https://doi.org/10.17221/103/2020-CJGPB

# TPR domain coding gene *ST2* may be involved in regulating tillering and fertility in rice

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## Electronic Supplementary Material (ESM)

The authors are fully responsible for both the content and the formal aspects of the electronic supplementary material. No editorial adjustments were made.

Table S1. Genetic analysis of *st2*

| Combinations | $F_1$ phenotype | $F_2$ population No. | Wild-type No. | Mutant No. | Separation ratio |
|---|---|---|---|---|---|
| *st2*/J10 | normal | 509 | 387 | 122 | $\chi^2 = 1.627 < \chi^2_{0.05,1} = 3.84$ |

Table S2. Molecular markers newly designed in this study

| Marker | Forward primer (5'→3') | Reverse primer (5'→3') |
|---|---|---|
| ZTQ35 | GCACATGCCCGCGTATATG | TTAGCATCCCAATGTGTAGGAG |
| ZTQ27 | GCAGCTAGTGCAAGACGGAG | GATGAGCCGTATGATCCGC |
| W25-28 | ACAGCTTTGTAGCAGTAACAGGATT | TCTACTCAATAATAGAATCAAACAGAGCT |
| FL-1 | GAGTATCAGACGATCAGACACCAC | CATTTGCCGTCGAATTGAT |
| W25-38 | GCACACAGGCTCAGCTACC | ACCTATGCCATGTTGCCAT |

Table S3. Primers used for the quantitative real-time PCR analysis

| Primer | Forward primer (5'→3') | Reverse primer (5'→3') | References |
|---|---|---|---|
| *UBIQUITIN5* | ACCACTTCGACCGCCACTACT | ACGCCTAAGCCTGCTGGTT | Chen et al. 2018 |
| *ST2* | CATATCTGCAGAGCGCAATT | CTTGGTAATCCATTGCCTGC | |

Table S4. Primers for the vector construction

| Primer | The sequence |
|---|---|
| ST2-GFP-*Xba*IF | AGTCCGGAGCTAGCTCTAGAATGAGGCGGCTGCCCAAAT |
| ST2-GFP-*BamH*IR | CCCTTGCTCACCATGGATCCTTCTCGGTCTTGGAATTTAGT |

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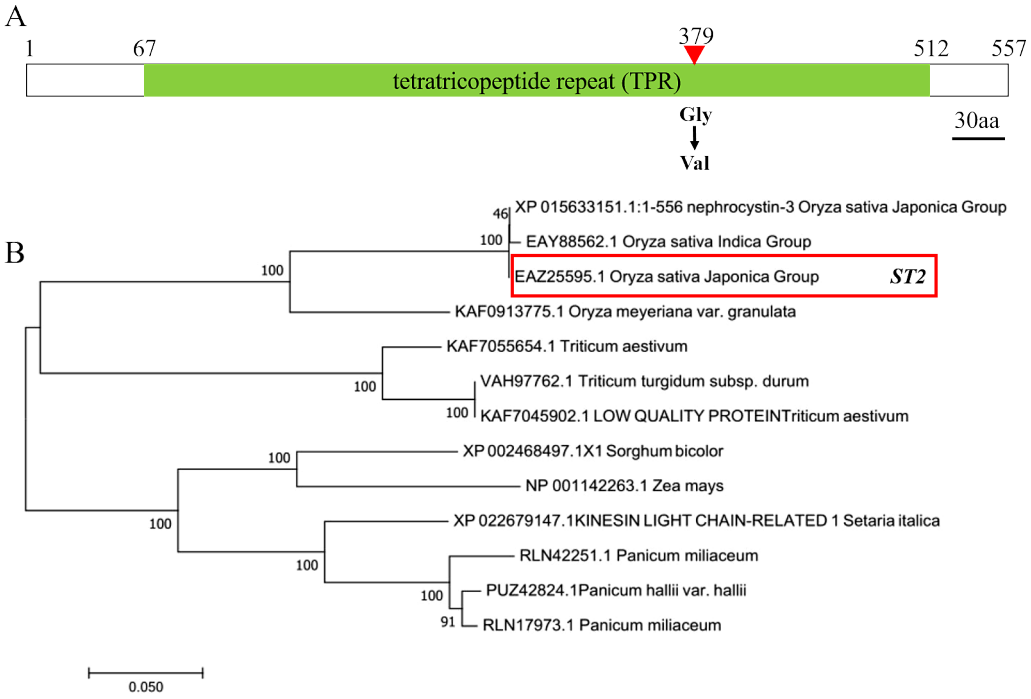


Figure S1. Analysis of the amino acid level of *ST2*

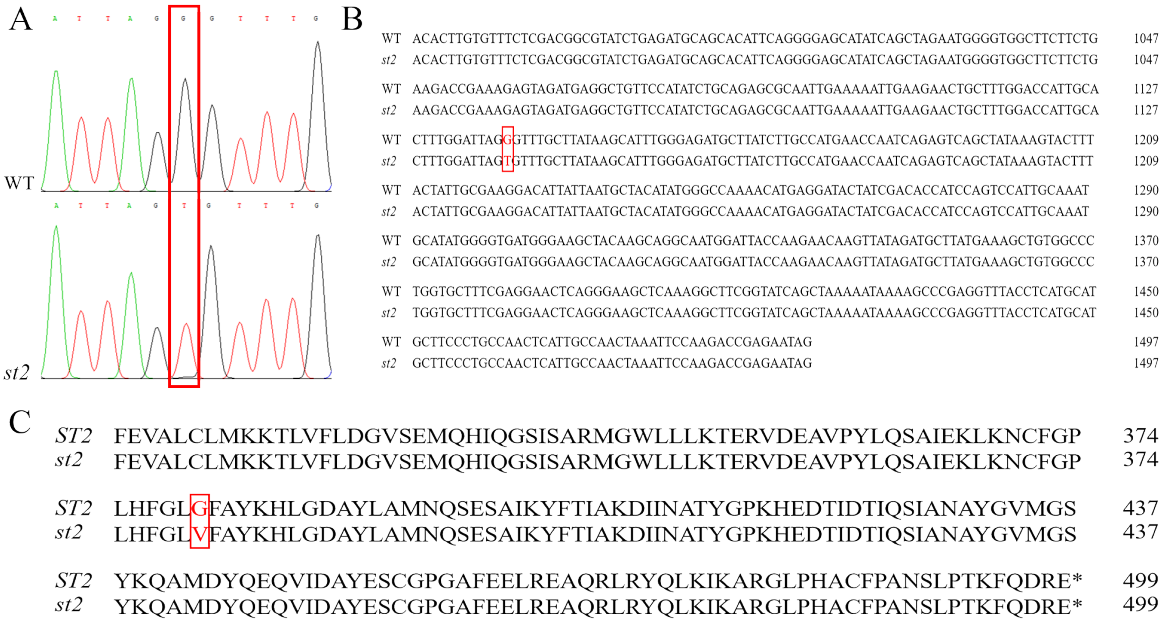


Figure S2. Detection of the mutation sites in *st2*: sequencing peak map (A), mutation of the DNA level (B), mutation of the protein level (C)

## REFERENCES

Chen X., Zhu M., Gu F., Liu M., Zhang Y., Xing Y., Du D., Xiao Y., Zhu X., He G. (2018): Identification and gene fine mapping of starch accumulation and early senescent leaf mutant *esl10* in rice. Crop Science, 58: 204–217.