

Supplementary material

Table S1. Number of alleles for the twelve loci genotyped in meagre broodstocks

	No of alleles sampled										
	Stock	Stock	Stock	Stock	Stock	Stock	Stock	Stock	Stock	Stock	Stock
	A	B	C	D	E	F	G	H	I	J	K
Cascmic14	4	5	4	3	5	4	5	4	5	3	5
Soc-11	5	7	4	5	6	5	8	4	6	4	7
Soc-35	5	5	4	3	3	5	6	2	4	3	4
Soc-405	3	3	3	3	2	3	3	2	4	3	3
Soc-42	7	9	6	6	3	6	8	3	10	3	6
Soc-431	4	4	3	3	3	4	4	3	3	3	4
Soc-44	2	5	5	2	3	3	4	3	4	3	5
Uba-005	2	3	2	2	3	2	3	2	3	2	3
Uba-006	5	6	4	3	4	6	6	1	4	2	5
Uba-042	3	5	3	3	3	3	4	2	3	2	3
Uba-050	6	6	3	4	4	5	5	2	4	3	4
Uba-054	2	2	2	2	2	2	2	2	3	2	2
Average	4,00	5,00	3,58	3,25	3,42	4,00	4,83	2,50	4,42	2,75	4,25

Table S2. Statistical summary of the performance of Coancestry software methods in the exploratory analysis of the 11 stocks for method selection. The coefficient of linear correlation between all methods as well as their variance is given.

Correlation Coefficient	TrioML	Wang	LynchLi	LynchRd	Ritland	QuellerGt	DyadML
TrioML	1,00000						
Wang	0,75285	1,00000					
LynchLi	0,76592	0,97722	1,00000				
LynchRd	0,87778	0,78018	0,78216	1,00000			

Ritland	0,63836	0,56091	0,58056	0,74478	1,00000		
QuellerGt	0,83700	0,87577	0,90519	0,88152	0,70389	1,00000	
DyadML	0,97694	0,77075	0,78289	0,90031	0,65864	0,85956	1,00000
Mean	0,13352	-0,01644	-0,01833	-0,00107	-0,00114	0,00271	0,14685
Variance	0,03442	0,11605	0,12933	0,05389	0,03443	0,08412	0,03852

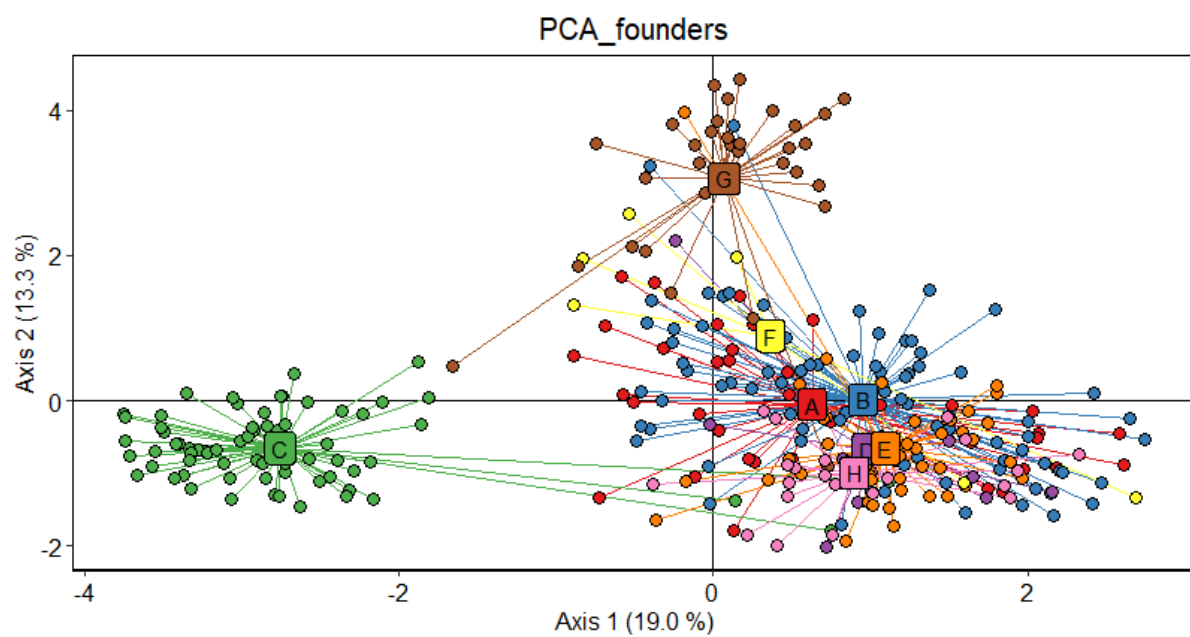


Figure S1. PCA analysis only for the eight breeder stocks A to H

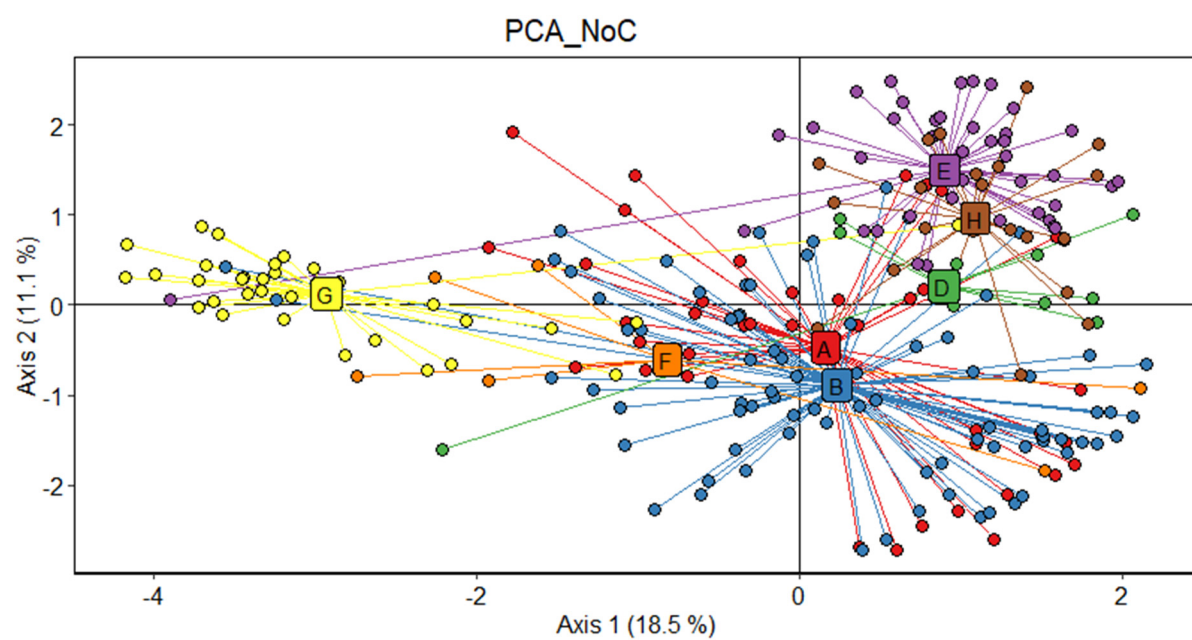


Figure S2. PCA analysis using the breeder stocks A, B, D, E, F, G, H to highlight the resolution in cluster 2 from DAPC analysis of Figure 4