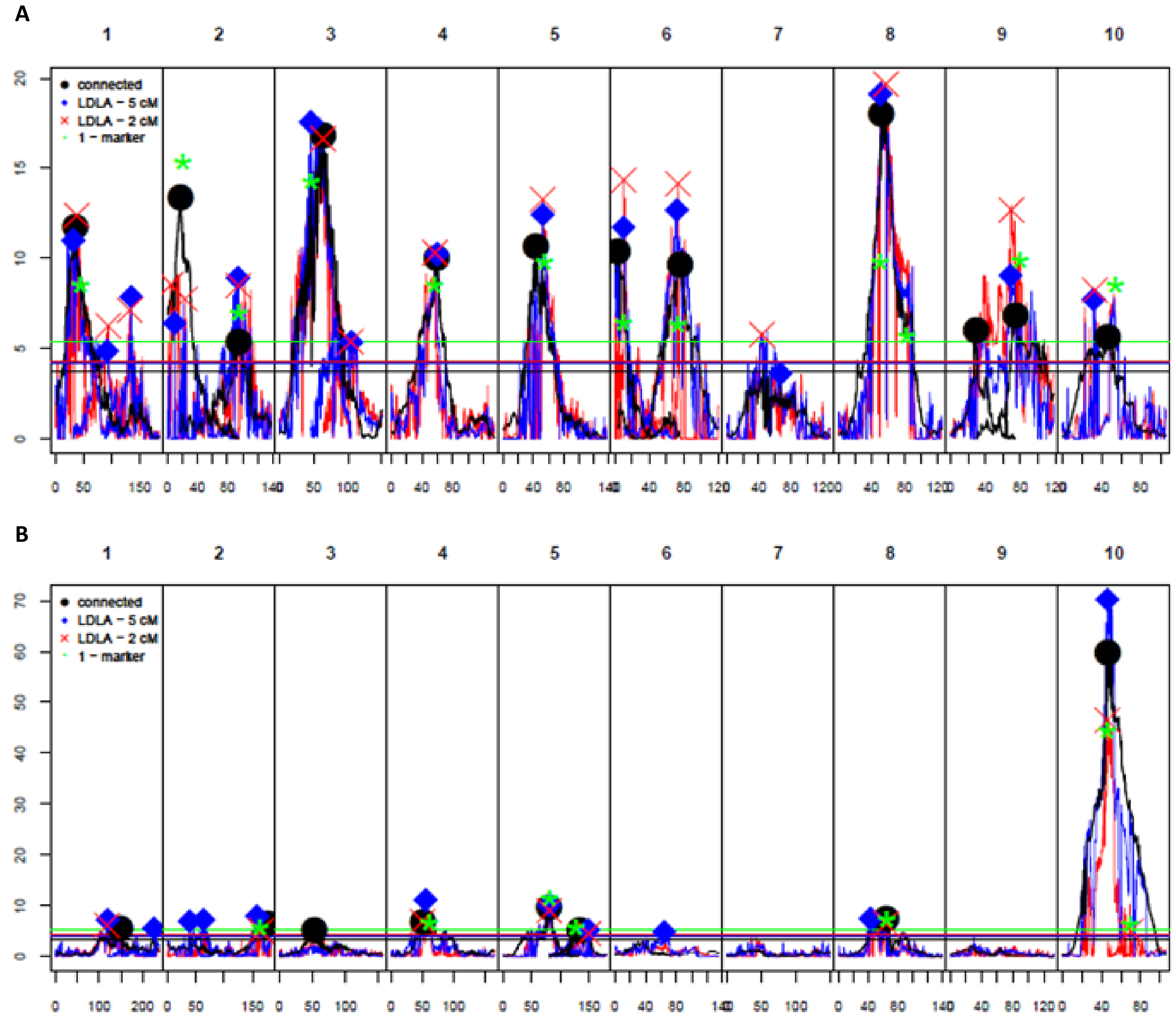

Figure S1 Results of the QTL detection with each model for DMC for **(A)** the dent design and **(B)** the flint design. The -log10(p-values) of the connected model are represented by black lines, the QTL positions of the connected models by black dots. The -log10(p-values) of the LDLA – 5 cM model are represented by blue lines and the QTL positions by blue diamonds. The -log10(p-values) of the LDLA – 2 cM model are represented by red lines and the QTL positions by red crosses. The -log10(p-values) of the QTL detected by the LDLA – 1-marker model are represented by green stars. Horizontal lines correspond to the threshold values of the different models.

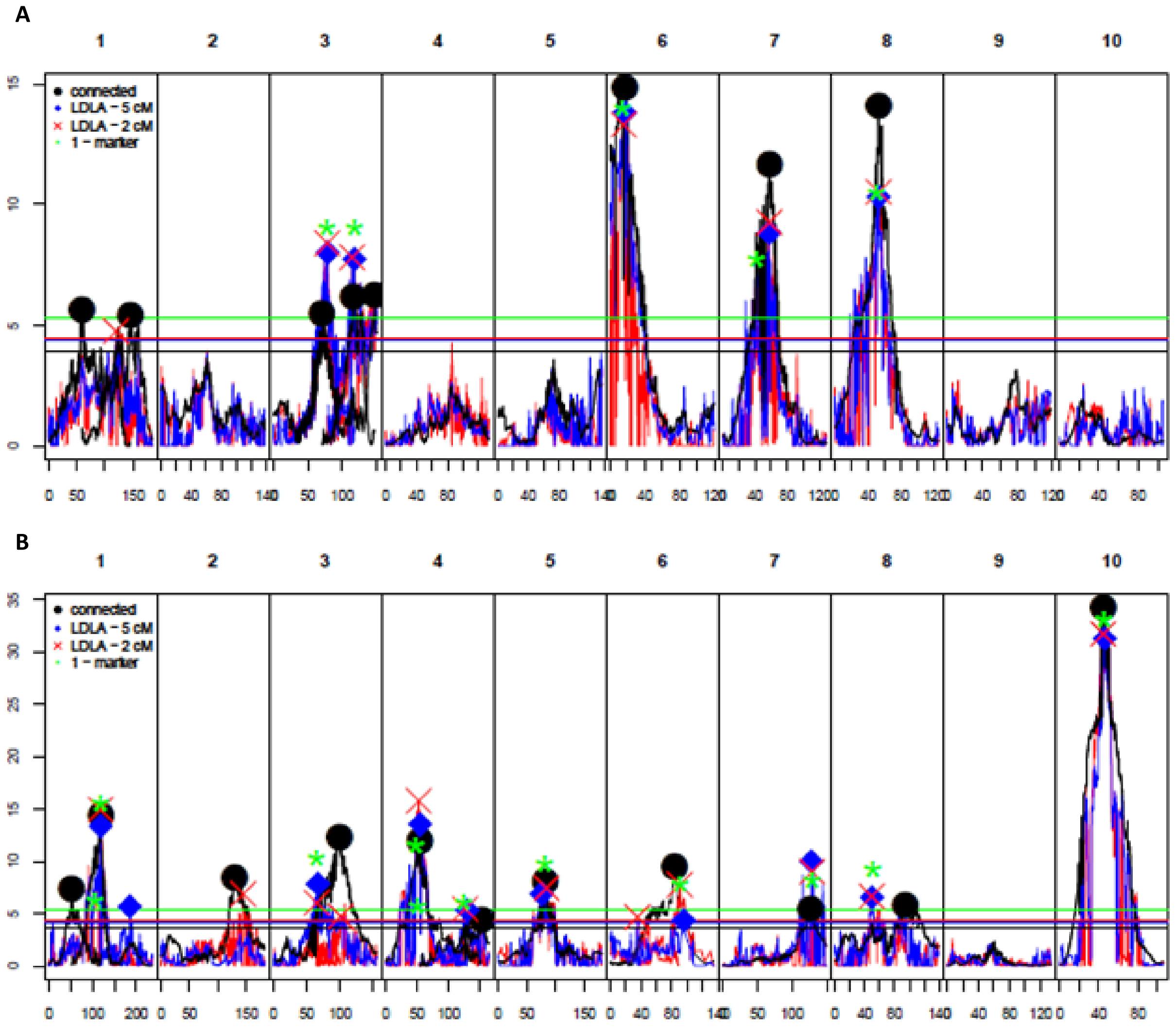

Figure S2 Results of the QTL detection with each model for DMY for **(A)** the dent design and **(B) the** flint design. The results for the dent design are in the superior part, flint in the inferior part. The -log10(p-values) of the connected model are represented by black lines, the QTL positions of the connected models by black dots. The - log10(p-values) of the LDLA – 5 cM model are represented by blue lines and the QTL positions by blue diamonds. The - log10(p-values) of the LDLA – 2 cM model are represented by red lines and the QTL positions by red crosses. The - log10(p-values) of the QTL detected by the LDLA – 1-marker model are represented by green stars. Horizontal lines correspond to the threshold values of the different models.

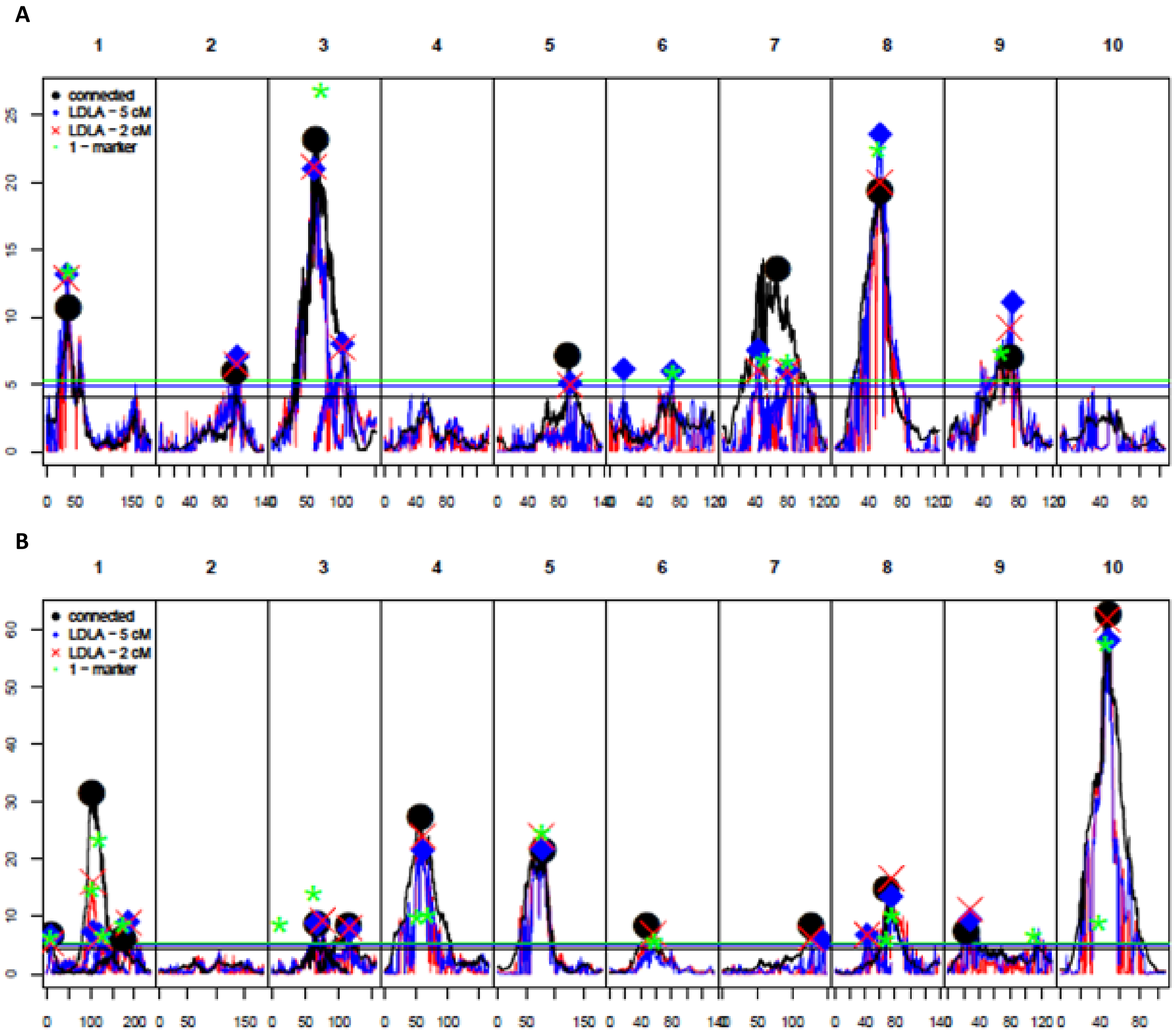

Figure S3 Results of the QTL detection with each model for DtTAS for **(A)** the dent design and **(B) the** flint design. The -log10(p-values) of the connected model are represented by black lines, the QTL positions of the connected models by black dots. The -log10(p-values) of the LDLA – 5 cM model are represented by blue lines and the QTL positions by blue diamonds. The -log10(p-values) of the LDLA – 2 cM model are represented by red lines and the QTL positions by red crosses. The -log10(p-values) of the QTL detected by the LDLA – 1-marker model are represented by green stars. Horizontal lines correspond to the threshold values of the different models.

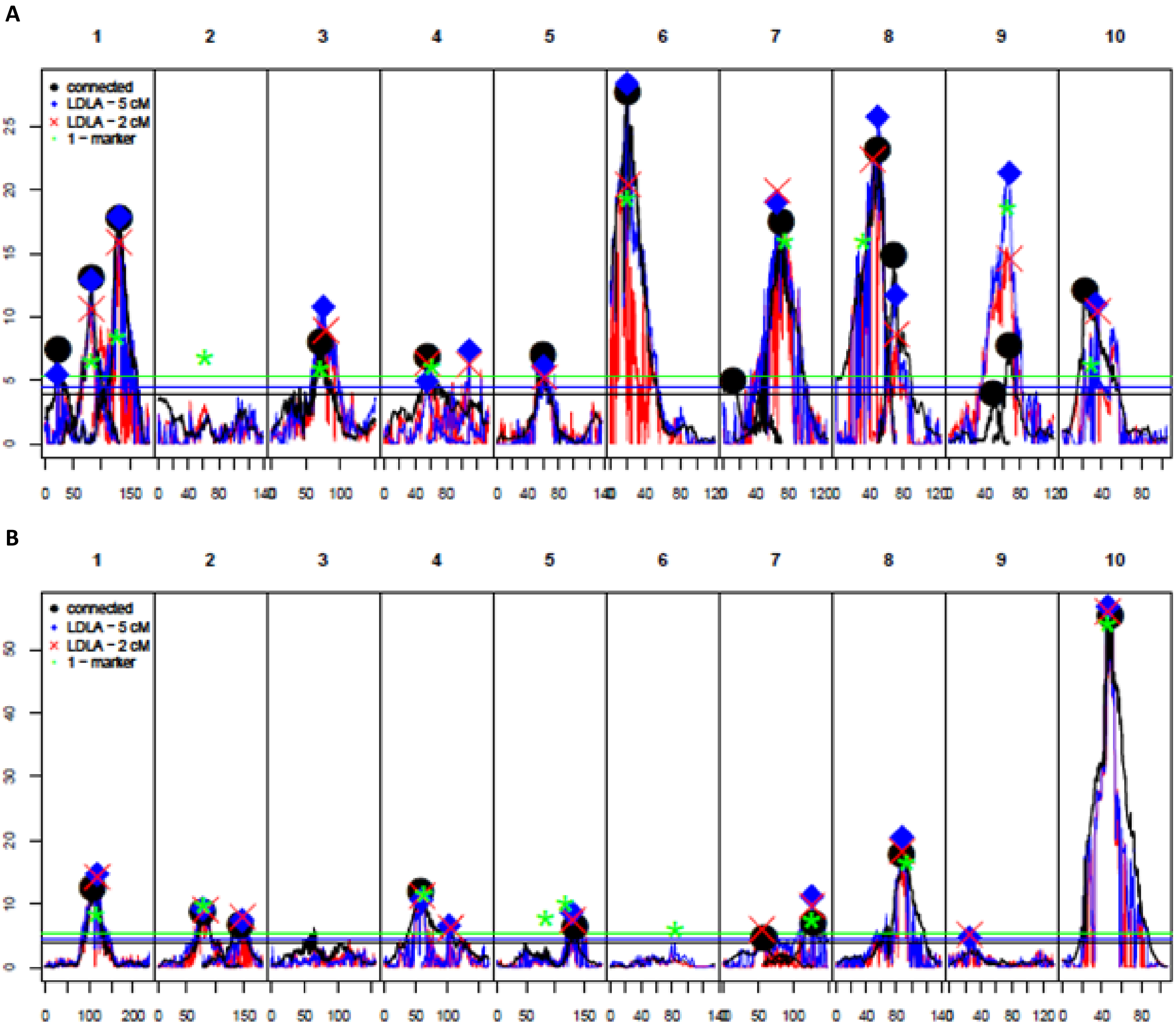

Figure S4 Results of the QTL detection with each model for PH for **(A)** the dent design and **(B) the** flint design. The -log10(p-values) of the connected model are represented by black lines, the QTL positions of the connected models by black dots. The -log10(p-values) of the LDLA – 5 cM model are represented by blue lines and the QTL positions by blue diamonds. The -log10(p-values) of the LDLA – 2 cM model are represented by red lines and the QTL positions by red crosses. The -log10(p-values) of the QTL detected by the LDLA – 1-marker model are represented by green stars. Horizontal lines correspond to the threshold values of the different models.

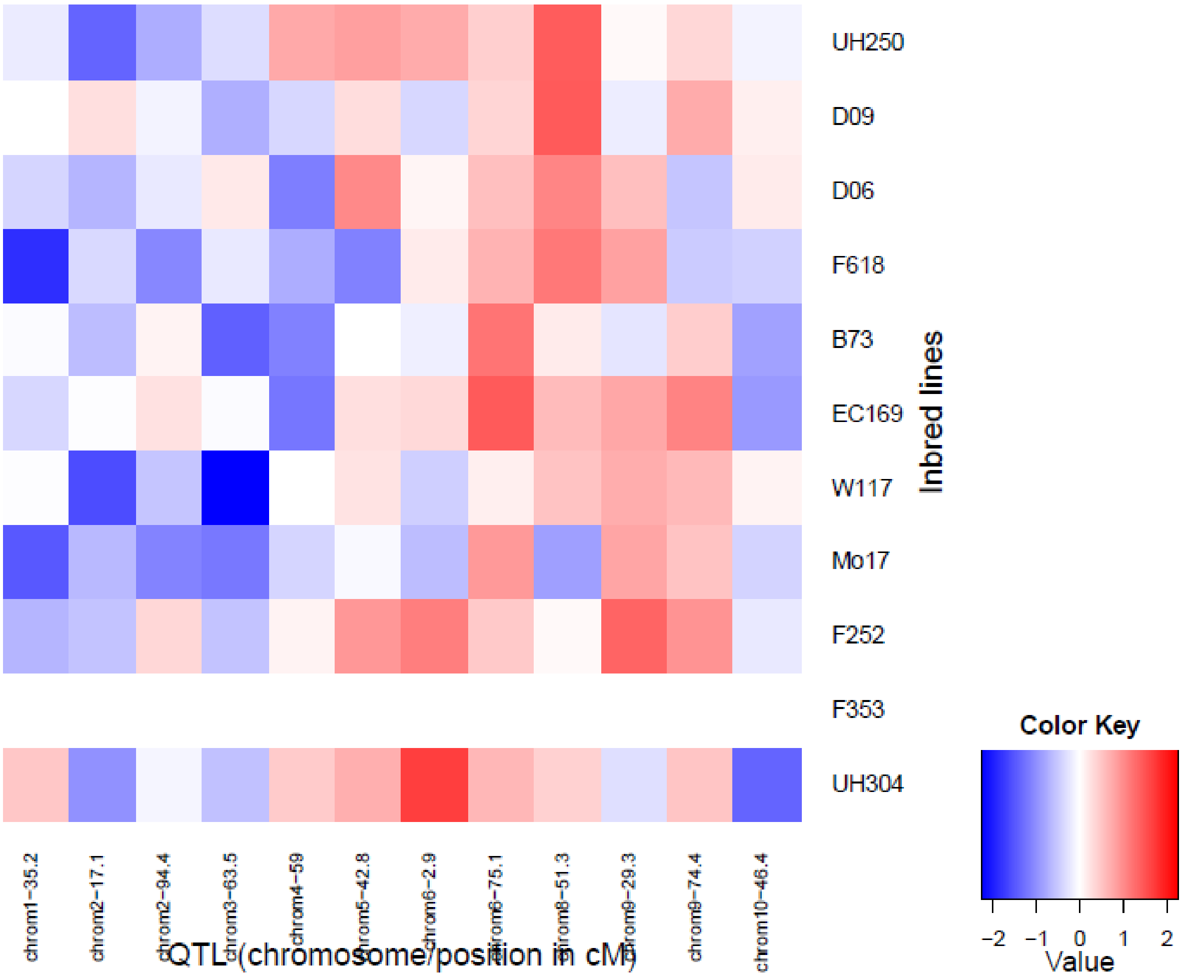

Figure S5 Allelic effects for the different dent lines for the QTL detected for DMC with the connected model. Allelic effects are estimated in contrast to the central line allelic effect (F353), which was set to zero.

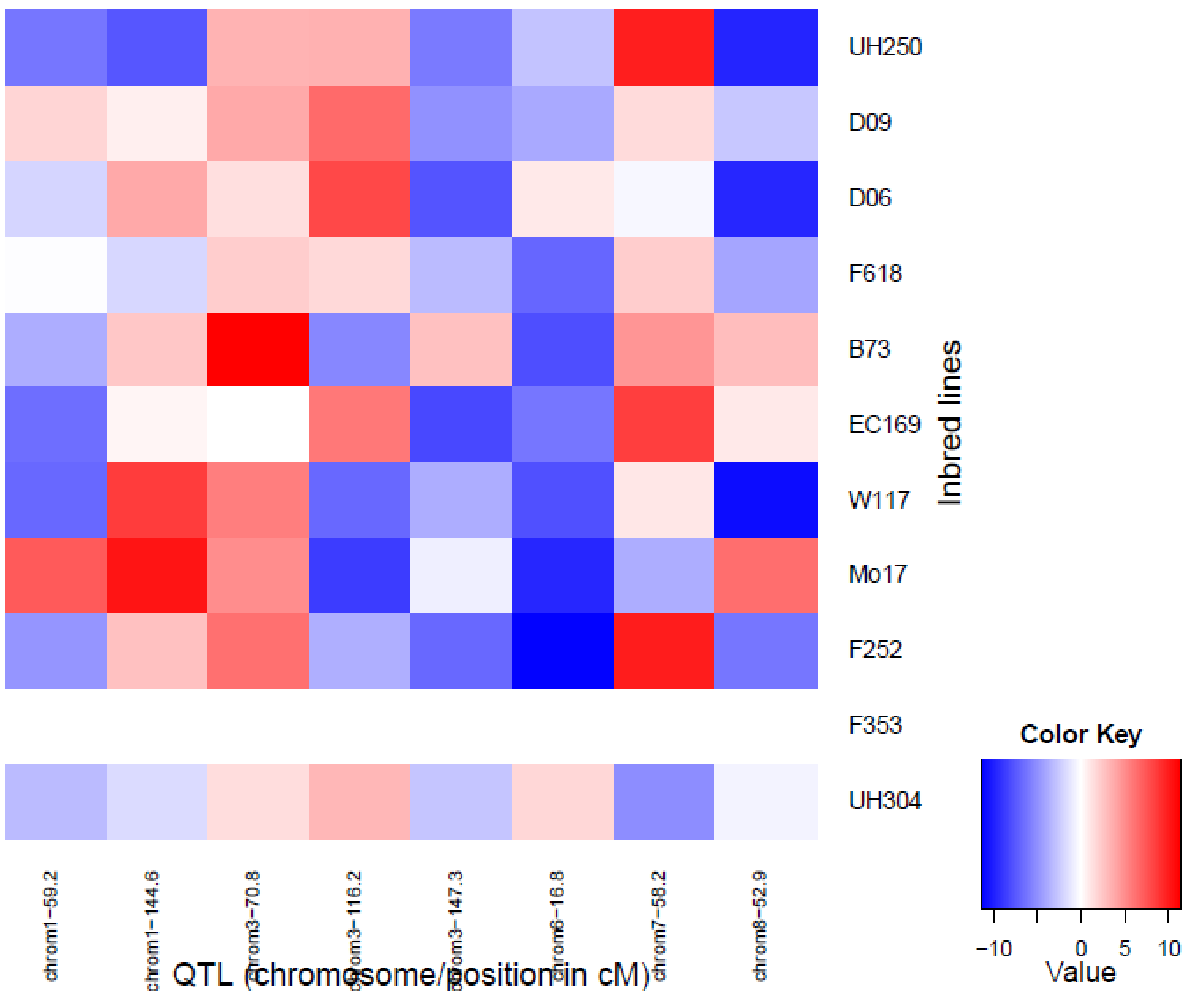

Figure S6 Allelic effects for the different dent lines for the QTL detected for DMY with the connected model. Allelic effects are estimated in contrast to the central line allelic effect (F353), which was set to zero.

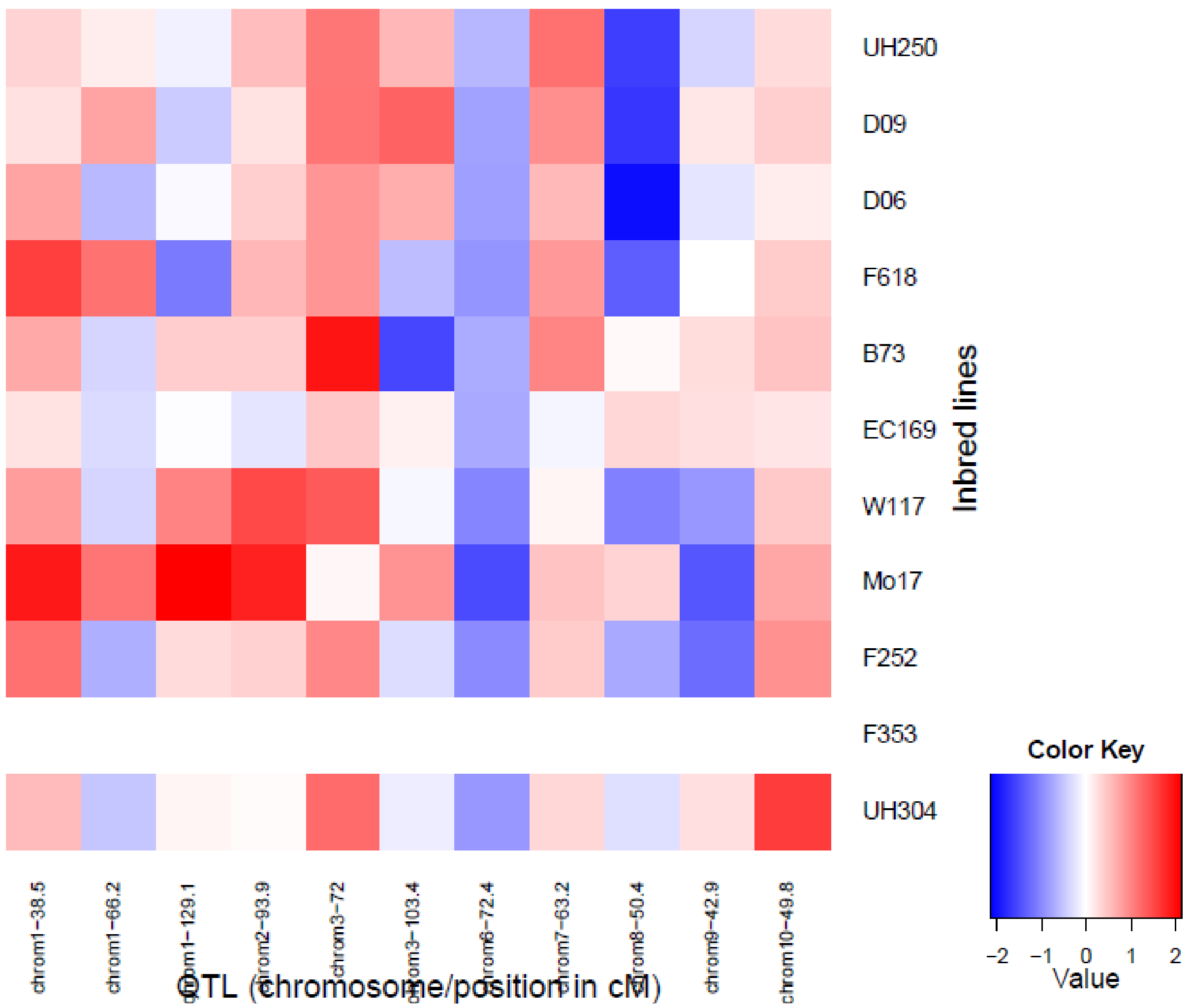

Figure S7 Allelic effects for the different dent lines for the QTL detected for DtSILK with the connected model. Allelic effects are estimated in contrast to the central line allelic effect (F353), which was set to zero.

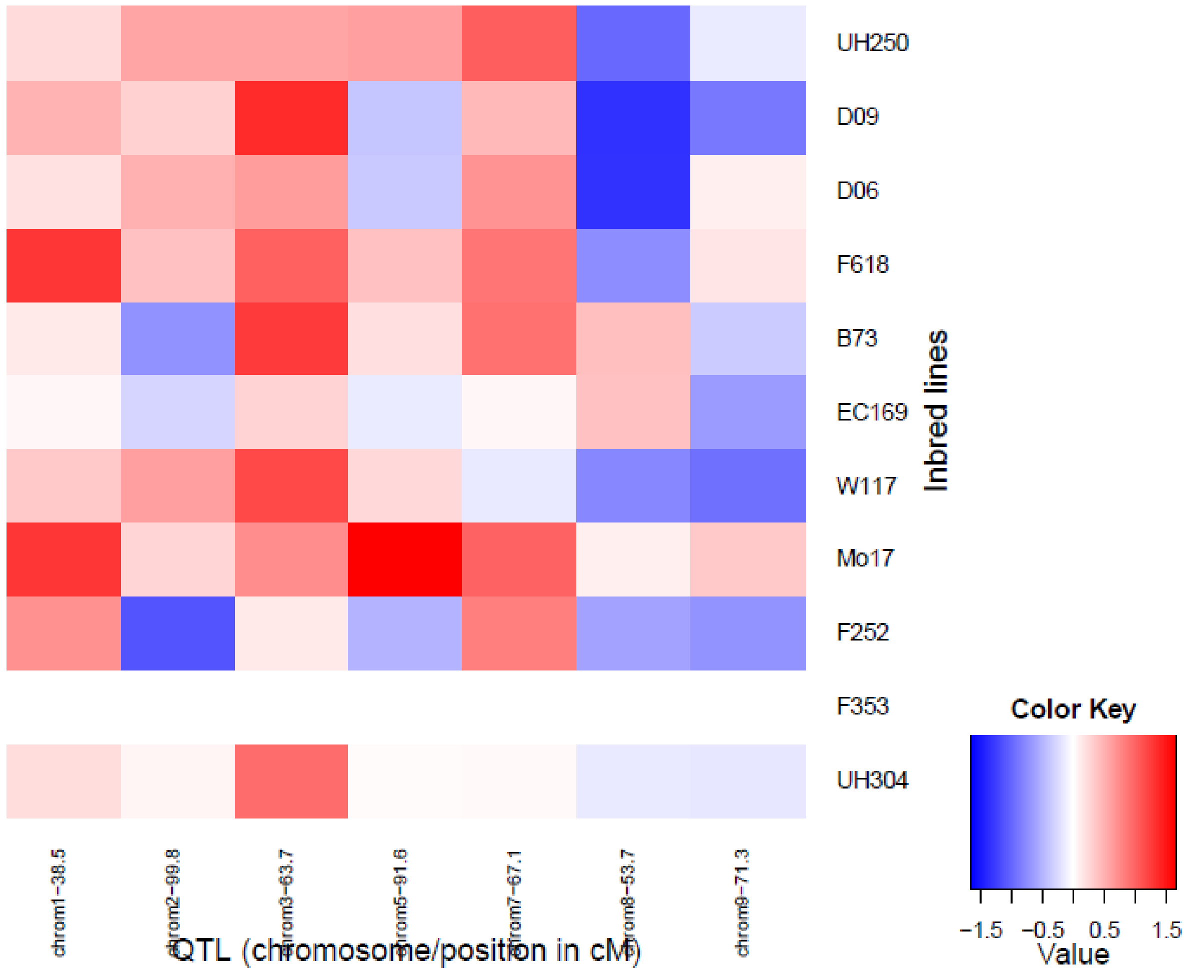

Figure S8 Allelic effects for the different dent lines for the QTL detected for DtTAS with the connected model. Allelic effects are estimated in contrast to the central line allelic effect (F353), which was set to zero.

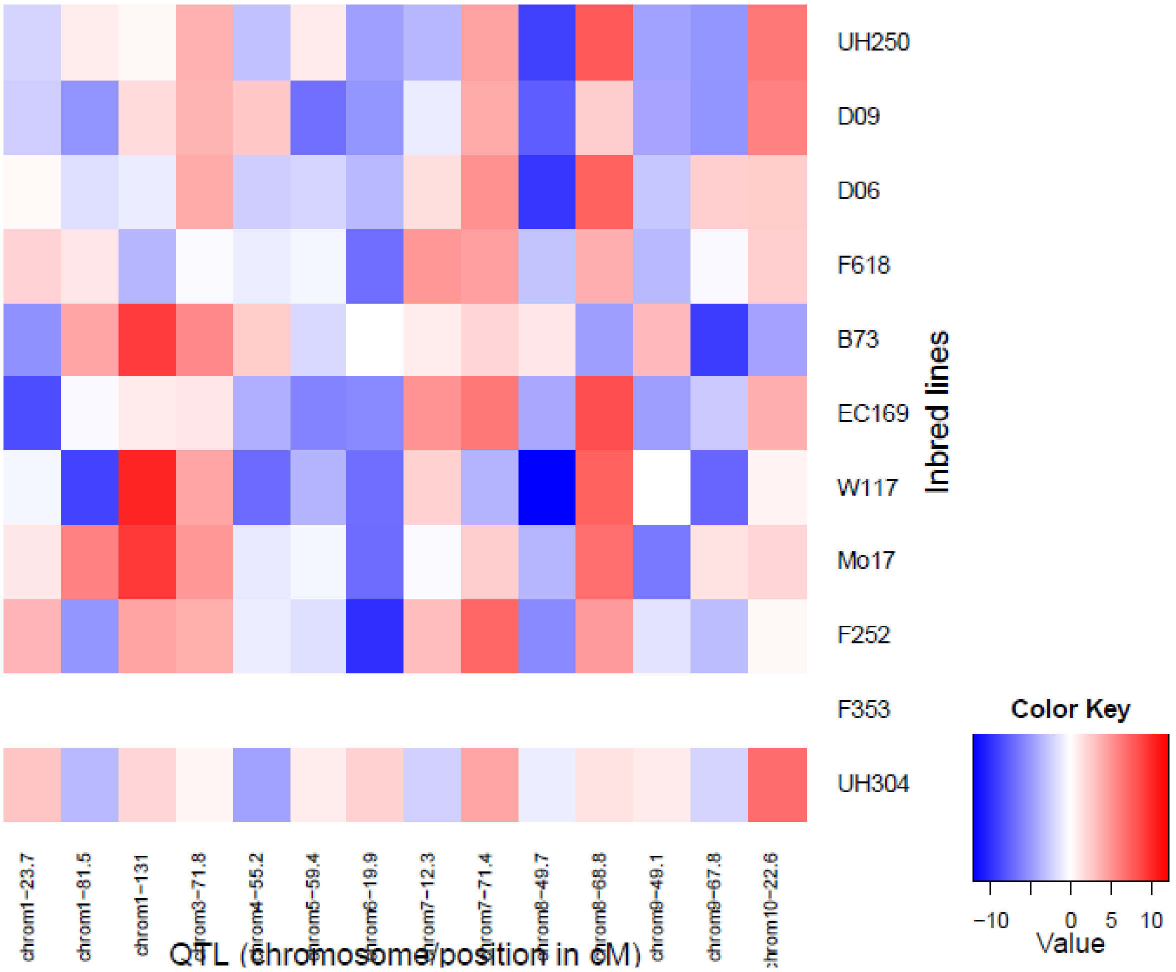

Figure S9 Allelic effects for the different dent lines for the QTL detected for PH with the connected model. Allelic effects are estimated in contrast to the central line allelic effect (F353), which was set to zero.

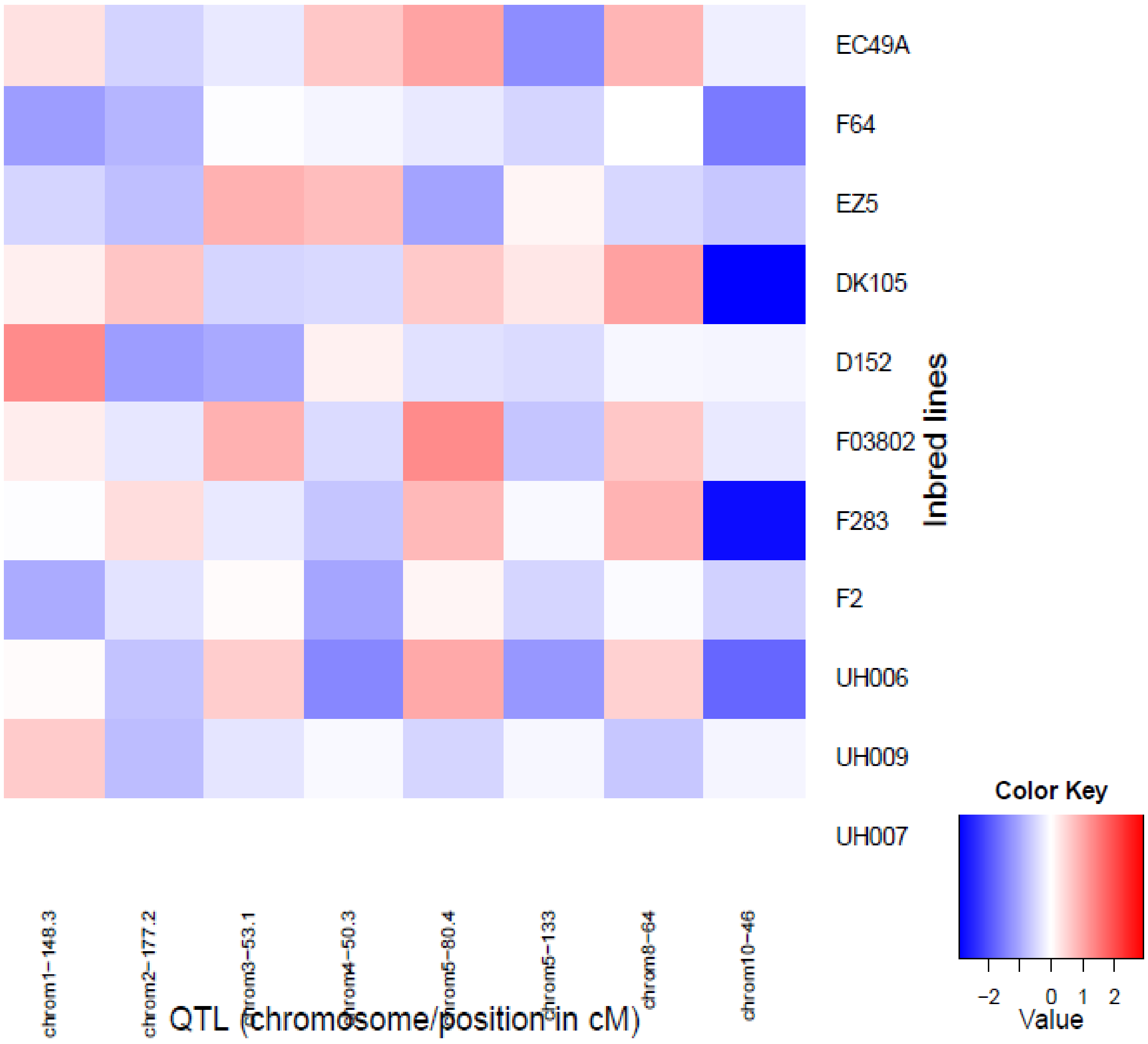

Figure S10 Allelic effects for the different flint lines for the QTL detected for DMC with the connected model. Allelic effects are estimated in contrast to the central line allelic effect (F353), which was set to zero. Allelic effects estimated for EP44 were not shown because the population where it segregates was too small (17 individuals) to obtain a reliable estimation.

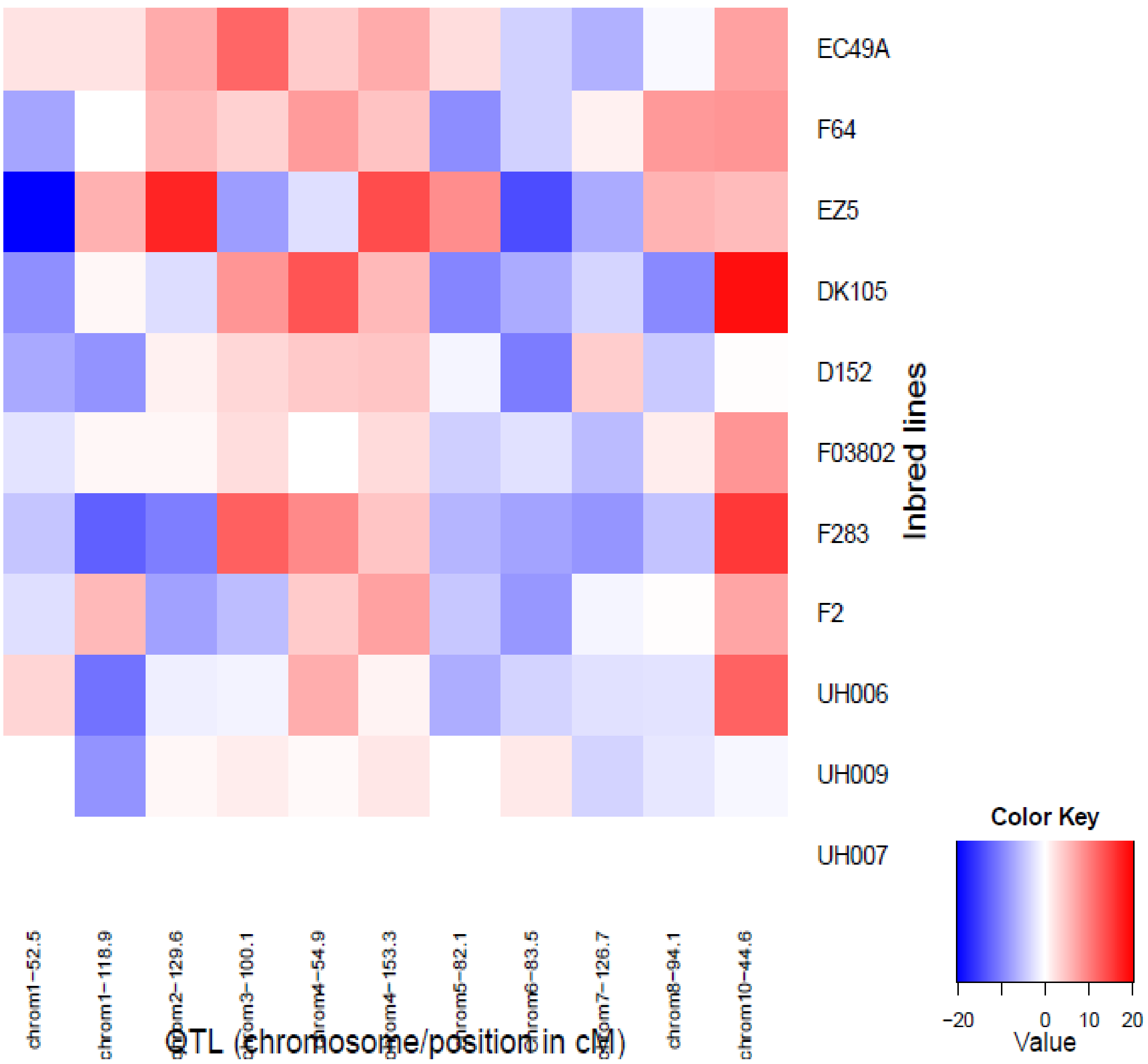

Figure S11 Allelic effects for the different flint lines for the QTL detected for DMY with the connected model. Allelic effects are estimated in contrast to the central line allelic effect (F353), which was set to zero. Allelic effects estimated for EP44 were not shown because the population where it segregates was too small (17 individuals) to obtain a reliable estimation.

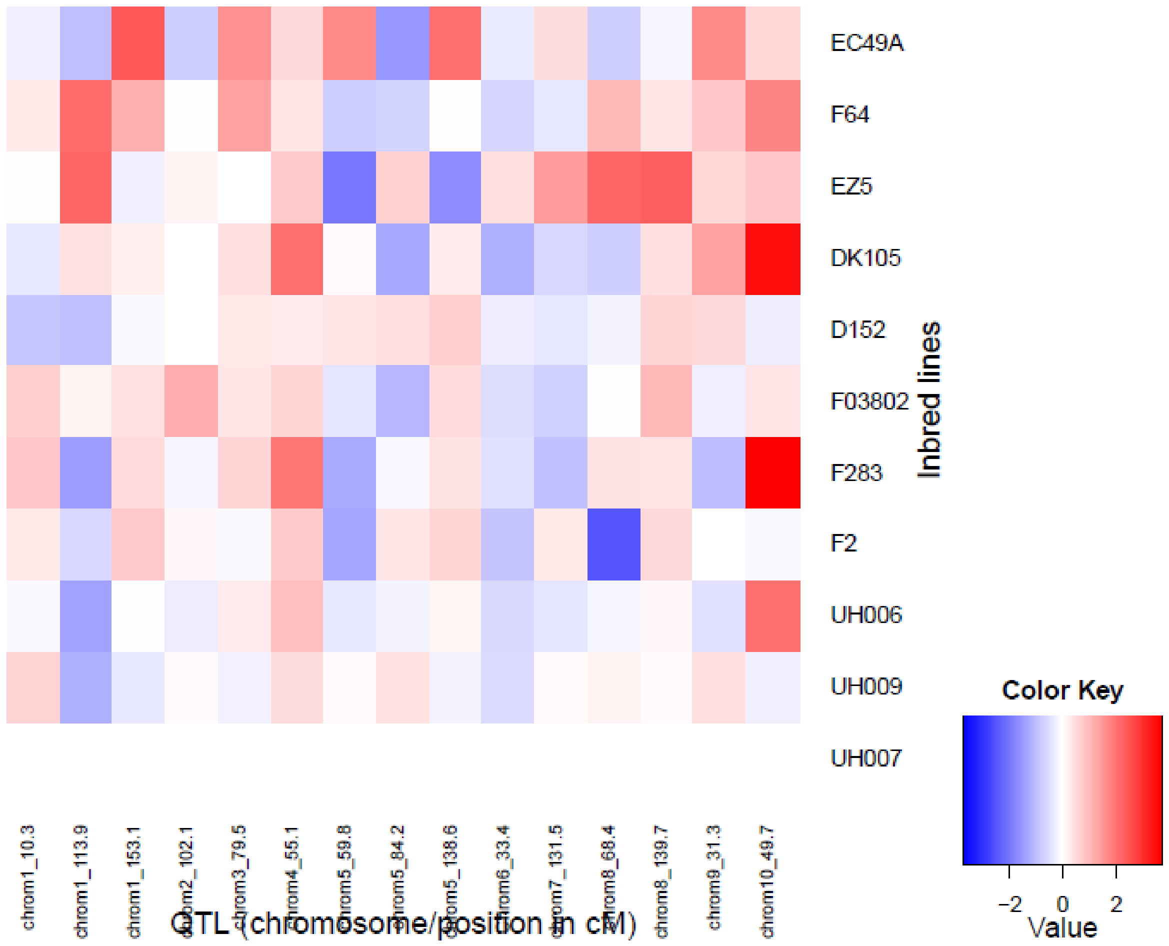

Figure S12 Allelic effects for the different flint lines for the QTL detected for DtSILK with the connected model. Allelic effects are estimated in contrast to the central line allelic effect (F353), which was set to zero. Allelic effects estimated for EP44 were not shown because the population where it segregates was too small (17 individuals) to obtain a reliable estimation.

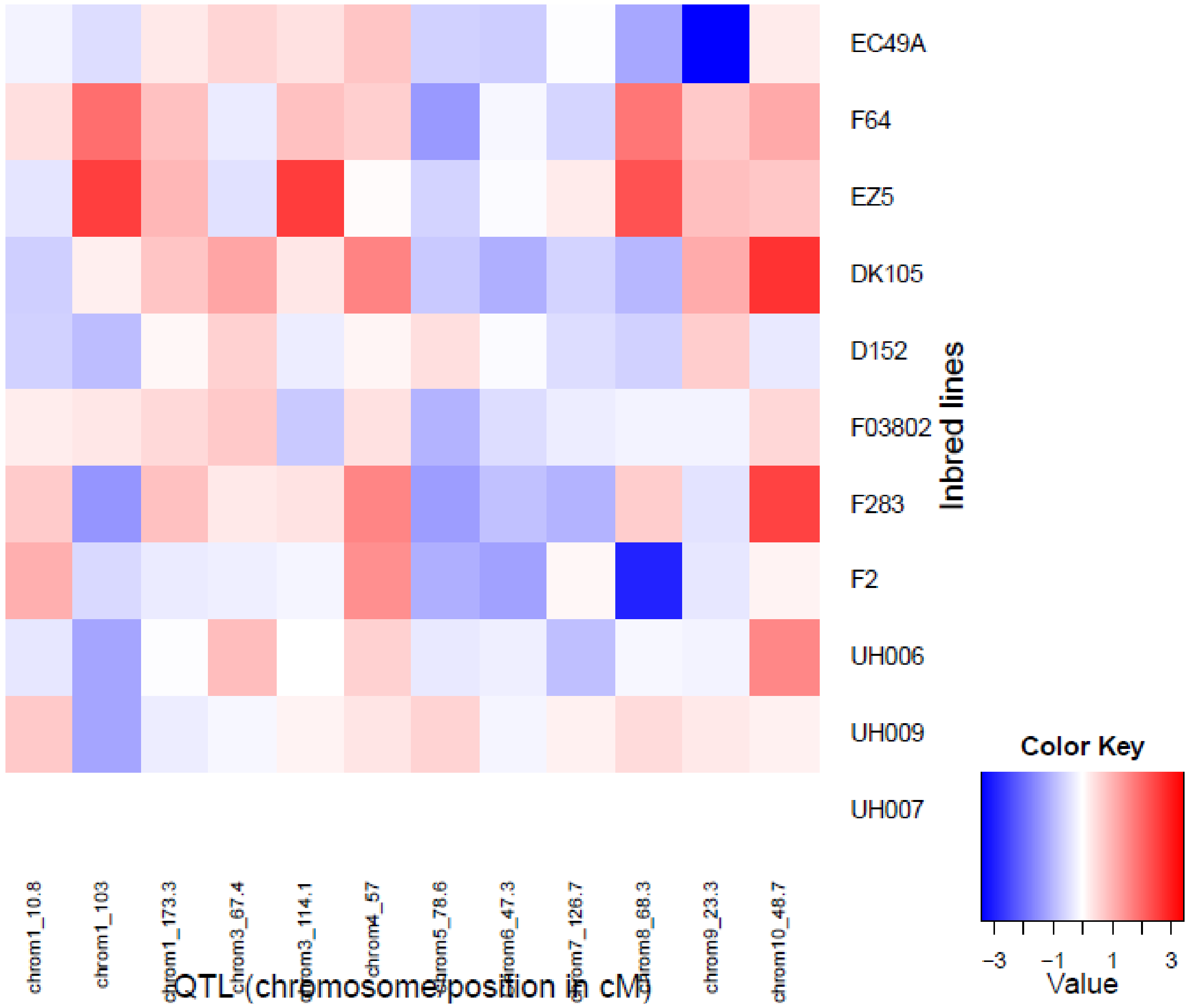

Figure S13 Allelic effects for the different flint lines for the QTL detected for DtTAS with the connected model. Allelic effects are estimated in contrast to the central line allelic effect (F353), which was set to zero. Allelic effects estimated for EP44 were not shown because the population where it segregates was too small (17 individuals) to obtain a reliable estimation.

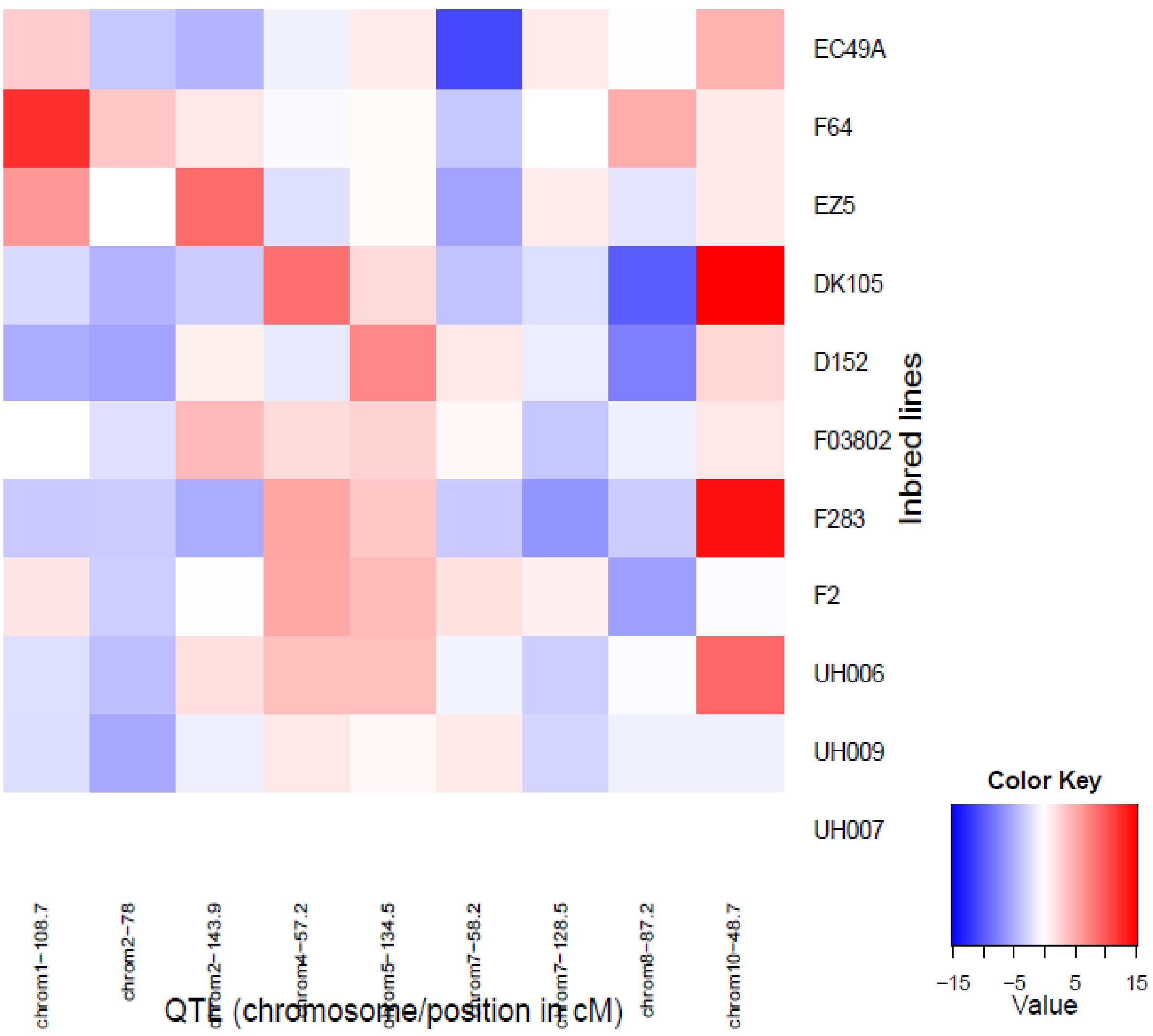

Figure S14 Allelic effects for the different flint lines for the QTL detected for PH with the connected model. Allelic effects are estimated in contrast to the central line allelic effect (F353), which was set to zero. Allelic effects estimated for EP44 were not shown because the population where it segregates was too small (17 individuals) to obtain a reliable estimation.

Table S1 Composition of the dent and flint designs with the number of DH lines in each family which were used for obtaining the consensus maps and the one which were phenotyped.

Dent design			**Flint design**		
Central line F353			Central line UH007		
Founder	Genotyped lines	Phenotyped lines	Founder	Genotyped lines	Phenotyped lines
B73	73	64	D152	112	72
D06	103	99	EC49A	53	29
D09	105	100	EP44	34[a]	17
EC169	77	66	EZ5	50	26
F252	105	96	F03802	129	129
F618	108	104	F2	77	54
Mo17	63	53	F283	134	133
UH250	99	94	F64	108	64
UH304	86	81	UH006	114	94
W117	100	84	UH009	117	98
			DK105	115	95
Total	**919**	**841**	**Total**	**1009**	**811**

[a] Population not used for mapping as too small

Table S2 Threshold values for the –log(p-value) for all the models and traits for the dent and flint groups and for the joint connected study.

	DMC	DMY	DtSILK	DtTAS	PH	**Mean**
Dent						
Connected	3.71	3.91	3.88	4.11	3.83	**3.89**
LDLA - 5cM	4.18	4.38	4.62	4.87	4.42	**4.49**
LDLA - 2cM	4.26	4.46	4.61	4.94	4.50	**4.55**
LDLA – 1-marker [a]	5.64	5.64	5.64	5.64	5.64	**5.64**
Flint						
Connected	3.43	3.65	4.15	4.37	3.83	**3.89**
LDLA - 5cM	4.07	4.20	4.84	5.13	4.53	**4.55**
LDLA - 2cM	4.30	4.36	5.04	5.23	4.60	**4.71**
LDLA – 1-marker [a]	5.61	5.61	5.61	5.61	5.61	**5.61**
Joint						
Connected	3.49	3.94	4.02	4.85	3.74	**4.00**

[a] The threshold value for the LDLA – 1-marker corresponded to a Bonferroni threshold for a genome-wide risk of 10 %. The other thresholds were calculated using 5,000 intra-family permutations of the phenotypes for a type I risk of 10 % across all families and the total genome.

Table S3 Results of the QTL detection in the flint design using the connected model. For each detected QTL, we showed its genetic position on the flint consensus map, its confidence interval, its level of significance and the partial percentage of variance explained. We also showed the name of one of the markers located at the detected position and their range of physical position(s) on the B73 v2 genome (Gore et al. 2009).

Trait	Nb	Chr	Marker	Physical position (kb)	Genetic position (cM)	Confidence interval	-log10(p)	R² (%)
DMC (%)	1	1	PZE_101172677	216581	148.3	142-149	5.4	3.2
	2	2	PZE_102191415	234096	177.2	176-181	6.6	3.6
	3	3	PZE_103033917	26445 - 138643	53.1	53-58	5.1	3
	4	4	PZE_104021549	18916 - 23142	50.3	49-55	6.7	3.7
	5	5	PZE_105085637	107137 - 138073	80.4	79-84	9.8	4.9
	6	5	PZE_105150268	201762	133	129-138	5.3	3.1
	7	8	PZE_108060399	107884 - 113068	64	50-65	7.4	4
	8	10	PZE_110049849	93025 - 115573	46	46-49	59.6	26.5
DMY (dt.ha-1)	1	1	PZE_101038989	25879 - 26917	52.5	52-54	7.4	3.8
	2	1	PZE_101147651	191513	118.9	117-120	14.4	6.4
	3	2	PZE_102152279	198891	129.6	127-141	8.5	4.2
	4	3	PZE_103137887	191279 - 196563	100.1	96-101	12.4	5.7
	5	4	PZE_104021283	22836	54.9	54-57	12.1	5.6
	6	4	PZE_104152609	237454 - 237702	153.3	127-154	4.5	2.7
	7	5	PZE_105078335	88752 - 139163	82.1	81-85	8.1	4.1
	8	6	PZE_106097864	151579	83.5	82-84	9.5	4.6
	9	7	PZE_107127708	170248	126.7	123-131	5.5	3.1
	10	8	PZE_108105216	159953	94.1	92-111	6	3.2
	11	10	PZE_110047350	88553 - 97551	44.6	44-45	34.2	14.2
DtSILK (d)	1	1	PZE_101005818	4452	10.3	9-12	6.9	2.2
	2	1	PZE_101143233	184616	113.9	101-115	26.3	6.7
	3	1	PZE_101181658	226175	153.1	148 -198	4.6	1.6
	4	2	PZE_102129781	178613 - 179981	102.1	101-162	5.4	1.8
	5	3	PZE_103121610	69965 - 179545	79.5	61-80	6.8	2.1
	6	4	PZE_104027603	23555 - 38027	55.1	52-57	31.8	8
	7	5	PZE_105033399	17477 - 18623	59.8	54-60	6.7	2.1
	8	5	PZE_105093579	135624 - 150088	84.2	80-86	7.3	2.2
	9	5	PZE_105163109	204822 - 205566	138.6	132-140	5.3	1.8
	10	6	PZE_106049962	99771	33.4	27-42	8	2.4
	11	7	PZE_107130719	171824	131.5	125-133	5.6	1.9
	12	8	PZE_108067425	119151	68.4	65-91	5.3	1.8
	13	8	PZE_108135936	175699 - 175734	139.7	117-140	6.1	2
	14	9	PZE_109009942	11080 - 11080	31.3	31-32	13	3.5

	15	10	PZE_110049100	91959 - 127347	49.7	49-50	94.6	27.5
DtTAS (d)	1	1	PZE_101005766	4609	10.8	9-13	6.8	2.5
	2	1	PZE_101108474	115220 - 161708	103	100-103	31.7	9
	3	1	PZE_101198020	246399 - 250557	173.3	164-175	6.2	2.3
	4	3	PZE_103098655	158895	67.4	67-68	9	3
	5	3	PZE_103153521	206703	114.1	110-115	8.5	2.9
	6	4	PZE_104025625	30431 - 37023	57	52-57	27.6	7.9
	7	5	PZE_105068746	71898 - 87721	78.6	78-79	21.6	6.3
	8	6	PZE_106061581	111966 - 112514	47.3	46-49	8.5	2.9
	9	7	PZE_107127708	170248	126.7	124-130	8.5	2.9
	10	8	PZE_108066752	118422 - 119082	68.3	68-69	15	4.6
	11	9	PZE_109007521	8233	23.3	23-38	7.6	2.6
	12	10	PZE_110048157	90243 - 122268	48.7	46-49	62.7	18.6
PH (cm)	1	1	PZE_101127891	162428 - 178788	108.7	108-109	12.7	5.4
	2	2	PZE_102074552	39031 - 55241	78	18-85	9	4.1
	3	2	PZE_102169535	213168	143.9	140-145	6.9	3.3
	4	4	PZE_104022475	23556 - 24765	57.2	55-60	12	5.1
	5	5	PZE_105151348	202416	134.5	132-136	6.4	3.2
	6	7	PZE_107061937	118305	58.2	53-62	4.9	2.6
	7	7	PZE_107128331	170536	128.5	121-129	7.2	3.4
	8	8	PZE_108098736	155052	87.2	87-92	17.8	7.1
	9	10	PZE_110048157	90243 - 122268	48.7	46-49	55.4	21.7

Table S4 Results of the QTL detection in the flint design using the LDLA – 5 cM model. For each detected QTL, we showed its genetic position on the flint consensus map, its confidence interval, its level of significance and the partial percentage of variance explained. We also showed the name of one of the markers located at the detected position and their range of physical position(s) on the B73 v2 genome (Gore et al. 2009).

Trait	Nb	Chr	Marker	Physical position (kb)	Genetic position (cM)	-log10(p)	R² (%)
DMC (%)	1	1	PZE_101147104	190602	119.4	7.3	2.9
	2	1	PZE_101250881	295590	225.9	5.6	2.2
	3	2	PZE_102025627	11947	39.2	7	1.8
	4	2	PZE_102046822	24366	63.7	7.3	3.4
	5	2	PZE_102183284	225854	157.9	8	3
	6	4	PZE_104021283	22836	54.9	11.2	4.8
	7	5	PZE_105085637	107137 - 138073	80.4	10.2	4.3
	8	5	PZE_105165365	208891 - 209048	148.7	5.2	1.6
	9	6	PZE_106076029	131411 - 134098	64.2	4.9	2.3
	10	8	PZE_108018911	18447	43.1	7.5	2.9
	11	10	PZE_110049849	93025 - 115573	46	70.2	29.2
DMY (dt.ha^{-1})	1	1	PZE_101147651	191513	118.9	13.3	5.7
	2	1	PZE_101213494	263732	185.2	5.7	2.6
	3	3	PZE_103098382	158668 - 159808	66.8	7.9	4.1
	4	4	PZE_104020618	21905	55	13.5	6.3
	5	4	PZE_104123129	200190	129.8	5.3	2.9
	6	5	PZE_105068572	71700 - 72614	75.9	6.9	3.7
	7	6	PZE_106107736	156986	95.6	4.3	1.2
	8	7	PZE_107128866	170819	127.8	10	3.5
	9	8	PZE_108029326	27221 - 66473	50.1	6.6	3.4
	10	10	PZE_110045930	86778 - 109582	46.3	31.3	14.3
DtSILK (d)	1	1	PZE_101005818	4452	10.3	5.2	1.2
	2	1	PZE_101146834	190143	119.1	34.3	8.1
	3	1	PZE_101199192	248322	171.8	15	3.9
	4	2	PZE_102179704	222468	154.6	10.1	2.4
	5	3	PZE_103098382	158668 - 159808	66.8	8.2	2.4
	6	3	PZE_103121610	69965 - 179545	79.5	7.8	2
	7	4	PZE_104062511	44504 - 124929	62.6	31.7	8.1
	8	5	PZE_105078445	86146 - 140781	80.7	18.6	4.7
	9	5	PZE_105153835	204326 - 205504	137.6	10.9	2.4
	10	7	PZE_107133704	173181	139.3	7.6	1.6
	11	8	PZE_108066557	118189	68.7	7.4	1.9
	12	8	PZE_108133033	173617	133.8	6.6	1.1
	13	9	PZE_109009936	11079	31.6	11.6	2.8

	14	10	PZE_110048157	90243 - 122268	48.7	98.7	29.1
DtTAS (d)	1	1	PZE_101005765	4609	10	6.5	1.8
	1	1	PZE_101109004	116312 - 158005	105.3	7.3	2.5
	2	1	PZE_101147104	190602	119.4	6.9	2.2
	3	1	PZE_101213102	263154	185.3	9	2.7
	4	3	PZE_103098655	158895	67.4	8.9	2.7
	5	3	PZE_103158635	210426	116.9	7.7	2.2
	6	4	PZE_104044703	33362 - 96313	60.7	21.6	6.8
	7	5	PZE_105066936	69125 - 83278	77.8	21.9	6.5
	8	7	PZE_107136925	174718	144.3	5.7	1.3
	9	8	PZE_108019174	18351	42.8	6.8	2
	10	8	PZE_108073574	128549 - 128753	75.2	13.4	3.9
	11	9	PZE_109009220	10008 - 10009	28.4	9.5	2.4
	12	10	PZE_110048157	90243 - 122268	48.7	58.1	18.3
	13	1	PZE_101005765	4609	10	6.5	1.8
PH (cm)	1	1	PZE_101146427	189406	118.5	14.7	5.2
	2	2	PZE_102074552	39031 - 55241	78	9.3	3.8
	3	2	PZE_102173058	216192	146.8	7.4	2.9
	4	4	PZE_104045760	68246 - 68323	58.7	10.6	4.4
	5	4	PZE_104103602	179801 - 180054	102.8	6.6	2.4
	6	5	PZE_105150122	201632	128.7	8.7	2.7
	7	7	PZE_107128144	170420 - 170496	126.6	11.2	3.2
	8	8	PZE_108092331	149305 - 155644	87.8	20.5	7.8
	9	9	PZE_109008703	9311	25.5	4.8	1.3
	10	10	PZE_110049849	93025 - 115573	46	56.8	21.7

TableS5 Results of the QTL detection in the flint design using the LDLA – 2 cM model. For each detected QTL, we showed its genetic position on the flint consensus map, its confidence interval, its level of significance and the partial percentage of variance explained. We also showed the name of one of the markers located at the detected position and their range of physical position(s) on the B73 v2 genome (Gore et al. 2009).

Trait	Nb	Chr	Marker	Physical position (kb)	Genetic position (cM)	-log10(p)	R^2 (%)
DMC (%)	1	1	PZE_101146598	189773	118	6.2	2.5
	2	2	PZE_102185359	229130 - 229288	165	5	1.7
	3	4	PZE_104018885	18916 - 23142	50.3	6.9	3.4
	4	5	PZE_105085637	107137 - 138073	80.4	9.1	4.6
	5	5	PZE_105163718	208374	149.2	4.5	1.9
	6	8	PZE_108063241	113068 - 113206	64.1	6.5	3.2
	7	10	PZE_110049849	93025 - 115573	46	46.5	20.8
	8	10	PZE_110089009	139036	69.9	5	1.4
DMY (dt.ha^{-1})	1	1	PZE_101146427	189406	118.5	14.9	5.3
	2	2	PZE_102172077	215135	144.9	6.9	2.5
	3	3	PZE_103097999	157939	65.4	6	1.9
	4	3	PZE_103142979	198520 - 198581	101.6	4.7	2.5
	5	4	PZE_104023433	26403 - 26403	52.7	15.8	5.8
	6	4	PZE_104122410	199546 - 199546	126.5	5.4	2.6
	7	5	PZE_105092759	133339 - 159961	84.4	7.4	3.7
	8	6	PZE_106050624	100745 - 103709	35.4	4.6	2.2
	9	6	PZE_106103665	155178	90.5	7.8	3.4
	10	7	PZE_107128846	170819	128.9	9	2.9
	11	8	PZE_108027746	26074 - 29164	49.5	6.7	3.4
	12	10	PZE_110047350	88553 - 97551	44.6	31.7	13.4
DtSILK (d)	1	1	PZE_101005818	4452	10.3	5.6	1.4
	2	1	PZE_101147104	190602	119.4	33.6	9.2
	3	1	PZE_101199859	248854 - 249092	173.9	14.2	4.1
	4	2	PZE_102181292	222435 - 223721	156.5	6.3	1.6
	5	3	PZE_103118006	176570	78.5	10.9	3
	6	3	PZE_103167997	216529	126.6	9.2	1.9
	7	4	PZE_104044892	42641 - 134020	62.5	29.6	8.8
	8	5	PZE_105039522	24542	63.6	18	5.4
	9	8	PZE_108133033	173617	133.8	9.2	2.1
	10	9	PZE_109010021	11134	30.1	11.9	2.9
	11	10	PZE_110060375	114622 - 114653	48.6	89.7	29.6
DtTAS(d)	1	1	PZE_101005770	4610	10.5	5.3	1.5
	2	1	PZE_101109004	116312 - 158005	105.3	16	4.7
	3	1	PZE_101147248	190703	121.1	6.4	1.7
	4	1	PZE_101213479	263702 - 265655	186.8	8.9	2.3

	5	3	PZE_103109418	170117 - 171781	75.9	9.3	2.1
	6	3	PZE_103157683	209726	116.3	8	2.1
	7	4	PZE_104044703	33362 - 96313	60.7	24	7.2
	8	5	PZE_105063310	62822 - 82069	76	24	7.1
	9	6	PZE_106064975	117082 - 122646	56.3	6.9	2.2
	10	7	PZE_107128144	170420 - 170496	126.6	6.1	1.4
	11	8	PZE_108019174	18351	42.8	6.8	1.9
	12	8	PZE_108073574	128549 - 128753	75.2	16.7	4.5
	13	9	PZE_109009220	10008 - 10009	28.4	11.2	2.5
	14	10	PZE_110049001	89438 - 108230	47.2	61.8	18.8
PH (cm)	1	1	PZE_101144184	187342 - 187381	118.6	14.2	4.6
	2	2	PZE_102076936	51554 - 59013	83	9.1	3.7
	3	2	PZE_102175167	217650	147.7	8	2.7
	4	4	PZE_104028514	34558 - 80248	60.2	11.3	4.8
	5	4	PZE_104104676	180887	105.6	6.2	1.5
	6	5	PZE_105144284	198198	130.3	7.5	1.9
	7	7	PZE_107057864	111123 - 112763	55.4	6	2.2
	8	7	PZE_107128144	170420 - 170496	126.6	9.7	2.8
	9	8	PZE_108092331	149305 - 155644	87.8	18.3	6.6
	10	9	PZE_109008133	8741	25.8	5.2	1.5
	11	10	PZE_110049849	93025 - 115573	46	56	21.3

Table S6 Results of the QTL detection in the flint design using the LDLA – 1-marker model. For each detected QTL, we showed its genetic position on the flint consensus map, its confidence interval, its level of significance and the partial percentage of variance explained. We also showed the name of one of the markers located at the detected position and their range of physical position(s) on the B73 v2 genome (Gore et al. 2009).

Trait	Nb	Chr	Marker	Physical position (kb)	Genetic position (cM)	-log10(p)	R^2 (%)
DMC (%)	1	2	PZE_102185353	229130	164.2	5.7	1.7
	2	4	PZE_104033064	40693	60	6.7	2.1
	3	5	PZE_105079359	90584	80.6	11.5	3.9
	4	5	PZE_105143697	197846	126.4	5.7	1.7
	5	8	PZE_108063319	113212	63.6	7.2	2.3
	6	10	PZE_110050010	94199	45.9	44.3	18.0
	7	10	PZE_110086343	137505	68.9	6.3	1.9
DMY (dt.ha^{-1})	1	1	PZE_101128881	164375	105.8	6.3	1.8
	2	1	PZE_101144216	187381	118.6	15.6	5.2
	3	3	PZE_103097999	157939	65.4	10.3	3.3
	4	4	PZE_104017088	17150	48.7	11.4	3.7
	5	4	PZE_104021665	23190	51.4	5.8	1.7
	6	4	PZE_104122007	198999	124	6.0	1.7
	7	5	PZE_105094114	137392	81.5	9.7	3.1
	8	6	PZE_106104239	155466	90.7	7.8	2.4
	9	7	PZE_107128846	170819	128.9	8.2	2.5
	10	8	PZE_108028156	29898	51.1	9.1	2.9
	11	10	PZE_110050010	94199	45.9	33.0	12.2
DtSILK (d)	1	1	PZE_101004387	3883	8.5	8.2	1.5
	2	1	PZE_101088198	79735	90.5	10.0	1.9
	3	1	PZE_101106156	109635	102.4	17.1	3.6
	4	1	PZE_101151084	194731	125.8	9.4	1.8
	5	1	PZE_101200614	249700	173.1	11.3	2.2
	6	3	PZE_103098779	158974	61.9	11.3	2.2
	7	4	PZE_104021514	23073	51	9.0	1.7
	8	4	PZE_104079162	153502	69	10.8	2.1
	9	4	PZE_104152590	237693	155.7	6.4	1.1
	10	5	PZE_105069912	74335	76.8	21.1	4.6
	11	5	PZE_105143119	197706	127.6	5.7	1.0
	12	7	PZE_107128331	170536	128.5	6.5	1.2
	13	8	PZE_108070056	122950	71	12.0	2.4
	14	9	PZE_109009591	10597	30.3	7.1	1.3
	15	10	PZE_110016138	16504	38.6	11.2	2.2
	16	10	PZE_110050010	94199	45.9	45.7	11.1
DtTAS(d)	1	1	PZE_101004387	3883	8.5	6.1	1.2

	2	1	PZE_101115961	138907	103.5	14.5	3.3
	3	1	PZE_101144216	187381	118.6	23.2	5.6
	4	1	PZE_101160171	202307	128	6.7	1.3
	5	1	PZE_101200614	249700	173.1	8.5	1.8
	6	3	PZE_103007349	4064	11.7	8.6	1.8
	7	3	PZE_103098779	158974	61.9	14.0	3.2
	8	4	PZE_104021514	23073	51	9.7	2.1
	9	4	PZE_104079162	153502	69	10.0	2.1
	10	5	PZE_105069912	74335	76.8	24.7	6.0
	11	6	PZE_106066817	119166	57.4	5.5	1.0
	12	8	PZE_108067255	118970	68.8	5.8	1.1
	13	8	PZE_108074213	129415	75.5	10.3	2.2
	14	9	PZE_109111133	151251	109.1	6.5	1.3
	15	10	PZE_110018448	22128	38.9	8.9	1.9
	16	10	PZE_110050010	94199	45.9	57.5	16.1
PH (cm)	1	1	PZE_101145493	188172	115.6	8.3	2.4
	2	2	PZE_102074558	55249	79.5	9.8	3.0
	3	4	PZE_104042538	60023	63.1	11.6	3.6
	4	5	PZE_105091638	129996	83.4	7.8	2.3
	5	5	PZE_105134752	195420	117.6	9.9	3.0
	6	6	PZE_106097959	151785	84.1	6.1	1.7
	7	7	PZE_107127637	170111	126.3	7.4	2.1
	8	8	PZE_108105216	159953	94.1	16.6	5.3
	9	10	PZE_110050010	94199	45.9	53.9	20.6

Table S7 Results of the QTL detection in the dent design using the connected model. For each detected QTL, we showed its genetic position on the dent consensus map, its confidence interval, its level of significance and the partial percentage of variance explained. We also showed the name of one of the markers located at the detected position and their range of physical position(s) on the B73 v2 genome (Gore et al. 2009).

Trait	Nb	Chr	Marker	Physical position (kb)	Genetic position (cM)	Confidence interval	-log10(p)	R² (%)
DMC (%)	1	1	PZE_101031077	19101	35.2	32-39	11.7	4.8
	2	2	PZE_102011868	5425	17.1	16-18	13.4	5.3
	3	2	PZE_102149235	195177 - 197936	94.4	88-100	5.4	2.6
	4	3	PZE_103091082	150173 - 165855	63.5	58-64	16.8	6.5
	5	4	PZE_104079076	153406	59	57-61	10	4.2
	6	5	PZE_105026024	13303 - 13313	42.8	42-45	10.6	4.4
	7	6	PZE_106002839	3588 - 3869	2.9	1-6	10.4	4.3
	8	6	PZE_106098045	151822	75.1	72-79	9.6	4.1
	9	8	PZE_108058161	103705 - 103897	51.3	51-58	18	6.9
	10	9	PZE_109009836	10943	29.3	27-30	6	2.8
	11	9	PZE_109096235	141951	74.4	70-76	6.8	3.1
	12	10	PZE_110048796	91481 - 107902	46.4	27-53	5.7	2.7
DMY (dt.ha-1)	1	1	PZE_101071870	54342	59.2	57-62	5.7	3.8
	2	1	PZE_101215677	266310 - 266369	144.6	123-160	5.5	3.7
	3	3	PZE_103108908	169730 - 172477	70.8	66-76	5.5	3.7
	4	3	PZE_103160673	211719 - 212707	116.2	115-129	6.2	4
	5	3	PZE_103185177	229665	147.3	146-148	6.3	4.1
	6	6	PZE_106038467	86549	16.8	9-20	14.9	8
	7	7	PZE_107066645	123598 - 126465	58.2	57-61	11.7	6.6
	8	8	PZE_108057442	102536 - 108663	52.9	52-53	14.2	7.7
DtSILK (d)	1	1	PZE_101033622	21685	38.5	32-39	11.6	4.7
	2	1	PZE_101081841	69289 - 70518	66.2	65-67	4.6	2.3
	3	1	PZE_101194503	241368 - 244469	129.1	128-133	6.6	3
	4	2	PZE_102148927	195747 - 196529	93.9	93-96	9.1	3.8
	5	3	PZE_103110415	170772 - 174828	72	65-72	15.9	6.1
	6	3	PZE_103147207	201536 - 202769	103.4	101-110	5.5	2.6
	7	6	PZE_106095147	150309	72.4	70-74	13	5.1
	8	7	PZE_107072681	129265	63.2	43-67	8.4	3.6
	9	8	PZE_108057885	103311	50.4	50-54	26.4	9.6
	10	9	PZE_109020361	18684 - 20598	42.9	38-45	5	2.5
	11	10	PZE_110057591	110540 - 120784	49.8	49-52	7.2	3.2
DtTAS (d)	1	1	PZE_101033622	21685	38.5	36-39	10.8	5.4
	2	2	PZE_102157405	204235	99.8	99-100	6	3.4

	3	3	PZE_103101981	162179 - 167076	63.7	61-65	23.2	10.4
	4	5	PZE_105144068	198031	91.6	91-96	7.3	3.9
	5	7	PZE_107076807	132075	67.1	48-68	13.7	6.5
	6	8	PZE_108058411	104281 - 104625	53.7	50-55	19.4	8.8
	7	9	PZE_109092637	139196 - 140154	71.3	56-74	7.1	3.9
PH (cm)	1	1	PZE_101018818	10905	23.7	21-24	7.5	3
	2	1	PZE_101133561	172881 - 172940	81.5	80-84	13.2	4.7
	3	1	PZE_101196829	245032 - 245219	131	127-133	17.9	6.1
	4	3	PZE_103110278	170548	71.8	69-73	8.1	3.2
	5	4	PZE_104073340	138154 - 144727	55.2	53-58	6.9	2.8
	6	5	PZE_105065019	66038 - 79496	59.4	58-60	7.1	2.9
	7	6	PZE_106040994	89408 - 91643	19.9	19-20	27.7	9.1
	8	7	PZE_107005418	3665 - 3667	12.3	2-16	5.1	2.2
	9	7	PZE_107080996	135892	71.4	71-72	17.6	6
	10	8	PZE_108056028	100939 - 102711	49.7	49-52	23.3	7.7
	11	8	PZE_108078317	130737 - 134065	68.8	68-69	14.9	5.2
	12	9	PZE_109025803	25986	49.1	48-50	4	1.9
	13	9	PZE_109086708	134570 - 135460	67.8	67-70	7.8	3.1
	14	10	PZE_110008028	6072	22.6	22-26	12.2	4.4

Table S8 Results of the QTL detection in the dent design using the LDLA – 5 cM model. For each detected QTL, we showed its genetic position on the dent consensus map, its confidence interval, its level of significance and the partial percentage of variance explained. We also showed the name of one of the markers located at the detected position and their range of physical position(s) on the B73 v2 genome (Gore et al. 2009).

Trait	Nb	Chr	Marker	Physical position (kb)	Genetic position (cM)	-log10(p)	R^2 (%)
DMC (%)	1	1	PZE_101028121	16789 - 17963	31.6	11	3.9
	2	1	PZE_101150204	193868 - 194764	92	4.9	2
	3	1	PZE_101202934	249700 - 251159	134.9	7.9	3.1
	4	2	PZE_102006385	3379	9.6	6.4	1.5
	5	2	PZE_102150016	196649	94	8.9	2.9
	6	3	PZE_103038564	33572 - 56014	46	17.6	6.4
	7	3	PZE_103151042	204999	105	5.4	2.3
	8	4	PZE_104081311	155805	59.6	10.2	4
	9	5	PZE_105047074	35783 - 36699	52.3	12.4	4.9
	10	6	PZE_106007445	18846 - 21466	9.9	11.7	4.3
	11	6	PZE_106096901	150891	71.7	12.7	4.6
	12	7	PZE_107040665	154074	66.8	3.6	1.7
	13	8	PZE_108057885	103311	50.4	19.1	6.1
	14	9	PZE_109089324	137410	68.6	9	3.5
	15	10	PZE_110012467	10879	31.8	7.7	2.2
DMY ($dt.ha^{-1}$)	1	3	PZE_103116584	175989	78.9	8	3.9
	2	3	PZE_103162977	213416	117.8	7.8	4.3
	3	6	PZE_106038467	86549	16.8	13.8	8.1
	4	7	PZE_107066645	123598 - 126465	58.2	8.8	5.6
	5	8	PZE_108057442	102536 - 108663	52.9	10.3	5.8
DtSILK (d)	1	1	PZE_101033622	21685	38.5	22.6	7.2
	2	1	PZE_101205734	251079 - 254464	136.4	6.7	2.4
	3	2	PZE_102152020	198672	94.5	15	4.5
	4	3	PZE_103086165	142732 - 157202	61.7	10	3.6
	5	3	PZE_103122617	180515	78.6	16.3	4.7
	6	5	PZE_105049624	41635 - 58706	56.3	4.8	2.2
	7	6	PZE_106094705	149930	71	16.5	5.4
	8	7	PZE_107045046	25471 - 104886	43.9	7.4	3
	9	7	PZE_107107125	158951 - 158952	82.1	5.8	2
	10	8	PZE_108058411	104281 - 104625	53.7	27.7	8.9
	11	9	PZE_109098496	143352	77.3	5.5	2
	12	10	PZE_110057591	110540 - 120784	49.8	8	3.1
DtTAS(d)	1	1	PZE_101032015	19641 - 21075	35.7	13.2	4.8
	2	2	PZE_102159907	206081 - 207151	102.9	7.1	2.8
	3	3	PZE_103098157	158352	60.8	21	7.6

	4	3	PZE_103143600	199245 - 201331	102.2	8	3.1
	5	5	PZE_105143985	197957 - 200116	95.6	5.1	2
	6	6	PZE_106033981	79499 - 86347	16	6.1	2.7
	7	6	PZE_106092387	148530 - 150461	72	6	2.5
	8	7	PZE_107045046	25471 - 104886	43.9	7.6	3.4
	9	7	PZE_107099124	152685 - 155704	79.9	6.1	2.7
	10	8	PZE_108062375	111291	54.3	23.6	8.3
	11	9	PZE_109094832	141175	73.4	11.1	3.9
PH (cm)	1	1	PZE_101018868	10962	21.4	5.5	2.1
	2	1	PZE_101133356	172811	81.4	12.9	4.4
	3	1	PZE_101196829	245032 - 245219	131	17.9	6.1
	4	3	PZE_103111112	171438 - 175550	75.5	10.8	3.9
	5	4	PZE_104073340	138154 - 144727	55.2	4.9	2
	6	4	PZE_104136077	202589 - 227111	109.7	7.4	2.6
	7	5	PZE_105068432	70082 - 86033	60.4	6.1	2.7
	8	6	PZE_106040975	89403 - 89404	19.3	28.4	9.3
	9	7	PZE_107076796	132076	65.4	19	6.3
	10	8	PZE_108056028	100939 - 102711	49.7	25.7	8.2
	11	8	PZE_108079422	133563 - 138524	71.4	11.7	4.1
	12	9	PZE_109085253	133933	68.1	21.3	7.2
	13	10	PZE_110014332	11179 - 13553	33.8	11	3.3

Table S9 Results of the QTL detection in the dent design using the LDLA – 2 cM model. For each detected QTL, we showed its genetic position on the dent consensus map, its confidence interval, its level of significance and the partial percentage of variance explained. We also showed the name of one of the markers located at the detected position and their range of physical position(s) on the B73 v2 genome (Gore et al. 2009).

Trait	Nb	Chr	Marker	Physical position (kb)	Genetic position (cM)	-log10(p)	R^2 (%)
DMC (%)	1	1	PZE_101036345	23712	38	12.4	4
	2	1	PZE_101154088	194939 - 197272	93.9	6.2	2.3
	3	1	PZE_101203104	250888	131.9	7.1	2.8
	4	2	PZE_102002360	1724	4.7	8.5	2
	5	2	PZE_102017964	8279	23.4	7.7	2.2
	6	2	PZE_102152020	198672	94.5	8.5	3
	7	3	PZE_103093079	154090 - 160936	63.9	16.7	5.4
	8	3	PZE_103148259	202185	104.1	5.4	2
	9	4	PZE_104076988	151510 - 151684	56.9	10.3	3.5
	10	5	PZE_105047074	35783 - 36699	52.3	13.3	4.9
	11	6	PZE_106020123	14400 - 24611	10	14.3	4.4
	12	6	PZE_106097959	151785	73.1	14.1	4.3
	13	7	PZE_107045895	24563 - 103626	43.6	5.8	2.4
	14	8	PZE_108061901	110744 - 115294	57.2	19.7	6.4
	15	9	PZE_109091148	138616 - 138617	69.6	12.7	4.2
	16	10	PZE_110012769	11241	33	8.2	2.2
DMY ($dt.ha^{-1}$)	1	1	PZE_101183895	228556	119.6	4.8	2.3
	2	3	PZE_103113115	172857 - 178134	78.3	8.4	4
	3	3	PZE_103159262	210755 - 210760	114.6	7.8	3.7
	4	6	PZE_106032535	75517 - 86627	15.5	13.3	6.9
	5	7	PZE_107069530	126351	58.1	9.3	5
	6	8	PZE_108057745	103023 - 103457	53	10.5	5.8
DtSILK (d)	1	1	PZE_101035008	19696 - 22646	37.8	22	6.9
	2	1	PZE_101205734	251079 - 254464	136.4	7.4	2.2
	3	2	PZE_102151348	197954	94.7	12.9	4.1
	4	3	PZE_103086165	142732 - 157202	61.7	10.2	3.7
	5	3	PZE_103122617	180515	78.6	16.3	4.7
	6	5	PZE_105049624	41635 - 58706	56.3	4.9	2.3
	7	6	PZE_106095370	150525 - 150588	72.6	17.5	5.1
	8	7	PZE_107045046	25471 - 104886	43.9	8.7	3.3
	9	7	PZE_107106025	158126	81.1	6.1	2
	10	8	PZE_108062521	111781	54.6	28.2	8.9
	11	9	PZE_109098632	143808	78.5	6.1	2.1
	12	10	PZE_110057591	110540 - 120784	49.8	7.8	3
DtTAS(d)	1	1	PZE_101032015	19641 - 21075	35.7	12.9	5

	2	2	PZE_102161022	207043	102.3	6.5	2.6
	3	3	PZE_103098157	158352	60.8	21.2	8.3
	4	3	PZE_103143600	199245 - 201331	102.2	7.8	3.2
	5	5	PZE_105143697	197846 - 200369	95.5	5	2.2
	6	7	PZE_107045046	25471 - 104886	43.9	6.1	2.9
	7	7	PZE_107099124	152685 - 155704	79.9	6	2.9
	8	8	PZE_108058411	104281 - 104625	53.7	20	7.6
	9	9	PZE_109090152	137787 - 138020	70.1	9.2	3.7
PH (cm)	1	1	PZE_101132703	171230 - 178401	82.3	10.6	4.1
	2	1	PZE_101196829	245032 - 245219	131	15.9	6
	3	3	PZE_103119393	178152 - 178564	79.1	8.9	2.8
	4	4	PZE_104073794	145614	55.7	6.4	2.5
	5	4	PZE_104138654	204861 - 226068	109.4	6.2	2.5
	6	5	PZE_105070660	74660 - 145496	61.9	5.2	2.5
	7	6	PZE_106044620	93734	20.4	20.4	6.4
	8	7	PZE_107077092	132190	66.5	19.9	6.5
	9	8	PZE_108038271	26346 - 65101	43.6	22.4	8.1
	10	8	PZE_108081297	133441 - 143002	71.9	8.6	3.3
	11	9	PZE_109085253	133933	68.1	14.6	5.4
	12	10	PZE_110013838	12922	35.9	10.4	4.2

Table S10 Results of the QTL detection in the dent design using the LDLA – 1-marker model. For each detected QTL, we showed its genetic position on the dent consensus map, its confidence interval, its level of significance and the partial percentage of variance explained. We also showed the name of one of the markers located at the detected position and their range of physical position(s) on the B73 v2 genome (Gore et al. 2009).

Trait	Nb	Chr	Marker	Physical position (kb)	Genetic position (cM)	-log10(p)	R² (%)
DMC (%)	1	1	PZE_101043094	29355	43.3	8.5	2.6
	2	2	PZE_102015152	6459	20.9	15.3	5.1
	3	2	PZE_102150016	196649	94	6.9	2.0
	4	3	PZE_103038375	33073	45.8	14.2	4.7
	5	4	PZE_104077580	151818	57	8.5	2.6
	6	5	PZE_105043990	31444	54.4	9.7	3.0
	7	6	PZE_106020569	16293	9.3	6.4	1.9
	8	6	PZE_106092387	148530	72	6.3	1.8
	9	8	PZE_108054499	97030	50.2	9.8	3.1
	10	8	PZE_108104357	159498	81.9	5.6	1.6
	11	9	PZE_109098884	143900	78.9	9.8	3.1
	12	10	PZE_110073412	130077	53.5	8.5	2.6
DMY (dt.ha^{-1})	1	3	PZE_103115334	175353	78.1	9.0	3.6
	2	3	PZE_103162977	213416	117.8	9.0	3.7
	3	6	PZE_106031833	74460	14.6	14.0	6.0
	4	7	PZE_107026145	29198	41.6	7.7	3.0
	5	8	PZE_108054494	97029	50.5	10.4	4.3
DtSILK (d)	1	1	PZE_101032230	19696	37.8	8.8	2.4
	2	1	PZE_101076734	60701	61	11.4	3.3
	3	2	PZE_102150016	196649	94	8.9	2.5
	4	3	PZE_103104448	165863	71.3	15.7	4.7
	5	3	PZE_103132614	188530	91.1	8.1	2.2
	6	5	PZE_105054634	51432	55.4	6.4	1.7
	7	6	PZE_106092387	148530	72	13.8	4.1
	8	7	PZE_107023943	25471	43.9	13.0	3.8
	9	8	PZE_108026961	27634	45.5	5.7	1.5
	10	8	PZE_108063387	113292	57.3	10.1	2.9
	11	10	PZE_110062675	117753	50.1	6.9	1.8
DtTAS(d)	1	1	PZE_101035341	23055	39.2	13.3	4.6
	2	3	PZE_103104448	165863	71.3	26.8	10.1
	3	6	PZE_106092387	148530	72	5.8	1.8
	4	7	PZE_107061937	118305	50.8	6.8	2.1
	5	7	PZE_107100713	155251	79.6	6.7	2.1
	6	8	PZE_108057325	102454	51.5	22.5	8.3
	7	9	PZE_109071914	116752	59.8	7.3	2.3

PH (cm)	1	1	PZE_101132469	170852	80.9	6.5	1.9
	2	1	PZE_101191970	238427	127.1	8.4	2.6
	3	2	PZE_102068532	46438	61.8	6.8	2.0
	4	3	PZE_103104448	165863	71.3	6.0	1.7
	5	4	PZE_104082879	156995	61.4	6.0	1.7
	6	6	PZE_106040890	89137	19.4	19.4	6.7
	7	7	PZE_107084200	139526	76.4	15.9	5.4
	8	8	PZE_108014288	14088	32	15.9	5.4
	9	9	PZE_109080822	128851	65.9	18.5	6.4
	10	10	PZE_110009551	7563	29.4	6.3	1.8

Table S11 Results of the QTL detection in the joint analysis using the connected model. For each detected QTL, we showed its genetic position on the dent-flint consensus map, its confidence interval, its level of significance and the partial percentage of variance explained. We also showed the name of one of the markers located at the detected position and their range of physical position(s) on the B73 v2 genome (Gore et al. 2009).

Trait	Nb	Chr	Marker	Physical position (kb)	Genetic position (cM)	-log10(p)	R^2 (%)
DMC (%)	1	1	PZE_101032230	19696 - 19975	41.3	8.5	2.3
	2	1	PZE_101103995	104611 - 113689	93.3	5.2	1.7
	3	1	PZE_101202934	251103 - 251159	160.4	4.5	1.6
	4	1	PZE_101247063	292581	200.4	4.3	1.5
	5	2	PZE_102012595	5556	17.2	21.4	4.5
	6	2	PZE_102178263	220854	131.3	6.9	2
	7	3	PZE_103033638	26310 - 30050	45.4	9.3	2.5
	8	3	PZE_103100449	160755	65.5	7.5	2.1
	9	4	PZE_104032843	40344 - 65470	54.6	13.8	3.3
	10	4	PZE_104143137	231732	130.7	4.4	1.6
	11	5	PZE_105025123	12581	42.6	17.6	3.8
	12	6	PZE_106005094	6514	6.3	10.1	2.6
	13	6	PZE_106082658	139918 - 142454	66	11.8	2.9
	14	7	PZE_107012564	9201	33.9	4.7	1.6
	15	8	PZE_108063387	112547 - 113298	63.4	21.7	4.5
	16	9	PZE_109010670	11079 - 11504	30.8	3.9	1.5
	17	9	PZE_109096248	141983	82.5	5.4	1.7
	18	10	PZE_110047687	89209 - 111680	47.7	68.5	12.5
DMY (dt.ha-1)	1	1	PZE_101145302	188026 - 188087	109.4	12.2	3.6
	2	1	PZE_101215394	266047	170.9	10.4	3.2
	3	2	PZE_102013856	5997 - 6049	18.5	5.2	2.1
	4	2	PZE_102066516	44332	67.4	7.2	2.6
	5	3	PZE_103010658	5853	21.6	7.6	2.6
	6	3	PZE_103098655	158895 - 161562	65.7	9.5	3.1
	7	3	PZE_103162977	213416	120.4	5.3	2.1
	8	4	PZE_104025845	28986 - 32061	51.5	13.5	3.9
	9	5	PZE_105103128	155811 - 160460	78	8.8	2.9
	10	6	PZE_106037747	81440 - 86559	18.3	9.9	3.1
	11	6	PZE_106050075	99944	34	11.4	3.4
	12	6	PZE_106106971	156749	88.4	9.2	3
	13	7	PZE_107025551	28013 - 100690	44.8	8.3	2.8
	14	7	PZE_107127637	170111 - 170248	119.3	5.9	2.3
	15	8	PZE_108060398	107884 - 111781	62.1	12.1	3.6
	16	10	PZE_110043381	82670 - 84599	43.2	38.6	8.9
DtSILK (d)	1	1	PZE_101005770	4452 - 4610	9.4	6.4	1.8

	2	1	PZE_101034085	21984 - 21992	42.7	10	2.3
	3	1	PZE_101105390	102985 - 118116	93.6	19.2	3.7
	4	1	PZE_101195591	244158 - 244596	155.9	11.2	2.5
	5	2	PZE_102161485	206123 - 207224	123	13.3	2.8
	6	3	PZE_103098655	158895 - 161562	65.7	12.7	2.7
	7	3	PZE_103128597	185274 - 187610	93.2	9.1	2.2
	8	4	PZE_104025181	29345 - 30933	51.8	22.8	4.2
	9	5	PZE_105050638	42662 - 51518	61.2	16.8	3.3
	10	6	PZE_106097991	151792	77.3	11.7	2.6
	11	7	PZE_107072354	128648 - 128709	68.9	14.8	3.1
	12	8	PZE_108061059	107884 - 109378	60.7	27.9	5
	13	9	PZE_109010476	11398	30.3	11.4	2.5
	14	9	PZE_109094832	141175	82.6	5.1	1.6
	15	10	PZE_110047800	89438 - 106051	47.4	93	15.2
DtTAS(d)	1	1	PZE_101033489	21569 - 22464	43	12.1	2.5
	2	1	PZE_101140981	182104 - 184245	105	41.4	6.6
	3	1	PZE_101216412	267537 - 267568	171.5	12.3	2.5
	4	3	PZE_103098655	158895 - 161562	65.7	30.9	5.1
	5	3	PZE_103152007	205694	109.8	11.3	2.4
	6	4	PZE_104022348	23525 - 25988	49.6	25.7	4.4
	7	5	PZE_105059330	58137 - 72409	66	29.1	4.9
	8	5	PZE_105138874	193728	108.2	7.8	1.9
	9	6	PZE_106090469	147428	71.3	6.8	1.7
	10	7	PZE_107040665	66316 – 171898	75.4	13.6	2.7
	11	7	PZE_107130789	171926	126.3	6.2	1.6
	12	8	PZE_108018453	18973	42.2	11.8	2.4
	13	8	PZE_108070788	123843	69.2	20.3	3.6
	14	9	PZE_109020361	20598 - 20829	47.7	10.7	2.3
	15	9	PZE_109089874	137784	78	10.3	2.2
	16	9	PZE_109119196	153947	120.8	6.8	1.7
	17	10	PZE_110050293	94969 - 106961	47.5	77	12
PH (cm)	1	1	PZE_101021455	12363	29.3	5.1	1.4
	2	1	PZE_101106839	111278 - 150672	93.9	20.8	3.7
	3	1	PZE_101184213	229073	145.9	13.7	2.7
	4	2	PZE_102011812	5379	17.1	5.9	1.6
	5	2	PZE_102076989	59015 - 62213	74.2	20.2	3.6
	6	2	PZE_102169349	212884	128.1	9.6	2.1
	7	3	PZE_103017768	10455	33.7	8.1	1.9
	8	3	PZE_103132826	188571 - 188925	94.8	11.8	2.5
	9	3	PZE_103175533	221582 - 221583	135.2	7.1	1.8
	10	4	PZE_104022152	23948 - 24979	49.7	13.8	2.7
	11	4	PZE_104132688	215436 - 227111	120.7	9	2

12	5	PZE_105084182	101590 - 150275	73.1	9.6	2.1
13	5	PZE_105152260	203315	120.3	7.4	1.8
14	6	PZE_106049618	98629	30.4	21.2	3.8
15	7	PZE_107072030	128141 - 128146	66.4	18	3.3
16	7	PZE_107126258	168905	115.7	10.4	2.3
17	8	PZE_108009237	9875	25.6	7.3	1.8
18	8	PZE_108056704	101776 - 102656	57	8.1	1.9
19	8	PZE_108096469	152593 - 153140	85.5	17.3	3.2
20	9	PZE_109077113	124694 - 130885	70.9	19.7	3.6
21	10	PZE_110047799	89438 - 97551	46.6	77.4	12.2