

## Supplementary Materials

### Conservation implications of strong population structure despite admixture in the endangered seagrass *Zostera capensis*

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**Table S1.** Kinship coefficients ( $\phi$ ) of three pairs of *Zostera capensis* leaf blades with high kinship coefficients ( $\phi > 0.33$ ) and sequenced in adjacent wells. Kinship coefficients ( $\phi$ ) were calculated for a dataset of 2 401 SNPs using --relatedness2 in VCFtools v3.0 (Danecek et al. 2011), which is based on the method of (Manichaikul et al. 2010).

Pair	Sample 1	Sample 2	Kinship coefficient ( $\phi$ )
1	KA15	BU12	0.472769
2	NA7	NA8	0.412791
3	NA5	NA19	0.330846

**Table S2.** Kinship coefficients ( $\phi$ ) of 10 pairs and 1 trio (11 groups) of *Zostera capensis* leaf blades related above the threshold of “identical genotypes” ( $\phi > 0.354$ , Manichaikul et al. 2010). Kinship coefficients ( $\phi$ ) were calculated for a dataset of 2 401 SNPs using --relatedness2 in VCFtools v3.0 (Danecek et al. 2011), which is based on the method of (Manichaikul et al. 2010).

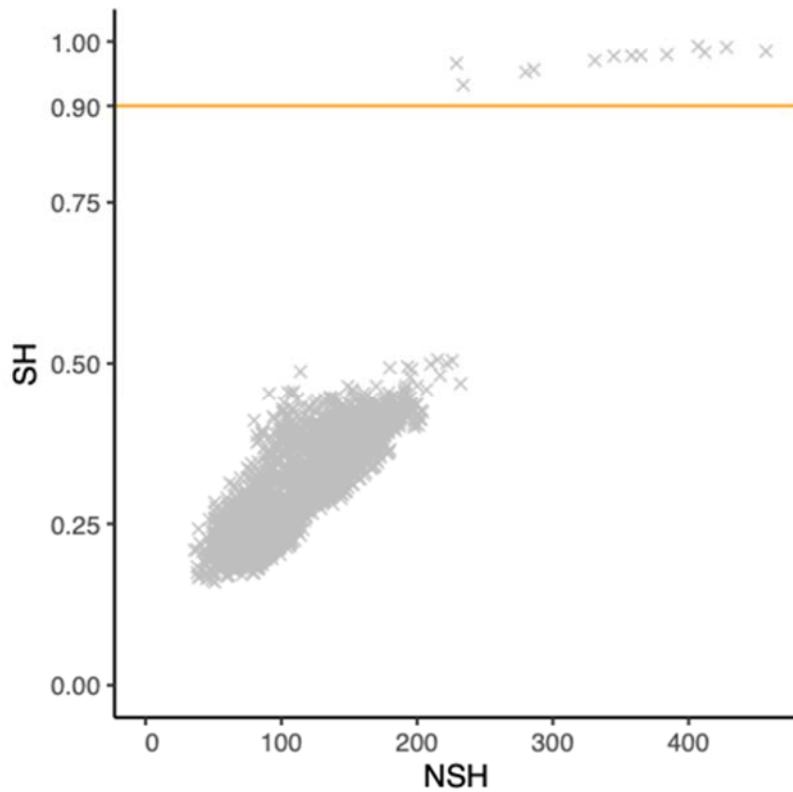
Group	Sample 1	Sample 2	Kinship coefficient ( $\phi$ )
1	BU4	BU6	0.493656
2	KA8	KA6	0.489818
3	SW4	SW6	0.486413
4	BU5	BU15	0.482436
5	NAE2	NA15	0.477178
6	NA2	NA3	0.475880
7	KA18	KA19	0.475467
8	NA4	NAL1	0.471510
9	BU19	BU20	0.453365
5	NA20	NA15	0.432678
5	NA20	NAE2	0.429448
10	NA11	NA10	0.429448
11	SW5	SW15	0.368504

**Table S3.** The number of sample pairs within and between five estuaries of *Zostera capensis* in the southeastern Cape that met the kinship coefficient ( $\phi$ ) inference criteria of the following degrees of relatedness: identical genotype/self:  $\phi > 0.354$ , 1st degree relatedness:  $\phi = 0.122$ - $0.354$ , 2nd degree relatedness:  $\phi = 0.088$ - $0.177$ , 3rd degree relatedness:  $\phi = 0.044$ - $0.088$ , unrelated:  $<0.044$  (Manichaikul et al. 2010). Estuary names are followed by the number of individual blades ( $n_{\text{estuary}1}$  or  $n_{\text{estuary}2}$ ) considered in each estuary. Kinship coefficients ( $\phi$ ) were generated for a dataset of 2 401 SNPs using --relatedness2 in VCFtools v3.0 (Danecek et al. 2011), which is based on the method of Manichaikul et al. (2010).

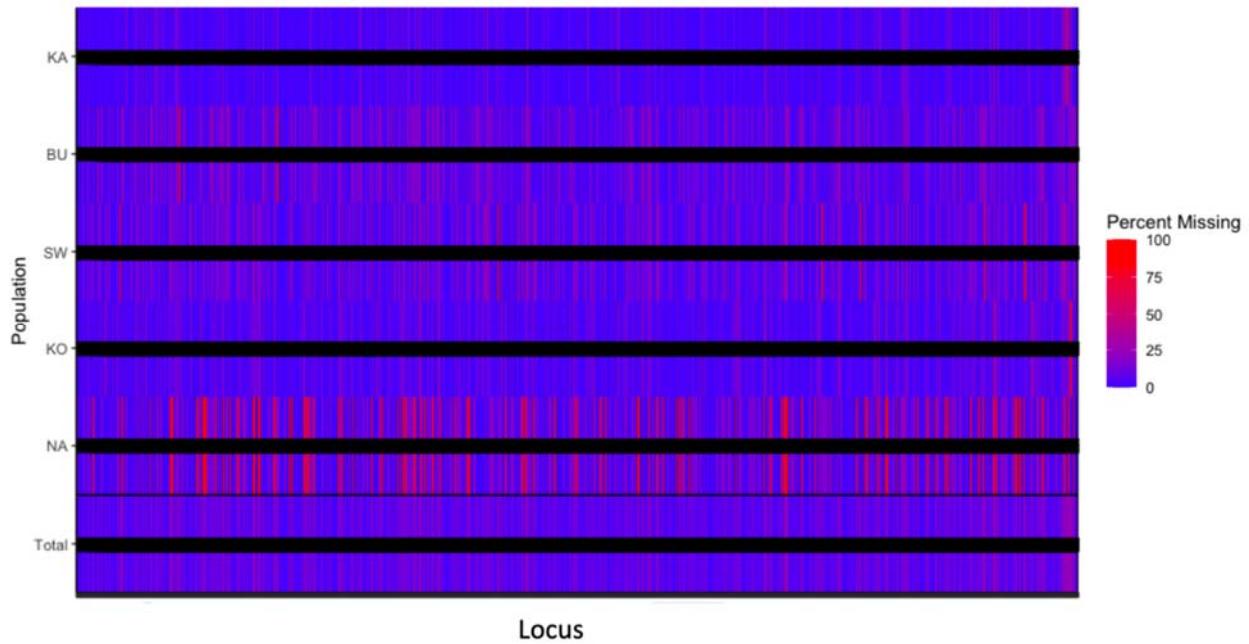
Estuary 1	$n_{\text{estuary}1}$	Estuary 2	$n_{\text{estuary}2}$	identical/ self	1st degree	2nd degree	3rd degree	unrelated
Swartkops	19	Swartkops	19	2	0	13	67	89
Swartkops	19	Bushmans	16	0	0	0	0	304
Swartkops	19	Kariega	17	0	0	0	0	323
Swartkops	19	Kowie	17	0	0	0	0	323
Swartkops	19	Nahoon	15	0	0	0	0	285
Bushmans	16	Bushmans	16	3	0	13	43	61
Bushmans	16	Kariega	17	0	0	15	12	245
Bushmans	16	Kowie	17	0	0	0	0	272
Bushmans	16	Nahoon	15	0	0	0	0	240
Kariega	17	Kariega	17	2	0	3	32	99
Kariega	17	Kowie	17	0	0	0	0	287
Kariega	17	Nahoon	15	0	0	0	0	255
Kowie	17	Kowie	17	0	0	8	34	94
Kowie	17	Nahoon	15	0	0	0	0	255
Nahoon	15	Nahoon	15	6	0	0	24	75
<b>Totals</b>				<b>13</b>	<b>0</b>	<b>52</b>	<b>214</b>	<b>3207</b>

**Table S4.** The 10 pairs and 1 trio (11 groups) of *Zostera capensis* leaf blades identified by the Jaccard Index approach (Yu et al. 2022) as having highly similar genotypes ( $SH > 0.90$ ). Jaccard indices were calculated based on shared heterozygosity according to the method of Yu et al. (2022) for a dataset of 2 401 SNPs.

Group	Sample 1	Sample 2	SH value
1	KA18	KA19	0.9927
2	BU4	BU6	0.9907
3	KA8	KA6	0.9849
4	BU5	BU15	0.9833
5	BU19	BU20	0.9796
6	NA2	NA3	0.9786
7	SW4	SW6	0.9781
8	NAE2	NA15	0.9773
9	NA4	NAL1	0.9707
10	NA11	NA10	0.9662
8	NA20	NA15	0.9565
8	NA20	NAE2	0.9524
11	SW5	SW15	0.9323



**Figure S1.** Number of SNPs for which two samples are identically heterozygous (NSH) against the shared heterozygosity value (SH) of each sample pair of *Zostera capensis* leaf blades calculated according to the approach of Yu et al. (2022) for a dataset of 2 401 SNPs. The 10 pairs and 1 trio of individual blades with SH indices > 0.90 were KA18 and KA19; BU4 and BU6; KA8 and KA6; BU5 and BU15; BU19 and BU20; NA2 and NA3; SW4 and SW6; NA4 and NAL1; NA11 and NA10; SW5 and SW5; NA15, NAE2 and NA20.



**Figure S2.** Average percent missing data for each locus across all five *Zostera capensis* populations (KA=Kariega, BU=Bushmans, SW=Swartkops, KO=Kowie, NA=Nahoon). Percent missing data was calculated and mapped using the R package *poppr* (Kamvar et al. 2015) and *adegenet* (Luu et al. 2017) for a dataset of 2 681 SNPs.

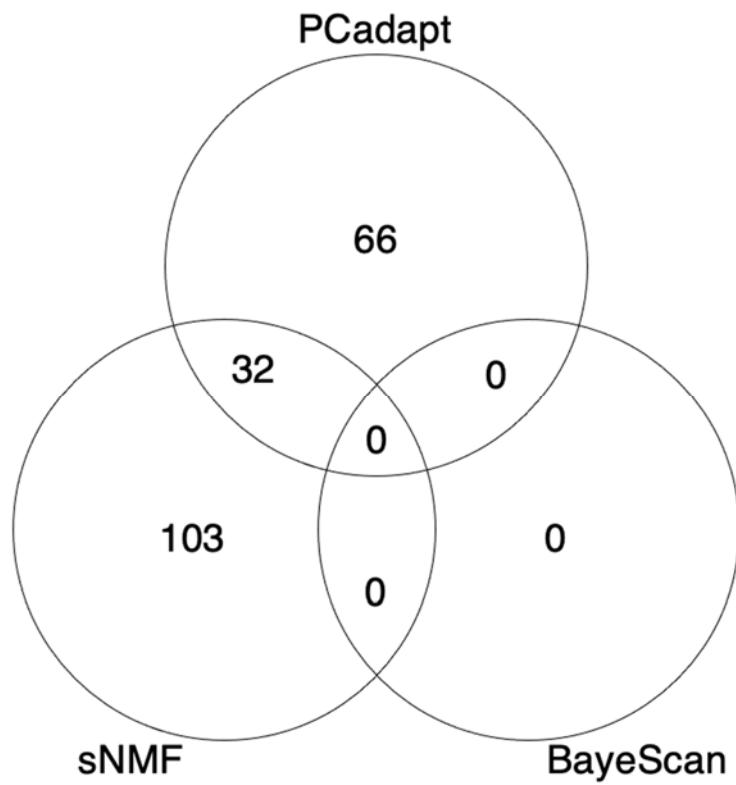
**Table S5.** Average missing data for each *Zostera capensis* population. Percent missing data was calculated using the R packages *poppr* (Kamvar et al. 2015) and *adegenet* (Luu et al. 2017) for a dataset of 2 681 SNPs.

Population	Average missing data (%)
Swartkops	4.2
Bushmans	10.1
Kariega	9.8
Kowie	6.3
Nahoon	21.2

**Table S6.** Average missing data for each *Zostera capensis* individual (n = 72). Percent missing data was calculated using the R packages *poppr* (Kamvar et al. 2015) and *adegenet* (Luu et al. 2017) for a dataset of 2 681 SNPs.

Individual	Population	Missing data (%)
P01-A04-na-SW9	Swartkops	4.0
P01-B02-na-SW11	Swartkops	1.4
P01-C04-na-SW10	Swartkops	2.3
P01-C06-na-SW4	Swartkops	3.2
P01-C09-na-SW2	Swartkops	23.7
P01-C10-na-SW14	Swartkops	11.1
P01-C11-na-SW3	Swartkops	6.5
P01-D04-na-SW19	Swartkops	1.8
P01-D05-na-SW5	Swartkops	36.1
P01-D06-na-SW8	Swartkops	21.1
P01-D09-na-SW1	Swartkops	13.3
P01-E04-na-SW18	Swartkops	1.8
P01-F02-na-SW17	Swartkops	1.4
P01-F04-na-SW13	Swartkops	24.4
P01-G01-na-SW12	Swartkops	1.6
P01-G06-na-SW16	Swartkops	11.2
P01-H02-na-SW7	Swartkops	1.7
P01-A03-na-BU4	Bushmans	1.3
P01-A05-na-BU14	Bushmans	36.0
P01-B05-na-BU11	Bushmans	40.7
P01-C01-na-BU7	Bushmans	1.3
P01-C05-na-BU19	Bushmans	12.0
P01-D01-na-BU3	Bushmans	1.4
P01-E05-na-BU8	Bushmans	3.5
P01-E06-na-BU2	Bushmans	2.1
P01-E10-na-BU18	Bushmans	9.2
P01-E11-na-BU10	Bushmans	2.5
P01-F06-na-BU16	Bushmans	23.4
P01-F11-na-BU17	Bushmans	5.4
P01-G03-na-BU5	Bushmans	1.5
P01-H03-na-BU13	Bushmans	1.3
P01-A01-na-KA2	Kariega	1.6
P01-A02-na-KA17	Kariega	1.2
P01-A07-na-KA5	Kariega	1.2

P01-B03-na-KA11	Kariega	0.4
P01-B04-na-KA13	Kariega	1.7
P01-B07-na-KA12	Kariega	3.3
P01-C07-na-KA1	Kariega	1.4
P01-D07-na-KA20	Kariega	11.2
P01-F03-na-KA7	Kariega	1.5
P01-F08-na-KA8	Kariega	2.8
P01-F09-na-KA14	Kariega	10.1
P01-F10-na-KA10	Kariega	6.0
P01-G05-na-KA4	Kariega	2.3
P01-G08-na-KA3	Kariega	17.2
P01-G11-na-KA18	Kariega	1.3
P01-H08-na-KA9	Kariega	4.6
P01-A06-na-KO4	Kowie	5.9
P01-A09-na-KO2	Kowie	7.5
P01-A12-na-KO6	Kowie	1.0
P01-B01-na-KO19	Kowie	2.6
P01-B06-na-KO7	Kowie	1.9
P01-C02-na-KO10	Kowie	4.1
P01-C03-na-KO18	Kowie	1.1
P01-D02-na-KO12	Kowie	2.6
P01-D03-na-KO16	Kowie	2.5
P01-E03-na-KO1	Kowie	2.3
P01-G02-na-KO20	Kowie	0.9
P01-G04-na-KO14	Kowie	1.7
P01-G09-na-KO9	Kowie	35.1
P01-G10-na-KO15	Kowie	3.7
P01-H04-na-KO3	Kowie	21.3
P01-H06-na-KO8	Kowie	10.2
P01-H09-na-KO17	Kowie	3.1
P01-A11-na-NA4	Nahoon	16.6
P01-B08-na-NA12	Nahoon	22.7
P01-B11-na-NA11	Nahoon	46.3
P01-B12-na-NA6	Nahoon	15.6
P01-C08-na-NA18	Nahoon	23.5
P01-D08-na-NA2	Nahoon	16.4
P01-G07-na-NA15	Nahoon	14.7
P01-H12-na-NAL2	Nahoon	14.2



**Figure S3.** The numerical breakdown of 201 putative outlier loci detected by each of three outlier detection methods (BayeScan v2.1, Foll & Gaggiotti 2008; PCadapt, Luu et al. 2017; sNMF, Fritchot et al. 2014) across a dataset of 2 681 SNPs.

**Table S7.** Population statistics of genomic diversity across five *Zostera capensis* populations calculated using the R packages *hierfstat* (Goudet et al. 2005) and *poppr* (Kamvar et al. 2015) from a) full (2 681 SNPs), b) neutral (2 649 SNPs) and c) outlier (32 SNPs) SNP datasets. N = number of leaf blades, Private = number of private SNPs,  $H_O$  = observed heterozygosity,  $H_E$ = expected heterozygosity and  $F_{IS}$ = inbreeding coefficient (SE = standard error).

a) Full dataset (2 681 SNPs)

Population	N	Private	$H_O$ ( $\pm$ SE)	$H_E$ ( $\pm$ SE)	$F_{IS}$ ( $\pm$ SE)
Swartkops	17	344	0.15 ( $\pm$ 0.00)	0.29 ( $\pm$ 0.00)	0.49 ( $\pm$ 0.01)
Bushman	14	20	0.17 ( $\pm$ 0.00)	0.32 ( $\pm$ 0.00)	0.47 ( $\pm$ 0.01)
Kariega	16	108	0.20 ( $\pm$ 0.00)	0.27 ( $\pm$ 0.00)	0.26 ( $\pm$ 0.01)
Kowie	17	124	0.18 ( $\pm$ 0.00)	0.28 ( $\pm$ 0.00)	0.36 ( $\pm$ 0.01)
Nahoon	8	121	0.13 ( $\pm$ 0.00)	0.27 ( $\pm$ 0.00)	0.51 ( $\pm$ 0.01)

b) Neutral dataset (2 649 SNPs)

Population	N	Private	$H_O$ ( $\pm$ SE)	$H_E$ ( $\pm$ SE)	$F_{IS}$ ( $\pm$ SE)
Swartkops	17	338	0.15 ( $\pm$ 0.00)	0.30 ( $\pm$ 0.00)	0.48 ( $\pm$ 0.01)
Bushman	14	20	0.17 ( $\pm$ 0.00)	0.31 ( $\pm$ 0.00)	0.47 ( $\pm$ 0.01)
Kariega	16	102	0.20 ( $\pm$ 0.00)	0.27 ( $\pm$ 0.00)	0.26 ( $\pm$ 0.01)
Kowie	17	124	0.18 ( $\pm$ 0.00)	0.28 ( $\pm$ 0.00)	0.35 ( $\pm$ 0.01)
Nahoon	8	116	0.13 ( $\pm$ 0.00)	0.27 ( $\pm$ 0.00)	0.52 ( $\pm$ 0.01)

c) Outlier dataset (32 SNPs)

Population	N	Private	$H_O$ ( $\pm$ SE)	$H_E$ ( $\pm$ SE)	$F_{IS}$ ( $\pm$ SE)
Swartkops	17	6	0.05 ( $\pm$ 0.01)	0.21 ( $\pm$ 0.03)	0.58 ( $\pm$ 0.06)
Bushman	14	0	0.04 ( $\pm$ 0.02)	0.22 ( $\pm$ 0.03)	0.58 ( $\pm$ 0.07)
Kariega	16	6	0.13 ( $\pm$ 0.03)	0.24 ( $\pm$ 0.04)	0.37 ( $\pm$ 0.05)
Kowie	17	0	0.05 ( $\pm$ 0.03)	0.16 ( $\pm$ 0.03)	0.37 ( $\pm$ 0.10)
Nahoon	8	5	0.14 ( $\pm$ 0.04)	0.24 ( $\pm$ 0.04)	0.45 ( $\pm$ 0.10)