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QTL mapping for plant height and yield components in common wheat under water-limited and full irrigation environments

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Supplementary Table 1. QTL × environment effects for GY, PH, KNS, NS and TKW

Trait	QTL	Marker	Distance	LOD(A)[a]	LOD(A/E)	PVE(A)[b]	PVE(A/E)	Add[c]
GY	*QGY.caas-3B.2*	*Xbarc251*	5.0	7.6	4.2	1.6	0.5	5.9
	QGY.caas-7A	*Xbarc121*	1.4	8.5	4.3	2.1	0.9	7.3
PH	*QPH.caas-4D*	*Xbarc105*	3.4	151.5	44.8	34.0	1.5	6.1
	QPH.caas-6A	*Xbarc103*	3.0	74.5	3.5	11.0	0.7	3.6
TKW	*QTKW.caas-1A.3*	*Xbarc119*	5.0	6.4	4.0	1.0	0.4	-0.3
	QTKW.caas-4B	*Xgwm251*	4.7	16.9	3.1	2.9	0.2	0.7
	QTKW.caas-4D	*Xbarc105*	2.4	31.9	5.0	5.5	2.1	0.9
	QTKW.caas-5B.1	*Xbarc74*	1.4	24.1	6.9	4.4	0.5	-0.9
	QTKW.caas-6A	*Xbarc103*	2.0	63.0	7.4	12.1	0.2	1.5
KNS	*QKNS.caas-1B*	*Xbarc61*	0.2	9.3	3.3	2.2	0.6	-0.5
	QKNS.caas-2A	*Xgwm95*	2.4	5.0	5.7	1.2	1.1	0.3
	QKNS.caas-5B.1	*Xgwm371*	0	8.3	3.3	1.8	0.5	0.4
	QKNS.caas-6A	*Xwmc256*	1.9	15.0	4.2	3.5	1.1	-0.6
	QKNS.caas-7D	*Xbarc126*	5.0	9.5	4.6	2.0	0.6	-0.4
NS	*QNS.caas-2D*	*Xgwm539*	1.6	8.7	4.9	2.2	1.2	9.4
	QNS.caas-4D	*Xbarc105*	1.4	8.4	6.6	2.1	1.3	-7.3
	QNS.caas-6A	*Xbarc103*	0	7.0	5.6	1.8	1.3	-6.9

[a]LOD(A) and LOD(A/E), LOD threshold of additive and additive/environment effects, respectively

[b]PVE(A) and PVE(A/E), phenotypic variation explained by additive QTL and by additive/environments, respectively

[c]Add, additive effect of QTL allele

Supplementary Table 2. Average phenotypic values of lines for markers positions on chromosomes 4D and 6A

Trait	Environment	6A						4D						4D/6A		
		Xbarc103			*Xwmc256*			*Rht-D1*			*Xbarc105*			*Xbarc103/Xbarc105*		
		0	2	±	0	2	±	0	2	±	0	2	±	0	2	±
PH	LI	67.9	73.6	8.4 **	67.3	73.8	9.7 **	68.6	76.5	11.5 **	65.6	76.6	16.8**	61.9	79.6	28.6**
	FI	79.1	86.2	9.0 **	75	83.6	11.5 **	78.9	88.2	11.8 **	75.8	89.6	18.2 **	70.8	92.5	30.6**
TKW	LI	40.4	43.2	6.9 **	40.4	43.3	7.2 **	41.6	42.9	3.1 **	41.2	42. 7	3.6 **	39.0	44.4	13.8**
	FI	42	45	7.1 **	41.4	44.9	8.5 **	43.1	44.2	2.6 **	42.4	44	3.8 **	40.2	46.3	15.2**
KNS	LI	33.8	32.6	-3.6*	33.2	32.7	-1.5*	33.3	32.7	-1.8*	33.86	32.6	-3.7**	32.8	31.2	-4.9**
	FI	33	32.2	-2.4*	32.7	32.3	-1.2	32.7	32.3	-1.2	33.21	32	-3.6**	32.5	31.4	-3.4*
NS	LI	413.6	409.8	-0.9	412.5	404.3	-2.0*	418.9	401.8	-4.1**	412.1	407.8	-1	438.6	410.3	-6.5**
	FI	499.9	477.5	-4.5**	487.7	478.5	-1.9*	494.7	480.8	-2.8**	496.6	476.4	-4.1**	531.4	478.4	-10.0**
GY	LI	317.5	317.8	0.1	329.4	327.1	-0.7	318.6	314.9	-1.2	329.0	326.7	-0.7	305.1	311.6	2.1*
	FI	436.6	438.0	0.3	436.1	438.1	0.5	439.4	436.4	-0.7	440.5	440.7	-0	426.2	437.3	2.6*

** and *, significant at P=0.01 and P=0.05, respectively.

0, genotype same as Aikang 58; 2, genotype same as Jingdong 8.

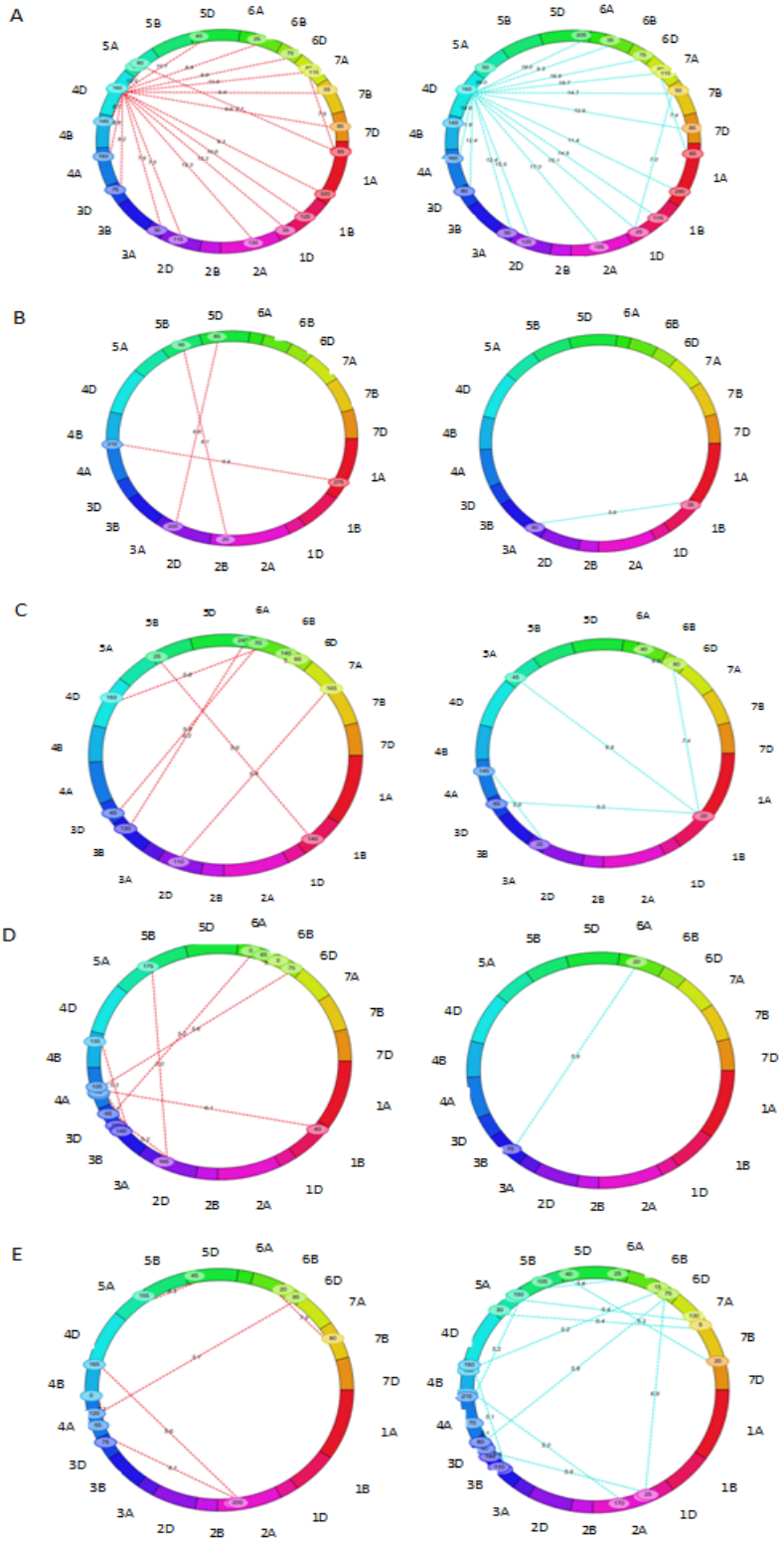
±, percent increase compared to 0 genotype.

PROC MIXED was used in ANOVA by residual maximum likelihood estimation, and mean was estimated by least squares means, line as random effect, marker as fixed effect.

LI, limited irrigation; FI, full irrigation.

PH, TKW, KNS and NS were average across four environments.

PH, plant height; *TKW*, thousand kernel weight; *KNS*, kernel number of per spike; *NS*, spike number per m^2; GY, grain yield



Supplementary Fig. 1. Epistatic effects of QTLs the $F_{2:4}$ population from Jingdong 8/Aikang 58; left, limited irrigation; right, full irrigation: A, PH; B, TKW; C, KNS; D, NS; E, GY.