

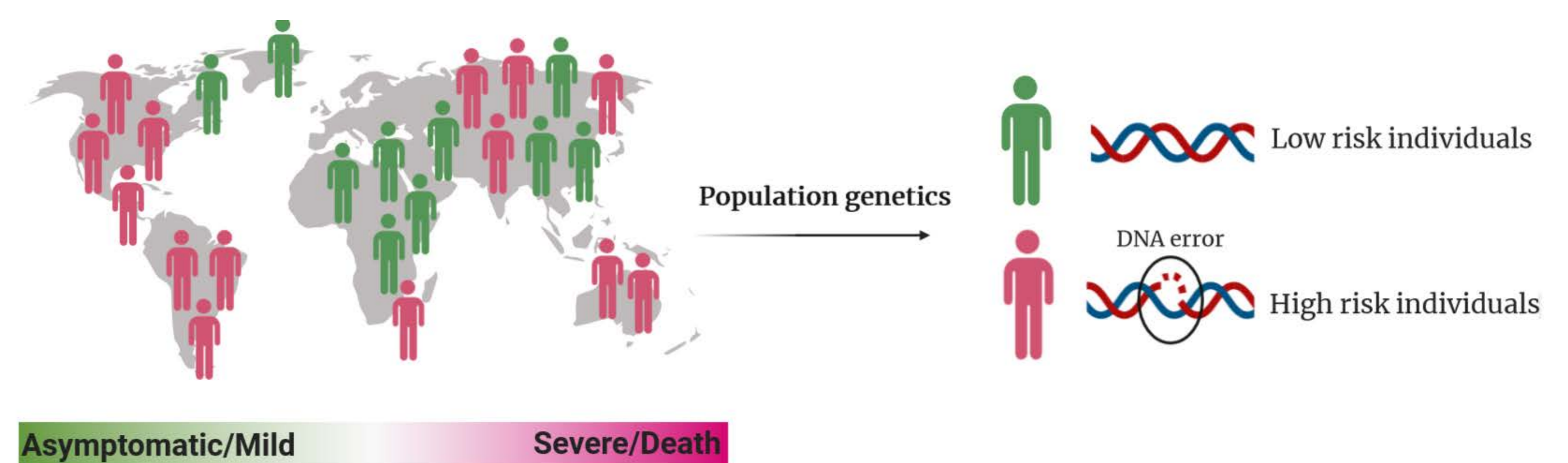
# Host genetic variants potentially associated with SARS-CoV-2 A multi-population analysis

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## INTRODUCTION

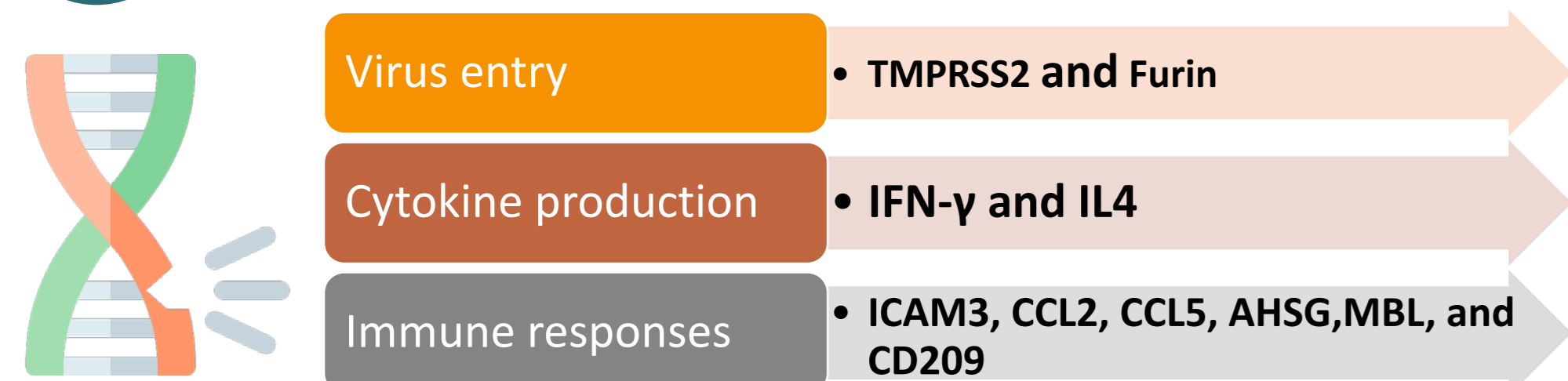
Clinical outcomes of coronavirus disease 2019 (COVID-19), caused by the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) showed enormous inter-individual and inter-population differences, possibly due to host genetics differences. Earlier studies identified single nucleotide polymorphisms (SNPs) associated with SARS-CoV-1 in Eastern Asian (EAS) populations. Importantly, these variants could have a potential effect on SARS-CoV-2 outcomes.



**Study Aim:** To explore the frequency of a set of genetic polymorphisms that could affect SARS-CoV-2 susceptibility or severity in the Qatari population, in comparison to other populations

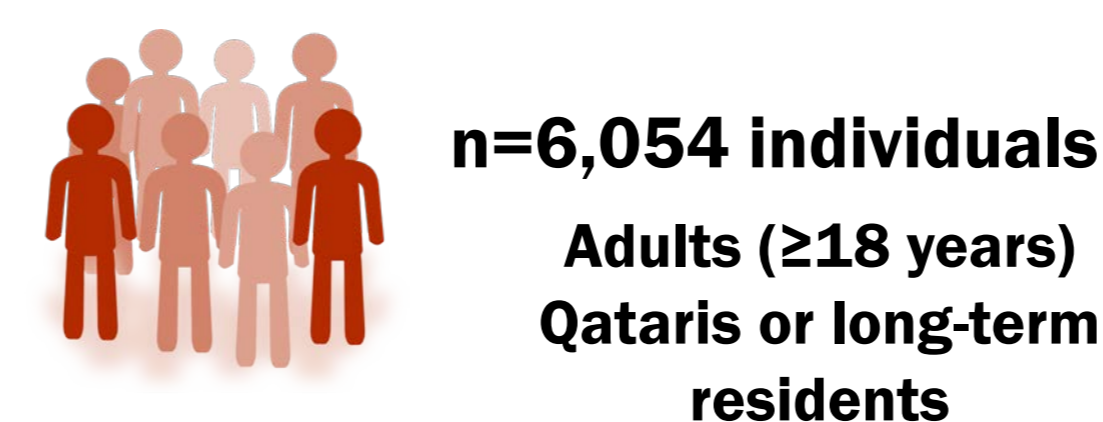
## METHODS

### 1 SNPs selection



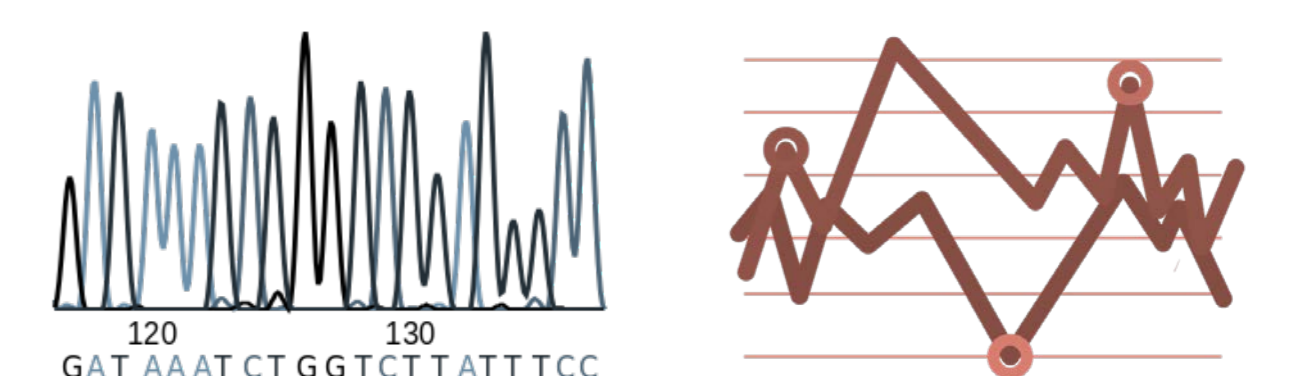
SNPs that were previously associated with SARS-CoV-1 were extracted from Genome wide association studies (GWAS).

### 2 Study population and Genomics data



Whole-genome sequences individuals who had previously participated in Qatar Genome Project (QGP) were obtained

### 3 Analysis



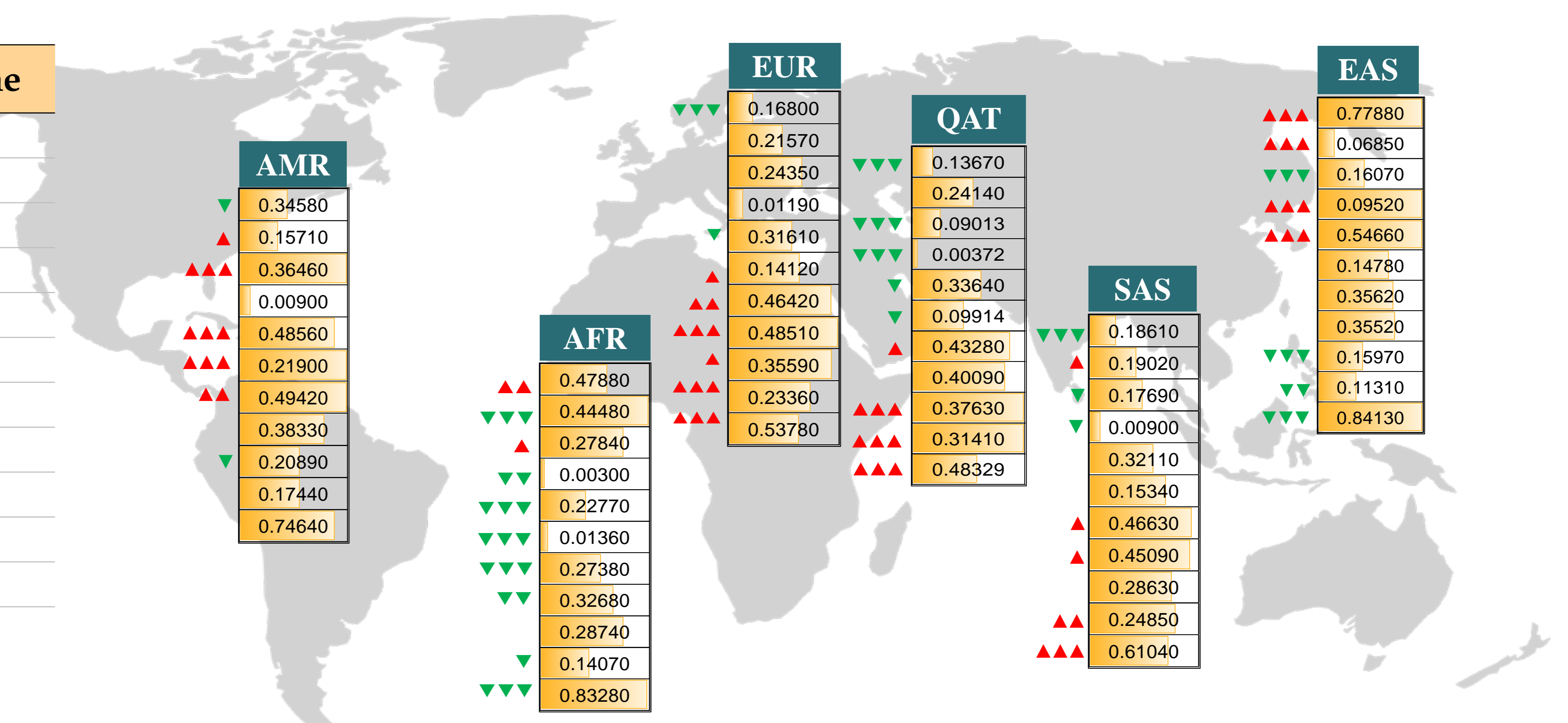
Sequences were used to calculate the allelic frequencies (AF) and compare it to the global AF from the 1000Genome project (n=2504)

## RESULTS

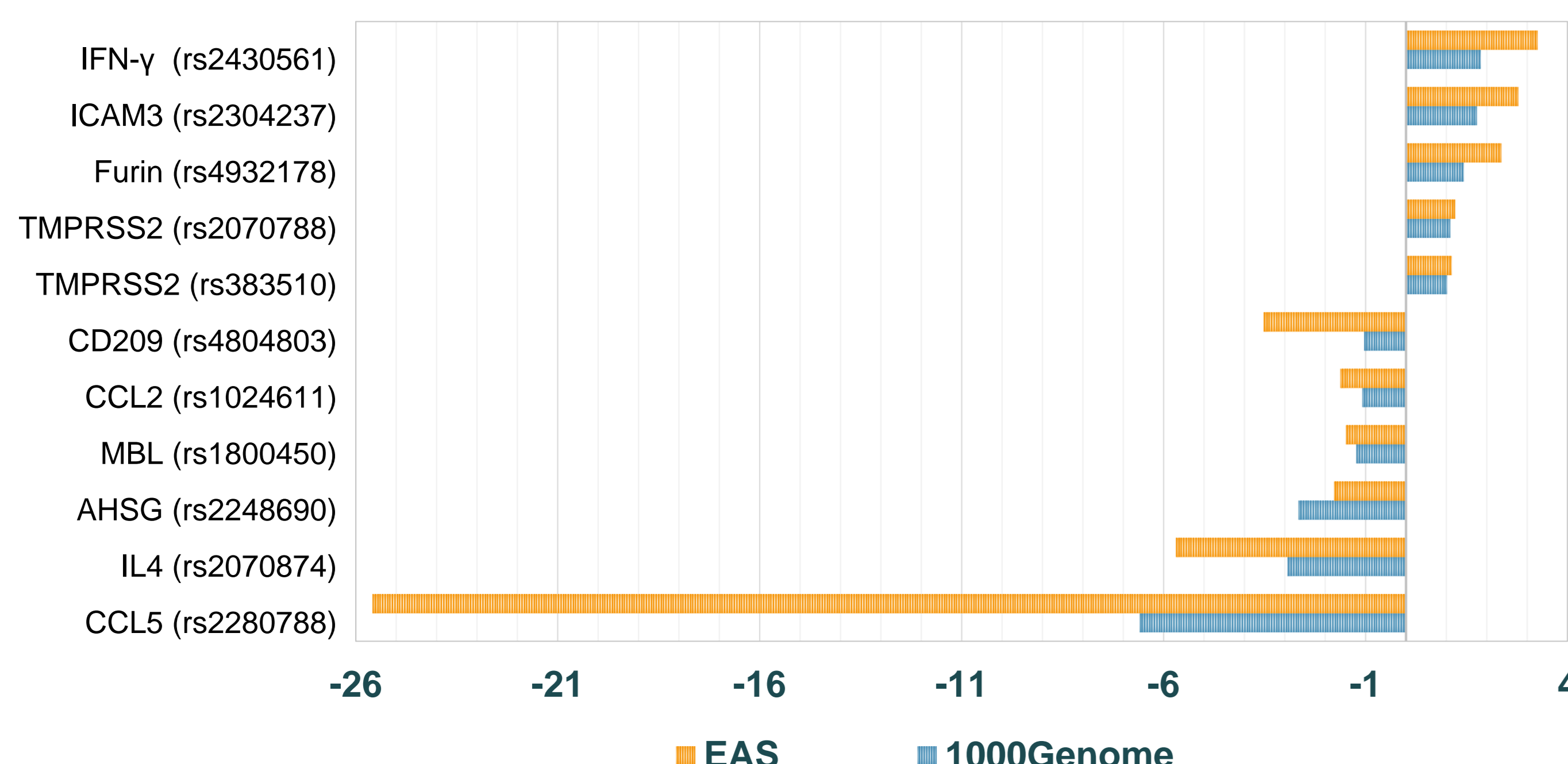
### 1 Allelic frequencies of SARS-CoV-1-associated genetic variants among different populations

Gene	SNP ID	AF 1000Genome
IL4	rs2070874	0.4012
CD209	rs4804803	0.2334
AHSG	rs2248690	0.2398
CCL5	rs2280788	0.0245
CCL2	rs1024611	0.3636
MBL	rs1800450	0.122
TMPRSS2	rs2070788	0.3968
TMPRSS2	rs383510	0.3964
Furin	rs4932178	0.2644
ICAM3	rs2304237	0.1795
IFN-γ	rs2430561	0.7198

▲ Higher susceptibility to SARS-CoV  
▼ Lower susceptibility to SARS-CoV



### 2 Fold differences in the risk allelic frequencies of SARS-CoV-1-related SNPs among Qatari population in comparison to 1000Genome and Eastern Asian populations.



## CONCLUSIONS

- Host genetic variants that could influence SARS-CoV-2 susceptibility or severity are distributed differently across populations.
- Qatari genomes had higher frequencies of risk variants that potentially increase SARS-CoV-2 susceptibility, but a much lower frequency of severity-related mutations.
- Africans seem to carry the lowest ratios of SARS-CoV-2 risk mutations.
- Clues on COVID-19 clinical variability could lie in the human genome
- Results from this work emphasize the importance of understanding the interplay between host genetic factors and response to infections, which could have important implications on public health infections control and therapeutics.