

Erratum to: Genetic structure of a QTL hotspot on chromosome 2 in sweet cherry indicates positive selection for favorable haplotypes

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In the original publication, the numbers assigned to each haplotype in Fig. 2 and its expanded version (Supplementary Fig. S2) are not consistent with the numbers used in the article. The haplotype numbers are corrected and the haplotypes are reordered according to these new numbers in the attached revised Fig. 2 and Supplementary Fig. S2.

Fig. 2 Marker allele composition of each haplotype across the five haploblocks for the sweet cherry QTL hotspot on chromosome 2 illustrated using the smallest number of markers needed to differentiate the haplotypes. SSR alleles

are recorded as fragment sizes in base pairs. Haplotypes were assigned by the PediHaplotyper software (Voorrips et al. 2016). Haplotypes containing missing marker scores were omitted from the table. The complete marker composition is in Supplementary Fig. S2

Supplementary Fig. S2 Marker allele composition of each haplotype across five haploblocks for the sweet cherry QTL hotspot on chromosome 2. SSR alleles are recorded as fragment sizes in base pairs. The smallest subset of markers needed to differentiate the haplotypes within each haploblock are highlighted in red font. Haplotypes were assigned by the PediHaplotyper software (Voorrips et al., 2016). Haplotypes containing missing marker scores were omitted from the table

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Haploblock	Marker	Physical position (bp)	Genetic position (cM)	Haplotypes											
				2	3	4	5	6	7	8					
HB-B	ss490549037	14,319,252	13.5	G	A	G	G	A	G	G					
	ss490549048	15,023,181	18.2	A	A	A	G	G	G	G					
	ss490559387	15,186,205	19.3	C	C	C	C	C	A	C					
	ss490559390	15,186,239	19.3	A	G	G	G	G	A	A					
HB-C				2	3	4	5	6	7	8					
	ss490547150	16,515,942	24.8	A	A	A	A	G	A	A					
	ss490547158	17,249,525	28.3	A	G	A	A	A	G	G					
	ss490549121	17,503,996	28.6	G	G	A	G	G	A	G					
ss490549138	17,704,790	28.9	C	A	A	A	C	A	C						
HB-D				2	3	4	5	6	7	11	12	14			
	ss490549172	17,862,597	29.0	C	A	C	C	C	C	A	A	A			
	ss490549192	17,940,428	29.0	G	G	G	G	G	G	G	A	G			
	CPSCT038	18,416,459	29.3	190	204	192	190	192	206	202	192	192			
	ss490556813	18,601,465	29.5	A	A	G	A	A	A	A	A	A			
	ss490556816	18,676,414	29.5	C	C	A	A	A	A	C	A	A			
HB-E				2	3	6	7	8	9	10	14	15	16	19	
	ss490549227	18,948,924	29.7	A	G	A	A	A	G	G	A	A	A	A	
	ss490549238	19,068,803	30.8	G	G	A	G	A	G	A	A	A	A	A	
	ss490549258	19,200,549	31.9	A	G	G	A	G	A	A	G	A	A	G	
	ss490549287	19,324,328	32.8	G	A	A	G	A	A	G	G	G	G	G	
	ss490549331	19,470,895	33.4	G	G	A	A	G	A	G	A	A	G	G	
HB-F				2	3	6	7	8	9	10	13	14	16	17	
	BPPCT034	20,068,024	40.2	255	235	223	237	223	225	223	225	221	255	250	
	ss490549443	20,126,852	40.3	A	C	A	A	A	C	C	A	A	A	A	
ss490549569	20,455,988	42.9	C	C	A	A	C	C	A	C	A	A	A		

Haploblock	Marker	Physical position (bp)	Genetic position (cM)	Haplotypes															
				2	3	4	5	6	7	8									
HB-B	ss490549037	14,319,252	13.5	G	A	G	G	A	G	G									
	ss490549044	14,872,352	17.2	G	G	G	G	G	A	G									
	ss490549048	15,023,181	18.2	A	A	A	G	G	G	G									
	ss490549052	15,185,727	19.3	C	A	A	A	A	C	C									
	ss490559387	15,186,205	19.3	C	C	C	C	C	C	C									
	ss490559390	15,186,239	19.3	A	G	G	G	G	A	A									
HB-C	ss490547150	16,515,942	24.8	A	A	A	A	G	A	A									
	ss490549109	17,033,717	26.9	G	A	G	G	G	G	A									
	ss490547158	17,249,525	28.3	A	G	A	A	A	G	G									
	ss490549121	17,503,996	28.6	G	G	A	G	G	A	G									
	ss490549138	17,704,790	28.9	C	A	A	A	C	A	C									
	HB-D	ss490549172	17,862,597	29.0	C	A	C	C	C	C	A	A	A						
ss490549176		17,868,204	29.0	A	G	G	G	G	G	A	A	G							
ss490549184		17,905,928	29.0	A	A	A	A	A	C	A	C	A							
ss490549187		17,907,446	29.0	C	C	C	C	C	C	A	C	A							
ss490549192		17,940,428	29.0	G	G	G	G	G	G	G	A	G							
ss490556795		18,223,481	29.2	G	A	G	G	G	G	G	G	G							
CPSCT038		18,416,459	29.3	190	204	192	190	192	206	202	192	192							
ss490556804		18,493,620	29.4	A	C	C	C	C	C	C	C	C							
ss490550555		18,509,392	29.4	C	A	C	C	C	A	A	C	C							
ss490556813		18,601,465	29.5	A	A	G	A	A	A	A	A	A							
ss490556816		18,676,414	29.5	C	C	A	A	A	A	C	A	A							
HB-E		ss490556819	18,732,420	29.6	G	G	A	G	A	A	A	A	G	G	A				
	ss490549216	18,914,293	29.7	G	G	A	G	A	G	G	A	G	G	A					
	ss490549219	18,932,477	29.7	A	G	G	A	G	G	G	G	A	A	G					
	ss490549227	18,948,924	29.7	A	G	A	A	A	G	G	A	A	A	A					
	ss490549238	19,068,803	30.8	G	G	A	G	A	G	A	A	A	A	A					
	ss490549258	19,200,549	31.9	A	G	G	A	G	A	A	G	A	A	G					
	ss490549278	19,288,458	31.9	A	G	G	A	G	G	A	G	A	A	A					
	ss490549287	19,324,328	32.8	G	A	A	G	A	A	G	G	G	G	G					
	ss490549323	19,449,927	33.3	G	G	A	A	G	G	G	A	G	G	G					
	ss490549327	19,450,637	33.3	G	G	G	A	G	G	G	A	G	G	G					
	ss490549331	19,470,895	33.4	G	G	A	A	G	A	G	A	A	G	G					
	ss490549350	19,559,740	33.8	G	G	A	G	A	G	A	C	G	G	G					
	ss490549371	19,675,328	34.2	A	C	C	C	C	C	C	C	C	C	C					
	ss490549379	19,694,934	34.2	A	G	G	G	G	G	G	G	G	G	G					
	ss490549383	19,719,211	35.1	G	G	A	A	A	A	A	A	G	A	A	A				
	HB-F	ss490547208	19,790,626	37.7	A	G	A	A	A	G	A	G	A	A	G				
ss490549403		19,790,626	37.7	A	G	A	A	A	G	A	G	A	A	G					
BPPCT034		20,068,024	40.2	255	235	223	237	223	225	223	225	221	255	250					
ss490549443		20,126,852	40.3	A	C	A	A	A	C	C	A	A	A	A					
ss490559440		20,192,101	40.3	G	A	G	G	G	A	G	G	G	G	G					
ss490549474		20,220,616	40.3	G	A	G	G	G	G	A	G	G	G	G					
ss490549565		20,451,849	42.9	A	A	G	G	A	A	G	A	G	G	G					
ss490549569		20,455,988	42.9	C	C	A	A	C	C	A	C	A	A	A					