Table S1. Genetic correlations between variables observed for the number of inflorescences, the number of fruit harvested and the mass of fruit harvested. For variable abbreviations, see Table 1.

	Y_inf_2	*Y_inf_3*	*Y_inf_4*	*Y_inf_5*	*Y_inf_6*	*Y_inf_7*	*Y_inf*	*Y_fruit_2*	*Y_fruit_3*	*Y_fruit_4*	*Y_fruit_5*	*Y_fruit_6*	*Y_fruit_7*	*Y_fruit*	*Y_mass_3*	*Y_mass_4*
Y_inf_2	1															
Y_inf_3	0,38	1														
Y_inf_4	-0,34	-0,11	1													
Y_inf_5	-0,32	0,20	-0,31	1												
Y_inf_6	-0,51	-0,67	0,26	-0,35	1											
Y_inf_7	-0,57	-0,21	-0,28	0,40	-0,13	1										
Y_inf	-1,00	-0,37	0,34	0,33	0,51	0,57	1									
Y_fruit_2	-0,17	-0,30	0,04	-0,19	0,35	0,04	0,16	1								
Y_fruit_3	0,00	0,50	-0,40	0,50	-0,32	0,16	0,00	-0,11	1							
Y_fruit_4	-0,20	-0,11	0,51	-0,18	0,22	-0,17	0,19	-0,08	-0,30	1						
Y_fruit_5	0,19	0,27	-0,27	0,44	-0,54	0,19	-0,17	-0,59	0,22	-0,26	1					
Y_fruit_6	0,06	-0,18	0,23	-0,43	0,36	-0,33	-0,07	-0,22	-0,49	0,17	-0,34	1				
Y_fruit_7	0,13	0,31	-0,18	0,34	-0,48	0,18	-0,12	-0,70	0,30	-0,18	0,56	-0,43	1			
Y_fruit	0,17	0,31	-0,05	0,21	-0,36	-0,04	-0,16	-1,00	0,12	0,06	0,61	0,20	0,70	1		
Y_mass_3	0,06	0,64	-0,32	0,50	-0,44	0,11	-0,05	-0,26	0,83	-0,16	0,32	-0,50	0,46	0,28	1	
Y_mass_4	-0,22	-0,10	0,60	-0,20	0,22	-0,20	0,21	-0,13	-0,33	0,90	-0,16	0,15	-0,10	0,11	-0,20	1
Y_mass_5	0,19	0,28	-0,12	0,42	-0,59	0,15	-0,17	-0,44	0,10	-0,20	0,82	-0,30	0,44	0,45	0,19	-0,09
Y_mass_6	0,04	-0,19	0,17	-0,38	0,32	-0,24	-0,05	-0,25	-0,46	0,05	-0,27	0,95	-0,35	0,24	-0,51	0,06
Y_mass_7	0,17	0,16	-0,24	0,31	-0,44	0,20	-0,15	-0,35	0,15	-0,23	0,40	-0,38	0,66	0,37	0,18	-0,23
Y_mass	0,18	0,19	0,03	0,07	-0,27	-0,08	-0,17	-0,76	-0,17	0,01	0,35	0,48	0,37	0,76	-0,07	0,08
CY_Inf	-0,99	-0,38	0,34	0,33	0,50	0,57	0,99	0,16	0,00	0,18	-0,16	-0,06	-0,11	-0,16	-0,06	0,21
CY_fruit	0,17	0,31	-0,04	0,21	-0,36	-0,04	-0,16	-1,00	0,12	0,07	0,60	0,20	0,70	1,00	0,28	0,12
CY_mass	0,19	0,19	0,04	0,07	-0,28	-0,09	-0,18	-0,76	-0,16	0,02	0,35	0,48	0,37	0,76	-0,07	0,08
PI_Inf	0,11	0,72	0,04	0,36	-0,68	0,11	-0,09	-0,35	0,39	-0,05	0,39	-0,34	0,48	0,36	0,58	-0,02
PI_fruit	0,01	0,43	-0,25	0,46	-0,43	0,22	0,00	-0,16	0,67	-0,03	0,35	-0,67	0,48	0,16	0,72	-0,04
PI_mass	-0,03	0,42	-0,24	0,45	-0,38	0,22	0,03	-0,14	0,62	-0,02	0,31	-0,67	0,48	0,14	0,74	-0,03
BBI_inf	0,31	0,33	-0,62	0,42	-0,50	0,19	-0,30	-0,25	0,46	-0,47	0,53	-0,28	0,33	0,27	0,42	-0,49
BBI_fruit	0,24	0,24	-0,35	0,28	-0,45	0,16	-0,23	-0,15	0,33	-0,42	0,43	-0,31	0,30	0,16	0,29	-0,41
BBI_mass	0,25	0,20	-0,34	0,23	-0,42	0,14	-0,25	-0,10	0,30	-0,45	0,38	-0,28	0,26	0,11	0,20	-0,44
NFI	0,28	0,36	0,07	0,04	-0,33	-0,24	-0,27	-0,55	0,07	0,16	0,24	-0,05	0,56	0,55	0,28	0,13
NSI	0,33	0,37	0,01	0,06	-0,37	-0,23	-0,33	-0,43	0,07	0,09	0,22	-0,10	0,49	0,43	0,25	0,08
NSF	0,23	0,15	-0,03	0,03	-0,21	-0,14	-0,23	0,03	0,04	0,00	0,00	-0,08	0,03	-0,03	0,08	-0,02

	Y_mass_5	*Y_mass_6*	*Y_mass_7*	*Y_mass*	*CY_Inf*	*CY_fruit*	*CY_mass*	*PI_Inf*	*PI_fruit*	*PI_mass*	*BBI_inf*	*BBI_fruit*	*BBI_mass*	*NFI*	*NSI*	*NSF*
Y_inf_2																
Y_inf_3																
Y_inf_4																
Y_inf_5																
Y_inf_6																
Y_inf_7																
Y_inf																
Y_fruit_2																
Y_fruit_3																
Y_fruit_4																
Y_fruit_5																
Y_fruit_6																
Y_fruit_7																
Y_fruit																
Y_mass_3																
Y_mass_4																
Y_mass_5	1															
Y_mass_6	-0,24	1														
Y_mass_7	0,37	-0,34	1													
Y_mass	0,40	0,54	0,47	1												
CY_Inf	-0,17	-0,05	-0,14	-0,17	1											
CY_fruit	0,46	0,24	0,36	0,76	-0,16	1										
CY_mass	0,41	0,54	0,46	1,00	-0,17	0,77	1									
PI_Inf	0,44	-0,33	0,34	0,23	-0,11	0,36	0,22	1								
PI_fruit	0,24	-0,70	0,39	-0,15	-0,01	0,17	-0,14	0,56	1							
PI_mass	0,20	-0,72	0,37	-0,18	0,01	0,14	-0,19	0,60	0,96	1						
BBI_inf	0,46	-0,24	0,36	0,18	-0,29	0,27	0,17	0,32	0,43	0,40	1					
BBI_fruit	0,36	-0,29	0,25	0,00	-0,22	0,15	-0,01	0,21	0,32	0,29	0,61	1				
BBI_mass	0,36	-0,25	0,25	0,00	-0,23	0,11	-0,01	0,16	0,27	0,23	0,59	0,95	1			
NFI	0,25	-0,07	0,20	0,27	-0,28	0,55	0,28	0,38	0,22	0,23	0,10	0,05	0,05	1		
NSI	0,27	-0,14	0,26	0,23	-0,32	0,43	0,23	0,39	0,22	0,24	0,16	0,12	0,11	0,82	1	
NSF	0,11	-0,12	0,13	0,03	-0,23	-0,02	0,03	0,12	0,06	0,08	0,15	0,12	0,10	0,07	0,54	1

Table S2. List of 120 candidate genes related to flowering identified *in silico* in the 'Golden Delicious' apple genome. For each gene, the table displays the gene prediction number in the apple genome browser, the name of the gene in apple, the gene position in Mb on the apple physical map (Chr, Chromosome) (Figure S3), the accession number, the name and the E-value of the closest related gene in *Arabidopsis* and in *Malus* (E-value lower than 1E-30). Names were attributed to MDP numbers when no apple EST was described before, according their similarity with *Arabidopsis* and *Malus.* When necessary, suffixes were added to existing names to specify the number of copies of the gene in the *Malus* genome.

***Malus* gene prediction #**	***Malus* name**	**Chr**	**Position**	**Reference gene in Arabisopsis**			**Reference gene in *Malus***			
				Arabidopsis accession #	**Arabidopsis name**	**E-value**	**Malus accession #**	***Malus* name**	**E-value**	**Reference**
FT / TFL1 familly										
MDP0000867916	*MdBFTa*	1	25,417	Q9FIT4	*AtBFT*	6,00E-66	BAG31957	*MdCEN*	7,00E-71	Mimida *et al.* 2009
MDP0000812208	*MdBFTb*	7	23,619	Q9FIT4	*AtBFT*	2,00E-65	BAG31958	*MdCEN*	2,00E-68	Mimida *et al.* 2009
MDP0000761080	*MdCENa*	10	29,915	Q9ZNV5	*AtCEN*	3,00E-77	BAG31957	*MdCENa*	2,00E-100	Mimida *et al.* 2009
MDP0000127457	*MdCENb*	13	23,355	Q9ZNV5	*AtCEN*	2,00E-69	BAG31958	*MdCENb*	7,00E-92	Mimida *et al.* 2009
MDP0000132050	*MdFT1*	12	31,575	Q9SXZ2	*AtFT*	2,00E-75	BAI77730	*MdFT*	8,00E-100	Kotoda *et al.* 2010
MDP0000139278	*MdFT2*	4	22,898	Q9SXZ2	*AtFT*	7,00E-32	ADP69290	*MdFT2*	9,00E-48	
MDP0000240165	*MdLHP1a*	2	27,276	Q946J8	*AtLHP1*	4,00E-56	BAF75818	*MdLHP1a*	0,00E+00	Mimida *et al.* 2007
MDP0000293596	*MdLHP1b*	17	23,582	Q946J8	*AtLHP1*	1,00E-54	BAF75820	*MdLHP1b*	0,00E+00	Mimida *et al.* 2007
MDP0000449224	*MdMFTa*	6	23,696	Q9XFK7	*AtMFT*	5,00E-79	ACF18114	*MdTFL1*	5,00E-47	
MDP0000208806	*MdMFTb*	14	28,244	Q9XFK7	*AtMFT*	1,00E-37				
MDP0000255437	*MdTFL1*	12	1,917	P93003	*AtTFL1*	4,00E-73	BAG31955	*MdTFL1*	5,00E-100	Mimida *et al.* 2009
MDP0000126761	*MdTFL1a*	4	8,861	P93003	*AtTFL1*	8,00E-72	ACF18114	*MdTFL1*	9,00E-100	
MADS-Box genes										
MDP0000324166	*MdMADS1a*	10	26,500	P17839	*AtAGL1*	2,00E-98	CAC80858	*MdMADS-C*	1,00E-132	Van der Linden *et al* . 2002
MDP0000250080	*MdMADS1b*	5	5,903	P17839	*AtAGL1*	9,00E-83	CAC80858	*MdMADS-C*	1,00E-119	Van der Linden *et al* . 2002
MDP0000324259	*MdAGL1a*	9	12,044	P29381	*AtAGL1*	1,00E-91	ADL36737	*MdMADS*	8,00E-144	
MDP0000242009	*MdAGL1b*	17	12,161	P29381	*AtAGL1*	2,00E-77	AAQ03090	*MdAGL*	9,00E-126	
MDP0000289836	*MdMADS2.1*	14	26,876	Q38876	*AtAGL8*	4,00E-78	ABB22023	*MdMADS2.1*	1,00E-145	Cevik *et al.* 2010
MDP0000218020	*MdMADS2.2*	6	22,210	Q38876	*AtAGL8*	1,00E-66	ABB22022	*MdMADS2.2*	6,00E-127	Cevik *et al.* 2010
MDP0000326906	*MdMADS3*	13	3,730	P29383	*AtAGL3*	4,00E-63	ADL36747	*MdMADS*	1,00E-130	
MDP0000137561	*MdMADS4a*	10	10,038	P47927	*AtAP2*	5,00E-99	AAD51423	*MdMADS4*	0,00E+00	Sung *et al.* 2000
MDP0000200319	*MdMADS4b*	4	8,775	P47927	*AtAP2*	2,00E-81	AAD51423	*MdMADS4*	2,00E-87	Sung *et al.* 2000
MDP0000163645	*MdMADS4c*	12	17,665	P47927	*AtAP2*	8,00E-78	AAD51423	*MdMADS4*	5,00E-86	Sung *et al.* 2000
MDP0000204900	*MdMADS4d*	15	24,190	P47927	*AtAP2*	1,00E-76	AAD51423	*MdMADS4*	0,00E+00	Sung *et al.* 2000
MDP0000268317	*MdMADS11a*	0		Q38836	*AtAGL11*	1,00E-62	BAG48168	*MdMADS*	3,00E-78	
MDP0000300752	*MdMADS11b*	14	21,621	Q38836	*AtAGL11*	4,00E-36	ADL36741	*MdMADS*	5,00E-36	
MDP0000254052	*MdMADS15a*	7	1,626	Q38847	*AtAGL15*	4,00E-61	ADL36752	*MdMADS*	1,00E-39	
MDP0000156783	*MdMADS15b*	2	34,644	Q38847	*AtAGL15*	4,00E-60	ADL36752	*MdMADS*	2,00E-33	
MDP0000144516	*MdMADS15c*	10	14,826	Q38847	*AtAGL15*	3,00E-42	ADL36738	*MdMADS*	1,00E-33	
MDP0000135652	*MdMADS15d*	14	10,808	Q38847	*AtAGL15*	1,00E-34	CAC80858	*MdMADS-C*	8,00E-33	Van der Linden *et al* . 2002
MDP0000270062	*MdMADS19*	10	4,239	O82743	*AtAGL19*	1,00E-52	ADL36739	*MdMADS*	2,00E-97	
MDP0000475549	*MdAGL21*	5	29,588	Q9SZJ6	*AtAGL21*	9,00E-37				
MDP0000527190	*MdMADS24a*	8	23,937	O82794	*AtAGL24*	8,00E-37	ADL36743	*MdMADS*	1,00E-86	
MDP0000322567	*MdMADS24b*	16	17,757	O82794	*AtAGL24*	1,00E-36	ADL36743	*MdMADS*	6,00E-84	
MDP0000434703	*MdAGL62a*	0		Q9FKK2	*AtAGL62*	3,00E-59				

Malus gene prediction #	*Malus* name	Chr	Position	Reference gene in Arabisopsis			Reference gene in *Malus*			
				Arabidopsis accession #	Arabidopsis name	E-value	Malus accession #	*Malus* name	E-value	Reference
MDP0000221590	*MdAGL62b*	14	4,254	Q9FKK2	*AtAGL62*	5,00E-39				
MDP0000696333	*MdAGL62c*	5	6,460	Q9FKK2	*AtAGL62*	9,00E-32				
MDP0000846004	*MdAGL80a*	15	38,525	Q9FJK3	*AtAGL80*	4,00E-52				
MDP0000925348	*MdAGL80b*	8	24,292	Q9FJK3	*AtAGL80*	6,00E-52				
MDP0000299637	*MdAGL80c*	6	1,686	Q9FJK3	*AtAGL80*	9,00E-37				
MDP0000129298	*MdAGL80d*	4	18,445	Q9FJK3	*AtAGL80*	8,00E-33				
MDP0000013331	*MdAP1a*	16	2,317	P35631	*AtAP1*	3,00E-88	CAA04321	*MdMADS*	5,00E-140	Yao *et al.* 1999
MDP0000269921	*MdAP1b*	13	3,705	P35631	*AtAP1*	2,00E-75	ACD69426	*MdAP1*	5,00E-120	
MDP0000133037	*MdAP3a*	6	14,318	P35632	*AtAP3*	3,00E-56	BAC11907	*MdMADS*	4,00E-131	Kitahara *et al.* 2004
MDP0000224779	*MdAP3b*	5	20,431	P35632	*AtAP3*	3,00E-56	BAC11907	*MdMADS*	4,00E-131	Kitahara *et al.* 2004
MDP0000315938	*MdAP3c*	2	12,242	P35632	*AtAP3*	2,00E-55	CAC80856	*MdMADS-B*	6,00E-137	Van der Linden *et al* . 2002
MDP0000220168	*MdAP3d*	8	1,390	P35632	*AtAP3*	3,00E-55	ADL36746	*MdMADS*	5,00E-95	
MDP0000286643	*MdPI*	8	20,663	P48007	*AtPI*	2,00E-63	CAC28022	*MdPI*	3,00E-120	Yao *et al.* 2001
MDP0000366022	*MdSEP1a*	7	5,046	P29382	*AtSEP1*	4,00E-100	CAA04919	*MdMADS*	6,00E-146	Yao *et al.* 1999
MDP0000280009	*MdSEP1b*	16	2,322	P29382	*AtSEP1*	8,00E-63	AAL57045	*AHAP2*	3,00E-117	
MDP0000326390	*MdSEP2a*	14	26,820	P29384	*AtSEP2*	2,00E-77	ADL36749	*MdMADS*	4,00E-148	
MDP0000366019	*MdSEP2b*	9	4,405	P29384	*AtSEP2*	2,00E-65	ADL36751	*MdMADS*	8,00E-117	
MDP0000220008	*MdSEP3a*	16	6,489	O22456	*AtSEP3*	3,00E-89	ADL36740	*MdMADS*	6,00E-121	
MDP0000370413	*MdSEP3b*	13	8,469	O22456	*AtSEP3*	6,00E-69	ADL36740	*MdMADS*	2,00E-80	
MDP0000316609	*MdAGL12*	10	26,792	Q38841	*AtAGL12*	1,00E-58	BAI49494	*MdSOC1-like*	1,00E-33	Kotoda *et al.* 2010
MDP0000314765	*MdSOC1a*	2	21,545	O64645	*AtSOC1*	3,00E-65	BAI49494	*MdSOC1-like*	3,00E-116	Kotoda *et al.* 2010
MDP0000060753	*MdSOC1b*	7	23,211	O64645	*AtSOC1*	1,00E-49	ABI74449	*MdMADS*	3,00E-81	
MDP0000144597	*MdSOC1-like*	1	25,034	O64645	*AtSOC1*	6,00E-46	ABI74449	*MdMADS*	6,00E-127	
MDP0000209705	*MdSVPa*	4	0,414	Q9FVC1	*AtSVP*	4,00E-81	ADL36738	*MdMADS*	2,00E-113	
MDP0000233948	*MdSVPb*	11	18,050	Q9FVC1	*AtSVP*	3,00E-81	ADL36738	*MdMADS*	9,00E-124	
MDP0000278738	*MdTT16a*	0		Q8RYD9	*AtTT16*	5,00E-41	BAI49495	*MdSOC1-like*	3,00E-31	Kotoda *et al.* 2010
MDP0000183226	*MdTT16b*	5	8,952	Q8RYD9	*AtTT16*	1,00E-37				
Flowering genes										
MDP0000492089	*MdAFL1*	11	20,414	Q00958	*AtLFY*	6,00E-121	BAB83096	*MdAFL1*	0,00E+00	Wada *et al.* 2002
MDP0000186703	*MdAFL2*	14	20,091	Q00958	*AtLFY*	2,00E-123	BAD10955	*MdAFL*	0,00E+00	
MDP0000897253	*MdCLV1a*	12	21,126	Q9SYQ8	*AtCLV1*	0,00E+00	AAC36318	*LRPKm1*	5,00E-176	Komjanc *et al.* 1999
MDP0000804361	*MdCLV1b*	8	0,794	Q9SYQ8	*AtCLV1*	0,00E+00	AAC36318	*LRPKm1*	4,00E-174	Komjanc *et al.* 1999
MDP0000618819	*MdCLV1c*	15	2,607	Q9SYQ8	*AtCLV1*	0,00E+00	ABO61511	*LRPKm1*	0,00E+00	Cova *et al.* 2001
MDP0000523939	*MdCLV1d*	2	20,785	Q9SYQ8	*AtCLV1*	0,00E+00	ABO61511	*LRPKm1*	0,00E+00	Cova *et al.* 2001
MDP0000275265	*MdCLV1e*	5	9,674	Q9SYQ8	*AtCLV1*	0,00E+00	ABO61514	*LRPKm1*	1,00E-175	Cova *et al.* 2001
MDP0000272100	*MdEFL3a*	8	10,751	O82804	*AtEFL3*	2,00E-92				
MDP0000127365	*MdEFL3b*	15	0,999	O82804	*AtEFL3*	7,00E-94				
MDP0000237496	*MdFCAa*	16	8,301	O04425	*AtFCA*	3,00E-142				
MDP0000211002	*MdFCAb*	13	12,457	O04425	*AtFCA*	3,00E-109				
MDP0000281110	*MdGIa*	10	3,053	Q9SQI2	*AtGI*	0,00E+00				

Malus gene prediction #	*Malus* name	Chr	Position	Reference gene in Arabisopsis			Reference gene in *Malus*			
				Arabidopsis accession #	Arabidopsis name	E-value	Malus accession #	*Malus* name	E-value	Reference
MDP0000171530	*MdGIb*	11	31,035	Q9SQI2	*AtGI*	0,00E+00				
MDP0000209424	*MdLDa*	3	32,459	Q38796	*AtLD*	0,00E+00				
MDP0000161239	*MdLDb*	11	34,178	Q38796	*AtLD*	2,00E-148				
MDP0000145072	*MdLDc*	17	17,434	Q38796	*AtLD*	6,00E-37				
MDP0000238744	*MdVRN1a*	3	18,460	Q8L3W1	*AtVRN1*	8,00E-106				
MDP0000555456	*MdVRN1b*	15	43,121	Q8L3W1	*AtVRN1*	8,00E-105				
MDP0000298218	*MdVRN1c*	2	14,200	Q8L3W1	*AtVRN1*	9,00E-33				
MDP0000192438	*MdVRN1d*	11	6,899	Q8L3W1	*AtVRN1*	7,00E-31				
MDP0000208349	*MdVRN2-1*	6	6,504	Q8W5B1	*AtVRN2*	2,00E-88	ACG69838	*MdVRN2-1*	0,00E+00	
MDP0000333597	*MdVRN2-2*	15	9,984	Q8W5B1	*AtVRN2*	8,00E-50	ACG69838	*MdVRN2-1*	4,00E-115	
Squamosa protein-like										
MDP0000919694	*MdSPL1*	13	11,724	Q9SMX9	*AtSPL1*	0,00E+00	ADL36823	*MdSPL*	3,00E-30	
MDP0000155354	*MdSPL2*	13	8,433	Q9S840	*AtSPL2*	5,00E-69	ADL36823	*MdSPL*	5,00E-34	
MDP0000865739	*MdSPL4a*	9	32,944	Q9S7A9	*AtSPL4*	3,00E-33	ADL36827	*MdSPL*	6,00E-98	
MDP0000255162	*MdSPL4b*	17	19,390	Q9S7A9	*AtSPL4*	2,00E-31	ADL36827	*MdSPL*	5,00E-63	
MDP0000861601	*MdSPL5a*	3	27,507	Q9S758	*AtSPL5*	4,00E-37	ADL36826	*MdSPL*	2,00E-88	
MDP0000158607	*MdSPL5b*	11	28,811	Q9S7A9	*AtSPL4*	5,00E-35	ADL36826	*MdSPL*	2,00E-107	
MDP0000171877	*MdSPL6a*	13	3,766	Q94JW8	*AtSPL6*	8,00E-44	ADL36824	*MdSPL*	3,00E-32	
MDP0000146640	*MdSPL6b*	6	22,075	Q94JW8	*AtSPL6*	2,00E-42	ADL36824	*MdSPL*	2,00E-37	
MDP0000193702	*MdSPL6c*	16	2,350	Q94JW8	*AtSPL6*	4,00E-41	ADL36823	*MdSPL*	2,00E-30	
MDP0000589558	*MdSPL6d*	14	26,755	Q94JW8	*AtSPL6*	3,00E-40	ADL36823	*MdSPL*	7,00E-36	
MDP0000181940	*MdSPL7a*	16	13,411	Q8S9G8	*AtSPL7*	1,00E-175				
MDP0000271587	*MdSPL7b*	13	16,866	Q8S9G8	*AtSPL7*	3,00E-107				
MDP0000803116	*MdSPL8*	7	9,568	Q8GXL3	*AtSPL8*	1,00E-59	ADL36823	*MdSPL*	5,00E-31	
MDP0000297978	*MdSPL9*	14	7,327	Q700W2	*AtSPL9*	2,00E-55	ADL36823	*MdSPL*	1,00E-177	
MDP0000262141	*MdSPL11*	7	9,638	Q9FZK0	*AtSPL11*	4,00E-30	ADL36823	*MdSPL*	8,00E-32	
MDP0000323003	*MdSPL12a*	10	28,220	Q9S7P5	*AtSPL12*	4,00E-32	ADL36825	*MdSPL*	1,00E-58	
MDP0000255201	*MdSPL12b*	5	4,579	Q9S7P5	*AtSPL12*	5,00E-29	ADL36825	*MdSPL*	1,00E-84	
MDP0000263766	*MdSPL13a*	6	17,180	Q8LFW6	*AtSPL13*	5,00E-58	ADL36824	*MdSPL*	0,00E+00	
MDP0000210138	*MdSPL13b*	14	21,647	Q8LFW6	*AtSPL13*	5,00E-54	ADL36824	*MdSPL*	0,00E+00	
MDP0000170630	*MdSPL13c*	9	0,702	Q8LFW6	*AtSPL13*	1,00E-34	ADL36824	*MdSPL*	3,00E-37	
MDP0000142582	*MdSPL13d*	17	0,605	Q8LFW6	*AtSPL13*	1,00E-34	ADL36824	*MdSPL*	5,00E-37	
MDP0000176265	*MdSPL13e*	16	6,527	Q8LFW6	*AtSPL13*	1,00E-36	ADL36824	*MdSPL*	4,00E-51	
MDP0000149339	*MdSPL14*	6	0,365	Q8RY95	*AtSPL14*	0,00E+00	ADL36824	*MdSPL*	5,00E-31	
Phytochrome										
MDP0000245413	*MdPHYAa*	4	18,271	P14712	*AtPHYA*	0,00E+00				
MDP0000170095	*MdPHYAb*	12	26,883	P14712	*AtPHYA*	0,00E+00				
MDP0000285110	*MdPHYBa*	16	8,633	P14713	*AtPHYB*	0,00E+00				
MDP0000184687	*MdPHYBb*	13	13,719	P14713	*AtPHYB*	0,00E+00				

Malus gene prediction #	*Malus* name	Chr	Position	Reference gene in Arabisopsis			Reference gene in *Malus*			
				Arabidopsis accession #	Arabidopsis name	E-value	Malus accession #	*Malus* name	E-value	Reference
MDP0000289028	*MdPHYC*	1	1,799	P14714	*AtPHYC*	2,00E-136				
MDP0000319396	*MdPHYEa*	5	6,243	P42498	*AtPHYE*	0,00E+00				
MDP0000279583	*MdPHYEb*	10	26,272	P42498	*AtPHYE*	0,00E+00				
Constance-like										
MDP0000202669	*MdCOL1*	1	26,862	Q940T9	*AtCOL4*	1,00E-111	ACD69427	*MdCOL1*	0,00E+00	Hättasch *et al.* 2008
MDP0000298635	*MdCOL2a*	17	5,396	Q96502	*AtCOL2*	3,00E-117	ADL36677	*MdCOL*	0,00E+00	
MDP0000297093	*MdCOL2b*	9	4,850	Q96502	*AtCOL2*	2,00E-109	ADL36677	*MdCOL*	0,00E+00	
MDP0000687337	*MdCOL4a*	0		Q940T9	*AtCOL4*	2,00E-109	ADL36664	*MdCOL*	0,00E+00	
MDP0000901915	*MdCOL4b*	11	33,378	Q940T9	*AtCOL4*	6,00E-81	ADL36664	*MdCOL*	1,00E-140	
MDP0000713113	*MdCOL5a*	16	20,659	Q9FHH8	*AtCOL5*	2,00E-86	ADL36670	*MdCOL*	0,00E+00	
MDP0000294359	*MdCOL5b*	2	19,905	Q9FHH8	*AtCOL5*	2,00E-85	ADL36670	*MdCOL*	2,00E-140	

Table S3. Accession numbers of gene predictions in the apple genome and sequences of primers developed for candidate gene mapping in the population STKxGS.

Gene name	Primer	Accession #	Segregation type in STK×GS population	Primer sequence	
Flowering Locus T	*MdFT1*	MDP0000132050	aa x ab	F	CTGCCATGAAGGAACCCTTA
				R	CACCAAAACAAAGCGATGAA
Mother of FT	*MdMFTa*	MDP0000449224	ab x aa	F	CTCGTGCCCATTTCAACAC
				R	ACCACACCATCCCCTCTATG
Brother of FT	*MdBFTa*	MDP0000867916	ab x ab	F	TCGTATCTATTTCCGCGTCA
				R	GGGAGGAGGGAGAGAAAAGA
Terminal Flower 1	*MdTFL1a*	MDP0000126761	ab x aa	F	GCTACGAGCCAACAAAACAA
				R	AGGCAACCGATATTTTCACC
Terminal Flower 2	*MdLHP1a*	MDP0000240165	ab x aa	F	CATTTCAGTGGCTTTGGTAGC
				R	CGGAGATGTTGCTCGTAAAA
	MdLHP1b	MDP0000293596	aa x ab	F	AGGGAGATTTGGGACAACAA
				R	CCTGATGCTCTTGCTCTTGA
Centroradialis	*MdCENa*	MDP0000761080	aa x ab	F	GCCCAAATTCACATCAATCC
				R	CACCATTTTCGTGCTGCTAA
Agamous Like	*MdAGL12*	MDP0000316609	ef x eg	F	TTTTGAAGGAAGGAGTTCTGAC
				R	CCCACACATTTAGTTGTTACTTTGG
Apetala	*MdAP1b*	MDP0000269921	ab x aa	F	GCTGAAGCGCATAGAGAACA
				R	CCCCTTGTTGGAGAAGACAA
	MdMADS4a	MDP0000137561	ab x aa	F	TGCAGCTTCTACTCCGAACA
				R	TTTGGTGGGAAATTGTGAGA
Pistillata	*MdPI*	MDP0000286643	ab x ab	F	TCCCTCTCTCTCTTCACCATTT
				R	AATCCCATTCCTCCTCTTGG
Short vegetative phase	*MdSVPa*	MDP0000209705	ab x ab	F	GAGCAGTTCATCGGCAGTAAG
				R	TCGTTCATTCTCTTCCGTCA
Supressor of Constance	*MdSOC1-like*	MDP0000144597	aa x ab	F	CGTGGATGGAGTTTTCACCT
				R	ATGCTACTTTGGCTCCGGTA
	MdSOC1b	MDP0000060753	ab x aa	F	GGGTGAGGCTTGAGTCCTTT
				R	CCGAAACTCTTCCCATACACC
			aa x ab	F	TCAATCAACTCCACCCACCT
				R	TGCAAACAGACCCAGAAAAA
Clavata	*MdCLV1b*	MDP0000804361	ef x eg	F	ATCCTTTTCCGCCCACTC
				R	TTCGGCAACATCATTCGTAG
	MdCLV1c	MDP0000618819	ef x eg	F	TGCACGAATTGTATTAGCGTTT
				R	CGAATTTGCCTTTTGCACTT
Early Flowering 3	*MdEFL3a*	MDP0000272100	aa x ab	F	GCAGAGAGGAAACAGCAGGA
				R	ACCGAGACATGCGAAAGAAA
	MdEFL3b	MDP0000127365	ab x aa	F	GGAAATCCACAGCCAACTCT
				R	TCCTCCACAAACTGGTCCTC
Leafy	*MdAFL1*	MDP0000492089	aa x ab	F	AAGGACGACGACATGGACAA
				R	AGGCTCCGTCACAATGAA
	MdAFL2	MDP0000186703	aa x ab	F	AAGAACGGCCTCGATTACCT
				R	TCGTACCTTGGTGGGACATT
Vernalization	*MdVRN1a*	MDP0000238744	ab x aa	F	GCCAGGGATGGTATGAGTTT
				R	CTGGGGTGAGATTTTGCAGT
	MdVRN1b	MDP0000555456	ab x aa	F	GCAAAGATGGTGTGCGTCT
				R	TCCTCATTAGAGATGAAGGGAAGT
	MdVRN2-1	MDP0000208349	ef x eg	F	TGAAGGCAATGGAAACAAGA
				R	AAGCAAGGCGTACAAAGAGG
	MdVRN2-2	MDP0000333597	aa x ab	F	TCTCTGTGAAGACCGAAAACC
				R	ATAGCAACCGCCTCCTCTAC
Squamosa protein-like	*MdSPL8*	MDP0000803116	ab x aa	F	GAGCACCGTACCAAAATGCT
				R	TGAGCTGAAGAGCCTGAAGA
Phytochrome	*MdPHYAa*	MDP0000245413	aa x ab	F	TGCATGGTATGTCACTCATTACTCT
				R	TTTTGTTCCTCTTTGCCTGA
	MdPHYEb	MDP0000279583	aa x ab	F	ACCAGGTGACGGTGCTAAAT
				R	CGCGACTTTTGTGTTTGTGT
Luminidependens	*MdLDc*	MDP0000145072	aa x ab	F	GGAGATGGAGATTGGGACCT
				R	TGGGAGAGAGGATTGACACC
DELLA	*MdRGL1b*	DQ007886	ab x aa	F	TCAGGAAGTGGGATGGAAAC
				R	CGAGTCAAACAGGGTCGAGT
	MdRGL2a	DQ007883	ab x aa	F	CGGAGACCGAGAGTACGAGA
				R	GAGTGTGTGGACGAGTTGGA
	MdRGL2b	DQ007884	aa x ab	F	ACCGGCGCTATGAGAAAAG
				R	GTAAATCCGACGAGCCAGAG
	MdRGL3a	DQ007887	ef x eg	F	GATTGACCGGCATTGGAC
				R	TCATCTCGATTGGGGAGTTC
	MdRGL3b	DQ007888	aa x ab	F	AGGTGAGCCCGAAAGAGG
				R	CTGCTCCACAACCGTCACTA

Gene name	Primer	Accession #	Segregation type in STK×GS population	Primer sequence	
Gibberellin 2-oxidase	*MdGA2ox3a*	MDP0000137705	aaxab	F	GGAGAGGGAGAGCAACTTCA
				R	TGCAAAAGGAAAGATACAGGAAA
	MdGA2ox2b	MDP0000145827	aaxab	F	CTTCCATAACACACTCTCACAACA
				R	CTCCCAAGTTAGCAAAAACAGTAAG
	MdGA2ox4b	MDP0000226405	abxab	F	GAACAGCTCGGCAGTGAGT
				R	CAGATGCGGGTAGTGATTGA
	MdGA2ox8a	MDP0000179396	aaxab	F	ACCGAAAAAGTGACCCACAG
				R	TGCAAAAATCAGACTCAAGAAAA
Gibberellin 3-oxidase	*MdGA3ox1b*	MDP0000716315	ab x aa	F	GCATGTGGGCAGTGATTAGA
				R	GCATCATTTTCTTGCAGGTATT
	MdGA3ox-like-b	MDP0000155229	ab x aa	F	CACAGGTGGAATTGAGGTGA
				R	GGAAATGACGGGCTAATCTG
Gibberellin 20-oxidase	*MdGA20ox1a*	MDP0000248981	ab x aa	F	GGGTCGTGAATGTGTGAAAA
				R	AAATTAGTCGGGCGTTTGGT
	MdGA20ox1b	MDP0000136940	ab x aa	F	GCTCTGCCCCATACCAATAA
				R	TTGAGTTGTTTCAAGGTTGCTC
	MdGA20ox1c	MDP0000280240	ef x eg	F	TGAACCCAGCAGTTCGTAGTT
				R	GGACAAAGGCAAAGTTAGAGGA
Cytokinin Oxidase	*MdCKX1a*	MDP0000318353	aa x ab	F	TTCAATTCTCCACATTCACACC
				R	CCCTTCCATAACCACCAAGA
			ab x aa	F	AGCACTTTCATCCGTGTTCC
				R	CTTTCAAGCCTCCCAACTGA
	MdCKX7b	MDP0000279125	ab x aa	F	ACACAGAGCAAAGCAAGCAA
				R	CGGTTAGGCTTCGATTCTCC
Indole Acetic Acid	*MdIAA103*	MDP0000295589	aa x ab	F	TCCTCAAACCCTCCATCAAC
				R	TCGGATTGCAGTGGTCTTTT
	MdIAA127A	MDP0000456476	ab x aa	F	TTGGAACTGAAGGAGCGAAA
				R	CCAGGAAGCCCAAGTCTAAGT
	MdIAA106	MDP0000176753	aaxab	F	CTCTGATGCCCTAGCCAAAA
				R	AGAGAGGTGACTCCGCACAC
	MdIAA33	MDP0000146848	aaxab	F	CCATCTTTTTCTGCCCTGTT
				R	CAAACTACAGTCCAAGGTATCACATC
Auxin Respons Factor	*MdARF3*	MDP0000179650	aaxab	F	TTCAAAGGAAGCACTCCAAA
				R	TGCGTGAATACGATGGGTAG
	MdARF104	MDP0000185253	ab x aa	F	GAAGTTTTTAATTGTGACGGGAAC
				R	GACGCTTGTGTCTGTGTTTG
Transport Inhibitor Response 1	*MdAFB6*	MDP0000305861	ab x aa	F	GGGTCGTGAATGTGTGAAAA
				R	AAATTAGTCGGGCGTTTGGT
CAROTENOID CLEAVAGE DIOXYGENASE	*MdCCD8b*	MDP0000219296	ef x eg	F	CCGCTTCCCGTAGATTAGAG
				R	TCAAGGAACAAAACCCCATC
	MdCCD7b		ab x aa	F	TGCTCACATGGTCTGTTGGT
				R	TGCATCAGCTCCTCCAATCT
	NZSNP187650	MDP0000232736	aa x ab	F	TCCACCCCATCAATTTTCTT
				R	TTTTGGGTCAATGGTTTCGT
	NZSNPQ06942	MDP0000139203	aaxab	F	GATCATATTTTCCAGCACACTCA
				R	CCAACGATCTCACCCAGTTT

Table S4. List of 55 candidate genes related to gibberellin and cytokinin oxidases and to Carotenoid Cleavage Dioxygenase identified *in silico* in the 'Golden Delicious' apple genome. For each gene, the table displays the gene prediction number in the apple genome browser, the name of the gene in apple, the gene position in Mb on the apple physical map (Chr, Chromosome) (Figure S3), the accession number, the name and the E-value of the closest related gene in *Arabidopsis* and in *Malus* (E-value lower than 1E-30). Names were attrib-uted to MDP numbers when no apple EST was described before according their similarity with *Arabidopsis* and *Malus* . When necessary, suffixes were added to existing names to specify the number of copies of the gene in the *Malus* genome.

				Reference gene in *Arabisopsis*			Reference gene in *Malus*			
***Malus* gene prediction #**	***Malus* name**	**Chr**	**Position**	***Arabidopsis* accession #**	***Arabidopsis* name**	**E-value**	**Malus accession #**	***Malus* name**	**E-value**	**Reference**
Gibberelin oxidase										
MDP0000248981	*MdGA20ox1a*	1	24,897	Q39111	*AtGA20ox2*	1,00E-148	BAB20975	*MdGA20ox*	0,00E+00	Kusaba *et al.* 2001
MDP0000136940	*MdGA20ox1b*	2	21,725	Q39110	*AtGA20ox1*	2,00E-142	BAB20975	*MdGA20ox*	2,00E-162	Kusaba *et al.* 2001
MDP0000280240	*MdGA20ox1c*	7	23,081	Q39111	*AtGA20ox2*	2,00E-145	BAB20975	*MdGA20ox*	0,00E+00	Kusaba *et al.* 2001
MDP0000128715	*MdGA20ox1d*	11	18,766	Q39110	*AtGA20ox1*	1,00E-76	BAB20975	*MdGA20ox*	6,00E-94	Kusaba *et al.* 2001
MDP0000142765	*MdGA20ox2*	15	43,373	Q39110	*AtGA20ox1*	5,00E-47	BAB20975	*MdGA20ox*	5,00E-45	Kusaba *et al.* 2001
MDP0000508761	*MdGA20ox4*	12	23,736	Q39110	*AtGA20ox1*	8,00E-46	BAB20975	*MdGA20ox*	9,00E-46	Kusaba *et al.* 2001
MDP0000136905	*MdGA20ox5*	15	3,025	Q39111	*AtGA20ox2*	2,00E-93	BAB20975	*MdGA20ox*	2,00E-99	Kusaba *et al.* 2001
MDP0000322440	*MdGA2ox2a*	5	6,655	Q9XFR9	*AtGA2ox2*	3,00E-126	FJ571521	*MdGA2ox*	7,00E-135	Zhao *et al.* 2010
MDP0000145827	*MdGA2ox2b*	10	25,855	Q9XFR9	*AtGA2ox2*	2,00E-117	FJ571521	*MdGA2ox*	1,00E-129	Zhao *et al.* 2010
MDP0000137705	*MdGA2ox3a*	10	19,867	Q8LEA2	*AtGA2ox1*	2,00E-108	FJ571521	*MdGA2ox*	0,00E+00	Zhao *et al.* 2010
MDP0000185333	*MdGA2ox3b*	5	14,153	Q8LEA2	*AtGA2ox1*	6,00E-108	FJ571521	*MdGA2ox*	0,00E+00	Zhao *et al.* 2010
MDP0000735747	*MdGA2ox4a*	16	8,036	Q9XFR9	*AtGA2ox2*	7,00E-77	FJ571521	*MdGA2ox*	3,00E-86	Zhao *et al.* 2010
MDP0000226405	*MdGA2ox4b*	13	12,25	Q9XFR9	*AtGA2ox2*	2,00E-69	FJ571521	*MdGA2ox*	5,00E-83	Zhao *et al.* 2010
MDP0000161181	*MdGA2ox6a*	17	24,286	Q9XFR9	*AtGA2ox2*	3,00E-76	FJ571521	*MdGA2ox*	3,00E-94	Zhao *et al.* 2010
MDP0000145841	*MdGA2ox6b*	9	31,364	Q9XFR9	*AtGA2ox2*	1,00E-50	FJ571521	*MdGA2ox*	1,00E-62	Zhao *et al.* 2010
MDP0000283742	*MdGA2ox7a*	3	24,937	O49561	*AtGA2ox8*	2,00E-85	BAB20975	*MdGA20ox*	5,00E-35	Kusaba *et al.* 2001
MDP0000317686	*MdGA2ox7b*	11	25,436	O49561	*AtGA2ox8*	2,00E-58	BAB20975	*MdGA20ox*	7,00E-31	Kusaba *et al.* 2001
MDP0000179396	*MdGA2ox8a*	10	31,39	O49561	*AtGA2ox8*	4,00E-126	BAB20975	*MdGA20ox*	3,00E-39	Kusaba *et al.* 2001
MDP0000177939	*MdGA2ox8b*	5	1,676	O49561	*AtGA2ox8*	5,00E-119	BAB20975	*MdGA20ox*	1,00E-40	Kusaba *et al.* 2001
MDP0000269990	*MdGA2ox8c*	16	7,343	O49561	*AtGA2ox8*	3,00E-99	BAB20975	*MdGA20ox*	3,00E-36	Kusaba *et al.* 2001
MDP0000132878	*MdGA2ox8d*	13	0,466	O49561	*AtGA2ox8*	1,00E-63	BAB20975	*MdGA20ox*	5,00E-26	Kusaba *et al.* 2001
MDP0000381531	*MdGA3ox1a*	8	6,696	Q39103	*AtGA3ox1*	2,00E-128	FJ571520	*MdGA3ox*	0,00E+00	Zhao *et al.* 2010
MDP0000716315	*MdGA3ox1b*	9	21,448	Q39103	*AtGA3ox1*	9,00E-124	FJ571520	*MdGA3ox*	0,00E+00	Zhao *et al.* 2010
MDP0000424553	*MdGA3ox2a*	2	30,314	Q9ZT84	*AtGA3ox2*	7,00E-102	FJ571520	*MdGA3ox*	1,00E-148	Zhao *et al.* 2010
MDP0000316943	*MdGA3ox2b*	7	4,325	Q39103	*AtGA3ox1*	2,00E-104	FJ571520	*MdGA3ox*	3,00E-150	Zhao *et al.* 2010
MDP0000320360	*MdGA3ox3*	15	11,474	Q9SVS8	*AtGA3ox3*	7,00E-101	FJ571520	*MdGA3ox*	4,00E-107	Zhao *et al.* 2010
MDP0000262840	*MdGA3ox4a*	12	13,233	Q39103	*AtGA3ox1*	8,00E-82	FJ571520	*MdGA3ox*	4,00E-94	Zhao *et al.* 2010
MDP0000130015	*MdGA3ox4b*	15	5,037	Q39103	*AtGA3ox1*	1,00E-82	FJ571520	*MdGA3ox*	9,00E-96	Zhao *et al.* 2010
MDP0000233590	*MdGA3ox5*	2	30,310	Q39103	*AtGA3ox1*	3,00E-98	FJ571520	*MdGA3ox*	5,00E-133	Zhao *et al.* 2010
MDP0000166016	*MdGA3ox-like-a*	11	6,286	O49561	*AtGA2ox8*	3,00E-45	FJ571520	*MdGA3ox*	2,00E-33	Zhao *et al.* 2010
MDP0000155229	*MdGA3ox-like-b*	1	28,963	O49561	*AtGA2ox8*	5,00E-48	FJ571520	*MdGA3ox*	8,00E-31	Zhao *et al.* 2010

Malus gene prediction #	*Malus* name	Chr	Position	Reference gene in *Arabisopsis*			Reference gene in *Malus*			
				Arabidopsis accession #	*Arabidopsis* name	E-value	Malus accession #	*Malus* name	E-value	Reference
Cytokinin Oxidase										
MDP0000318353	*MdCKX1a*	13	32,756	O22213	*AtCKX1*	0,00E+00				
MDP0000223673	*MdCKX1b*	14	12,131	O22213	*AtCKX1*	0,00E+00				
MDP0000293966	*MdCKX1c*	2	34,338	O22213	*AtCKX1*	0,00E+00				
MDP0000256199	*MdCKX1d*	7	2,018	O22213	*AtCKX1*	4,00E-166				
MDP0000271354	*MdCKX3*	15	14,868	Q9LTS3	*AtCKX3*	1,00E-141				
MDP0000213431	*MdCKX4*	15	37,144	Q9FUJ2	*AtCKX4*	3,00E-153				
MDP0000250917	*MdCKX5a*	12	21,638	Q67YU0	*AtCKX5*	0,00E+00				
MDP0000234983	*MdCKX5b*	8	1,462	Q67YU0	*AtCKX5*	0,00E+00				
MDP0000238100	*MdCKX7a*	15	0,257	Q9FUJ1	*AtCKX7*	0,00E+00				
MDP0000279125	*MdCKX7b*	8	9,500	Q9FUJ1	*AtCKX7*	3,00E-143				
Carotenoid Cleavage Dioxygenase										
MDP0000164529	*MdCCD1a*	7	0,98	O65572	*AtCCD1*	0,00E+00	ABY47995	*MdCCD4*	1,00E-94	Huang *et al.* 2009
MDP0000224062	*MdCCD1b*	2	35,434	O65572	*AtCCD1*	0,00E+00	ABY47995	*MdCCD4*	1,00E-93	Huang *et al.* 2009
MDP0000174621	*MdCCD1c*	0		O65572	*AtCCD1*	3,00E-120	ABY47995	*MdCCD4*	5,00E-47	Huang *et al.* 2009
MDP0000547655	*MdCCD4a*	16	4,234	O49675	*AtCCD4*	0,00E+00	ABY47995	*MdCCD4*	0	Huang *et al.* 2009
MDP0000555220	*MdCCD4b*	14	18,104	O49675	*AtCCD4*	0,00E+00	ABY47995	*MdCCD4*	0	Huang *et al.* 2009
MDP0000147391	*MdCCD4c*	17	11,066	O49675	*AtCCD4*	1,00E-174	ABY47995	*MdCCD4*	0	Huang *et al.* 2009
MDP0000744887	*MdCCD4d*	15	38,519	O49675	*AtCCD4*	8,00E-108	ABY47995	*MdCCD4*	4,00E-119	Huang *et al.* 2009
MDP0000197409	*MdCCD7a*	2	26,2	Q7XJM2	*AtCCD7*	4,00E-113				
MDP0000227870	*MdCCD8a*	8	14,415	Q8VY26	*AtCCD8*	0,00E+00				
MDP0000219296	*MdCCD8b*	15	3,345	Q8VY26	*AtCCD8*	0,00E+00				
MDP0000813805	*MdNCED3a*	10	19,947	Q9LRR7	*AtNCED3*	0,00E+00	ABY47995	*MdCCD4*	6,00E-101	Huang *et al.* 2009
MDP0000228070	*MdNCED3b*	8	19,341	Q9LRR7	*AtNCED3*	0,00E+00	ABY47995	*MdCCD4*	4,00E-100	Huang *et al.* 2009
MDP0000929213	*MdNCED5a*	5	7,442	Q9C6Z1	*AtNCED5*	0,00E+00	ABY47995	*MdCCD4*	2,00E-96	Huang *et al.* 2009
MDP0000386460	*MdNCED5b*	5	6,722	Q9C6Z1	*AtNCED5*	0,00E+00	ABY47995	*MdCCD4*	3,00E-95	Huang *et al.* 2009

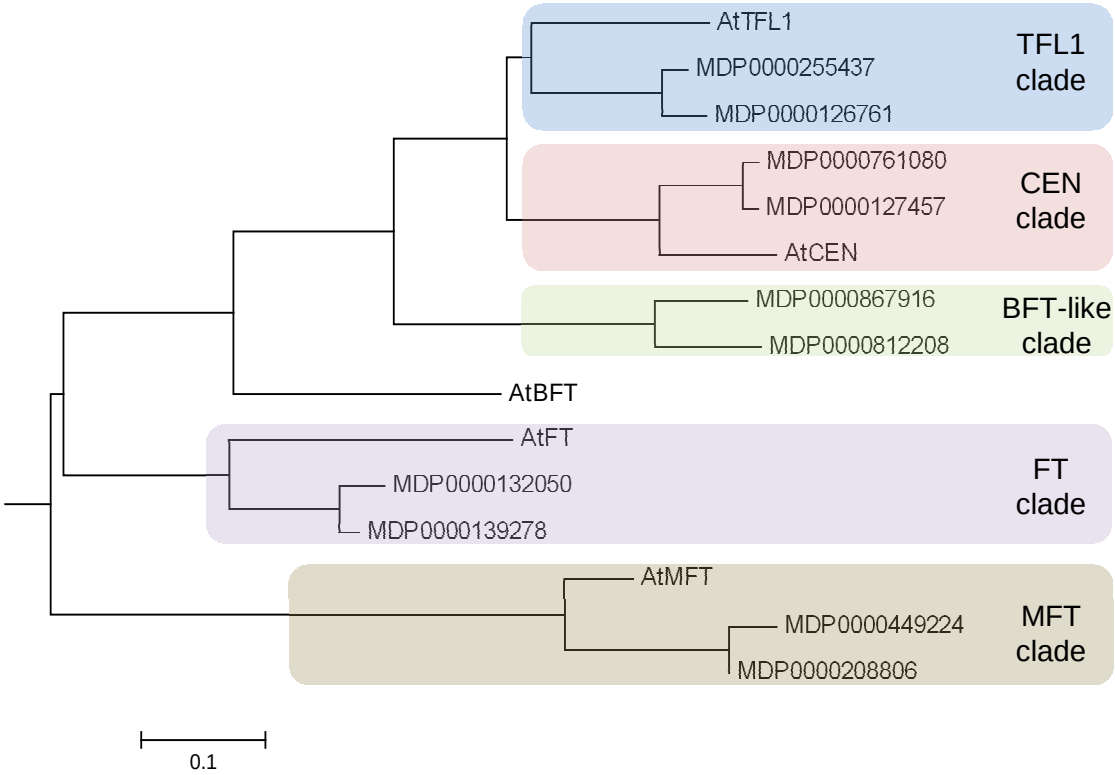

Figure S1A. Phylogenetic analysis of *FT/TFL1* family members from *Arabidopsis thaliana* and *Malus* x *domestica*.

Protein sequences were obtained from GenBank: *AtFT* (Q9SXZ2), *AtMFT* (Q9XFK7), *AtBFT* (Q9FIT4), *AtCEN* (Q9ZNV5) and *AtTFL1* (P93003). *Malus* x *domestica* gene predictions (MDP) were isolated from the 'Golden Delicious' apple genome sequence using BLASTP. Phylogenetic trees were created using the Phylogeny.fr platform (http://www.phylogeny.fr) (Dereeper et al., 2008). The unit for the scale bar displays branch lengths (0.1 substitutions/site).

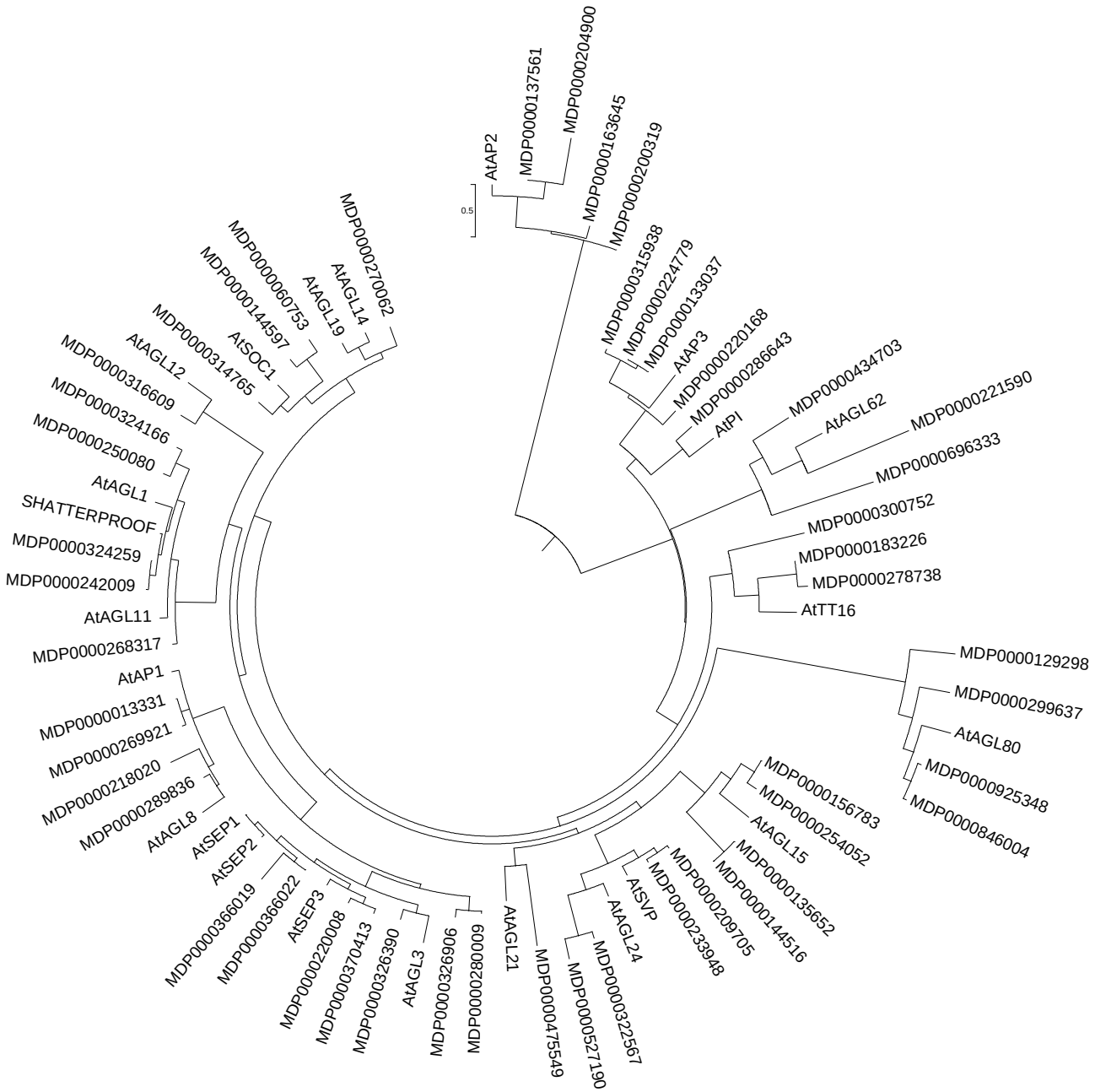

Figure S1B. Phylogenetic analysis of *MADS-box* family members from *Arabidopsis thaliana* and *Malus* x *domestica*.

Protein sequences were obtained from GenBank: *AtAGL1* (P29381), *AtAGL3* (P29383), *AtAGL8* (Q38876), *AtAGL11* (Q38836), *AtAGL12* (Q38841), *AtAGL15* (Q38847), *AtAGL19* (O82743), *AtAGL21* (Q9SZJ6), *AtAGL24* (O82794), *AtAGL62* (Q9FKK2), *AtAGL80* (Q9FJK3), *AtAP1* (P35631), *AtAP2* (P47927), *AtAP3* (P35632), *AtPI* (P48007), *AtSEP1* (P29382), *AtSEP2* (P29384), *AtSEP3* (O22456), *AtSOC1* (O64645), *AtSVP* (Q9FVC1) and *AtTT16* (Q8RYD9). *Malus* x *domestica* gene predictions (MDP) were isolated from the 'Golden Delicious' apple genome sequence using BLASTP. Phylogenetic trees were created using the Phylogeny.fr platform (http://www.phylogeny.fr) (Dereeper et al., 2008). The unit for the scale bar displays branch lengths (0.5 substitutions/site).

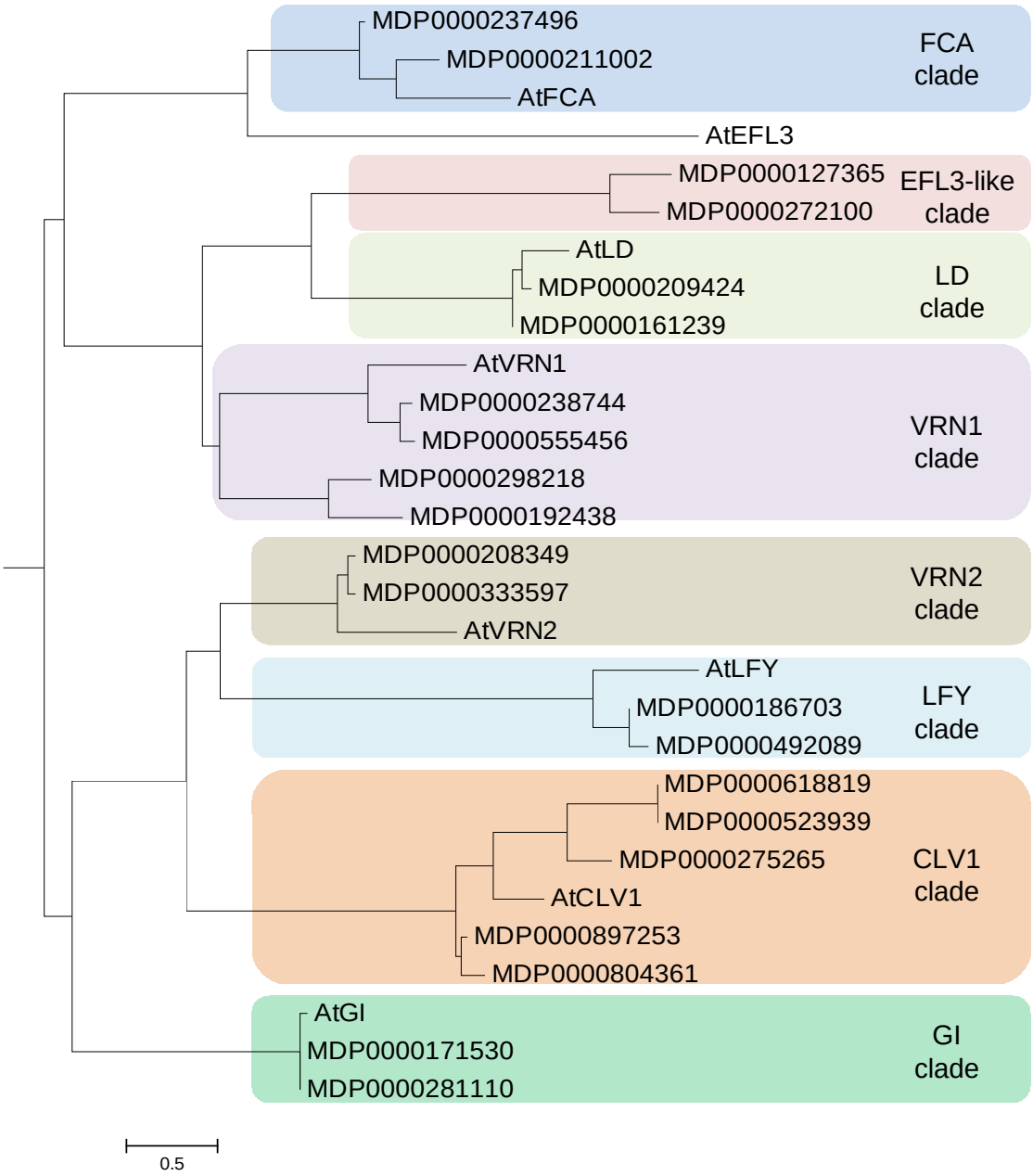

Figure S1C. Phylogenetic analysis of flowering genes of different gene families from *Arabidopsis thaliana* and *Malus* x *domestica*.

Protein sequences were obtained from GenBank: AtLFY (Q00958), AtCLV1 (Q9SYQ8), AtEFL3 (O82804), AtFCA (O04425), AtGI (Q9SQI2), AtLD (Q38796), AtVRN1 (Q8L3W1) and AtVRN2 (Q8W5B1). Malus x domestica gene predictions (MDP) were isolated from the 'Golden Delicious' apple genome sequence using BLASTP. Phylogenetic trees were created using the Phylogeny.fr platform (http://www.phylogeny.fr) (Dereeper et al., 2008). The unit for the scale bar displays branch lengths (0.5 substitutions/site).

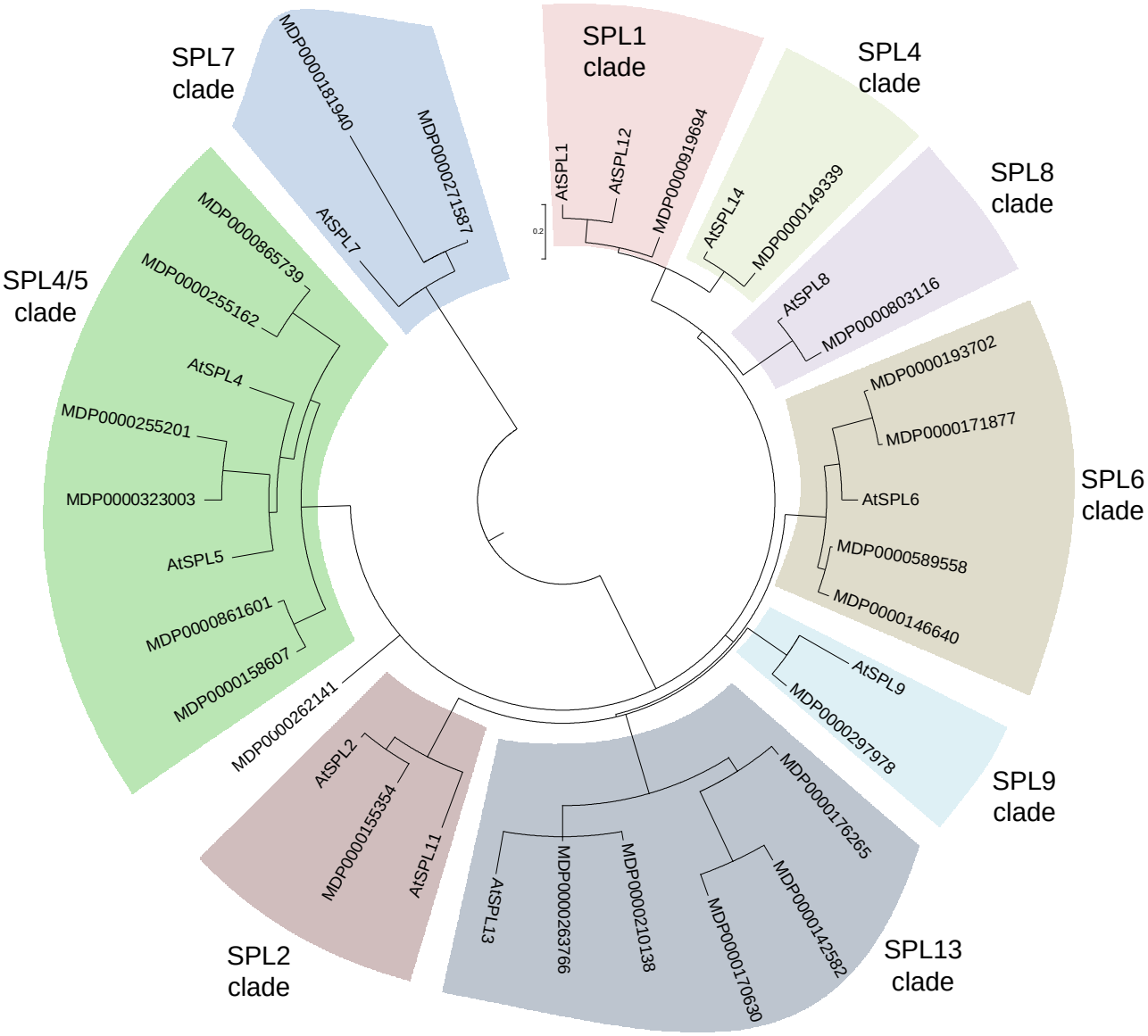

Figure S1D. Phylogenetic analysis of the *Squamosa Protein-Like* family from *Arabidopsis thaliana* and *Malus* x *domestica*.

Protein sequences were obtained from GenBank: *AtSPL1* (Q9SMX9), *AtSPL2* (Q9S840), *AtSPL4* (Q9S7A9), *AtSPL5* (Q9S758), *AtSPL6* (Q94JW8), *AtSPL7* (Q8S9G8), *AtSPL8* (Q8GXL3), *AtSPL9* (Q700W2), *AtSPL11* (Q9FZK0), *AtSPL12* (Q9S7P5), *AtSPL13* (Q8LFW6) and *AtSPL14* (Q8RY95). *Malus* x *domestica* gene predictions (MDP) were isolated from the 'Golden Delicious' apple genome sequence using BLASTP. Phylogenetic trees were created using the Phylogeny.fr platform (http://www.phylogeny.fr) (Dereeper et al., 2008). The unit for the scale bar displays branch lengths (0.2 substitutions/site).

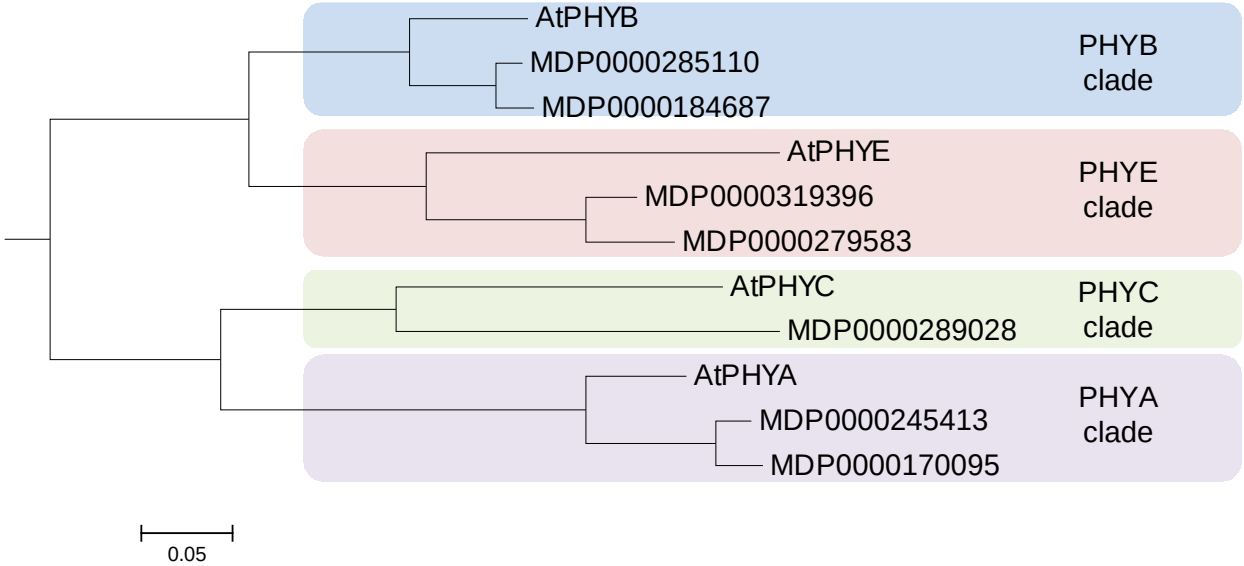

Figure S1E. Phylogenetic analysis of the *Phytochrome* family from *Arabidopsis thaliana* and *Malus* x *domestica*.

Protein sequences were obtained from GenBank: *AtPHYA* (P14712), *AtPHYB* (P14713), *AtPHYC* (P14714) and *AtPHYE* (P42498). *Malus* x *domestica* gene predictions (MDP) were isolated from the 'Golden Delicious' apple genome sequence using BLASTP. Phylogenetic trees were created using the Phylogeny.fr platform (http://www.phylogeny.fr) (Dereeper et al., 2008). The unit for the scale bar displays branch lengths (0.05 substitutions/site).

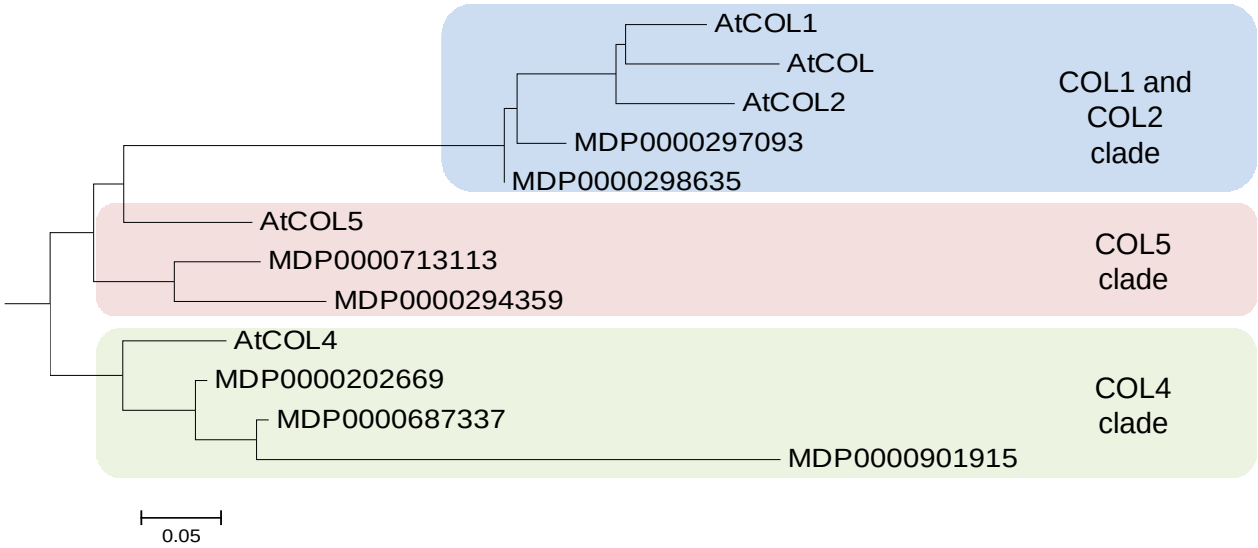

Figure S1F. Phylogenetic analysis of the *Constance-like* family from *Arabidopsis thaliana* and *Malus* x *domestica*.

Protein sequences were obtained from GenBank: *AtCOL2* (Q96502), *AtCOL4* (Q940T9) and *AtCOL5* (Q9FHH8). *Malus* x *domestica* gene predictions (MDP) were isolated from the 'Golden Delicious' apple genome sequence using BLASTP. Phylogenetic trees were created using the Phylogeny.fr platform (http://www.phylogeny.fr) (Dereeper et al., 2008). The unit for the scale bar displays branch lengths (0.05 substitutions/site).

Figure S2A. Phylogenetic analysis of the *Gibberellin Oxidase* family members from *Arabidopsis thaliana* and *Malus* x *domestica*.

Protein sequences were obtained from GenBank: *AtGA20ox1* (Q39110), *AtGA20ox2* (Q39111), *AtGA20ox3* (Q39112), *AtGA3ox1* (Q39103), *AtGA3ox2* (Q9ZT84), *AtGA3ox3* (Q9SVS8), *AtGA2ox1* (Q8LEA2), *AtGA2ox2* (Q9XFR9) and *AtGA2ox8* (O49561). *Malus* x *domestica* gene predictions (MDP) were isolated from the 'Golden Delicious' apple genome sequence using BLASTP. Phylogenetic trees were created using the Phylogeny.fr platform (http://www.phylogeny.fr) (Dereeper et al., 2008). The unit for the scale bar displays branch lengths (0.2 substitutions/site).

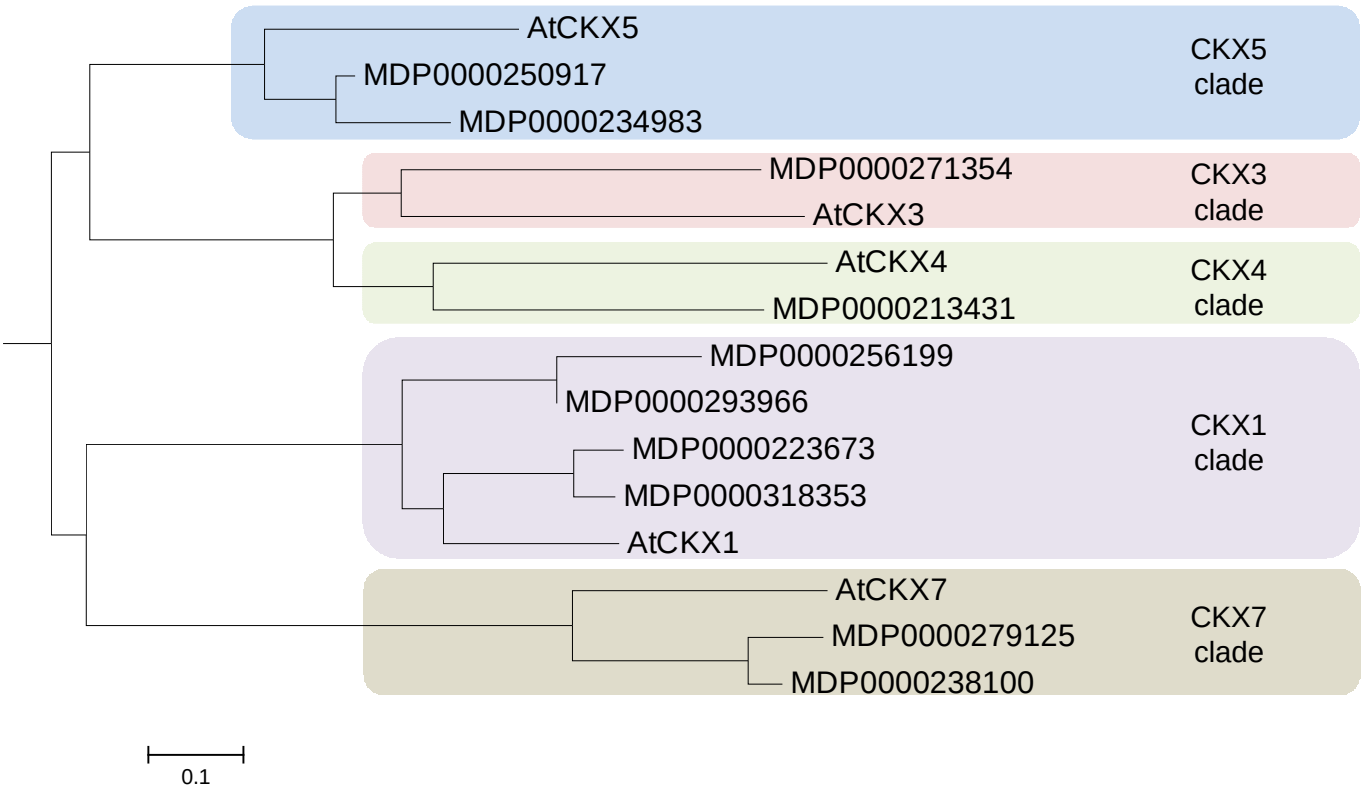

Figure S2B. Phylogenetic analysis of the *Cytokinin Oxidase* family members from *Arabidopsis thaliana* and *Malus* x *domestica*.

Protein sequences were obtained from GenBank: *AtCKX1* (O22213), *AtCKX3* (Q9LTS3), *AtCKX4* (Q9FUJ2), *AtCKX5* (Q67YU0), and *AtCKX7* (Q9FUJ1). *Malus* x *domestica* gene predictions (MDP) were isolated from the 'Golden Delicious' apple genome sequence using BLASTP. Phylogenetic trees were created using the Phylogeny.fr platform (http://www.phylogeny.fr) (Dereeper et al., 2008). The unit for the scale bar displays branch lengths (0.1 substitutions/site).

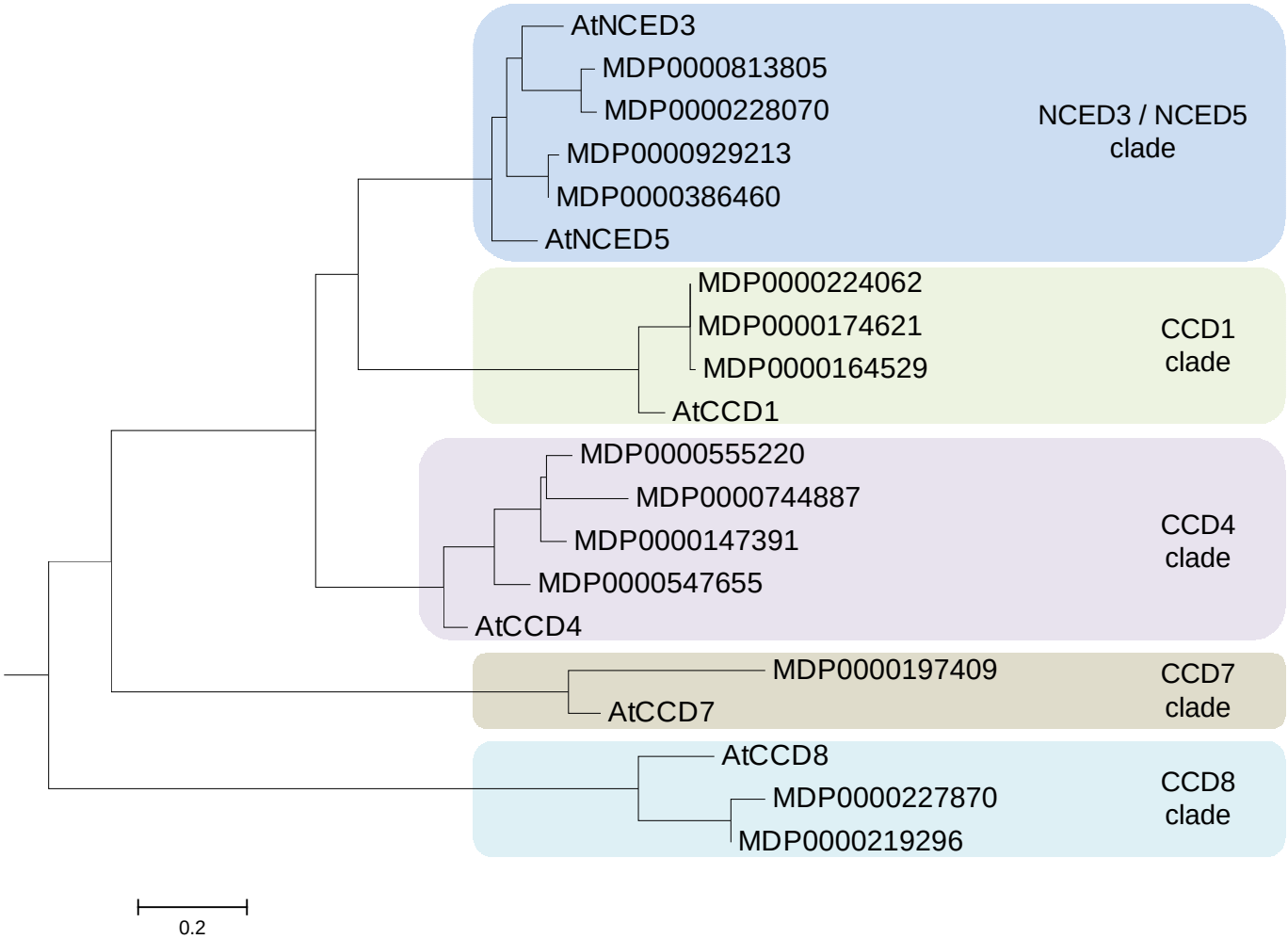

Figure S2C. Phylogenetic analysis of the *Carotenoid Cleavage Dioxygenase* family members from *Arabidopsis thaliana* and *Malus* x *domestica*.

Protein sequences were obtained from GenBank: *AtCCD1* (O65572), *AtCCD4* (O49675), *AtCCD7* (Q7XJM2), *AtCCD8* (Q8VY26), *AtNECD3 (*Q9LRR7) and *AtNECD5* (Q9C6Z1). *Malus* x *domestica* gene predictions (MDP) were isolated from the 'Golden Delicious' apple genome sequence using BLASTP. Phylogenetic trees were created using the Phylogeny.fr platform (http://www.phylogeny.fr) (Dereeper et al., 2008). The unit for the scale bar displays branch lengths (0.2 substitutions/site).

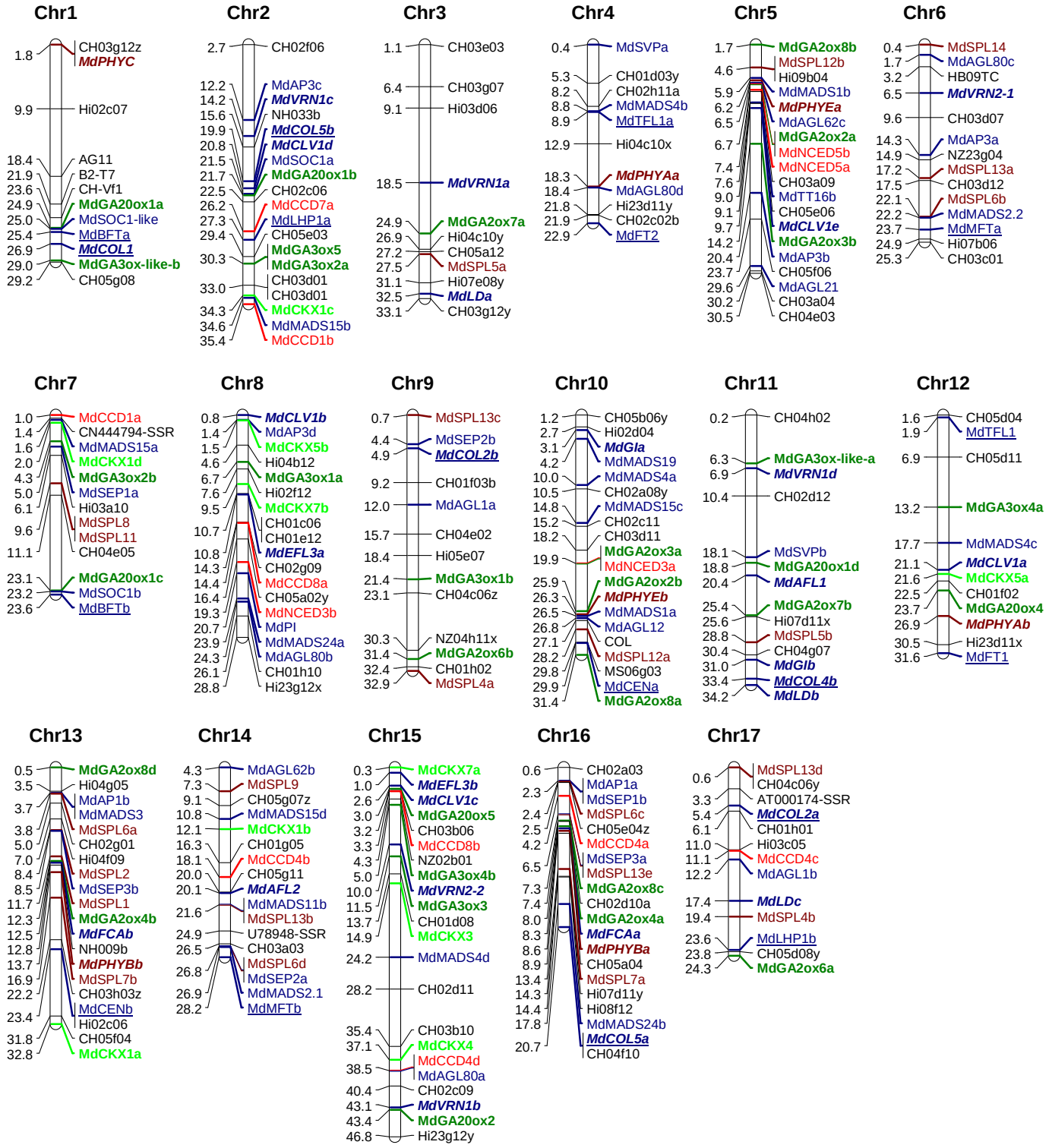

Figure S3. Physical position (Mb) of genetic markers (black) and candidate genes on the 17 chromosomes (Chr) of the apple genome ('Golden Delicious'). Candidate gene families are represented in different colours: *FT/TFL1*, blue underlined; *MASD-box*, blue; flowering genes from different gene families, blue bold italic; *Squamosa*, brown; *Phytochrome*, brown bold italic; *Constance-like*, blue bold italic underlined; *Gibberellin Oxidase*, green bold; *Cytokinin Oxidase*, light green bold and *Carotenoid Cleavage Dioxygenase*, red.

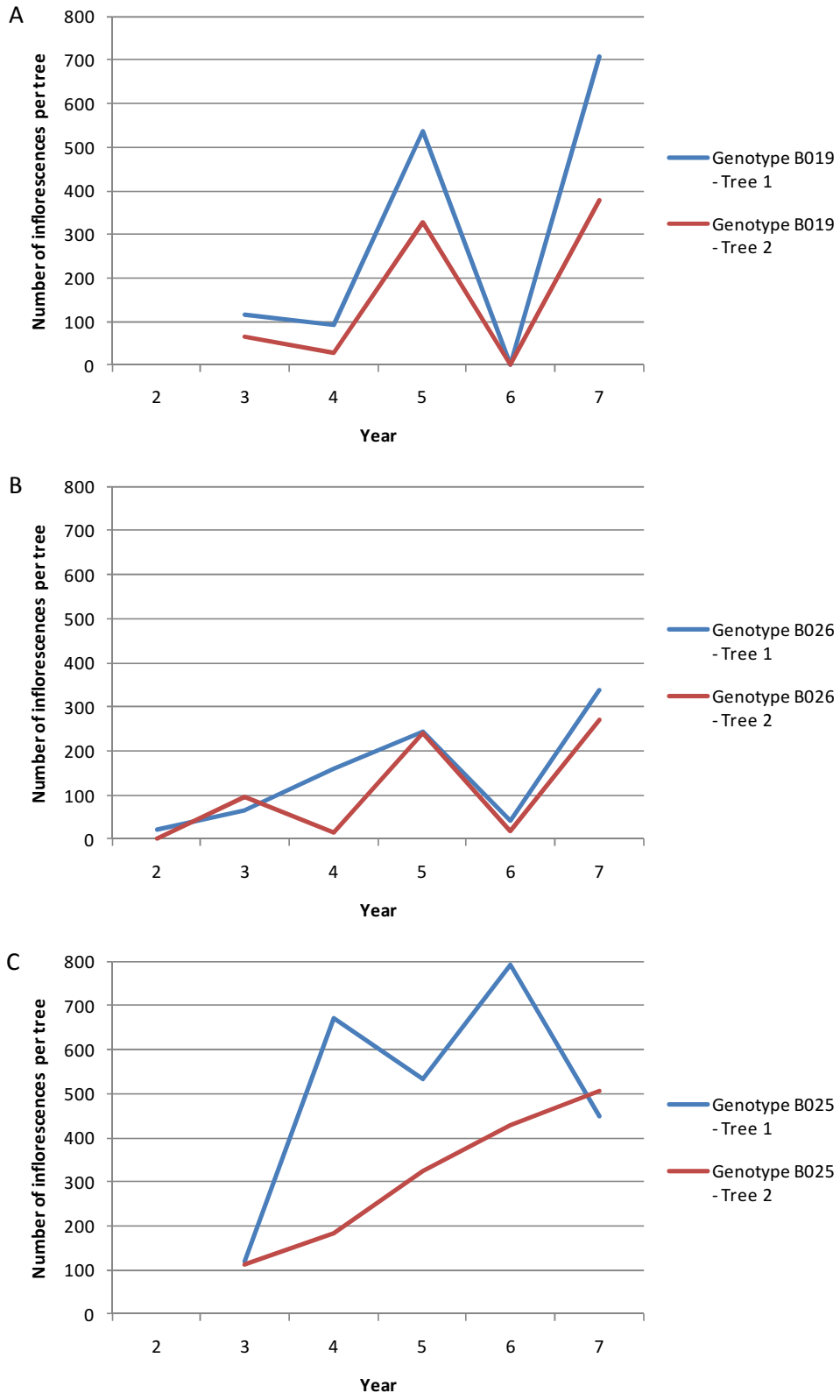

Figure S4. Variability of the number of inflorescences per tree between replicates of the same genotype. (A) A genotype (B019) with very similar bearing behavior for both replicates. In total, 48 genotypes displayed this pattern; (B) A genotype (B044) with similar bearing behavior for both replicates differentiated by one year of production. In total, 47 genotypes displayed this pattern and (C) A genotype (B025) with contrasted bearing behavior for both replicates. In total, 15 genotypes displayed this pattern.