



ERRATUM

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 PediHaplotype 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 PediHaplotype software (Voorrips et al., 2016). Haplotypes containing missing marker scores were omitted from the table

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Haplotype	Marker	Physical position (bp)	Genetic position (cM)	Haplotypes												
				2	3	4	5	6	7	8	9	10	11	12	13	14
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						
HB-D	ss490549138	17,704,790	28.9	C	A	A	A	C	A	C						
	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						
	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				
HB-E	ss490556816	18,676,414	29.5	C	C	A	A	A	A	C	A	A				
				2	3	6	7	8	9	10	14	15	16	17		
	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		
HB-F	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		
	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		

Haplloblock	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	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				
	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				2	3	4	5	6	7	11	12	14		
	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	A	C	A	C		
	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				2	3	6	7	8	9	10	14	15	16	19
	ss490556819	18,732,420	29.6	G	G	A	G	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	G	A	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	G	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	G	G	G
HB-F	ss490549350	19,559,740	33.8	G	G	A	G	G	A	G	G	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	A	A	A	A	A	G	A	A	A	A
				2	3	6	7	8	9	10	13	14	16	17
	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
HB-F	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	G	A	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