SUPPLEMENTARY INFORMATION FOR

On the Origin and Spread of Feral Pigeons

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Suplementary Notes

Sampling effort. To investigate the genomic patterns of current pigeon populations of different evolutionary histories, we intentionally targeted our sampling to cover four distinct categories (Figure 1). Furthermore, to help root the evolutionary relationships between these groups, we also included a small number of individuals representing the Columba livia intermedia (Strickland, 1844) subspecies. Specifically in this regard, we sampled five populations from Sri Lanka, where two of them were from urban localities (Colombo and Trincomalee), one was from a Conservation National Park (Pigeon Island) and two others were captive populations maintained by local breeders (Wattala and Wellawatte) (Supplementary Fig.

1). To check for data reproducibility, we sequenced two of the samples twice (Tehran_16-GBS and Perth_02-GBS) to serve as replicates. Finally, to serve as external outgroups, we also generated data from five samples of (*Columba palumbus Linnaeus, 1758*) captured in Copenhagen (Denmark), one captive sample of (*Streptopelia risoria* Linnaeus, 1758), and additionally incorporated previously published whole genome resequence data from a Columba rupestris8. (we also included the WGS library to serve as another replicate) (Supplementary Spreadsheet).

Methods

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References
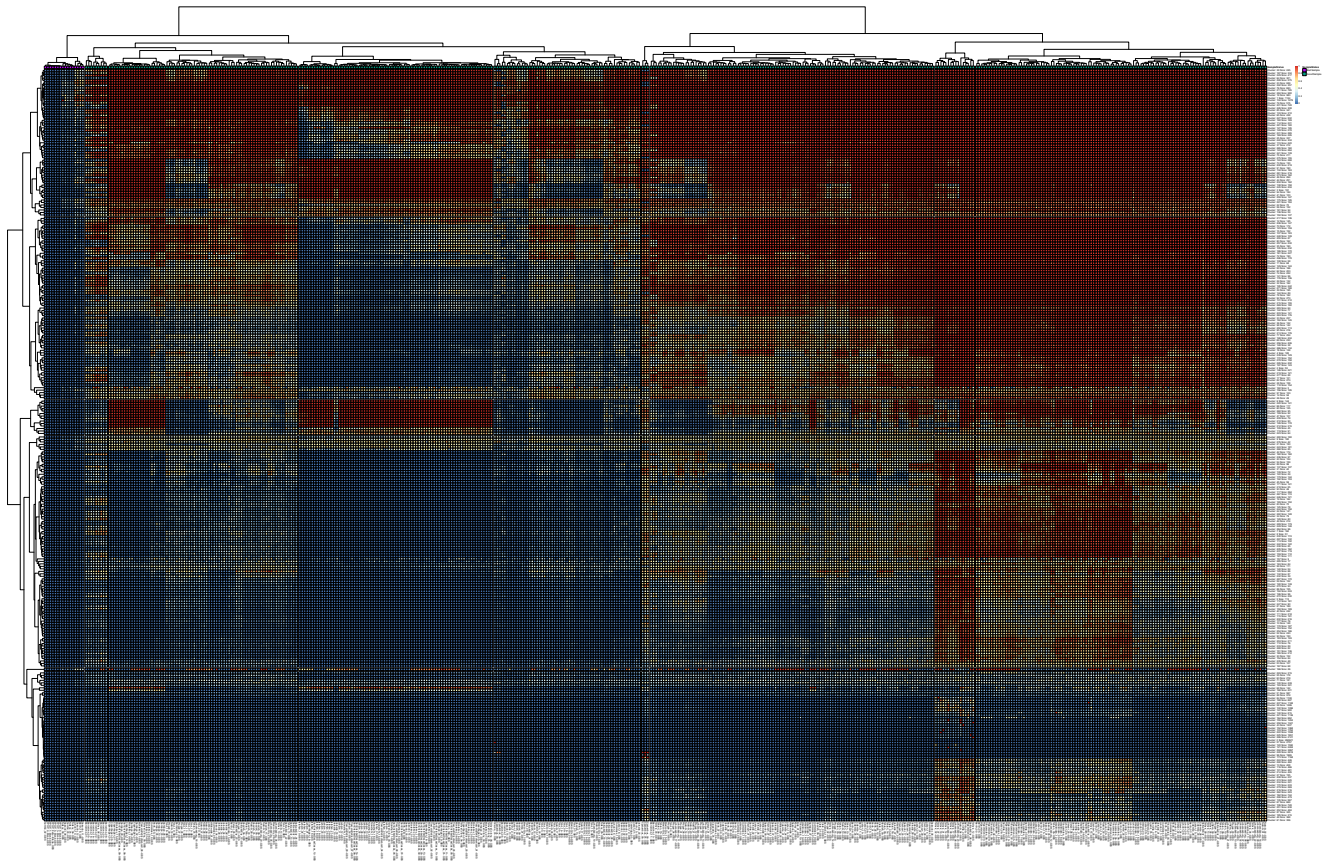
Supplementary Fig. 1. Coverage heatmap. Heatmap based on the presence/absence matrix. Individual samples are represented by each column, whereas clusters of loci are represented by the rows.
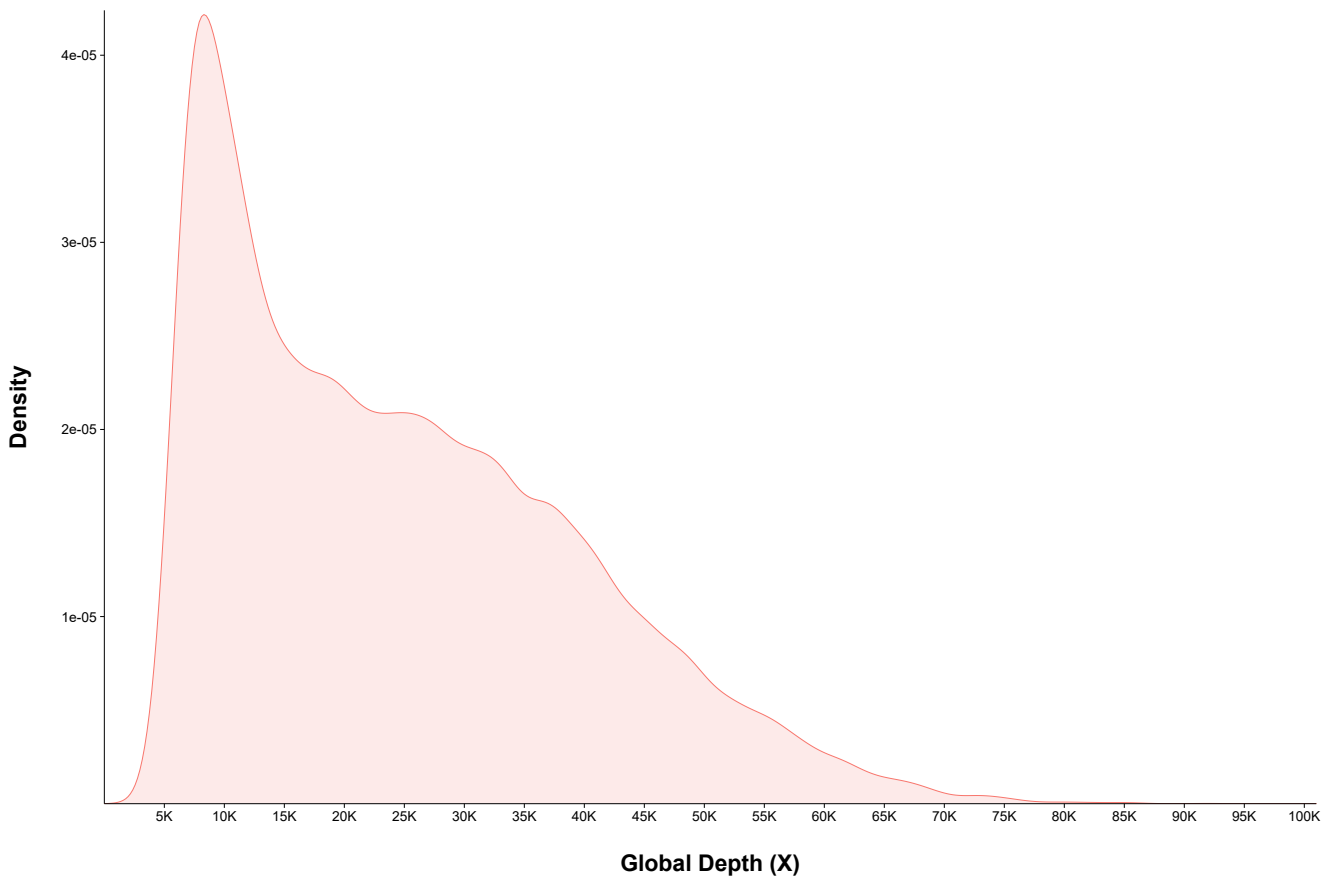
Supplementary Fig. 1. Global depth distribution. Heatmap based on the presence/absence matrix. Individual samples are represented by each column, whereas clusters of loci are represented by the rows.
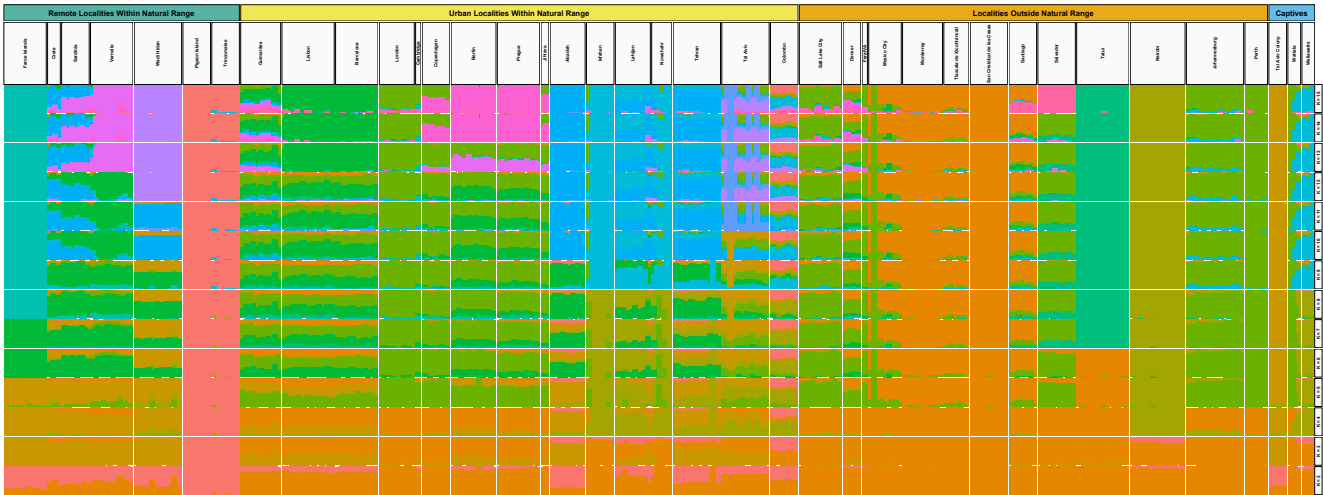

Fig. 3 Estimation of Admixture proportions. Individuals are represented by columns, while rows depict the Admixture proportions based on the assumption of different numbers of ancestral populations (K = 2 - 15). Individuals are sorted by sampling locality (light grey upper labels) and grouped per biological status
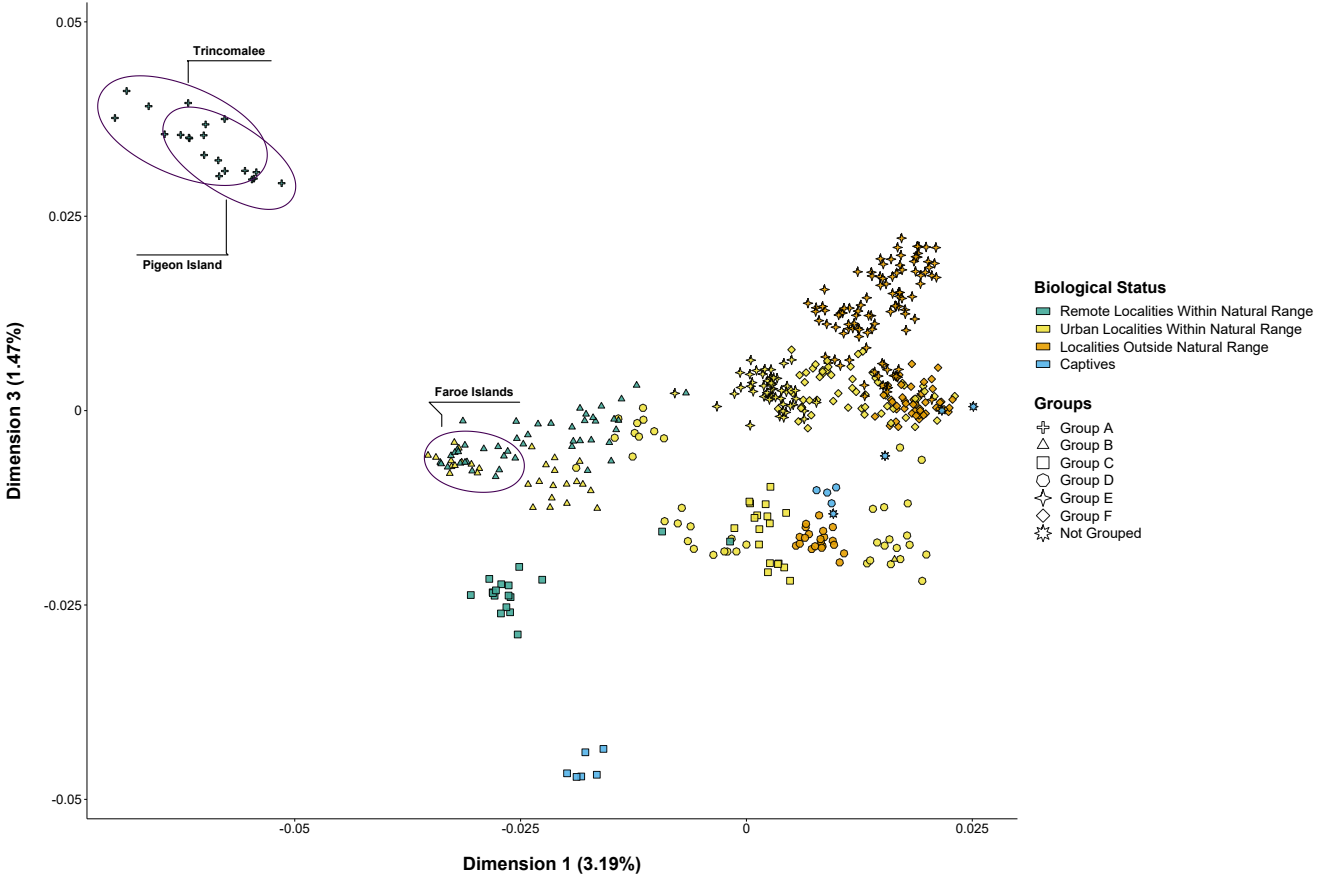
Fig. 2 Multidimensional scaling analysis. a) Dimensions 1 and 3 are plotted. b) Dimensions 2 and 3 are plotted. Each point on the plot represents a single individual. The ellipses represent the rough distribution of the two most distinct groups.