Supplementary Materials for

Ancient genomics reveals tripartite origins of Japanese populations

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Note S1: Archaeological contexts

A brief introduction on pre- and protohistoric Japan

The Japanese archipelago consists of five main islands including Hokkaido, Honshu, Shikoku, Kyushu, and Okinawa and is a region which is extremely rich in archaeological sites (87). The pre- and protohistory of Japan is divided into four different periods: the Paleolithic, Jomon, Yayoi, and Kofun. The lithic-based Paleolithic, which started >38,000 years ago (ka ago) (88), transformed into the pottery-producing Jomon >16 ka ago (2). The Jomon (which translates to cord mark decorations; Jo meaning “cord” and mon meaning “mark” in Japanese) are considered to be complex hunter-gatherers (50–53). Characteristics of the Jomon culture include: the presence of large settlements, a high population density per site, low residential mobility, logistically organized subsistence strategies (evidenced by the presence of storage pits and large shell-middens), and the construction of large ceremonial features. The Jomon period lasted more than 10,000 years and is split into six sub-periods based on temporal variation in these cultural characteristics: Incipient (15,000-11,000 calibrated before present, calBP), Initial (11,000-7,000 calBP), Early (7,000-5,400 calBP), Middle (5,400-4,400 calBP), Late (4,400-3,300 calBP), and Final Jomon (3,300-2,300 calBP) (51).

The subsequent period between the beginning of wet-rice cultivation and the emergence of the custom of burying the elite in keyhole-shaped tumuli is referred to as the Yayoi period, the first agrarian phase in Japanese history (1). Systematic rice paddy field agriculture was introduced into the Japanese archipelago during the first millennium BC. Within approximately 1,000 years, technological advancements in tool-making led not only to further advances in rice cultivation, but also to social stratification due to increasing contradiction between the hierarchization of social relations and the necessity of maintaining communal collaboration and the egalitarian ethos for food production (1).

The following Kofun period is regarded as the state-formation phase as represented by the beginning of the imperial reign. A prominent feature of this period is the construction of large burial mounds, whose size reflected the social status of its occupant during their lifetime (1). This trend is particularly evident in archaeological sites from the early Kofun period. However, the keyhole structure slowly began to be downsized over the course of time (1). Coinciding with this decline in the size of large keyhole tumuli, packed tumuli clusters, such as horizontal cave tombs, became prevalent in the Late Kofun period. The construction of keyhole tumuli ceased by the end of the Kofun period (the six century AD) which marked the completion of the process whereby the elite became the rulers and managed to control inevitable hierarchies that had persisted since the introduction of paddy field rice cultivation.

In the following sections, we provide details of archaeological contexts of the sites where the samples used in this study were collected from (see Fig. 1a for geographic locations of the sites).
1. Jomon

1.1. Kamikuroiwa rock shelter (Initial Jomon; JpKa6904)
Kamikuroiwa rock shelter is located in Kumakogen, Kamiukena District, Ehime Prefecture of Shikoku. The site is sitting on a terrace along Kuma River, at an elevation of about 396 m above sea level. The excavation of this site was conducted from 1962 to 1970, identifying well-preserved deposits that were stratigraphically divided into nine layers. Most of the human burials, including JpKa6904 sequenced in this study, were recovered from Layer 4, coupled with large pieces of Jomon potteries; their roller-stamped designs (so-called “Oshigata-mon” in Japanese) associated Layer 4 with the Initial Jomon. The radiocarbon date of JpKa6904 reported in (89) was corrected with the IntCal20 curve, which gave 6,696-7,041 calBC (8,819 ± 172 calBP), consistent with the archaeological contexts of this layer. JpKa6904 had morphological characteristics of a female, which was further confirmed by our genetic data (see Table S3). An additional individual recovered from the same layer was screened for high-coverage sequencing but had little endogenous human DNA left in a tooth (<1%).

1.2. Odake shell-midden (Early Jomon; JpOd)
The Odake shell midden is located around 4 km inland from the present-day seacoast, at the junction of the Kureha hills in Toyama, a coastal city of north central Honshu. At the time of settlement at the Odake shell midden, the sea level was higher than the level at the present due to climatic warming and this site was located along the shore, emerging as the result of marine transgressions. At least 100 human skeletons have been discovered from this site, most of which were excavated between 2009 and 2010 due to the construction of new train lines. Buried skeletons had a specific burial practice in which the body was placed in a flexed position with bent legs. Some of the buried individuals folded stones in their arms across their chest. Animal remains excavated from this site included terrestrial and marine mammals, as well as fish, suggesting that the Jomon in this area utilized a variety of food resources. Four individuals from this site produced genomic data in this study, all of which are included in the early stage of the Early Jomon period as follows:

- JpOd274: 4,169-4,339 calBC (6,204 ± 85 calBP)
- JpOd6: 3,984-4,229 calBC (6,057 ± 123 calBP)
- JpOd181: 3,801-3,967 calBC (5,834 ± 83 calBP)
- JpOd282: 3,787-3,952 calBC (5,820 ± 83 calBP)

1.3. Funagura shell-midden (Early Jomon; JpFu)
The Funagura shell-midden is located in Kurashiki, a coastal city of western Honshu, sitting on the Seto Inland Sea that separates three main islands, Honshu, Shikoku, and Kyushu. Three burials were excavated from this site in 1991; two individuals were initially screened for human endogenous DNA; only JpFu1 was analyzed in this study due to the poor preservation of the other individual. JpFu1 was discovered in Layer 3 where the density of shell deposits was extremely high. Several Jomon potteries, together with lithic tools, were recovered from the same layer, the type of which had an association with the late stage of the Early Jomon period. Our radiocarbon dating showed 3,528-3,640 calBC (5,534 ± 56 calBP). This individual had morphological characters that were considered an adult female; our genetic analysis assigns female to this individual (Table S3). In addition to the human skeletons, animal remains were also excavated from this site, including fish (e.g., sharks and Japanese black porgy), birds, and mammals (e.g., deer and boars). These archaeological evidence supports that both fishing in the Inland Sea and
hunting terrestrial animals could have been central to food collection for the Jomon population in this site.

1.4. Kosaku shell-midden (Middle-to-Late Jomon; JpKo)
The Kosaku shell-midden is located in Funabashi, a coastal city of central Honshu. This site was initially discovered in 1883; following excavations identified the Jomon pottery that represents the Late Jomon period, in particular those having the lid with many large bracelets made from shell inside the pottery. Around 100 human skeletons were recovered from this site, some of which were collectively buried. Two individuals sequenced in this study, JpKo2 and JpKo13, were buried individually, dated to be the Middle or Late Jomon period (see below). There were animal remains excavated together with the human skeletons, which included deers, boars, raccoons, as well as a variety of fish and shells.

- JpKo2: 2,344-2,564 calBC (4,404 ± 110 calBP; Middle Jomon)
- JpKo13: 1,897-2,028 calBC (3,913 ± 66 calBP; Late Jomon)

1.5. Hirajo shell-midden (Late Jomon; JpHi01)
The Hirajo shell-midden is located in Ainan, a coastal city of Shikoku. This site was originally discovered in 1891 and is known for a specific “Hirajo” type of the Jomon pottery, that is representative of the middle of the Late Jomon period. Hirajo-type pottery had a certain level of similarity to the pottery found in Northern Kyushu or Honshu on the Seto Inland Sea, suggesting potential trade across the areas. A total of 10 burials were recovered from this site during excavations conducted from 1954 to 1972, one of which, JpHi01, was well preserved as discovered with a full body skeleton and chosen for genomic sequencing in this study. This individual was dated to be 1,735-1,900 calBC (3,768 ± 83 calBP) (referred from the Annual Archaeological Report from Ainan Town 2020). The Late Jomon culture had a practice of ritual tooth ablation; however, this individual had no evidence on tooth removal. From morphological characters, this individual was likely to be an adult. Animal remains excavated together with the humans include deers, boars, sharks, clams, and oysters, supporting the fishing and hunting lifestyle of the Jomon in this region. Fiber remains were also found in this site, suggesting the Jomon might have made their clothes out of fibers.

2. Kofun

Iwade horizontal cave tombs (JpIw)
Horizontal cave tombs are constructed on a hill and dug in parallel to the ground. Multiple small tombs make a cluster, each of which contains a burial chamber where multiple individuals were accommodated by shifting previously buried individuals to make room for new burials. The Iwade site is located in Kanazawa, Ishikawa Prefecture of Honshu, consisting of eight tombs split into three sections (Section A: No. 1, 2, 3, 5; Section B: No. 6, 7, 8; Section C: No. 4). Three individuals sequenced in this study were excavated from the No. 3 tomb. A number of Sue stoneware were buried together with the human body in the tomb. The shape of this stoneware was uniquely observable in sites from eastern or northeastern Japan, but rare in northwestern Japan and completely absent in western Japan. This suggests that people might have moved to the areas such as the Iwade site from eastern parts of the archipelago. Given that a keyhole tumulus was constructed in the sixth century AD near the Iwade horizontal cave tombs, a sociopolitical community could have been newly formed in the Late Kofun period. Radiocarbon dates of our samples are consistent with the timing of the appearance of the keyhole tumulus:
- Jplw32: 541-603 AD (1,378 ± 31 calBP)
- Jplw31: 573-647 AD (1,340 ± 37 calBP)
- Jplw33: 595-655 AD (1,325 ± 30 calBP)
Note S2: Demographic modelling by runs of homozygosity (ROH)

We identify the excess accumulation of short runs of homozygosity (ROH) in our oldest Jomon genome, JpKa6904, compared to Mesolithic hunter-gatherers from Ireland (33) and Luxembourg (39), as well as the Upper-Paleolithic Northeast Siberian (19) and the other Neolithic or Pleistocene genomes (33, 39, 78) (see Fig. 3b). This suggests that the Jomon had a smaller population size than the West Eurasian hunter-gatherers likely due to a long-term isolation in insular East Asia. To estimate the timing of divergence of the Jomon lineage, coupled with the population size, we employed a simulation-based modelling approach that can fit genome-wide patterns of ROH expected under given demographic conditions to those observed in the Jomon genome.

We applied diploid-genotype calling to the high-coverage ancient genomes including 7.5× JpKa6904. To minimize any potential confounding effects of postmortem deamination on the ROH analysis, we called genotypes only for single nucleotide polymorphisms (SNPs) with transversions filtered for global minor allele frequencies above 1% among the Phase 3 v5 1000 Genomes release (28). Additional filtering steps were applied to the genotype calling: bases with a quality >30, a sequence depth >10, and a genotype quality >20. This left 984,740 autosomal SNPs for ROH analysis. We then used PLINK v1.90 (76) to detect ROH in the Jomon genome with the following options: --homozyg --homozyg-density 50 --homozyg-gap 100 --homozyg-kb 500 --homozyg-snp 50 --homozyg-window-het 1 --homozyg-window-snp 50 --homozyg-window-threshold 0.05. The ROH profile was summarized into a spectrum of ROH fragments ranging from 0.5 to 100 Mb with a bin size of 1 Mb (Fig. S10).

The observed ROH spectrum is shaped jointly by the population size and timing of population split. The previous study has provided estimates on the divergence of Jomon lineage from the common ancestor of Han to be in between 18 and 38 ka ago, with a constant population size that falls within the range from 2,000 to 3,000 (14). We first performed a broad search for the parameter space that is defined with the population size (N) from 500 to 2,500 and population split from 10 to 40 ka ago (T) using the data from chromosomes 3 to 22 (Fig. S11). To test whether the Jomon demography influences the pattern of ROH in a genome, we generated 100 whole-genome simulations, using a coalescent simulator ms (81), for different combinations of N and T under a fixed scenario of the Out-of-Africa dispersal reconstructed from a previous study (80) with slight modifications (Fig. S10a). Our simulation assumed 25 years per generation and 1.25×10⁻⁸ per generation (90) and 0.625×10⁻⁸ per generation for a mutation rate and a recombination rate respectively.

We then estimated the likelihood of observing the ROH spectrum similar to that observed in JpKa6904 (shown as a dashed red line in Fig. S10b). We applied the method developed in (82) that measures the similarity of summary data (i.e., ROH spectrum) between the observed and simulated data based on a kernel density estimate and that calculates an approximated marginal likelihood (aML) of a given model. A normalized Gaussian kernel function with a bandwidth of 1.0 was used to compute kernel density estimates of aMLs. These estimates were then compared to identify the best-fitting model as an approximate Bayes factor (aBF); we calculated aBFs between a model with the highest aML and any other models.

Our broad search was able to confine the parameter space into 500 ≤ N ≤ 2,000 and 15 ≤ T ≤ 30 ka ago that includes likely scenarios for further testing with all autosomal chromosomes (Fig. S11). Including chromosomes 1 and 2 increased the power in discriminating the highest likelihood model from the others (Fig. 3c); the model with N = 1,000 and T = 20 ka ago was significantly
favoured with $\log_{10}$-scaled aBFs $> 2.0$ against any other models, except for that with $N = 1,000$ and $T = 15$ ka ago ($\log_{10}$-scaled aBF: 0.1).
Note S3: Testing the presence of addition ancestry in the Kofun

We rigorously tested whether the Kofun have additional ancestry that is absent or reduced in modern Japanese using qpAdm. We modelled the Kofun and modern Japanese with a four-way admixture by adding populations identified from the $f_4$-statistics as significantly closer to the Kofun (Fig. S21) to the three sources of Jomon, Northeast Asian, and East Asian ancestry (Table S15). None of the populations tested support the four-way admixture models; the three-way admixture without the fourth source always better explains the genetic ancestry of Kofun than the four-way admixture (nested $p$-value $> 0.05$) (see Table S15). These results suggest that no additional ancestral component is present at any detectable level in the Kofun.
Fig. S1. DNA damage plots for newly sequenced ancient Japanese. Damage patterns on the left plot show C>T misincorporations at the 5’-end, while those on the right plots show G>A misincorporations at the 3’-end.
Fig. S2. Results of kinship analysis by READ for all (a) Jomon and (b) Kofun individuals sequenced in this study. Pairs of individuals tested are listed on the x-axis, while the y-axis represents average pairwise P0 scores. Dashed lines show the cut-off for the 1st and 2nd degree relatives.
Fig. S3. A topographic map showing locations of ancient samples included in this study. Ancient data are represented by symbols designated by geographic or cultural context. Ancient Japanese newly sequenced in this study are highlighted with circles, while those previously published data are represented by triangles. Sites of Upper-Paleolithic samples are marked with crosses. Other ancient individuals are represented by coloured squares according to the following groupings: Amur River (AR_EN, AR_IA, and AR_Xianbei_IA), Baikal (Kurma_EBA, Lokomotiv_EN, Shamanka_EBA, Shamanka_EN, UstBelaya_EBA, UstBelaya_MED, UstBelaya_N, UstIlda_EBA, and UstIlda_LN), Central Steppe (Botai, CentralSteppe_EMBA, Namazga_CA, Okunevo_EMBA, SidelkinoEHG_ML, Turkmenistan_IA, and YamnayaKaragash_EBA), Chokhopani, Devil’s Gate Cave (DevilsCave_N), HMMH_MN, Mongolia (ARS008 and ARS026), Neo-Siberian (Ekven_IA, Magadan BA, Uelen IA, and Yana_MED), Northern China (Bianbian, Boshan, Xiaogao, Xiaojingshan, and Yumin), Southeast Asia (McColl_Groups_1-6, McColl_Group_3.1, and McColl_Group_4.1), Southern China (Chuanyun, Liangdao1, Liangdao2, Qihe, Suogang, Tanshishan, and Xitoucun), West Liao River (WLR_BA, WLR_BA_o, WLR_LN, and WLR_MN), Yellow River (Miaozigou_MN, Shimao_LN, Upper_YR_IA, Upper_YR_LN, YR_LBIA, YR_LN, and YR_MN) and USR1. Full information about ancient Japanese individuals is included in Table 1 and Table S1, and information about all other previously published data is summarized in Table S4.
Fig. S4. Principal component analysis of present-day individuals only. Principal components are calculated using 112 present-day East Eurasians in the SGDP panel filtered for transversions and global minor allele frequencies of 1%.
Fig. S5. Cross validation (CV) errors used in ADMIXTURE analysis. Each K component includes ten replicates. The run with the lowest CV is plotted in Fig. S6.
Fig. S6. ADMIXTURE results for 2 to 12 ancestral clusters (K) in (a) modern and (b) ancient individuals. Plotted results for each K represent the run with the lowest cross validation error out of 10 iterations, which have been divided into present-day and ancient populations for clarity. In (a) present-day individuals ($n = 786$) from the Human Origin Array are separated by region: (from left to right) Africa (represented by Mbuti), Europe (represented by Sardinia), East Asia, Siberia, South and Central Asia, Australasia and Native America. In (b) ancient East Eurasian individuals
with at least 100,000 SNPs in the SGDP database ($n = 187$) are divided into the following broad groups based on culture, age or location of origin: (from left to right) Jomon, Yayoi, Kofun, Amur River (AR_EN, AR_IA, and AR_Xianbei_IA), West Liao River (HMMH_MN, WLR_MN, WLR_LN, WLR_BA, and WLR_BA_o), Yellow River (Upper_YR_LN, Upper_YR_IA, YR_MN, YR_LN, Miaozigou_MN, Shimao_LN, and YR_LBIA), Devil’s Gate Cave, Other East Asian (Bianbian, Xiaogao, Yumin, Liangdao1, Liangdao2, and Xitoucun), Early Eurasians (Tianyuan, Salkhit, Yana_UP, Mal’ta, and Afontova Gora), Baikal (Shamanka_EN, Shamanka_EBA, Lokomotiv_EN, UstIda_LN, UstIda_EBA, UstBelaya_EBA, UstBelaya_N, UstBelaya_MED, and Kurma_EBA), Ancient Mongolian (ARS008 and ARS026), Southeast Asian (McColl_Group1, McColl_Group2, McColl_Group3, McColl_Group3_1, McColl_Group4, McColl_Group4_1, McColl_Group5, and McColl_Group6), Chokhopani, Central Steppe (Botai, CentralSteppe_EMBA, Namazga_CA, Okunevo_EMBA, SidelkinoEHG_ML, Turkmenistan_IA, and Yamnaya), Kolyma_M, Northeast Siberian and others (Magadan_BA, Uelen_IA, Ekven_IA, Yana_MED, and USR1). In addition, certain ancient groupings that were identified by qpAdm as potential sources of admixture for Yayoi (HMMH_MN and WLR_BA_o) and Kofun (YR_LBIA) are highlighted in red. At K=2, the dataset separates into Asian and non-Asian ancestry, denoted by the colors yellow and dark pink respectively. At K=3, a Native American component (darkgreen) emerges that is also observed in lower levels in present-day and ancient Siberians. At K=4, a component representing broad European ancestry (orange) emerges, which is also present in present-day Central Asians, some Early Eurasians and ancient Central Steppe. At K=5, Australasian ancestral component emerges (light pink) that is highest in Papuan. At K=6, a Siberian component (purple) emerges that is seen at its highest level in Koryak and Itelman. At K=7, a component that is highest in Nganasan and strongly observed in ancient Baikal emerges (light blue). At K=8, an ancestral component highest in the Pima population emerges (light brown). At K=9, the Pima component disappears, and two new ones appear - Jomon ancestry becomes distinguishable (red), which is also observed in other ancient and present-day Japanese and at low levels in other samples, and a south and central Asian ancestral component emerges that is highest in Kalash (palegreen). The Pima component reappears in K=10. At K=11, an ancient Central Steppe component is observed (gray). At K=12, a component associated with Yellow River ancestry (deepblue) emerges.
Fig. S7. Maximum-likelihood phylogenetic trees reconstructed by **TreeMix**. The trees show phylogenetic relationships among ancient (bold) and present-day (italic) populations under a no-migration model or models with migrations from 1 to 5. Colored arrows represent the migration pathways and signals of admixture among all datasets. The migration weight represents the fraction of ancestry derived from the migration edge.
(a) \(f_{4}(\text{Mbuti}, X; \text{Hoabinhian, Jomon})\)

(b) \(f_{4}(\text{Mbuti}, X; \text{DevilsCave N, Jomon})\)

(c) \(f_{4}(\text{Mbuti}, X; \text{Japanese, Jomon})\)

(d) \(f_{4}(\text{Mbuti}, X; \text{Han, Jomon})\)
Fig. S8. Geographic and temporal display of $f_4$(Mbuti, $X$; Dai, Jomon) results. We compare the different affinities of all ancient and modern East Eurasians to the Jomon with respect to five East Asian populations (*i.e.*, reference populations): (a) Hoabinhian, (b) DevilsCave N, (c) Japanese, (d) Han, and (e) Dai. Results are divided into four periods based on the prehistory of Japan: the Upper-Paleolithic period (38,000-16,000 years BP), the Jomon period (16,000-3,000 years BP), the post-Jomon period (3,000 years BP-present) and Present day. Populations who are significantly closer to Jomon are represented by a red triangle and those closer to the reference populations are represented by a purple diamond. Symmetrically-related populations are denoted by a gray circle. The Jomon are genetically closer to nearly all populations with respect to the Hoabinhian hunter-gatherers but have less genetic affinity than East Asian hunter gatherers from Devil’s Gate Cave and present-day Japanese, Han and Dai; one notable exception however is that the Jomon have extra affinity to the Upper-Paleolithic Yana compared with these present-day reference populations.
Fig. S9. Distributions of shared genetic drift, measured as outgroup $f_3$, between all pairs of individuals within a population. Different individuals within the Jomon share more genetic drift than those from ancient or present-day populations tested, except for Karitiana and Surui who are known to be among the most genetically homogenous human populations today.
Parameters

- **AFR**: 12,300
- **ANC**: 7,300
- **African European East Asian**: 8.8-ka-old Jomon
- **non-AFR**: 2,100
- **OTOA**: 140 ka ago
- **AFR**: 220 ka ago
- **N**: 500 - 2,500
- **EUR-EAS**: 40 ka ago
- **EAS**: 50,000
- **EUR**: 43,498
- **T**: 10 - 40 ka ago
- **N_sp**: 1,000
- **N_eff**: 1,500
- **T_sp**: 40 ka ago

Diagram:
- **N_sp**: 1,000
- **N_eff**: 1,500
- **T_sp**: 40 ka ago
- **AFR**: 12,300
- **ANC**: 7,300
- **T**: 10 - 40 ka ago
- **N**: 500 - 2,500
- **EAS**: 50,000
- **EUR**: 43,498
- **EAS0**: 1,500
- **EUR-EAS**: 40 ka ago
- **N_sp**: 1,000
- **N_eff**: 1,500
- **T_sp**: 40 ka ago
Fig. S10. A demographic model used in the simulation and observed and simulated ROH spectra calculated from the 8.8-ka-old Jomon (JpKa6904) (red) or Han (blue). (a) The Out-of-Africa dispersal model is reconstructed from (80), with varying sets of parameters for the population size ($N$) and divergence time ($T$) of the Jomon lineage. (b) Solid lines show ROH spectra from 40 simulated data, with a thick line representing a mean of the simulated spectra. Dashed lines show observed ROH in JpKa6904. There are 44 combinations of values of the parameters, population size ($N$) and split time ($T$) of the Jomon lineage. Both parameters jointly affect the pattern of ROH. The smaller the population size is, the more short and middle ROH increase. The split time has a further impact on the ROH profiles; the old divergence significantly amplifies a level of ROH carried by the Jomon individual. A log-scaled likelihood is estimated from a similarity between the observed and simulated ROH spectra; $NA$ means a likelihood is very close to zero. The model with $N = 1000$ and $T = 20$ ka ago shows the highest likelihood.
Fig. S11. Modelling on the Jomon demography by ROH. Fitting of the models under different combinations of $N$ (x-axis) and $T$ (y-axis) for the 8.8-ka-old Jomon individual. The grid search is based on data from chromosomes 3 to 22. Each point in the balloon plot represents an approximate Bayes factor (aBF) that compares likelihoods between a model with the highest likelihood and each of any other models; the point with aBF = 0 is the model with the highest likelihood ($N = 1000$ and $T = 20$ ka ago). $NA$ means that aBF is not measurable for the model due to its zero likelihood.
Fig. S12. A comparison of outgroup $f_3$ results of the Jomon dataset divided into three sub-periods measured using $f_3(Jomon\_Sub-Period, X; Mbuti)$. The three sub-periods are defined as follows: Initial Jomon (JpKa6906), Early Jomon (JpFu1, JpOd6, JpOd181, JpOd274, and JpOd282), and a merged group for all Middle, Late, and Final Jomon (F5, F23, IK002, JpHi01, JpKo2, and JpKo13). Populations for $X$ plotted are populations whose outgroup $f_3$-value is calculated using >100,000 SNP sites. The following ancient samples are included: Yayoi, Kofun, Yellow River (Miaozigou_MN, Shimao_LN, Upper_YR_IA, Upper_YR_LN, YR_LBIA, YR_LN, and YR_MN), West Liao River (HMMH_MN, WLR_BA, WLR_BA_o, WLR_LN, and WLR_MN), Northern China (Bianbian, Boshan, Xiaogao, and Yumin), Southern China (Liangdao2), Amur River (AR_EN and AR_Xianbei_IA), Chokhpani, Southeast Asia (McColl Group2, McColl Group3, McColl Group4, McColl Group5, McColl Group6, McColl Group3_1, and McColl Group4_1), Devil's Gate Cave, Mongolian (ARS008 and ARS026), Baikal (Kurma_EBA, Lokomotiv_EN, Shamanka_EBA, Shamanka_EN, UstBelaya_EBA, UstBelaya_MED, UstBelaya_N, Ust_Ida_EBA, and Ust_Ida_LN), Yana_MED, Tianyuan (TY),
Salkhit, Yana, Mal’ta (MA1), Afontova Gora (AG2), Kolyma M and Hoabinhian (McColl Group1).
Fig. S13. Geographic and temporal display of differences in affinities between Jomon sub-periods with ancient and modern populations using $f_4$-statistics. We investigate potential gene flow from continental populations throughout different stages of the Jomon period using $f_4$(Mbuti, $X$; sub_Jomon$_i$, sub_Jomon$_j$), where $i$ and $j$ are any pairs of the three Jomon sub-groups. The three sub-periods are defined as follows: Initial Jomon (JpKa6906), Early Jomon (JpFu1, JpOd6, JpOd181, JpOd274, and JpOd282) and a merged group for all Middle, Late and Final Jomon (F5, F23, IK002, JpHi01, JpKo2, and JpKo13). Populations genetically closer to the later sub-period when compared to the earlier one with $Z > 3.0$ are designated by red triangles and those symmetrically related to both are designated by gray circles. The populations tested are split into four different periods, depending on their ages: Upper-Paleolithic (>16,000 years BP), Jomon (from 16,000 to 3,000 years BP), Post-Jomon (from 3,000 years BP to the present), and Present-day. There are almost no significant results in this analysis, suggesting that the Jomon were genetically isolated from the rest of the continent from the Initial to Final Jomon period. The Igorot population from the Philippines were found to be significantly closer to the Middle-Late-Final
Jomon subperiod when compared to Early Jomon; however this signal is not replicated with the comparison of Middle-Late-Final Jomon to Initial Jomon.
Fig. S14. A comparison of outgroup $f_3$ results for the Jomon dataset grouped by the island of origin measured using $f_3$(Jomon_Sub-Group, X; Mbuti). Jomon are separated into the three islands in the Japanese archipelago from which we have sample data: Honshu (JpFu1, JpOd6, JpOd274, JpOd282, JpOd181, IK002, JpKo2, and JpKo13), Shikoku (JpKa6904 and JpHi01) and Rebun Island (F5 and F23). Populations for X plotted are populations whose outgroup $f_3$-value is calculated using >100,000 SNP sites. The following ancients are included: the Jomon from the island not included in the comparison, Yayoi, Kofun, Yellow River (Miaozigou_MN, Shimao_LN, Upper_YR_IA, Upper_YR_LN, YR_LBIA, YR_LN, and YR_MN), West Liao River (HMMH_MN, WLR_BA, WLR_BA_o, WLR_LN, and WLR_MN), Northern China (Bianbian, Boshan, Xiaogao, Xiaojingshan, and Yumin), Southern China (Liangdao2), Amur River (AR_EN, AR_IA, and AR_Xianbei_IA), Chokhopani, Southeast Asia (McColl Group2, McColl Group3, McColl Group4, McColl Group5, McColl Group6, McColl Group3_1, and McColl Group4_1), Devil’s Gate Cave, Mongolian (ARS008 and ARS026), Baikal (Kurma_EBA, Lokomotiv_EN, Shamanka_EBA, Shamanka_EN, UstBelaya_EBA, UstBelaya_MED, UstBelaya_N, Ust_Ida_EBA, and Ust_Ida_LN), Yana_MED, Tianyuan (TY), Salkhit, Yana, Mal’ta (MA1),
Afontova Gora (AG2), Kolyma_M, and Hoabinhian (McColl Group1). The results show a remarkable level of consistency in results between each pair of islands; however there appears to be a slightly greater affinity for Yayoi samples (from northern Kyushu) to Honshu and Shikoku when compared to the geographically distant Rebun Island, which is consistent with Fig. 4c.
Fig. S15. A heatmap of pairwise outgroup $f_3$ comparisons between Jomon individuals grouped by archaeological site. Shared genetic drift is measured using outgroup $f_3$(any pair of archaeological sites; Mbuti), with multiple individuals originating from the same site grouped together: JpOd (JpOd6, JpOd181, JpOd274, and JpOd282), JpKo (JpKo2 and JoKo3) and Funadomari (F5 and F23). Site labels are colored according to the different islands on which they are located – Honshu samples are in green, Shikoku in yellow, and Rebun Island in red. There appears to be a slightly increased affinity within samples from Honshu, and the site representing the oldest individual (JpKa6904) and the most northerly site (Funadomari) separate from the others.
Fig. S16. Geographic and temporal display of $f_4$(Mbuti, X; Jomon, Yayoi) results. We compare the different affinities of all ancient and modern East Eurasians to the Jomon and the Yayoi. Results are divided into four periods based on the prehistory of Japan: the Upper-Paleolithic period (38,000-16,000 years BP), the Jomon period (16,000-3,000 years BP), the post-Jomon period (3,000 years BP-present) and Present-day. Populations that are significantly closer to Yayoi are marked by a triangle and a brown label and symmetrically-related populations are marked by a circle and a black label. The color within the shapes represents $f_4$-values, and only results based on >100,000 SNPs are plotted.
Fig. S17. A heatmap summary of outgroup $f_3$-statistics for all pairs of ancient and modern East Asians. Outgroup $f_3$-statistics are based on the form Outgroup $f_3$(Pop1, Pop2; Mbuti). We highlight three clusters: 1) the green square shows the high affinity of ancient Yellow River individuals and modern East Asians, 2) the blue square shows ancient and present-day individuals mainly from the Amur River basin and Baikal and 3) the black square shows the high affinity between the Jomon and Yayoi.
Fig. S18. Geographic and temporal display of $f_4$(Mbuti, X; Yayoi, Kofun) results. We compare the different affinities of all ancient and modern East Eurasians to the Yayoi and the Kofun. Results are divided into four periods based on the prehistory of Japan: the Upper-Paleolithic period (38,000-16,000 years BP), the Jomon period (16,000-3,000 years BP), the post-Jomon period (3,000 years BP-present) and Present-day. Populations that are significantly closer to the Kofun are marked by a triangle and a brown label and symmetrically-related populations are marked by a circle and a black label. The color within the shapes represents $f_4$-values, and only results based on >100,000 SNPs are plotted.
Fig. S19. Genetic ancestry of the Kofun modelled with two-way admixture. Samples from the Kofun period were modelled as two-way admixture between Yayoi and other source represented by Han, Korean, or YR_LBIA. Vertical bars represent ± 1 standard error estimated by qpAdm. The values of admixture proportions are shown in Table S9.
Fig. S20. Dating admixture in the Kofun individuals by the DATES program. Top: Estimated dates of admixture events (circles) and a mean calibrated age across three Kofun individuals (diamond) are plotted. Dating for two scenarios are presented: one in which the Kofun are derived from a single admixture event between Jomon and YR_LBIA, and another allowing for two separate events between the Jomon and Northeast Asian (N.EA.), and between the Jomon and East Asian (E.A.) ancestry. The estimates are converted to a number of years before present by adding the values to the mean age of samples, with an assumption of 25 years per generation. N.EA. and E.A. ancestry is represented by the West Liao River population (WLR_BA_o and HMMH_MN) or CHB in 1000 Genome Phase 3 respectively. The horizontal bars associated with the admixture dates show standard errors estimated by a weighted block jackknife method. Bottom: Ancestry covariances in the Kofun individuals. The plots show the exponential decay of weighted ancestry covariance (y-axis) with genetic distance (x-axis), in which a decay rate depends on the time since admixture. Fitting starts at a genetic distance of 0.45 centi Morgan (cM).
Fig. S21. Geographic and temporal display of $f_4$(Mbuti, X; Kofun, Japanese) results. We compare the different affinities of all ancient and modern East Eurasians to the Kofun and present-day Japanese. Results are divided into four periods based on the prehistory of Japan: the Upper-Paleolithic period (38,000-16,000 years BP), the Jomon period (16,000-3,000 years BP), the post-Jomon period (3,000 years BP-present) and Present-day. Populations that are significantly closer to the Japanese are marked by a diamond and a purple label and symmetrically-related populations are marked by a circle and a black label. The color within the shapes represents $f_4$-values, and only results based on >100,000 SNPs are plotted.
Fig. S22. Genetic ancestry of the Kofun and present-day Japanese population modelled as three-way admixture. The three-way admixture includes Jomon, Northeast Asian (represented by WLR_BA_o and HMMH_MN), and East Asian ancestry (represented by Han). Vertical bars represent ± 1 standard error estimated by \( qpAdm \). The values of admixture proportions for the Kofun and Japanese are shown in Tables S10 and S17.
### Table S1. Additional information on ancient Japanese samples.

| Associated Culture | Sample ID   | Lab.Code^a (Layer or Pit No.) | Age (BC or AD) Top: uncalibrated Bottom: calibrated | #Reads (BAM) | #SNPs (SGDP) | #SNPs (HOA) | Latitude | Longitude |
|--------------------|-------------|-------------------------------|------------------------------------------------------|--------------|--------------|-------------|---------|-----------|
|                |             |                               | Lower | Higher | Median |              |          |          |           |
| Jomon            | JpKa6904^b  | MTC-13800 (Layer 4)           | 5,960 | 6,056  | 6,008  | 441,555,803  | 3,672,440 | 593,322  | 33.61340  | 132.97460 |
|                  | JpOd274     | PLD-41178 (Layer 3)           | 3,425 | 3,477  | 3,451  | 78,075,659   | 2,770,870 | 460,505  | 36.72122  | 137.16677 |
|                  | JpOd6       | PLD-41176 (Layer 3)           | 3,282 | 3,336  | 3,309  | 6,3096,322   | 2,107,727 | 344,858  | 36.72122  | 137.16677 |
|                  | JpOd181     | PLD-41177 (Layer 3)           | 3,122 | 3,174  | 3,148  | 108,925,378  | 2,892,871 | 511,099  | 36.72122  | 137.16677 |
|                  | JpOd282     | PLD-41179 (Layer 3)           | 3,080 | 3,132  | 3,106  | 53,803,318   | 2,040,722 | 370,729  | 36.72122  | 137.16677 |
|                  | JpFu1       | PLD-39693 (Pit 1)             | 2,825 | 2,871  | 2,848  | 67,453,090   | 2,301,273 | 380,012  | 34.59220  | 133.77320 |
|                  | JpKo2       | PLD-39690 (Pit K2)            | 1,970 | 2,014  | 1,992  | 147,935,560  | 3,213,950 | 538,334  | 35.72088  | 139.96344 |
|                  | JpKo13      | PLD-39691 (Pit K13)           | 1,636 | 1,680  | 1,658  | 111,027,919  | 2,914,377 | 495,272  | 35.72088  | 139.96344 |
|                  | JpH01       | TKA-18417 (Burial No. 3)     | -     | -      | -      | 60,272,828   | 1,796,203 | 303,320  | 32.96353  | 132.56477 |
| Kofun            | Jplw32      | PLD-39692 (Pit 3)             | 418   | 458    | 438    | 258,117,426  | 3,630,288 | 589,026  | 36.61895  | 136.70233 |
|                  | Jplw31      | UBA40246 (Pit 3)              | 468   | 516    | 492    | 74,816,071   | 2,718,997 | 447,147  | 36.61895  | 136.70233 |
|                  | Jplw33      | UBA40248                      | 499   | 545    | 522    | 79,160,173   | 2,810,991 | 470,568  | 36.61895  | 136.70233 |
Abbreviations of Lab Code are as follows: Paleo Labo Co., Ltd, Japan (PLD), Research Center for Nuclear Science and Technology, University of Tokyo, Japan (MTC), Belfast 14CHRONO Centre, Ireland (UBA).

The radiocarbon dating results of JpKa6904 are referred from (89).

The radiocarbon dating results of JpHsi01 are referred from the Annual Archaeological Report from Ainan Town 2020, where only calibrated dates were reported.
| Sample ID | mtDNA Contamination rates | All sites | All sites without molecular damage |
|-----------|---------------------------|-----------|-----------------------------------|
| JpKa6904  | 1.461                     | JpKa6904  |                                   |
| JpOd274   | 1.131                     | JpOd274   |                                   |
| JpOd6     | 1.546                     | JpOd6     |                                   |
| JpOd181   | 0.909                     | JpOd181   |                                   |
| JpOd282   | 1.377                     | JpOd282   |                                   |
| JpFu1     | 2.152                     | JpFu1     |                                   |
| JpKo2     | 1.436                     | JpKo2     |                                   |
| JpKo13    | 1.495                     | JpKo13    |                                   |
| JpHi01    | 1.446                     | JpHi01    |                                   |
| Jplw32    | 0.405                     | Jplw32    |                                   |
| Jplw31    | 0.625                     | Jplw31    |                                   |
| Jplw33    | 0.748                     | Jplw33    |                                   |
### Table S3. Sexing results for newly sequenced data

| Sample ID | #Reads mapped to X chromosome | #Reads mapped to Y chromosome | #Total (X + Y) | Rx    | Ry   | SE   | Assigned Sex |
|-----------|-------------------------------|-------------------------------|---------------|-------|------|------|--------------|
| JpKa6904  | 21,685,400                    | 122,597                       | 21,807,997    | 0.994 | 0.006| 5.02E-10 | F            |
| JpFu1     | 3,265,205                     | 18,886                        | 3,284,091     | 0.994 | 0.006| 3.41E-09 | F            |
| JpKo2     | 7,234,163                     | 41,638                        | 7,275,801     | 0.994 | 0.006| 1.53E-09 | F            |
| JpKo13    | 5,435,655                     | 31,311                        | 5,466,966     | 0.994 | 0.006| 2.04E-09 | F            |
| JpHi01    | 2,907,655                     | 16,525                        | 2,924,180     | 0.994 | 0.006| 3.77E-09 | F            |
| JpOd274   | 1,933,203                     | 200,709                       | 2,133,912     | 0.906 | 0.094| 7.83E-08 | M            |
| JpOd6     | 3,060,597                     | 24,441                        | 3,085,038     | 0.992 | 0.008| 4.99E-09 | F            |
| JpOd181   | 2,593,378                     | 259,235                       | 2,852,613     | 0.909 | 0.091| 5.68E-08 | M            |
| JpOd282   | 1,275,323                     | 130,481                       | 1,405,804     | 0.907 | 0.093| 1.17E-07 | M            |
| JpIw31    | 3,670,669                     | 22,888                        | 3,693,557     | 0.994 | 0.006| 3.27E-09 | F            |
| JpIw32    | 6,595,047                     | 644,474                       | 7,239,521     | 0.911 | 0.089| 2.20E-08 | M            |
| JpIw33    | 3,939,727                     | 21,514                        | 3,961,241     | 0.995 | 0.005| 2.67E-09 | F            |
Table S4. A summary of all processed published data included in this analysis.

| Population Group | Individual IDs | Median calBP* | Removed as 1st degree relatives | #Inds included | Downloaded data format | Data type | References |
|------------------|----------------|---------------|---------------------------------|----------------|------------------------|-----------|------------|
| - Mal’ta (MA1)   | 24,157         | -             | 1                               | BAM WGS       |                        |           | Raghavan et al. (2014); (86) |
| - Alistova Gora (AG2) | 16,913         | -             | 1                               | BAM WGS       |                        |           |           |
| - Chokhpuni      | 2,775          | -             | 1                               | FASTQ WGS     |                        |           | Jeong et al. (2016); (91)    |
| - Satikhit       | 34,425         | -             | 1                               | BAM Capture   | Massilani et al. (2020); (92) |
| - Tianyuan (TY)  | 40,328         | -             | 1                               | BAM Capture   | Yang et al. (2017); (85) |
| - USB1           | 11,500*        | -             | 1                               | BAM WGS       | Moreno-Mayar et al. (2018); (78) |
| Botai           | BOT14, BOT15, BOT2016 | 5,399 - 5,161 | -                               | 3 FASTQ WGS   |                        |           |           |
| CentralSteppe EMBA | EBA1, EBA2     | 4,200*        | -                               | 2 FASTQ WGS   |                        |           |           |
| Kama_EBA        | DA354, DA358, DA360 | 4,169 - 4,078* | -                               | 3 FASTQ WGS   |                        |           |           |
| Lokomotiv_EN    | DA340, DA341, DA357, DA359 | 6,713*        | -                               | 4 FASTQ WGS   |                        |           |           |
| Namaza_CA       | DA379, DA380, DA381, DA383 | 5,263 - 5,173 | -                               | DA379 3 FASTQ WGS |                        |           |           |
| Okunevo_EMBA    | RISE515, RISE516, RISE662, RISE664, RISE666, RISE670, RISE671, RISE672, RISE673, RISE674, RISE675, RISE677, RISE680, RISE681, RISE683, RISE684, RISE685, RISE718, RISE719 | 4,555 - 3,963 | -                               | RISE516, RISE673 17 FASTQ WGS |                        |           |           |
| Shamanka_EBA    | DA334, DA335, DA336, DA337, DA338, DA339 | 3,871 - 3,706* | -                               | DA335, DA338 4 FASTQ WGS |                        |           | de Barros Dumgaard et al. (2018); (17) |
| Shamanka_EN     | DA245, DA246,DA247, DA248, DA249, DA250, DA251, DA252, DA253, DA362 | 7,123 - 6,319* | -                               | 10 FASTQ WGS   |                        |           |           |
| SidelkinoEHG_ML | Sidelkino      | 11,259        | -                               | 1 FASTQ WGS   |                        |           |           |
| Turkmenistan_JA | DA382          | 2,805         | -                               | 1 FASTQ WGS   |                        |           |           |
| UstIda_EBA      | DA343, DA353, DA356, DA361 | 3,854*        | -                               | 4 FASTQ WGS   |                        |           |           |
| UstIda_LN       | DA342, DA344, DA345, DA355 | 4,885*        | -                               | 4 FASTQ WGS   |                        |           |           |
| Yamnaya         | Yamnaya        | 4,900*        | -                               | 1 FASTQ WGS   |                        |           |           |
| McColl_Group1    | La368, Ma911 | 7,040 - 2,865* | -                               | 2 FASTQ WGS, Capture |                        |           | McColl et al. (2018); (12)  |
| McColl_Group2    | La364, La727, La898, Ma912, Vt832, Vt860 | -10,000 - 2,800* | -                               | 6 FASTQ WGS, Capture |                        |           |           |
| McColl_Group3    | Vt777, Vt779, Vt781, Vt796, Vt808 | 2,275 - 2,242* | -                               | 4 FASTQ WGS   |                        |           |           |
| McColl_Group3_1  | Th551, Vt719 | 1,687 - 223* | -                               | 1 FASTQ WGS, Capture |                        |           |           |
| Sample Group | Sample Code | Total Reads | Read Error | Library Type |
|---------------|-------------|-------------|-------------|--------------|
| McColl_Group4 | Th519, Th521, Th530, Th705 | 1,792 - 1,736* | - | 4 FASTQ WGS |
| McColl_Group4 | V778 | 2,549* | - | 2 FASTQ WGS |
| McColl_Group5 | In661, In662 | 2,152 - 1,917* | - | 2 FASTQ WGS, Capture |
| McColl_Group6 | Ma554, Ma555, Phi534 | 1,877 - 299* | - | 3 FASTQ WGS, Capture |
| ARS008 | ARS008 | 3,172 | - | 1 FASTQ WGS |
| ARS026 | ARS026 | 2,962 | - | 1 FASTQ WGS |
| DevilsCave_N | NEO235, NEO236, NEO237, NEO238, NEO239, NEO240 | 7,658 - 7,515 | - | 4 FASTQ WGS |
| Elven_IA | NEO241, NEO242, NEO243, NEO246, NEO247, NEO248, NEO249, NEO250, NEO251, NEO253 | 2,229 - 1,646 | - | 10 FASTQ WGS |
| Kolyma_M | Kolyma1 | 9,769 | - | 1 FASTQ WGS |
| Yana_MED | Yana_young | 766 | - | 1 FASTQ WGS |
| Yana_UP | Yana1, Yana2 | 31,630 | - | 2 FASTQ WGS |
| Magadan_BA | M9984, M10831 | 3,065 - 3,000 | - | 2 FASTQ WGS |
| Uelen_IA | NEO234, NEO233 | 2,816 - 1,774 | - | 2 FASTQ WGS |
| UstBelaya_EBA | NEO230, NEO231, NEO232, NEO298 | 4,862 - 4,546 | - | 4 FASTQ WGS |
| UstBelaya_MED | NEO299 | 598 | - | 1 FASTQ WGS |
| UstBelaya_N | NEO229 | 6,579 | - | 1 FASTQ WGS |
| AR_EN | WQM4, ZLNJ-2 | 7,443 - 7,350 | - | 2 FASTQ WGS |
| AR_IA | ZLNJ-1 | 1,843 | - | 1 FASTQ WGS |
| AR_Xianbei_IA | MGS-M6, MGS-M7L, MGS-MTR | 1,800* | MGS-M7L | 2 FASTQ WGS |
| HMBJH_Min | HMF32 | 5,615 | - | 1 FASTQ WGS |
| Miaozigou_Min | MZG016-1, MZG016, MZG023 | 5,500* | - | 3 FASTQ WGS |
| Shimao_LN | SM-SGDLM27, SM-SGDLM6, SM-SGDLM7X | 4064 - 4,000* | - | 3 FASTQ WGS |
| Upper_YR_IA | DCZ-M17IV, DCZ-M21III, DCZ-M22IV, DCZ-M6 | 2,000 - 1,852* | - | 4 FASTQ WGS |
| Upper_YR_LN | JCKM1-1, LJM14, LJM2, LJM25, LJM3, LJM4, LJM5 | 4,800 - 3,800* | LJM5 | 6 FASTQ WGS |
| WLR_BA | 91KLH11, 91KLH18 | 2,813 - 2,650* | - | 2 FASTQ WGS |
| WLR_BA_o | 91KLM2 | 2,650* | - | 1 FASTQ WGS |
| WLR_LN | EDMI24, EDMI39, EDMI76 | 4,000 - 3,554 | - | 3 FASTQ WGS |
| WLR_MN | BLSM27S, BLSM41, BLSM45 | 5,300 - 5,168 | - | 3 FASTQ WGS |
| YR_LIBA | HHTM13, HHTW13, DXNTM2, JXNTM23, LOM41, LOM79 | 3,000 - 2,153* | - | 6 FASTQ WGS |

* Denotes trimmed reads
| YR_LN        | HJTM107, HJTM109, PLTM310, PLTM311, PLTM312, PLTM313, WD-WTH16, WD-WT352 | 4.110 - 3.700* | PLTM312 | 7 | FASTQ | WGS |
|--------------|--------------------------------------------------------------------------|----------------|----------|---|--------|-----|
| YR_MN        | WGH35-1, WGM20, WGM35, WGM43, WGM30, WGM765, WGM94, XW-MIR18             | 6.056 - 5.180  | -        | 8 | FASTQ | WGS |
| Xiaocun      | L5705, L5700, L5692, L5706, L5704, L5703, L5701                           | 4.372 - 4.329  | -        | 7 | BAM   | Capture |
| Xiaojingshan | XJIS309_M7, XJIS1311_M16, XJIS309_M4                                   | 7.661 - 7.797  | -        | 3 | BAM   | Capture |
| Tanahisan    | L7415, L7417, L4698, L5694                                             | 4.472 - 4.318  | -        | 4 | BAM   | Capture |
| Suyang       | SuogangB1, SuogangB3                                                    | 4.530*         | -        | 2 | BAM   | Capture |
|              | Boshan                                                                  | 8,180          | -        | 1 | BAM   | Capture |
|              | Yumin                                                                   | 8,375          | -        | 1 | BAM   | Capture |
|              | Xiaogao                                                                  | 8,684          | -        | 1 | BAM   | Capture |
|              | Liangdasi1                                                               | 8,190          | -        | 1 | BAM   | Capture |
|              | Bianbian                                                                | 9,513          | -        | 1 | BAM   | Capture |
|              | Liangdasi2                                                               | 7,575          | -        | 1 | BAM   | Capture |
|              | Chuanyun                                                                 | 308            | -        | 1 | BAM   | Capture |
|              | Qihe                                                                     | 8,394          | -        | 1 | BAM   | Capture |

*The values show the most recent and oldest ages if multiple samples were sequenced from the same site in a previous study. The asterisks indicate that the age is not calibrated.*
Table S5. Modelling on the genetic ancestry of the Jomon individuals as a mixture of two sources by *qpWave* and *qpAdm*.

| Left populations: | Rank 0 (Single ancestor) | Rank 1 (Two ancestors) | Rank 2 (Full model) | Tail probability | Admixture proportions (± 1 standard error) |
|-------------------|--------------------------|------------------------|---------------------|------------------|------------------------------------------|
| Hoabinhian DevilsCave_N | Tail | Tail-diff | Tail | Tail-diff | Tail | Tail-diff | Hoabinhian | DevilsCave_N |
|                    | 1.20E-169 | 2.75E-05 | 1.85E-168 | 2.758E-05 | 2.81E-05 | - | - |
### Table S6. Results for $f_4$-tests with the form of $f_4$(Mbuti, Yana; Jomon, X).

| Pop1 | Pop2 | Pop3 | Pop4 (X) | $f_4$  | sd   | Z-score (bold if $Z < -3.0$) |
|------|------|------|----------|-------|------|-----------------------------|
| Mbuti | Yana | Jomon | Ami      | -0.000755 | 0.000263 | -2.871                      |
|       |      |       | Atayal   | -0.001147 | 0.000307 | -3.729                      |
|       |      |       | Dai      | -0.000892 | 0.000244 | -3.656                      |
|       |      |       | Daur     | -0.000933 | 0.000308 | -3.032                      |
|       |      |       | Han      | -0.000954 | 0.000263 | -3.628                      |
|       |      |       | Japanese | -0.000804 | 0.000239 | -3.366                      |
|       |      |       | Korean   | -0.000772 | 0.000258 | -2.998                      |
|       |      |       | Lahu     | -0.000948 | 0.000266 | -3.561                      |
|       |      |       | Miao     | -0.00087 | 0.000263 | -3.312                      |
|       |      |       | Mongola  | -0.000819 | 0.000293 | -2.796                      |
|       |      |       | Oroqen   | -0.000674 | 0.000271 | -2.49                       |
|       |      |       | She      | -0.000734 | 0.000287 | -2.562                      |
|       |      |       | Tu       | -0.001025 | 0.000263 | -3.901                      |
|       |      |       | Tujia    | -0.001048 | 0.000271 | -3.867                      |
|       |      |       | Xibo     | -0.000937 | 0.000261 | -3.593                      |
|       |      |       | Burmese  | -0.001301 | 0.000322 | -4.041                      |
|       |      |       | Cambodian| -0.001120 | 0.000267 | -4.195                      |
|       |      |       | Dusun    | -0.001059 | 0.000270 | -3.914                      |
|       |      |       | Kinh     | -0.001085 | 0.000276 | -3.931                      |
|       |      |       | Thai     | -0.001248 | 0.000269 | -4.643                      |
|       |      |       | Yi       | -0.00071 | 0.000269 | -2.639                      |
|       |      |       | DevilsCave_N | -0.00003 | 0.00026 | -0.126                      |
|       |      |       | Shamanka_EN | 0.00038 | 0.00024 | 1.574                      |
|       |      |       | Lokomotiv_EN | 0.00035 | 0.00027 | 1.287                      |
Table S7. Modelling on the genetic ancestry of the Yayoi individuals as a mixture of two sources by *qpWave* and *qpAdm*.

| Left populations: | qpWave | qpAdm (Target: Yayoi) |
|-------------------|--------|-----------------------|
| - Yayoi           |        |                       |
| - Jomon           |        |                       |
| - Additional source |      |                       |
| Additional source | Tail   | Tail-diff | Tail | Tail-diff | Tail | Tail-diff | Admixture proportions (± 1 standard error) | Jomon | Additional source |
|                   |        |           |      |           |      |           |                                               |       |                 |
| **Right populations without a subset of Jomon** |        |           |      |           |      |           |                                               |       |                 |
| WLR_BA_o          | 5.39E-23 | 1 | 3.61E-01 | 4.15E-25 | 1 | 3.61E-01 | 3.64E-01 | 0.584 ± 0.076 | 0.416 ± 0.076 |
| HMMH_MN           | 2.72E-17 | 1 | 2.01E-01 | 1.01E-18 | 1 | 2.01E-01 | 2.02E-01 | 0.506 ± 0.088 | 0.494 ± 0.088 |
| UstBelaya_EBA     | 2.43E-23 | 1 | 4.64E-05 | 1.05E-20 | 1 | 4.64E-05 | 0.00E+00 | - | - |
| Ekven_IA          | 1.32E-27 | 1 | 1.45E-05 | 0.00E+00 | - | - |           |    |
| Even              | 6.99E-14 | 1 | 2.77E-02 | 5.62E-14 | 1 | 2.77E-02 | 2.80E-02 | - | - |
| Lokomotiv_EN      | 3.15E-23 | 1 | 8.01E-02 | 2.24E-24 | 1 | 8.01E-02 | 8.10E-02 | 0.550 ± 0.101 | 0.450 ± 0.101 |
| Shamanka_EN       | 3.24E-33 | 1 | 1.86E-02 | 6.80E-34 | 1 | 1.86E-02 | 1.90E-02 | - | - |
| **Northeast Asian ancestry (WLR_BA_o + HMMH_MN)** | 3.46E-28 | 1 | 2.64E-01 | 2.77E-30 | 1 | 2.64E-01 | 2.66E-01 | 0.613 ± 0.074 | 0.387 ± 0.074 |

| **Right populations with a subset of Jomon** |        |           |      |           |      |           |                                               |       |                 |
| WLR_BA_o          | 0 | 1 | 4.65E-01 | 0 | 1 | 4.65E-01 | 4.67E-01 | 0.542 ± 0.021 | 0.458 ± 0.021 |
| HMMH_MN           | 0 | 1 | 3.47E-01 | 0 | 1 | 3.47E-01 | 3.49E-01 | 0.491 ± 0.021 | 0.509 ± 0.021 |
| UstBelaya_EBA     | 0 | 1 | 9.02E-05 | 0 | 1 | 9.02E-05 | 0.00E+00 | - | - |
| Ekven_IA          | 0 | 1 | 8.23E-07 | 0 | 1 | 8.23E-07 | 0.00E+00 | - | - |
| Even              | 0 | 1 | 3.22E-02 | 0 | 1 | 3.22E-02 | 3.30E-02 | - | - |
| Lokomotiv_EN      | 0 | 1 | 1.62E-01 | 0 | 1 | 1.62E-01 | 1.64E-01 | 0.598 ± 0.019 | 0.402 ± 0.019 |
| Shamanka_EN       | 0 | 1 | 5.19E-02 | 0 | 1 | 5.19E-02 | 5.30E-02 | 0.623 ± 0.019 | 0.377 ± 0.019 |
| **Northeast Asian ancestry (WLR_BA_o + HMMH_MN)** | 3.46E-28 | 0 | 1 | 3.94E-01 | 0 | 1 | 3.96E-01 | 0.587 ± 0.02 | 0.413 ± 0.02 |

**Note:** Source population is highlighted by bold if the admixture is supported from modelling with a given set of the reference populations or by bold and red if the admixture is supported from modelling with and without a subset of Jomon included in the reference populations.
Table S8. Modelling on the genetic ancestry of the Kofun individuals as a mixture of two sources by *qpWave* and *qpAdm*.

| Left populations: |  |  |  |  | qpWave |  |  |  |  | Tail probability | qpAdm (Target: JpIw) |  |  |
|-------------------|-----------------------|-----------------------|-----------------------|-----------------------|-----------------------|-----------------------|-----------------------|-----------------------|-----------------------|-----------------------|-----------------------|-----------------------|
| - JpIw | - Jomon | - Additional source | Rank 0 (Single ancestor) | Rank 1 (Two ancestors) | Rank 2 (Full model) | Tail probability | Jomon | Additional source |
| Additional source | Tail | Tail-diff | Tail | Tail-diff | Tail | Tail-diff | Admixture proportions (± 1 standard error) |

**Right populations without a subset of Jomon**

|  |  |  |  |  | Tail | Tail-diff | Tail | Tail-diff | Tail | Tail-diff | Tail probability | Jomon | Additional source |
|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|
| WLR_BA_o | 4.25E-108 | 1 | 1.64E-07 | 2.87E-104 | 1 | 1.64E-07 | 0.00E+00 | - | - |
| HMMH_MN | 6.21E-107 | 1 | 7.73E-14 | 2.20E-96 | 1 | 7.73E-14 | 0.00E+00 | - | - |
| Lokomotiv_EN | 8.86E-133 | 1 | 3.65E-24 | 8.34E-112 | 1 | 3.65E-24 | 0.00E+00 | - | - |
| Northeast Asian ancestry (WLR_BA_o + HMMH_MN) | 4.09E-112 | 1 | 1.42E-15 | 8.27E-100 | 1 | 1.42E-15 | 0.00E+00 | - | - |

**Right populations with a subset of Jomon**

|  |  |  |  |  | Tail | Tail-diff | Tail | Tail-diff | Tail | Tail-diff | Tail probability | Jomon | Additional source |
|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|
| WLR_BA_o | 0 | 1 | 5.26E-08 | 0 | 1 | 5.26E-08 | 0.00E+00 | - | - |
| HMMH_MN | 0 | 1 | 1.60E-17 | 0 | 1 | 1.60E-17 | 0.00E+00 | - | - |
| Lokomotiv_EN | 0 | 1 | 6.75E-53 | 0 | 1 | 6.75E-53 | 0.00E+00 | - | - |
| Northeast Asian ancestry (WLR_BA_o + HMMH_MN) | 0 | 1 | 9.55E-18 | 0 | 1 | 9.55E-18 | 0.00E+00 | - | - |
Table S9. Modelling on the genetic ancestry of the Kofun individuals as a mixture of two sources by \textit{qpWave} and \textit{qpAdm}.

| Left populations: | \textit{qpWave} | \textit{qpAdm} (Target: JpIw) | Admixture proportions (+1 standard error) |
|-------------------|-----------------|-----------------------------|------------------------------------------|
| - JpIw            | Rank 0 (Single ancestor) | Rank 1 (Two ancestors) | Rank 2 (Full model) | Tail probability | Yayoi | Additional source |
| - Yayoi           | Tail | Tail-diff | Tail | Tail-diff | Tail | Tail-diff | 0.775 ± 0.046 | 0.225 ± 0.046 |
| - Additional source | | | | | | | 0.748 ± 0.059 | 0.307 ± 0.056 |

Right populations without a subset of Jomon

| Han | 2.59E-25 | 1 | 2.25E-01 | 3.42E-27 | 1 | 2.25E-01 | 2.32E-01 | 0.775 ± 0.046 | 0.225 ± 0.046 |
| Korean | 2.47E-20 | 1 | 6.01E-02 | 3.44E-21 | 1 | 6.01E-02 | 6.30E-02 | 0.748 ± 0.059 | 0.225 ± 0.059 |
| YR_LBIA | 4.43E-24 | 1 | 4.02E-01 | 2.54E-26 | 1 | 4.02E-01 | 4.06E-01 | 0.693 ± 0.056 | 0.307 ± 0.056 |
| Uygar | 1.43E-290 | 1 | 5.20E-02 | 2.49E-294 | 1 | 5.20E-02 | 6.20E-02 | 1.031 ± 0.004 | -0.031 ± 0.004 |
| Burmese | 2.96E-09 | 1 | 3.23E-01 | 1.89E-10 | 1 | 3.23E-01 | 3.27E-01 | -1.215 ± 1.328 | 2.215 ± 1.328 |
| Atayal | 2.50E-51 | 1 | 1.37E-09 | 1.58E-44 | 1 | 1.37E-09 | 0.00E+00 | - | - |
| Daur | 2.26E-12 | 1 | 5.51E-03 | 1.49E-11 | 1 | 5.51E-03 | 7.00E-03 | - | - |
| Lahu | 1.62E-15 | 1 | 7.48E-05 | 8.16E-13 | 1 | 7.48E-05 | 0.00E+00 | - | - |
| Miao | 1.21E-23 | 1 | 2.94E-03 | 4.94E-23 | 1 | 2.94E-03 | 3.00E-03 | - | - |
| Mongola | 1.50E-13 | 1 | 1.21E-02 | 3.38E-13 | 1 | 1.21E-02 | 1.40E-02 | - | - |
| Oroqen | 7.65E-18 | 1 | 3.44E-05 | 7.13E-15 | 1 | 3.44E-05 | 0.00E+00 | - | - |
| She | 4.08E-26 | 1 | 7.35E-03 | 4.56E-26 | 1 | 7.35E-03 | 8.00E-03 | - | - |
| Tu | 7.38E-17 | 1 | 1.07E-05 | 2.55E-13 | 1 | 1.07E-05 | 0.00E+00 | - | - |
| Tuja | 3.17E-21 | 1 | 2.30E-02 | 1.37E-21 | 1 | 2.30E-02 | 2.50E-02 | - | - |
| Xibo | 4.20E-11 | 1 | 9.19E-03 | 1.84E-10 | 1 | 9.19E-03 | 1.00E-02 | - | - |
| Cambodian | 1.19E-33 | 1 | 7.78E-05 | 1.43E-31 | 1 | 7.78E-05 | 0.00E+00 | - | - |
| Dusun | 7.57E-51 | 1 | 9.31E-11 | 8.12E-43 | 1 | 9.31E-11 | 0.00E+00 | - | - |
| Kinh | 2.91E-36 | 1 | 1.43E-09 | 3.37E-29 | 1 | 1.43E-09 | 0.00E+00 | - | - |
| Thai | 2.04E-32 | 1 | 9.29E-10 | 4.41E-25 | 1 | 9.29E-10 | 0.00E+00 | - | - |
| Yi | 4.41E-14 | 1 | 1.08E-03 | 1.46E-12 | 1 | 1.08E-03 | 1.00E-03 | - | - |
| Aleut | 5.37E-292 | 1 | 3.52E-02 | 1.56E-295 | 1 | 3.52E-02 | 4.30E-02 | - | - |
| Altaian | 2.86E-70 | 1 | 1.35E-02 | 1.43E-71 | 1 | 1.35E-02 | 1.90E-02 | - | - |
| Eskimo_Chaplin | 1.84E-56 | 1 | 1.03E-03 | 3.57E-56 | 1 | 1.03E-03 | 2.00E-03 | - | - |
| Eskimo_Naukan | 4.26E-110 | 1 | 7.34E-03 | 1.40E-111 | 1 | 7.34E-03 | 1.00E-02 | - | - |
| Eskimo_Sireniki | 1.84E-107 | 1 | 4.27E-03 | 1.25E-108 | 1 | 4.27E-03 | 6.00E-03 | - | - |
| Even | 3.30E-75 | 1 | 6.82E-03 | 3.24E-76 | 1 | 6.82E-03 | 9.00E-03 | - | - |
| Hezhen | 1.36E-14 | 1 | 3.25E-04 | 1.57E-12 | 1 | 3.25E-04 | 0.00E+00 | - | - |
| Itelman | 3.62E-73 | 1 | 6.28E-04 | 6.56E-73 | 1 | 6.28E-04 | 1.00E-03 | - | - |
| Tabularar | 3.21E-234 | 1 | 2.19E-02 | 3.26E-237 | 1 | 2.19E-02 | 2.70E-02 | - | - |
| Ulchi | 7.99E-18 | 1 | 2.67E-04 | 8.26E-16 | 1 | 2.67E-04 | 0.00E+00 | - | - |
| ARS008 | 7.96E-65 | 1 | 6.54E-04 | 1.87E-64 | 1 | 6.54E-04 | 1.00E-03 | - | - |
| ARS026 | 7.70E-244 | 1 | 3.81E-02 | 3.37E-247 | 1 | 3.81E-02 | 4.80E-02 | - | - |
| Lokomotiv_EN | 1.25E-47 | 1 | 6.86E-06 | 1.02E-44 | 1 | 6.86E-06 | 0.00E+00 | - | - |
| Shamanka_EBA | 2.88E-104 | 1 | 1.16E-04 | 1.48E-103 | 1 | 1.16E-04 | 0.00E+00 | - | - |
| Shamanka_EN | 2.59E-62 | 1 | 4.79E-07 | 2.09E-58 | 1 | 4.79E-07 | 0.00E+00 | - | - |
| Ust_Ida_EBA | 3.28E-128 | 1 | 1.86E-04 | 5.62E-128 | 1 | 1.86E-04 | 0.00E+00 | - | - |
| Ust_Ida_LN | 1.95E-142 | 1 | 8.41E-04 | 4.36E-143 | 1 | 8.41E-04 | 1.00E-03 | - | - |
| DevilsCave_N | 2.65E-17 | 1 | 3.10E-08 | 3.40E-11 | 1 | 3.10E-08 | 0.00E+00 | - | - |
| UstBelaya_N | 1.86E-26 | 1 | 7.33E-06 | 4.68E-23 | 1 | 7.33E-06 | 0.00E+00 | - | - |
| UstBelaya_EBA | 8.94E-112 | 1 | 2.94E-04 | 1.30E-111 | 1 | 2.94E-04 | 0.00E+00 | - | - |
| Ekven_IA | 3.18E-185 | 1 | 7.52E-04 | 3.94E-186 | 1 | 7.52E-04 | 1.00E-03 | - | - |
| Yana_MED | 8.01E-63 | 1 | 9.30E-04 | 1.34E-62 | 1 | 9.30E-04 | 1.00E-03 | - | - |
| McCell_Group2 | 3.58E-48 | 1 | 3.29E-08 | 8.99E-43 | 1 | 3.29E-08 | 0.00E+00 | - | - |
| McCell_Group3 | 1.05E-39 | 1 | 1.06E-09 | 1.41E-32 | 1 | 1.06E-09 | 0.00E+00 | - | - |
| McCell_Group4 | 1.29E-18 | 1 | 1.99E-02 | 8.81E-19 | 1 | 1.99E-02 | 2.20E-02 | - | - |
| Boshan | 6.25E-13 | 1 | 3.10E-04 | 9.03E-11 | 1 | 3.10E-04 | 0.00E+00 | - | - |
| AR_EN | 2.07E-19 | 1 | 3.81E-09 | 1.95E-12 | 1 | 3.81E-09 | 0.00E+00 | - | - |
| AR_Xianbei_IA | 1.81E-21 | 1 | 8.07E-08 | 7.08E-16 | 1 | 8.07E-08 | 0.00E+00 | - | - |
| HMMH_MN | 4.11E-22 | 1 | 3.87E-10 | 3.42E-14 | 1 | 3.87E-10 | 0.00E+00 | - | - |
| WLR_MN | 1.34E-17 | 1 | 2.13E-07 | 2.46E-12 | 1 | 2.13E-07 | 0.00E+00 | - | - |
| WLR_LN | 4.27E-15 | 1 | 4.75E-02 | 1.49E-15 | 1 | 4.75E-02 | 4.80E-02 | - | - |
| WLR_BA | 9.14E-14 | 1 | 3.56E-03 | 8.26E-13 | 1 | 3.56E-03 | 4.00E-03 | - | - |
| WLR_BA_o | 2.85E-15 | 1 | 1.56E-07 | 8.04E-10 | 1 | 1.56E-07 | 0.00E+00 | - | - |
| Miaozigou_MN | 1.61E-22 | 1 | 6.20E-06 | 6.41E-19 | 1 | 6.20E-06 | 0.00E+00 | - | - |
| Shimao_LN | 3.10E-19 | 1 | 3.91E-06 | 2.55E-15 | 1 | 3.91E-06 | 0.00E+00 | - | - |
| Upper_YR_LN | 1.20E-37 | 1 | 2.53E-10 | 7.83E-30 | 1 | 2.53E-10 | 0.00E+00 | - | - |
| Upper_YR_IA | 5.65E-20 | 1 | 3.64E-02 | 1.56E-20 | 1 | 3.64E-02 | 3.80E-02 | - | - |
| YR_MN | 6.12E-25 | 1 | 6.12E-06 | 2.08E-21 | 1 | 6.12E-06 | 0.00E+00 | - | - |
| YR_LN | 7.84E-27 | 1 | 4.77E-02 | 8.03E-28 | 1 | 4.77E-02 | 4.90E-02 | - | - |

Right populations with a subset of Jomon

| Han | 2.45E-240 | 1 | 2.54E-01 | 1.85E-245 | 1 | 2.54E-01 | 2.62E-01 | 0.736 ± 0.017 | 0.264 ± 0.017 |
| Korean | 2.37E-190 | 1 | 8.36E-02 | 2.28E-194 | 1 | 8.36E-02 | 8.70E-02 | 0.710 ± 0.020 | 0.290 ± 0.020 |
| YR_LBIA | 3.54E-214 | 1 | 5.11E-01 | 1.01E-219 | 1 | 5.11E-01 | 5.16E-01 | 0.680 ± 0.020 | 0.320 ± 0.020 |
| Language     | Value     |
|--------------|-----------|
| Uygur        | 0.00E+00  |
| Burmese      | 4.59E-154 |
| Atayal       | 3.73E-202 |
| Daur         | 1.32E-178 |
| Lahu         | 1.80E-208 |
| Miao         | 8.66E-214 |
| Mongola      | 6.37E-202 |
| Oroqen       | 8.07E-191 |
| She          | 5.35E-230 |
| Tu           | 3.40E-230 |
| Tujia        | 8.78E-210 |
| Xibo         | 8.61E-186 |
| Cambodian    | 1.33E-218 |
| Dusun        | 1.26E-232 |
| Kinh         | 2.36E-250 |
| Thai         | 1.62E-249 |
| Yi           | 3.62E-190 |
| Aleut        | 0.00E+00  |
| Altaian      | 8.80E-223 |
| Eskimo Chaplin | 1.21E-217 |
| Eskimo_Naukan | 6.49E-315 |
| Eskimo_Sireniki | 4.10E-286 |
| Even         | 3.83E-283 |
| Hezhen       | 4.05E-192 |
| Itelmen      | 1.27E-225 |
| Tubalar      | 0.00E+00  |
| Ulchi        | 1.41E-157 |
| ARS008       | 1.42E-212 |
| ARS026       | 0.00E+00  |
| Lokomotiv_EN | 3.94E-225 |
| Shamanka_EBA | 1.02E-289 |
| Shamanka_EN  | 8.56E-266 |
| Ust_Ida_EBA  | 4.28E-296 |
| Ust_Ida_LN   | 0.00E+00  |
| DevilsCave_N | 1.91E-149 |
| Source Population | Value 1       | Value 2       | Value 3       | Value 4       | Value 5       | Value 6       | Value 7       | Value 8       | Value 9       | Value 10      | Value 11      | Value 12      | Value 13      | Value 14      |
|-------------------|---------------|---------------|---------------|---------------|---------------|---------------|---------------|---------------|---------------|---------------|---------------|---------------|---------------|---------------|
| UstBelaya_N       | 1.04E-173     | 1             | 1.73E-22      | 7.72E-155     | 1             | 1.73E-22      | 0.00E+00      | -             | -             |               |               |               |               |               |
| UstBelaya_EBA     | 7.93E-304     | 1             | 3.89E-73      | 4.00E-234     | 1             | 3.89E-73      | 0.00E+00      | -             | -             |               |               |               |               |               |
| Ekven_IA          | 0.00E+00      | 1             | 1.09E-85      | 0.00E+00      | 1             | 1.09E-85      | 0.00E+00      | -             | -             |               |               |               |               |               |
| Yana_MED          | 9.84E-198     | 1             | 1.84E-62      | 2.14E-138     | 1             | 1.84E-62      | 0.00E+00      | -             | -             |               |               |               |               |               |
| McColl_Group2     | 2.99E-239     | 1             | 1.01E-41      | 4.56E-201     | 1             | 1.01E-41      | 0.00E+00      | -             | -             |               |               |               |               |               |
| McColl_Group3     | 1.33E-199     | 1             | 2.63E-31      | 7.88E-172     | 1             | 2.63E-31      | 0.00E+00      | -             | -             |               |               |               |               |               |
| McColl_Group4     | 4.42E-182     | 1             | 1.33E-19      | 2.95E-166     | 1             | 1.33E-19      | 0.00E+00      | -             | -             |               |               |               |               |               |
| Boshan            | 6.41E-122     | 1             | 4.22E-04      | 2.45E-122     | 1             | 4.22E-04      | 0.00E+00      | -             | -             |               |               |               |               |               |
| AR_EN             | 1.00E-163     | 1             | 5.58E-13      | 1.02E-154     | 1             | 5.58E-13      | 0.00E+00      | -             | -             |               |               |               |               |               |
| AR_Xianbei_IA     | 8.94E-167     | 1             | 4.32E-16      | 1.65E-154     | 1             | 4.32E-16      | 0.00E+00      | -             | -             |               |               |               |               |               |
| HMMH_MN           | 1.80E-159     | 1             | 3.73E-16      | 4.42E-147     | 1             | 3.73E-16      | 0.00E+00      | -             | -             |               |               |               |               |               |
| WLR_MN            | 6.59E-170     | 1             | 3.22E-07      | 3.42E-167     | 1             | 3.22E-07      | 0.00E+00      | -             | -             |               |               |               |               |               |
| WLR_IA            | 2.70E-163     | 1             | 7.90E-02      | 4.68E-167     | 1             | 7.90E-02      | 8.00E-02      | 0.440 ± 0.026 | 0.560 ± 0.026 |               |               |               |               |               |
| WLR_BA            | 1.75E-166     | 1             | 6.91E-03      | 7.88E-169     | 1             | 6.91E-03      | 7.00E-03      | -             | -             |               |               |               |               |               |
| WLR_BA_o          | 5.58E-142     | 1             | 2.63E-07      | 6.31E-139     | 1             | 2.63E-07      | 0.00E+00      | -             | -             |               |               |               |               |               |
| Miaozigou_MN      | 7.84E-183     | 1             | 6.67E-07      | 1.43E-180     | 1             | 6.67E-07      | 0.00E+00      | -             | -             |               |               |               |               |               |
| Shimao_LN         | 1.67E-172     | 1             | 7.90E-06      | 2.24E-171     | 1             | 7.90E-06      | 0.00E+00      | -             | -             |               |               |               |               |               |
| Upper_YR_LN       | 1.11E-240     | 1             | 9.54E-16      | 2.97E-229     | 1             | 9.54E-16      | 0.00E+00      | -             | -             |               |               |               |               |               |
| Upper_YR_IA       | 1.62E-210     | 1             | 5.73E-02      | 1.96E-214     | 1             | 5.73E-02      | 5.90E-02      | 0.662 ± 0.021 | 0.338 ± 0.021 |               |               |               |               |               |
| YR_MN             | 3.78E-208     | 1             | 6.28E-06      | 3.64E-207     | 1             | 6.28E-06      | 0.00E+00      | -             | -             |               |               |               |               |               |
| YR_LN             | 4.83E-225     | 1             | 4.53E-02      | 6.56E-229     | 1             | 4.53E-02      | 4.70E-02      | -             | -             |               |               |               |               |               |

**Note:** Source population is highlighted by bold if the admixture is supported from modelling with a given set of the reference populations or by bold and red if the admixture is supported from modelling with and without a subset of Jomon included in the reference populations.
Table S10 Modelling on the genetic ancestry of the Kofun individuals as a mixture of three sources by \textit{qpWave} and \textit{qpAdm}.

| Left populations: | \textit{qpWave} | \textit{qpAdm} (Target: JpIw) |
|-------------------|-----------------|-----------------------------|
| - JpIw            | Rank            | Admixture proportions (± 1 standard error) |
| - Jomon           | Probability     | Jomon | Second source | Third source |
| - Two more sources| 0 | 1 | 2 | 3 | Tail | 0.150 ± 0.038 | 0.215 ± 0.088 | 0.636 ± 0.068 |
|                   | 1.20E-155 | 1.29E-19 | 3.91E-01 | 1 | 3.94E-01 | | |
|                   | 8.23E-141 | 2.00E-21 | 3.91E-01 | | | | |
|                   | Tail-diff 1 | 9.00E-02 | 0.282 ± 0.076 | -0.415 ± 0.249 | 1.133 ± 0.193 |
| Right populations without a subset of Jomon | | | | |
| Han               | Tail-diff 1 | 9.00E-02 | 0.282 ± 0.076 | -0.415 ± 0.249 | 1.133 ± 0.193 |
| Korea             | Tail-diff 1 | 1.61E-15 | 8.84E-02 | | | |
| YR_LBIA           | Tail-diff 1 | 7.83E-01 | 0.216 ± 0.043 | -0.306 ± 0.139 | 1.090 ± 0.112 |
|                   | 1.33E-155 | 2.09E-13 | 7.82E-01 | 1 | 7.83E-01 | | |
|                   | 1.45E-147 | 1.83E-15 | 7.82E-01 | | | |
| Right populations with a subset of Jomon | | | | |
| Han               | Tail-diff 1 | 4.81E-01 | 0.139 ± 0.010 | 0.231 ± 0.071 | 0.631 ± 0.066 |
| Korea             | Tail-diff 1 | 2.20E-02 | - | - | - |
| YR_LBIA           | Tail-diff 1 | 1.43E-19 | 2.149E-02 | | | |
|                   | 0 | 1 | 0 | 1.132E-29 | 4.772E-01 | 4.81E-01 | | 0.139 ± 0.010 | 0.231 ± 0.071 | 0.631 ± 0.066 |
|                   | 1 | 0 | 8.008E-20 | 2.149E-02 | 2.20E-02 | - | - | - |
| Note: Source population is highlighted by bold if the admixture is supported from modelling with a given set of the reference populations or by bold and red if the admixture is supported from modelling with and without a subset of Jomon included in the reference populations.
Table S11. Testing fittings of three-way versus two-way admixture to the genetic ancestry of the Kofun by *qpAdm* with the third source represented by Han.

| Source combinations | Degree of freedom | Tail probability | $x^2$ | $P$-value for the nested model (Three-way vs. Two-way models) |
|---------------------|-------------------|------------------|-------|---------------------------------------------------------------|
| **Left populations:** |                   |                  |       |                                                               |
| Jomon               |                   |                  |       |                                                               |
| Northeast Asian ancestry (WLR\_BA\_o + HMMH\_MN) | 5 | 3.94E-1 | 5.186 | -                                                             |
| Han                 |                   |                  |       |                                                               |
| **Models**          |                   |                  |       |                                                               |
| Three-way           | 5                  | 3.94E-1          | 5.186 | -                                                             |
| Two-way             | 6                  | 9.90E-2          | 10.665| 1.90E-2                                                        |
| Two-way             | 6                  | 2.00E-2          | 20.541| 8.91E-5                                                        |
| Two-way             | 6                  | 2.42E-15         | 80.822| 0.00E+00                                                       |
| **Right populations without a subset of Jomon** |                   |                  |       |                                                               |
| Three-way           | 5                  | 3.94E-1          | 5.186 | -                                                             |
| Two-way             | 6                  | 9.90E-2          | 10.665| 1.90E-2                                                        |
| Two-way             | 6                  | 2.00E-2          | 20.541| 8.91E-5                                                        |
| Two-way             | 6                  | 2.42E-15         | 80.822| 0.00E+00                                                       |
| **Right populations with a subset of Jomon** |                   |                  |       |                                                               |
| Three-way           | 6                  | 4.81E-1          | 5.505 | -                                                             |
| Two-way             | 7                  | 4.58E-2          | 14.319| 2.99E-3                                                        |
| Two-way             | 7                  | 2.05E-29         | 151.414| 0.00E+00                                                     |
| Two-way             | 7                  | 1.68E-17         | 94.215| 0.00E+00                                                      |
Table S12. Modelling on the genetic ancestry of the Kofun individuals as a mixture of two sources (Jomon and additional source) by qpWave and qpAdm.

| Left populations: | qpWave | qpAdm (Target: JpIw) |
|-------------------|---------|-----------------------|
|                   | Rank 0 (Single ancestor) | Rank 1 (Two ancestors) | Rank 2 (Full model) | Tail probability | Admixture proportions (+ 1 standard error) |
|                   | Tail | Tail-diff | Tail | Tail-diff | Tail | Tail-diff | Jomon | Additional source |
| Additional source |       |         |       |         |       |         |       |                   |
| Han               | 3.43E-145 | 1 | 9.59E-02 | 1.80E-148 | 1 | 9.59E-02 | 9.70E-02 | 0.212 ± 0.031 | 0.788 ± 0.031 |
| YR_LBIA          | 6.23E-149 | 1 | 1.41E-01 | 1.74E-152 | 1 | 1.41E-01 | 1.42E-01 | 0.149 ± 0.027 | 0.851 ± 0.027 |
| Burmese          | 4.28E-98 | 1 | 2.99E-01 | 1.15E-101 | 1 | 2.99E-01 | 3.00E-01 | -0.169 ± 0.088 | 1.169 ± 0.099 |
| Atayal           | 5.97E-157 | 1 | 3.04E-35 | 7.92E-125 | 1 | 3.04E-35 | 0.00E+00 | 0.304 ± 0.054 | 0.696 ± 0.054 |
| Daur             | 8.79E-98 | 1 | 6.46E-04 | 7.31E-98 | 1 | 6.46E-04 | 1.00E-03 | -0.355 ± 0.135 | 1.355 ± 0.135 |
| Korean           | 1.92E-131 | 1 | 1.92E-02 | 1.16E-133 | 1 | 1.92E-02 | 2.00E-02 | 0.177 ± 0.035 | 0.823 ± 0.035 |
| Lahu             | 5.62E-114 | 1 | 7.38E-05 | 3.80E-113 | 1 | 7.38E-05 | 0.00E+00 | 0.504 ± 0.048 | 0.946 ± 0.048 |
| Miao             | 1.28E-132 | 1 | 3.31E-04 | 1.03E-132 | 1 | 3.31E-04 | 0.00E+00 | 0.184 ± 0.036 | 0.816 ± 0.036 |
| Mongola          | 1.41E-101 | 1 | 1.71E-03 | 3.36E-102 | 1 | 1.71E-03 | 2.00E-03 | -0.247 ± 0.076 | 1.247 ± 0.076 |
| Oroqen           | 1.82E-104 | 1 | 2.47E-09 | 1.23E-98  | 1 | 2.47E-09 | 0.00E+00 | -0.398 ± 0.116 | 1.398 ± 0.116 |
| She              | 1.61E-132 | 1 | 6.10E-04 | 6.37E-133 | 1 | 6.10E-04 | 1.00E-03 | 0.243 ± 0.033 | 0.757 ± 0.033 |
| Tu               | 1.46E-106 | 1 | 4.40E-08 | 4.25E-102 | 1 | 4.40E-08 | 0.00E+00 | -0.268 ± 0.096 | 1.268 ± 0.096 |
| Tuja             | 3.33E-123 | 1 | 1.23E-02 | 4.25E-125 | 1 | 1.23E-02 | 1.30E-02 | 0.191 ± 0.034 | 0.809 ± 0.034 |
| Uygur            | 0.00E+00 | 1 | 1.23E-23 | 0.00E+00 | 1 | 1.23E-23 | 0.00E+00 | 1.565 ± 0.053 | -0.565 ± 0.053 |
| Xibo             | 1.40E-106 | 1 | 4.41E-03 | 9.38E-108 | 1 | 4.41E-03 | 5.00E-03 | -0.093 ± 0.063 | 1.093 ± 0.063 |
| Cambodian        | 4.07E-113 | 1 | 1.51E-15 | 7.58E-101 | 1 | 1.51E-15 | 0.00E+00 | -0.799 ± 0.189 | 1.799 ± 0.189 |
| Dusun            | 5.56E-159 | 1 | 1.17E-41 | 2.03E-120 | 1 | 1.17E-41 | 0.00E+00 | 0.177 ± 0.057 | 0.823 ± 0.057 |
| Khil             | 4.45E-142 | 1 | 1.47E-19 | 6.80E-126 | 1 | 1.47E-19 | 0.00E+00 | 0.19 ± 0.042 | 0.81 ± 0.042 |
| Thai             | 2.38E-120 | 1 | 2.37E-20 | 3.48E-103 | 1 | 2.37E-20 | 0.00E+00 | -0.286 ± 0.102 | 1.286 ± 0.102 |
| Yi               | 7.39E-110 | 1 | 2.45E-04 | 1.39E-109 | 1 | 2.45E-04 | 0.00E+00 | 0.074 ± 0.042 | 0.926 ± 0.042 |
| Aleut            | 0.00E+00 | 1 | 4.80E-25 | 0.00E+00 | 1 | 4.80E-25 | 0.00E+00 | 1.544 ± 0.051 | -0.544 ± 0.051 |
| Altaian          | 2.35E-156 | 1 | 1.52E-22 | 3.35E-137 | 1 | 1.52E-22 | 0.00E+00 | 3.221 ± 0.796 | -2.221 ± 0.796 |
| Eskimo_Chaplin   | 7.07E-141 | 1 | 9.23E-23 | 2.14E-121 | 1 | 9.23E-23 | 0.00E+00 | 88.014 ± 6552.437 | -87.014 ± 6552.437 |
| Eskimo_Naukan    | 5.20E-203 | 1 | 4.19E-24 | 1.58E-182 | 1 | 4.19E-24 | 0.00E+00 | 4.443 ± 1.317 | -3.443 ± 1.317 |
| Eskimo_Sireniki  | 3.40E-184 | 1 | 1.57E-30 | 4.81E-157 | 1 | 1.57E-30 | 0.00E+00 | 5.059 ± 1.801 | -4.059 ± 1.801 |
| Even             | 5.07E-162 | 1 | 5.12E-19 | 1.56E-146 | 1 | 5.12E-19 | 0.00E+00 | -6.139 ± 3.613 | 7.139 ± 3.613 |
| Hezhen           | 1.22E-101 | 1 | 8.29E-05 | 9.75E-101 | 1 | 8.29E-05 | 0.00E+00 | -0.216 ± 0.076 | 1.216 ± 0.076 |
| Itelman          | 7.29E-154 | 1 | 7.04E-29 | 3.20E-128 | 1 | 7.04E-29 | 0.00E+00 | 11.759 ± 13.954 | -10.759 ± 13.954 |
| Location          | P-value   | Theta      | 95% CI     | p-value   | Theta      | 95% CI     |
|-------------------|-----------|------------|------------|-----------|------------|------------|
| Tubalar           | 1.22E-295 | 2.58E-24  | 2.37E-275  | 2.58E-24  | 0.00E+00   | 1.735 ± 0.078 |
| Ulchi             | 1.91E-106 | 1.10E-06   | 1.69E-103  | 1.10E-06  | 0.00E+00   | -0.463 ± 0.113 |
| ARS008            | 1.60E-142 | 3.12E-26   | 1.66E-119  | 3.12E-26  | 0.00E+00   | 41.448 ± 239.75 |
| ARS026            | 4.31E-303 | 1.84E-24   | 1.11E-282  | 1.84E-24  | 0.00E+00   | 1.524 ± 0.049 |
| Lokomotiv_EN      | 8.86E-133 | 3.65E-24   | 8.34E-112  | 3.65E-24  | 0.00E+00   | -0.871 ± 0.205 |
| Shamanka_EBA      | 7.32E-176 | 9.13E-34   | 2.24E-145  | 9.13E-34  | 0.00E+00   | 35.296 ± 108.781 |
| Shamanka_EN       | 2.12E-145 | 4.85E-41   | 2.15E-107  | 4.85E-41  | 0.00E+00   | -0.987 ± 0.29 |
| Ust_Ida_EBA       | 1.40E-208 | 2.24E-42   | 1.57E-169  | 2.24E-42  | 0.00E+00   | 10.111 ± 9.893 |
| Ust_Ida_LN        | 1.33E-208 | 1.83E-35   | 1.48E-176  | 1.83E-35  | 0.00E+00   | 3.669 ± 0.797 |
| DevilsCave_N      | 2.49E-110 | 1.39E-08   | 2.31E-105  | 1.39E-08  | 0.00E+00   | -0.31 ± 0.074 |
| UstBelaya_N       | 1.46E-112 | 5.57E-12   | 5.20E-104  | 5.57E-12  | 0.00E+00   | 1.31 ± 0.074 |
| UstBelaya_EBA     | 1.67E-174 | 1.77E-37   | 3.01E-140  | 1.77E-37  | 0.00E+00   | 14 ± 15.745 |
| Ekven_IA          | 6.14E-259 | 8.06E-42   | 1.17E-220  | 8.06E-42  | 0.00E+00   | 3.213 ± 0.594 |
| Yana_MED          | 1.42E-146 | 1.31E-21   | 2.60E-128  | 1.31E-21  | 0.00E+00   | -5.453 ± 4.083 |
| McColl_Group2     | 2.49E-126 | 7.88E-32   | 1.61E-97   | 7.88E-32  | 0.00E+00   | -0.521 ± 0.135 |
| McColl_Group3     | 5.64E-126 | 2.21E-29   | 1.21E-99   | 2.21E-29  | 0.00E+00   | -0.087 ± 0.034 |
| McColl_Group4     | 3.28E-99  | 1.35E-05   | 2.16E-97   | 1.35E-05  | 0.00E+00   | 1.234 ± 0.048 |
| Boshan            | 1.32E-101 | 2.95E-04   | 2.46E-101  | 2.95E-04  | 0.00E+00   | 0.005 ± 0.014 |
| AR_EN             | 6.18E-109 | 3.26E-10   | 3.24E-102  | 3.26E-10  | 0.00E+00   | 1.096 ± 0.034 |
| AR_Xianbei_IA     | 2.53E-111 | 7.78E-12   | 6.50E-103  | 7.78E-12  | 0.00E+00   | -0.09 ± 0.029 |
| HMMH_MN           | 6.21E-107 | 7.73E-14   | 2.20E-96   | 7.73E-14  | 0.00E+00   | -0.151 ± 0.071 |
| WLR_MN            | 5.57E-113 | 1.13E-07   | 5.06E-109  | 1.13E-07  | 0.00E+00   | 0.111 ± 0.05 |
| WLR_LN            | 8.34E-110 | 1.35E-02   | 1.28E-111  | 1.35E-02  | 1.40E-02   | 0.049 ± 0.017 |
| WLR_BA            | 1.24E-113 | 9.53E-04   | 4.37E-114  | 9.53E-04  | 1.00E-03   | 0.054 ± 0.03 |
| WLR_BA_o          | 4.25E-108 | 1.64E-07   | 2.87E-104  | 1.64E-07  | 0.00E+00   | -0.017 ± 0.052 |
| Miaozigou_MN      | 5.58E-128 | 5.24E-09   | 1.00E-122  | 5.24E-09  | 0.00E+00   | 0.074 ± 0.022 |
| Shimao_LN         | 3.66E-119 | 8.73E-08   | 3.83E-115  | 8.73E-08  | 0.00E+00   | 0.104 ± 0.039 |
| Upper_YR_LN       | 3.25E-145 | 9.06E-22   | 8.85E-127  | 9.06E-22  | 0.00E+00   | 0.144 ± 0.038 |
| Upper_YR_IA       | 4.69E-130 | 1.03E-02   | 6.42E-132  | 1.03E-02  | 1.10E-02   | 0.138 ± 0.031 |
| YR_MN             | 2.98E-131 | 2.39E-08   | 9.85E-127  | 2.39E-08  | 0.00E+00   | 0.133 ± 0.034 |
| YR_LN             | 1.30E-149 | 4.88E-03   | 3.06E-151  | 4.88E-03  | 5.00E-03   | 0.173 ± 0.029 |

**Right populations with a subset of Jomon**

| Location          | P-value   | Theta      | 95% CI     | p-value   | Theta      | 95% CI     |
|-------------------|-----------|------------|------------|-----------|------------|------------|
| Han               | 0.00E+00  | 4.90E-02   | 0.00E+00   | 4.90E-02  | 5.00E-02   | 0.158 ± 0.009 |
| YR_LBIA           | 0.00E+00  | 1.51E-01   | 0.00E+00   | 1.51E-01  | 1.54E-01   | 0.125 ± 0.008 |

**Results**

- The table compares the genetic diversity and differentiation among various populations, primarily focusing on a subset of Jomon populations.
- Significant p-values (e.g., 1.40E-208) indicate strong evidence against the null hypothesis of no genetic differentiation.
- The 95% confidence interval (CI) provides a range for the estimated theta value, indicating the uncertainty.
- The results show a high degree of genetic diversity and differentiation across the compared populations.
| Language    | p-value  | Value  | p-value  | Value  | p-value  | Value  | p-value  | Value  | p-value  | Value  | p-value  | Value  |
|-------------|----------|--------|----------|--------|----------|--------|----------|--------|----------|--------|----------|--------|
| Burmese     | 0.00E+00 | 1.01E-04 | 0.00E+00 | 1.01E-04 | 0.143 ± 0.011 | 0.857 ± 0.011 |
| Atayal      | 0.00E+00 | 6.44E-37 | 0.00E+00 | 6.44E-37 | 0.147 ± 0.012 | 0.853 ± 0.012 |
| Daur        | 0.00E+00 | 5.13E-11 | 0.00E+00 | 5.13E-11 | 0.15 ± 0.011 | 0.85 ± 0.011 |
| Korean      | 0.00E+00 | 2.18E-02 | 0.00E+00 | 2.18E-02 | 2.20E-02 | 0.141 ± 0.01 | 0.859 ± 0.01 |
| Lahu        | 0.00E+00 | 1.61E-05 | 0.00E+00 | 1.61E-05 | 0.159 ± 0.01 | 0.841 ± 0.01 |
| Miao        | 0.00E+00 | 5.27E-04 | 0.00E+00 | 5.27E-04 | 1.00E-03 | 0.152 ± 0.01 | 0.848 ± 0.01 |
| Mongola     | 0.00E+00 | 7.20E-13 | 0.00E+00 | 7.20E-13 | 0.00E+00 | 0.14 ± 0.01 | 0.86 ± 0.01 |
| Oroqen      | 0.00E+00 | 1.02E-20 | 0.00E+00 | 1.02E-20 | 0.121 ± 0.011 | 0.879 ± 0.011 |
| She         | 0.00E+00 | 1.30E-04 | 0.00E+00 | 1.30E-04 | 0.00E+00 | 0.167 ± 0.009 | 0.833 ± 0.009 |
| Tu          | 0.00E+00 | 7.12E-18 | 0.00E+00 | 7.12E-18 | 0.158 ± 0.01 | 0.842 ± 0.01 |
| Tuja        | 0.00E+00 | 1.39E-02 | 0.00E+00 | 1.39E-02 | 1.40E-02 | 0.155 ± 0.01 | 0.845 ± 0.01 |
| Uygur       | 0.00E+00 | 9.88E-324 | 0.00E+00 | 9.88E-324 | 0.152 ± 0.014 | 0.848 ± 0.014 |
| Xibo        | 0.00E+00 | 3.15E-06 | 0.00E+00 | 3.15E-06 | 0.131 ± 0.01 | 0.869 ± 0.01 |
| Cambodian   | 0.00E+00 | 1.34E-39 | 0.00E+00 | 1.34E-39 | 0.144 ± 0.011 | 0.856 ± 0.011 |
| Dusun       | 0.00E+00 | 7.29E-41 | 0.00E+00 | 7.29E-41 | 0.162 ± 0.01 | 0.838 ± 0.01 |
| Kinh        | 0.00E+00 | 5.41E-19 | 0.00E+00 | 5.41E-19 | 0.00E+00 | 0.17 ± 0.009 | 0.83 ± 0.009 |
| Thai        | 0.00E+00 | 1.27E-31 | 0.00E+00 | 1.27E-31 | 0.162 ± 0.01 | 0.838 ± 0.01 |
| Yi          | 0.00E+00 | 9.90E-05 | 0.00E+00 | 9.90E-05 | 0.00E+00 | 0.151 ± 0.009 | 0.849 ± 0.009 |
| Aleut       | 0.00E+00 | 1.07E-319 | 0.00E+00 | 1.07E-319 | 0.148 ± 0.017 | 0.852 ± 0.017 |
| Altaian     | 0.00E+00 | 6.57E-80 | 0.00E+00 | 6.57E-80 | 0.121 ± 0.013 | 0.879 ± 0.013 |
| Eskimo_Chiplin | 0.00E+00 | 4.65E-67 | 0.00E+00 | 4.65E-67 | 0.00E+00 | 0.118 ± 0.014 | 0.882 ± 0.014 |
| Eskimo_Naukan | 0.00E+00 | 3.01E-129 | 0.00E+00 | 3.01E-129 | 0.107 ± 0.013 | 0.893 ± 0.013 |
| Eskimo_Sireniki | 0.00E+00 | 4.25E-126 | 0.00E+00 | 4.25E-126 | 0.00E+00 | 0.121 ± 0.013 | 0.879 ± 0.013 |
| Even        | 0.00E+00 | 7.24E-94 | 0.00E+00 | 7.24E-94 | 0.115 ± 0.011 | 0.885 ± 0.011 |
| Hezhen      | 0.00E+00 | 4.95E-12 | 0.00E+00 | 4.95E-12 | 0.123 ± 0.01 | 0.877 ± 0.01 |
| Itelman     | 0.00E+00 | 2.53E-78 | 0.00E+00 | 2.53E-78 | 0.09 ± 0.014 | 0.91 ± 0.014 |
| Tabalar     | 0.00E+00 | 4.30E-256 | 0.00E+00 | 4.30E-256 | 0.135 ± 0.015 | 0.865 ± 0.015 |
| Ulchi       | 0.00E+00 | 3.80E-17 | 0.00E+00 | 3.80E-17 | 0.07 ± 0.013 | 0.93 ± 0.013 |
| ARS008      | 0.00E+00 | 8.13E-75 | 0.00E+00 | 8.13E-75 | 0.105 ± 0.012 | 0.895 ± 0.012 |
| ARS026      | 0.00E+00 | 4.84E-262 | 0.00E+00 | 4.84E-262 | 0.103 ± 0.016 | 0.897 ± 0.016 |
| Lokomotiv_EN | 0.00E+00 | 6.75E-53 | 0.00E+00 | 6.75E-53 | 0.087 ± 0.01 | 0.913 ± 0.01 |
| Shamanka_EBA | 0.00E+00 | 6.10E-117 | 0.00E+00 | 6.10E-117 | 0.105 ± 0.011 | 0.895 ± 0.011 |
| Shamanka_EN  | 0.00E+00 | 2.83E-69 | 0.00E+00 | 2.83E-69 | 0.111 ± 0.01 | 0.889 ± 0.01 |
| Ust_Lda_EBA | 0.00E+00 | 4.90E-143 | 0.00E+00 | 4.90E-143 | 0.089 ± 0.011 | 0.911 ± 0.011 |
| Ust_Lda_LN  | 0.00E+00 | 2.83E-158 | 0.00E+00 | 2.83E-158 | 0.114 ± 0.012 | 0.886 ± 0.012 |
| Source Population | T1 | T2 | F1  | F2  | p-value  | F1  | F2  | p-value |
|-------------------|----|----|-----|-----|----------|-----|-----|---------|
| DevilsCave_N      | 0.00E+00 | 1  | 1.29E-10 | 0.00E+00 | 1  | 1.29E-10 | 0.00E+00 | 0.073 ± 0.01 | 0.927 ± 0.01 |
| UstBelaya_N       | 0.00E+00 | 1  | 1.94E-23 | 0.00E+00 | 1  | 1.94E-23 | 0.00E+00 | 0.05 ± 0.008 | 0.95 ± 0.008 |
| UstBelaya_EBA     | 0.00E+00 | 1  | 2.64E-123 | 0.00E+00 | 1  | 2.64E-123 | 0.00E+00 | 0.113 ± 0.011 | 0.887 ± 0.011 |
| Ekven_IA          | 0.00E+00 | 1  | 8.14E-203 | 0.00E+00 | 1  | 8.14E-203 | 0.00E+00 | 0.126 ± 0.012 | 0.874 ± 0.012 |
| Yana_MED          | 0.00E+00 | 1  | 2.01E-68 | 0.00E+00 | 1  | 2.01E-68 | 0.00E+00 | 0.08 ± 0.011 | 0.92 ± 0.011 |
| McColl_Group2     | 0.00E+00 | 1  | 2.02E-50 | 0.00E+00 | 1  | 2.02E-50 | 0.00E+00 | 0.095 ± 0.01 | 0.905 ± 0.01 |
| McColl_Group3     | 0.00E+00 | 1  | 3.49E-36 | 0.00E+00 | 1  | 3.49E-36 | 0.00E+00 | 0.067 ± 0.005 | 0.933 ± 0.005 |
| McColl_Group4     | 0.00E+00 | 1  | 3.40E-21 | 0.00E+00 | 1  | 3.40E-21 | 0.00E+00 | 0.084 ± 0.007 | 0.916 ± 0.007 |
| Boshan            | 0.00E+00 | 1  | 3.12E-04 | 0.00E+00 | 1  | 3.12E-04 | 0.00E+00 | 0.024 ± 0.003 | 0.976 ± 0.003 |
| AR_EN             | 0.00E+00 | 1  | 1.31E-15 | 0.00E+00 | 1  | 1.31E-15 | 0.00E+00 | 0.053 ± 0.005 | 0.947 ± 0.005 |
| AR_Xianbei_IA     | 0.00E+00 | 1  | 8.26E-18 | 0.00E+00 | 1  | 8.26E-18 | 0.00E+00 | 0.04 ± 0.005 | 0.96 ± 0.005 |
| HMMH_MN           | 0.00E+00 | 1  | 1.60E-17 | 0.00E+00 | 1  | 1.60E-17 | 0.00E+00 | 0.071 ± 0.01 | 0.929 ± 0.01 |
| WLR_MN            | 0.00E+00 | 1  | 2.78E-08 | 0.00E+00 | 1  | 2.78E-08 | 0.00E+00 | 0.112 ± 0.01 | 0.888 ± 0.01 |
| WLR_LN            | 0.00E+00 | 1  | 2.46E-02 | 0.00E+00 | 1  | 2.46E-02 | 2.60E-02 | 0.05 ± 0.004 | 0.95 ± 0.004 |
| WLR_BA            | 0.00E+00 | 1  | 1.41E-03 | 0.00E+00 | 1  | 1.41E-03 | 1.00E-03 | 0.08 ± 0.007 | 0.92 ± 0.007 |
| WLR_BA_o          | 0.00E+00 | 1  | 5.26E-08 | 0.00E+00 | 1  | 5.26E-08 | 0.00E+00 | 0.079 ± 0.01 | 0.921 ± 0.01 |
| Miaozigou_MN      | 0.00E+00 | 1  | 8.37E-09 | 0.00E+00 | 1  | 8.37E-09 | 0.00E+00 | 0.053 ± 0.005 | 0.947 ± 0.005 |
| Shimao_LN         | 0.00E+00 | 1  | 2.21E-07 | 0.00E+00 | 1  | 2.21E-07 | 0.00E+00 | 0.114 ± 0.009 | 0.886 ± 0.009 |
| Upper_YR_LN       | 0.00E+00 | 1  | 2.12E-21 | 0.00E+00 | 1  | 2.12E-21 | 0.00E+00 | 0.12 ± 0.008 | 0.88 ± 0.008 |
| Upper_YR_IA       | 0.00E+00 | 1  | 1.43E-02 | 0.00E+00 | 1  | 1.43E-02 | 1.50E-02 | 0.115 ± 0.008 | 0.885 ± 0.008 |
| YR_MN             | 0.00E+00 | 1  | 6.15E-08 | 0.00E+00 | 1  | 6.15E-08 | 0.00E+00 | 0.119 ± 0.008 | 0.881 ± 0.008 |
| YR_LN             | 0.00E+00 | 1  | 2.80E-03 | 0.00E+00 | 1  | 2.80E-03 | 3.00E-03 | 0.127 ± 0.008 | 0.873 ± 0.008 |

Note: Source population is highlighted by bold if the admixture is supported from modelling with a given set of the reference populations or by bold and red if the admixture is supported from modelling with and without a subset of Jomon included in the reference populations.
Table S13. Testing fittings of three-way versus two-way admixture to the genetic ancestry of the Kofun by \textit{qpAdm} with the third source represented by YR_LBIA.

| Left populations: | Models | Degree of freedom | Tail probability | $x^2$ | P-value for the nested model (Three-way vs. Two-way models) |
|-------------------|--------|-------------------|------------------|------|----------------------------------------------------------|
| Target: JpIw      |        |                   |                  |      |                                                          |
| Sources:          |        |                   |                  |      |                                                          |
| - Jomon           |        |                   |                  |      |                                                          |
| - Northeast Asian (WLR_BA_o and HMMH_MN) | |                   |                  |      |                                                          |
| - YR_LBIA        |        |                   |                  |      |                                                          |
| Right populations without a subset of Jomon | | 5 | 7.83E-1 | 2.454 | - |
| Three-way (Jomon, Northeast Asian, and YR_LBIA) | | 6 | 1.46E-1 | 9.520 | 7.86E-3 |
| Two-way (Jomon and YR_LBIA) | | 6 | 1.45E-6 | 37.430 | 3.34E-9 |
| Two-way (Northeast Asian and YR_LBIA) | | 6 | 2.13E-15 | 81.088 | 0.00E+00 |
| Right populations with a subset of Jomon | | 6 | 2.34E-1 | 8.059 | - |
| Three-way (Jomon, Northeast Asian, and YR_LBIA) | | 7 | 1.49E-1 | 10.764 | 1.00E-1 |
| Two-way (Jomon and YR_LBIA) | | 7 | 4.10E-18 | 97.188 | 0.00E+00 |
| Two-way (Northeast Asian and HYR_LBIAan) | | 7 | 1.55E-17 | 94.391 | 0.00E+00 |
Table S14. Testing fittings of two-way admixture to the genetic ancestry of the Yayoi and Kofun by *qpAdm*.

| Left populations: Target: Yayoi or JpIw Sources: | qpWave | qp-Adm |
|-----------------------------------------------|--------|--------|
|                                              | Rank 0 (Single ancestor) | Rank 1 (Two ancestors) | Rank 2 (Full model) | Tail probability | Admixture proportions (± 1 standard error) |
|                                              | Tail | Tail-diff | Tail | Tail-diff | Tail | Tail-diff | Jomon | YR_LBIA |
| Right populations with a subset of Jomon       |      |          |      |          |      |          |       |         |
| Yayoi                                        | 0    | 1        | 3.88E-01 | 0 | 1 | 3.88E-01 | 3.89E-01 | 0.626 ± 0.019 | 0.374 ± 0.019 |
| JpIw                                         | 0    | 1        | 1.51E-01 | 0 | 1 | 1.51E-01 | 1.54E-01 | 0.125 ± 0.008 | 0.875 ± 0.008 |
Table S15. Testing fittings of three-way versus four-way admixture to the genetic ancestry of the Kofun by *qpAdm*.

| Left populations: | Three-way admixture (Jomon, Northeast Asian, and East Asian ancestry) | Four-way admixture | \(P\)-value for nested model |
|-------------------|---------------------------------------------------------------------|---------------------|-----------------------------|
| Target: JpIw      |                                                                     |                     |                             |
| Sources:          |                                                                     |                     |                             |
| - Jomon           |                                                                     |                     |                             |
| - Northeast Asian ancestry (WLR\_BA\_o + HMMH\_MN) |                     |                     |                             |
| - East Asian ancestry (Han) |                     |                     |                             |
| - Additional source |                                                                  |                     |                             |

| Additional source | \(\chi^2\)-value | Degree of freedom | \(\chi^2\)-value | Degree of freedom | \(P\)-value |
|-------------------|------------------|------------------|------------------|------------------|------------|

**Right populations without a subset of Jomon**

| Population       | \(\chi^2\)-value | Degree of freedom | \(\chi^2\)-value | Degree of freedom | \(P\)-value |
|------------------|------------------|------------------|------------------|------------------|------------|
| ARS026           | 5.182            | 5                | 4.936            | 4                | 0.620      |
| Shamanka\_EBA    | 5.197            | 5                | 3.681            | 4                | 0.218      |
| Shamanka\_EN     | 5.181            | 5                | 4.693            | 4                | 0.485      |
| Ust\_Ida\_EBA   | 5.166            | 5                | 4.130            | 4                | 0.309      |
| Namazga\_CA     | 5.263            | 5                | 5.257            | 4                | 0.938      |
| Okunevo\_EMBA   | 5.245            | 5                | 4.713            | 4                | 0.466      |
| UstBelaya\_EBA  | 5.192            | 5                | 4.619            | 4                | 0.449      |
| Yana\_MED       | 5.145            | 5                | 4.807            | 4                | 0.561      |
| McColl\_Group2  | 5.179            | 5                | 3.216            | 4                | 0.161      |
| McColl\_Group3  | 5.176            | 5                | 5.191            | 4                | 1.000      |
| Miaozigou\_MN   | 5.164            | 5                | 3.470            | 4                | 0.193      |
| Upper\_YR\_LN   | 5.179            | 5                | 3.911            | 4                | 0.260      |
| YR\_MN          | 5.205            | 5                | 2.177            | 4                | 0.082      |
| YR\_LN          | 5.170            | 5                | 5.216            | 4                | 1.000      |
| YR\_LBIA        | 5.184            | 5                | 2.416            | 4                | 0.096      |

**Right populations with a subset of Jomon**

| Population       | \(\chi^2\)-value | Degree of freedom | \(\chi^2\)-value | Degree of freedom | \(P\)-value |
|------------------|------------------|------------------|------------------|------------------|------------|
| ARS026           | 5.527            | 6                | 5.470            | 5                | 0.811      |
| Shamanka\_EBA    | 5.690            | 6                | 4.852            | 5                | 0.360      |
| Shamanka\_EN*    | 32.111 (5.723)   | 6 (6)            | 5.843            | 5                | 0.000 (1.000) |
| Ust\_Ida\_EBA   | 5.589            | 6                | 4.985            | 5                | 0.437      |
| Namazga\_CA*    | 101.784 (9.735)  | 6 (6)            | 5.925            | 5                | 0.000 (0.051) |
| Okunevo\_EMBA*  | 97.024 (8.482)   | 6 (6)            | 5.598            | 5                | 0.000 (0.089) |
| UstBelaya\_EBA  | 6.170            | 6                | 5.419            | 5                | 0.386      |
| Yana\_MED       | 5.612            | 6                | 5.495            | 5                | 0.732      |
| McColl\_Group2  | 6.328            | 6                | 6.164            | 5                | 0.686      |
| Population       | FST  | N  | P  | Q  | D  |
|------------------|------|----|----|----|----|
| McColl_Group3    | 6.391| 6  | 6.524 | 5  | 1.000 |
| Miaozigou_MN     | 6.315| 6  | 6.401 | 5  | 1.000 |
| Upper_YR_LN      | 9.218| 6  | 5.735 | 5  | 0.062 |
| YR_MN            | 7.132| 6  | 5.361 | 5  | 0.183 |
| YR_LN            | 7.588| 6  | 6.653 | 5  | 0.334 |
| YR_LBIA          | 8.747| 6  | 7.590 | 5  | 0.282 |

*These populations have an alternative model of three-way admixture shown in the parentheses that includes Jomon, East Asian ancestry, and additional source tested, instead of Jomon, Northeast Asian, and East Asian ancestry, likely due to their shared ancestry with the source population representing Northeast Asian ancestry (WLR_BA_o + HMMH_MN).*
Table 16. Modelling on the genetic ancestry of modern Japanese only by Kofun ancestry (no admixture) or by a mixture of two sources by \textit{qpAdm}.

| Left populations: | No admixture (JpIw) | Two-way admixture (JpIw and additional source) | \(P\)-value for nested model |
|-------------------|----------------------|-----------------------------------------------|-------------------------------|
| Target: Japanese Sources: | | | |
| - JpIw | Additional source | \(\chi^2\)-value | Degree of freedom | \(\chi^2\)-value | Degree of freedom |
| Yayoi | 7 | 3.929 | 6 | 2.670 | 0.262 |
| Jomon | 7 | 3.914 | 6 | 3.235 | 0.410 |
| Han | 7 | 3.922 | 6 | 2.577 | 0.246 |
| Tuja | 7 | 3.917 | 6 | 3.464 | 0.301 |
| Atayal | 7 | 3.901 | 6 | 3.895 | 0.938 |
| Daur | 7 | 3.903 | 6 | 2.627 | 0.259 |
| Korean | 7 | 3.918 | 6 | 3.428 | 0.484 |
| Lahu | 7 | 3.913 | 6 | 3.723 | 0.663 |
| Miao | 7 | 3.918 | 6 | 2.718 | 0.273 |
| Mongola | 7 | 3.916 | 6 | 2.858 | 0.304 |
| Oroqen | 7 | 3.915 | 6 | 2.125 | 0.181 |
| She | 7 | 3.916 | 6 | 3.206 | 0.399 |
| Tu | 7 | 3.918 | 6 | 2.420 | 0.221 |
| Xibo | 7 | 3.917 | 6 | 2.589 | 0.249 |
| Burmese | 7 | 3.903 | 6 | 2.381 | 0.217 |
| Cambodian | 7 | 3.914 | 6 | 3.799 | 0.735 |
| Dusun | 7 | 3.914 | 6 | 3.810 | 0.747 |
| Kinh | 7 | 3.918 | 6 | 3.697 | 0.638 |
| Thai | 7 | 3.917 | 6 | 3.930 | 1.000 |
| Yi | 7 | 3.917 | 6 | 3.872 | 0.832 |
| Aleut | 7 | 3.912 | 6 | 2.183 | 0.189 |
| Altaian | 7 | 3.905 | 6 | 2.272 | 0.201 |
| Chukchi | 7 | 3.902 | 6 | 2.390 | 0.219 |
| Eskimo_Chaplin | 7 | 3.902 | 6 | 2.155 | 0.186 |
| Eskimo_Naukan | 7 | 3.913 | 6 | 2.267 | 0.200 |
| Eskimo_Sireniki | 7 | 3.912 | 6 | 2.177 | 0.188 |
| Even | 7 | 3.920 | 6 | 2.460 | 0.227 |
| Hezhen | 7 | 3.917 | 6 | 2.999 | 0.338 |
| Population   | N  | R  | S  | L  | D  |
|--------------|----|----|----|----|----|
| Itelman      | 7  | 3.905 | 6  | 1.943 | 0.161 |
| Mansi        | 7  | 3.910 | 6  | 2.276 | 0.201 |
| Russian      | 7  | 3.905 | 6  | 2.479 | 0.232 |
| Tubalar      | 7  | 3.911 | 6  | 2.344 | 0.211 |
| Ulchi        | 7  | 3.915 | 6  | 2.016 | 0.168 |
| **Right populations with a subset of Jomon** | | | | | |
| Yayoi        | 8  | 4.404 | 7  | 3.234 | 0.279 |
| Jomon        | 8  | 4.397 | 7  | 3.599 | 0.372 |
| Han          | 8  | 4.397 | 7  | 3.126 | 0.260 |
| Tujia        | 8  | 4.390 | 7  | 3.548 | 0.359 |
| Atayal       | 8  | 4.371 | 7  | 4.154 | 0.641 |
| Daur         | 8  | 4.373 | 7  | 4.392 | 1.000 |
| Korean       | 8  | 4.392 | 7  | 3.538 | 0.355 |
| Lahu         | 8  | 4.385 | 7  | 3.752 | 0.426 |
| Miao         | 8  | 4.392 | 7  | 3.165 | 0.268 |
| Mongola      | 8  | 4.389 | 7  | 4.391 | 1.000 |
| Oroqen       | 8  | 4.388 | 7  | 4.261 | 0.722 |
| She          | 8  | 4.390 | 7  | 3.354 | 0.309 |
| Tu           | 8  | 4.391 | 7  | 4.405 | 1.000 |
| Xibo         | 8  | 4.391 | 7  | 4.383 | 0.929 |
| Burmese      | 8  | 4.372 | 7  | 4.351 | 0.885 |
| Cambodian    | 8  | 4.386 | 7  | 4.325 | 0.805 |
| Dusun        | 8  | 4.386 | 7  | 3.889 | 0.481 |
| Kinh         | 8  | 4.392 | 7  | 3.692 | 0.403 |
| Thai         | 8  | 4.390 | 7  | 4.062 | 0.567 |
| Yi           | 8  | 4.391 | 7  | 3.868 | 0.470 |
| Aleut        | 8  | 4.384 | 7  | 3.413 | 0.324 |
| Altaian      | 8  | 4.375 | 7  | 3.719 | 0.418 |
| Chukchi      | 8  | 4.371 | 7  | 3.484 | 0.346 |
| Eskimo_Chaplin | 8  | 4.372 | 7  | 3.724 | 0.421 |
| Eskimo_Naukan | 8  | 4.386 | 7  | 3.707 | 0.410 |
| Eskimo_Sireniki | 8  | 4.384 | 7  | 3.628 | 0.385 |
| Even         | 8  | 4.395 | 7  | 4.034 | 0.548 |
| Hezhen       | 8  | 4.391 | 7  | 4.393 | 1.000 |
| Itelman      | 8  | 4.375 | 7  | 3.509 | 0.352 |
| Language  | Value1 | Value2 | Value3 | Value4 |
|-----------|--------|--------|--------|--------|
| Mansi     | 8      | 4.382  | 7      | 3.432  | 0.330  |
| Russian   | 8      | 4.374  | 7      | 3.442  | 0.334  |
| Tubalar   | 8      | 4.384  | 7      | 3.527  | 0.355  |
| Ulchi     | 8      | 4.387  | 7      | 3.836  | 0.458  |
Table S17. Modelling on the genetic ancestry of present-day Japanese as a mixture of three sources by *qpWave* and *qpAdm*.

| Left populations: | qpWave |          | qpAdm (Target: Japanese) |          |
|-------------------|---------|----------|--------------------------|----------|
|                   |         | Probability | Admixture proportions (± 1 standard error) |          |
|                   |         | Rank | Jomon | Northeast Asian ancestry | East Asian ancestry |
|                   |         | 0 | 1 | 2 | 3 | Tail | 0 | 1 | 0.131 ± 0.035 | 0.156 ± 0.077 | 0.713 ± 0.061 |
|                   |         | Tail | 1.69E-154 | 7.15E-19 | 7.68E-01 | 1 | 7.71E-01 |
|                   |         | Tail-diff | 1 | 1.90E-140 | 3.36E-21 | 7.68E-01 |
| Right populations without a subset of Jomon | Tail | 0 | 3.047E-26 | 8.370E-01 | 1 | 8.40E-01 |
| Right populations with a subset of Jomon | Tail | 1 | 0 | 2.761E-29 | 8.370E-01 |

**Note:** Source population is highlighted by bold if the admixture is supported from modelling with a given set of the reference populations or by bold and red if the admixture is supported from modelling with and without a subset of Jomon included in the reference populations.
Table S18. Test of the genetic continuity between Kofun and present-day Japanese.

| Model          | Drift parameter | Log-likelihood |
|----------------|-----------------|----------------|
|                | $t_1$ (JPT)     | $t_2$ (Kofun)  |                 |
| Continuity     | 0.009           | -              | -3,697,125.918  |
|                | (fixed as $t_2 = 0$) |               |                 |
| Non-continuity | 0.004           | 0.015          | -3,696,423.430  |
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