

Figure S1. Schematic representation of the *oscoila* double mutant lines.

OsCOIIa and *OsCOIIb* gene structures and the CRISPR-Cas9 target sites are shown. The insertion and deletion sites of two allelic mutations (*oscoila-1/b-1*, *oscoila-1/b-2*) generated by two gRNAs are shown in comparison with the wild-type (WT) sequence.

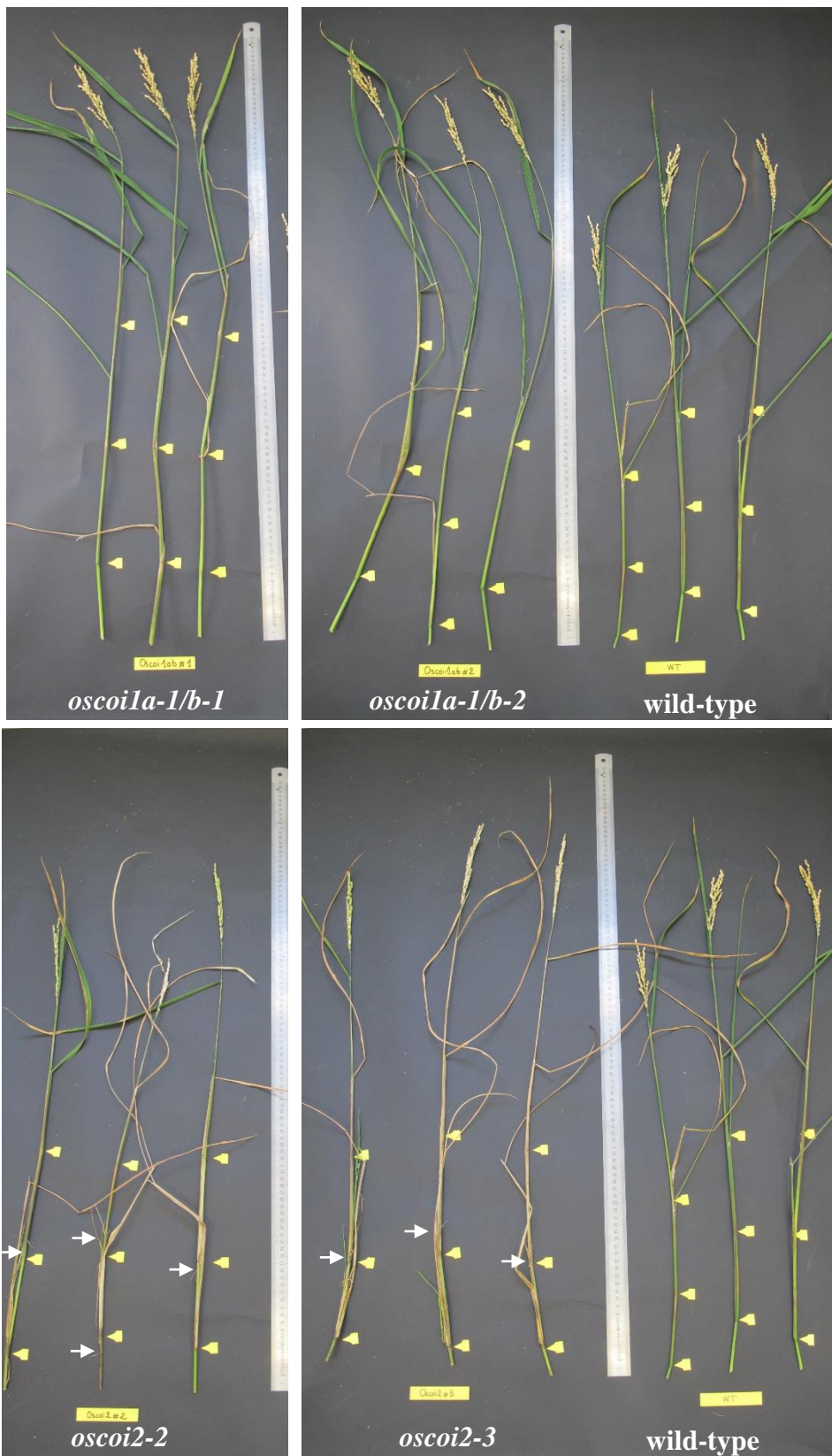


Figure S2. Images of wild type, *oscoi1a-1/b-1*, *oscoi1a-1/b-2*, *oscoi2-2* and *oscoi2-3* show panicle phenotypes.
 Yellow arrows show nodes 1, 2 and 3. White arrows indicate adventitious roots from nodes.

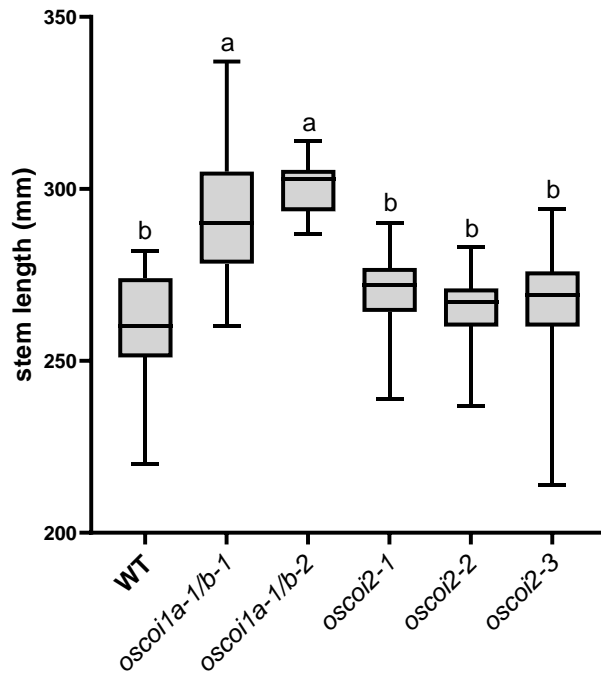


Figure S3. Quantification of stem length of the WT and *oscoi* mutant plantlets.

Quantification of stem length of the WT and *oscoi* mutants plantlets. Letters indicate significant differences between lines (21 < n < 24, One way-ANOVA with Tuckey's multiple comparisons test, $p < 0.05$). In the boxplots, whiskers denote minimum/maximum values, the box defines the interquartile range and the centre line represents the median.

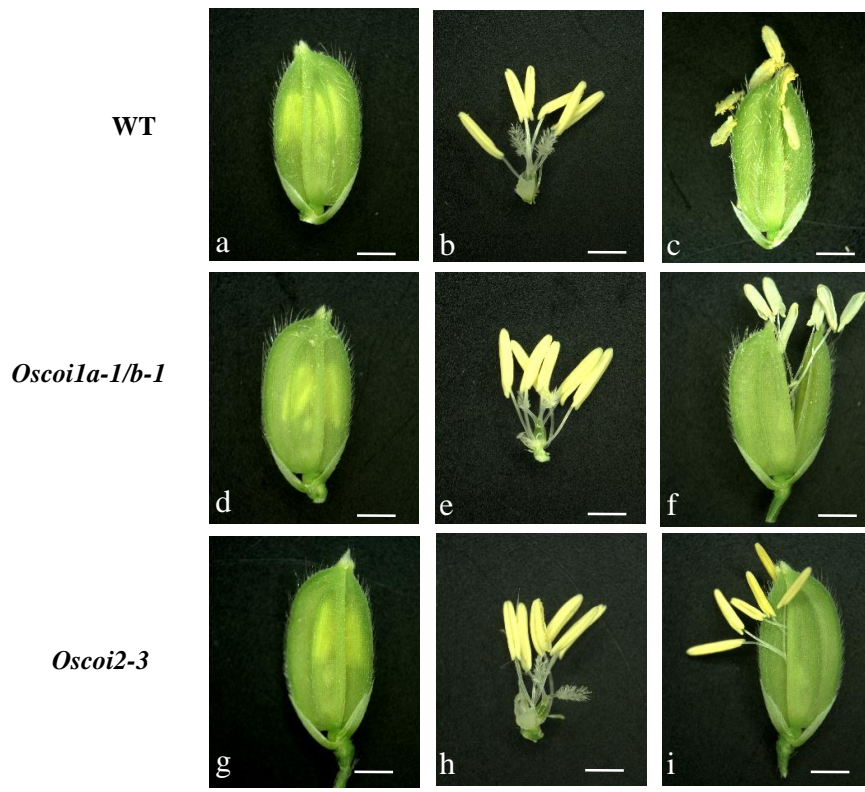


Figure S4. Comparison of anther dehiscence between the wild-type and the *oscoi* mutants.

Close spikelet before anthesis (a, b, d, e, g and h) and after widely opened spikelet (c, f, i).

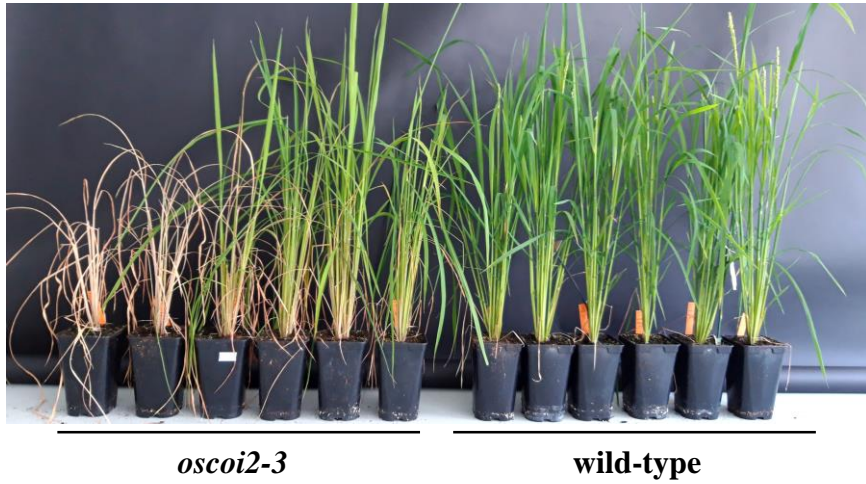


Figure S5. Image of wild-type and *oscoi2-3* mutant plants showing mortality at reproductive stage.

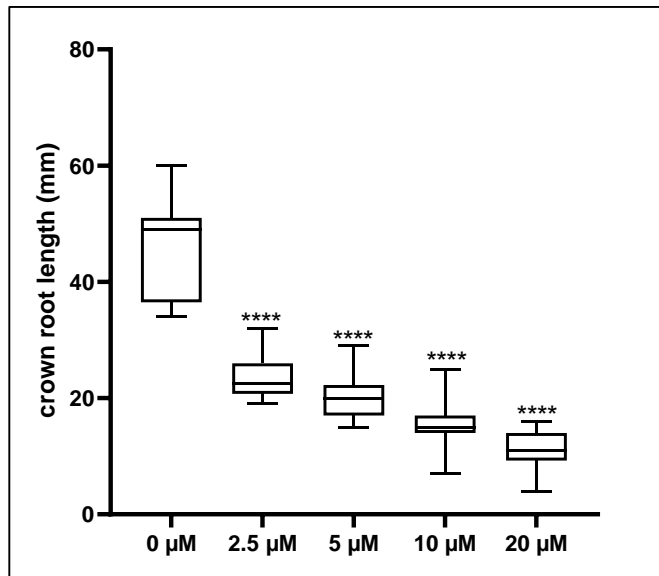


Figure S6. JA dose-dependent effect on crown root length

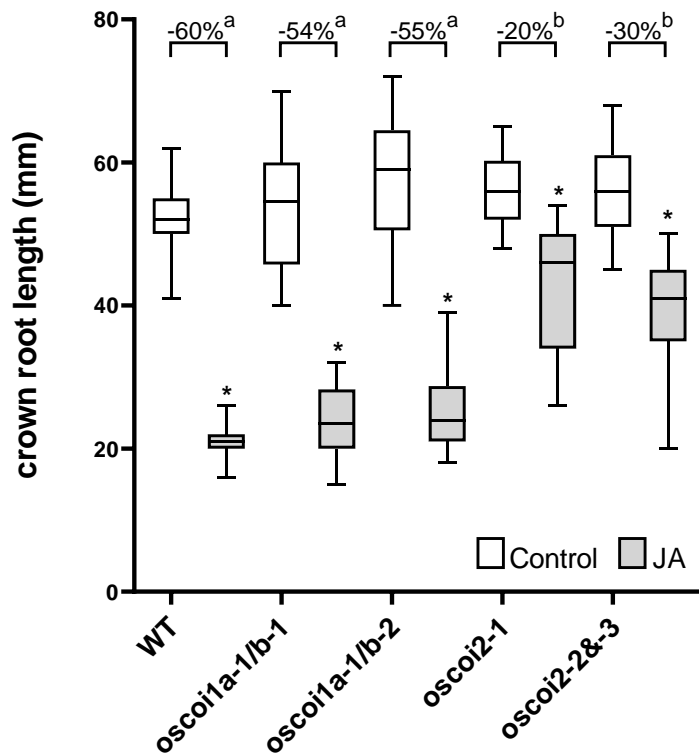


Figure S7. Crown root growth inhibition assay by JA application on WT and T2 *oscoi* mutants. Effect of JA on crown root length of the WT, two allelic mutations of the double mutant *oscoi1a/oscoi1b* (*oscoi1a-1/b-1* and *oscoi1a-1/b-2*) and two mutants of *OsCOI2* (*oscoi2-1*, *oscoi2-2&-3* heterozygous line). In the boxplots, whiskers denote minimum/maximum values, the box defines the interquartile range and the center line represents the median. Asterisks indicate significant differences between treated and control plants (One way-ANOVA with Bonferroni's multiple comparisons test, $p < 0.05$). The plot values are the means of the crown roots. Percentage of crown root growth inhibition by JA from the WT, *oscoi1a-1/b-1*, *oscoi1a-1/b-2*, *oscoi2-1* and *oscoi2-2&-3* heterozygous line. Letters (a, b) indicate significant differences between lines (One way-ANOVA with Tuckey's multiple comparisons test, $p < 0.05$)

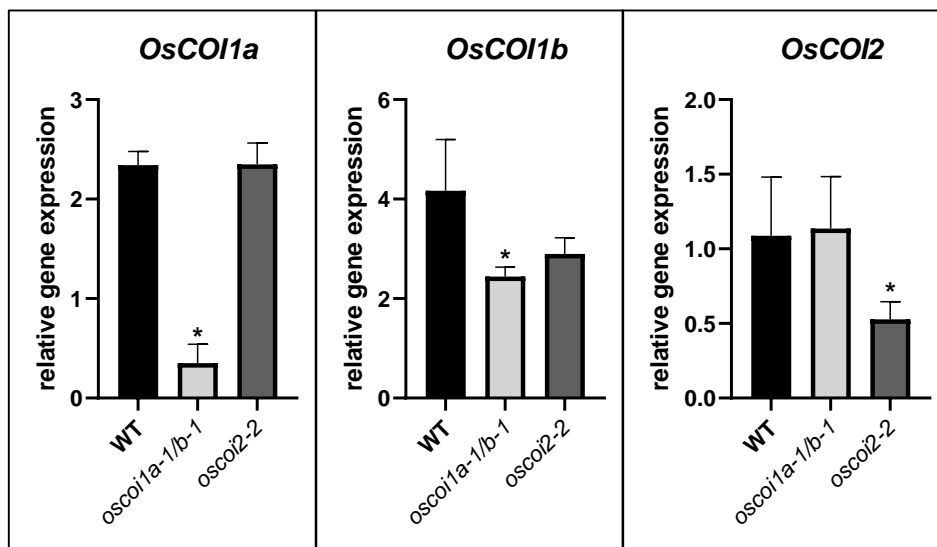


Figure S8. Relative expression of *OsCOI* genes in WT and *oscoi* mutants in crown root tips

Gene name	Locus or Target	Forward primer	Reverse primer	Amplicon size	Use
<i>OsCOI1a</i>	LOC_Os01g63420	GATGCCCTCCCTGAGATACA	CCACACAGGGTTCTCCATCT	158 bp	qPCR
<i>OsCOI1b</i>	LOC_Os05g37690	CAGGCCTTGCTATATTGGA	CAGGGGAAGGCATACCTCGTA	188 bp	qPCR
<i>OsCOI2</i>	LOC_Os03g15880	ATGGGTGCAAGGATACAAGG	TGCAAGAATCTGTGCCTGAC	133 bp	qPCR
<i>OsAOC</i>	LOC_Os03g32314	AAGAGGAATCGAGGACAAGATATTTG	AAGCCTCTTCTGTTCGGATCA	75 bp	qPCR
<i>OsJAZ5</i>	LOC_Os04g32480	CGAGGCAACTAAAGCAAAAGGA	TGAGTGGCTCTTTGGCAAAATT	71 bp	qPCR
<i>OsJAZ8</i>	LOC_Os09g26780	GAAGGCTCAACAGCTGACCAT	TTGGTGGACGGGAAGTTCTC	69 bp	qPCR
<i>OsMYC2</i>	LOC_Os10g42430	CTAGCGAGGAAACCAATCG	CCATCCATCCATCCTAACAC	158 bp	qPCR
<i>OsWRKY71</i>	LOC_Os02g08440	CGGCAAAAGACGCTTGTAAAC	TCGGGACCGAAGCAAATTTG	106 bp	qPCR
<i>OsPR5</i>	LOC_Os12g43380	CTGGCGGAGTTCACCATC	GCAGGAGAAGCTCATGGC	87 bp	qPCR
<i>OsPR10</i>	LOC_Os03g18850	CGGACGCTTACAACATAATCG	AAACAAAACCATCTCCGACAG	174 bp	qPCR
<i>OsPLT1</i>	LOC_Os04g55970	AACATTCGGCACTGAGGAGG	CTCCCGATTGGAAGTTGCT	141 pb	qPCR
<i>OsPLT6</i>	LOC_Os11g19060	TCCAGACGTCACAGGTTTCG	CGGGAGACCATGAAAGCCAT	94 pb	qPCR
<i>OsEXPB7</i>	LOC_Os03g01270	GTCAGTATCCAGGGCTGACG	CGTACTCCACAGTATCGCC	81 bp	qPCR
<i>OsEXP13</i>	LOC_Os02g16730	CAAGTGAGCCACCTGATCGAT	ACCCCCATCAGCATCCAAATT	153 pb	qPCR
<i>OsXTH12</i>	LOC_Os06g48180	AGTGCACTGCCAAGTAGGAAA	TCTTCCTCGTATCCTTTTCCCA	133 pb	qPCR
<i>OsCYCB1</i>	LOC_Os01g59120	CTCTCAAGCACCACTGGA	CTTGCTCTCAGGGGCGTAG	92 pb	qPCR
<i>OsCDKB1</i>	LOC_Os01g67160	GTCCGTTGGTTGCATCTTCG	GTTACTCCAGGCCACTGCTC	132 pb	qPCR
<i>OsCDKB2</i>	LOC_Os08g40170	CGCTCGTTCACTGTCCCTCT	CCACAGACCAGATGTCAACCG	121 pb	qPCR
<i>EXP</i>	LOC_Os06g11070	TCCATCTGCTCCCGTTGTTGTG	AAAGAGTTCGCCACCAACCGTC	273 bp	qPCR
<i>OsCOI1a</i>	target 1	TGGAAGAGTGCCATATTACTG	TCAAACACAATTAATCAATGC	496 bp	identify mutations
<i>OsCOI1b</i>	target 2	TGTCATACTTTAGCTCACTGG	ACGTAAGTCTTAAGGAGCACA	477 bp	identify mutations
<i>OsCOI2</i>	targets 1 and 2	CCATGGCGTACTCCACCACG	GAGAGAACTCCTAAGACGTAG	462 bp	identify mutations
<i>OsCOI2</i>	targets 3 and 4	CCATATGTTGTCAATTTGCAG	CAGCGCTGGACCAGCTGACAG	485 bp	identify mutations
<i>Cas9</i>	T-DNA	GGATGATGGCATATGCAGCAG	GAGTGTGAGGTCCTGTTGGT	1216 bp	check T-DNA insertion
<i>HPT</i>	T-DNA	CTCGGAGGGCGAAGAATCTC	GCTCCAGTCAATGACCGCTG	759 bp	check T-DNA insertion

Table S1. List of primers used for qPCR and plant genotyping.