

Supplementary Tables

Supplementary Table S1. Comparison of agronomic traits between wild type WYJ7 and mutant *tscd5* (mean \pm SD, n = 9).

Agronomic Characters	Wild type	Mutant
Plant height/cm	92.17 \pm 1.87	85.11 \pm 3.41**
Tillering number	10 \pm 1.09	9 \pm 1.83
Panicle length/cm	18.14 \pm 0.81	17.38 \pm 0.56*
No.of primary rachis branches	14.44 \pm 0.88	14.22 \pm 0.83
No.of secondary rachis branches	35.89 \pm 1.76	33 \pm 2.96*
Grain length/cm	7.13 \pm 0.3	7.04 \pm 0.31
Grain width/mm	3.3 \pm 0.15	3.11 \pm 0.23*
1000-grain weight/g	30.81 \pm 0.1	27.94 \pm 0.07**
Seed setting rate/%	92.41 \pm 2.46	85.52 \pm 4.47**

* Significance at $P < 0.05$, ** extremely significance at $P < 0.01$.

Supplementary Table S2. Genetic analysis of the *tscd5* mutant in F₂ population.

Cross	F ₁	F ₂		χ^2 (3:1)	P-Value
		Wild-type	Mutant		
<i>tscd5</i> /WYJ7	Normal	694	227	0.061	0.805
<i>tscd5</i> /93-11	Normal	1178	376	0.536	0.464

Supplementary Table S3. Primers for fine mapping in this study.

Marker	Forward primer sequence (5'-3')	Reverse primer sequence (5'-3')
B5-6	CATTAAGCAACCTCCTAGCCA	CAATAGAGCCTCTTGATTTAGC
B5-9	AACCACCTAGGTTTCTCCCC	TAGCAACGAGGTTATTGGGC
B5-10	AAACAACGACGTCCCTGATC	GTGCCTCCGTGGTTATGAAC
B5-12	ATCCCGTGTGTTGGCTTAGAATC	TCCAAACATCAGAAAGCAAGCAC
B5-13	TTACCACAAGGATTCTCGTCG	TCCACGGTTAAGATAAATGCATC
ZL-2	CGCCTTTATGAGGAGGAGATGG	AAACTCTTCGACACGCCTTGC
ZL-4	GACGAAGGTGACGTAGACCG	GACGCCTCTAGAAAGCGAG
ZL-5	CCTACGTGGCATACCATTCAGC	GCCTCAGTCCACTGCTCACC
ZL-8	GCGCTCCGAGAATTCGTGAGG	GACCAGCGAGTCGTCGTCATGG
ZL-9	TCAAGCTGCATTAGGAAGACACC	AACTTAGCTGAAACGCAACACG
RM440	GGTAGGCACCAAAGAGTTTGACG	GGCATCACCTTATCCAATCACC

Supplementary Table S4. Primers for vector construction in this study.

Primer	Sequence (5'→3')	Restriction enzyme
TSCD5-COM-F	ACGAATTCGAGCTCGGTACCTTAGTCCCGATTATTTCACCCG	KpnI
TSCD5-COM-R	TCGACTCTAGAGGATCCTAGATCCGGTGCCACATCTATA	BamHI
TSCD5-OE-F	TTCGAGCTCGGTACCATGGCGCTCACGACGTTCTCCA	KpnI
TSCD5-OE-R	GCAGGTCGACTCTAGACTACGCGTTGGGCACCGTCATG	XbaI
TSCD5-GFP-F	TTACAATTACAGTCGAATGGCCTCCGACCTGCGCCCGC	Sall

TSCD5-GFP-R	TGGATCCTCTAGAGTCAGAATGATCTGAAGACGCCTTC	
TSCD5-GUS-F	GCAGGCATGCAAGCTTTATTTGGACACATGCATGGAGT	<i>HindIII</i>
TSCD5-GUS-R	CTCAGATCTACCATGGTGCTCCTCCTCCTCAACGC	<i>NcoI</i>

Supplementary Table S5. Primers for qRT-PCR in this study.

Gene	Forward primer sequence (5'-3')	Reverse primer sequence (5'-3')
<i>Osh36</i>	GCACGGAGGCGAACGA	TTGAGCGGTAGCACCCATT
<i>OsI57</i>	ACCCTAAAGTAAATGAAGTC	CCTGCTCTTGCTTTGTTA
<i>OsI85</i>	GAGCAACGGCGTGAGAGA	GCGGCGGTAGAGGAGATG
<i>OsWRKY23</i>	TCCAGTTCCTCTCCAGTTCTAA	CACATTGTTCTCCTTTTCTTCCC
<i>OsWRKY72</i>	CACCACAAATCACATCTACTCCG	GCTGAAGGGAAGAGAGGTGAG
<i>OsNAC2</i>	AAAAACAACCGCATTTGGCAG	AGTCCTCATCTCCTCTGTCTAATCC
<i>SGR</i>	AGGGGTGGTACAACAAGCTG	GCTCCTTGCGGAAGATGTAG
<i>AOX1a</i>	CTTCGCATCGGACATCCATTA	TCCTCGGCAGTAGACAAACATC
<i>AOX1b</i>	CCTGCTCAGTTTCATCACCATCA	GCATAAAACGGAGTGACAATAGC
<i>APX1</i>	AGGTGCCACAAGGAAAGATCTGGT	TCAGCAGGGCTTTGTCACTAGGAA
<i>APX2</i>	TGGGAAGATGCCACAAGGAGAGAT	TCCGCAGCATATTTCTCCACCAGT
<i>CATA</i>	CAACCGCAACGTCGACAACCTTCTT	TTACCCGGCAGCATCAGGTAGTTT
<i>CATB</i>	GCTTGCTTTCTGCCCAGCGATAAT	AAATAGTTTGGGCCAAGACGGTGC
<i>HEMA</i>	ATGGAGGCCCAAACAATCATC	GCGTAGGACCTCAGCTTCTTGA
<i>GSA</i>	GCTCTCCGTGACTTGACGAAAC	CCGAAGTATTCTTGAGCCCCA
<i>HEME1</i>	GATCCCTTGAGAACAGCAGCTG	CATTGTAAACCTCTTCCCGCAA
<i>CHLD</i>	CGCATGCAGAATGCGAAAG	CCTCAGCAAAATCTCCACGAAA
<i>DVR</i>	CGAGCCCAGGTTTCATCAAGGTGC	CCTCCCGATCTTGCCGAACCTCC
<i>CHLH</i>	AACTGGATGAGCCAGAAGAGA	AAATGCAAAAGACTTGCGACT
<i>PORA</i>	ATGGCTCTCCAAGTTCAG	TGGCTCACGCTAAGGAAC
<i>PORB</i>	CCGCAAGGAGGGAGCGGTG	CCCTCTTGGTGCTAAGGCCG
<i>CAO1</i>	GACACCTTCATCTGGGCTTCAA	CGAGAGACATCCGGTAGAGC
<i>NYC1</i>	CATGCAACACCAACAAAAGG	GACCATTCCAGGAGAAGCAG
<i>NYC3</i>	TCTATCTAGGTGCCAAAGGC	ATTCTGGCACCTGCTGTTTC
<i>RCCR1</i>	CGCATTTCTCATGGAATTT	CTTCTCACGCTGTTTGTTCA
<i>PCCR</i>	GGATCGACGATTGATTTTCATG	GTCGAGGCGTTCAGAAAGAT
<i>PAO1</i>	AAGCCTCCGATGTTACCGAAA	CGAGGGTTTCCAGAATTTGA
<i>HSA1</i>	AATCAGGTGACGCCATTGTTG	GCATGTTTCATTGCAGTATGCA
<i>RpoTp</i>	TCCTCATGTGAGCAAGGAT	GAAAGAATGTCTGGACTTTG
<i>POLP1</i>	ACCGGTGCTTTCAGGCTTGG	GCTGACTGATAATCACACG
<i>RpoA</i>	CGCATCAATTTGCGTCAAAG	GTTAGCTATAGGTTGTGCCGTATCAA
<i>RpoB</i>	CAAGTTTTTCGGAGCCGAGAT	GCTAAAGATCCAGTAAGTCCAACGT
<i>RpoC1</i>	TCCGTCGGAACAACAATCTTG	TCCACGGCTTCTTGTACCAAT
<i>RpoC2</i>	ATGCATCGCAGGTACACCAA	CCCTCGCGTAAATTGCTTTG
<i>rps7</i>	GCCAAAATCCATTCCAATTC	GGAGATGTACACGAGGAGATTG
<i>rps15</i>	AGATACGGAGACTTGCTTCA	GCTCCCTAATATCCAAGTACT
<i>V1</i>	AGAATCAGCGCGAGAAGAGAACCT	TACACCAGCTTTGGAGGAGCTGAA
<i>V2</i>	AGCAGATCCGTGATTACATGGCGA	TGCTCTTCACTCTCTGCAACCAA

<i>TCM5</i>	TCCGCTGCGATTCTTGCT	TCCTCTGCTCGTCCGTCAT
<i>RbcL</i>	CTTGGCAGCATTCCGAGTAA	ACAACGGGCTCGATGTGATA
<i>rbcS</i>	TCCGCTGAGTTTTGGCTATTT	GGACTTGAGCCCTGGAAGG
<i>psaA</i>	GCGAGCAAATAAAACACCTTTC	GTACCAGCTTAACGTGGGGAG
<i>psbA</i>	CCCTCATTAGCAGATTCGTTTT	ATGATTGTATTCCAGGCAGAGC
<i>CAB1R</i>	AGATGGGTTTAGTGCGACGAG	TTTGGGATCGAGGGAGTATTT
<i>CAB2R</i>	TGTTCTCCATGTTTCGGCTTCT	GCTACGGTCCCCACTTCACT
<i>LchP2</i>	GAAGAAGATCAAGAACGGCC	TTGCCGGGGACGAAGTTGGT
<i>Lhcb1</i>	CCATGTTCTCCATGTTTCGGCTTCT	TAGGCCCAGGCGTTGTTGTTGA
<i>Lhcb4</i>	TACCTGCAGTTCGAGCTGGAC	AGGCCGAACACCTCGGTGTA
<i>TSCD5</i>	GAAGCAAATCGGAGGGTCG	ATGAGGTCGTGATGTTGTG
<i>Histone</i>	GGTCAACTTGTTGATTCCCCTCT	AACCGCAAAATCCAAAGAACG
