

# SUPPLEMENTARY INFORMATION FOR

## On the Origin and Spread of Feral Pigeons

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### Supplementary 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 rupestris*<sup>8</sup>. (we also included the WGS library to serve as another replicate) (Supplementary Spread-

sheet).

**Sequencing data and filtering.**

**Population genetics statistics.**

**Phylogenetic relationships among feral pigeon populations.**

**Population structure among pigeon populations.**

**Contribution of pigeon breeds to current non-domesticated populations.**

### Discussion

### Methods

**Sequencing data generation and processing.**

**Data analysis.**

**Population genetics statistics.**

**Phylogenetic reconstruction.**

**Inference of Population Structure.**

**Contribution of pigeon breeds to current non-domesticated populations.**

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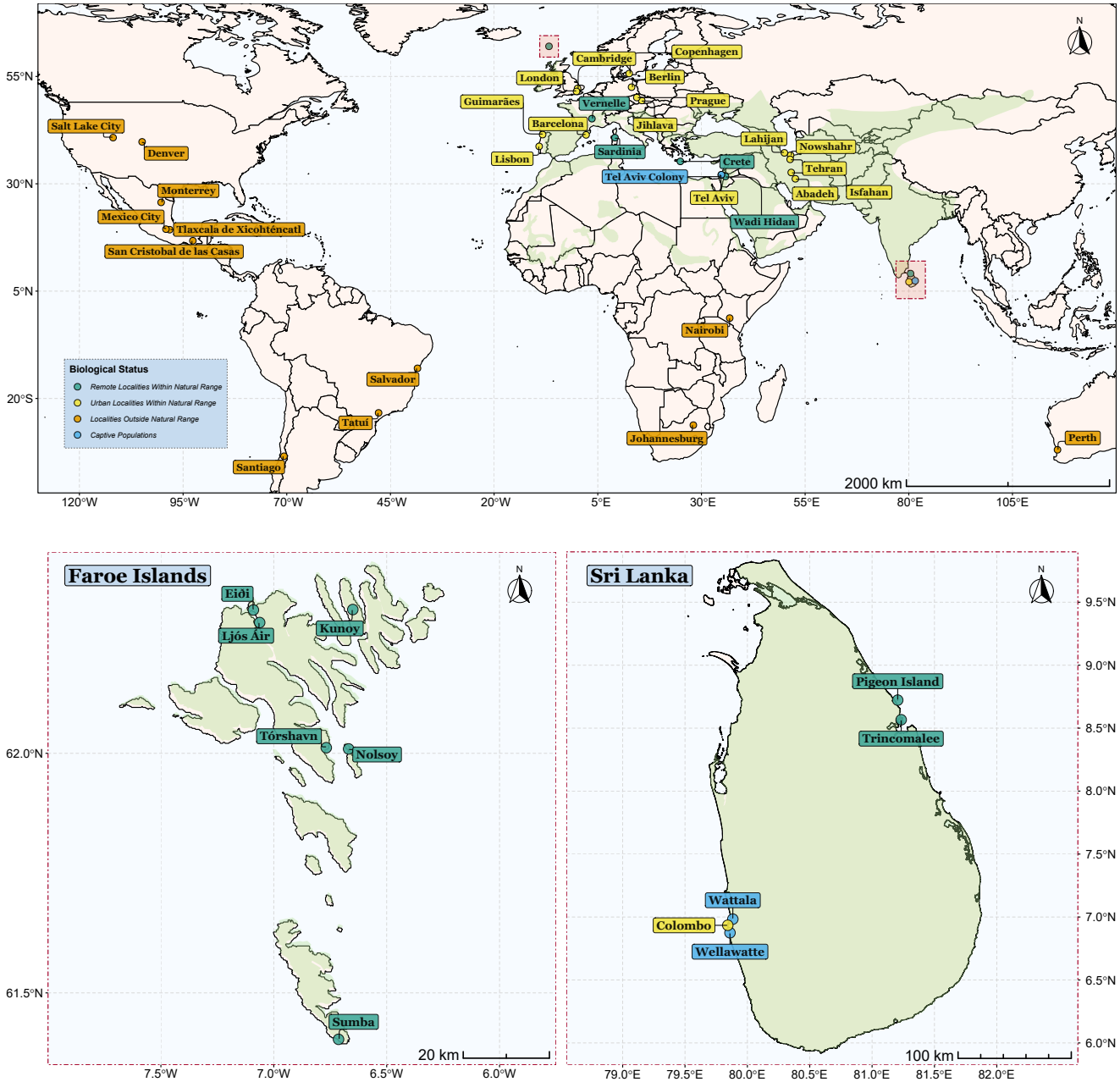


Fig. 1 Map of sampling effort. This is a trial attempt.

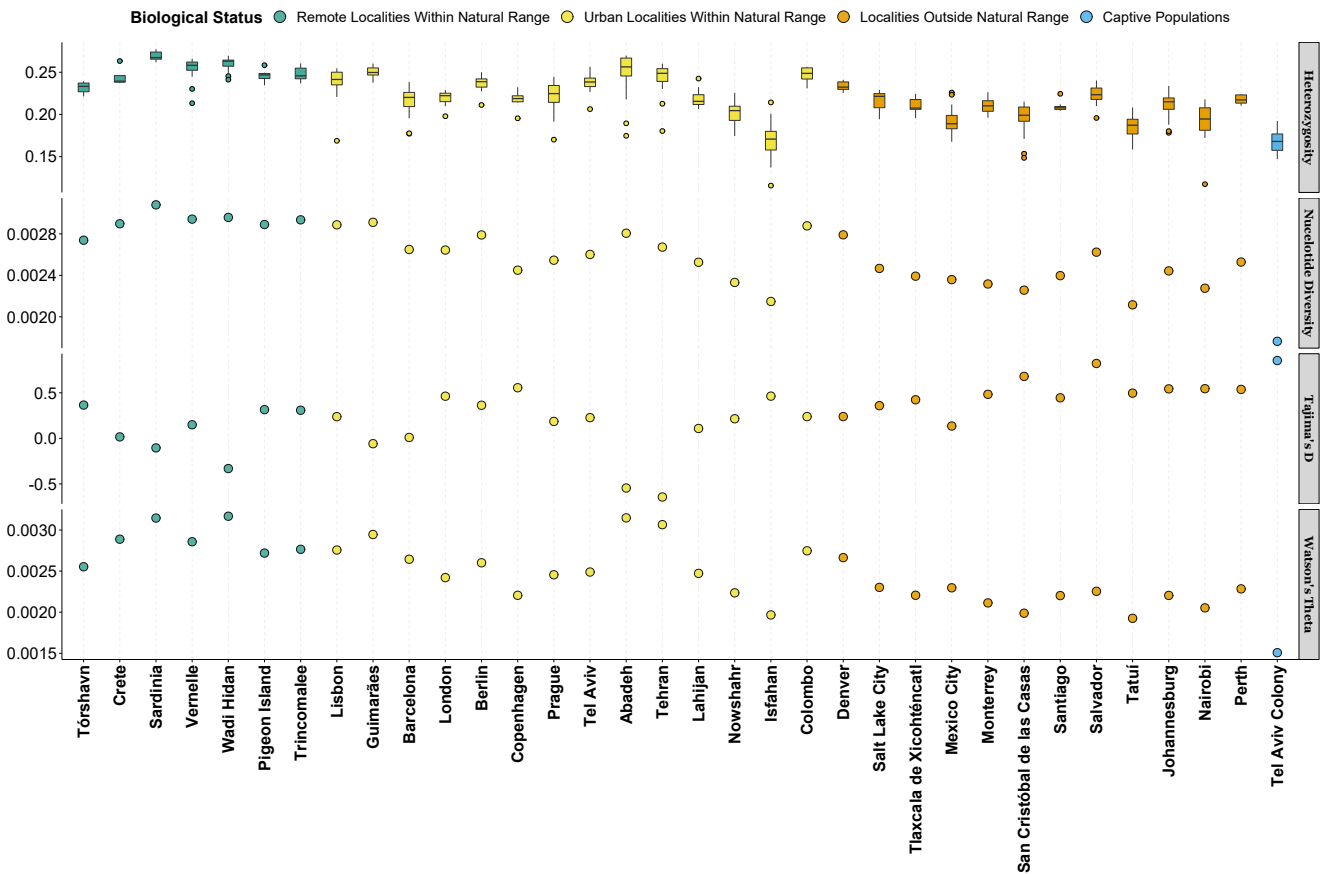


Fig. 2 Map of sampling effort. This is a trial attempt.

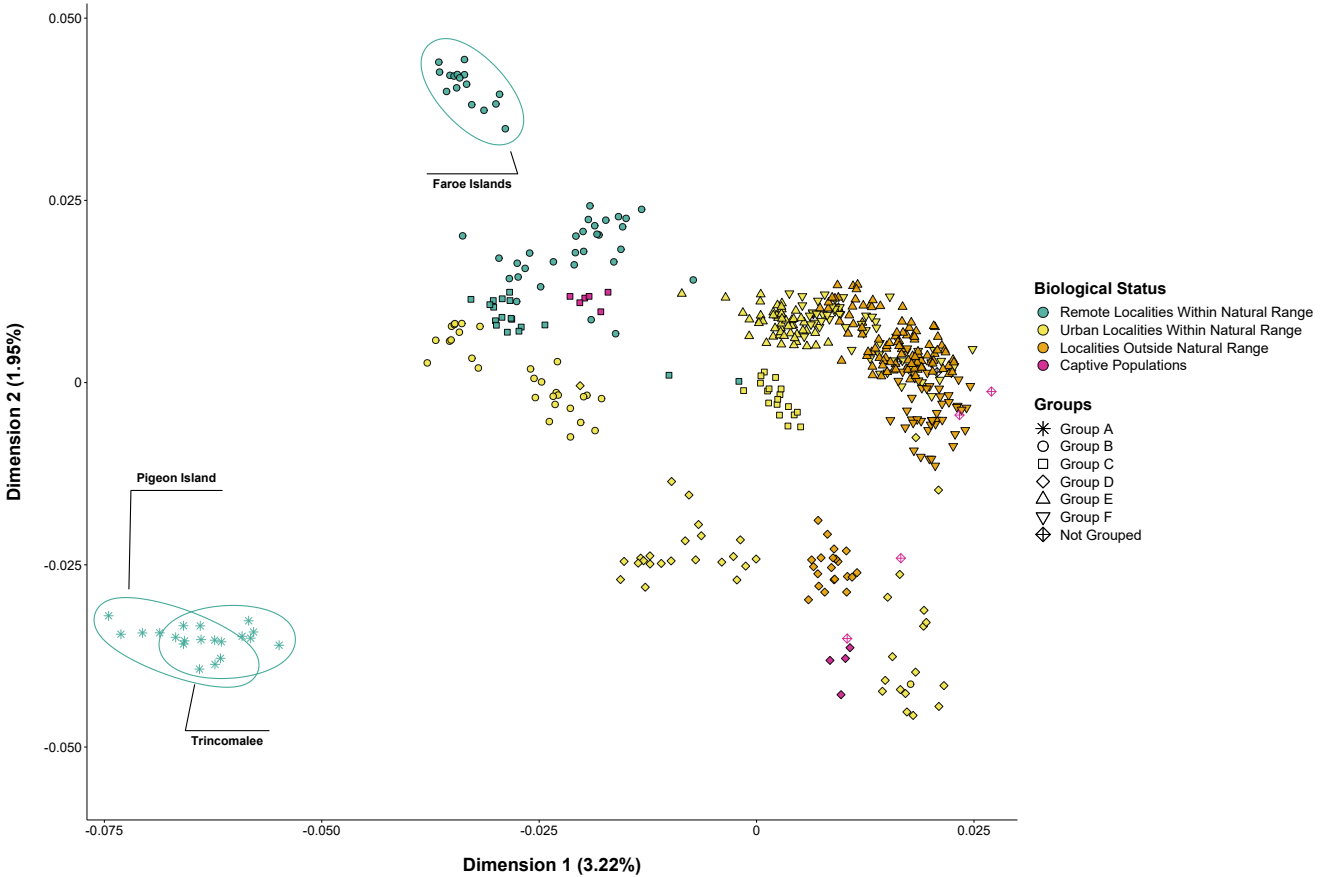
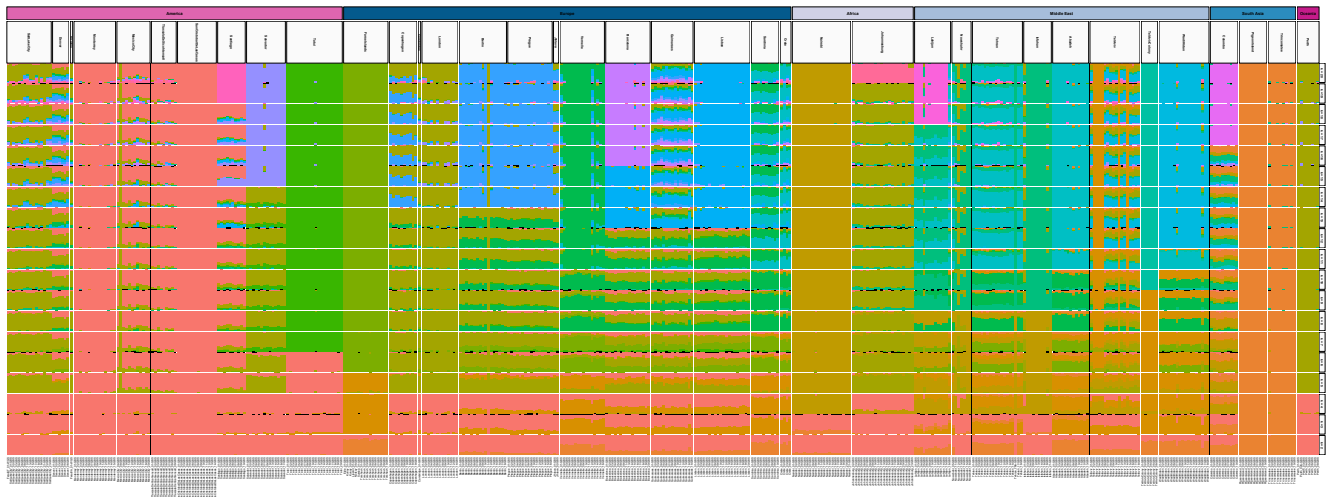


Fig. 2 Map of sampling effort. This is a trial attempt.



**Fig. 3 Map of sampling effort.** This is a trial attempt.

## References

### Data Availability

All demultiplexed GBS sequencing data is publicly available at SRA (Project Number: PRJNA495951), as well as additional data uploaded to the University of Copenhagen's long term storage ([https://sid.erda.dk/wsgi-bin/lis.py?share\\_id=aKqQoJvH4Y](https://sid.erda.dk/wsgi-bin/lis.py?share_id=aKqQoJvH4Y)).

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### Author Contributions

M.T.P.G. conceived the project and obtained financial support. M.T.P.G., G.P. and F.G.V. designed the study. G.P. led

the project. M.T.P.G., G.P., M.T.O., T.dF.R., P.H., P.N., C.S., I.L.R., S.S.S., K.M., C. L.-F., G.S., R.F., J.D., J. F., N.H., F.K., R. D., A.H., M.B.A. M. C. A.-A. and P. R. E. contributed to sampling. M.D.S. collected and provided the breed samples. G.P. performed the vast majority of DNA extraction and QC. K.M. performed DNA extraction and QC on Sri Lanka samples. G.P. and F.G.V. conducted the computational analyses assisted by M.D.M. G.P., F.G.V., M.T.O. and M.T.P.G. interpreted the results. G.P. wrote the first draft of the manuscript with great input from M.T.P.G. and F.G.V. All authors critically reviewed and approved the final manuscript.

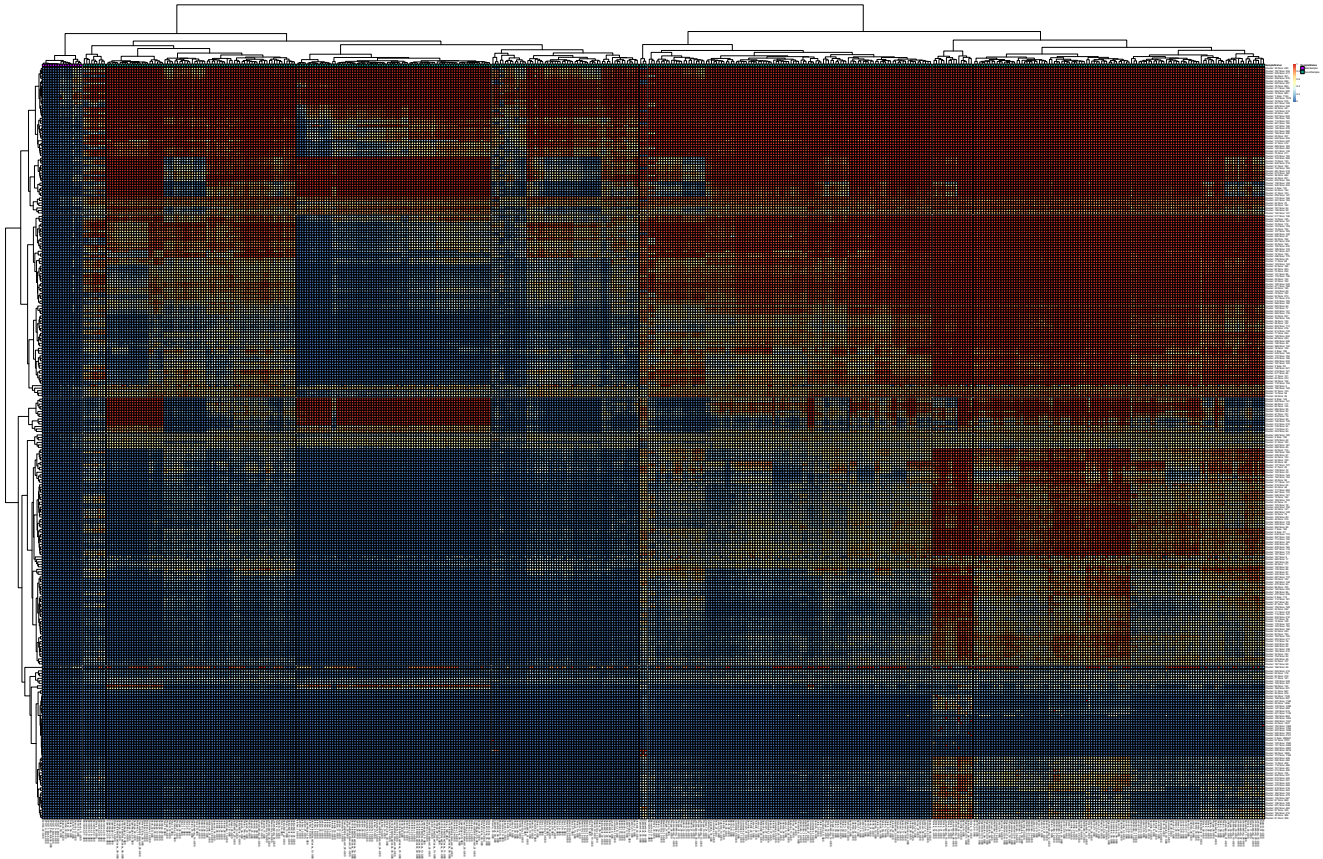
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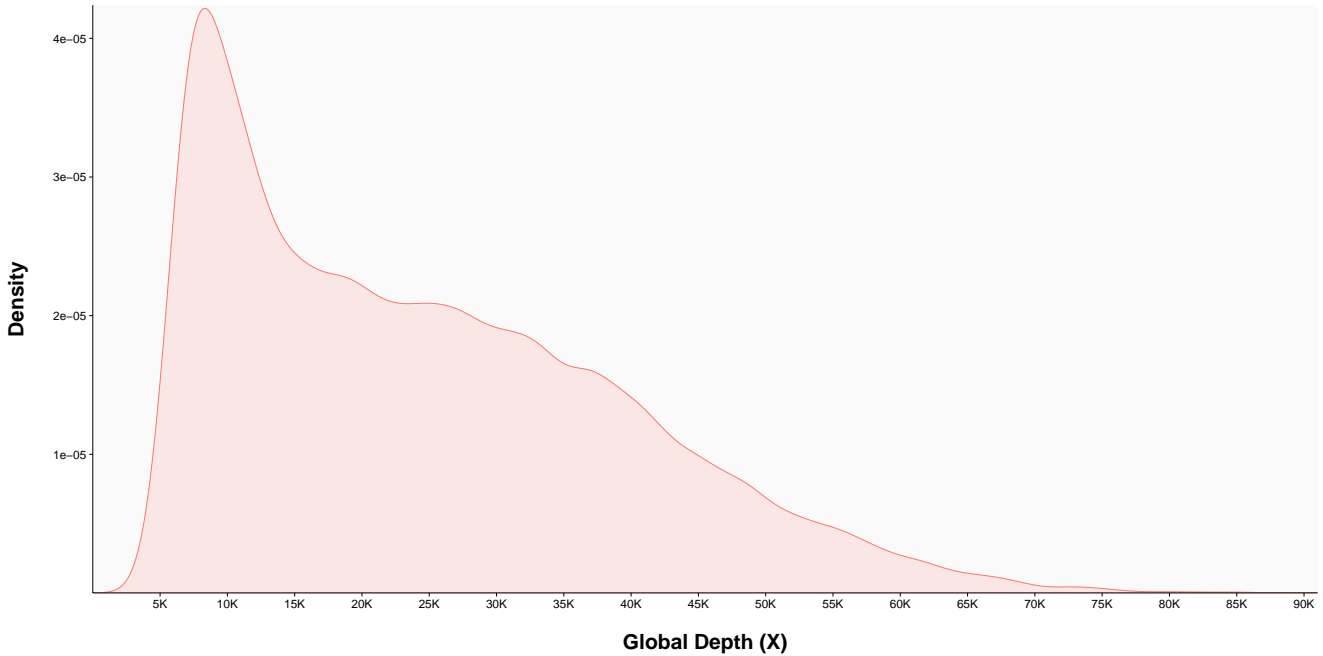
### Competing Interests

We have no competing interests.





**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.



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