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Detection of genomic loci associated with days to heading in tropical japonica rice through QTL-seq

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Electronic Supplementary Material (ESM)

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Table S1. Data quality summary of sequencings

Sample	Raw reads	Raw data (Gb)	Effective	Error	Q20	Q30	GC
					(%)		
Bulk early DTH	174 509 304	26.2	99.38	0.03	96.58	91.08	43.57
Bulk late DTH	159 419 210	23.9	99.35	0.03	96.83	91.57	43.28
Rojolele Srinuk	163 324 612	24.5	99.40	0.03	96.79	91.45	43.29
Rojolele	41 399 292	6.2	99.11	0.03	96.51	90.92	42.97

DTH – days to heading; Q20 – reads with base call accuracy ≥ 99%; Q30 – reads with base call accuracy ≥ 99.9%; GC– guanine and cytosine content

Table S2. Regions with the top five lowest and highest average Δ(SNP-index)

Chr	Δ SNP index	Chromosome region (bp)
Chr7	0.473787159	29 500 000
Chr3	0.453300796	10 000 000
Chr7	0.448138775	29 000 000
Chr7	0.445472309	30 000 000
Chr3	0.414317865	10 500 000
Chr3	–0.545549398	30 500 000
Chr3	–0.575891622	28 500 000
Chr3	–0.57876862	27 000 000
Chr3	–0.579709464	27 500 000
Chr3	–0.597415698	28 000 000