

	MSQ4	MSQ13	QrOst1	QpD12	QpZag15	QpZag9	QpZag46	QpZag110	QpZag36	QrZag20	QrZag11	QrZag7	QmAj1
MSQ4	X												
MSQ13	0.2	X											
QrOst1	0.02	0.93	X										
QpD12	0.16	0.64	0.07	X									
QpZag15	0.03	0.87	0.35	0.07	X								
QpZag9	0.82	0.28	0.64	0.16	0.41	X							
QpZag46	0.58	0.28	0.75	0.91	0.65	0.99	X						
QpZag110	0.41	0.89	0.98	0.66	0.48	0.29	0.89	X					
QpZag36	0.71	0.93	0.83	0.53	0.61	0.55	<1.43e-09	0.76	X				
QrZag20	0.46	0.18	0.45	0.08	0.39	0.7	0.04	0.74	0.58	X			
QrZag11	0.3	0.19	0.2	0.49	0.01	0.01	0.05	0.61	0.46	0.24	X		
QrZag7	0.39	0.05	0	0.33	<0.002654	0.65	0.91	0.87	0.57	0.37	0.95	X	
QmAj1	0.42	0.81	0.03	0.19	0.35	0.54	0.3	0.73	0.74	0.34	0.64	0.09	X

Table S3: Linkage disequilibrium among pairs of loci

Results of the linkage disequilibrium among pairs of loci and 17 populations, showing the p-values for the G-test with the null hypothesis of independence among genotypes. Values below $p=0.05$ are considered statistically significant.