**GWAS summary statistics of Jomon proportion in Japanese**

General information:

* **Sample size**: 161,155 samples
* **Genotyping array**: the Illumina HumanOmniExpressExome BeadChip or a combination of the Illumina HumanOmniExpress and HumanExome BeadChips.
* **Sample QC**: We excluded (i) individuals with lower call rates (< 99%), (ii) closely related individuals with genetic relatedness ≥ 0.178 calculated from a genetic related matrix (GRM) by GCTA (version 1.93.3beta2). We included samples of the estimated Japanese ancestry using PCA.
* **Variant QC**: We excluded variants with (i) call rate < 99%, (ii) *P* value for Hardy-Weinberg equilibrium (HWE) < 1.0 × 10-6, (iii) number of heterozygotes < 5, and (iv) a concordance rate < 99.5% or a non-reference concordance rate between GWAS array and whole genome sequencing.
* **Phasing and imputation**: Eagle and Minimac3
* **Imputation reference**: Combined panel of 1000 Genomes Project Phase 3 version 5 genotype (*n* = 2,504) and Japanese whole-genome sequencing data (*n* = 1,037)
* **Post-imputation QC**: We excluded imputed variants with *Rsq* < 0.7 and minor allele frequency < 1.0%.
* **Association test**: We adopted the following correction methods: (i) GCTA-fastGWA with the adjustment of covariates: age, age2, sex, the top 20 PCs, 45 disease status, geographic regions, and PCA clusters; (ii) fixed-effect meta-analysis of Mainland summary data including individuals from the Mainland and EA\_admix clusters (*n* = 151,075) and of Ryukyu summary data including individuals from the Ryukyu, Ryukyu admix, and Hokkaido\_sub clusters (*n* = 10,080) using METAL (version 2020-05-05); and (iii) double genomic control correction method using METAL. Computing *Z* score for each variant by considering the sign of the beta coefficient and the associated *p*-value, we left the variants with positive Z score.

Uploaded file

| **File name** | **Descriptions** |
| --- | --- |
| Jomon\_related\_SNP\_SummaryData\_2024.txt.gz | Results for 3,454,920 autosomal chromosome variants |

Columns

| **#** | **column name** | **Descriptions** |
| --- | --- | --- |
| 1 | SNP | marker name (CHR:POS:REF:ALT) |
| 2 | CHR | chromosome |
| 3 | POS | position (hg19) |
| 4 | REF | REF allele |
| 5 | ALT | ALT allele |
| 6 | A1 | The effect allele (A1 is equal to ALT.) |
| 7 | AF1 | allele frequency of A1 allele (ALT) |
| 8 | N | sample size in total |
| 9 | CHISQ | Chi square statistics |
| 10 | BETA | effect size of A1 allele |
| 11 | SE | standard error of BETA |
| 12 | P | P value from METAL |

Reference

If you use the summary statistics, please cite the following paper;  
Yamamoto K et al. Genetic Legacy of Ancient Hunter-Gatherer Jomon in Japanese Populations. *Nature Communications* 2024.