Table S4: Alternative splits for each node of the regression tree (figure 2), explaining allelic richness (A) and expected heterozygosity (H_e). Alternative splitting variables are listed (Variable), as are the percent variances explained by each split (VarEx) and to which side of the regression tree each group splits at each node.

Variable	VarEx	To the left	To the right
Allelic richness (A)			
Split 1			
Glacial range area	66.1%	<3.5e5 km^2	≥ 3.5e5 km^2
Glacial refugia count	47.4%	<21.9	≥ 21.9
Modern range patch count	41.8%	<58	≥ 58
Modern range area	37.5%	<8.4e5 km^2	≥ 8.4e5 km^2
Modern range contiguity	32.3%	≥ 0.86	<0.86
Split 2			
Glacial range contiguity	8.6%	<0.85	≥ 0.85
Modern range contiguity	8.3%	<0.86	≥ 0.86
Glacial refugia count	8.2%	≥ 15	<15
Glacial range area	7.4%	<1.4e5 km^2	≥ 1.4e5 km^2
Modern range area	6.6%	≥ 5.5e5 km^2	<5.5e5 km^2
Split 3			
Dispersal mechanism	3.7%	all others	wind
Glacial refugia count	3.6%	<64	≥ 64
Glacial contiguity	2.6%	≥ 0.84	<0.84
Modern range patch count	1.6%	<101	≥ 101
Glacial range area	1.6%	<9.7e5 km^2	≥ 9.7e5 km^2
Expected heterozygosity (H_e)			
Split 1			
Glacial refugia count	26.7%	<64	≥ 64
Glacial range contiguity	25.2%	≥ 0.84	<0.84
Modern range contiguity	14.7%	≥ 0.86	<0.86
Glacial range area	12.3%	<2.1e5 km^2	≥ 2.1e5 km^2
Modern range patch count	9.4%	<101	≥ 101
Split 2			
Modern range area	20.8%	≥ 4.3e5 km^2	<4.3e5 km^2
Glacial range contiguity	13.1%	≥ 0.86	<0.86
Modern range contiguity	7.3%	≥ 0.85	<0.85
Modern range patch count	7.2%	≥ 20	<20
Glacial range area	4.1%	≥ 0.8e5 km^2	<0.8e5 km^2
Split 3			
Glacial range area	16.3%	<1.4e5 km^2	≥ 1.4e5 km^2
Glacial refugia count	7.5%	<22	≥ 22
Succession	7.1%	early, late	middle
Glacial range contiguity	5.5%	≥ 0.86	≥ 0.86
Modern range patch count	5.2%	<36	≥ 36