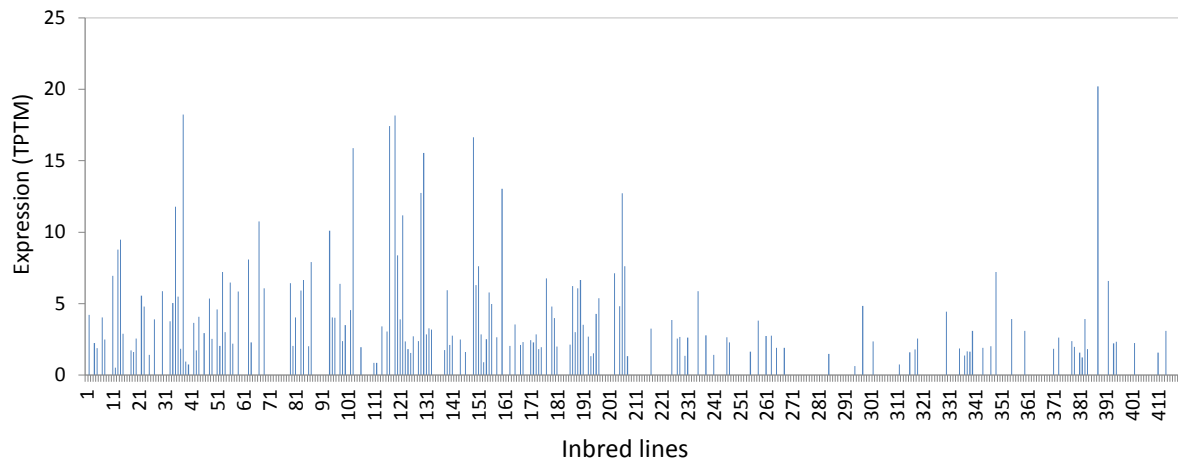
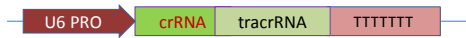


**Figure S1.** Maize *ARGOS8* gene expression. The transcript abundance of *ARGOS8* in various tissues of maize inbred PH184C was measured by RNA sequencing. Samples were taken from the plants at the developmental stage of V10, VT/R1 and R4. TPTM, transcript per ten million.



**Figure S2.** Comparison of *ARGOS8* gene expression among 419 maize inbred lines. The *ARGOS8* transcript levels in leaves of 3-week-old seedlings were measured by RNA sequencing. TPTM, transcript per ten million.

(a)



(b)

*CR1*

GC GTGCATCG ATCCATCGCG TTTTAGAGCT AGAAATAGCA AGTTAAAATA AGGCTAGTCC GTTATCAACT TGAAAAAGTG GCACCGAGTC GGTGCT

*CR2*

GCATCATATC TATCCGTAGC CGTTTTAGAG CTAGAAATAG CAAGTTAAAA TAAGGCTAGT CCGTTATCAA CTTGAAAAAG TGGCACCGAG TCGGTGCT

*CR3*

GTTACTTCTC TAAGCACGGC GTTTTAGAGC TAGAAATAGC AAGTTAAAAT AAGGCTAGTC CGTTATCAAC TTGAAAAAGT GGCACCGAGT CCGGTGCT

**Figure S3.** Single guide RNA genes used in editing the genomic sequence of *ARGOS8*. (a) Scheme illustrating the structure of a single guide RNA (sgRNA) gene. (b) DNA sequences of the transcription region in the sgRNA genes *CRISPR RNA1 (CR1)*, *CR2* and *CR3*. U6 PRO, maize U6 polymerase III promoter; crRNA, CRISPR RNA (in red font) functioning as a guide; tracrRNA, trans-activating CRISPR RNA, the sgRNA scaffold.

>ID189\_HR1 junction PCR product (P1/P2), *ARGOS8-v1*

GCGCCATCCCTAAAGGTAAGTAACTAAACAGAACACAATTTTCTTAGGCCATCTCCAGCAGGCTGTGTAACAGCCGTGCAAAATGTTGTTTTGCA  
CTGTTTGTACAGTGAAGTTTTAAATAAAGAGTAAGATAGGAAATGAGATAAAGAGTATTCTGGAGATAGTCTTATACATCACCGTAGCAACGCATT  
AATATATACCTAGTTAATATTATATGATTTAAATTTTATCTTAAATACTTGACGCTCTATGAGTTTAGTAGTTTATAATACATATTTATCTTCTTAA  
TACATGAACATCCTTTTTAGAATACGTCATAGGACGATACCAGTACGGAGGATCTAGGCAAACAACATAAGAATCGAGCGAGTGCTAGGAGCATC  
TCTAAAAGACTAATAAAATAACTCGTAAAGTTAAATTTTATAGATACTCAAGAGTAAATAAATACTATTTAACAGACTCGTTATTTGACTCATCAATATACC  
CTTCAAATTGACTCTCTCACTATCTAAACTTGGCTAGCCACTATGACTAACTAACTAGATAGATATTTTGGTGGAGTAAGATGCTATATATAAAGTG  
TAATATTTATAAAATGATAAATAAAAAGCTAAAAATAAAGAGTTACTTCTCTAAGCACGGCTGGATTTTCAGGCCTCTAGTCTCTACTAGTACTAGCT  
ACACGACGTGCACGCATGCATCAGCATCAACAAGTACAGCAGCACACGCTGCACGCGCCGGGAACCCACTGATCCCCCTTCCCGCGCGC  
GGTTTGATTTCTTCTGTTACGATCCATATCTGAGGGCTGTTTCGGTTATCCCAACACACATGATTGGATGGGATTGAAAAAAAATGAGAA  
GAAGTTTGACTTGTGGGATCAAACCCATCCAATCCACTCAATCCACATGGATTGAGAGCTAACCGAACAAAGCCCTCATAGTACATACCTGGTA  
CGGATCCATATCATAGTACATAGTCCAGTAGAATAGAAGGTGATCCGACCCGCGCGCTTGCCTGTTTTCCCGGTCCATTGAACCTGCCAACCC  
TCCTAACACAGGCACGCAAAACCGCGGCTCCGCGCCACCCGCGCACCTGCCCTGCCGACCTCTCCAACCCAAATCCAGGGGGGGG  
GGGGGACCATGCGTGCATCGATCCATGCTCGTGCCAAGCGTCACTTACGATTAGC

>ID189\_HR2 junction PCR product (P5/P4), *ARGOS8-v1*

ACCGTCCTATCTCTGCATCATCTATCTGTGCTAGTTTCTGCGTCTTCTCAAATATTTCCGGCCTGTGTAGCATGTGACTGATAATATGATTTTGCA  
GCTTCTGCATAAGAACAACAAATCAAAAGCTTGATCAGCTCGGTGCTACAAAACCTCAACAACCAAGTTTCCATGAGCGCTGGCGCGCGGGTCCG  
GCGGGGCGGTGTGAGGGCAAATTTATATAGTCTAGTGGTACCCGGCTACGGATAGATATGATGCTGCACTGCACATTGGCTATATCTGAGG  
CTCTGCGCGCGCTTGGCCAGTGTCTGTCTGCGGGCGATGCCGAGGAAGGAAAGCGCGGTGGCGACGACACCATTGGCCGGGGGCAA  
GGTGGCGCGCTGCTGGCCAGCGCGCGCGCTGCTGCTGCTGCCGCTGGCGCTGCCGCGCTGCCGCGCGCCACGCAGCTGTTGTTG  
TCCCCGTGGTCTGCTCCTCGTGGCGTCCCTCGCTTCTGCCCGCGCGACCCCTCGCGTCCGCGATGCATGCCGCGACCCACGGGCTGTT  
CGGGACCACTGGATCACCGCACCTATGTTGACGCTGACGATGAGAGATCTGCTGATCGACGCTCGGCTTGCATGGCGCTCGGAATCAAGCAG  
TTCGCACACAC

>ID664\_HR1 junction PCR product (P1/P2), *ARGOS8-v2*

GCGCCATCCCTAAAGGTAAGTAACTAAACAGAACACAATTTTCTTAGGCCATCTCCAGCAGGCTGTGTAACAGCCGTGCAAAATGTTGTTTTGCA  
CTGTTTGTACAGTGAAGTTTTAAATAAAGAGTAAGATAGGAAATGAGATAAAGAGTATTCTGGAGATAGTCTTATACATCACCGTAGCAACGCATT  
AATATATACCTAGTTAATATTATATGATTTAAATTTTATCTTAAATACTTGACGCTCTATGAGTTTAGTAGTTTATAATACATATTTATCTTCTTAA  
TACATGAACATCCTTTTTAGAATACGTCATAGGACGATACCAGTACGGAGGATCTAGGCAAACAACATAAGAATCGAGCGAGTGCTAGGAGCATC  
TCTAAAAGACTAATAAAATAACTCGTAAAGTTAAATTTTATAGATACTCAAGAGTAAATAAATACTATTTAACAGACTCGTTATTTGACTCATCAATATACC  
CTTCAAATTGACTCTCTCACTATCTAAACTTGGCTAGCCACTATGACTAACTAACTAGATAGATATTTTGGTGGAGTAAGATGCTATATATAAAGTG  
TAATATTTATAAAATGATAAATAAAAAGCTAAAAATAAAGAGTTACTTCTCTAAGCACGCTCGTGTCCAAGCGTCACTTACGATTAGC

>ID664\_HR2 junction PCR product (P5/P4), *ARGOS8-v2*

ACCGTCCTATCTCTGCATCATCTATCTGTGCTAGTTTCTGCGTCTTCTCAAATATTTCCGGCCTGTGTAGCATGTGACTGATAATATGATTTTGCA  
GCTTCTGCATAAGAACAACAAATCAAAAGCTTGATCAGCTCGGTGCTACAAAACCTCAACAACCAAGTTTCCATGGTACGGATAGATATGATGCT  
GCACTGCACATTGGCTATATCTGAGGCTCCTGCGCGCGCTTGGCCAGGTGTCTGTCTGCGGGCGATGCCGAGGAAGAGGAAGCCGCGGTGG  
CGACGACGACCATGCCGGGGGCAAGGTGGCGCGCTGCTGGCCAGCGCGCCGCGCTGCTGCTGCTGCCGCTGCCGCTGCCGCGCTGCC  
GCCGCGCCACGCAGCTGTTGTTGTCGCCGTGTTGCTGCTCCTCGTGGCGTCCCTCGCTTCTGCCCGCGCGACCCCTCGCGTCCCG  
ATGCATGCCGCGACCCAGGTCGTTCCGGACCACTGGATCACCGCACCTATGTTGACGCTGACGATGAGAGATCTGCTGATCGACGCTCGGCT  
TGCAATGGCGCGTGGAAATCAAGCAGTTTCGCACAC

>ID336\_PCR product (P1/P4), *ARGOS8-v3*

GCGCCATCCCTAAAGGTAAGTAACTAAACAGAACACAATTTTCTTAGGCCATCTCCAGCAGGCTGTGTAACAGCCGTGCAAAATGTTGTTTTGCA  
CTGTTTGTACAGTGAAGTTTTAAATAAAGAGTAAGATAGGAAATGAGATAAAGAGTATTCTGGAGATAGTCTTATACATCACCGTAGCAACGCATT  
AATATATACCTAGTTAATATTATATGATTTAAATTTTATCTTAAATACTTGACGCTCTATGAGTTTAGTAGTTTATAATACATATTTATCTTCTTAA  
TACATGAACATCCTTTTTAGAATACGTCATAGGACGATACCAGTACGGAGGATCTAGGCAAACAACATAAGAATCGAGCGAGTGCTAGGAGCATC  
TCTAAAAGACTAATAAAATAACTCGTAAAGTTAAATTTTATAGATACTCAAGAGTAAATAAATACTATTTAACAGACTCGTTATTTGACTCATCAATATACC  
CTTCAAATTGACTCTCTCACTATCTAAACTTGGCTAGCCACTATGACTAACTAACTAGATAGATATTTTGGTGGAGTAAGATGCTATATATAAAGTG  
TAATATTTATAAAATGATAAATAAAAAGCTAAAAATAAAGAGTTACTTCTCTAAGCACTCGTGGCGCGGGTCCGGCGGGGGCTGCTGTGAGG  
GCAAATTTATATAGGTCTAGTGGTACCCGGCTACGGATAGATATGATGCTGCACTGCACATTGGCTATATCTGAGGCTCCTGCGCGCGCTTGGC  
CAGGTGTCTGTCTGCGGGCGATCCGCGAGGAAGGAAAGCGCGGTGGCGACGACCATGGCCGGGGCAAGGTGGCGCGCTGCTGGC  
CACGGCGCGCGCTGCTGCTGCTGCCGCTGGCGCTGCCCGCTGCCGCGCCACGCAGCTGTTGTTGCTCCCCGTGGTCTGCTGCT  
CCTCGTGGCGTCCCTCGCTTCTGCCCGCGCGACCCCTCGCGTCCGCGATGCATGCCGCGACCCAGGGTCTTCCGGACCACTGGATCACC  
GCACCTATGTTGACGCTGACGATGAGAGATCTGCTGATCGACGCTCGGCTTGCATGGCGCTCGGAATCAAGCAGTTTCGCACA

**Figure S4.** DNA sequences of the junction PCR products amplified from *ARGOS8* variants

**Table S1.** Frequency of the GOS2 promoter insertion with one target site and the promoter swap with two target sites in T0 maize plants

	Insertion	Swap
Target sites	CTS1	CTS2 and CTS3
No. of embryos bombarded	1050	1150
No. of shoots regenerated	194	334
No. of shoots with CTS modified	190	172 *
No. of shoots positive with junction PCR	7	23
HR1 junction-PCR positive	2	9
HR2 junction-PCR positive	3	11
Both junction-PCR positive	2	3
No. of T0 plants regenerated	3	8
HR1 junction-PCR positive	1	3
HR2 junction-PCR positive	1	3
Both junction-PCR positive	1	2

\* Both CRISPR-RNA target site 2 (CTS2) and CTS3 were modified.

**Table S2.** Primers and probes used for generation and characterization of *ARGOS8* genome editing variants

Target	PCR type	Primer name	Primer type	Primer sequence (5'-3')
CTS1	qPCR	P11	Forward	CCTCTCCAACCCCAAATCCA
		P12	Reverse	CCACTAGACCTATATAAATTTGCCCTCA
			Probe	CGCCAGCGATGGAT
CTS2	qPCR	P13	Forward	TGTGAGGGCAAATTTATATAGGTCTAGTG
		P14	Reverse	AGCCTCAGATATAGCCAATGTGCA
			Probe	CCGGCTACGGATAGA
CTS3	qPCR	P15	Forward	AGATAGATATTTTGGTGGAGTAAGATGCT
		P16	Reverse	GCTAGTACTAGTAGAGGACTAGAGGCCTG
			Probe	AATCCAGCCGTGCTT
HR1 junction	PCR	P1	Forward	GCGCCATTCCCTAAAGGTAAC
		P2	Reverse	GCTAATCGTAAGTGACGCTTGGA
HR2 junction	PCR	P5	Forward	ACCGTCCTTATCTCTGCATCATCT
		P4	Reverse	GTGTGCGAACTGCTTGATCCG
HR2 junction	PCR	P3	Forward	GCTCGTGTCCAAGCGTCACTTACGATTAGCT
		P4	Reverse	GTGTGCGAACTGCTTGATCCG
<i>ARGOS8</i> locus	Long PCR	P1	Forward	GCGCCATTCCCTAAAGGTAAC
		P4	Reverse	GTGTGCGAACTGCTTGATCCG
Cas9	PCR	P21	Forward	AACTGGTGGACAGCACAGACAA
		P22	Reverse	GAAGTGGCCGCGAACT
			Probe	CTCGGCATATGAT
sgRNA	PCR	P23	Forward	CTAATCACAAGAGTGGAGCGTACCTT
		P24	Reverse	AGCCTTATTTAACTTGCTATTTCTAGCTCT
			Probe	CCGAGCCGCAAGCA
PMI	PCR	P25	Forward	CGCCGGAGATATCGTTTCA
		P26	Reverse	CCTCTCCGAGCAGAGTCGATT
			Probe	CTCAATCACATCACGCA
ODP2	PCR	P27	Forward	TTGGTGTTACTTCTGCAGGTCGA
		P28	Reverse	AGAGGGAGAAAGCGAGCCAGT
			Probe	ATCCATGGCCACTGTGAA
WUS	PCR	P29	Forward	CTCCCTGCACCTGCCATG
		P30	Reverse	GCTGCCGCTGCCTCCTC
			Probe	CGCTGAGATAGAGGCATG

**Table S3.** Plant height (PLTHT), ear height (EARHT) and grain moisture (MST) of *ARGOS8* genome edited variants and wild type under flowering stress, grain-filling stress and optimal (well-watered) conditions.

	PLTHT (cm)	EARHT (cm)	MST %
<i>Flowering Stress (FS)</i>			
<i>ARGOS8-v1</i>	213.1	94.2	20.1
<i>ARGOS8-v2</i>	213.1	95.0	20.4
WT	213.5	92.8	20.3
<i>Optimal (OPT)</i>			
<i>ARGOS8-v1</i>	273.3	143.0	21.4
<i>ARGOS8-v2</i>	275.6*	144.5*	21.6
WT	273.0	141.3	21.5
<i>Grain-filling Stress (GFS)</i>			
<i>ARGOS8-v1</i>	nd	nd	18.2*
<i>ARGOS8-v2</i>	nd	nd	18.7
WT	nd	nd	19.0

Asterisks indicate predicted difference significant at  $P < 0.1$ . nd, not determined.