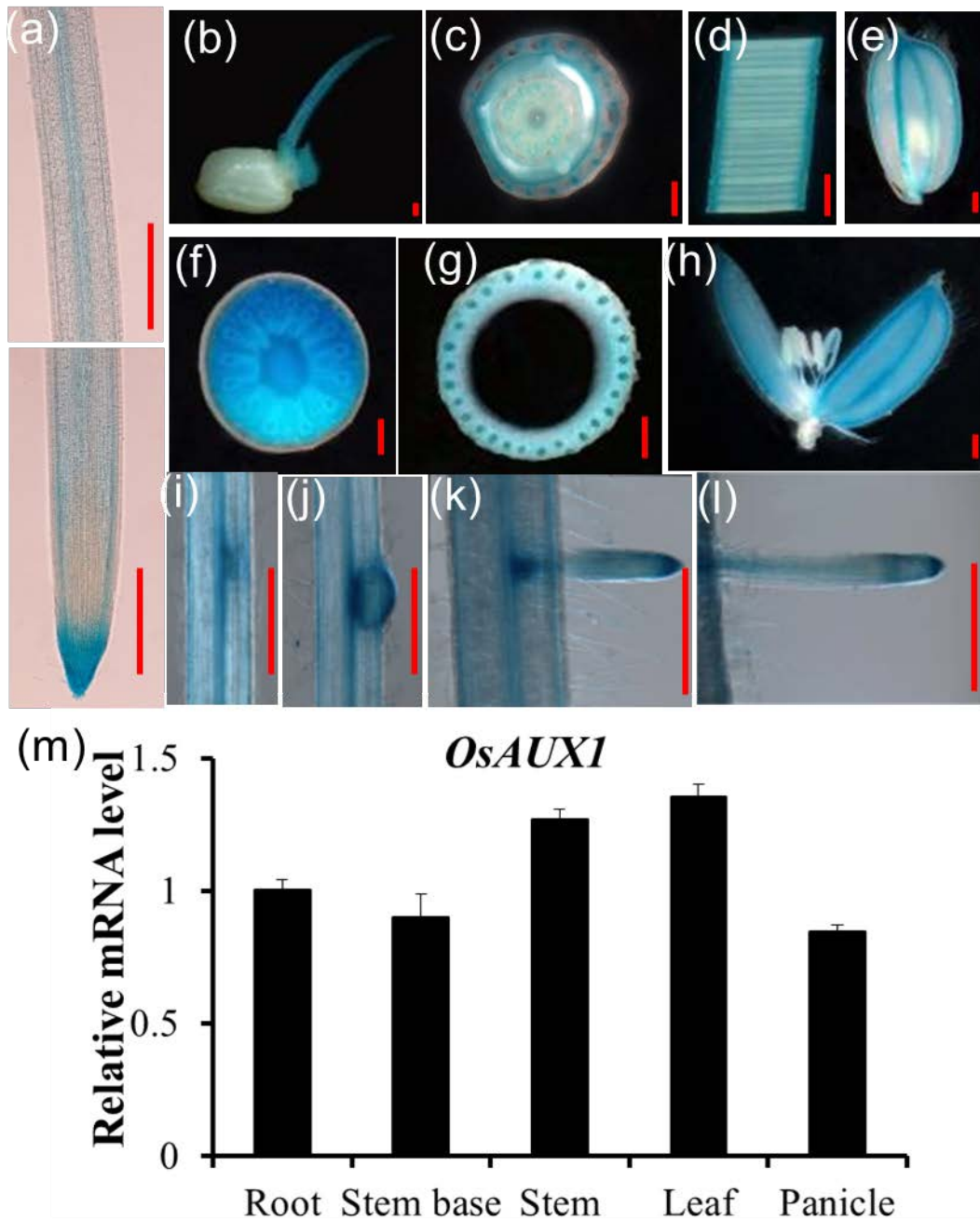**Figure S1.** Root hair length in WT and osaux1-1 mutant under various treatments.

Root hair length of WT and *osaux1-1* under Control, 1μM IAA, 0.1μM 2, 4-D and 0.1μM NAA

treatments for 3 days. Ten seedlings were measured at each treatment. Means marked

with different letters indicate significant differences using Duncan's multiple range

mean comparisons at 5% alpha.

Figure S2. Expression pattern of *OsAUX1*.

(a-k)The expression pattern of *OsAUX1*, as revealed by promoter GUS fusion analysis in transgenic seedlings . Region of PR maturation (a), germinated seed (b), stem base (c),leaf(d), glume(e), stem node(f), stem(g) , flower(h), LR from initiation to mature (i-l).Bar=500μm for (a-k) .(m)Quantitative reverse transcription PCR of *OsAUX1* expression in various tissues. Total RNA was extracted from the root, stem base, stem, mature leaf and panicle of the wild-type.

Experiments were analyzed using three independent biological repeats.
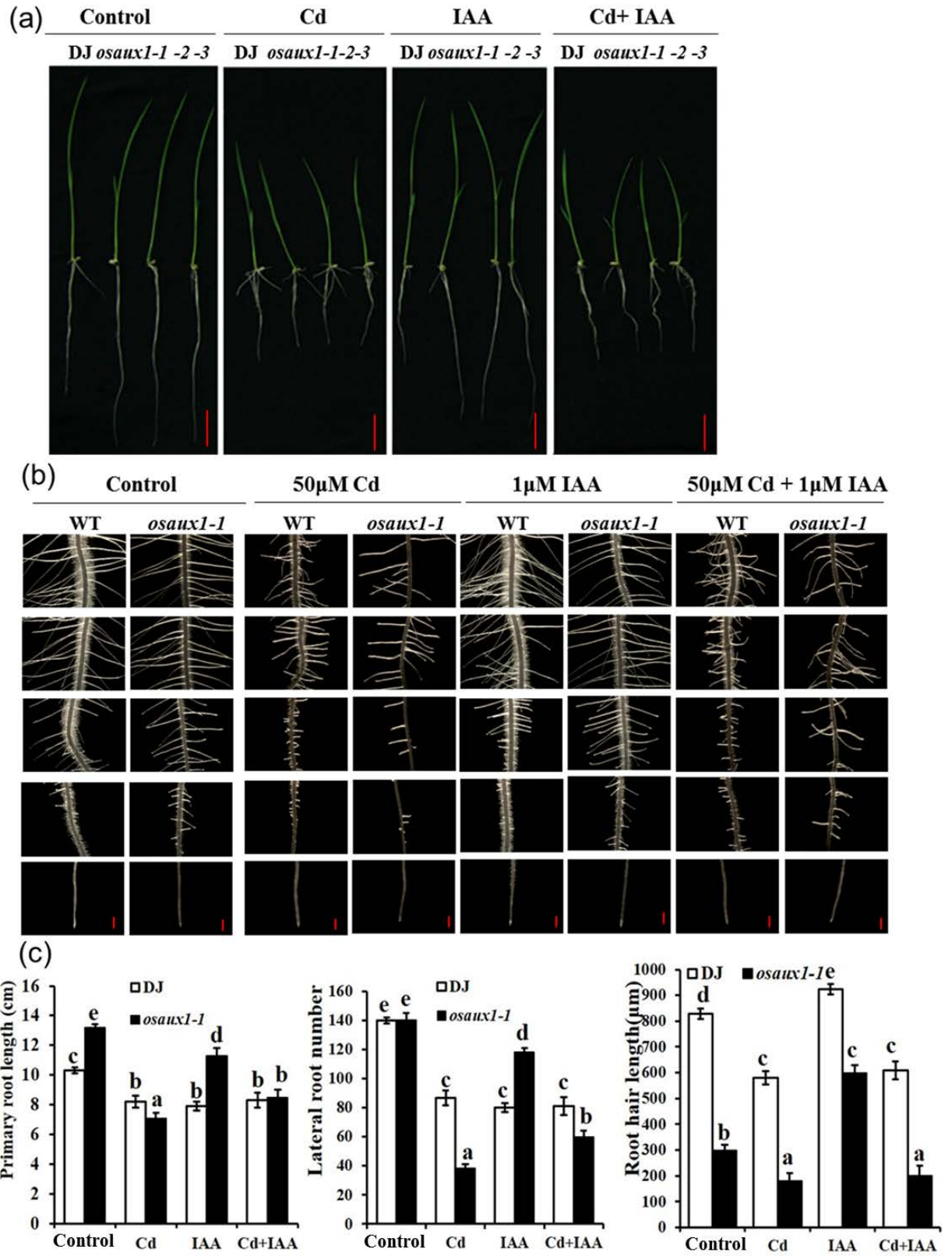
Figure S3. Phenotype of WT and *osaux1* under Cd and IAA co-treatment

(a) Phenotype of WT and *osaux1* under Cd and IAA cotreament. Left to right, WT, *osaux1-1, osaux1-2* and *osaux1-3* growth in Control, 50μM CdCl₂, 1μM IAA, and 50μM CdCl₂ plus 1μM IAA for 7 days. Bar=2cm.

(b) Phenotype of LR and RH in WT and *osaux1* under Cd and IAA cotreament. Left to right, WT and *osaux1-1* mutant planted in Control, 50μM CdCl₂, 1μM IAA, and 50μM CdCl₂ plus 1μM IAA for 7 days. Bar=1mm. These phenotypes were observed with a Leica MZ95 stereomicroscope.

(c) Statistics of roots phenotype. PR length, the number of LR and RH length was measured in WT and *osaux1* planted in Control, 50μM CdCl₂, 1μM IAA, and 50μM CdCl₂ plus 1μM IAA for 7 days. Ten seedlings were measured at each parameter. Means marked with different letters indicate significant differences using Duncan's multiple range mean comparisons at 5% alpha.

Table S1. PR lengths of 7 days seedling of WT, *osaux1* mutants and *OsAUX1* over-expression lines under various treatments.

PR length (cm)	DJ	*osaux1-1*	*osaux1-2*	*osaux1-3*	*OsAUX1-O1*	*OsAUX1-O2*	*OsAUX1-O3*
Control	10.21±0.58	13.91±0.54**	13.86±0.32**	13.88±0.44**	7.12±0.45**	7.25±0.34**	7.85±0.55**
IAA treatment	7.21±0.25	11.19±0.45**	11.31±0.36**	11.40±0.42**	4.12±0.24**	4.75± 0.28**	4.95±0.32**
2.4-D treatment	4.42±0.18	8.30±0.45**	8.52±0.25**	8.64±0.55**	1.54±0.12**	2.05±0.15**	2.15±0.18**
NAA treatment	2.24±0.15	2.12±0.18	2.25±0.21	2.23±0.18	1.25±0.14**	1.55±0.14**	1.65±0.14**
NPA treatment	4.31±0.25	8.56±0.45**	8.55±0.34**	8.58 ±0.42**	1.56±0.12**	2.15±0.25**	2.23±0.22**

All values are the averages of 10 seedlings for 7 days plants (±SD).

* Significant difference from wild type at 5% by student's *t* test.

** Significant difference from wild type at 1% by student's *t* test.

Table S2. LR number of 7 days seedling of WT, *osaux1* mutants and *OsAUX1*-overexpression lines under various treatments.

PR length (cm)	DJ	*osaux1-1*	*osaux1-2*	*osaux1-3*	*OsAUX1-O1*	*OsAUX1-O2*	*OsAUX1-O3*
Control	140±5	138±9	140±8	142±9	65±4**	70±4**	78±5**
IAA treatment	68±4	116±5**	118±4**	121±4**	25±5**	30±5**	30±6**
2.4-D treatment	57±6	107±5**	113±6**	109±7**	10±2**	15±1**	15±1**
NAA treatment	40±2	40±3	39±3	40±5	15±2**	18±2**	18±3**
NPA treatment	40±4	92±5**	95±5**	95±7**	8±1**	8±1**	8±1**

All values are the averages of 10 seedlings for 7 days plants (±SD).

* Significant difference from wild type at 5% by student's *t* test.

** Significant difference from wild type at 1% by student's *t* test.

Table S3. Primers used in this study.

Name	Primer sequences (5'-3')
OVAUX1 U/L	GAGCTCATGGTGCCGCGCGAGCAGGC/GGATCCGTGGTGCGGCAATGGCACCG
35S:ORF$_{AUX1}$-GFP U/L	GAGCTCATGGTGCCGCGCGAGCAGGC/GGATCCGTGGTGCGGCAATGGCACCG
ProAUX1-GUS U/L	AAGCTTTGAGACAAATAGAGTAGATT/GGATCCGCTGACCACGCCGCCCTTCC
ProAUX1-GFP U/L	GAATTCTGAGACAAATAGAGTAGATT/GAGCTCGCTGACCACGCCGCCCTTCC
osaux1-1 LP / RP	TGGACCGCCTACCTAATCAG/TTTGCTTACACTGTGACGGC
osaux1-2 LP / RP	AACAAAAACATGCATGCAGC/ATCTTGACAATGCCCCTCAC
osaux1-3 LP / RP	TATTTGTCGGCTCCTCCATC/AAGCGTCGATGAAATCCATC
Ngus-RB	AACGCTGATCAATTCCACAG
AUX1-qRT U/L	GCCTGCGCGAGTAACATCTA/CAGCACCAGCTTGGTTGGAC
AUX2-qRT U/L	CTCTTCTACGGGCTGTTGGG/CGTCCTCTTGTCCAGCTTGT
AUX3-qRT U/L	TTGGAATTTTGCAGGTGGCG/ACCACTGGATGACGTGGTTC
AUX4-qRT U/L	GGCCTTCAACTGCACGTTTT/GATGTACCAGGCGGTGTAGG
AUX5-qRT U/L	GACAAGCGGACATGGACCTA/AGATCATCTTGAACCGCCGC
OsACTIN U/L	TCAGCAACTGGGATGATATGGAG/GCCGTTGTGGTGAATGAGTAAC
OsCyCB1;1-qRT U/L	AATGTTGCCGCTCTGGGAAA/GATGACATGCTCGGGCGGAGG
OsHMA3-qRT U/L	GCAAGTCAAGCCACCCAATG/ACGCCCTTGATCATCTCACC
OsHMA5-qRT U/L	GGGGCTAATCATGGGGTACT/GAACTCCTGTCTTCGCGTTC
OsHMA6-qRT U/L	ATAATGGAGGAGGCCGAACT/CCTGCCTTTTCATGTGGAGT
OsHMA9-qRT U/L	CAGTAATCGGAGGGACAATG/GTGATGAAACGGTGAAGAGG