SUPPLEMENTAL

Table S1. The range of nucleotides and variants seen in each sample comparison for the training data set. F_{ST} estimations were calculated for each nucleotide in common between two samples (Individual A and Individual B). Then all F_{ST} values greater than 0 ($F_{ST} > 0$) were used to calculate the minimum, median, mean, and maximum. Additionally, the number of F_{ST} estimates higher than 0.10, 0.25, and 0.50 were determined for each comparison. S0## represents an individual, and R# represents the replicate.

Attached excel worksheet.

Table S2. Votes and rank of classes for sample S028_R3 for *per marker* and *overall* method. The total number of votes possible via SVM for the training data set was 25 votes. Sample S028_R3 had no classification obtaining 25 votes. For classes that received the same number of votes, the mean prediction percentage was used to break the tie.

Votes	Classification	Rank
24	S036	1
23	S029	2
22	S007	3
22	S004	4
22	S025	5
20	S008	6
20	S006	7
18	S001	8
18	S010	9
16	S028	10