

## GENOMIC LANDSCAPE OF THE GREAT STEPPE: GENETIC VARIANTS IN HEALTHY KAZAKH INDIVIDUALS

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Recent advancements in SNP genotyping have made it a cost-effective method for population genetics studies. Despite this, the Kazakh population remains underrepresented in genomic studies.

Earlier research, including the first whole-genome sequencing (WGS) of Kazakhs and admixture analysis of Kazakhs from Xinjiang, China, focused on smaller cohorts. As descendants of Silk Road travelers, Kazakhs present a unique opportunity to study genetic influences from both East and West. Thus, we present a comprehensive dataset of 224 healthy Kazakh individuals.

The primary aim of our study is to create a genomic reference database for the Kazakh population for various applications, including investigating the evolutionary history of Central Asian populations, and advancing biomedical research.

PCA analysis and Fst heatmap results highlight the unique genetic positioning of Kazakhs between East and West Eurasian populations, reflecting their geographical location along the historical Silk Road. Together, these findings reinforce the idea that Kazakhs present a unique blend of Eastern and Western influences, shaped by their histor-

ical and geographical context, yet maintaining their own distinct genetic signature.

Additionally, SNPs with differing Minor Allele Frequencies (MAFs) compared to European, East Asian, and South Asian populations. This allowed us to investigate genetic variants that distinguish Kazakhs from these populations using annotations from various medical databases to

explore their potential biological and health-related significance.

We present the largest genotyping study of the Kazakh population to date, comprising 224 healthy ethnically Kazakh individuals. This study advances genomic research on Central Asian populations, exploring the genetic position of Kazakhs within Eurasia and identifying specific

genetic variants that distinguish the Kazakh population in a biomedical context. This study offers valuable implications for population-specific health, disease susceptibility, and the development of precision medicine tailored to this group.

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