

Table S 2 Microsatellite markers used to infer the population structure of the *Malus* accessions used for the association analysis.

Marker	Linkage Groups	Genotype No	Allele No	Size Range	Gene Diversity	Heterozygosity
NZ02b01	15	43	14	216-260	0.8146	0.8495
CH03G04	14	55	18	119-148	0.8656	0.6611
NZ05g08	4	42	19	101-157	0.7394	0.3801
CH05f04	13	22	8	157-171	0.7346	0.7901
NZ28f04	12	15	6	95-113	0.7506	0.7923
CH01h02	9	39	18	217-259	0.7783	0.7391
CH03d02	11	45	26	152-247	0.7835	0.6452
Hi02f12	17	38	12	129-152	0.8394	0.6860
NZ23g04	6	51	18	86-118	0.7979	0.7978
CH01c06	8	39	13	154-189	0.8135	0.8138
Hi05b09	7	33	14	128-158	0.7590	0.8011
CH05a09	16	47	17	147-197	0.7653	0.8297