

1 **Supplementary Information**

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3 **Title**

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5 **Genotyping-by-sequencing based QTL mapping for rice grain yield under reproductive stage drought stress**
6 **tolerance**

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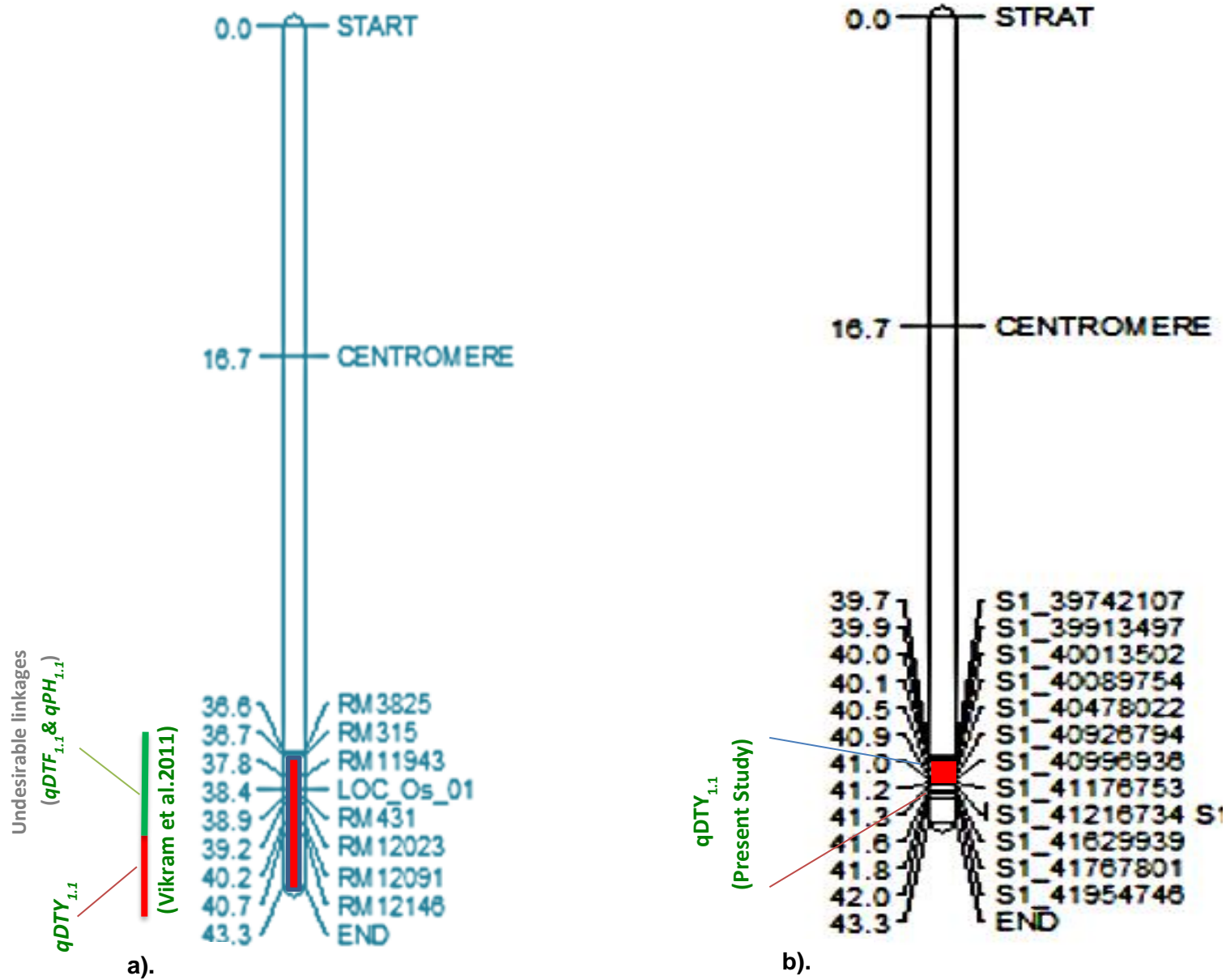
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Figure S1: A comparative map showing narrowed down genomic region of previously identified *qDTY_{1.1}* using high density linkage maps
 a). *qDTY_{1.1}* with undesirable linkages of early flowering and tallness (Vikram et al. 2011) located in genomic region of 36.75-40.70 Mb with QTL size of 3.95 Mb
 b). *qDTY_{1.1}* (present study) located nearly to 40 Mb genomic region with QTL size of 1.2 Mb size and free from undesirable linkages

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43 Supplementary Tables

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45 **Detailed Excel file has been attached (Table S1-S9)**

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48 **Table S1.** Summary of analyzed GBS data through TASSEL-GBS pipeline

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50 **Table S2.** Alignment of reads to reference genome in Swarna*2/Dular population.

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52 **Table S3.** Alignment of reads to reference genome in IR11N121*2/Aus 196.

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54 **Table S4.** Total SNPs generated in TASSEL GBS pipeline for Swarna*2/Dular population.

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56 **Table S5.** Total SNPs generated in TASSEL GBS pipeline for IR11N121*2/Aus 196 population.

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58 **Table S6.** Filtered, polymorphic SNPs used in linkage map construction for Swarna*2/Dular population.

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60 **Table S7.** Filtered, polymorphic SNPs used in linkage map construction for IR11N121*2/Aus 196 population.

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62 **Table S8.** Validation of *qDTY1.1* using flanking markers in 250 lines randomly selected from five mapping populations

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64 **Table S9.** Results of estimation of QTL effects among + QTL and - QTL lines

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