

SUPPORTING FIGURE LEGENDS:

Figure S1. Phenotype of *osabcb14* mutants and complemented transgenic lines under NAA treatment.

(a) Phenotype of seven-day seedlings under NAA treatment. Bar = 2 cm.

(b) Shoot length under indicated concentrations of NAA at seven-day.

(c) PR length under indicated concentrations of NAA at seven-day.

Figure S2. Expression of *OsABCB14* in roots responded to various treatments.

(a) *OsABCB14* expression of response to various treatments. Seven-day-old seedlings grown in normal culture solution were treated for 3 h with 1 μ M 2,4-D, 10 μ M IAA, 1 μ M NAA, 1 μ M 6-BA, 10 μ M ABA, 10 μ M GA₃, 1 mM SA, 1 μ M NPA or 10 μ M NOA. Total RNA from roots were analyzed with qRT-PCR.

(b)(c) Expression of *OsABCB14* in 1 μ M 2,4-D (b) or 10 μ M IAA treatments (c) at indicated time intervals. Seven-day-old seedlings grown in normal culture solution were exposed to 1 μ M 2,4-D (b) or 10 μ M IAA treatments (c) until roots were sampled at indicated time intervals. (a) to (c) All qRT-PCR experiments were analyzed using three independent biological repeats. *OsACTIN* gene was used as an internal control.

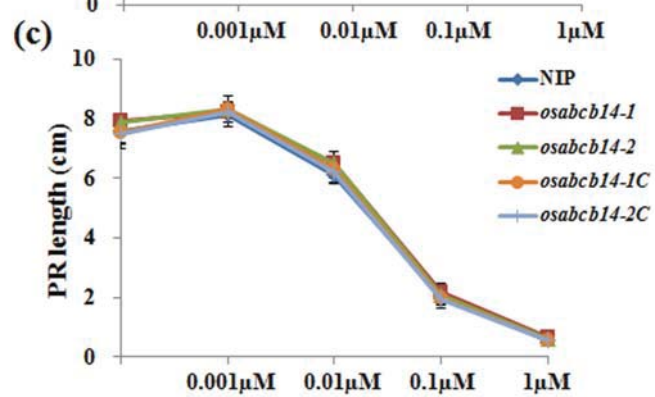
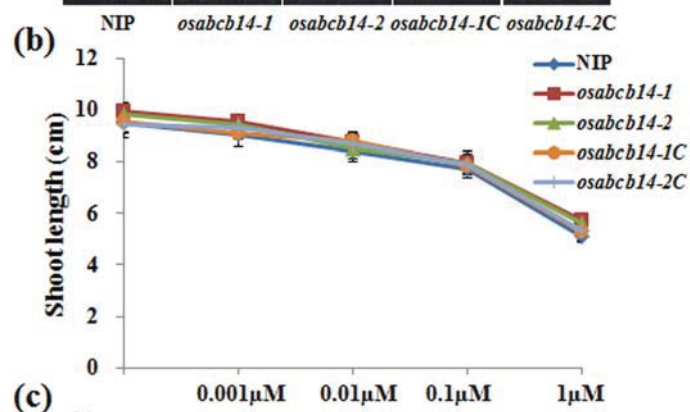
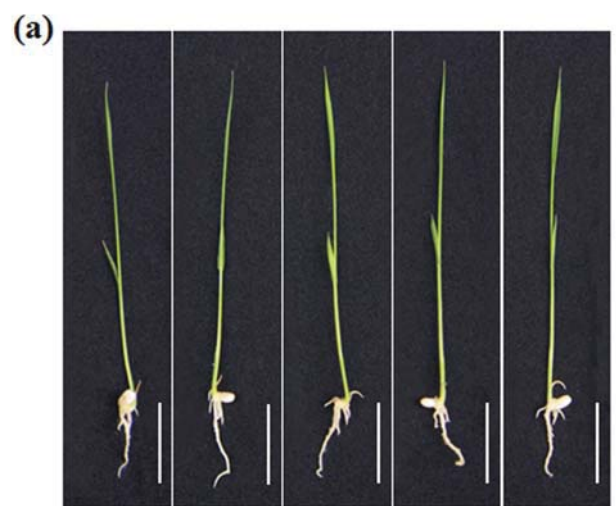
Figure S3. Mn, Cu, Zn, Mg and Ca concentrations (μ g/g) in shoot and root of *osabcb14* mutants.

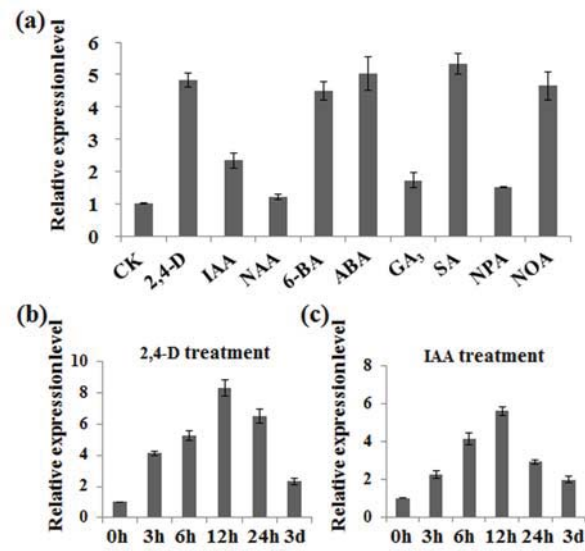
(a) to (e) Mn(a), Cu(b), Zn(c), Mg(d) and Ca(e) concentrations ($\mu\text{g/g}$) in shoot and root of *osabcb14* mutants. All experiments were analyzed using five independent biological repeats. * indicates significant difference at $P < 0.05$ and ** at $P < 0.01$.

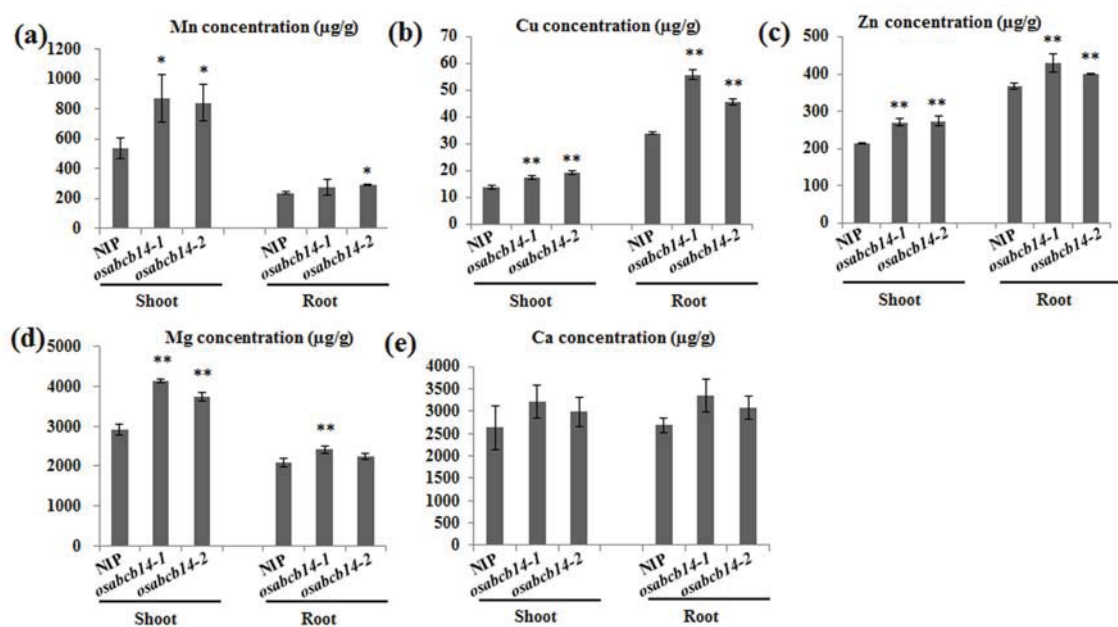
Figure S4. Relative expression of genes related to Fe uptake and transport in roots of NIP and *osabcb14* mutants.

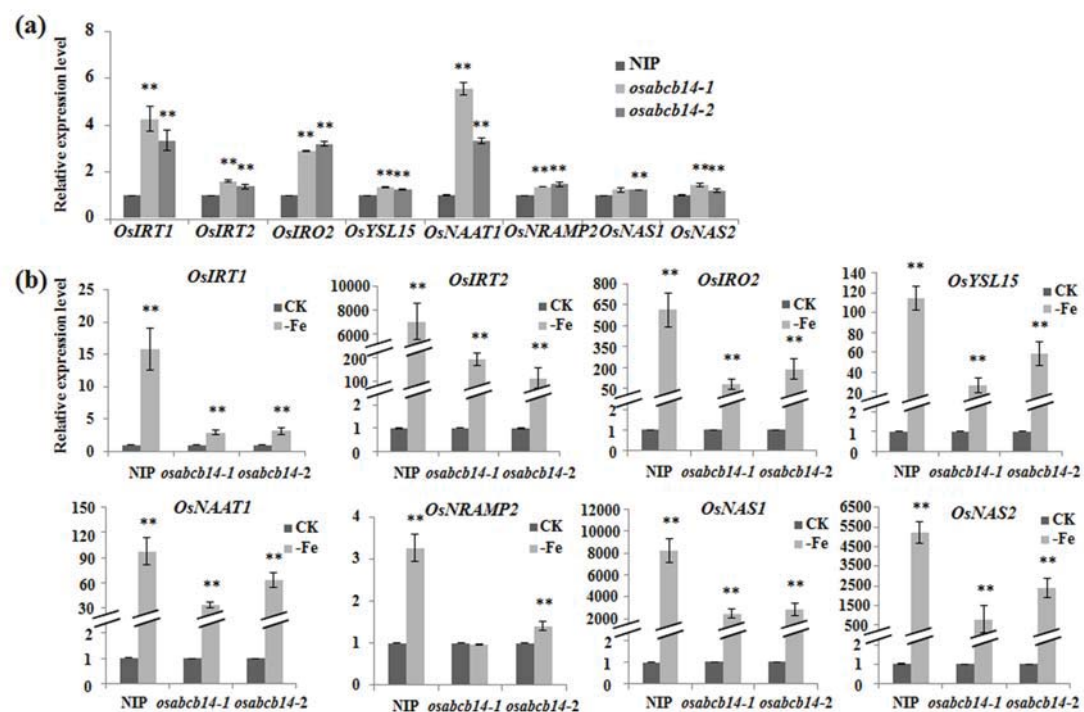
(a) qRT-PCR analysis for genes related to Fe response in roots of NIP and *osabcb14* mutants.

(b) qRT-PCR analysis for genes related to Fe response in roots of NIP and *osabcb14* mutants under CK and $-\text{Fe}$. (a)(b) All qRT-PCR experiments were analyzed using three independent biological repeats. *OsACTIN* gene was used as an internal control. CK: normal culture solution. * indicates significant difference at $P < 0.05$ and ** at $P < 0.01$.









Supporting Tables

Table S1. Primer sequences of *OsABCB14*

Name	Primer sequences (5'-3')
Tos17-tail6	AGGTTGCAAGTTAGTTAAGA
ABCB14-1U/L	TTTACCTGGGCAAAGTTGG/TACGGTGCGTTGACATGATT
ABCB14-2U/L	AATCATGTCAACGCACCGTA/TTGCAGGTCAAGTTTTGCTG
RTABCB14U1/L1	CAGAAACCGTGACTTCCGTGG/CATCATTCTCAAGATAGCAGC
qRTABCB14U1/L1	CAGAAACCGTGACTTCCGTGG/TAACCCTTAGGTGCTGGGTAC
RTABCB14U2/L2	ATGGCGGATGAGTCAGGGAG/AAGTTGCCGACCTTCTCGCCG
qRTABCB14U2/L2	ATGGCGGATGAGTCAGGGAG/TCGCCGAAGAGGAGGAAGAAC
RTABCB14U3/L3	AGATCGGCCTGGTGCAGCAG/GTGGTG TAGCTGCAGCTGCAG
qRTABCB14U3/L3	TGCTGCAGGAGGCGCTCGA/GTGGTG TAGCTGCAGCTGCAG
ABCB14-OU/L	CACCATGGCGGATGAGTCAGG/GCCGTGGTG TAGCTGCAGCT
ABCB14-proU/L	GTCGACCGAGTAGTTTATGCATAATG/GGTACCCACGCACGCTCA CCTCT

Table S2. Primer sequences for auxin-responsive genes.

Name	Primer sequences (5'-3')
qRTIAA1U/L	GCCGCTCAATGAGGCATT/GCTTCCA TTTCTTTCAATCCAA
qRTIAA3U/L	AACTGAACAACAACAAGAAGAA/GCAATGAGGAGATGAGATGA
qRTIAA9U/L	AAGAAAATGGCCAATGATGATCA/CCCATCACCATCCTCGTAGGT
qRTIAA20U/L	TTGTACGTGAACGGGATTATTTTG/CATGCTTATGAAATTGCTGAAACA

qRTIAA23U/L	GAAGATGTTCGTCGAGTC/GTCTTGGCGATAAGTTGA
qRTSAUR39U/L	CTAAGGTTGTCTGAGGAT/CAAGCACATCACATACTC

Table S3. Primer sequences for Fe-deficiency responsive genes.

Name	Primer sequences (5'-3')
qRTIRT1U/L	CGTCTTCTTCTTCTCCACCACGAC/GCAGCTGATGATCGAGTCTGACC
qRTIRT2U/L	CGTTCCACACGCGGGGCAGCAAG/CCCATCCCCTCGAACATCTGGTGG
qRTIRO2U/L	GGCTACCTGCATCAATGAC/GCTTTGTTCTGACGACTTT
qRTYSL15U/L	AACATAAGGGGGACTGGTAC/TGATTACCGCAATGATGCTTAG
qRTNAAT1U/L	AGACCAGGCTACCCAAACT/CACCTCTTTGATAGCGATCC
qRTNRAMP2U/L	ATCGCCATCAAGATCCTCAGCC/GTATCTCAACGCTTCACGGACT
qRTNAS1U/L	GGACGCGGTGTTTCGACAACTAC/GGGCGACGATGACGGAGTTGA
qRTNAS2U/L	ATCAACTCCGTCATCGTGGCTC/TTACTCGTCGTTGTCCCCTAGA