

## Supplementary Information

### Eelgrass *Zostera capensis* populations in KwaZulu-Natal, South Africa, harbour distinct genomic signals despite limited geographical distance

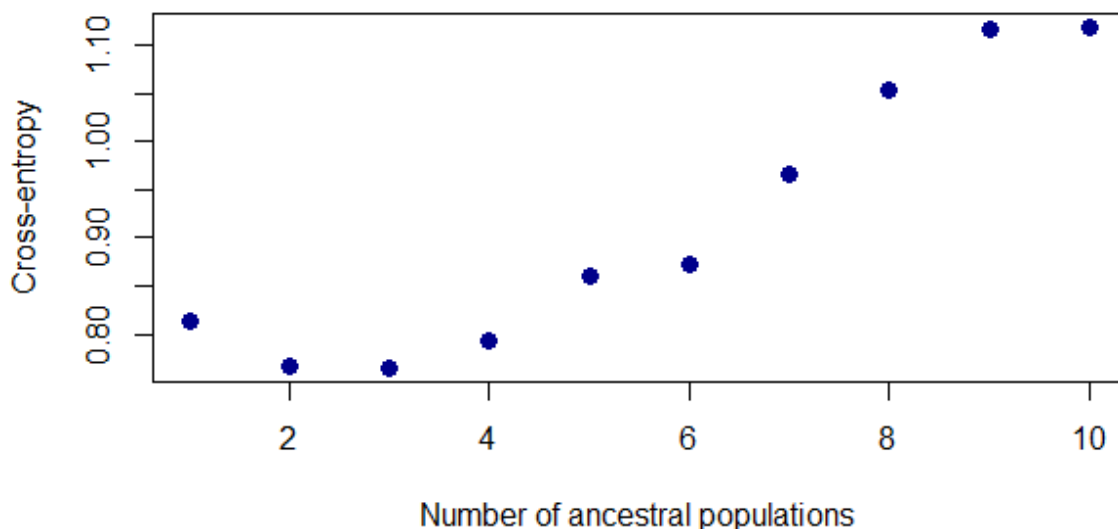
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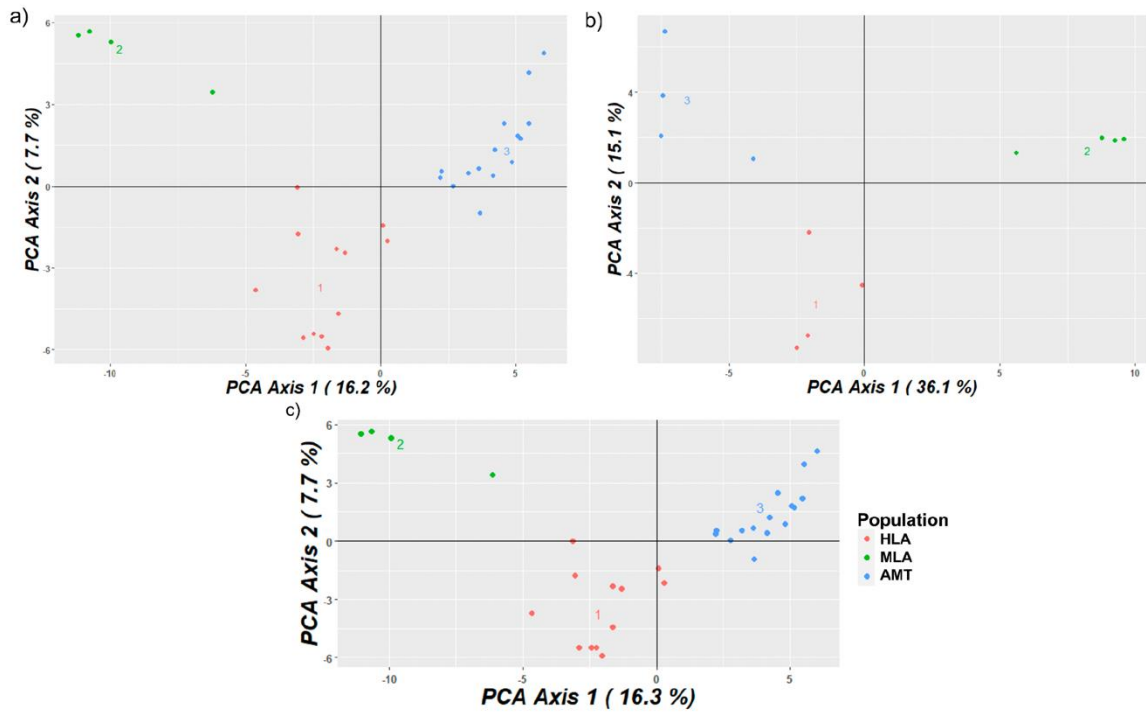
<https://doi.org/10.2989/1814232X.2023.2263503>

**Supplementary Table S1:** Summary of the difference between different sequence alignment methods. For the full dataset, all sampled individuals of *Zostera capensis* were analysed, but this only included four individuals from the Mlalazi Estuary. To ascertain whether sample size influenced downstream analyses, only four individuals from each population were included in the reduced dataset of samples. The full dataset of samples was analysed by aligning sequences to the *Z. marina* genome and also using a *de novo* approach, with the number of variants and missing data provided below

Sequence alignment method	<i>n</i>	Variants	Missing data (%)
<i>Zostera marina</i> reference	31	155	22.9
<i>De novo</i> full dataset	31	1 904	15.6
<i>De novo</i> reduced dataset	12	1 272	16.8



**Supplementary Figure S1:** Graph showing the number of clusters (*K*) and cross-entropy criterion; where the cross-entropy criterion minimum occurs is the most likely value of *K*. The sNMF analysis provided almost equal support for two or three clusters of eelgrass *Zostera capensis* populations, but with some admixture detected



**Supplementary Figure S2:** Principal coordinates analysis (PCoA) plots indicating population differentiation among eelgrass *Zostera capensis* populations at Mhlatuze (HLA), Mlalazi (MLA), and Amatikulu (AMT) estuaries: (a) population clustering with the full dataset; (b) population clustering with the reduced dataset; and (c) population clustering after the removal of putative outlier loci