

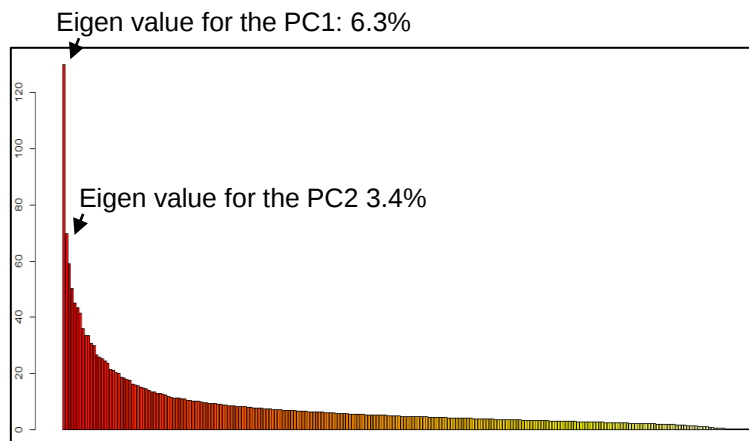


Figure S1. Distribution of eigen values in principal component analysis using genotypic data at 14,695 loci. The highest 256th of eigen values were shown in this figure.

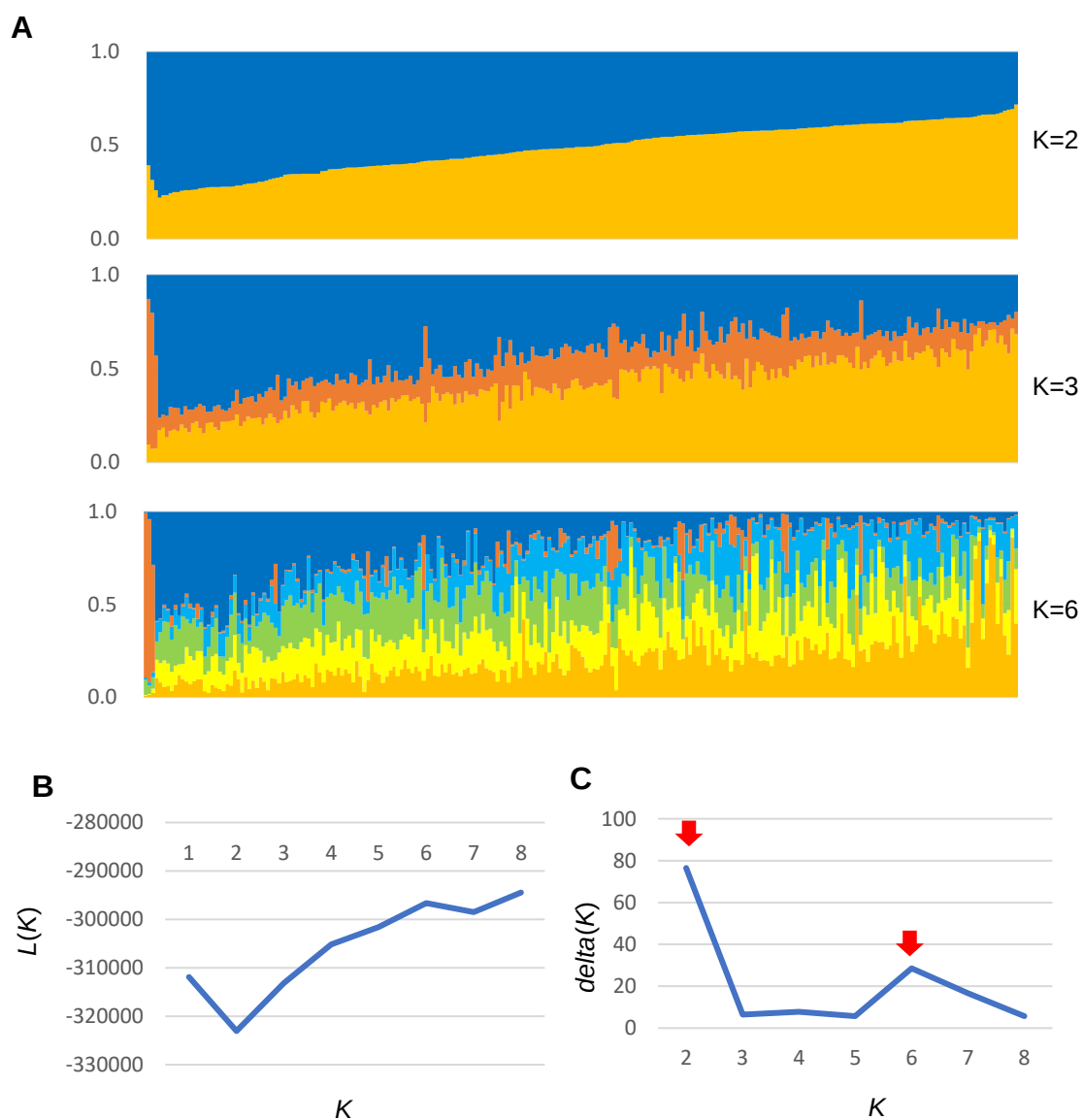
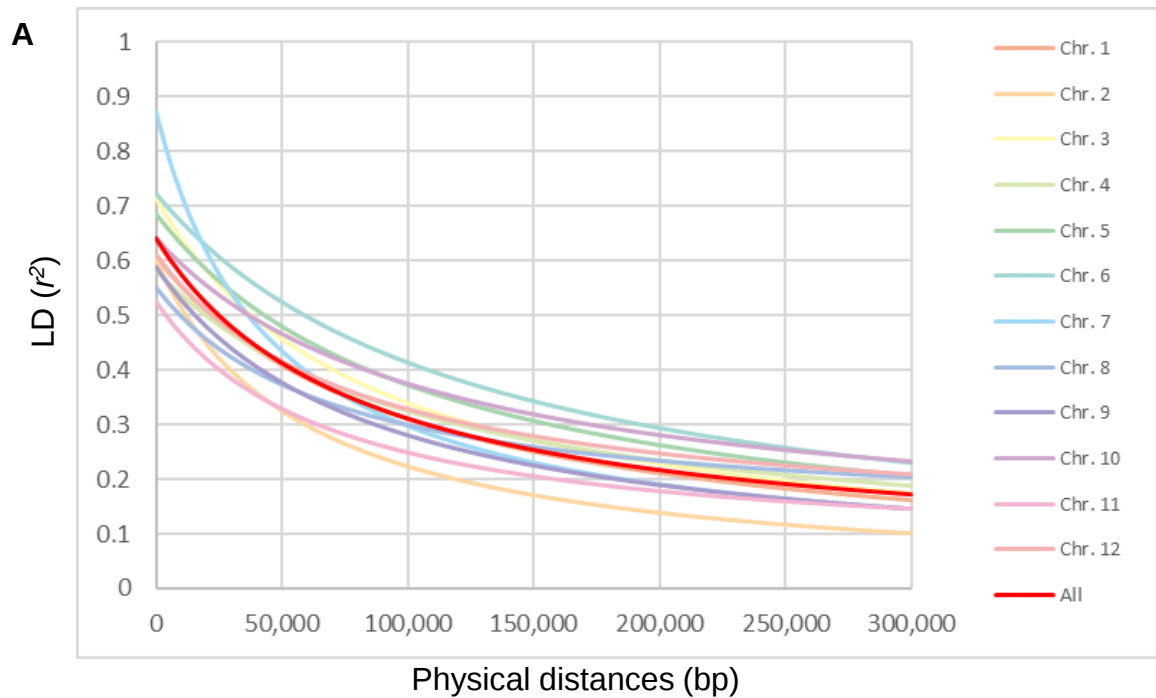


Figure S2. Bayesian clustering using 'Structure' software in the diversity panel 'G'. **(A)** Barplots of the accessions represented in the subpopulation portions when the number of subpopulation (K) is assumed as $K=2$, 3, and 6. **(B)** Average likelihood at each of K . **(C)** The local maximum of the delta (K) values. $K=2$ or $K=6$ is assumed the most optimum number of the subpopulation.



B

Chr.	DecayRate (r^2 /bp)	LDmax (r^2_{High})	LDmin (r^2_{Low})	DecayRate Lower confidence interval (r^2 /bp)	DecayRate Upper confidence interval (r^2 /bp)	LDmax Lower confidence interval (r^2_{High})	LDmax Upper confidence interval (r^2_{High})	LDmin Lower confidence interval (r^2_{Low})	LDmin Upper confidence interval (r^2_{Low})	Distance (d_{LD50})
1	1.0.E-05	0.608	0.015	9.8.E-06	1.0.E-05	0.604	0.613	0.013	0.017	90,714
2	1.7.E-05	0.602	0.005	1.4.E-05	1.9.E-05	0.523	0.617	0.000	0.012	56,310
3	1.2.E-05	0.715	0.022	1.2.E-05	1.2.E-05	0.713	0.718	0.021	0.024	74,931
4	9.3.E-06	0.583	0.046	9.0.E-06	9.6.E-06	0.579	0.587	0.044	0.049	80,295
5	9.2.E-06	0.687	0.033	9.1.E-06	9.5.E-06	0.684	0.692	0.031	0.035	90,247
6	7.9.E-06	0.724	0.021	7.8.E-06	8.0.E-06	0.722	0.728	0.020	0.023	113,095
7	2.2.E-05	0.872	0.035	1.5.E-05	2.0.E-05	0.773	0.850	0.002	0.026	39,030
8	1.4.E-05	0.552	0.121	1.3.E-05	1.5.E-05	0.544	0.561	0.118	0.124	33,085
9	1.2.E-05	0.589	0.023	1.2.E-05	1.9.E-05	0.623	0.760	0.001	0.026	72,102
10	9.2.E-06	0.641	0.085	9.0.E-06	9.4.E-06	0.638	0.644	0.083	0.088	67,590
11	1.5.E-05	0.525	0.058	1.4.E-05	1.5.E-05	0.516	0.534	0.057	0.061	45,855
12	1.3.E-05	0.612	0.103	1.2.E-05	1.3.E-05	0.606	0.614	0.101	0.105	43,969
Mean	1.2.E-05	0.643	0.047	1.1.E-05	1.3.E-05	0.627	0.660	0.041	0.049	67,269

Figure S3. Half LD decay from the maximum LD to the minimum LD by the physical distances between two markers.

(A) LD decay by the physical distances (bp) by each chromosome. (B) Estimation of half physical distances where LD reduce to halve between the maximum LD and minimum LD.

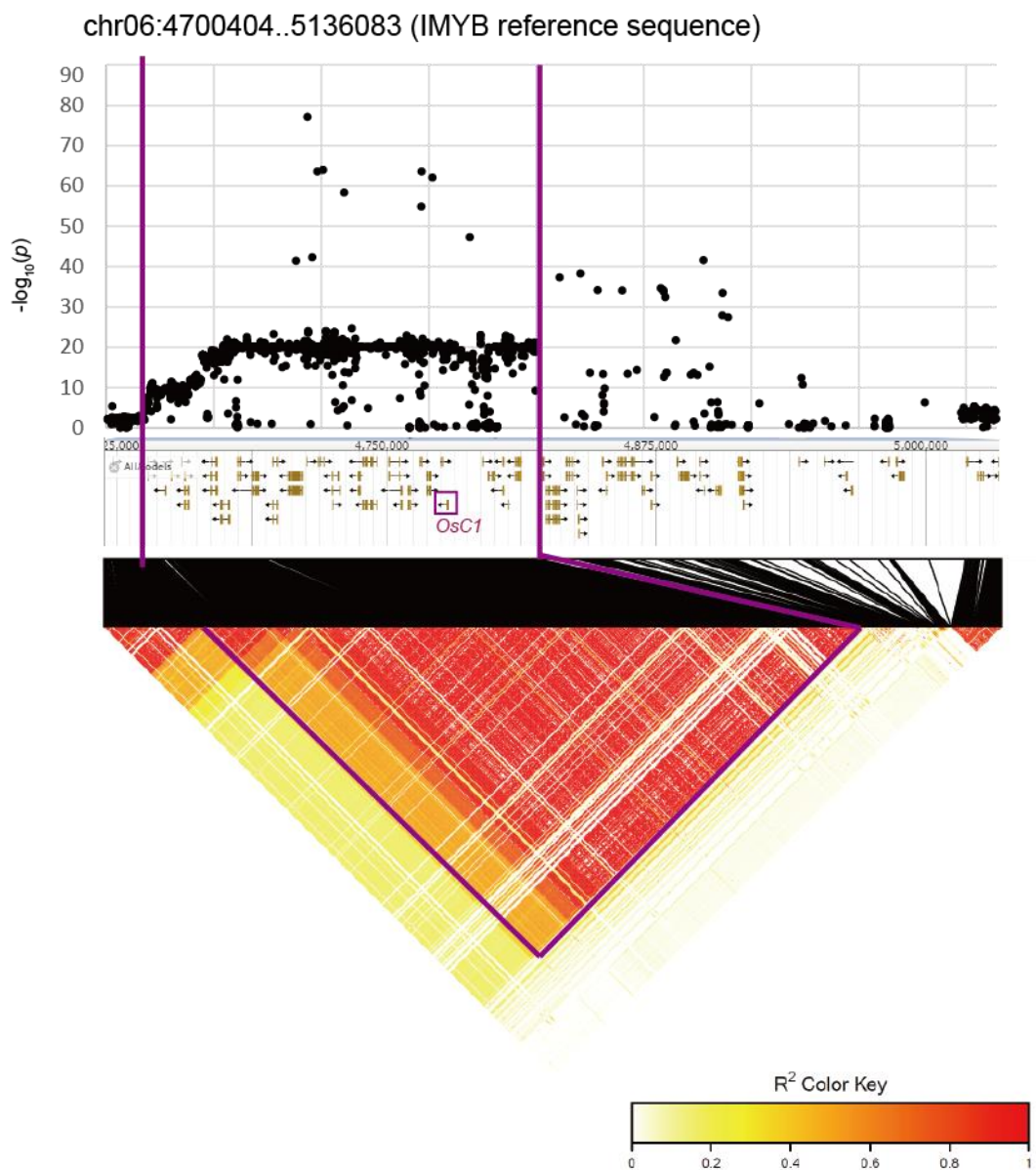


Figure S4. Genome-wide association and linkage disequilibrium structure around *qAPC6.3*.

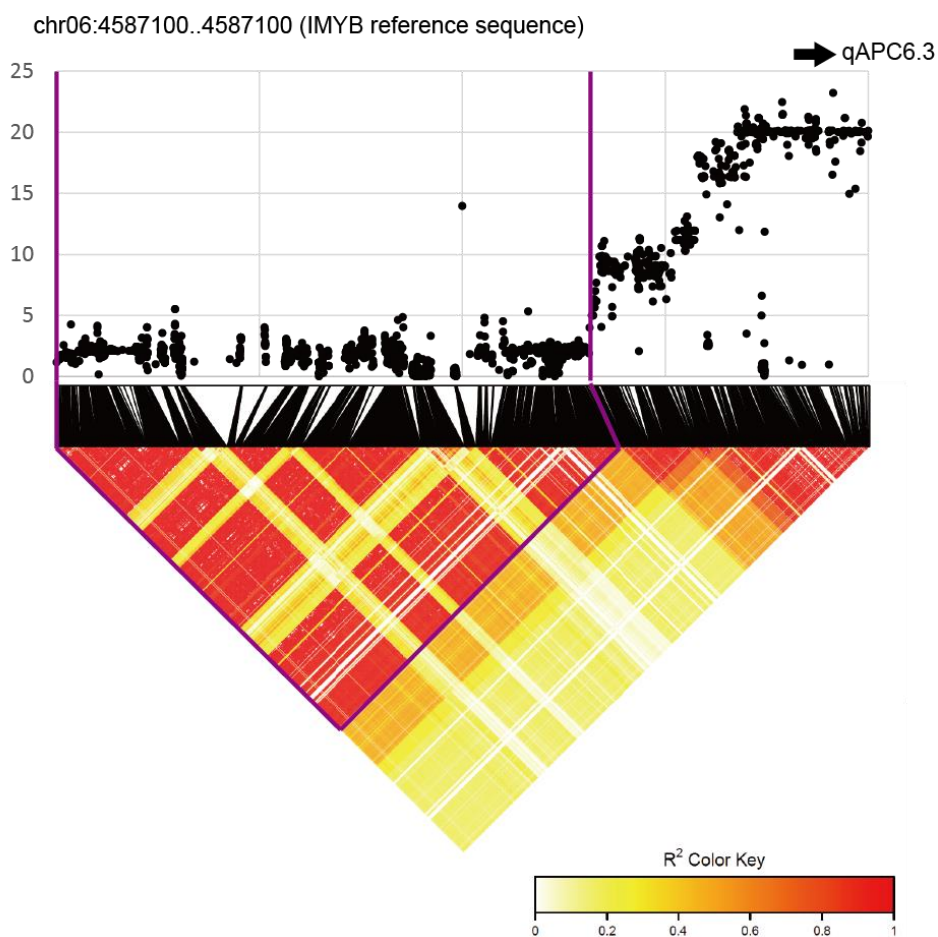


Figure S5. Genome-wide association and linkage disequilibrium structure around *qAPC6.2*.

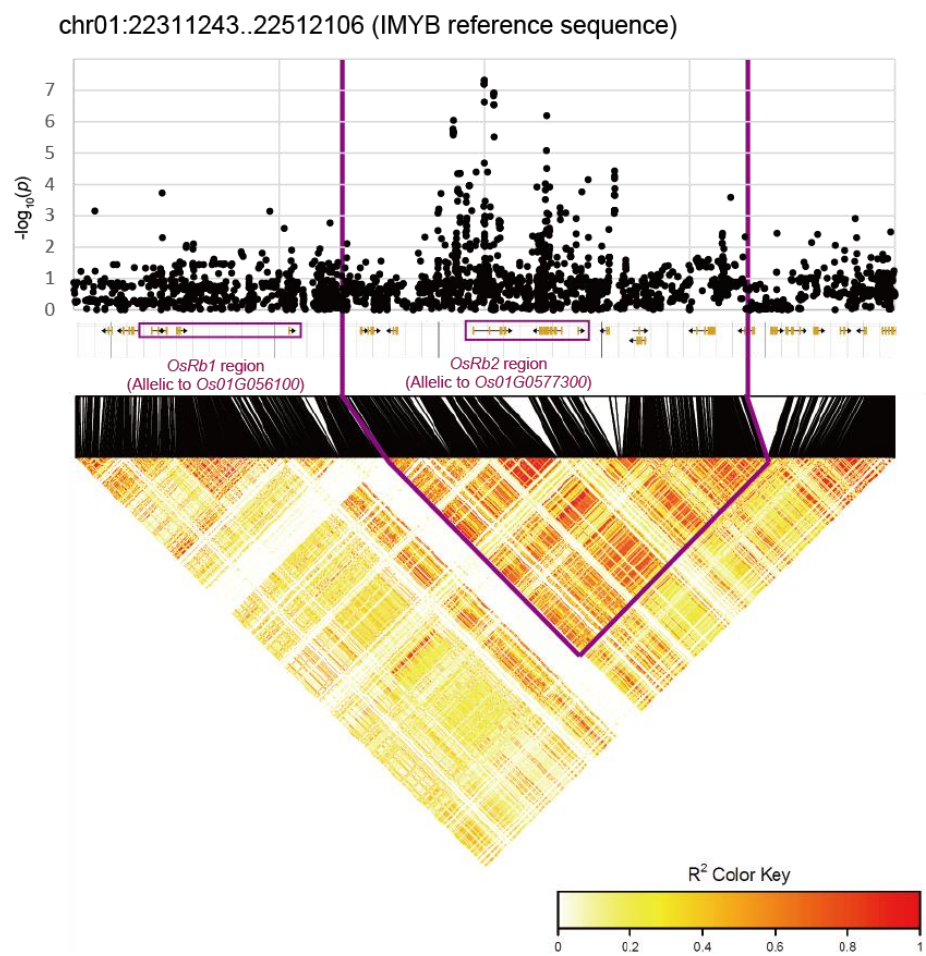


Figure S6. Genome-wide association and linkage disequilibrium structure around *qAPC1.1*.

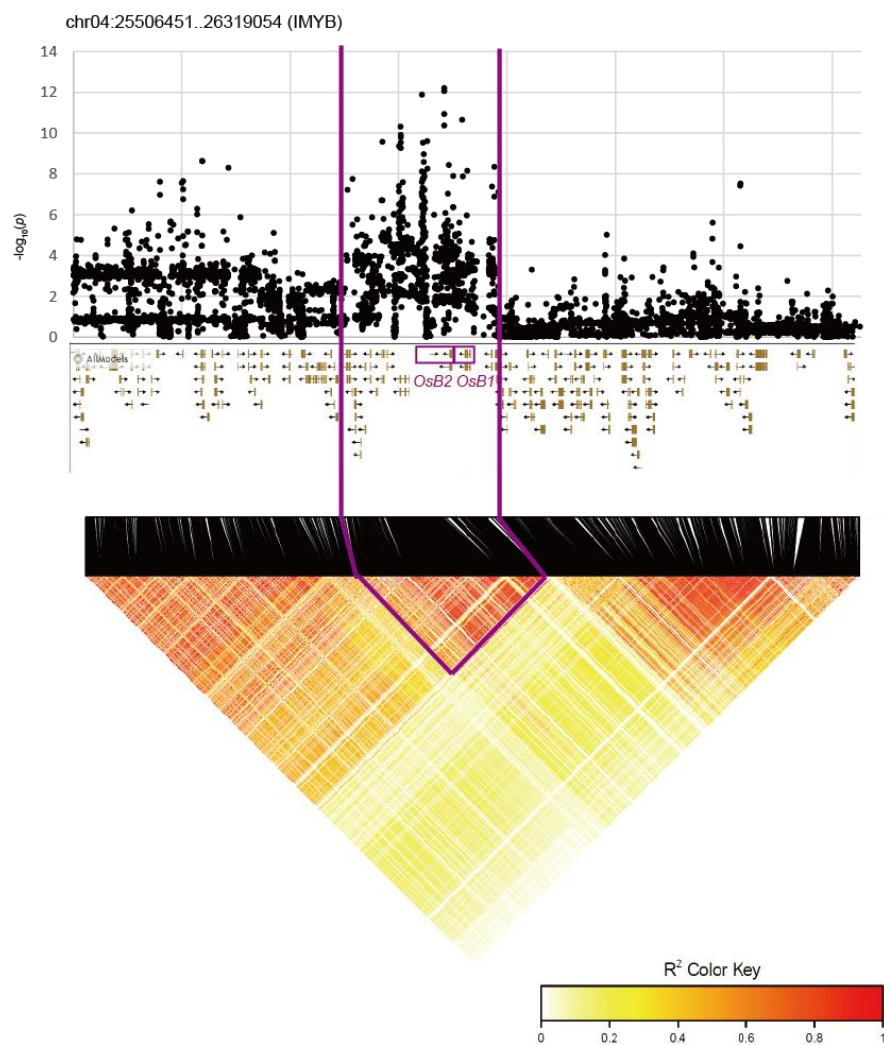


Figure S7. Genome-wide association and linkage disequilibrium structure around *qAPC4.1*.

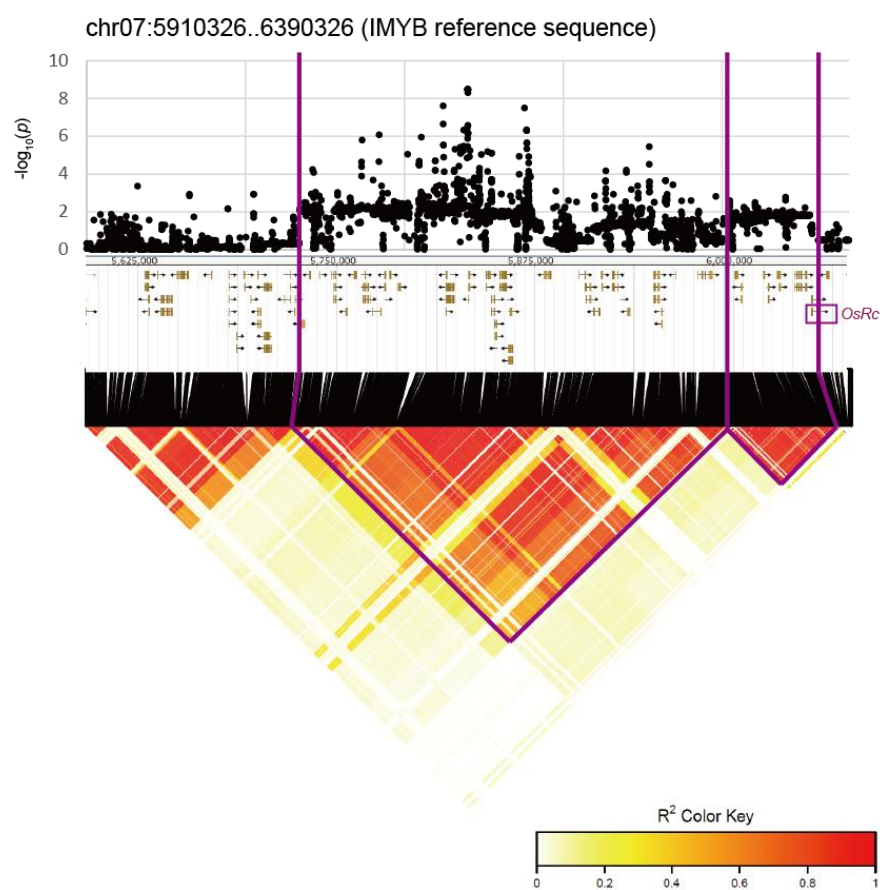


Figure S8. Genome-wide association and linkage disequilibrium structure around *qAPC7.1*.

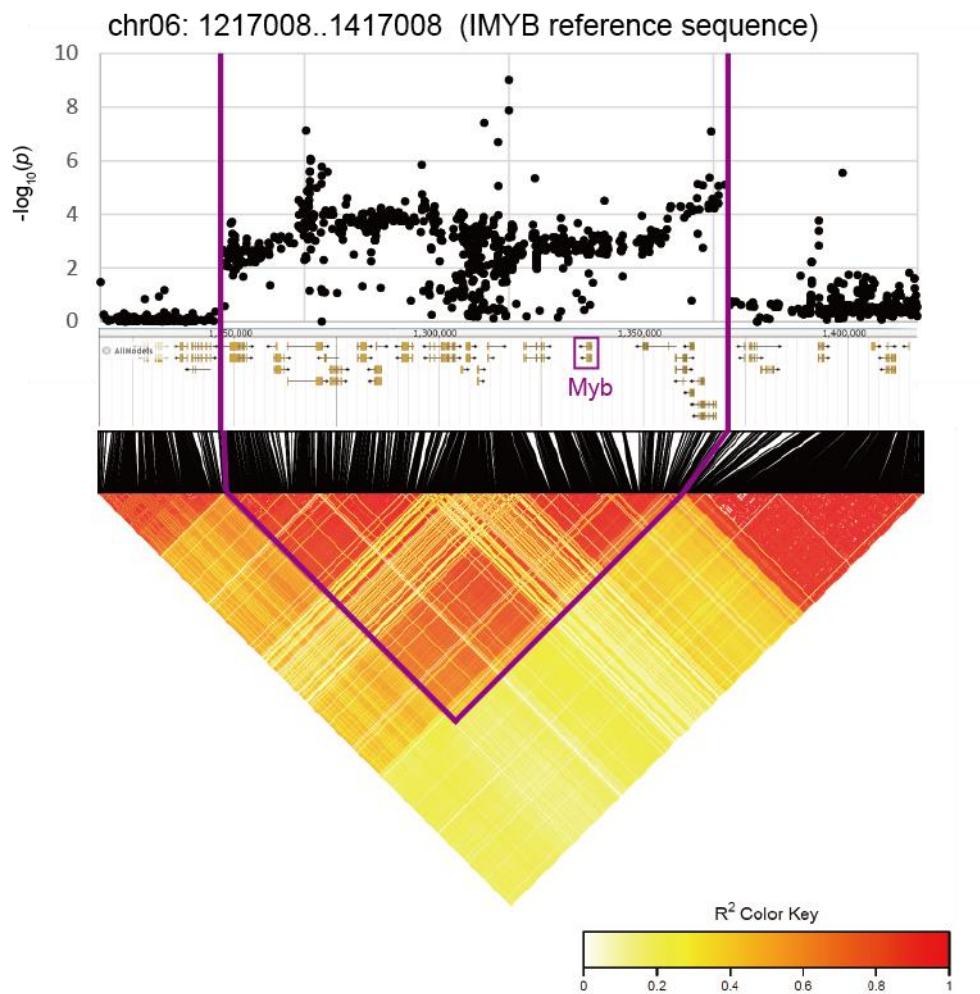


Figure S9. Genome-wide association and linkage disequilibrium structure around *qAPC6.1*.

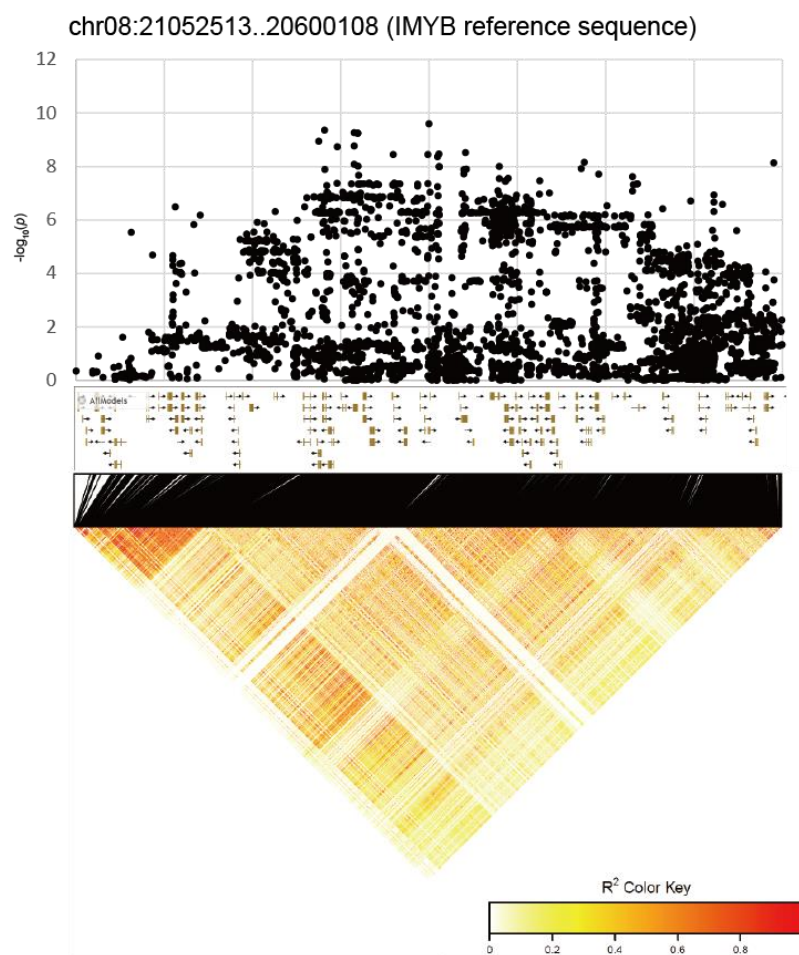


Figure S10. Genome-wide association and linkage disequilibrium structure around *qAPC8.1*.