S4 Table. Within-year QTL associated with heading date and plant height in the GADH population using the CIM and SIM with major genes as covariates.

Trait	QTL	LG	cM	Confidence interval (cM)	LOD	*P*-value	PVE (%)	Allele effect[a]
				CIM				
HD20	*Ppd-A1*	2A	13	10-16	6.7	0.0000	23.2	1.7
	Ppd-D1	2D	86	83-89	10.5	0.0000	34.0	2.0
	Qncb.hd-5A	5A.1	191	186-191	4.8	0.0016	7.9	1.0
	Qncb.hd-5B	5B	148	87-173	4.5	0.0024	12.2	-1.2
HD21	*Ppd-A1*	2A	13	10-16	6.8	0.0002	20.2	2.6
	Ppd-D1	2D	86	83-89	14.7	0.0000	42.5	3.7
	Qncb.hd-5B	5B	173	170-176	13.7	0.0000	36.1	-3.3
PH20	*Ppd-A1*	2A	13	10-16	5.6	0.0000	19.3	3.2
	Qncb.ph-2D	2D	88	83-89	9.8	0.0000	47.1	5.1
	Qncb.ph-5A	5A.1	189	151-201	3.5	0.0170	4.0	1.5
PH21	*Qncb.ph-2D*	2D	88	50-89	3.3	0.0282	30.9	3.8
				SIM with covariates				
HD20	*Qncb.hd-5A[c]*	5A.1	201	186-201	6.6	0.0000	8.4	1.0
HD21	*Qncb.hd-5B[c]*	5B	80	22-105	3.3	0.0340	13.1	-2.0
PH20	*Qncb.ph-2D[c]*	2D	40	29-61	4.1	0.0042	24.0	3.5
	Qncb.ph-5A[c]	5A.1	181	146-201	3.1	0.0414	4.4	1.5

Abbreviations: CIM = composite interval mapping; SIM = standard interval mapping; QTL = quantitative trait loci; LG = linkage group; cM = centimorgan; HD = heading day (days); PH = plant height (cm); HD20 = heading date 2020; HD21 = heading date 2021; PH20 = plant height 2020; PH21 = plant height 2021; LOD = logarithm of the odds at 0.05 level of probability, obtained through a 5,000-iteration permutation test; PVE = percentage of phenotypic variance explained by the QTL. [a]Estimated allele effect reported in terms of the AGS2033 parent. The estimated allele effect unit corresponds to each trait unit. [c] = covariate.