

## Supplementary Material

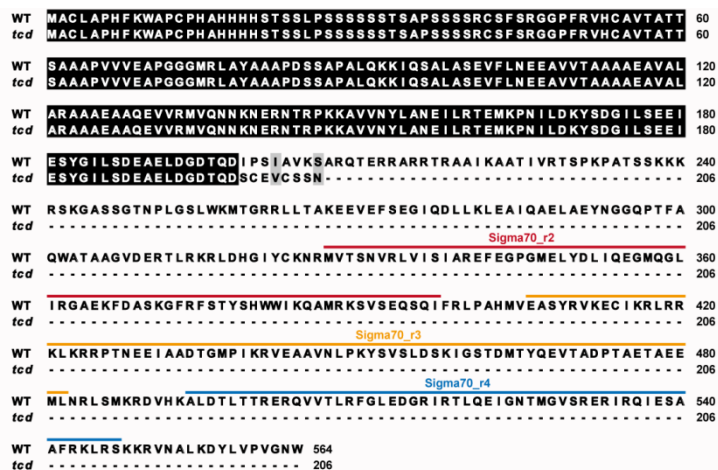
### ***OsSIG2A* is required for chloroplast development in rice (*Oryza sativa* L.) at low temperature by regulating plastid genes expression**

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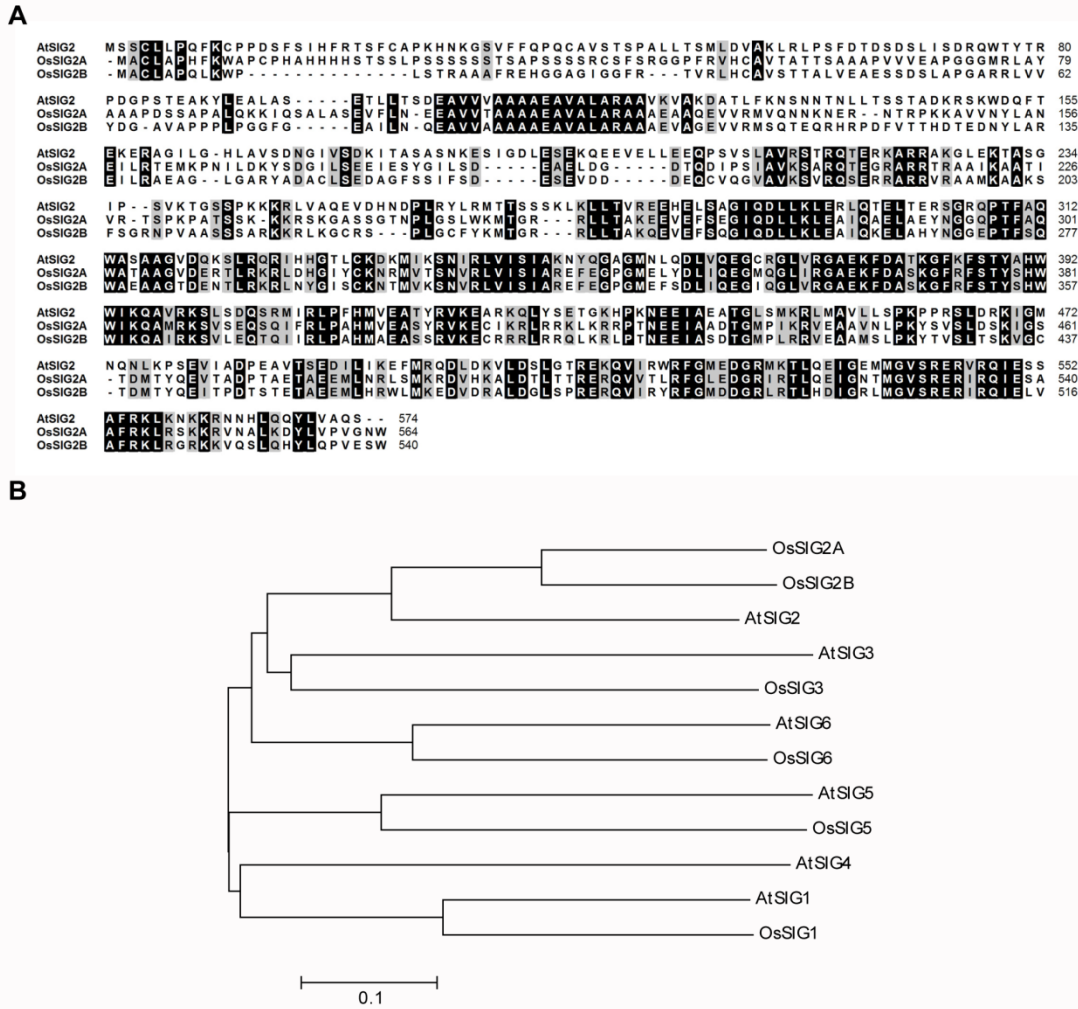
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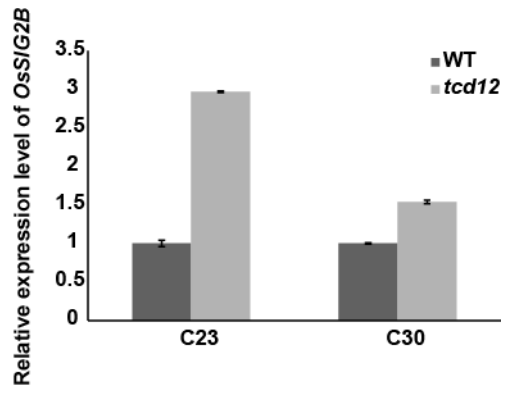
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**Fig. S1.** Amino acid sequence alignment of *OsSIG2A* protein and *tcd12* protein.



**Fig. S2.** Deduced amino acid sequence alignment (A) and evolutionary tree (B) of OsSIG2A and its homologs in rice and *Arabidopsis*.



**Fig. S3.** Relative expression level of *OsSIG2B* in WT and *tcd12* at C23 and C30.

**Table S1. Primer sequences**

| Marker                      | Forward sequence (5'-3')              | Reverse sequence (5'-3')                 |
|-----------------------------|---------------------------------------|--|
| Fine mapping primers        |                                       |  |
| RM536                       | TCTCTCCTCTGTTTGGCTC                   | ACACACCAACACGACCACAC                     |
| RM209                       | ATATGAGTTGCTGTCGTGCG                  | CAACTTGCATCCTCCCCTCC                     |
| RM6091                      | GCTGTCTCTGTCCTGAATCC                  | TGGTAGGCTGGTGACATGC                      |
| RM6272                      | AACATCTACTCCGCCACCAC                  | CAGCAAGCAGATGGTGGC                       |
| Y9                          | GCATAACAATCTTGTCGTG                   | GTTTGGTGATTCTGCTTA                       |
| Y7                          | GCCACTCTTCCGCCGACTG                   | AGGTAGTGGCGGCGGTGCG                      |
| Y13                         | GATCCGTCTTCAGCCTCCACTAC               | AGGCCACCAAGCGAACCA                       |
| Y12                         | AGGGCAGGACGAACGACGGC                  | CGAGAAGCCCAATCGAGGAGCA                   |
| Y17                         | AGGGATGCTTACCAAAT                     | GGTTAGAACAACATATCAGG                     |
| Y3                          | CCTGGAGACGAGGGTGGTG                   | CGCCCATCCATGATCCTTAA                     |
| Y4                          | AGTATTACATAGGGGAAAGAAG                | ATCACCAAGTAGCAACCAG                      |
| Vector construction Primers |                                       |  |
| TCD-A                       | TAGGTACCAGGCTGAGCTCTCGCGCCGCACTTCAAGT | ACGTAGGGGGGATAGAGCTCGTTACAACAGCCTCTTCATT |
| TCD-S                       | GAATTCGGGGGATCCTCGCGCCGCACTTCAAGT     | CAGGTGGAAGACGCGTGTACAACAGCCTCTTCATT      |
| GTCD                        | CGGTCCGGGGGATCCATGGCGTGCTCGCGCCGCACTT | TGCTCACCATGGATCCCAATTGCCTACTGGTAC        |
| Quantitative PCR Primers    |                                       |  |
| <i>TCD12</i>                | AGAGAAGAGCTCGGAGAACG                  | CTTTGAGGACGTTGCAGGTT                     |
| Ubq                         | GCTCCGTGGCGGTATCAT                    | CGGCAGTTGACAGCCCTAG                      |
| HEMA1                       | CACCAGTCTGAATCATAT                    | CTACCACTTCTCTAATCC                       |
| CAO1                        | GATCCATACCCGATCGACAT                  | CGAGAGACATCCGGTAGAGC                     |
| PORA                        | ATCACCAAGGGCTACGTCTC                  | GAGTTGTTGTTCCAGCTCCA                     |
| CHLD                        | GGAAAGAGAGGGCATTAG                    | CAATACGATCAAGTAAGTGTT                    |
| CHLI                        | AGTAACCTTGGTGCTGTG                    | AATCCATCAACATTCAACTCTG                   |
| CHLH                        | CTATACATTCGCCCACT                     | TATCACACAACCTCCCAAG                      |
| YGL1                        | TGGACAGTTGAAGATGTT                    | GAATAGGACGGTAAGGTT                       |
| rpoA                        | GTGGAAGTGTGTTGAATCAA                  | TCTCTTTGATCCGTAACTC                      |
| rpoB                        | TTTGGTTTCGATGTGCA                     | TATGGTCTAATCCGAGCGGT                     |
| rpoC1                       | CATAGATTAGGCATACAGGC                  | AATAGCGGGAGATAGGAG                       |
| rpoC2                       | AAAAGAGGAGGCTCGTGC                    | GATGTTGGCTAAGTGATTGA                     |
| V1                          | TCAGAACGAGAAGGATTCAGCA                | GGCAACAGCCACTAAAATTCT                    |
| V2                          | GAGGAGTTCCTCACGATGAT                  | AGCATCAATGATAGACTCC                      |
| V3                          | GTTAGATGCTTCACTACACAG                 | GTACCATTGCCAACATGGCAAC                   |
| PORA                        | TGTAAGGAGCTGGAACAACAA                 | GAGCACAGCAAAATCCTAGACG                   |
| psaA                        | GAGATACCACTTCCTCAT                    | ACTAAGAAATTCTGCGTATT                     |
| psbA                        | AAGTTTCTCTGATGGTATG                   | ATAGCACTGAATAGGGAA                       |

|       |                       |                      |
|-------|-----------------------|----------------------|
| psaB  | TTGGTATTGCTACCGCACAT  | CCGGACGTCCATAGAAAGAT |
| psbB  | TCATATTGCTGCGGGTACAT  | AGTTGCTGACCCATACCACA |
| psbC  | TACAACCTTGGCAAGAACGA  | TACGCCACCCACAGAATTTA |
| psaE  | AAGAGAGGCACCAAGGTGAA  | TAGCGAGTGTTGGGATCCTG |
| rbcS  | TCCGCTGAGTTTTGGCTATTT | GGACTTGAGCCCTGGAAGG  |
| rbcL  | GTTGAAAGGATAAGTTGA    | AATGGTTGTGAGTTTACG   |
| CAB1R | AGACGTTCCCAAGAACC     | GAGGAGCTCCGGGAAGAC   |
| CAB2R | GTTCTCCATGTTCCGGCTTCT | GACGAAGTTGGTGGCGTAG  |

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**Table S2. Genetic segregation analysis of *tcd12* mutants in the F<sub>2</sub> population**

| Cross                   | Observed number of F <sub>2</sub> plants |       |        | <i>P</i>    |
|-------------------------|--|-------|--------|-------------|
|                         | Total                                    | Green | Albino |             |
| <i>tcd12</i> /Nanjing11 | 2032                                     | 1509  | 523    | 0.44 > 0.05 |

**Table S3. Predicted genes at *tcd12*-containing region**

| ORF   | Locus        | Description   |
|-------|--------------|---|
| ORF1  | Os11g0444700 | Octicosapeptide/Phox/Bem1p domain containing protein                                    |
| ORF2  | Os11g0444800 | Conserved hypothetical protein  |
| ORF3  | Os11g0444900 | Octicosapeptide/Phox/Bem1p domain containing protein                                    |
| ORF4  | Os11g0445300 | Protein kinase, core domain containing protein  |
| ORF5  | Os11g0445475 | Similar to harpin-induced protein   |
| ORF6  | Os11g0446000 | Conserved hypothetical protein  |
| ORF7  | Os11g0446500 | Similar to Phospholipid-translocating P-type ATPase, flippase family protein, expressed |
| ORF8  | Os11g0447300 | GTP-binding protein, HSR1-related domain containing protein                             |
| ORF9  | Os11g0448000 | Protein kinase, catalytic domain domain containing protein                              |
| ORF10 | Os11g0448100 | Non-protein coding transcript   |
| ORF11 | Os11g0448400 | RNA polymerase sigma factor   |
| ORF12 | Os11g0448700 | Conserved hypothetical protein  |
| ORF13 | Os11g0449600 | Conserved hypothetical protein  |
| ORF14 | Os11g0450050 | Conserved hypothetical protein  |
| ORF15 | Os11g0450400 | Similar to Sulfotransferase domain containing protein, expressed                        |
| ORF16 | Os11g0451051 | Conserved hypothetical protein  |
| ORF17 | Os11g0451700 | Similar to Dehydrin DHN1 (M3) (RAB-17 protein)  |
| ORF18 | Os11g0452400 | Conserved hypothetical protein  |
| ORF19 | Os11g0453550 | Conserved hypothetical protein  |
| ORF20 | Os11g0453600 | Conserved hypothetical protein  |
| ORF21 | Os11g0453900 | Dehydrin RAB 16D  |
| ORF22 | Os11g0454000 | Dehydrin RAB 16C  |
| ORF23 | Os11g0454200 | Dehydrin RAB 16B  |
| ORF24 | Os11g0454250 | Similar to Calmodulin   |
| ORF25 | Os11g0454300 | Similar to Water-stress inducible protein RAB21   |
| ORF26 | Os11g0454650 | Non-protein coding transcript   |