# Supplementary Material

**Supplement Table. A1** Statistical analysis of TA

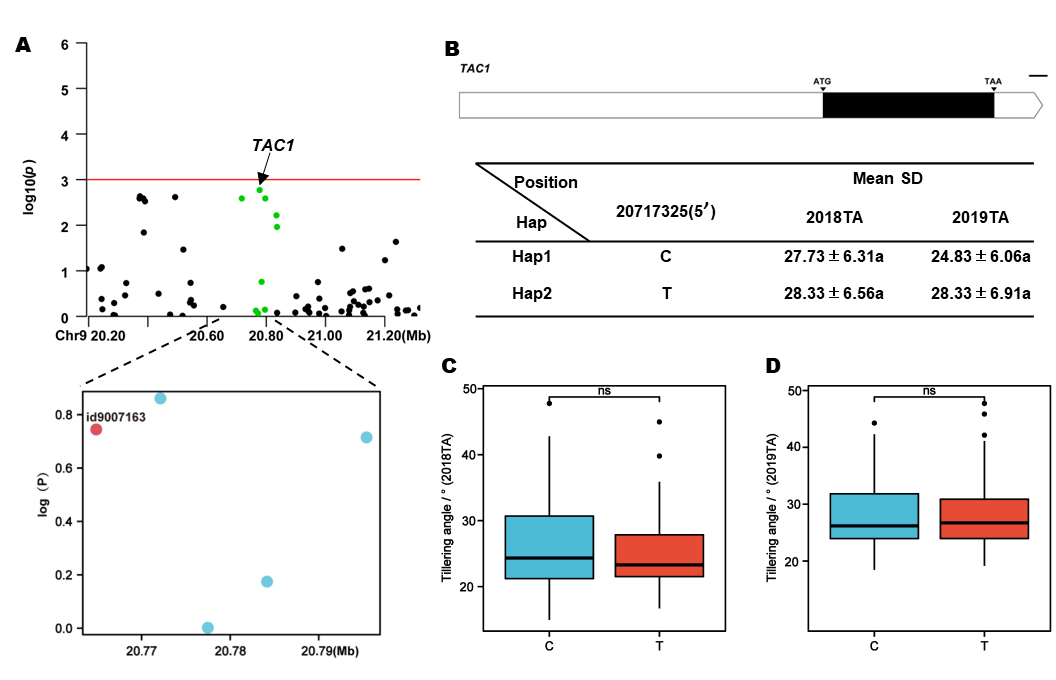
|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| year/site | phenotype | Variability | Mean | SD | CV (%) | Kurt | [skewness](javascript:;) |
| 2018 liuyang | TA | 9.63°-55.66° | 27.86a | 6.75 | 24.23% | 1.42 | 0.84 |
| 2019 liuyang | 14.59°-47.76° | 25.82a | 6.56 | 25.43% | 0.67 | 0.85 |

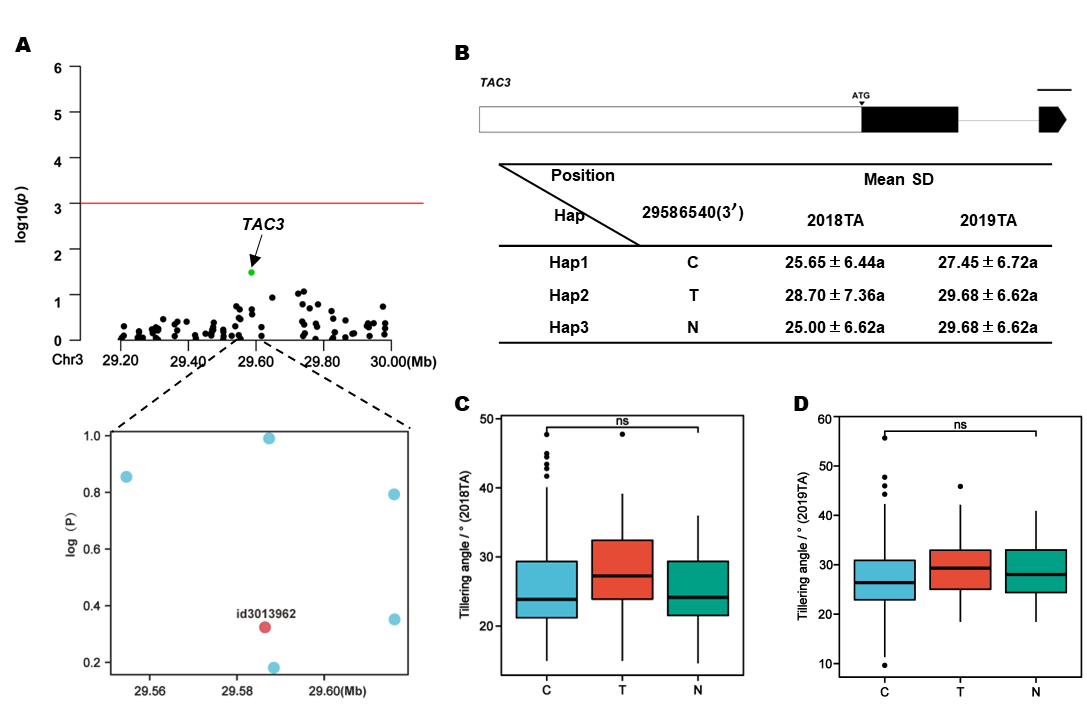
**Supplement Table. A2** Primer for RT–qPCR

|  |  |  |
| --- | --- | --- |
| Gene ID | Primer sequence (5'to3') | |
| *LOC\_Os01g67770* | F | AATGAAGGTCTTGTGTTGCATC | |
| R | GCTTTGGTTTTGTAAGCTCTGA | |
| *LOC\_Os02g35180* | F | CCTCCTCTTTCAAATACTCCCA | |
| R | CTCCCATCCTCTCAGGTCT | |
| *LOC\_Os09g38130* | F | TTAGCTGGAATGATTCAGCTCA | |
| R | ATTATAGTTATCTACGCGGGCC | |
| *OsActin* | F | CAGCCACACTGTCCCCATCTA | |
| R | AGCAAGGTCGAGACGAAGGA | |

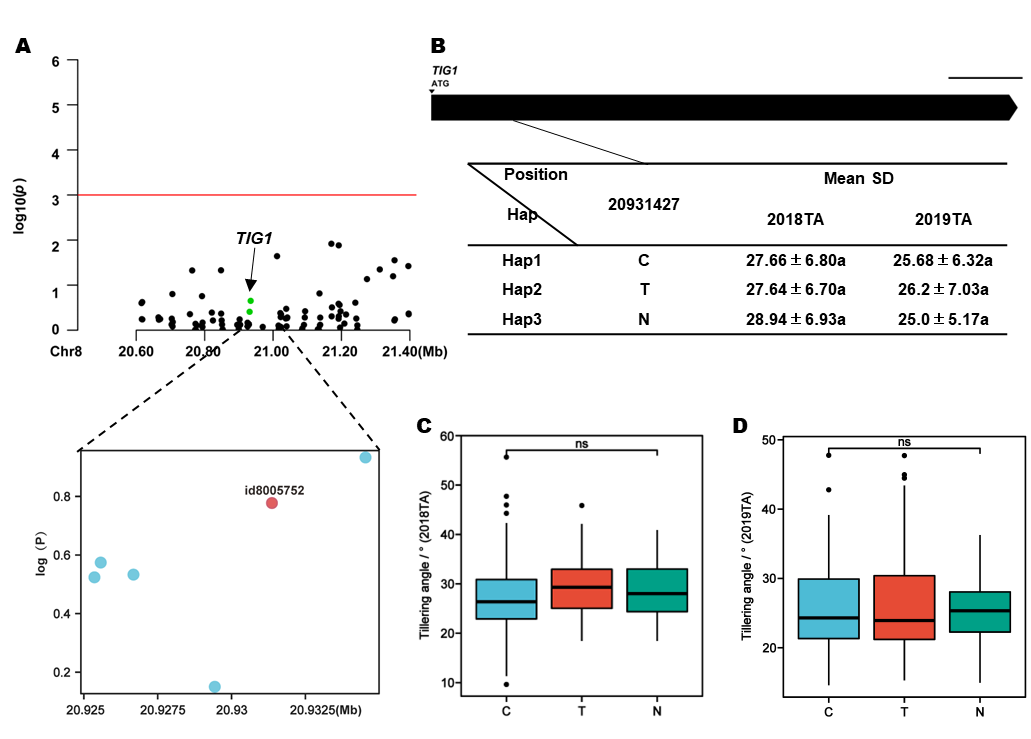
**Supplement Table. A3** Comparison of GWAS results with previously reported results of TA

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| QTL | Chr | Marker interval | LOD score | P value | R2(%) | Ref |
| *QTa1* | 1 | RG173/RG532 | 2.6 | - | 2.7 | Li.et al (1999) |
| *qTA1.1* | 1 | 1297448 | - | 1.64E-07 | - | Bai.et al (2022) |
| *qTA1.2* | 1 | 12048457 | - | 1.64E-07 | - | Bai.et al (2022) |
| *QTa2* | 2 | RG171-RG437 | 3.6 | - | 5.2 | Li.et al (1999) |
| *qTA-2* | 2 | C777-R1989 | 7.56 | - | 19.05 | Yu.et al (2005) |
| *qTA2* | 2 | RM13594–RM3512 | 4.26 | - | 39 | Zhao.et al (2022) |
| *qTA2.1* | 2 | 30414101 | - | 1.47E-12 | - | Bai.et al (2022) |
| *qTA6* | 6 | RM528–RM3343 | 3.12 | - | 37 | Zhao.et al (2022) |
| *qTA6.1* | 6 | 3234165 | - | 5.85E-08 | - | Bai.et al (2022) |
| *Ta* | 9 | RZ228-RG667 | 32.3 | - | 47.5 | Li.et al (1999) |
| *qTA-9a* | 9 | RG662-CT100 | 5.51 | - | 22.7 | Qian.et al (2001) |
| *qTA-9b* | 9 | G295-RG451 | 3.05 | - | 11.9 | Qian.et al (2001) |
| *qTA9-2* | 9 | RM107-RG667 | 22 | - | 19.5 | Shen.et al (2005) |
| *qTA -9* | 9 | XNpb108 -C570 | 10.5 | - | 32. 83 | Yu.et al (2005) |
| *TAC1* | 9 | P4-P5 | - |  | - | Yu.et al (2007) |
| *qTAC9* | 9 | RM201-RM7306 | 9.31 | - | 17.4 | He.et al (2017) |
| *qTA9* | 9 | RM6235–RM24288 | 4.27 | - | 27 | Zhao.et al (2022) |
| *qTA9-1* | 9 | RM3700–RM24288 | 7.08 | - | 37 | Zhao.et al (2022) |
| *qTA-12* | 12 | RG461-G148 | 5.71 | - | 20.9 | Qian.et al (2001) |

**Supplement** **Figure. A3** *TAC1* haplotype significance analysis. (**A**) Partial Manhattan map of *TAC1* on Chr.9; (**B**) Schematic representation of *TAC1* structure and the positions of 1 SNPs used for haplotype analysis, bar = 100bp; (**C**) and (**D**) Comparisons of TA values among accessions with different haplotypes in2018 and 2019. \*p ≤ 0.05, \*\*p ≤ 0.01.



**Supplement Figure. A4** *TAC3* haplotype significance analysis. (**A**) Partial Manhattan map of *TAC3* on Chr.3; (**B**) Schematic representation of *TAC3* structure and the positions of 1 SNPs used for haplotype analysis, bar = 100bp; (**C**) and (**D**) Comparisons of TA values among accessions with different haplotypes in2018 and 2019. \*p ≤ 0.05, \*\*p ≤ 0.01.



**Supplement Figure. A5***TIG1* haplotype significance analysis. (**A**) Partial Manhattan map of *TIG1* on Chr.8; (**B**) Schematic representation of *TIG1* structure and the positions of 1 SNPs used for haplotype analysis, bar = 100bp; (**C**) and (**D**) Comparisons of TA values among accessions with different haplotypes in2018 and 2019. \*p ≤ 0.05, \*\*p ≤ 0.01.