

## Supporting Information

**ESM Table S1** Pair-wise population  $F_{ST}$ -values. Only sites with five or more genotyped individuals are included. Values in bold are statistically significant after sequential Bonferroni correction ( $P < 0.05$ ).

	PAS	HEM	PAU	AVO	LUZ	PAL	OAK	RAM	YSA	JUL	ALP	LAW	DUL
PAS	-												
HEM	<b>0.076</b>	-											
PAU	<b>0.084</b>	<b>0.115</b>	-										
AVO	0.042	0.033	0.064	-									
LUZ	0.047	0.034	0.042	0.023	-								
PAL	<b>0.077</b>	<b>0.066</b>	<b>0.078</b>	<b>0.057</b>	0.020	-							
OAK	0.039	0.049	0.055	0.035	0.023	0.064	-						
RAM	0.049	0.045	<b>0.083</b>	0.016	0.033	0.040	0.023	-					
YSA	0.038	0.050	0.037	0.032	0.006	0.026	-0.001	0.028	-				
JUL	<b>0.050</b>	<b>0.047</b>	<b>0.065</b>	0.013	0.004	0.013	0.028	0.023	0.002	-			
ALP	<b>0.058</b>	<b>0.066</b>	<b>0.073</b>	0.028	0.027	0.038	0.035	0.022	0.021	0.029	-		
LAW	<b>0.057</b>	<b>0.068</b>	0.035	0.033	0.034	0.054	0.032	0.036	0.009	0.026	0.054	-	
DUL	<b>0.072</b>	<b>0.076</b>	0.049	0.019	0.035	0.055	0.052	0.033	0.042	0.038	0.029	0.059	-