

Fig. S1. Mean depth distribution across sites of the raw data before filtering

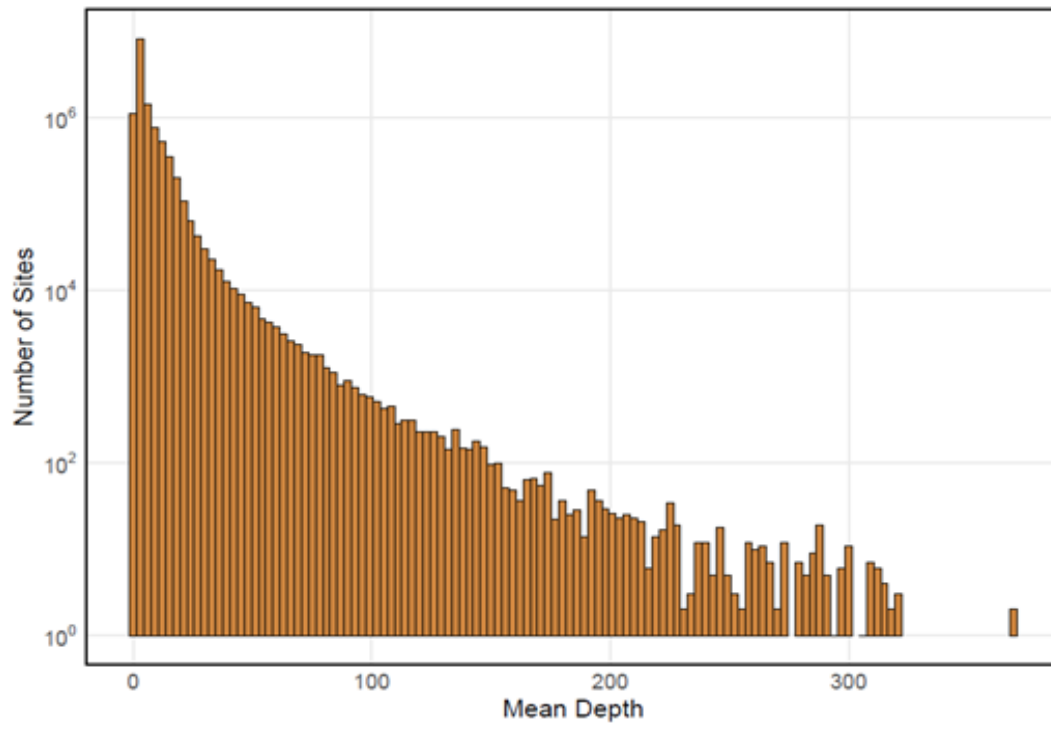


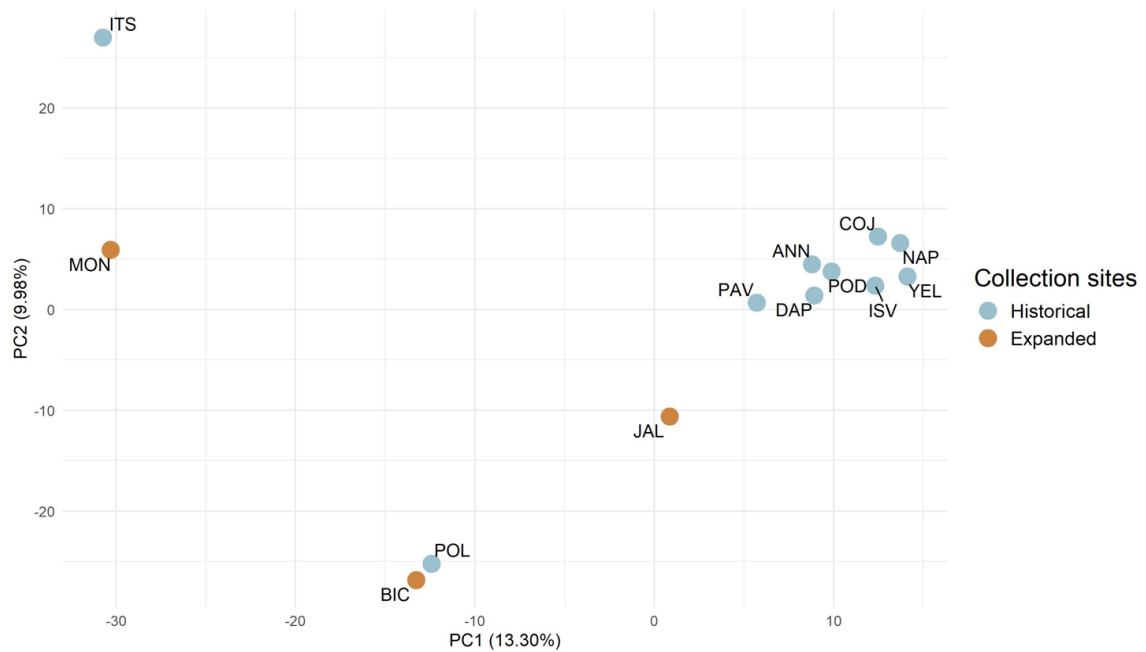
Table S1. Nucleotide diversity ( $\pi$ ) and Watterson's  $\theta_W$  calculated per pool using individual mpileup files and the Variance-sliding.pl function in PoPoolation v1.2.2, with the following parameters: –min-count 2 –min-coverage 20 –max coverage 200 –window-size 1000 –step-size 1000 –min-covered-fraction 0.2.

Populations North - South	$\pi$	Watterson's $\theta_W$
MON	0.013	0.016
BIC	0.014	0.018
JAL	0.016	0.019
COJ	0.017	0.018
NAP	0.013	0.013
ISV	0.015	0.015
YEL	0.009	0.010
ANN	0.016	0.019
POD	0.016	0.018
PAV	0.016	0.018
DAP	0.017	0.019
POL	0.014	0.017
ITS	0.017	0.020

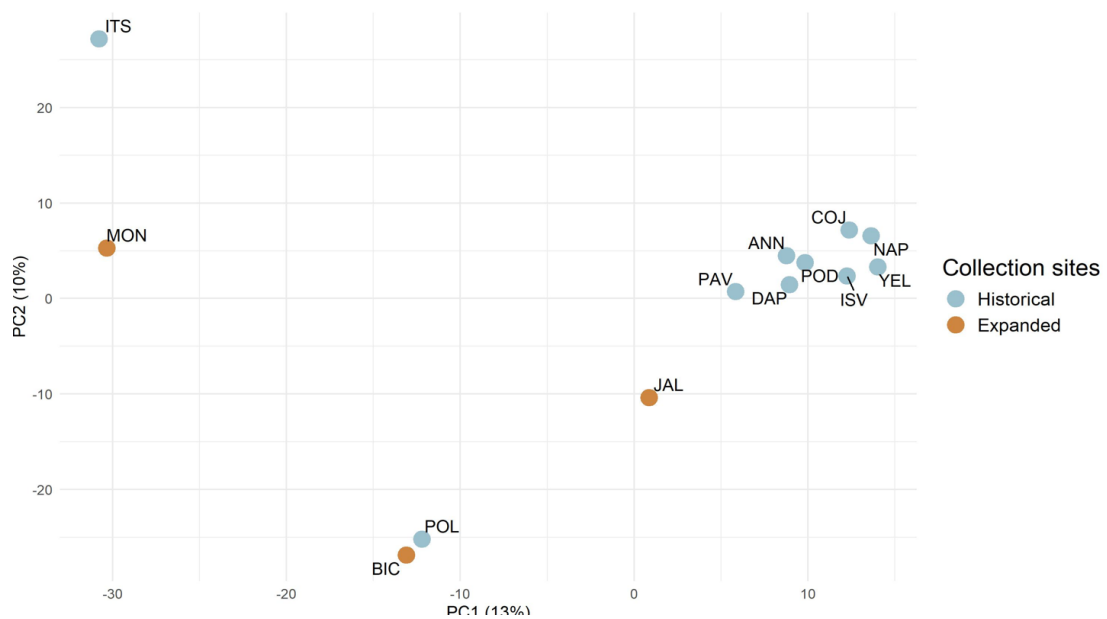


**Fig. S3.** Series of Principal Component Analysis (PCA) showing the first two axes of the genetic differentiation among the Kellet’s whelk populations in the expanded and historical distribution range considering different amount of missing data. The proportion of missing data allowed, from the most restrictive option (no missed data) to a more loose one (50% of missing data), was explored by using the filter `–max-missing` implemented in VCFtools. Regardless the amount of missing data allowed, all PCAs show the same pattern in which MON and ITS are the most distant populations, BIC and POL are very similar and populations from the Santa Barbara Channel cluster together.

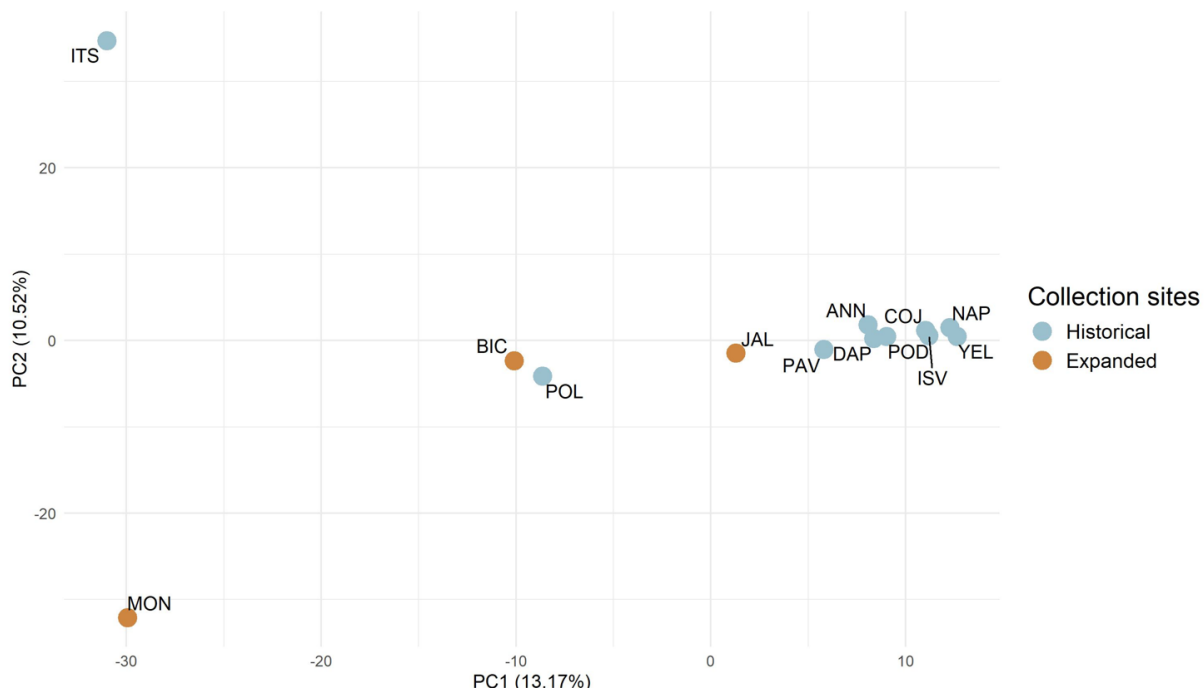
**50% of missing data allowed, number of SNPs 46949**



**25% of missing data allowed, number of SNPs 46737**



### 15% of missing data allowed, number of SNPs 42214



### No missing data allowed, number of SNPs 30717

