**Table S1. Primers used in this study**.

| Primer name | Primer sequences (5'-3') | Engineered restriction site (with underline) | Purpose |
|---|---|---|---|
| OsABCG18-P1 | CGGAATTCTATGCCGCCTCAGGAGTTGCATGGC | *EcoR* Ⅰ | For constructing OsABCG18 expression |
| OsABCG18-P2 | CGGGATCCTCACCTTGGCTTGAGGCGGTCCAAGG | *BamH* Ⅰ | |
| OsABCG18-P3 | CATGACCGGTGTAACTGCCTAAGGGAGTGCCTAG | *Age* Ⅰ | For cloning OsABCG18 promoter |
| OsABCG18-P4 | CATGCCATGGGGCGATCGATCGATGGATGAAAATC | *Nco* Ⅰ | |
| UBQ-F | GCACAAGCACAAGAAGGTGA | | The standard gene for qRT-PCR |
| UBQ-R | CCAAAGAACAGGAGCCTACG | | |
| G18CAS 1F | GGCAGTTCGAGGAGGTGGTGTACA | | The first crispr/Cas9 target site of g18 |
| G18CAS1R | AAACTGTACACCACCTCCTCGAAC | | |
| G18CAS2F | GGCAGGCGCACCTGCAGGACCGGA | | The second crispr/Cas9 target site of g18 |
| G18CAS2R | AAACTCCGGTCCTGCAGGTGCGCC | | |
| OsABCG18-P5 | GATCGTCTTCTCCTTCGCCAC | | For amplifying the first crispr/Cas9 target with OsABCG18-P1 |
| OsABCG18-P6 | GCAGTTCACGGTGCTGCTCCG | | For amplifying the first crispr/Cas9 target with OsABCG18-P2 |
| OsABCG18-P7 | CCACCGCGACTTCAGTTCTC | | for OsABCG18 qRT-PCR |
| OsABCG18-P8 | GGAGGTGTTGGTGGAAGAGGA | | |
| OsRR2-F | GACTACTGCATGCCGGAGATG | | for OsRR2 qRT-PCR |
| OsRR2-R | TTCTCCGACGACATGACCAC | | |
| OsRR6-F | ACCGACTACTGGATGCCCG | | for OsRR6 qRT-PCR |
| OsRR6-R | TCCGACGACATGATCACCAC | | |
| OsRR10-F | CATGTCCTGGCTGTGGATGA | | for OsRR10 qRT-PCR |
| OsRR10-R | TTGCTCCCGGAATCAACAGT | | |

**Table S2. Accession codes used in this study.**

.

| Gene | Genes locus | Gene | Genes locus |
|---|---|---|---|
| *UBQ* | LOC_Os01g45420 | *AtABCG1* | AT2G39350 |
| *OsRR2* | LOC_Os02g35180 | *AtABCG2* | AT2G37360 |
| *OsRR6* | LOC_Os04g57720 | *AtABCG3* | AT2G28070 |
| *OsRR10* | LOC_Os11g04720 | *AtABCG4* | AT4G25750 |
| *OsABCG1* | LOC_Os01g03144 | *AtABCG5* | AT2G13610 |
| *OsABCG2* | LOC_Os01g42900 | *AtABCG6* | AT5G13580 |
| *OsABCG3* | LOC_Os01g61940 | *AtABCG7* | AT2G01320 |
| *OsABCG4* | LOC_Os03g06139 | *AtABCG8* | AT5G52860 |
| *OsABCG5* | LOC_Os03g17350 | *AtABCG9* | AT4G27420 |
| *OsABCG6* | LOC_Os03g17370 | *AtABCG10* | AT1G53270 |
| *OsABCG7* | LOC_Os03g64200 | *AtABCG11* | AT1G17840 |
| *OsABCG8* | LOC_Os04g11820 | *AtABCG12* | AT1G51500 |
| *OsABCG9* | LOC_Os04g44610 | *AtABCG13* | AT1G51460 |
| *OsABCG10* | LOC_Os05g02870 | *AtABCG14* | AT1G31770 |
| *OsABCG11* | LOC_Os05g02890 | *AtABCG15* | AT3G21090 |
| *OsABCG12* | LOC_Os05g13520 | *AtABCG16* | AT3G55090 |
| *OsABCG13* | LOC_Os05g31910 | *AtABCG17* | AT3G55100 |
| *OsABCG14* | LOC_Os06g30730 | *AtABCG18* | AT3G55110 |
| *OsABCG15* | LOC_Os06g40550 | *AtABCG19* | AT3G55130 |
| *OsABCG16* | LOC_Os06g51460 | *AtABCG20* | AT3G53510 |
| *OsABCG17* | LOC_Os07g18874 | *AtABCG21* | AT3G25620 |
| *OsABCG18* | LOC_Os08g07010 | *AtABCG22* | AT5G06530 |
| *OsABCG19* | LOC_Os09g03939 | *AtABCG23* | AT5G19410 |
| *OsABCG20* | LOC_Os09g07670 | *AtABCG24* | AT1G53390 |
| *OsABCG21* | LOC_Os09g23640 | *AtABCG25* | AT1G71960 |
| *OsABCG22* | LOC_Os09g29660 | *AtABCG26* | AT3G13220 |
| *OsABCG23* | LOC_Os09g29670 | *AtABCG27* | AT3G52310 |
| *OsABCG24* | LOC_Os10g08014 | *AtABCG28* | AT5G60740 |
| *OsABCG25* | LOC_Os10g30610 | *CBL1* | AT4G17615 |
| *OsABCG26* | LOC_Os10g35180 | | |
| *OsABCG27* | LOC_Os11g07600 | | |
| *OsABCG28* | LOC_Os11g22350 | | |
| *OsABCG29* | LOC_Os12g22110 | | |
| *OsABCG30* | LOC_Os12g22284 | | |

**Table S3.※ Agronomic traits of wild-type and *osabcg18* mutant plants at mature stage (for Figure 7).**

| **Agronomic Trait** | **WT** | ***osabcg18-14*** | ***osabcg18-32*** | ***osabcg18-24*** |
|---|---|---|---|---|
| Plant height (cm) | 86.5 ±2.1 | 76.5 ±4.1 *** | 74.8 ±2.7 *** | 77.7 ±3.2 *** |
| Effective tiller number | 12.9 ±2.2 | 7.4 ±0.9 *** | 6.9 ±1.1 *** | 7.6 ±1.6 *** |
| Days to flowering | 79.7 ±1.4 | 82.6 ±1.2 *** | 83.9 ±1.2 *** | 84.0 ±1.4 *** |
| Setting rate (%) | 85.6 ±2.3 | 69.2 ±13.1 *** | 69.3 ±9.8 *** | 75.6 ±4.5 *** |
| Panicle length (cm) | 20.0 ±0.7 | 18.1 ±1.1 ** | 20.1 ±0.8 | 17.9 ±0.9 ** |
| Primary branches per panicle | 9.5 ±0.5 | 7.6 ±0.6 *** | 8.7 ±0.6 ** | 8.0 ±0.6 *** |
| Grain number per panicle | 101 ±11 | 73 ±11 *** | 66 ±10 *** | 74 ±11 *** |
| Grain length (mm) | 7.06 ±0.11 | 7.31 ±0.18 *** | 7.50 ±0.03 *** | 7.36 ±0.10 *** |
| Grain width (mm) | 3.21 ±0.14 | 3.32 ±0.05 ** | 3.32 ±0.04 ** | 3.33 ±0.04 ** |
| 1000 grain weight (g) | 23.4 ±1.6 | 25.0 ±1.50 ** | 27.0 ±0.5 *** | 24.7 ±0.8 ** |
| Grain number per plant | 773 ±138 | 560 ±257 *** | 534 ±134 *** | 462 ±144 *** |
| Grain weight per plant (g) | 17.5 ±3.4 | 13.4 ±6.5 *** | 14.1 ±3.4 *** | 11.2 ±3.5 *** |

※ Values are means ±SD (n = 15). ** and *** indicate the significant differences at $P < 0.01$ and $P < 0.001$, respectively (from *t*-test in one-way ANOVA).

**Table S4.※Agronomic traits of wild-type (Zhonghua 11, ZH11) and *OsABCG18* overexpression plants (for Figure 8).**

| Agronomic Trait | ZH11 | G18OE-10 | G18OE-14 | G18OE-25 |
|---|---|---|---|---|
| Plant height (cm) | 102.1 ±5.0 | 100.2 ±5.2 | 99.9 ±5.7 | 100.5 ±5.5 |
| Effective tiller number | 8.4 ±1.7 | 10.6 ±1.9 ** | 10.5 ±1.6 ** | 10.0 ±1.4* |
| Setting rate (%) | 86.3 ±8.3 | 80.7 ±10.6 ** | 84.2 ±6.6 | 80.4 ±7.2** |
| Panicle length (cm) | 21.4 ±1.2 | 22.1 ±1.3 * | 23.1 ±1.0 *** | 21.0 ±0.8 |
| Primary branches per panicle | 9.9 ±1.5 | 10.0 ±1.6 | 10.5 ±1.0 * | 10.4 ±0.9 |
| Grain number per panicle | 136 ±26 | 145 ±28 * | 152 ±17 ** | 142 ±22 |
| Grain length (mm) | 6.93 ±0.07 | 7.21 ±0.29 ** | 7.29 ±0.06 *** | 7.37 ±0.14*** |
| Grain width (mm) | 3.09 ±0.04 | 3.06 ±0.04 | 3.02 ±0.06 *** | 3.07 ±0.04 |
| 1000 grain weight (g) | 22.9 ±0.5 | 23.7 ±1.5 * | 24.0 ±0.9 *** | 23.40 ±0.6** |
| Grain number per plant | 840 ±188 | 975 ±205 * | 978 ±113 ** | 871±137 |
| Grain weight per plant (g) | 19.7 ±3.3 | 23.1 ±3.9 * | 23.3 ±2.5 ** | 20.3 ±2.4 |

※ Data are means ±SD (n ≥ 12). *, ** and *** indicate significant differences at $P < 0.05$, $P < 0.01$ and $P < 0.001$, respectively (from *t*-test in one-way ANOVA).