

Table S6. The QTLs detected in this study overlapped with the QTLs/genes reported previously.

QTL name	Chr.	Position range /bp	Known QTL ^a / association locus ^a	Flanking region /bp ^a	Reference
<i>qBRR5.1</i>	5	742,718-942,718	<i>qBR-5</i>	264,087-1,861,366	Weng et al. 2007
<i>qMRR11</i>	11	3,119,894-3,319,894	<i>qMR-11</i>	2,449,321-3,812,236	Weng et al. 2007
<i>qHMRR2</i>	2	33,924,415-34,124,415	<i>qHR2</i>	32,774,365-35,272,373	Hu et al.2011
				26,934,304-28,704,796	Tan et al. 2001
<i>qHMRR5</i>	5	27,851,340-28,051,340	<i>mr5</i>	22,671,210-33,689,061	Aluko et al. 2004
			<i>qMR-5b</i>	22,555,884-28,704,796	Weng et al. 2007
<i>qHMRR11</i>	11	24,733,345-24,933,345	<i>qHR11</i>	19,840,132-28,281,693	Yao et al. 2023

^aThe gene name, QTL name and the physical position (bp) was inferred from the database of Gramene website (<http://www.gramene.org/markers/>), BLAST (<http://blast.ncbi.nlm.nih.gov/Blast.cgi>) and the China Rice Data Center database (<http://www.ricedata.cn/gene/list/1499.htm>).