

Figure S1

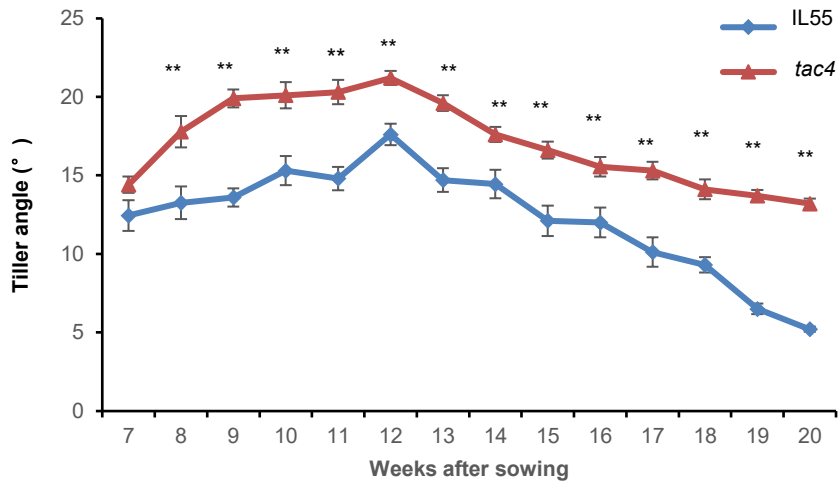


Figure S1. Kinetic analysis of tiller angle between IL55 and the *tac4* mutant. Error bars indicate SEM, $n = 10$. The double asterisks represent a significant difference determined by Student's *t*-test at $P < 0.01$.

Figure S2

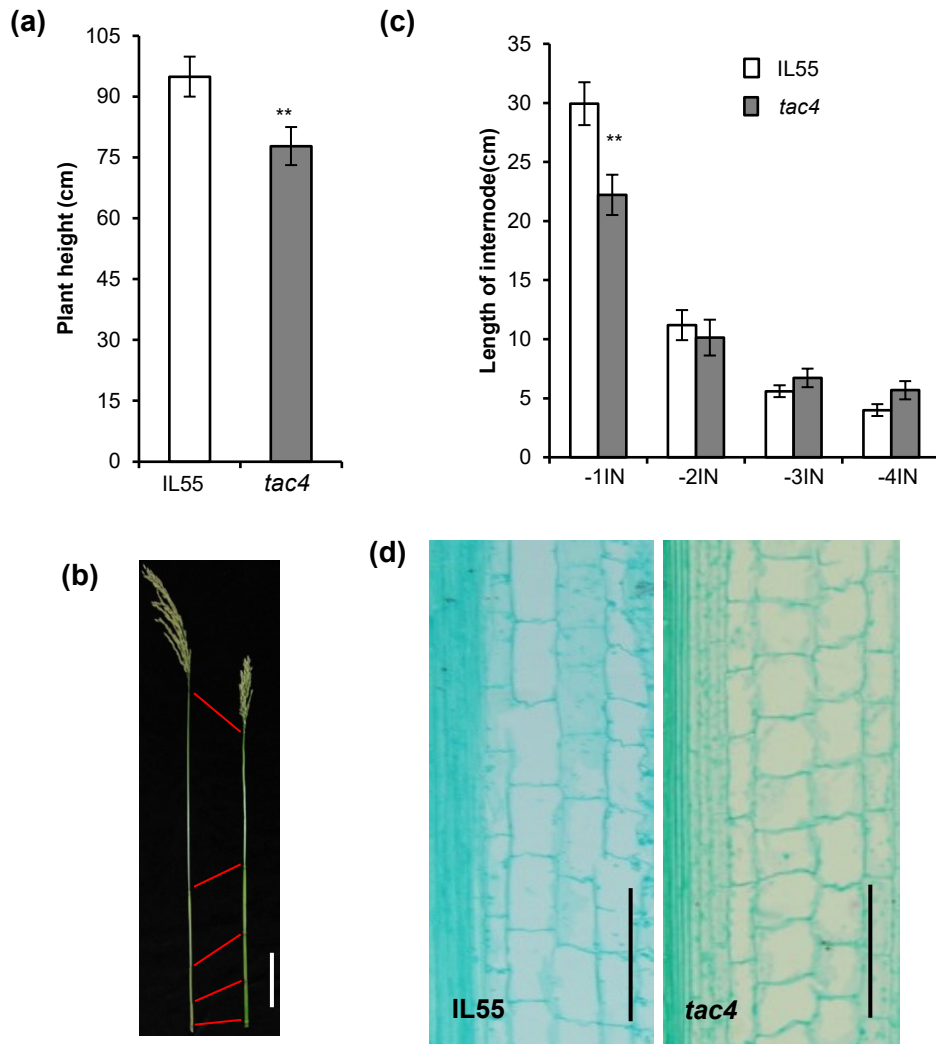


Figure S2. *TAC4* regulates plant height.

(a) Comparison of the plant height between IL55 and *tac4* mutant. (b-c) Internode length comparison. Scale bar, 10 cm. (d) Longitudinal sections of the uppermost internodes. Scale bar, 100 μm. Error bars indicate SD, $n = 20$. The double asterisks represent a significant difference determined by Student's *t* test at $P < 0.01$.

Figure S3

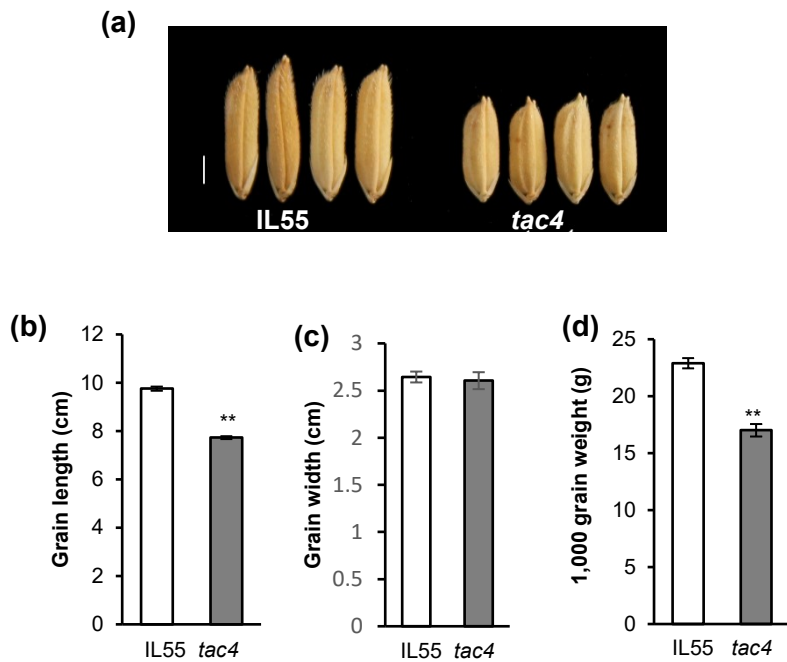


Figure S3. *TAC4* regulates grain size and weight.

(a) Grains of IL55 and *tac4*. Scale bar, 2 mm.

(b-d) Comparison of grain size and weight. The double asterisks represent a significant difference determined by Student's *t* test at $P < 0.01$.

Figure S4

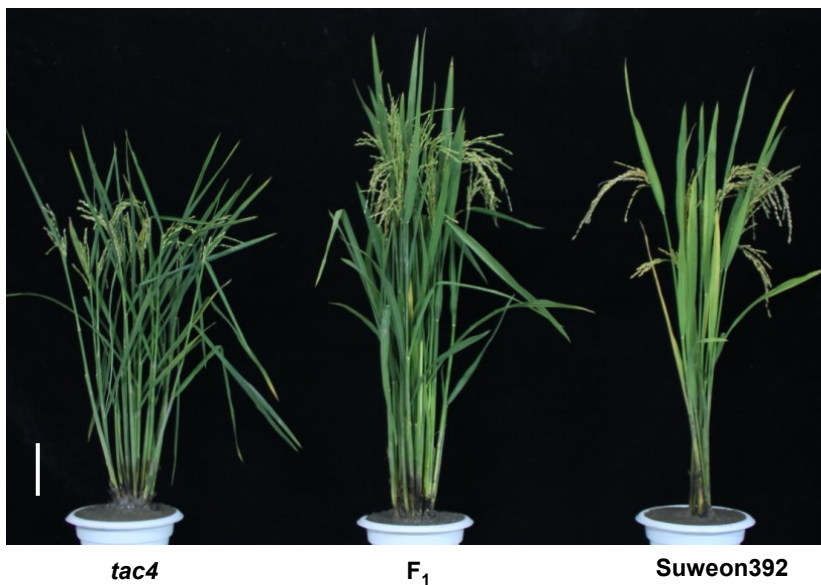


Figure S4. Phenotypic characterization of F₁ plants derived from a cross of between Suweon392 and the *tac4* mutant. Scale bar, 15 cm.

Figure S5

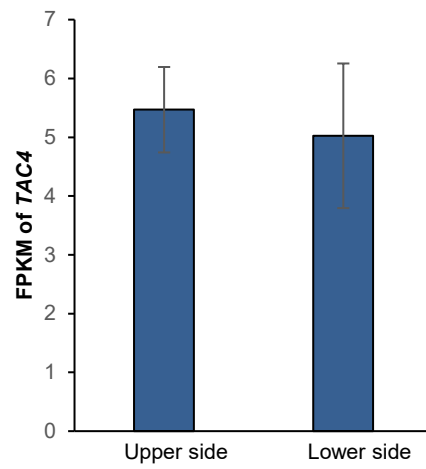


Figure S5. The FPKM values of *TAC4* in RNA-seq data of tiller bases of 70-day-old IL55. n=3

Figure S6

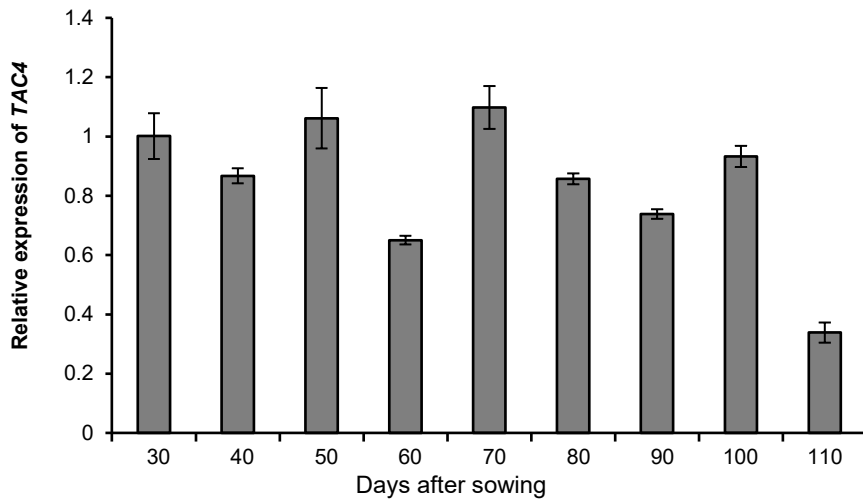


Figure S6. Kinetic analysis of the transcript abundance of *TAC4*. values are \pm SD ($n = 3$).

Figure S7

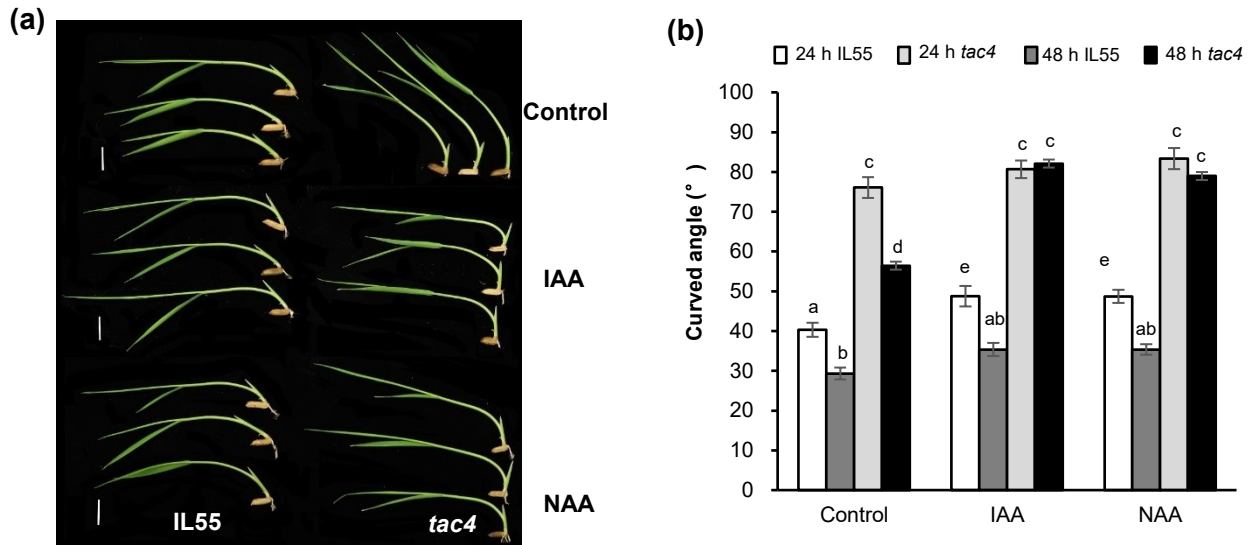


Figure S7. The gravity response of *tac4* can be rescued by an auxin application.

(a) Shoot curvature of IL55 and *tac4* at the seedling stage after 48 h of gravistimulation with or without application of auxin (IAA or NAA). Bar = 1 cm

(b) Shoot curvature comparisons after 24 h and 48 h of gravistimulation with or without application of auxin (5 mM IAA or 0.1 Mm NAA). Error bars indicate SEM; n = 20. Means with different letters are significantly different (P < 0.05; ANOVA).

Figure S8

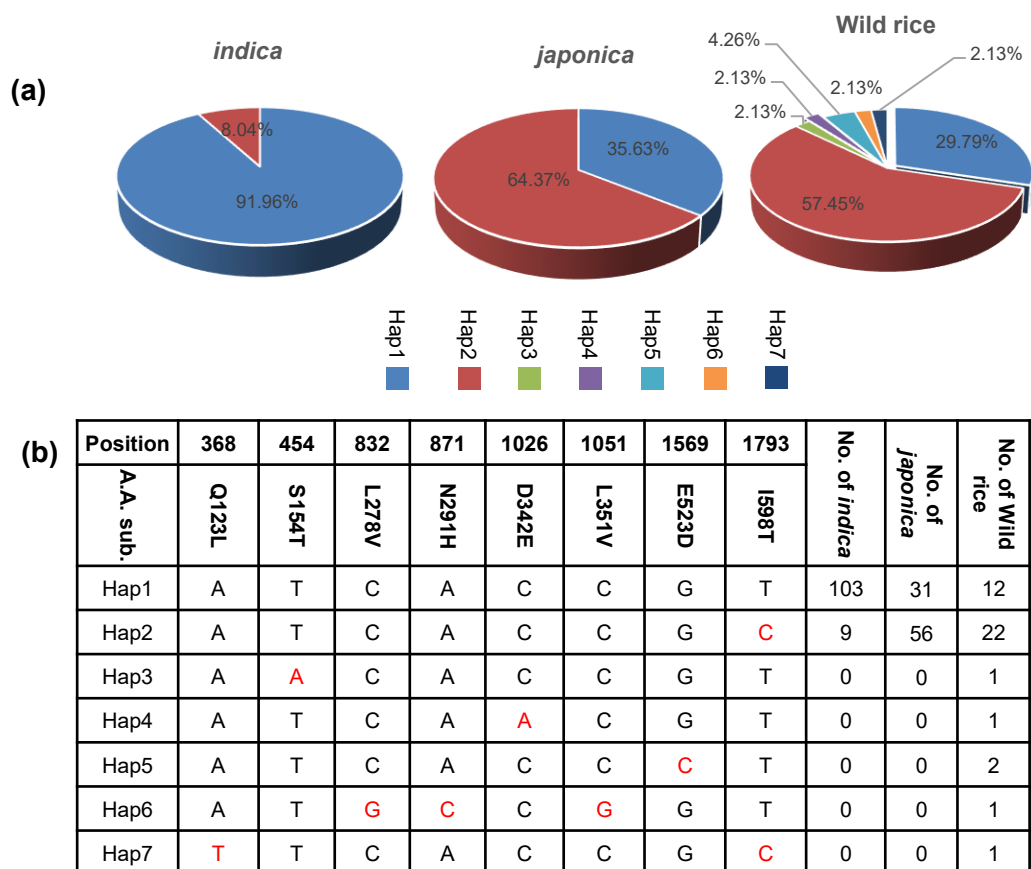


Figure S8. *TAC4* variants in wild and cultivated rice.

(a) Haplotype frequencies are shown as percentages for a core collection of wild and cultivated rice germplasms.

(b) The polymorphic nucleotides of Hap1–7 in the *TAC4* coding sequence

Figure S9

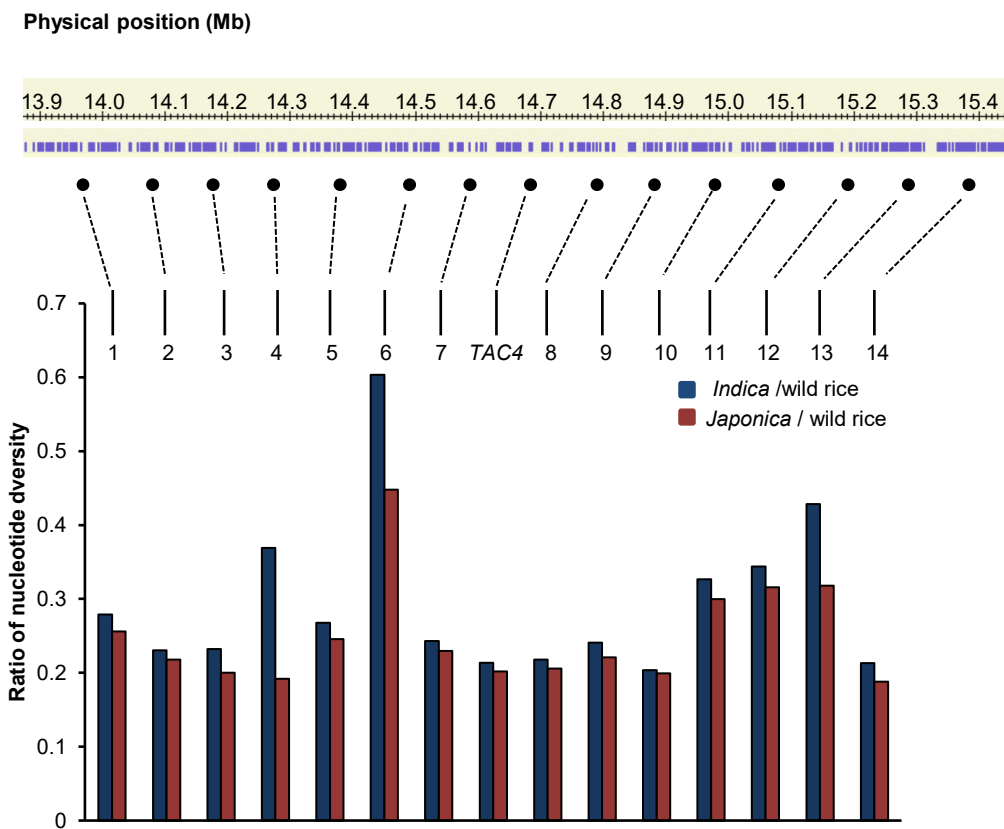


Figure S9. Comparison of diversity ratios surrounding the *TAC4* locus.

Figure S10

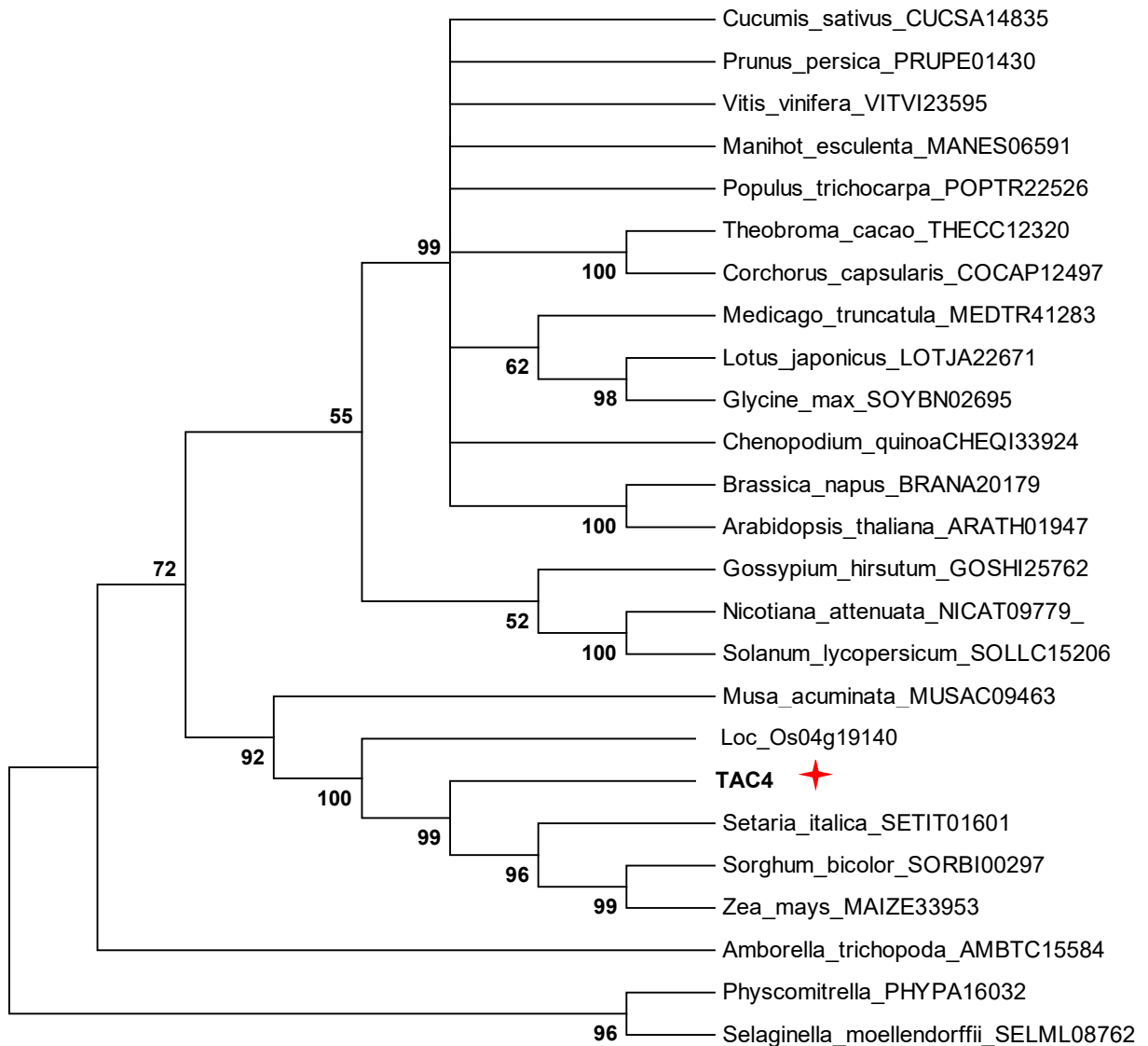


Figure S10. Phylogenetic tree of 25 homologs of TAC4 in land plants. The tree was constructed using MEGA 6.0 based on the neighbor joining method. The red asterisks indicates the position of TAC4.

Figure S11

TAC4	---- MSTA-AKEEAAAASAP----APAMGEEAAAARAAAKRYEGLLTVRAKAVKGGKAWYWAHLEPVLIPADTGVPPKAVKLRG	76
<i>Sorghum bicolor</i> _SORBI00297	---- MSTA-AKEEAAAASAP----APAMGEEAAAARAAAKRYEALLTVRAKAVKGGKAWYWAHLEPVLIPADTGVPPKAVKLRCA	77
<i>Zea mays</i> _MAIZE33953	---- MSTATAKEEAAAAA----APAMVGEAAAARAAAKRYEALLTVRAKAVKGGKAWYWAHLEPVLIPPAETGVPPKAVKLRCA	76
<i>Setaria italica</i> _SETIT01601	---- MSTASAKEEQAASASAAPAPAMGEEAAAARAAAKRYEALLTVRAKAVKGGKAWYWAHLEPVLIPADTGVPPKAVKLRCA	81
Loc_Os04g19140	MSAEEAGGASAEASGSGSAPAGAAVMPVCGEEAAAARAAAKRYDALMQRVRAKAVKGGKAWYWAHLEPVLIPPPGSGVPPKAVKLRCA	85
TAC4	LCSAVFASASNPSRTIASEHLKRGICPNFASPPPGAAASGSSGSHQQQTQQAALCALPPPNSTASSPIPISSIAPSSPRHHPHHS	161
<i>Sorghum bicolor</i> _SORBI00297	LCSAVFASASNPSRTIASEHLKRGICPNFAALPTGPAAGSGSQPSQHPSTTQQAACLALPSNSTASSPVPISIIAPSSPRHHCHHH	161
<i>Zea mays</i> _MAIZE33953	LCSAVFASASNPSRTIASEHLKRGICPNFASPPPGAGASALQPAQHPTPTQQAACLALPSNSTASSPVPISIIAPSSSRHHPHHH	162
<i>Setaria italica</i> _SETIT01601	LCSAVFASASNPSRTIASEHLKRGICPNFAAPPGPAAASGSSGSHPTTTPAQHQCLALPSNSTASSPIPISYIAPSSPRHHPHHS	166
Loc_Os04g19140	LCAATFASASNPSRTIASEHLKRCACPNFAAQQGAAAPHQAMTVQHQQTQQAALCALPPNSAASSVPIISSIPSSORHHPHHS	170
TAC4	QCCQPQSIIHHHHHSGSRKRHSMPAYTAAEPVSHHLLVVDPSLTVSPPLPALPPPQQPQSALVLSGGKEDLICALMLED	246
<i>Sorghum bicolor</i> _SORBI00297	SPQNPHHHQQQQQSGSRKRHTMPPAYTPADPVSHHLLVVDPSVYSPALPALPAAPPQHSSALVLSGGKDDLICALMLED	246
<i>Zea mays</i> _MAIZE33953	SPQNPHHHHHQQQQSGSRKRHSMPAYTAAEPVSHHLLVVDPSLTVSPALPALPAPPPHGSSALVLSGGKDDLICALMLED	247
<i>Setaria italica</i> _SETIT01601	QCCQQRHQHQHHHHHSGSRKRHSMPAYTPADPRSHHLLVVDPSVYSPALPALPAPPPHGSSALVLSGGKEDLICALMLED	251
Loc_Os04g19140	QCCQPQSIIHRHSTGGGRKRHALAAAYAAVEAAASHHLLVVDPSVYSPPTTPPALPAPRQVLSALVLSGGKEDLICALMLED	255
TAC4	VKRLKSPKASPGAMLPKQOADAALALLAEWFLLESSGGVSLSAVANPKLRSFLRVGLPELQRTDLGAGRLDARFAEARADATARY	331
<i>Sorghum bicolor</i> _SORBI00297	VKRLKSPKASPVAMPKQOADAAMVADWFLLESSPGVSLSAASHPKLRAFLRVGLPDLQRADLAGPRLDARFAEARADATARY	331
<i>Zea mays</i> _MAIZE33953	VKRLKSPKASPVTMPKQOADAALALLSDWFLLESSPGVSLSAASHPKLRAFLRVGLPDLQRADLAGPRLDARFAEARADATARY	332
<i>Setaria italica</i> _SETIT01601	VKRLKSPKASPAAMMPKAOADAALGLLADWFLLESSAGVSLSSASHPKLRAFLRVGLPDLQRADLAGPRLDARFAEARADATARY	336
Loc_Os04g19140	VKRLKSPVASPGAMLPKQQAFAALALLAEWFLLESSGVSLSAHEPKLKAFLRQVGLPELSRAELAGARLNARFAEARADAAARI	340
TAC4	RDALFFQLAADGWREQVVTLSVNLNGTGVFRAVVPVPAAPSDYAEVLIDAVASVSAAGSSNDLHHCAGIADRFKSKALRDL	416
<i>Sorghum bicolor</i> _SORBI00297	RDALFFQLAADGWREQVVTLSVNLNGTGVFRAVVPVPAAPSDYAEELMNAVASVSAAGSSNDLHHCAGIADRFKSKALRDL	416
<i>Zea mays</i> _MAIZE33953	RDALFFQLAADGWREQVVTLSVNLNGTGVFRAVVPVPAAPSDYAEELMNAVASVSAAGSSNDLHHCAGIADRFKSKALRDL	417
<i>Setaria italica</i> _SETIT01601	RDALFFQFAADGWREQVVTLSVNLNGTGVFRAVVPVPAAPSDYAEELMNAVASVSSAGSSNDLHHCAGIADRFKSKALRDL	421
Loc_Os04g19140	REARFFQLAADGWREQVVTLSVNLNGASVFERAVPTPAPASSDYAEQLMELIASSVASAGSSSEELHHCAGIADRFKSKALRDL	425
TAC4	ENKHHWVWNLSCQIHGFTRLMVDFARELPLFRSAAAKSAKLAAYFNAAKTVRSLLHKHQIQELGHASLLRVAHVPFNNGSDYRA	501
<i>Sorghum bicolor</i> _SORBI00297	ENKHYWVWNLCCQHSFTHLMVDFARELPLFRSATAKSAKLAAYFNAAKTVRSLLHKHQIQELGYASLLRVAHVPFNNGSNCRRA	501
<i>Zea mays</i> _MAIZE33953	ENKHYWVWNLSCQIHGFTRLMVDFARELPLFRSATAKSAKLAAYFNAAKTVRSLLHKHQIQELGHASLLRVAHVPFNNGSNCRNRA	502
<i>Setaria italica</i> _SETIT01601	ENKHHWVWNLSCQIHGFTRLMVDFARELPLFRSAAAKSAKLAAYFNAAKTVRSLLKQYQIQELGHASLLRVAHVPFNNGSDDFRA	506
Loc_Os04g19140	ENKHPWVWNLACQVHGLSRVDFARELPLFRSASANCAKLAAYFNAAKTVRSLLHKHQIQEIGHASLLRVAHVPFNNGSDYAA	510
TAC4	AFEMLEDLTSARPLQLAVHEESYKLVCIDDSAAREMADMDDGSFVSEVAVLVLKLIQMDVVKEMETDRPLVGCCPLVEELR	586
<i>Sorghum bicolor</i> _SORBI00297	AFDMLEDIENSAHPLHRAVQEDSYKLVCIDDSAAREIEMVHSEAFWIEVDAAVSLVKLIQMDVVKEMETDRPLVGCCPLVEELR	586
<i>Zea mays</i> _MAIZE33953	AFEMLEDLNSAHPLHRAVQEDSYKLVCIDDSAAREIEMVHSEAFWIEVDAAVSLVKLIQMDVVKEMETDRPLVGCCPLVEELR	587
<i>Setaria italica</i> _SETIT01601	AFEMLEDLNSAHPLHRAVQEDSYKLVCIDDSAAREMGEVHNEAFWIEVDAAVSLVKLIQMDVVKEMEGDRPLVGCCPLVEELR	591
Loc_Os04g19140	AFAMLEDLTSARPLQLAVHEESYKLVCIDDPAAREVGSVMKVAVFTEVBAASLVKLIQMDVVKEMEAERPLVGCCPLVEELR	595
TAC4	GKVRDWCQKFNIDEGAALNVVEKFRKRYHPAWSAAFLDPLYLKDAASGRYLPPFKCLTPDCEKDQVDRLLTRVMSREEAHLVLM	671
<i>Sorghum bicolor</i> _SORBI00297	SKVRDWCQKFNIDEGTVLNVLEKFRKRYHPAWSAAFLDPLYLKDAASGRYLPPFKCLTPDCEKDQVDRLLTRVMSREEAHLVLM	671
<i>Zea mays</i> _MAIZE33953	SKVRDWCQKFNIDEGAALNVLEKFRKRYHPAWSAAFLDPLYLKDAASGRYLPPFKCLTPDCEKDQVDRLLTRVMSREEAHLVLM	672
<i>Setaria italica</i> _SETIT01601	SKVRDWCQKFNIDEGIALNVVEKFRKRYHPAWSAAFLDPLYLKDAASGRYLPPFKCLAPDCEKDQVDRLLTRVMSQEEAHLALM	676
Loc_Os04g19140	GKVRDWCQKFNIDEGIAMNVVEVFRKRYHPAWSAAFLDPLYLKDVSGRYLPPFKYLTPEQDKDQVDRLLTRLVSPREEAHLALM	680
TAC4	ELMKWRSEGLDPLIYAQAVQVRQDPDSTGKMKVANKQSSRLVVIETCLSELKSLGKQAVRLLFLHATARSFRCTPSMVRWLCAPGSL	756
<i>Sorghum bicolor</i> _SORBI00297	ELMKWRSDGLDPLIYAQAVQVRQDPDSTGKMKVANKQSSRLVVIETCLSELKSLGKQAVRLLFLHATARSFRCTPSMVRWLCAPGSL	756
<i>Zea mays</i> _MAIZE33953	ELMKWRSDGLDPLIYAQAVQVRQDPDSTGKMKVANKQSSRLVVIETCLSELKSLGKQAVRLLFLHATARSFRCTPSMVRWLCAPGSM	757
<i>Setaria italica</i> _SETIT01601	ELMKWRSDGLDPLIYAQAVQVRQDPDSTGKMKVANKQSSRLVVIETCLSEFVKSLLGKQAVRLLFLHATARSFRCTPSMVRWLVSSPGL	761
Loc_Os04g19140	ELMKWRSEGLDPLIYAQAVQVRQDPDSTGKMRVANKQSSRLVVIETCLSDLKSLGKQAVRLLFLHATAKGFRCTAPPMSRVLTPAGSS	765
TAC4	AGGIDRAHRLVFVAANSKLERDDFSSDEDKDAELITEGDDVLENEPGS-LERSV-----	810
<i>Sorghum bicolor</i> _SORBI00297	ASGNDRAHRLAFVAANSKLERDDFSSDEDKDAELITEGDDVVNLPGN-AEPSSV-----	810
<i>Zea mays</i> _MAIZE33953	ASGNDRAHRLVFVAANSKLERDDFSSDEDKDAELITEGDDVLDVPGT-VEPSSV-----	811
<i>Setaria italica</i> _SETIT01601	ASSTNRAHRLVFVAANSKLERDDFSSDEDKDAELITEGDDFANEPGN-VEPSSVFWGGELGMRWRYALSFHDQVWLANDCLFC	845
Loc_Os04g19140	AAGIARAQRLVYVAANSKLERDDFSSDDDKDELITEGDDVLETEATASVDPSSV-----	820

Figure S11. Multiple alignment of TAC4 and its homologs. Conserved amino acids are highlighted in shades of black and gray: white letters with black background (100% identity), black letters with gray background (80% identity). The red asterisks indicates the position of *tac4* stop codon.

Figure S12

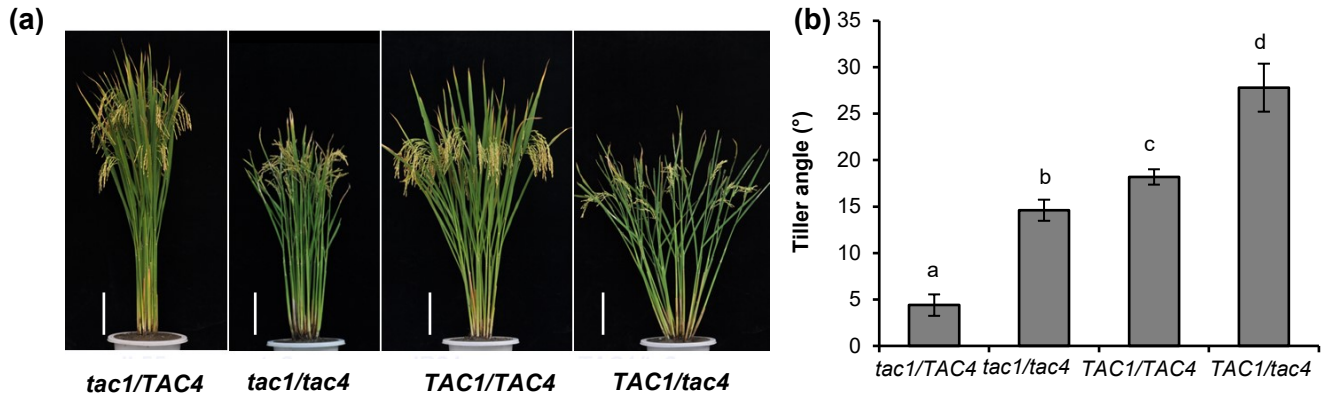


Figure S12. *TAC4*'s regulation of tiller angle is independent of *TAC1*.

(a) The morphology of *tac1/TAC4* (IL55), *tac1/tac4*, *TAC1/TAC4*, and *TAC1/tac4*. Scale bar, 20 cm.

(b) Comparison of tiller angle. Error bars indicate SEM, n = 5. Means with different letters are significantly different ($P < 0.05$; ANOVA).