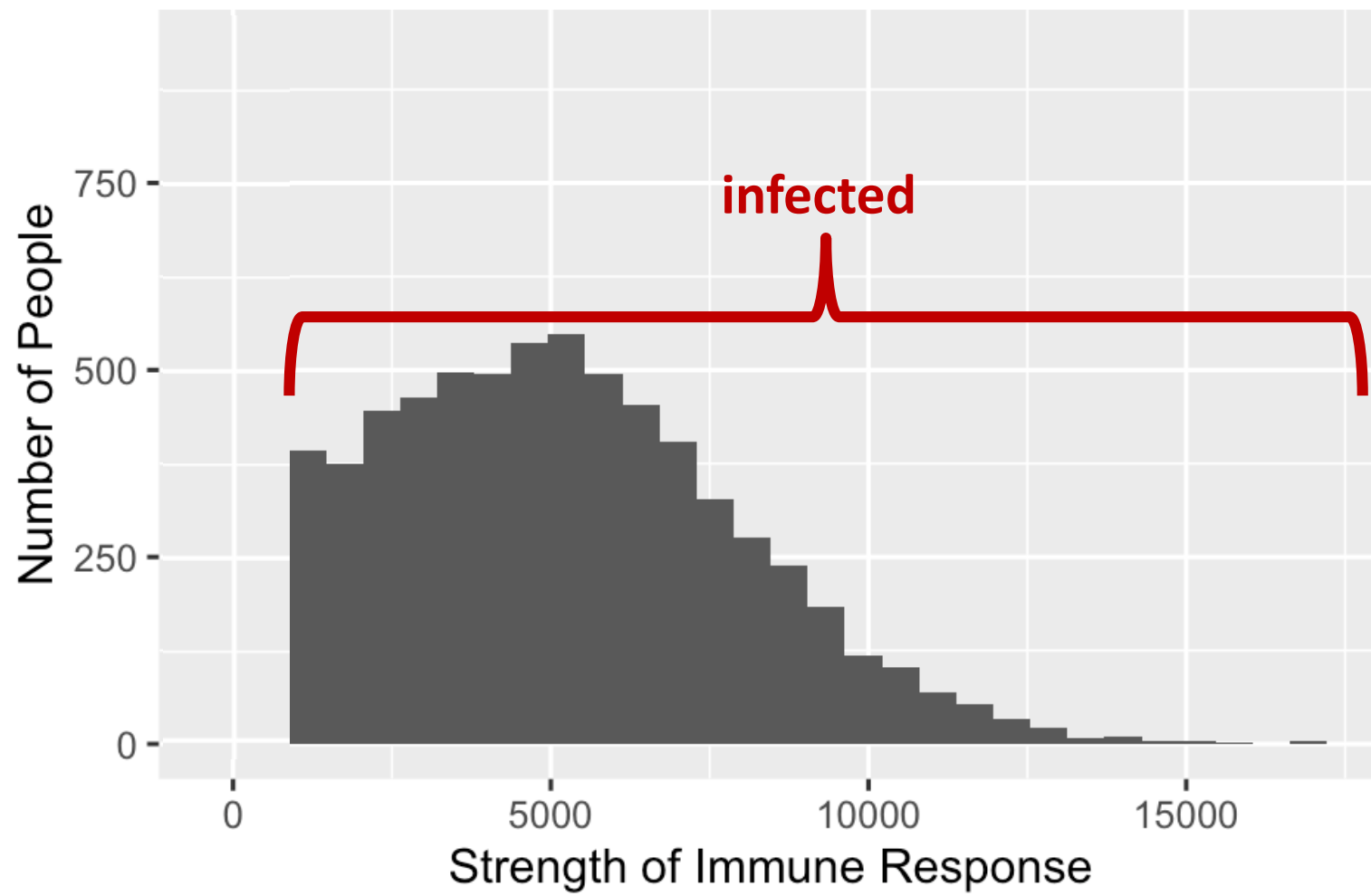


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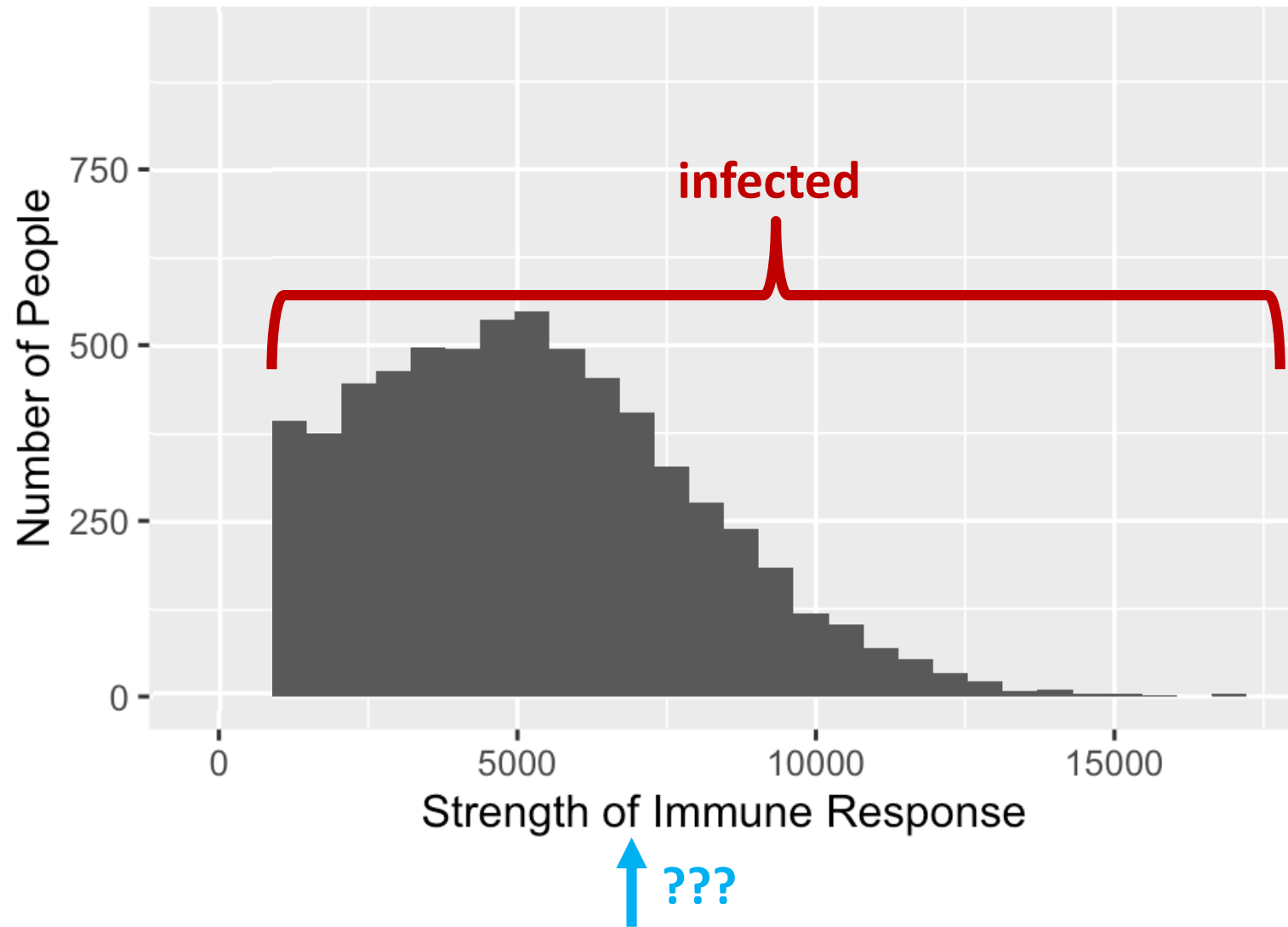
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Among infected individuals, what is the genetic basis of variability in immune response?





# Genome-Wide Association Study

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# Single- Nucleotide Polymorphism ("SNP")



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AA

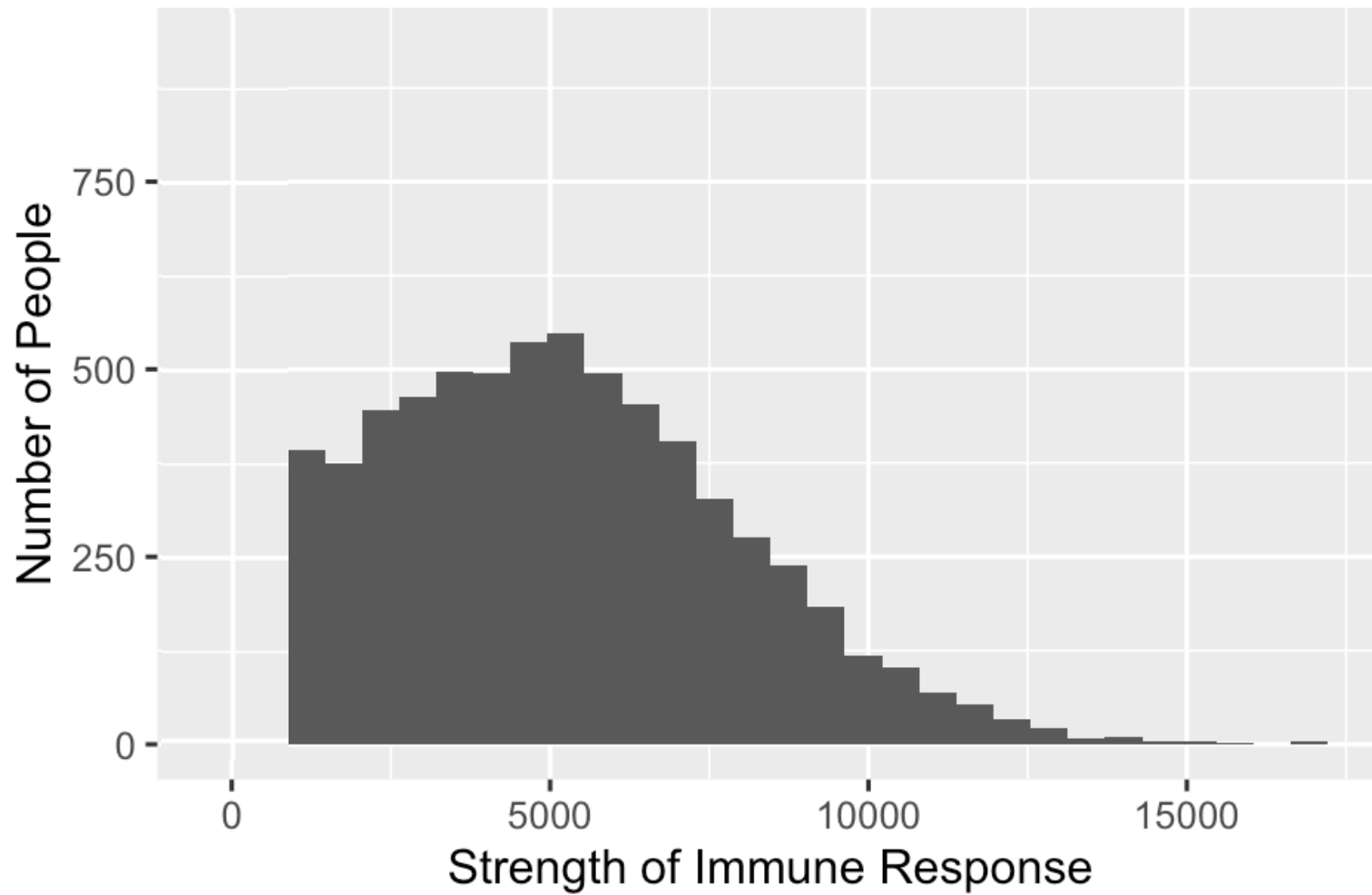
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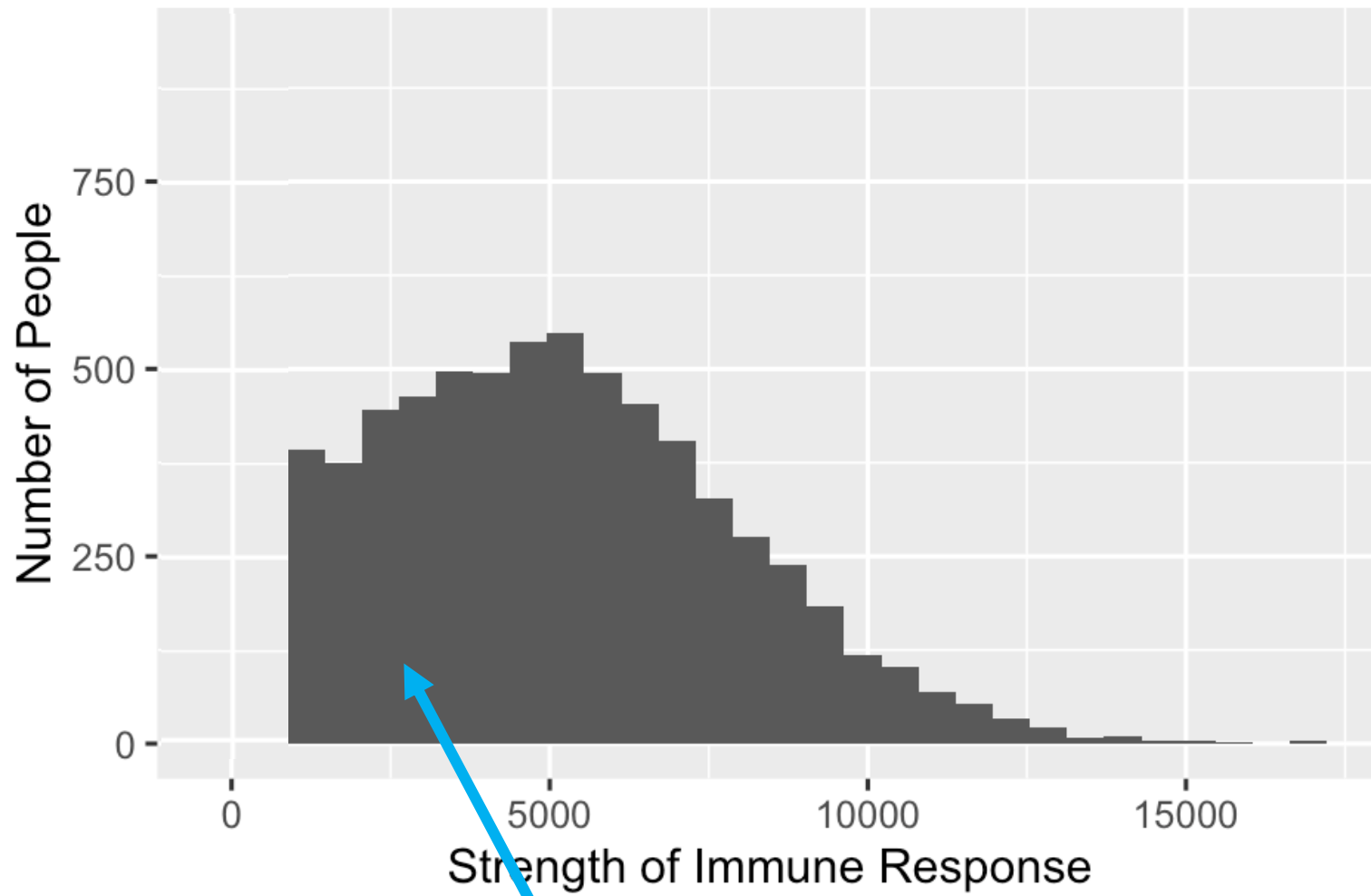


GG



**Single-  
Nucleotide  
Polymorphism  
("SNP")**

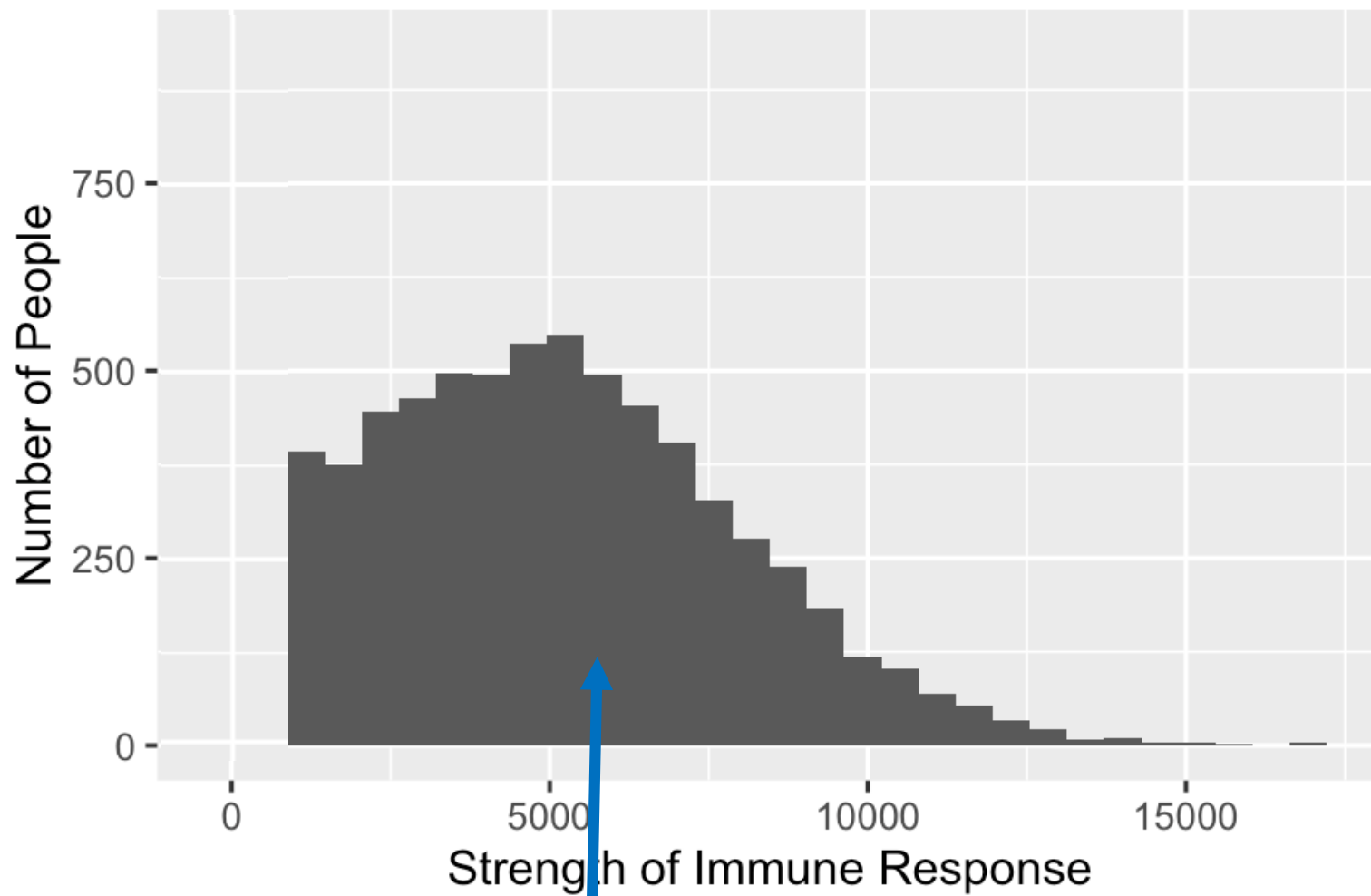




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**AA**

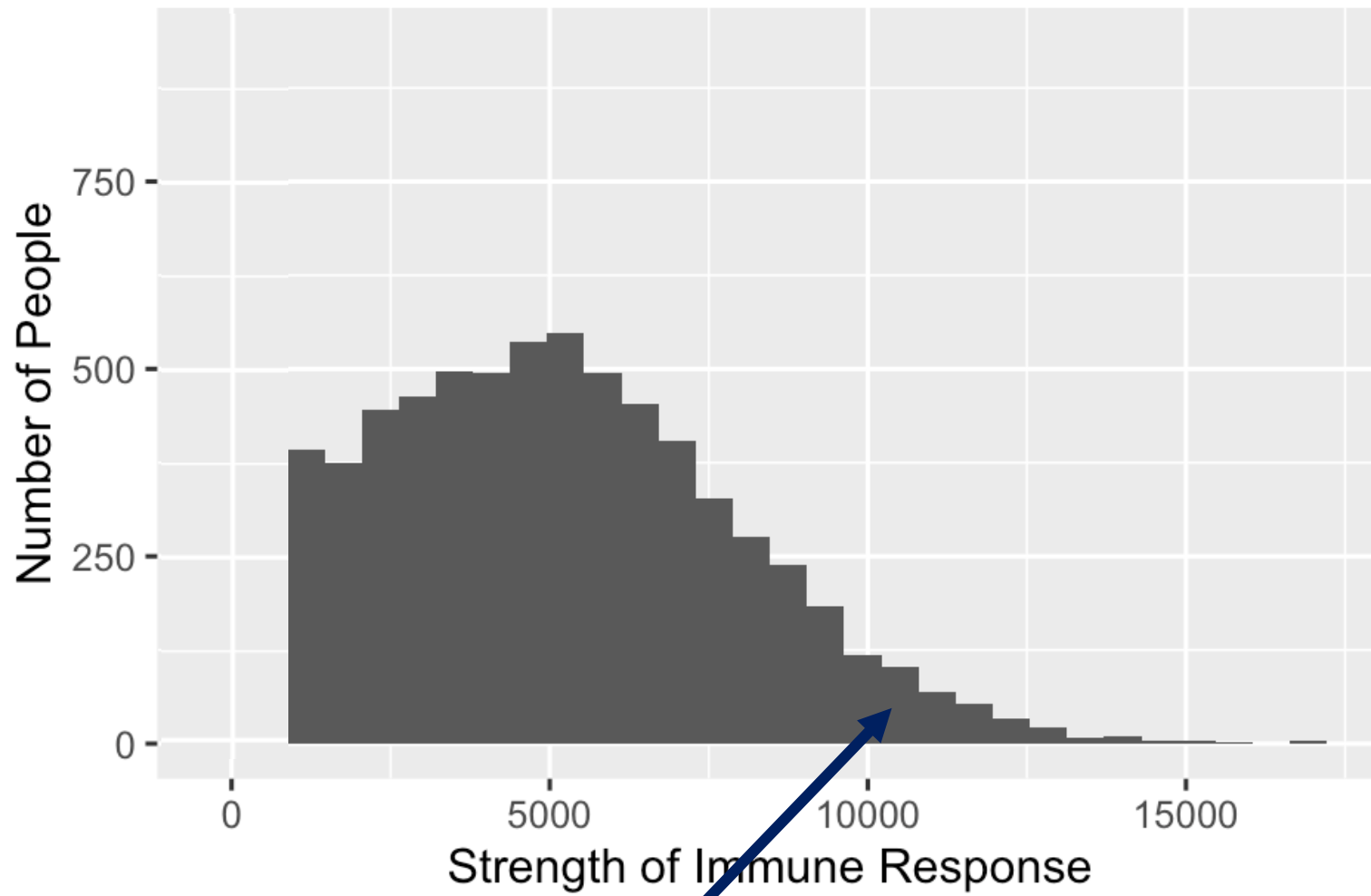


**Single-  
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**AG**

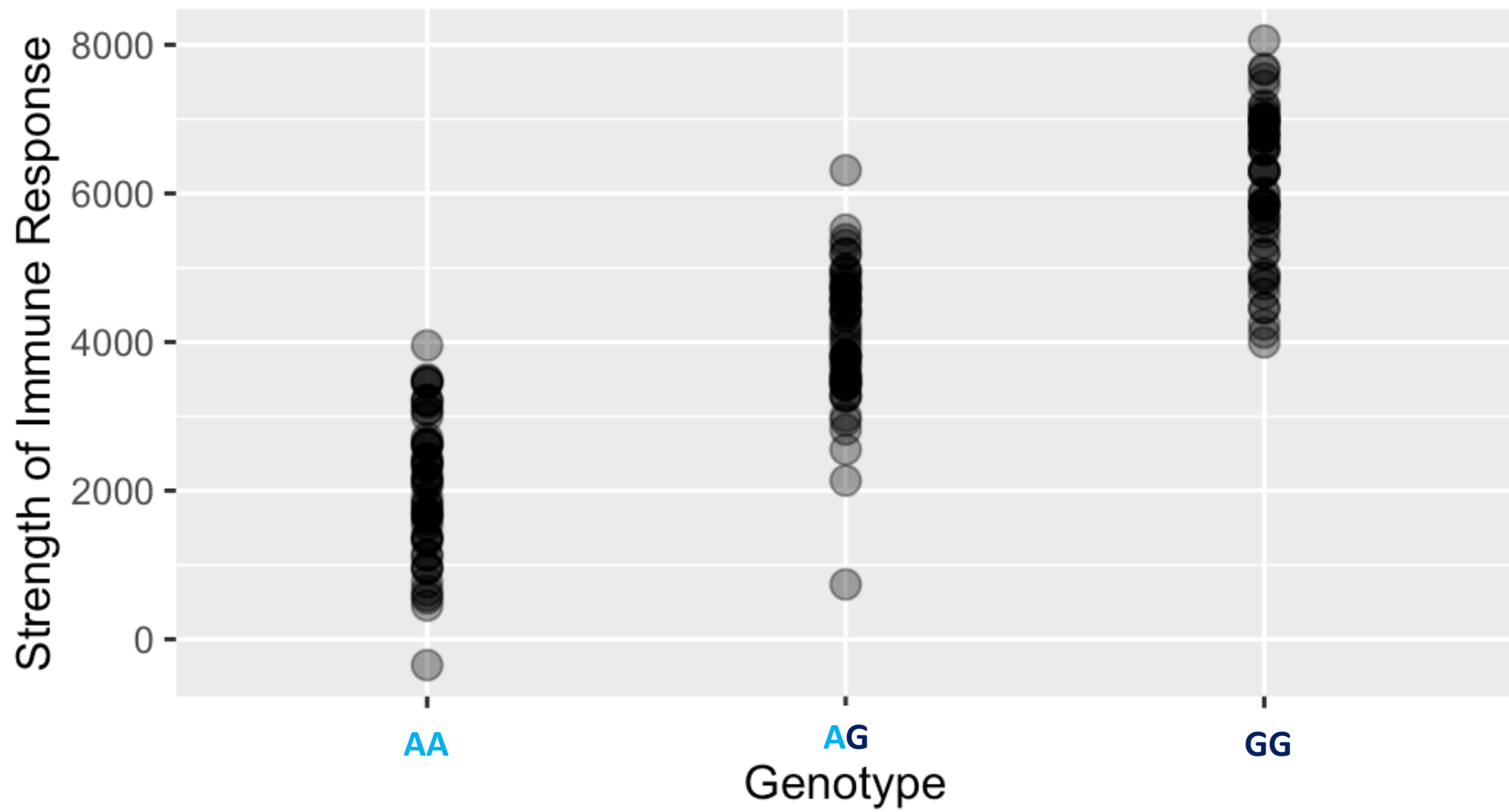


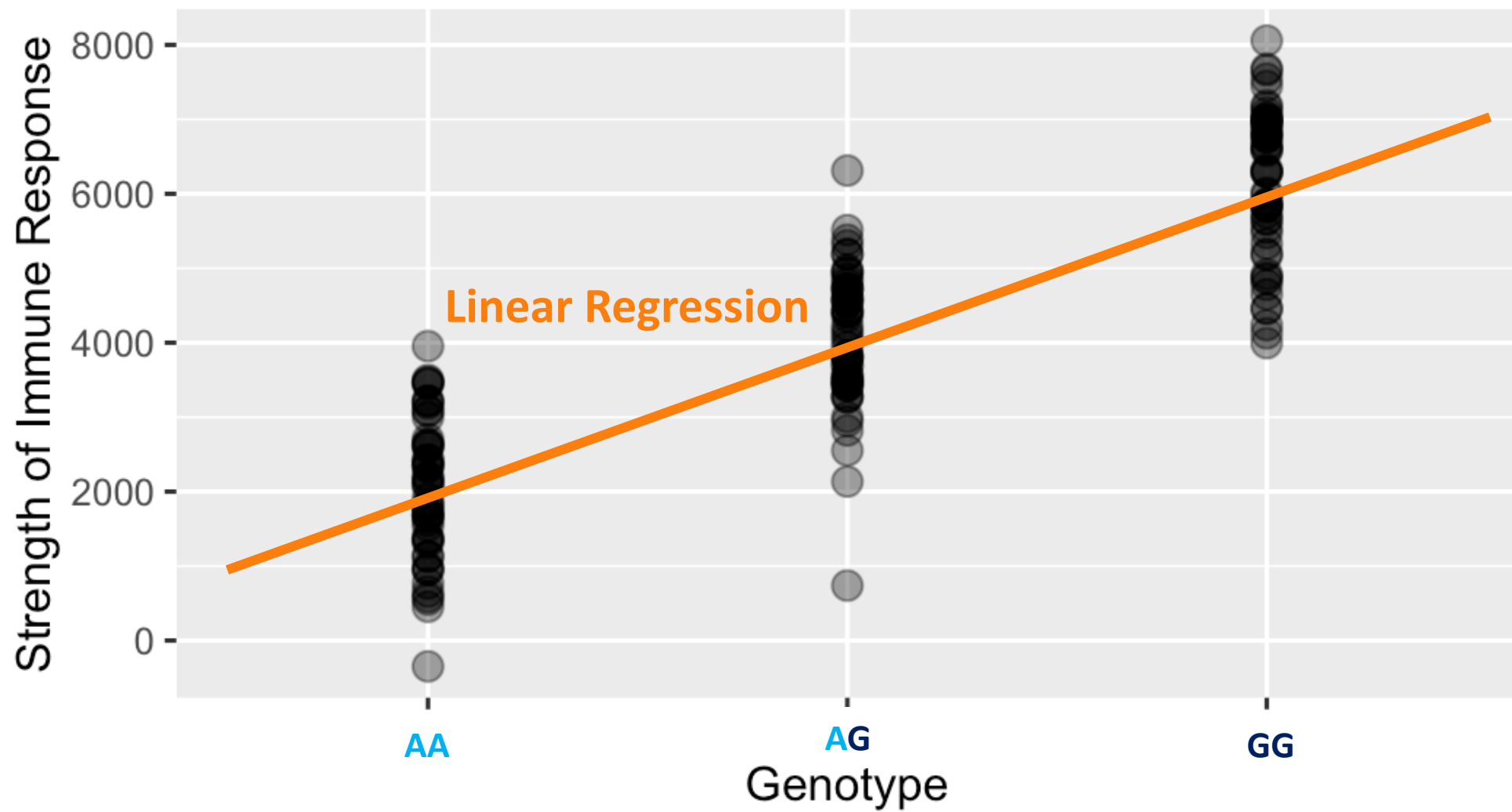


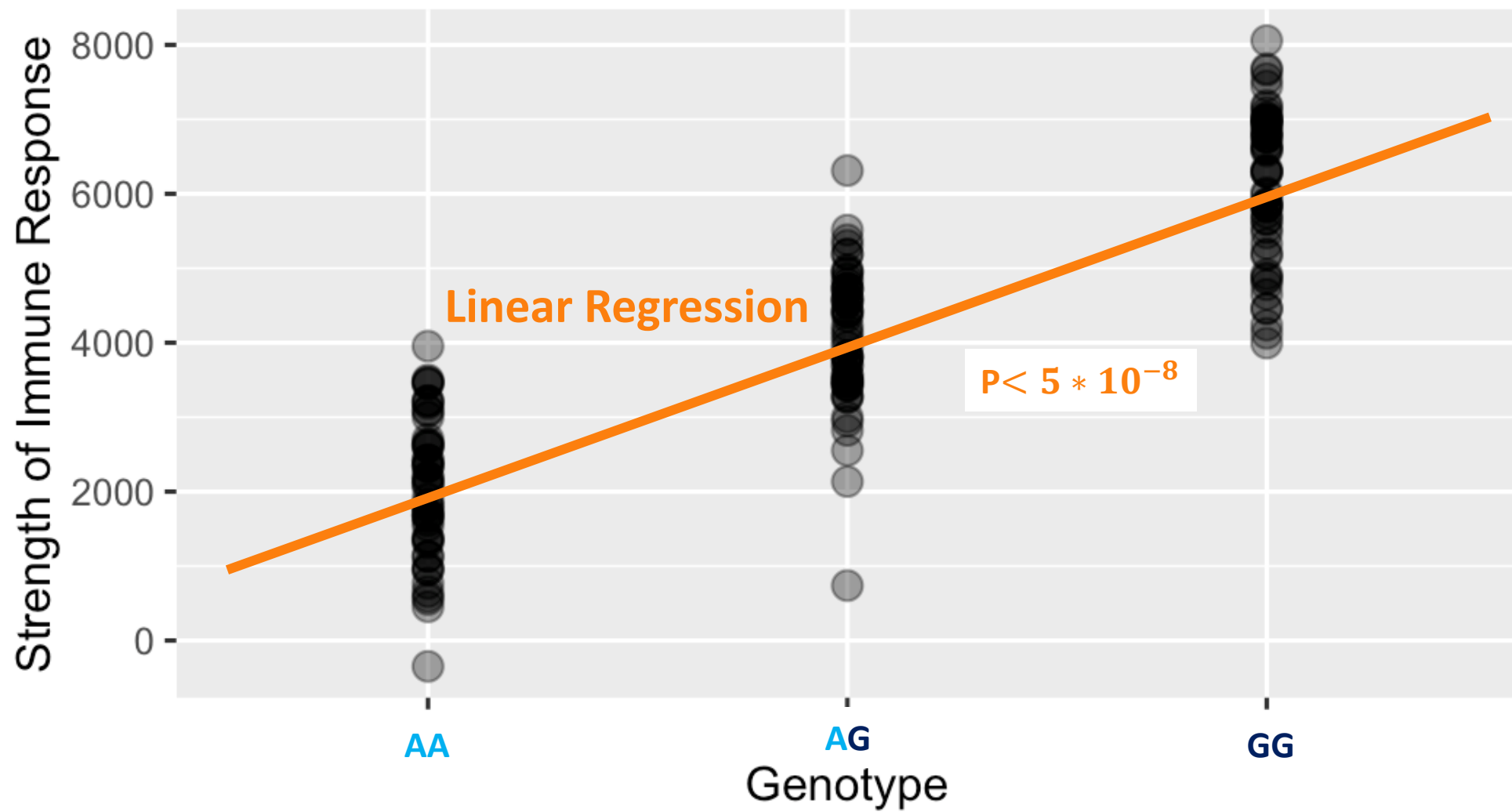
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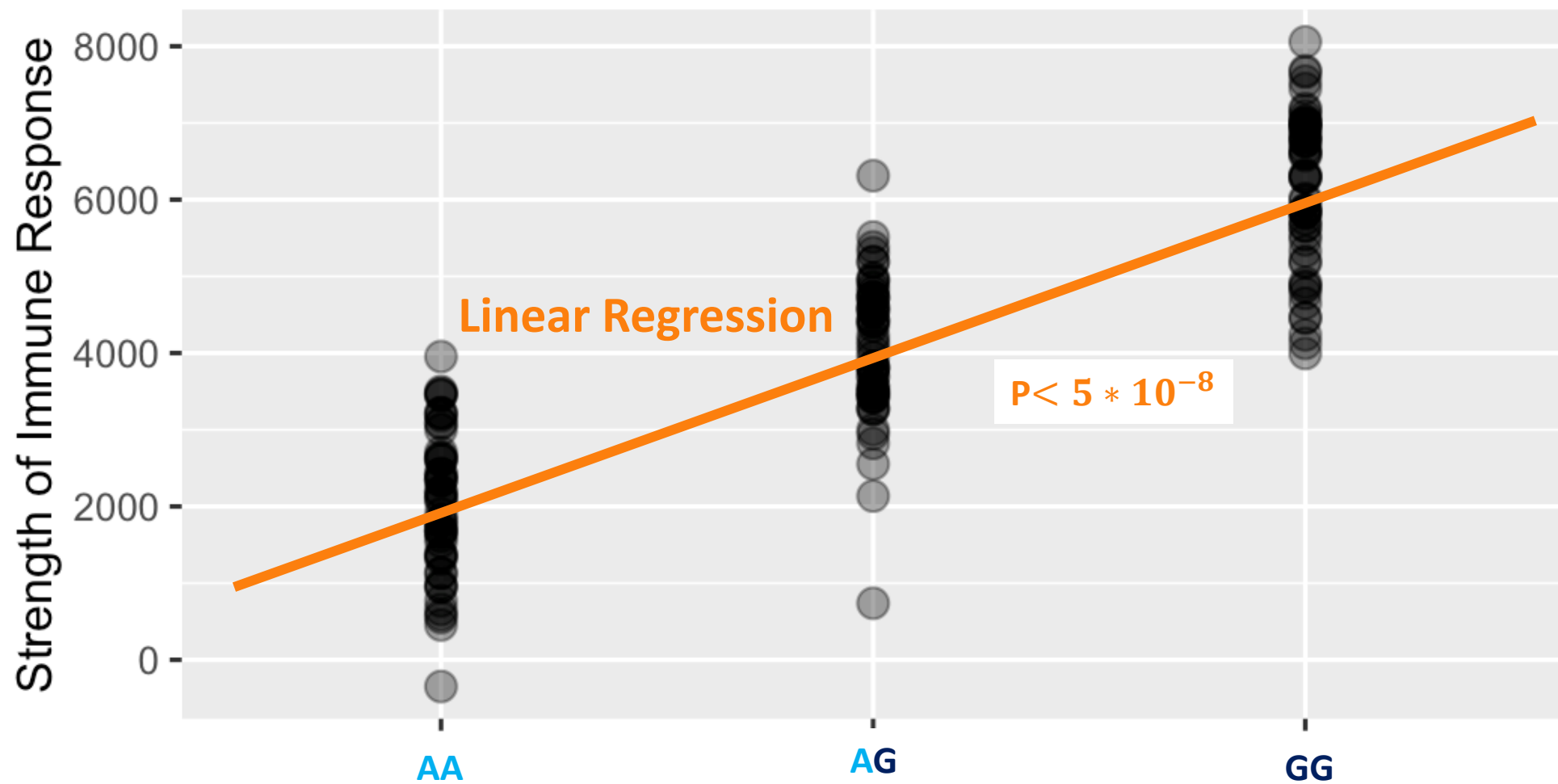


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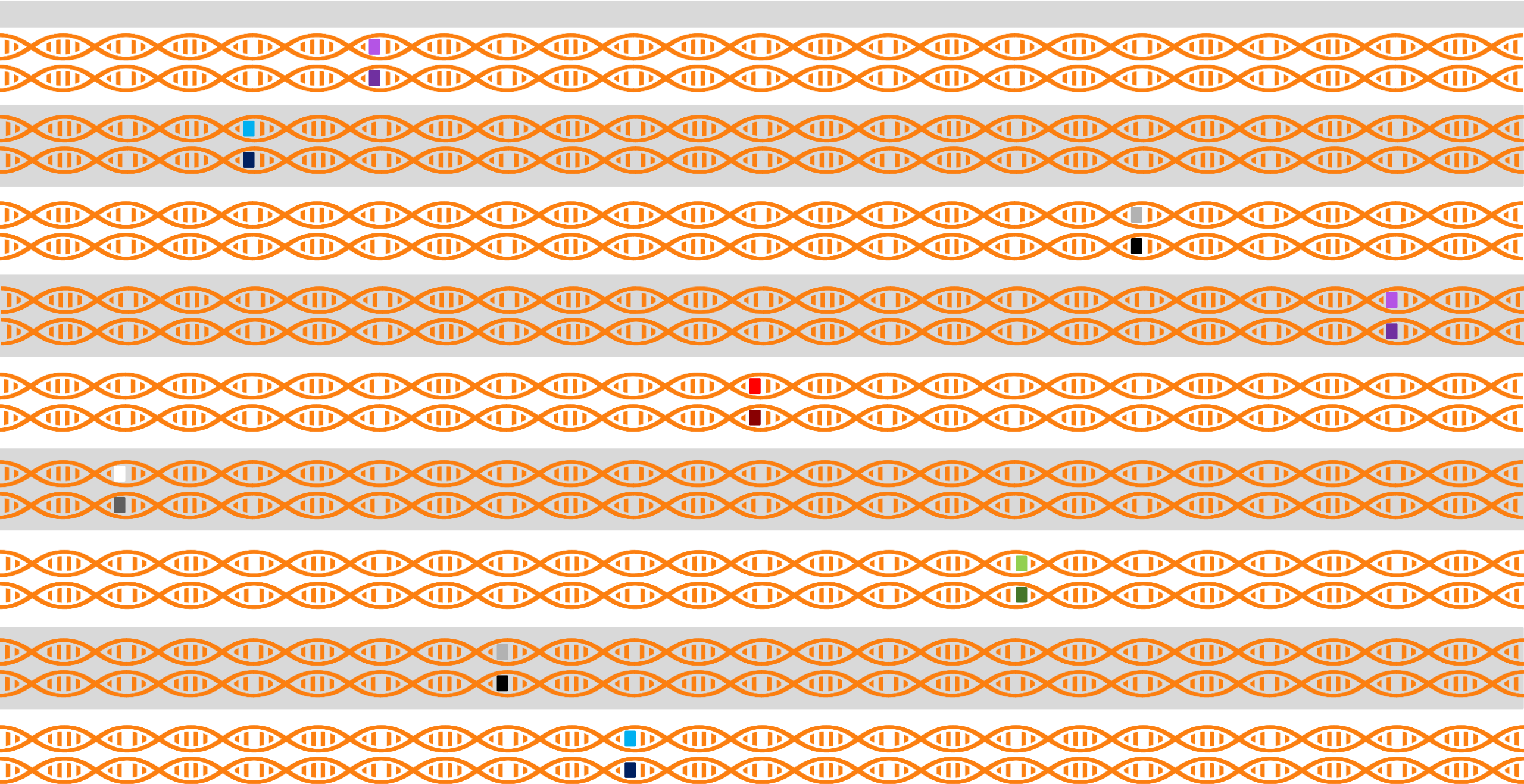






$$y = \beta_0 + \beta_1 \times (G \in \{0, 1, 2\}) + \beta_{\text{Age}} \times (\text{Age}) + \dots + \epsilon$$





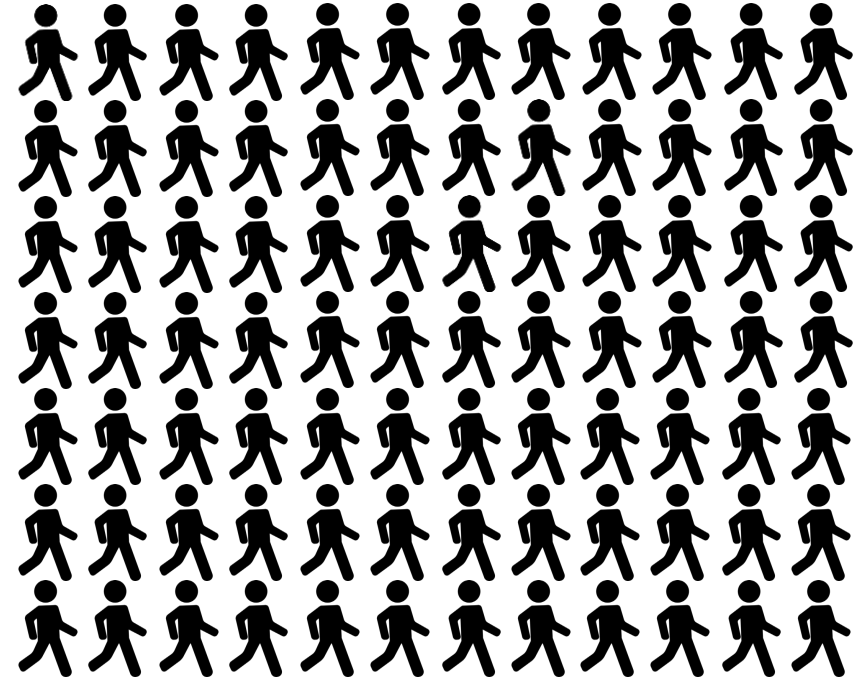
We analyzed many different SNPs throughout the genome.

# Data

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## UK Biobank:

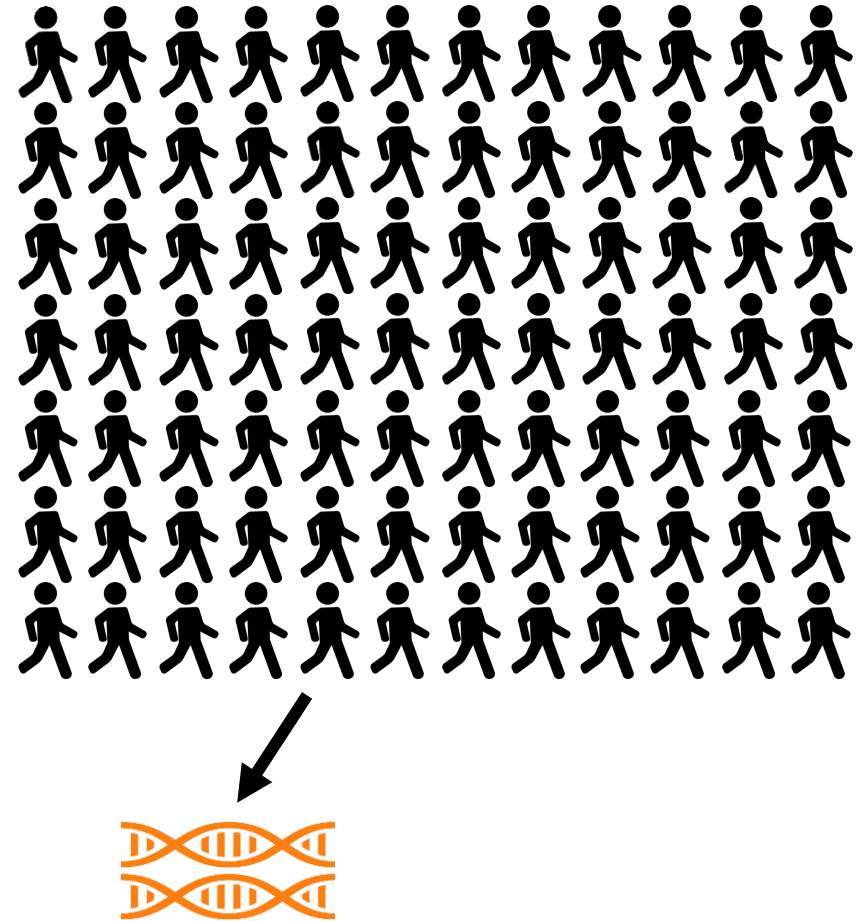
- ~500,000 individuals recruited (2006-2010)
- Aged 40-69 at time of recruitment



# Data

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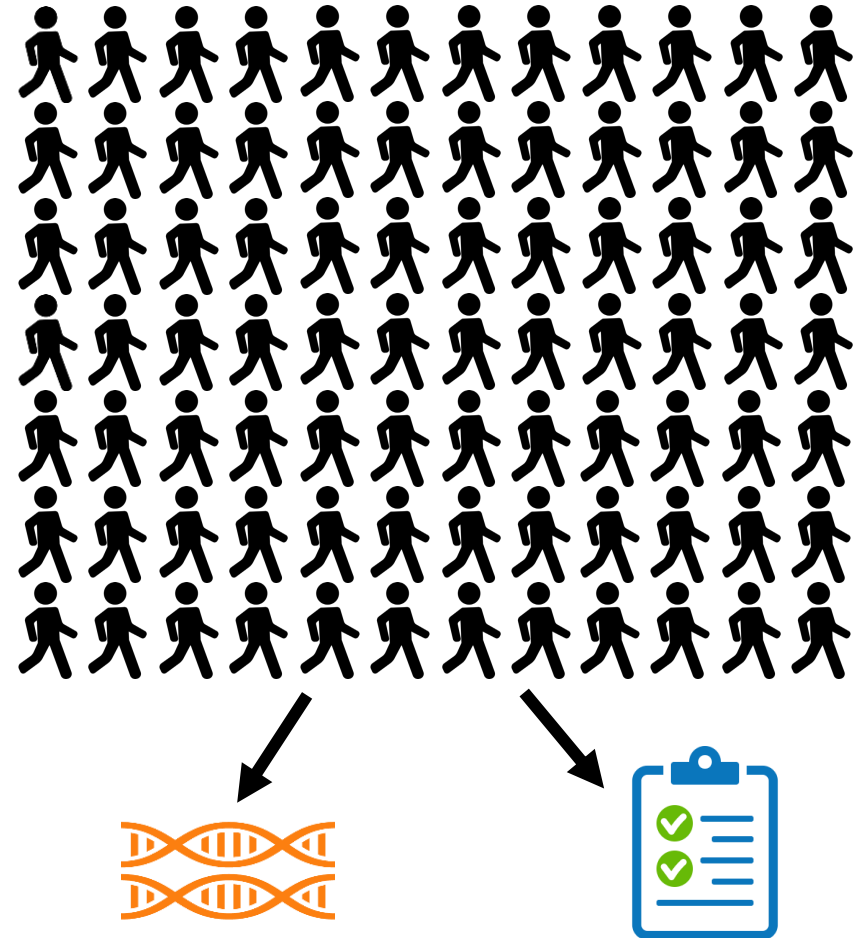




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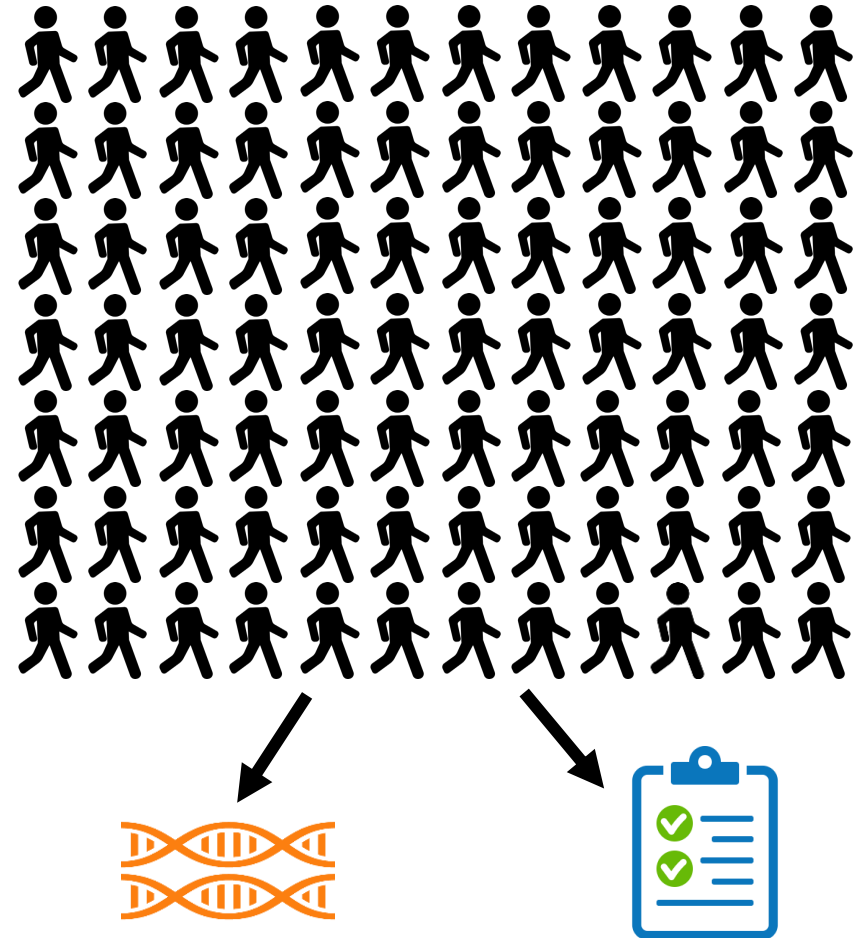
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## Pilot Study:

- ~8,000 individuals of European ancestry



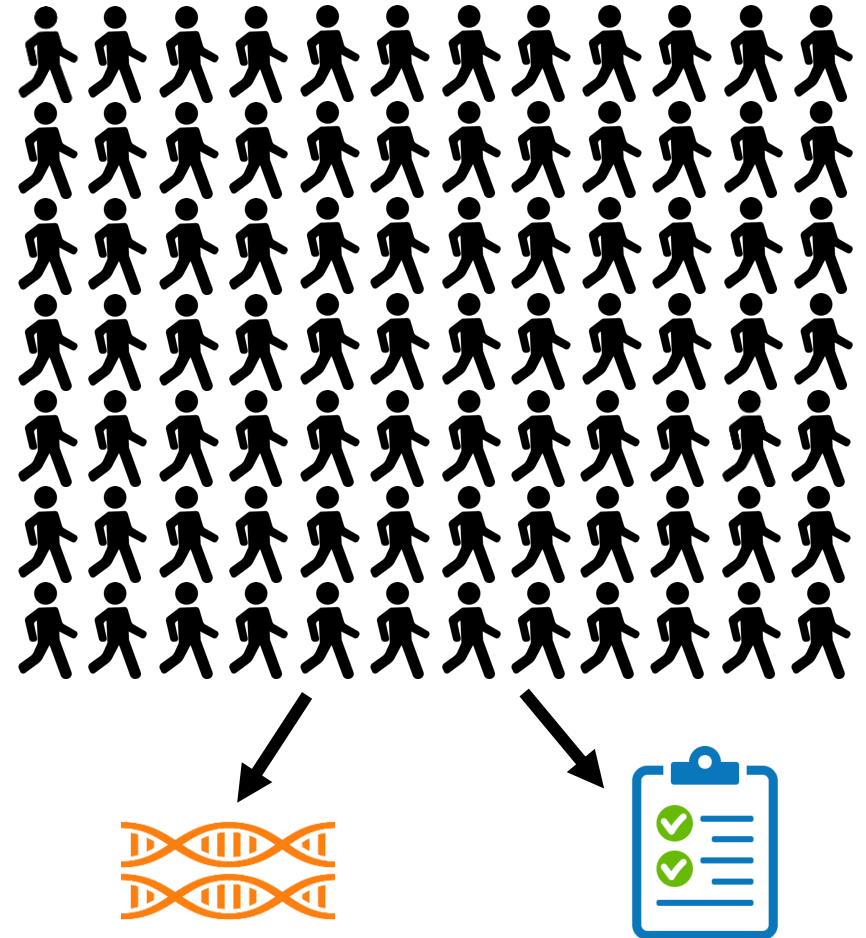
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- Thousands of phenotypes

## Pilot Study:

- ~8,000 individuals of European ancestry
- Hundreds of biomarkers
  - Includes 44 antibodies
  - 22 antibodies with seroprevalence  $>20\%$



# Data

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## 12 Pathogens:

- Herpes Simplex virus-1
- Varicella Zoster Virus (Chickenpox)
- Epstein-Barr Virus
- Human Cytomegalovirus
- Human Herpesvirus-6
- Human Herpesvirus-7
- Human Polyomavirus BKV
- Human Polyomavirus JCV
- Merkel Cell Polyomavirus
- *Chlamydia trachomatis*
- *Helicobacter pylori*
- *Toxoplasma gondii*

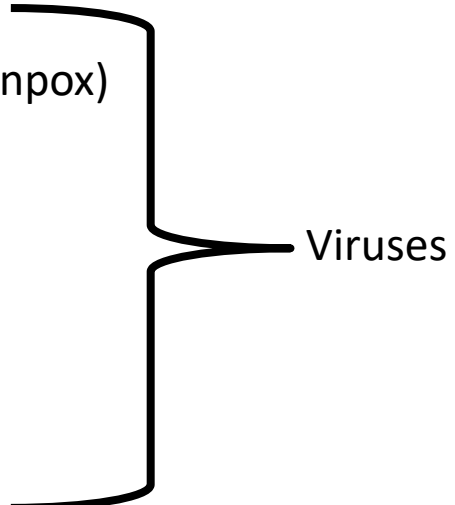
**Total of 22 antibodies against these pathogens**

**Each antigen's seroprevalence >20%**

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- Viruses

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- 
- The diagram uses curly braces to group the pathogens. A large brace on the right side of the first nine items (all viruses) is labeled 'Viruses'. A smaller brace on the right side of the last three items (all bacteria) is labeled 'Bacteria'.

**Total of 22 antibodies against these pathogens**

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- The diagram uses curly braces to group the pathogens into three categories:
- Viruses:** A large curly brace on the right groups the first nine pathogens (Herpes Simplex virus-1 through Merkel Cell Polyomavirus).
  - Bacteria:** A curly brace on the right groups the last two pathogens (*Chlamydia trachomatis* and *Helicobacter pylori*).
  - Parasite:** A horizontal line on the right connects the final pathogen (*Toxoplasma gondii*) to the label.

**Total of 22 antibodies against these pathogens**

**Each antigen's seroprevalence >20%**

# Data

---

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  - Varicella Zoster Virus (Chickenpox)
  - Epstein-Barr Virus
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- Viruses
- Bacteria
- Parasite

**These pathogens are risk factors for cancer and cardiovascular or neurodegenerative diseases.**

**Total of 22 antibodies against these pathogens**  
**Each antigen's seroprevalence >20%**



# Data

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## **Covariates for all regression models:**

- Age
- Sex
- Body mass index
- Genotyping array
- Antigen assay date
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$$y = \beta_0 + \beta_1 \times (G \in \{0, 1, 2\}) + \beta_{\text{Age}} \times (\text{Age}) + \cdots + \epsilon$$

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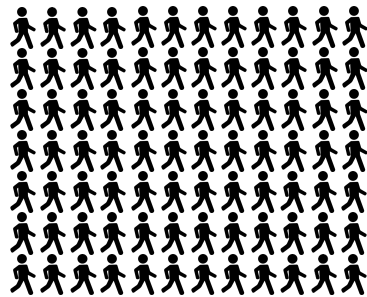
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# Methods - Summary

UK Biobank Data



N=8,000

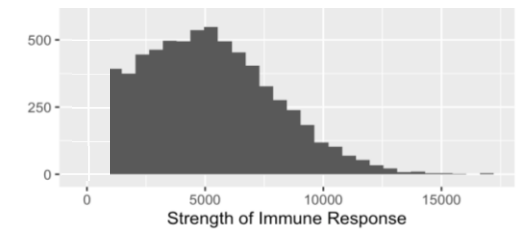


22 common  
antibodies  
(12 pathogens)



Genome-Wide  
Association Study

$$y = \beta_0 + \beta_1 \times (G \in \{0, 1, 2\}) + \dots + \epsilon$$



???



# Results

- Found associated SNPs for **17 antigens** against **10 pathogens**

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- **99** independent ( $R^2 < 0.05$ ) SNPs ( $P < 5 \times 10^{-8}$ )

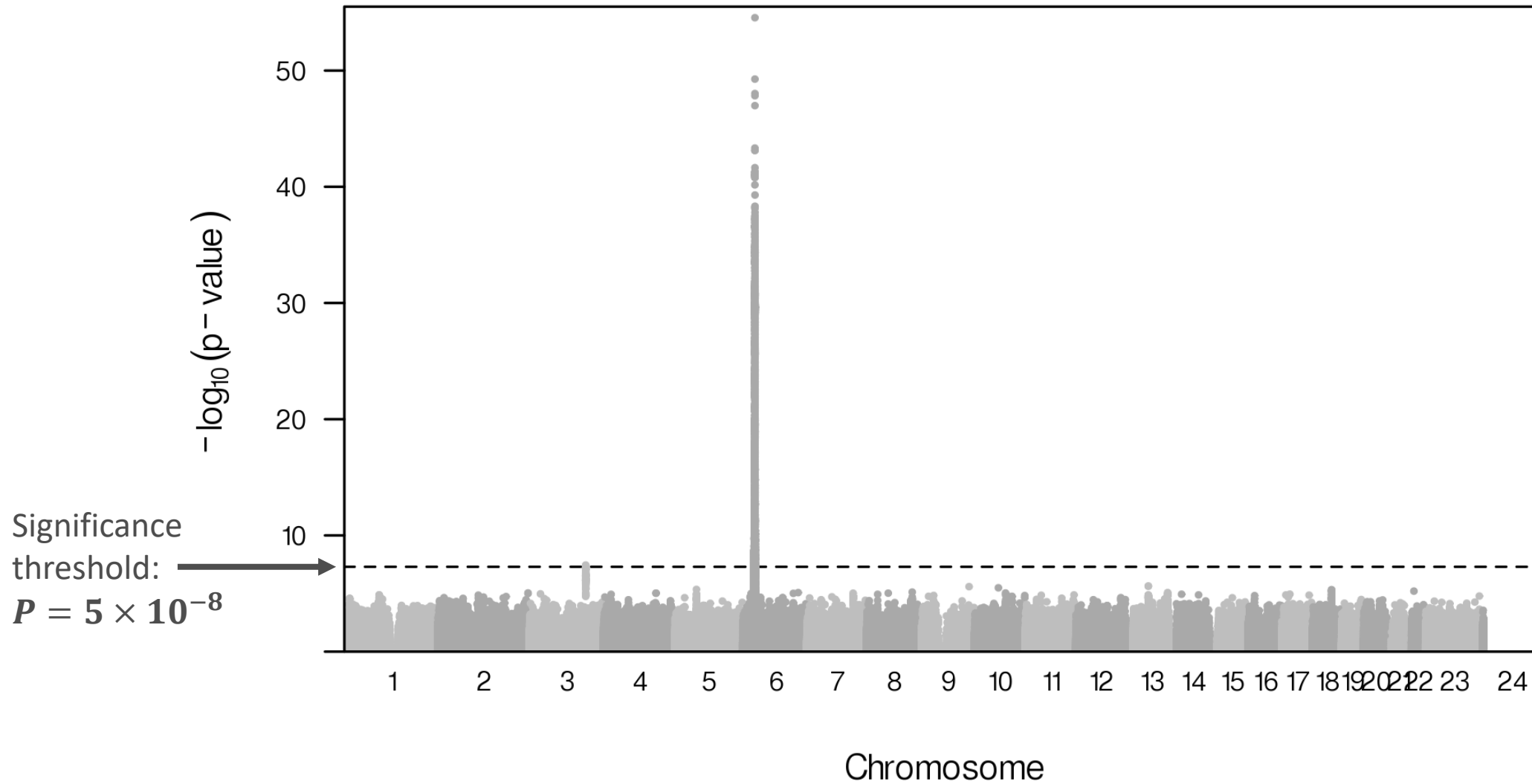
# Results

- Found associated SNPs for **17 antigens** against **10 pathogens**
- **99** independent ( $R^2 < 0.05$ ) SNPs ( $P < 5 \times 10^{-8}$ )
- **47** of these SNPs lie within genes (45 distinct genes)
  - Many genes associated with autoimmunity, inflammation, and vaccine response



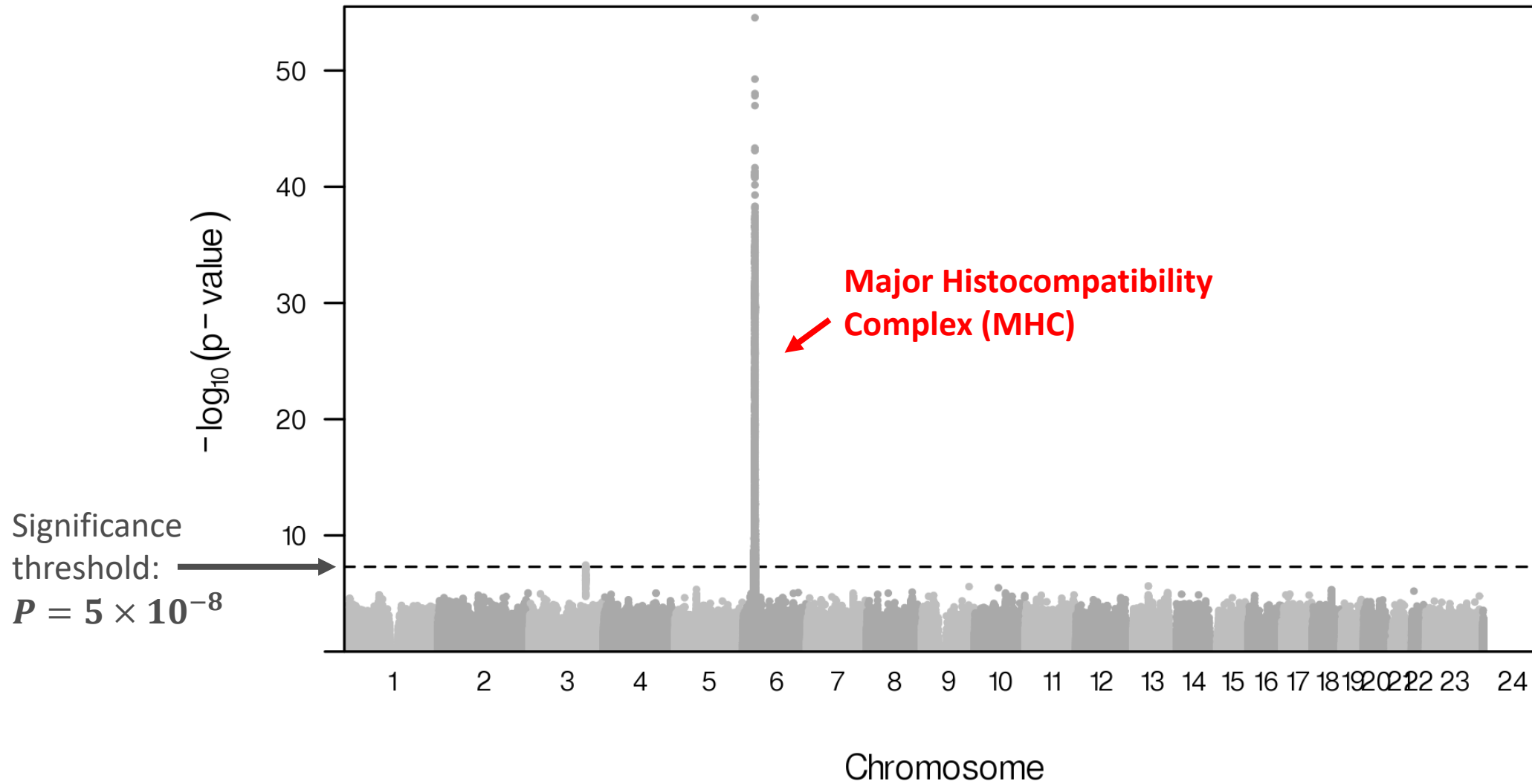
# EBNA-1 Antigen for N = 6845

## Epstein-Barr Virus



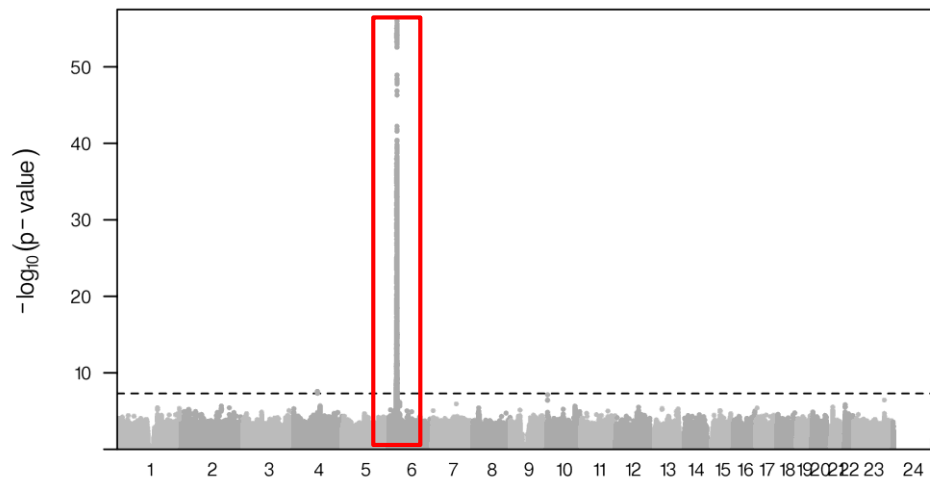
# EBNA-1 Antigen for N = 6845

## Epstein-Barr Virus



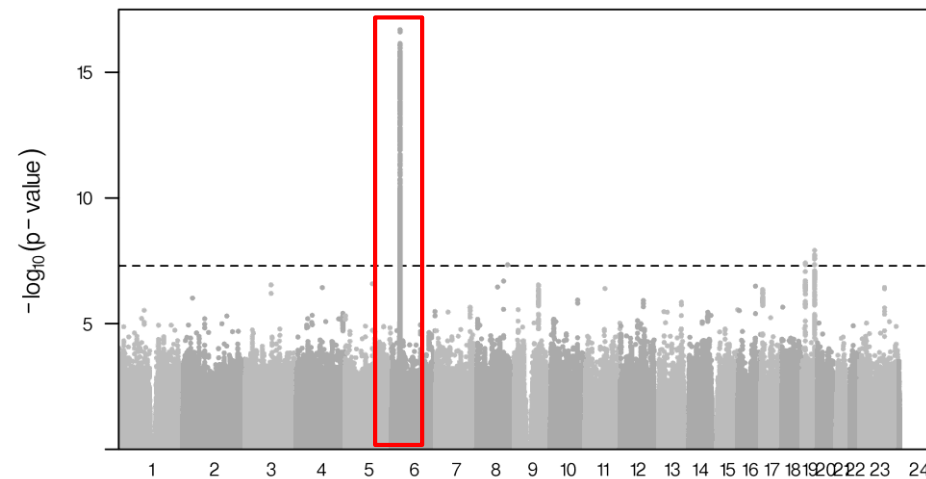
ZEBRA Antigen for  
Epstein-Barr Virus

N = 7033



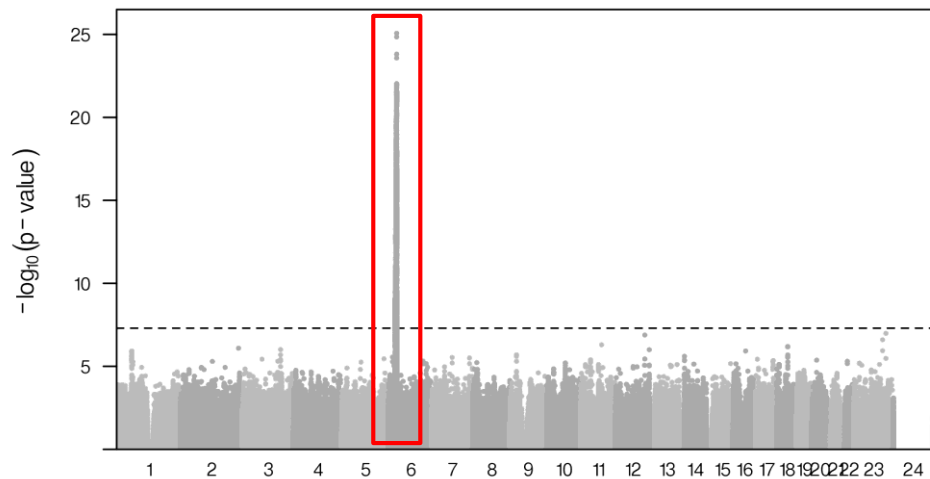
JC VP1 Antigen for  
Human Polyomavirus JCV

N = 4367



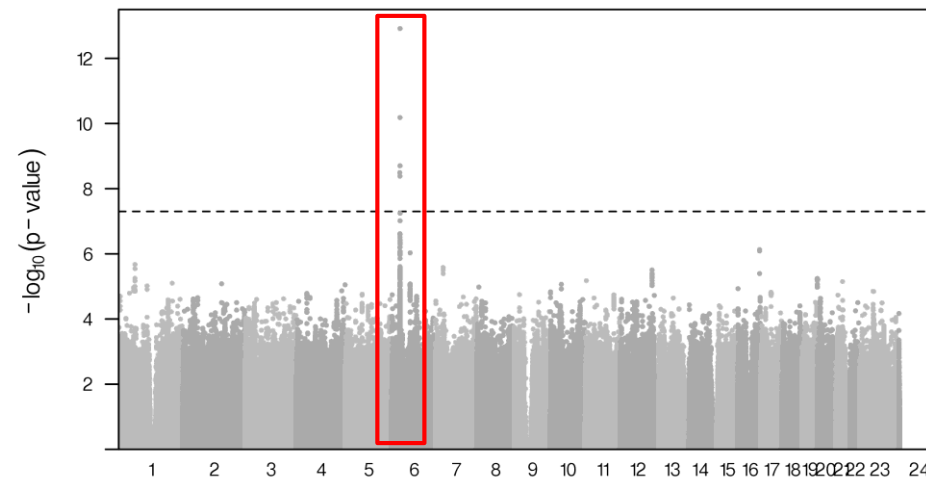
gE/gI Antigen for  
Varicella Zoster Virus

N = 7124



pp52 Antigen for  
Human Cytomegalovirus

N = 4881

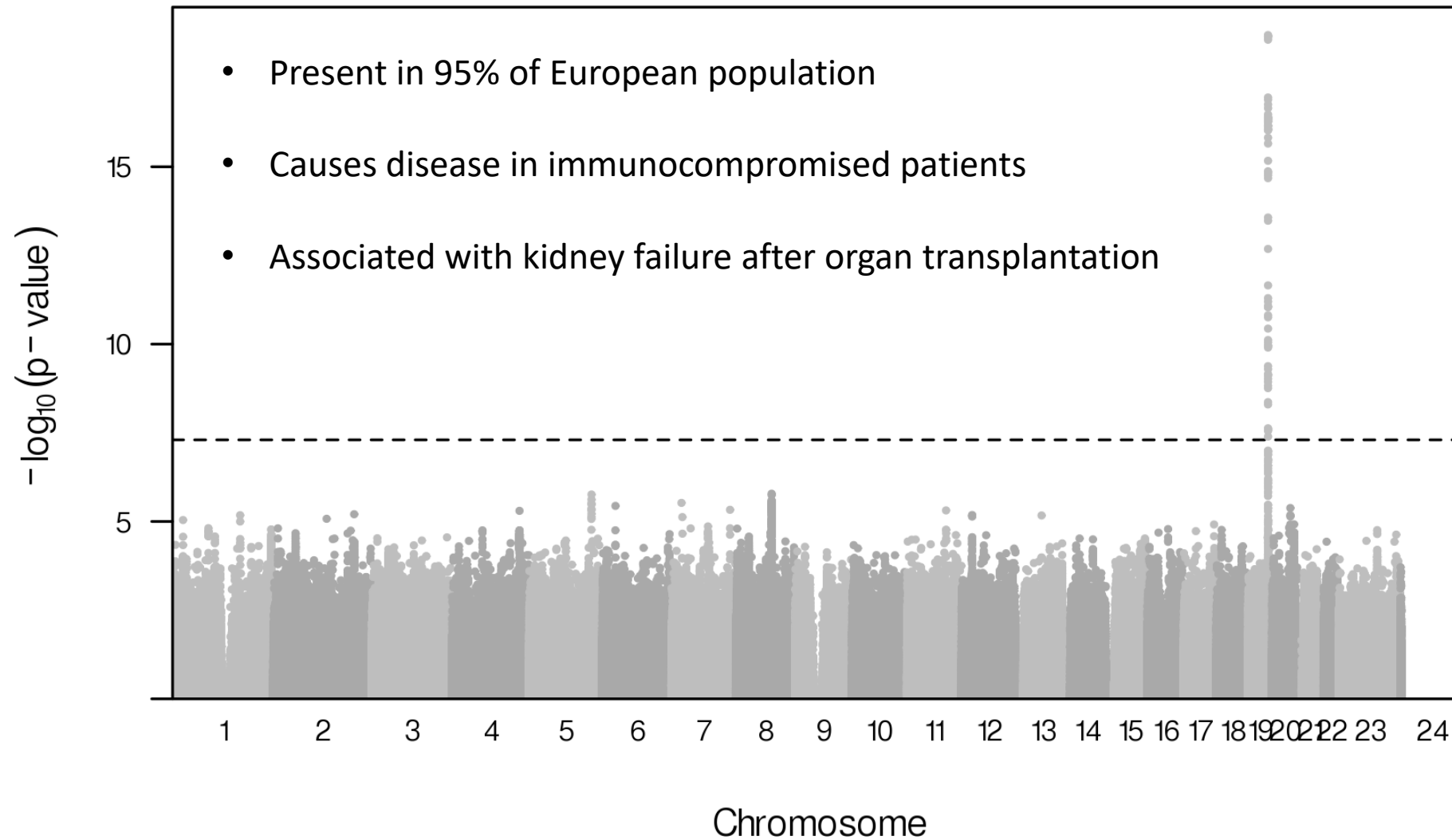


Chromosome

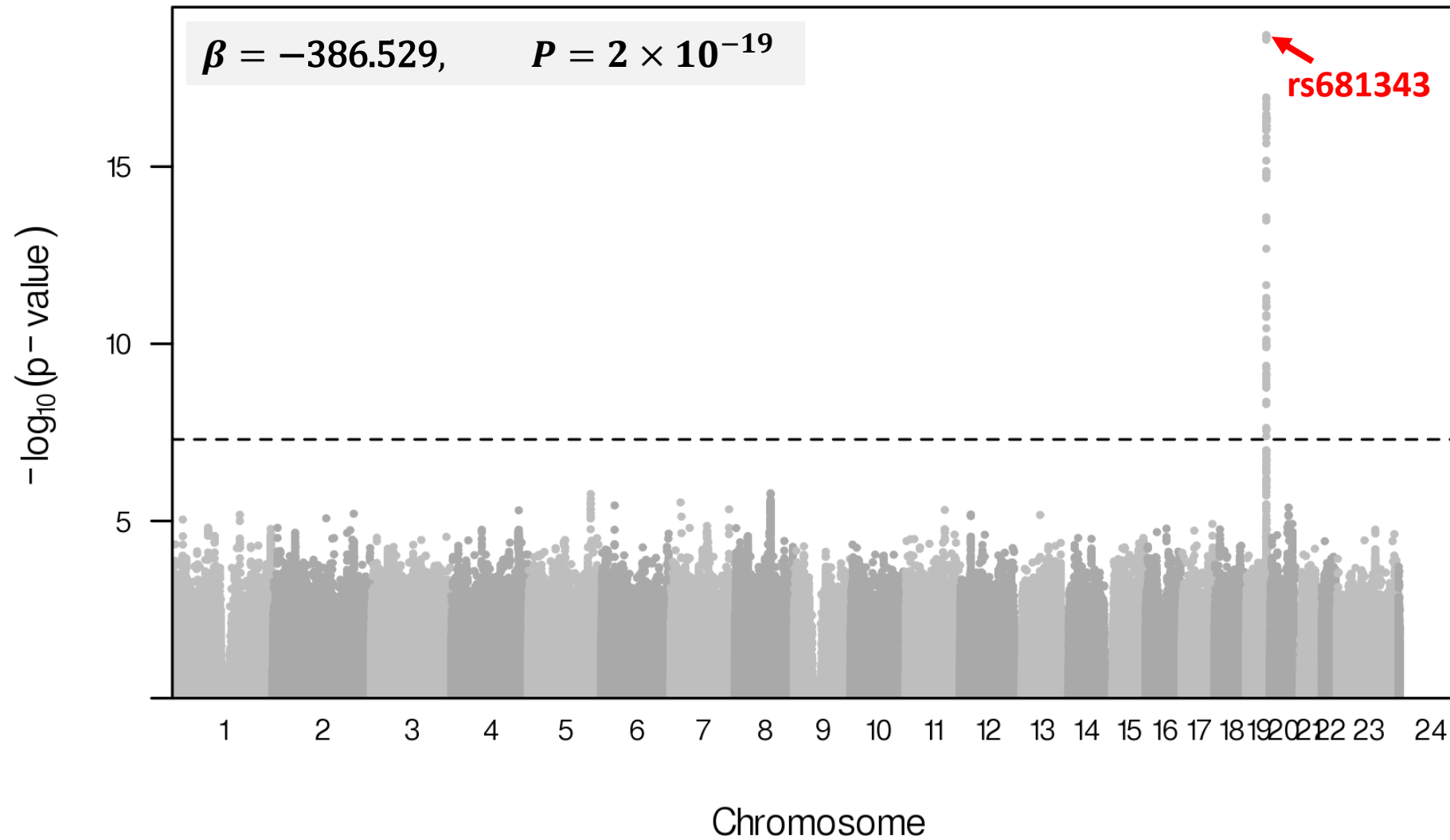
Chromosome

We identified **45** independent SNPs in the Major Histocompatibility Complex

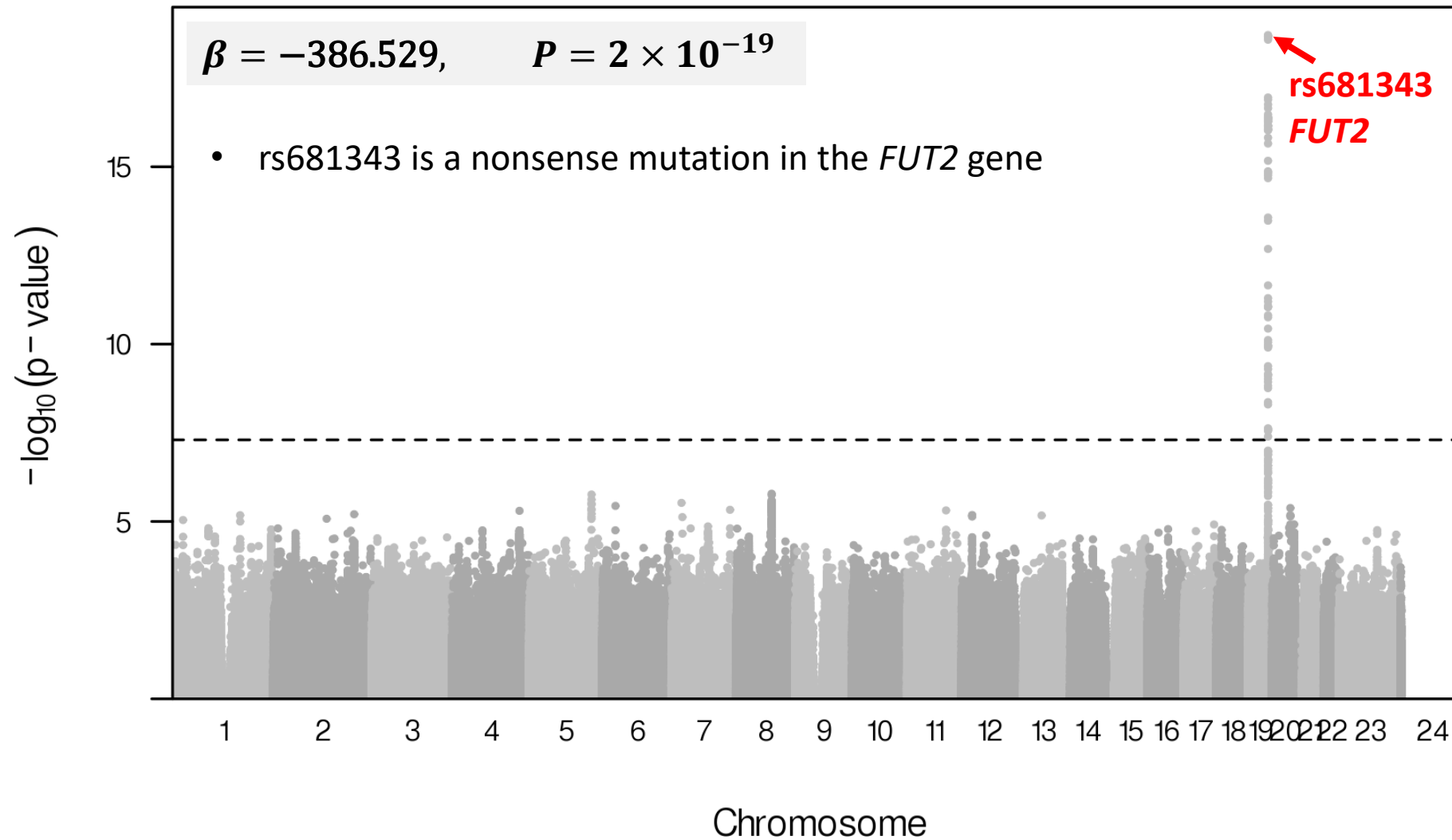
# BK VP1 Antigen for **N = 7349** **Human Polyomavirus BKV (PBKV)**



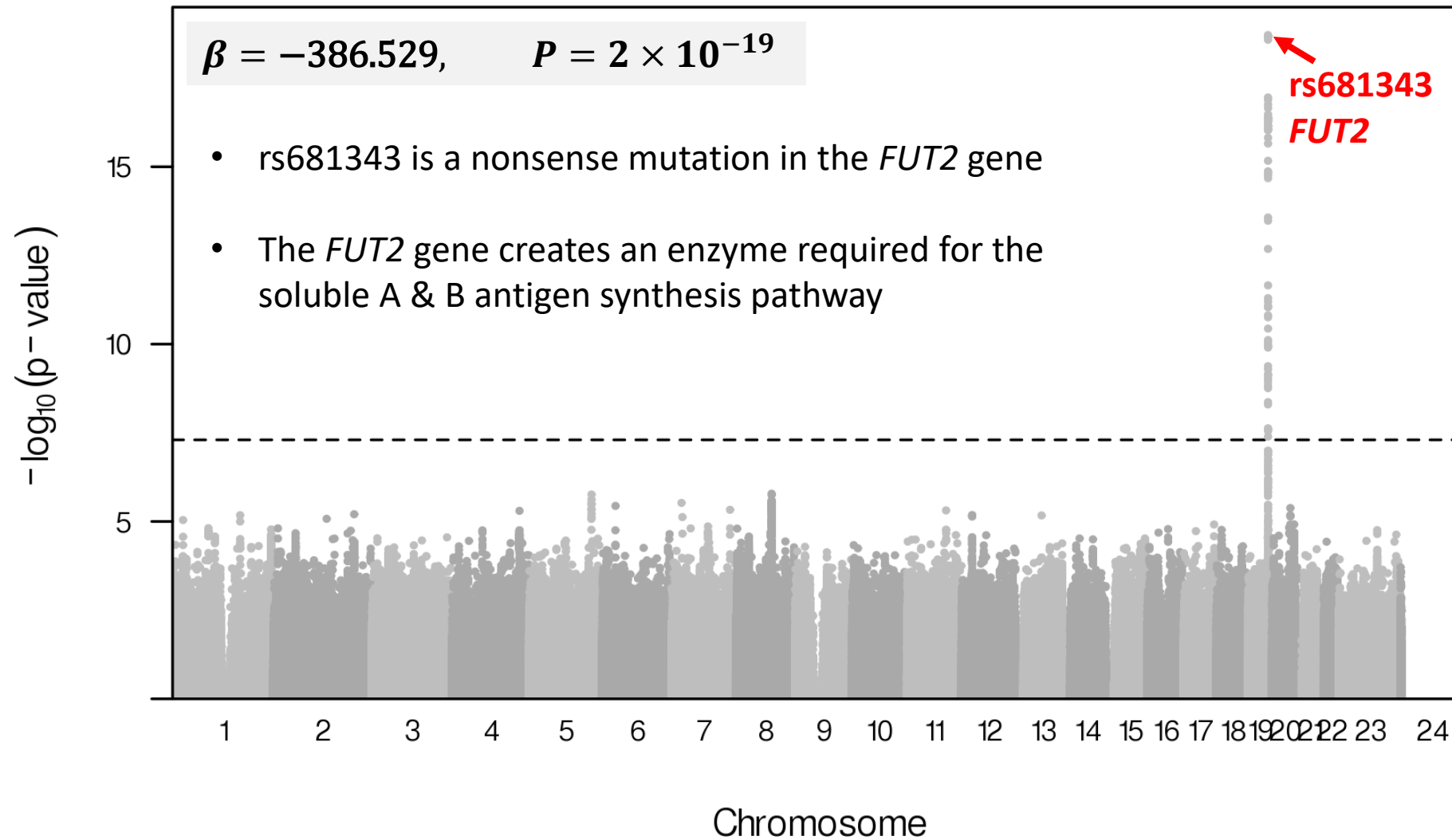
BK VP1 Antigen for **N = 7349**  
**Human Polyomavirus BKV (PBKV)**

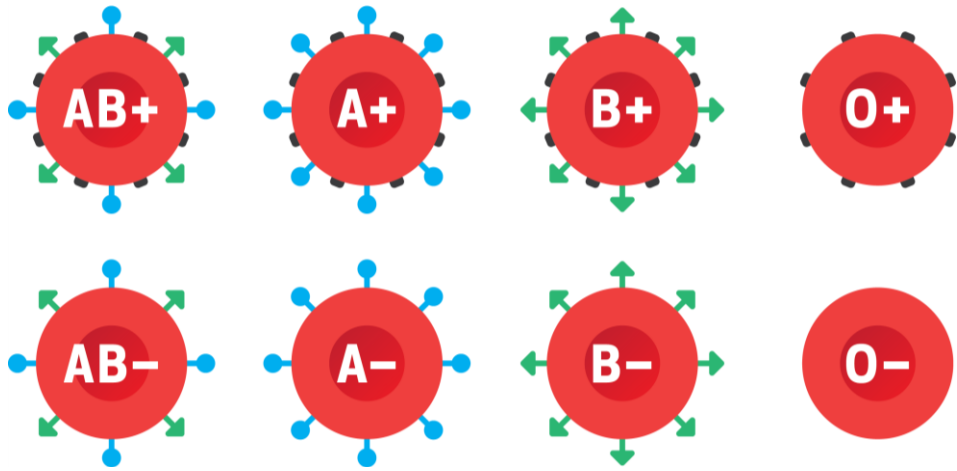


BK VP1 Antigen for **N = 7349**  
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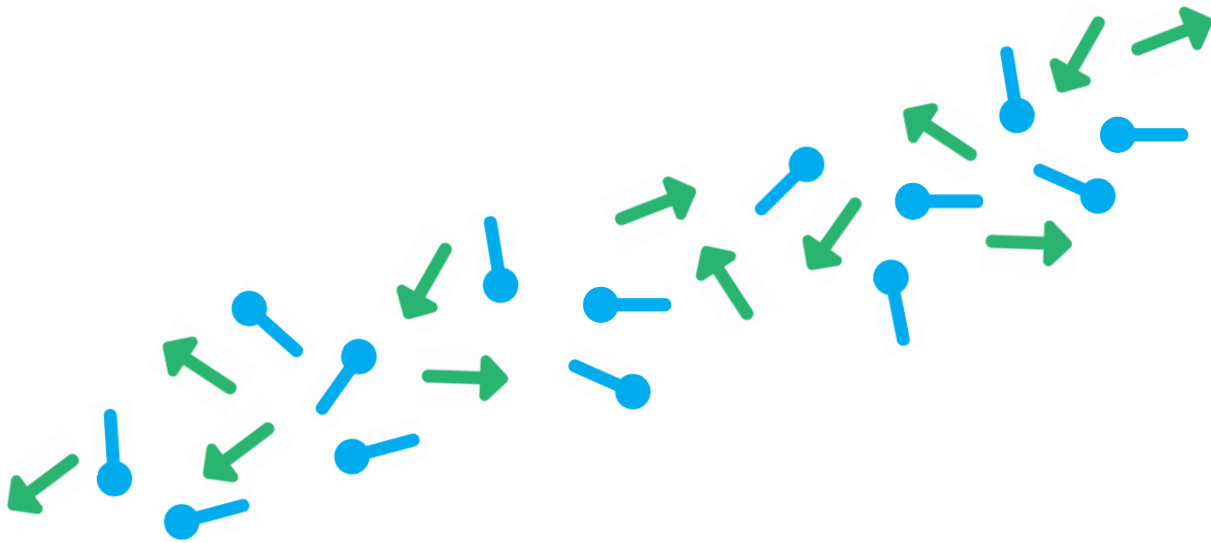
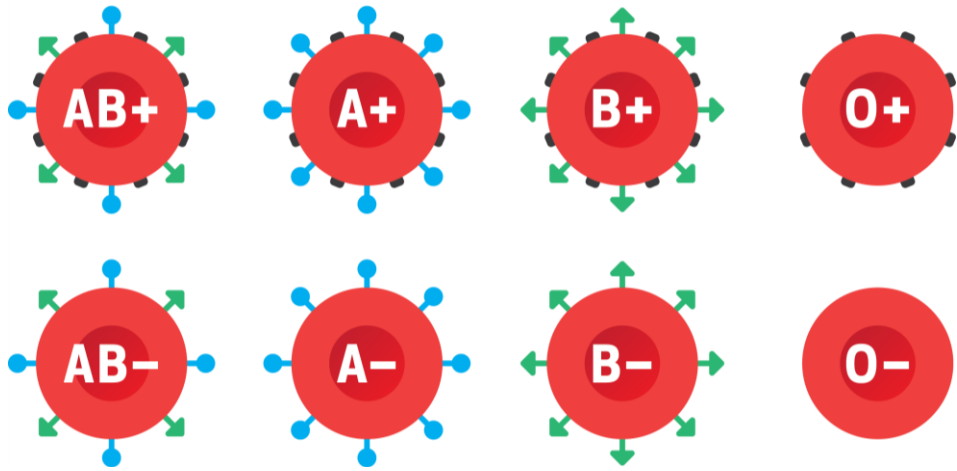


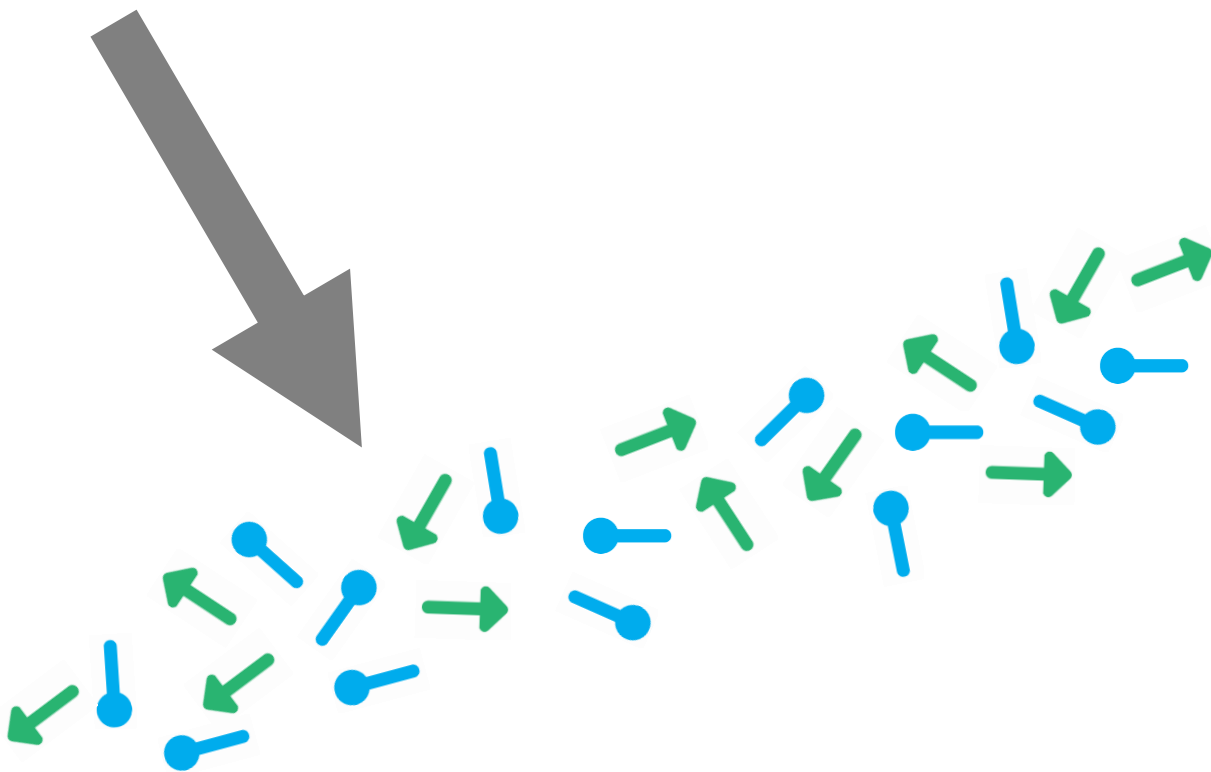
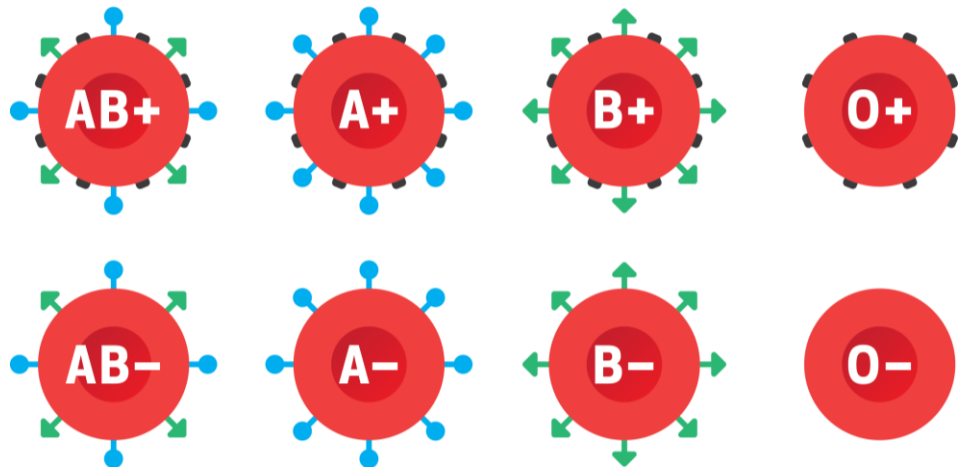
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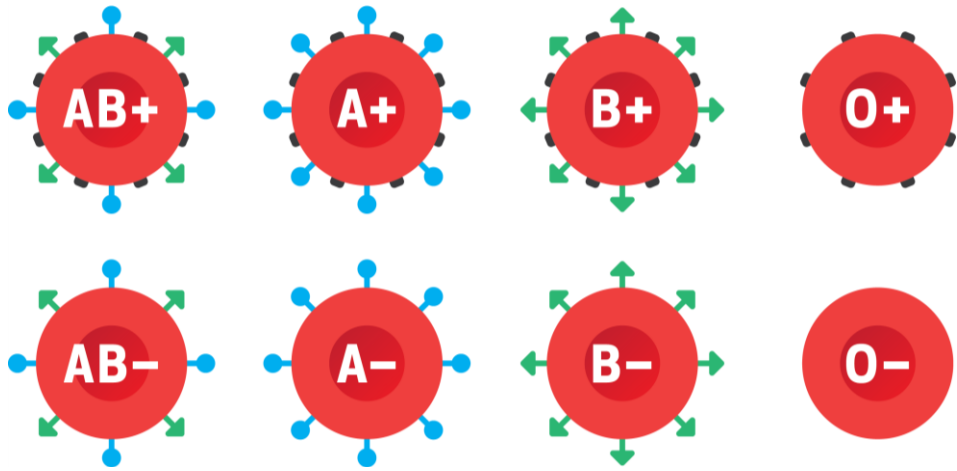




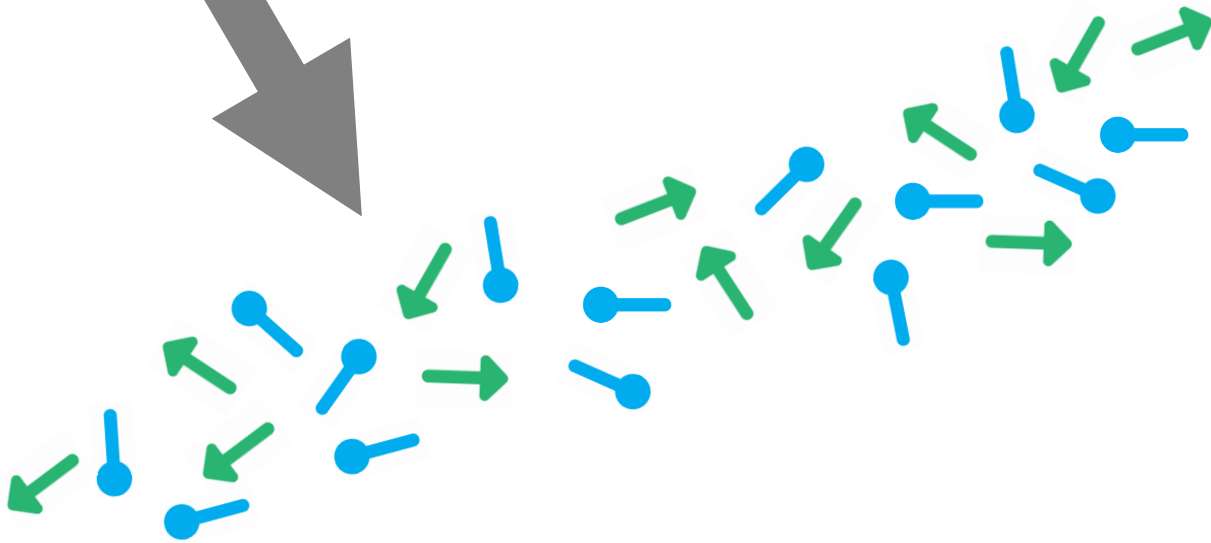


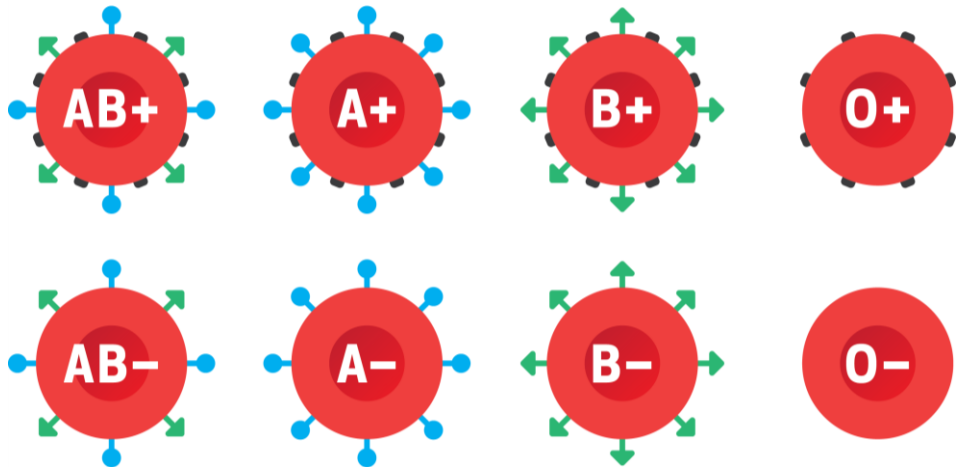




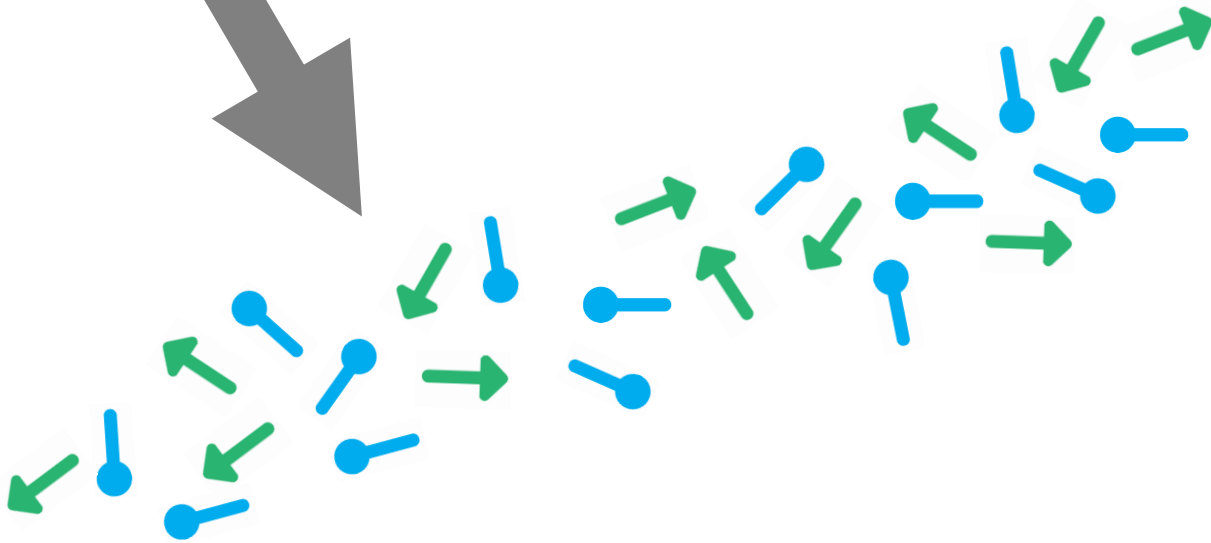


*FUT2* ( $\alpha$ 1,2fucosyltransferase )



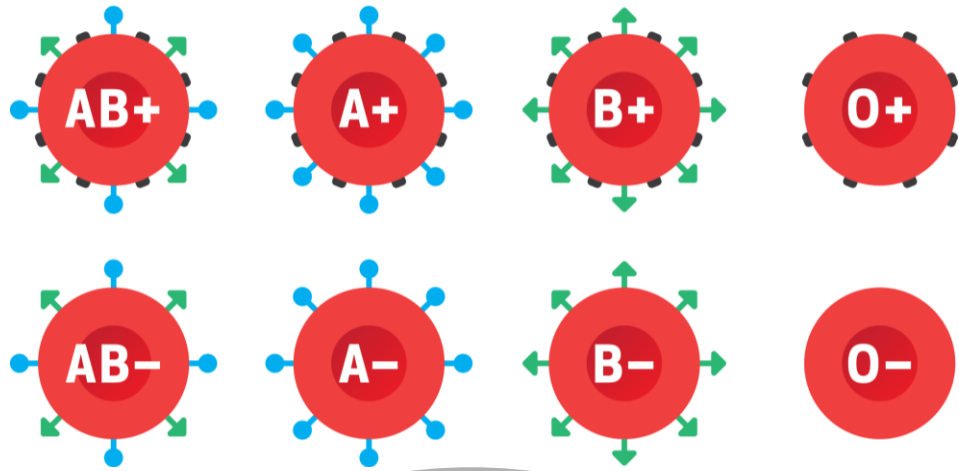


*FUT2* ( $\alpha$ 1,2fucosyltransferase )



20% of Europeans are homozygous for a **recessive nonsense mutation** ( $FUT2^{-/-}$ ) which results in a **nonfunctional enzyme**.

PMID:7876235

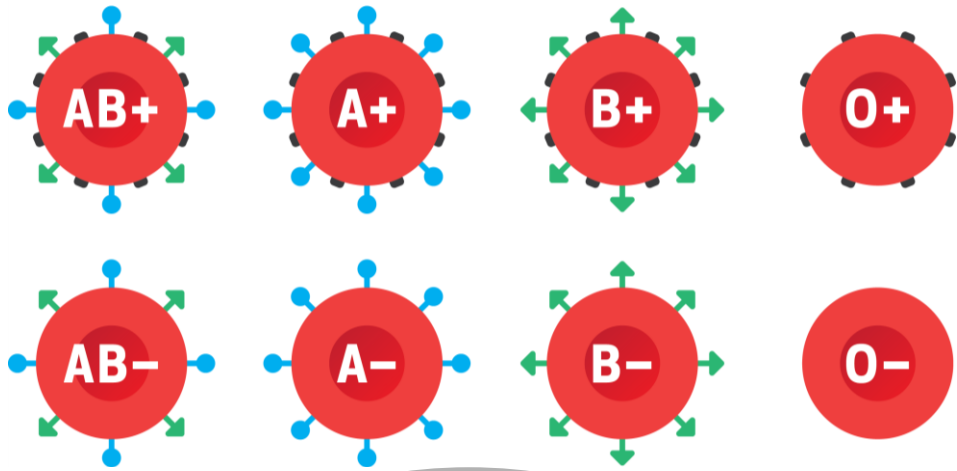


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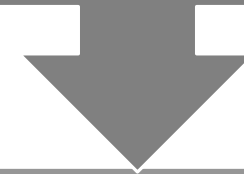
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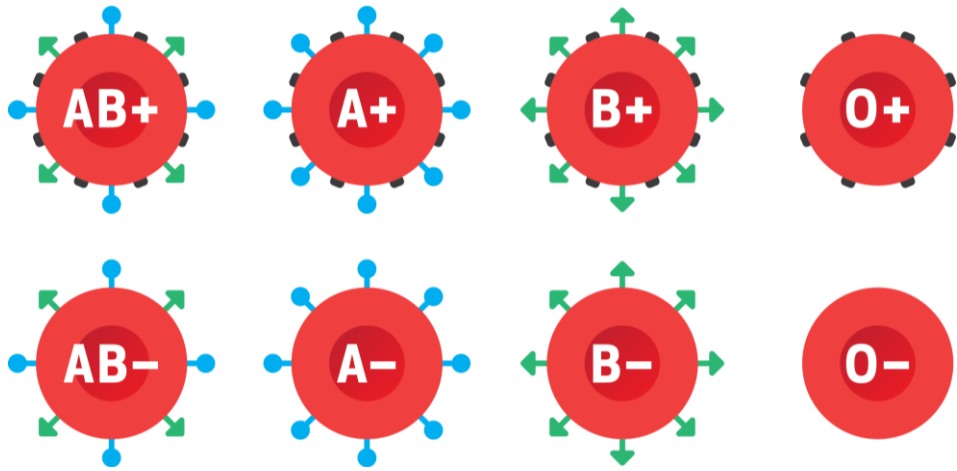
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These individuals are **highly resistant to norovirus** infection.

PMID: 16306606, 16973373





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PMID: 16306606, 16973373

The association of *FUT2* with Polyomavirus BKV suggests that **secreted histo-blood group antigens** could play a role in polyomavirus response.

# Conclusions



Different genes are associated with different antibodies.



# Conclusions



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Some of these genes could elucidate how the immune system interacts with specific pathogens.

## Future Directions



Genetic basis of pathogen-induced  
cancers & immune response

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Biological function of immune-response-associated genes

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Biological function of immune-response-associated genes



Personalized prevention (vaccines) & intervention (drug targets)

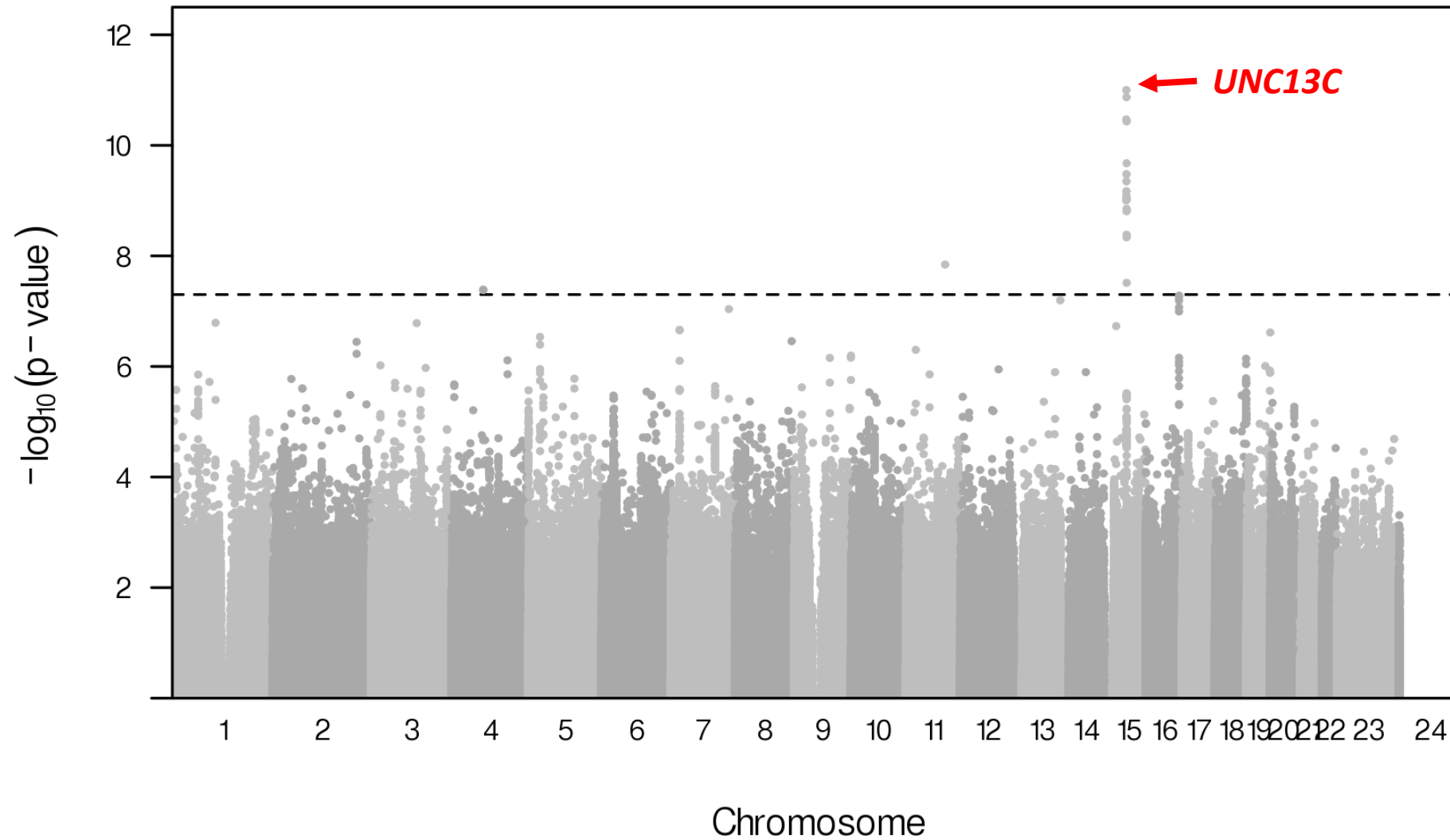
# Thank you!

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- Dr. Linda Kachuri & Dr. Sara Rashkin
- Dr. John Witte & The Witte Lab
- UCSF SRTP: Julia Clark & Dr. D'Anne Duncan
- Amgen Foundation



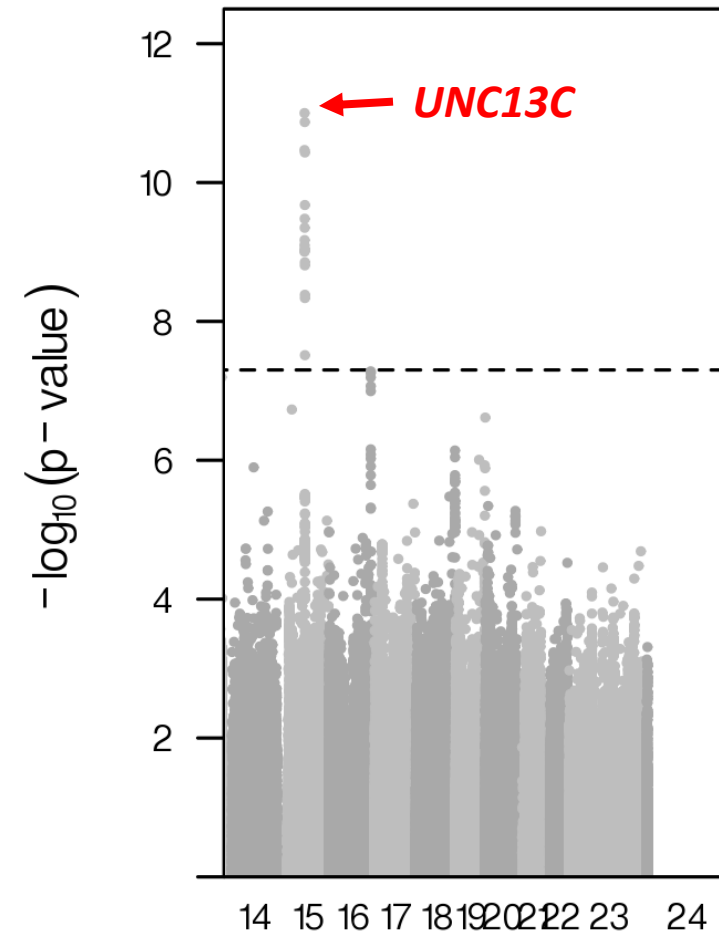
IE1B Antigen for **N = 6095**  
**Human Herpesvirus-6**



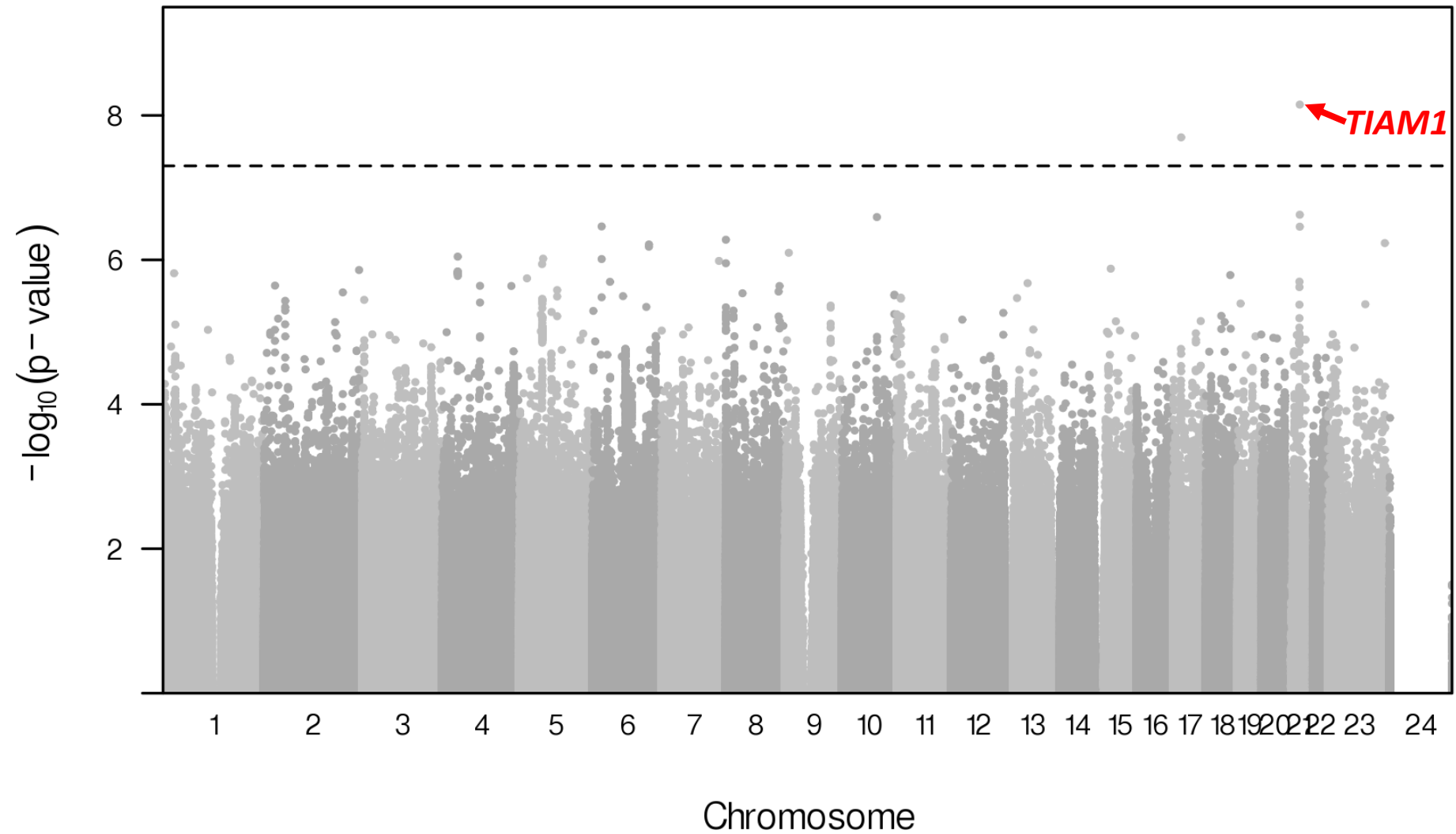


## rs118162566 – *UNC13C* Gene

- Related to immune response to IE1B antigen for Human Herpesvirus-6 ( $\beta = -506.2, P = 10^{-11}$ )
- *UNC13C* may play a role in vesicle maturation during exocytosis
- Appeared in same GWAS of antibody response to the **smallpox vaccine** (PMID: 22542470,  $P = 8 \times 10^{-7}$ )



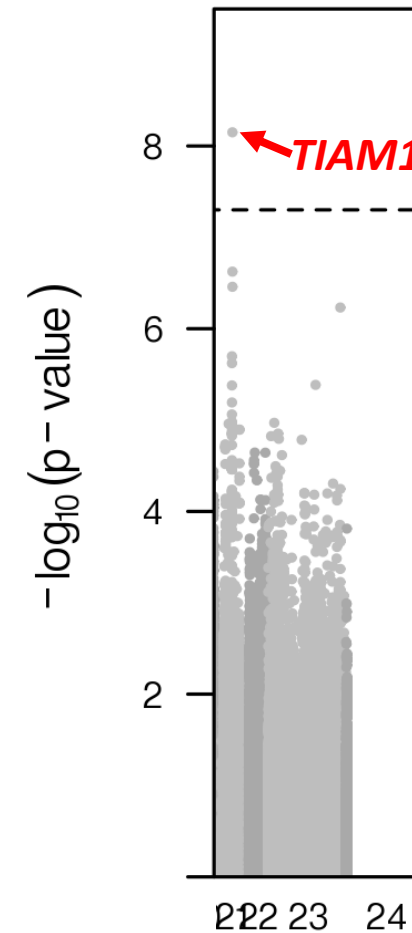
UreA Antigen for **N = 1891**  
***Helicobacter pylori***



## rs113552662 – *TIAM1* Gene

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- Related to immune response to UreA antigen for *Helicobacter pylori* ( $\beta = -2023, P = 7 \times 10^{-9}$ )
- *TIAM1* (**T Cell Lymphoma Invasion and Metastasis 1**) plays a role in cell invasion, metastasis, and carcinogenesis
- Appeared in GWAS of **HIV-1 virologic failure** (PMID: 25461247,  $P = 10^{-6}$ )



# rs681343 - Fucosyltransferase 2

- Related to immune response to BK VP1 antigen for Human Polyomavirus BKV ( $\beta = -386.529, P = 2 \times 10^{-19}$ )
- *FUT2* is an enzyme required for the soluble A & B antigen synthesis pathway

Also associated with:

- **Crohn Disease** (PMID: 26192919)
- Several **autoimmune diseases** (PMID: 26301688)
- **Infectious diseases** such as rotavirus, norovirus, and pneumonia (PMID: 24277741, 16306606, 2876155)

