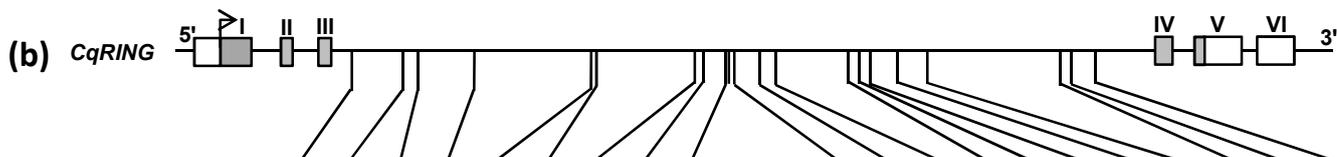
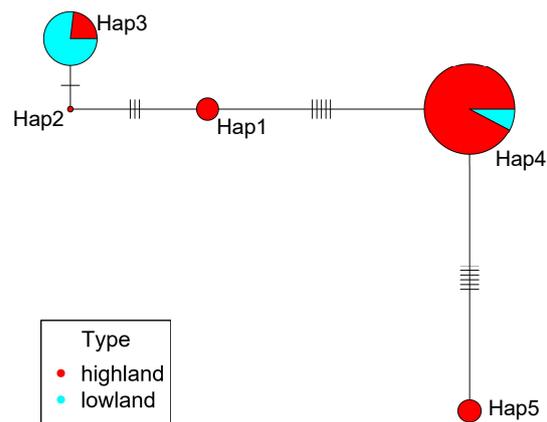
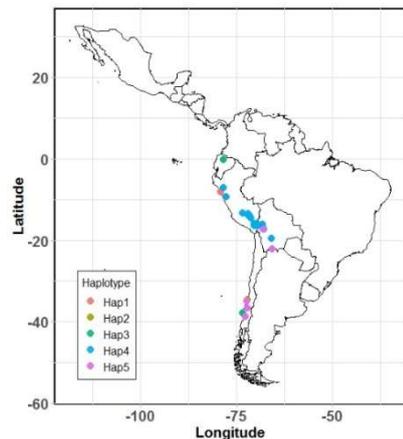


UTR/Exon/Intron	Exon 1	Exon 2					Exon 3	Intron 3	Exon 4	Intron 4					
SNP position	-1323	-93	587	773	779	1252	1520	1637	2152	2160	2543	3101	4243	4346	
AA substitution			Arg196Arg	Ile258Met	Val260Val	Asp345Gly		Ser440Ser							
Hap1	A	C	G	G	T	A	G	C	A	C	G	A	A	T	
Hap2	A	C	A	G	T	A	G	C	A	C	G	A	A	T	
Hap3	A	C	A	A	T	A	G	A	A	C	A	A	A	T	
Hap4	C	T	A	G	T	A	T	C	A	T	G	T	A	T	
Hap5	C	T	A	G	A	G	T	C	T	C	G	A	T	C	
Missense variant				*	*	*									



UTR/Exon/Intron	Intron 3																						
SNP position	539	749	813	1045	1523	1548	1955	1980	2082	2084	2114	2221	2281	2586	2625	2670	2772	2782	2908	3455	3499	3593	
AA substitution																							
Hap1	C	A	T	T	C	A	T	C	T	G	T	T	A	G	C	T	G	A	G	A	T	C	
Hap2	C	A	T	T	C	A	A	C	T	G	T	T	A	G	C	T	G	A	G	A	T	C	
Hap3	C	A	T	T	C	A	T	C	T	G	T	T	A	A	C	T	G	A	G	A	T	C	
Hap4	C	G	T	T	C	G	A	C	T	A	C	T	A	G	C	A	G	A	G	A	T	C	
Hap5	C	G	T	T	C	G	A	T	T	G	T	T	A	G	C	A	G	A	A	A	C	C	
Hap6	G	G	A	T	C	G	A	C	T	G	T	T	A	G	T	A	G	A	G	A	T	T	
Hap7	G	G	A	C	T	G	A	C	A	G	T	G	A	G	C	A	A	G	G	G	T	T	

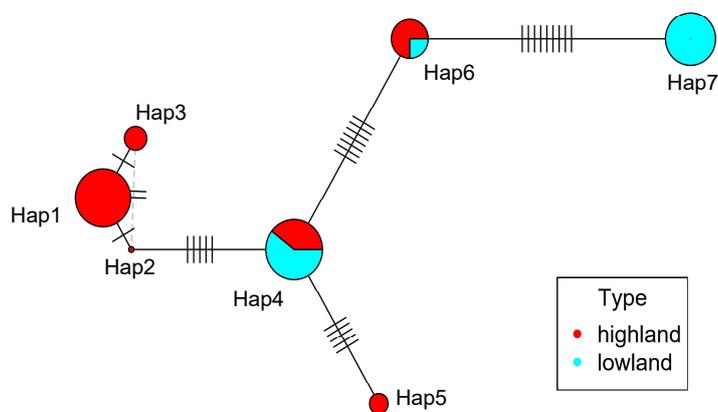
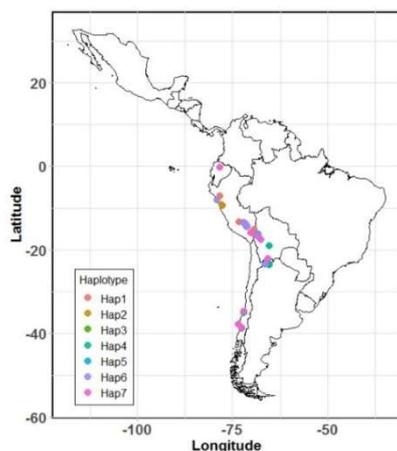


Figure 4-figure supplement 2: Haplotypes of two genes, *CqPP2C* (a) and *CqRING* (b) associated with seed size in quinoa. The geographic origin of the accessions and haplotype networks are displayed below the gene structure. The frequency of haplotypes is correspondent to the circle size. The color of the pie chart depicts the population. Crosslines represent the number of nucleotide polymorphisms between haplotypes.