

Table S1 Genome-wide association studies. Only regions with over 5% of WPPA were shown. The ADE model with BayesB was used for the association studies. CL, culm length; TW, total weight; BR, brix; CD, culm diameter; CN, culm number; PL, panicle length. A, additive; D, dominance.

Trait	Effect	Chromosome	Region (Mb)	Probability (%)
CL	A	1	10 - 11	5.1
		1	66 - 67	16.0
		1	67 - 68	6.5
		1	69 - 70	8.2
		3	30 - 31	7.0
		3	64 - 65	16.6
		4	16 - 17	6.0
		4	25 - 26	11.5
		6	5 - 6	9.4
		6	7 - 8	12.9
		6	13 - 14	5.1
		6	31 - 32	9.5
		6	40 - 41	10.1
		TW	D	9
A	1		14 - 15	7.2
	6		6 - 7	32.6
	6		13 - 14	95.3
BR	A	6	40 - 41	6.7
		9	31 - 32	5.2
		1	62 - 63	6.0
		3	30 - 31	9.1
CD	A	3	57 - 58	23.3
		8	14 - 15	5.4
		10	24 - 25	5.3
		1	50 - 51	15.3
		3	36 - 37	6.4
		3	67 - 68	63.0
		4	15 - 16	9.0
		4	50 - 51	13.1
		4	68 - 69	15.6
		5	54 - 55	28.8
		6	3 - 4	17.6
		6	5 - 6	43.4
		6	6 - 7	39.7
		6	7 - 8	8.5
		6	13 - 14	44.7
		6	36 - 37	7.4
6	38 - 39	5.2		
6	40 - 41	6.2		
7	0 - 1	8.4		
7	47 - 48	5.2		
8	60 - 61	5.2		

		10	8 - 9	6.8
		10	15 - 16	7.3
		10	24 - 25	8.3
		10	58 - 59	14.2
CN	A	1	50 - 51	6.2
		3	30 - 31	20.8
		4	16 - 17	6.6
		4	25 - 26	5.5
		5	4 - 5	9.0
		5	63 - 64	11.9
		6	13 - 14	6.7
		7	48 - 49	6.7
		9	31 - 32	9.4
		10	3 - 4	11.0
		10	20 - 21	7.1
		10	46 - 47	7.9
PL	A	1	19 - 20	53.7
		1	32 - 33	5.0
		1	47 - 48	18.9
		1	50 - 51	7.8
		1	53 - 54	47.2
		2	19 - 20	5.2
		2	26 - 27	7.0
		3	30 - 31	5.5
		3	36 - 37	16.9
		3	70 - 71	52.6
		6	13 - 14	5.8
		6	44 - 45	30.5
		6	47 - 48	92.1
		8	15 - 16	5.4
		9	3 - 4	7.6
		9	31 - 32	7.0
		10	3 - 4	5.3
