

Table S29 Summary of QTL for canopy temperature. Summary of quantitative trait loci (QTL) identified from multi-environment, inclusive composite interval mapping (ME-ICIM) for canopy temperature in the TM-1×NM24016 recombinant inbred line (RIL) population under two irrigation regimes, water-limited (WL) and well-watered (WW), with an experiment-wise Type I error rate of 5%. Marker positions are reported as centimorgans (cM).

Year ^a	Days ^b	Irrigation Regime ^c	Chr. ^d	LG ^e	Left marker	Left marker position (cM)	Right marker	Right marker position (cM)	Max LOD(A) ^f	Ave. LOD(A) ^g	Max PVE(A) ^h	Ave. PVE(A) ⁱ	Max additive effect ^j	Ave. additive effect ^k
2	8	WL/WW	A01	1	DPL1673a	33.71	SNP0366	40.44	5.82	4.36	10.98	6.22	-0.47	-0.29
2	8	WL/WW	A05	74	SNP0029	0.00	SNP0159	24.03	14.36	7.04	16.96	8.47	0.46	0.33
2	7	WL/WW	A06	21	SNP0146	9.23	SNP0426	20.03	5.89	4.72	12.59	7.16	-0.57	-0.31
2	14	WL/WW	A07	24	DPL0790a	0.00	CIR238a	16.60	9.29	5.50	13.77	8.51	-0.47	-0.33
3	12	WL/WW	A08	29	C2-003a	0.00	SNP0471	16.44	6.77	4.53	15.17	7.59	-0.62	-0.34
3	6	WL/WW	A09	32	SNP0093	20.32	SNP0003	35.83	5.67	4.21	7.47	5.35	0.44	0.25
2	8	WL/WW	A12	45	SNP0264	0.00	SNP0136	22.20	5.51	4.15	8.20	5.26	0.44	0.28
2	7	WL/WW	A13	55	MUSS181a	37.24	SNP0036	54.82	6.36	4.40	10.10	6.43	0.45	0.32
2	14	WL/WW	D01	24	DPL0790a	0.00	CIR238a	16.60	9.29	5.50	13.77	8.51	-0.47	-0.33
2	3	WL/WW	D01	65	SNP0268	12.64	SNP0465	24.70	4.10	3.77	4.67	4.35	-0.26	-0.24
2	9	WL/WW	D04	96	SHIN-1547	0.00	SNP0285	15.80	13.00	6.45	14.67	7.98	-0.51	-0.33
2	4	WW	D06	22	SNP0044	6.75	SNP0086	21.39	5.48	4.55	11.62	8.18	-0.47	-0.34
3	14	WL/WW	D10	88	DPL1903	0.00	SNP0120	19.69	6.85	4.36	13.48	6.36	0.46	0.30
3	14	WL/WW	D12	54	SNP0331	0.00	SNP0425	18.47	12.10	6.48	14.77	8.59	-0.51	-0.29

a. Year, number of years in which quantitative trait loci (QTL) were detected, years are 2010-2012.

b. Days, number of days across years on which data were collected, total of 19 unique days.

c. Irrigation regime, irrigation regime in which the QTL was identified.

d. Chr., chromosome on which marker is located.

e. LG, linkage group in which marker is located.

f. Max LOD(A), maximum logarithm of odds (LOD) for the QTL additive effect detected across all significant results for detected QTL.

g. Ave. LOD(A), average logarithm of odds (LOD) for the QTL additive effect averaged across all significant results for detected QTL.

h. Max PVE(A), maximum phenotypic variance explained by the additive effect of the detected QTL across all significant results, as a percentage.

i. Ave. PVE(A), average phenotypic variance explained by the additive effect of the detected QTL across all significant results, as a percentage.

j. Max additive effect, maximum additive effect when substituting a NM24016 allele with an allele from TM-1 across all significant results for detected QTL, reported as °C.

k. Ave. additive effect, average additive effect when substituting a NM24016 allele with an allele from TM-1, averaged across all significant results for detected QTL, reported as °C.