

SUPPLEMENTARY MATERIAL

Genetic homogeneity of the invasive lionfish across the Northwestern Atlantic and the Gulf of Mexico based on Single Nucleotide Polymorphisms

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Figure FS1. Heterozygosity graph. Graph of heterozygosity observed (Ho) versus expected (He) for 1,220 *P. volitans* SNPs included in this study. SNPs displaying larger and significant values of observed versus expected heterozygosity were removed from the database before further analyses.

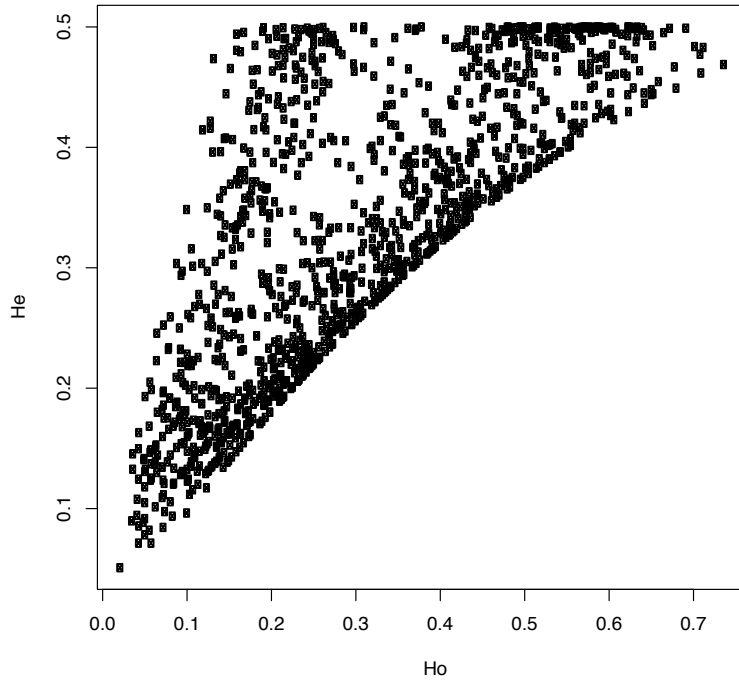


Figure FS2. Number of alleles from SNPs. Graph of the cumulative number of alleles from 1,220 SNPs of 162 *P. volitans* specimens related to population sample size.

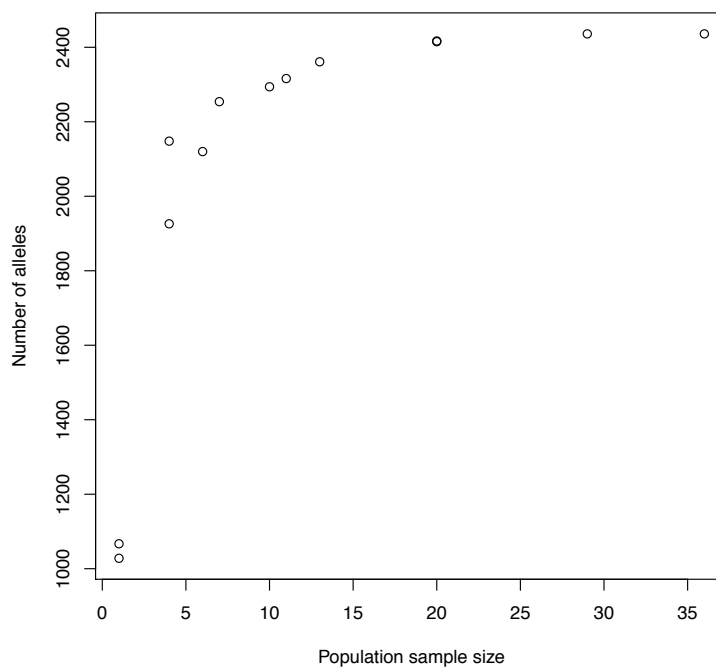


Figure FS3. Maximum likelihood phylogenetic tree. ML tree reconstructed from 1,220 SNPs and 162 different *P. volitans* genotypes. Different branch colours represent localities where genotypes were collected. Specimens are identified by their population code (as in Table 1) followed by an individual number. Only bootstrap support over 40% is represented on the nodes.

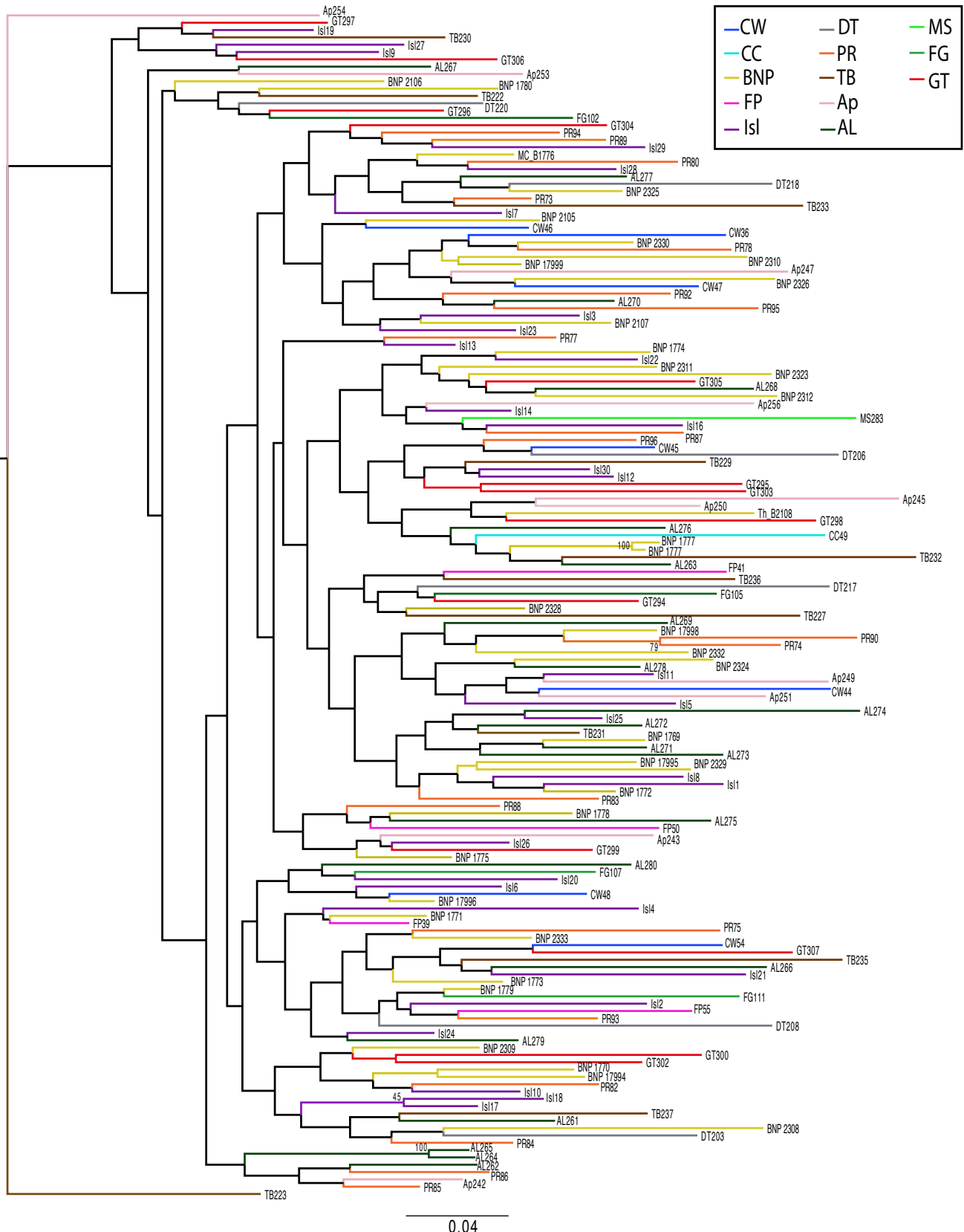


Figure FS4. Structure output for all K values. Values of the mean Log likelihood for each K (top left), optimal number of clusters detected according to the ad hoc statistic ΔK and represented as red circles (Delta K)(top right), and barplots from K=2 to K=8.

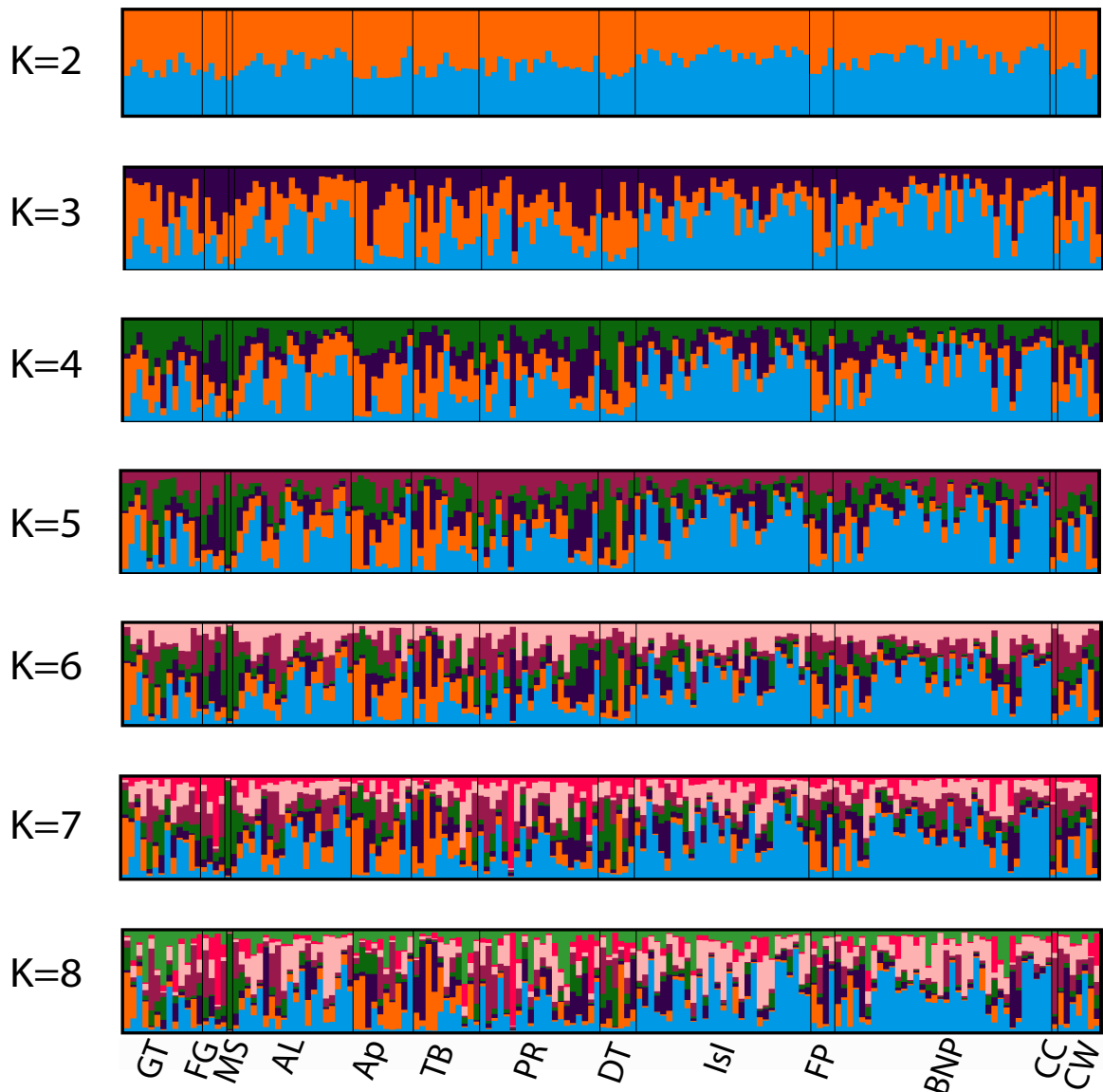
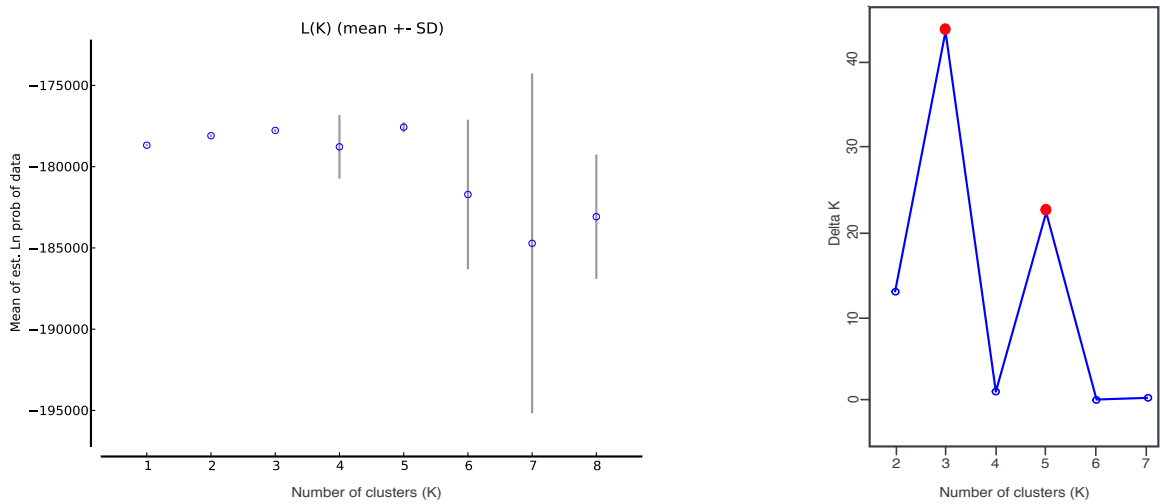


Table TS1. Results of analyses of molecular variance (AMOVAs) of lionfish from 1,207 neutral SNPs. Populations' grouping (Source of variation), degrees of freedom (d.f.), percentage of variation (% Var.), fixation indexes, and *p*-values.

Source of variation	d.f	% Var.	Fixation index	<i>p</i>-value
<i>PR and DT within NW Atlantic</i>				
Among groups	1	0	-0.001	0.84
Among populations within groups	11	0	-0.007	1.00
Within populations	149	0	-0.040	0.99
Within individuals	162	100	-0.048	0.99
<i>PR and DT within Gulf of Mexico</i>				
Among groups	1	0	-0.002	0.89
Among populations within groups	11	0	-0.006	1.00
Within populations	149	0	-0.040	0.99
Within populations	162	100	-0.049	0.99
<i>Without PR and DT</i>				
Among groups	1	0	-0.002	0.86
Among populations within groups	11	0	-0.006	1.00
Within populations	125	0	-0.049	0.99
Within populations	136	100	-0.057	0.99