

Introduction

The Canary Islands is a Spanish archipelago located in the Atlantic Ocean, 100 kilometers off Morocco. Due to its volcanic origin, it has not been connected to the mainland which implies an outstanding genetic makeup characterized by isolation and historical admixture.

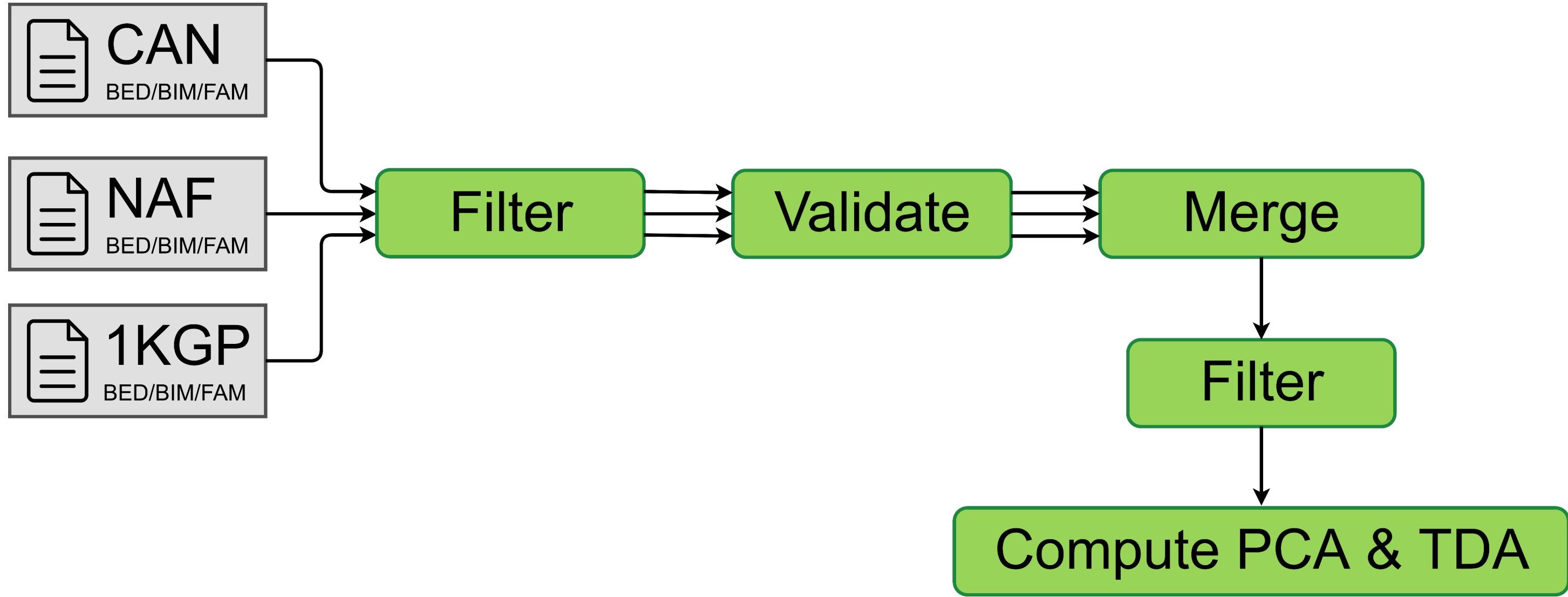
Recent studies¹ based on SNP array data, model-based ancestry estimations, and principal component analysis (PCA) have revealed the existence of a significant African influence and population isolation in current inhabitants of the Canary Islands. Furthermore, the smaller islands have showed an outlier behavior when runs of homozygosity are considered. This issue could be interpreted as the result of genetic isolation, reduced population size and inbreeding events.

Here, we reassess the Canary Islanders genomic diversity and structure based on alternative high-dimensional analysis techniques in order to increase the accuracy in genetic subdivision within the islands.

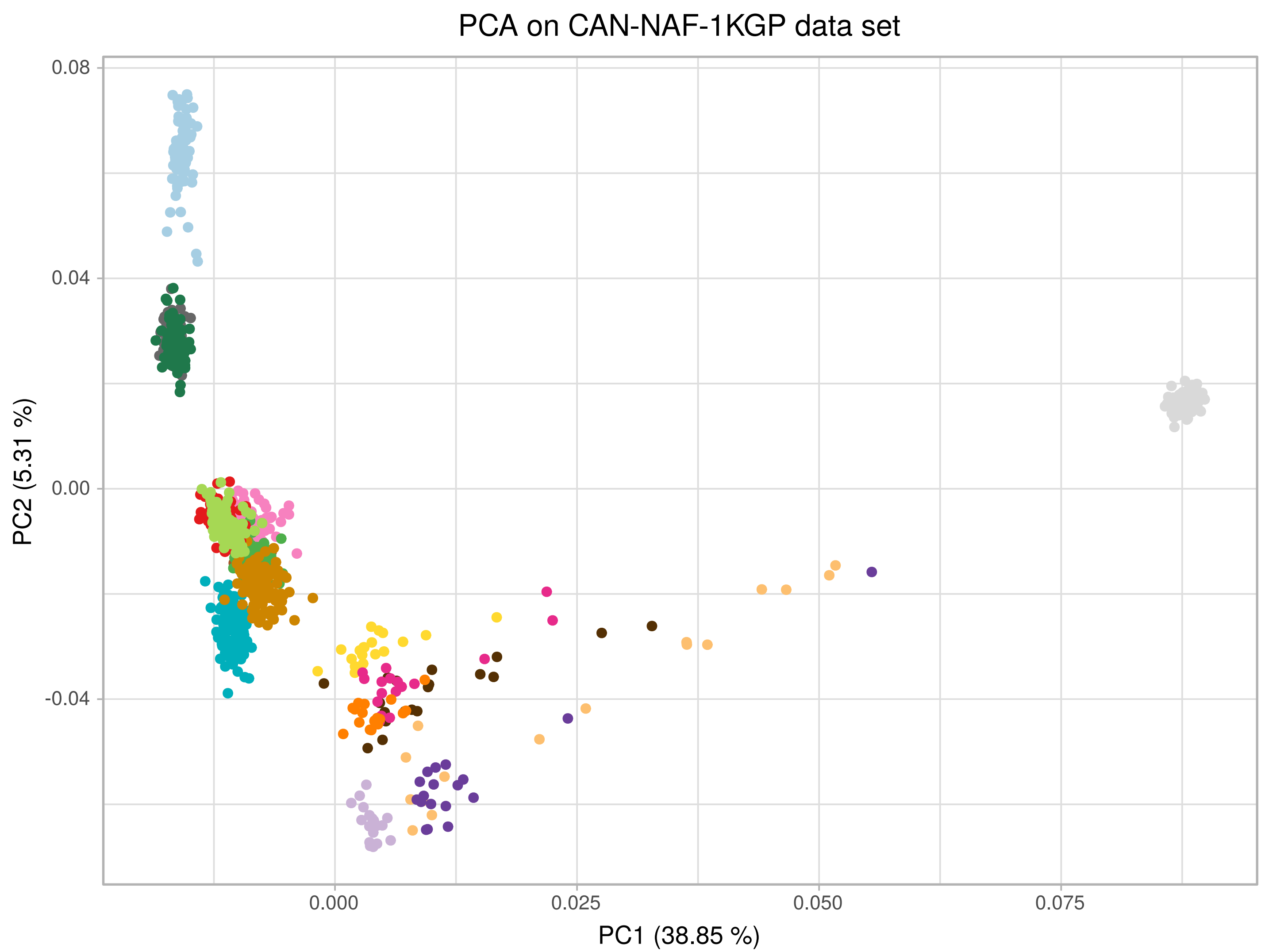
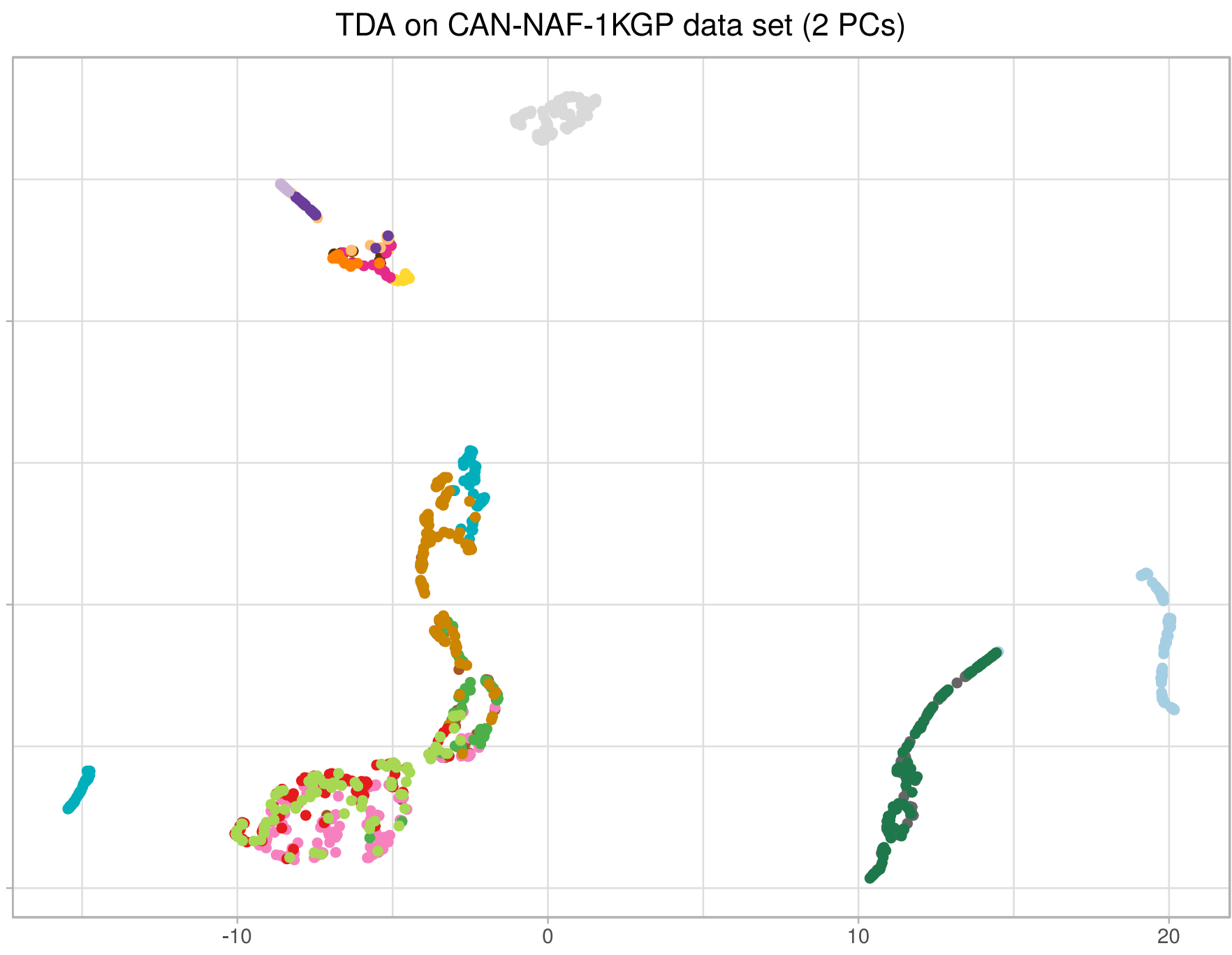
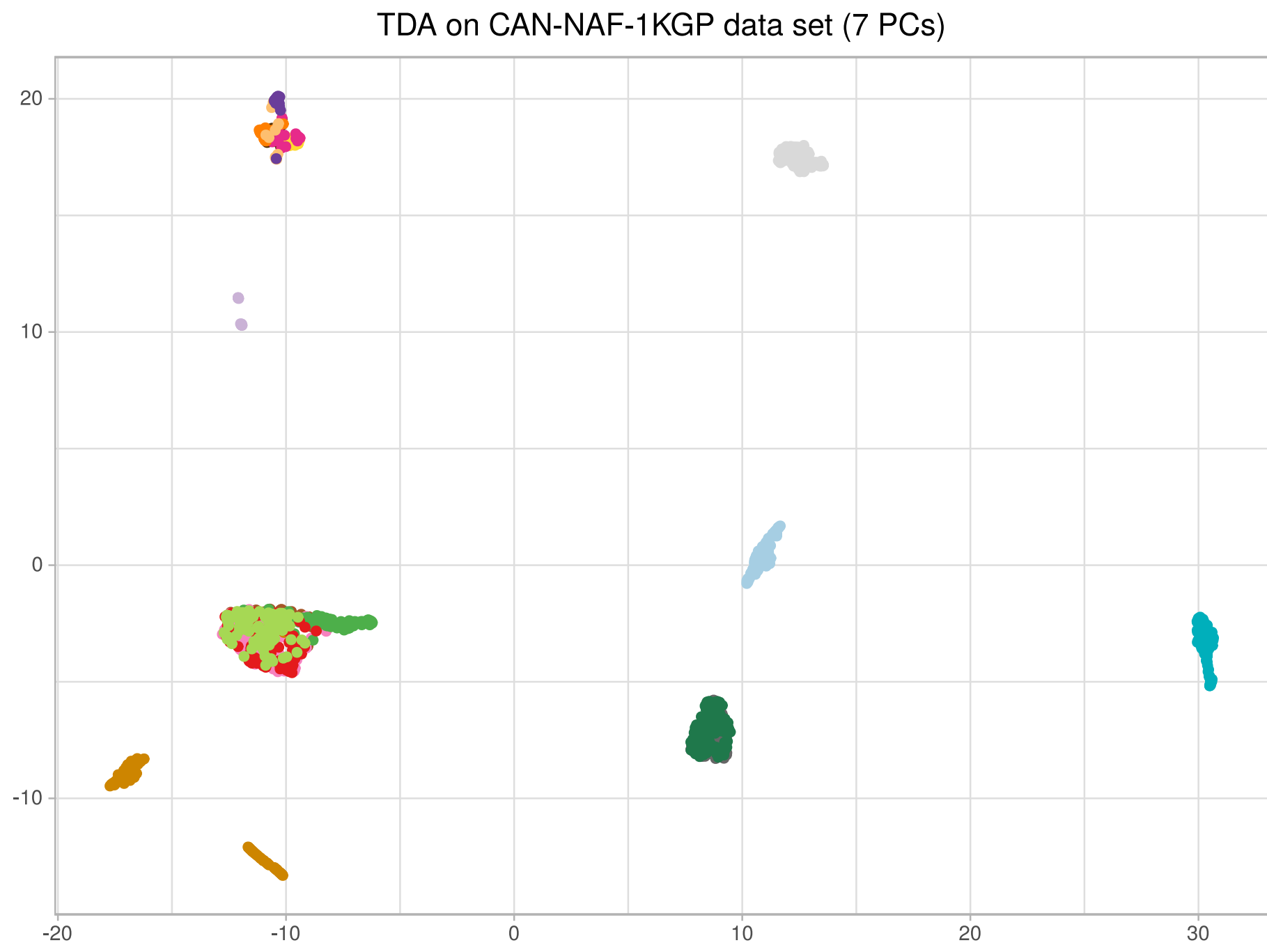
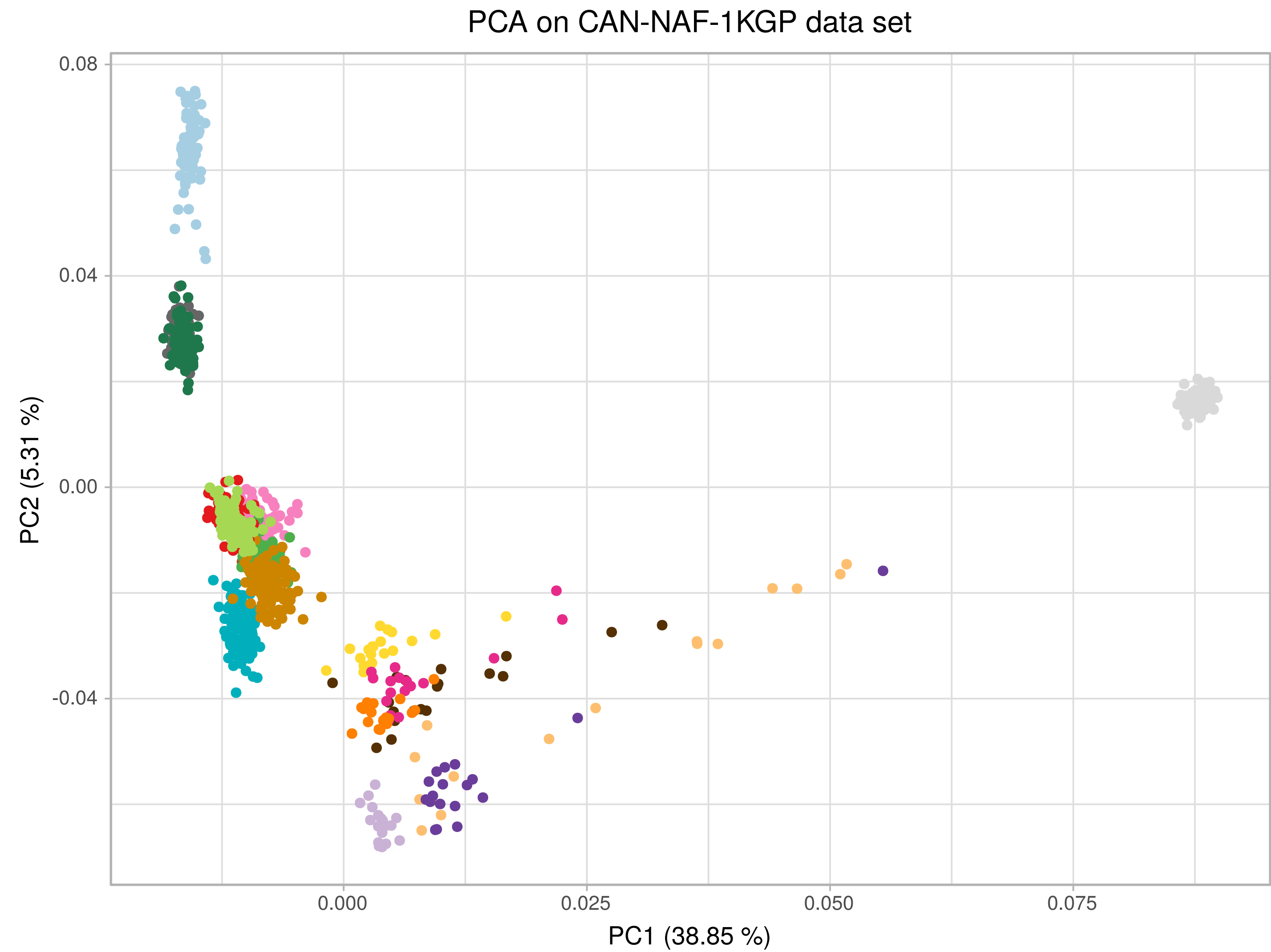
Materials and Methods

SNP array data from 618 Canary Islanders (CAN), and from 125 North-Africans (NAF) and SNP WGS data from 108 Yoruba and 289 European individuals from 1000 Genomes Project (1KGP) have been considered.

Data manipulation, principal components analysis (PCA) and topological data analysis (TDA) have been performed using PLINK v1.9, R software and umap3 v0.2.0 library for R as shown on fig. 1.



Results



Contact

Funding

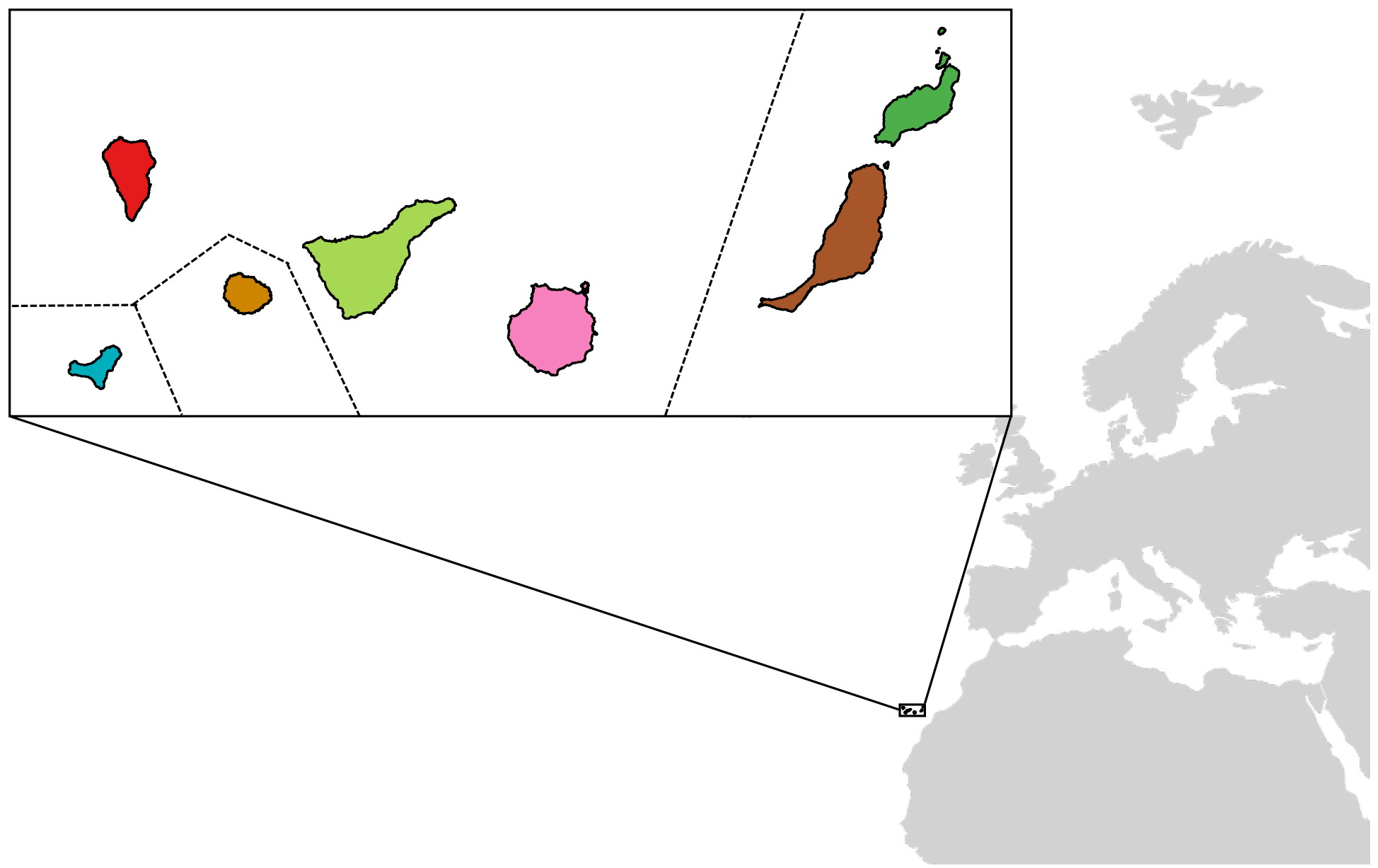
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The authors declare no conflict of interest



Conclusions

TDA has allowed us to disentangle in a better way the inherent subdivision of Canary Islands, where La Gomera shows a signature pattern in three different clusters. This trend has been previously observed in other studies⁴ so our next steps will be aimed to unravel uniqueness of La Gomera subpopulations.



References

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- The 1000 Genomes Project Consortium. *Nature* 2015; 526: 68-74
- Fregel et al. *Eur J Hum Genet* 2015; 23(9): 1236-1243.