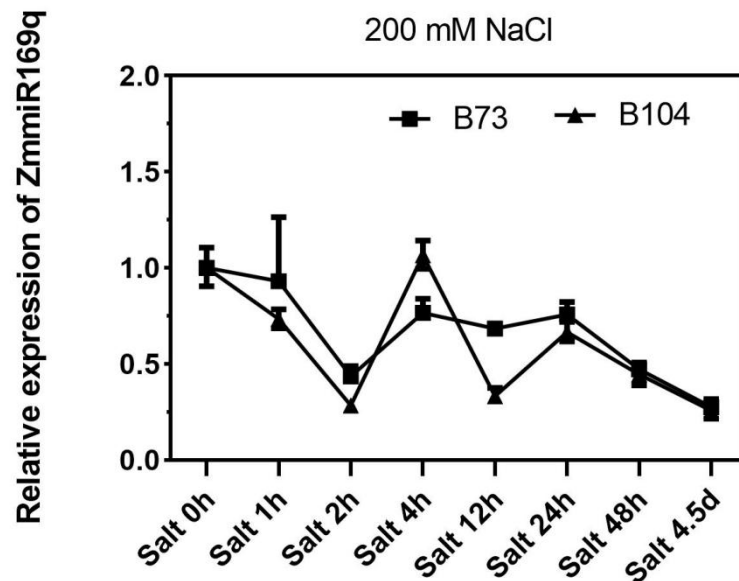
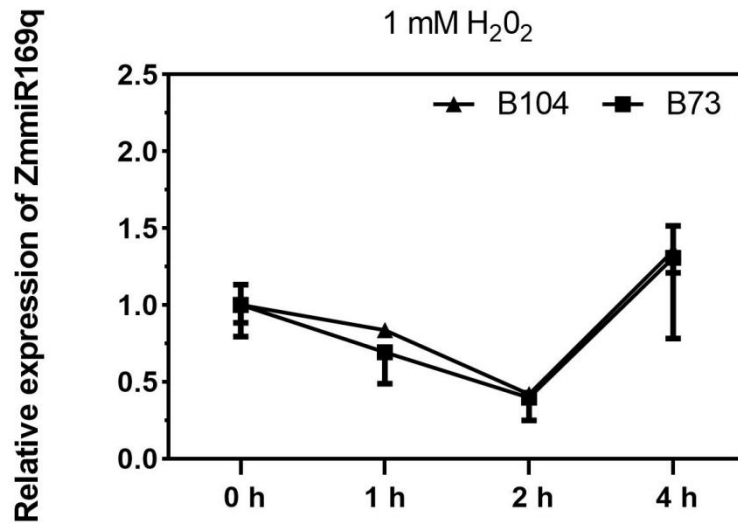


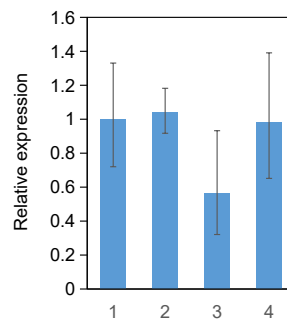
Supplemental Figure S1. Salt stress rapidly reduces ZmmiR169q expression in maize roots. Short-term high salinity induction (200 mM NaCl) assay of ZmmiR169q in the roots of *pmiR169q:GUS* transgenic plants assessed via histochemical staining. Strong GUS activity was observed in the *pmiR169q:GUS* root at 0 h, and GUS activity was reduced in the *pmiR169q:GUS* roots in response to salt stress. The GUS-staining assay of *pmiR169q:GUS* showed that the expression of ZmmiR169q was sharply reduced by 1 h of the high salinity treatment, and gradually increased after 4h, suggesting that ZmmiR169q might act as a responsive signal to salt stress. Bars = 1cm.



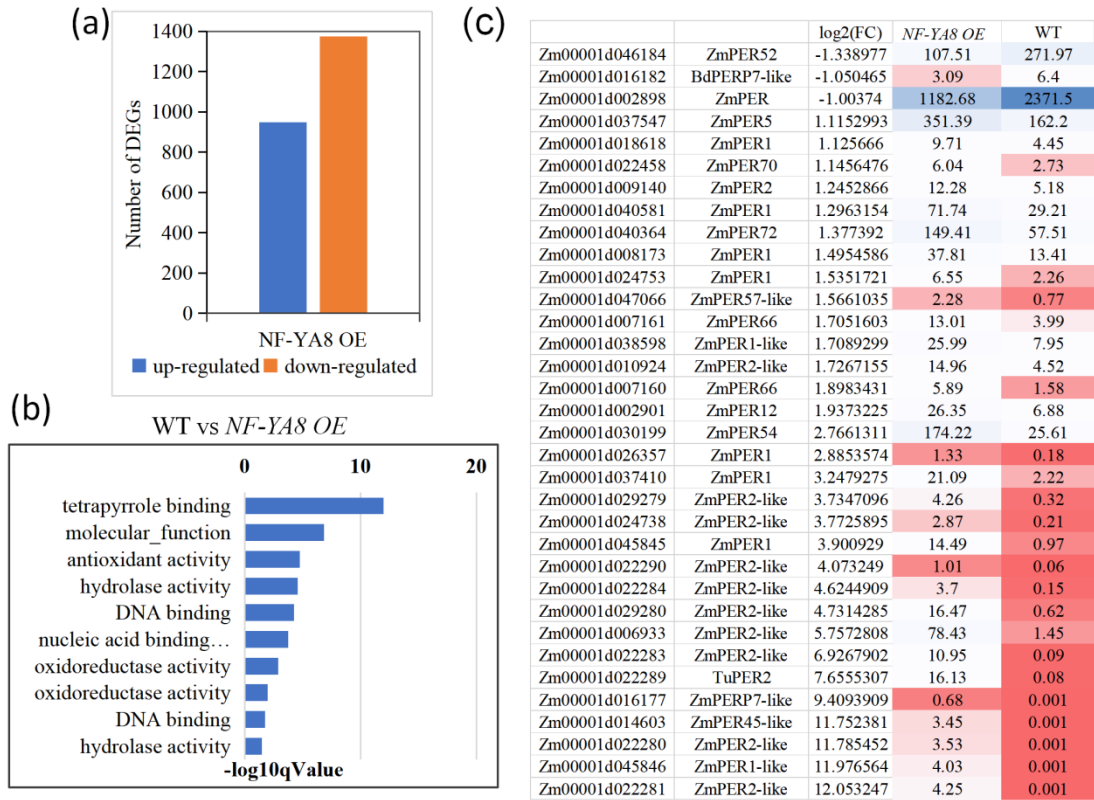
Supplemental Figure S2. The expression profiles of ZmmiR169q in B73 and B104 under 200 mM NaCl treatment. Short-term and long-term high salinity induction (200 mM NaCl) assay of ZmmiR169q in the roots of B73 and B104 assessed via RT-qCR. The results showed that the expression of ZmmiR169q in both B73 and B104 decreased and fluctuated slightly when the seedlings were treated under 200 mM NaCl from 1h to 24h, then declined gradually till 4.5d after salt treatment. In addition, ZmmiR169q expression patterns under salt are the same in both B73 and B104. Values are means \pm SD, n=3.



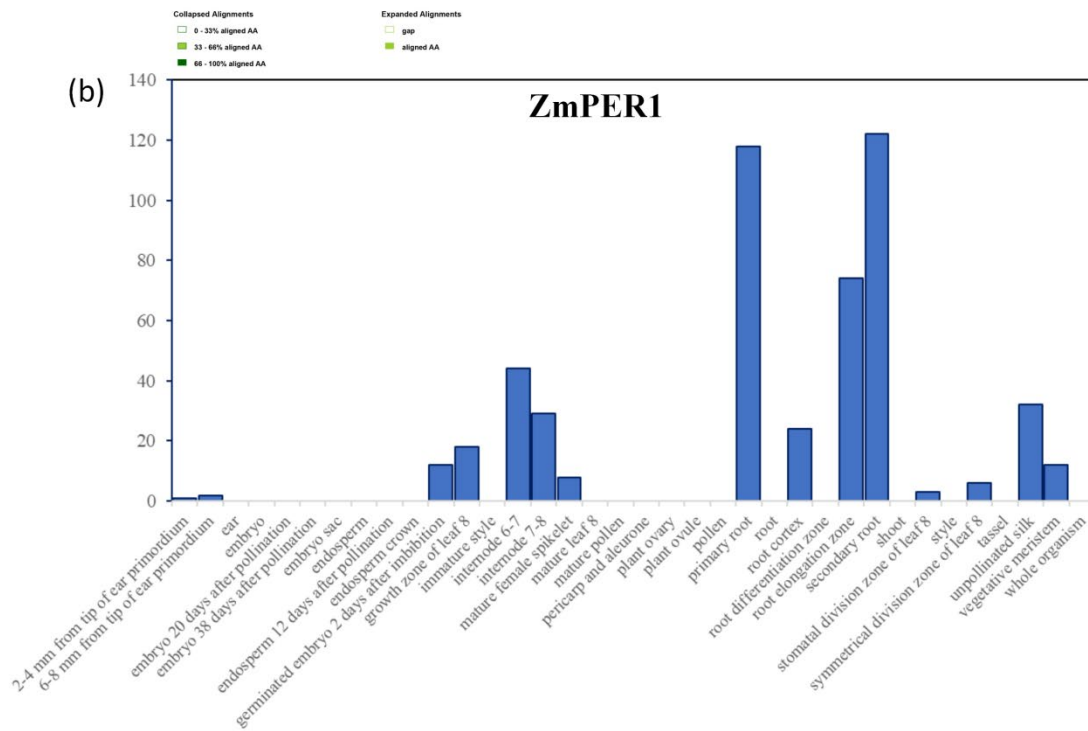
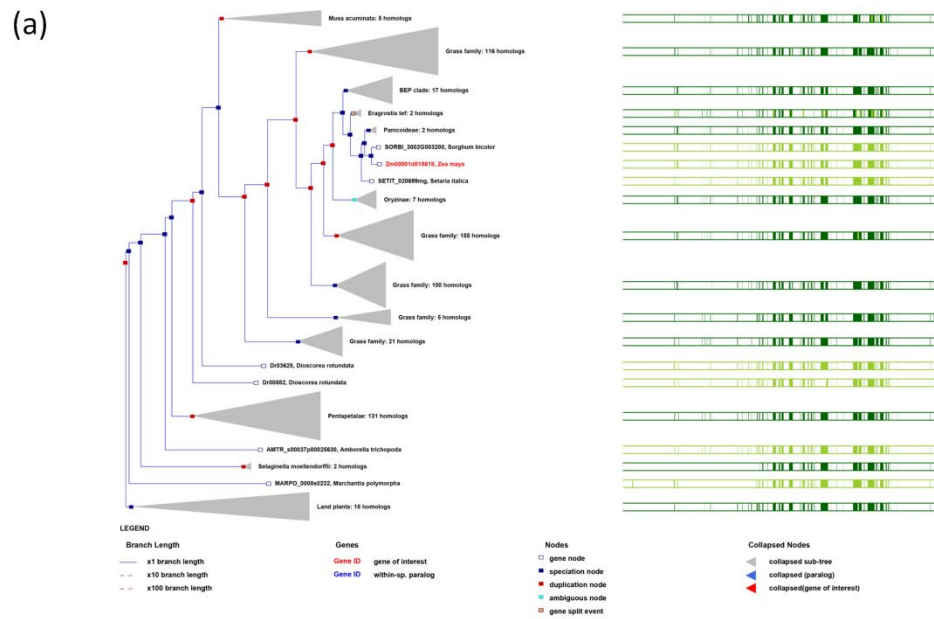
Supplemental Figure S3. The expression profiles of ZmmiR169q in B73 and B104 under 1 mM H₂O₂ treatment. Short-term oxidation stress response (1 mM H₂O₂) assay of ZmmiR169q in the roots of B73 and B104 assessed via RT-qPCR. ZmmiR169q expression patterns under 1 mM H₂O₂ treatment are the same in both B73 and B104. Values are means \pm SD, n=3.



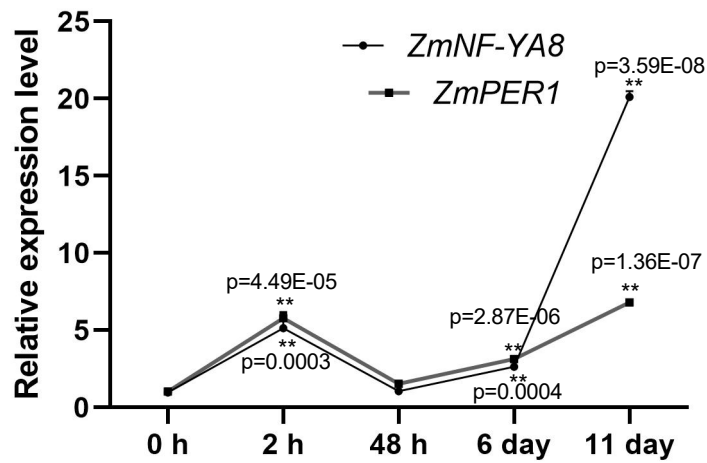
Supplemental Figure S4. Coexpression of zmmiR169q and ZmNF-YA8 gene in a transient expression system in *Nicotiana benthamiana* cells. Values are means \pm SD, n=3. Student's t-test, * P<0.05.



Supplemental Figure S5. *ZmNF-YA8* was involved in antioxidant pathway. (a) The number of genes differentially expressed in the different transgenic line compared with WT. (b) Gene ontology (GO) enrichment analysis of DEGs in the molecular function GO term. (c) Heatmap illustrating DEGs between *NF-YA8 OE* and WT related to oxidative stress and antioxidant pathway.

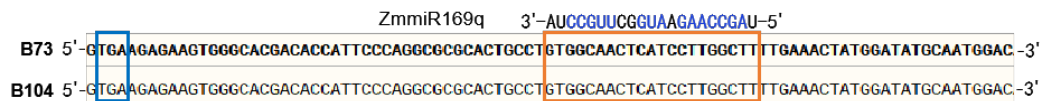


Supplemental Figure S6. Gene tree of *Zm0001d018618* and expression profiles in different tissues. (a) *Zm0001d018618* shares the highest similarity to the orthologue of sorghum. (b) *Zm0001d018618* preferentially expresses in root tissues.



Supplemental Figure S7. Expression profiles of *ZmNF-YA8* and *ZmPER1* in root of B104 under 200 mM NaCl treatment. Values are means \pm SD, n=3. Asterisks denote a statistically significant difference from the wild-type, Student's t-test, ** P<0.01.

Partial sequence of 3' UTR of *ZmNF-YA8*



Supplemental Figure S8. Alignment of ZmmiR169q target sites in the 3' UTR of *ZmNF-YA8* between B73 and B104

Supplemental Table S1. Mapping ratio of reference genome

Sample	Total reads	Unmapped reads	Unique mapped reads	Multiple mapped reads	Mapping ratio
NF-YA8 OE	28873258	5262193 (18.23%)	23290919 (80.67%)	320146 (1.11%)	81.77%
WT	31871210	8589031 (26.95%)	22983385 (72.11%)	298794 (0.94%)	73.05%
miR169q OE	23827196	6634399 (27.84%)	16966517 (71.21%)	226280 (0.95%)	72.16%

Supplemental Table S2. List of primers used in this study

Name	Sequence 5' -3'
P-miR169q-F	GTGTAGGGAGGTAAAGGTGC
P-miR169q-R	GGGAGATAGGCTCCTCATCT
P-YA8-F	AAACTGATGTAATAATGCGT
P-YA8-R	TATCTCCTTCCTCTCCCCTTC
Zma-miR169q-qPCR-F	GTAGCCAAGAATGGCTTGCCCT
Pri-miR169q-F	GCTCAATGCTTGCCCTGAAGC
Zma-miR169q-qPCR-F	GTAGCCAAGAATGGCTTGCCCT
Zm-NFYA8-qPCR-F	GCCTGTGGCAACTCATCCTT
Zm-NFYA8-qPCR-R	GGTCATGTTTCGATGGCTTCAC
Zm-PER1-qPCR-F	CGCTGCTCGCTCTCATCCA
Zm-PER1-qPCR-R	TTCATGTCCAGCCCAGCTGC
U6-FW	GGAGACATCCGATAAAAATTGG
U6-RW	GGACCATTCTCGATTGTGC
ZmActin1-F	ATGTTTCCTGGGATTGCCGAT
ZmActin1-R	CCAGTTTCGTCATACTCTCCCTTG
AD-Zm-NFYA8	CGAAGAAGTCCAAAGCTTCTG
AD-Zm-NFYA8-Arm-F	GTACCAGATTACGCTCATATGATGTGCCCTTTTACG
AD-Zm-NFYA8-Arm-R	CTACGATTATCTGCAGCTCGAGCCTTATGGTG
3C1F	AGCTTTGACTGATTGGGTAGAGTGACTGATTGGGTAGAGTGACTGATTGGGTAGAGC
3C1R	TCGAGCTCTACCAATCAGTCACTCTACCAATCAGTCACTCTACCAATCAGTCAA
3C2F	AGCTTTGGGACCAATGCAGCATTGGGACCAATGCAGCATTGGGACCAATGCAGCAC
3C2R	TCGAGTGCTGCATTGGTCCCAATGCTGCATTGGTCCCAATGCTGCATTGGTCCCAAA
3C3F	AGCTTAGAAGTATTGGATGTTAAGAAGTATTGGATGTTAAGAAGTATTGGATGTTAC
3C3R	TCGAGTAACATCCAATACTTCTTAACATCCAATACTTCTTAACATCCAATACTTCTA
3C4F	AGCTTCTTTAGCCAATTGTGTTCTTTAGCCAATTGTGTTCTTTAGCCAATTGTGTTTC
3C4R	TCGAGAACAACAATTGGCTAAAGAACAACAATTGGCTAAAGAACAACAATTGGCTAAAGA
3C5F	AGCTTGATGAACCAATATAAAGATGAACCAATATAAAGATGAACCAATATAAAGAT
3C5R	TCGAGTTTTATATTGGTTCATCTTTATATTGGTTCATCTTTATATTGGTTCATCA
3C2mF	AGCTTTGGGACTAGTTGCAGCATTGGGACTAGTTGCAGCATTGGGACTAGTTGCAGCAC

3C2mR	TCGAGTGCTGCAACTAGCCCAATGCTGCTAGTCCCAATGCTGCTAGTCCCAAA
3C4m-F	AGCTTCTTTAGCTAGTTGTGTCTTTAGCTAGTTGTGTCTTTAGCTAGTTGTGTTC
3C4m-R	TCGAGAACAACAAGCTAAAGAACAACAAGCTAAAGAACAACAAGCTAAAGA
3C5m-F	AGCTTGATGAAGTATATAAAGATGAAGTATATAAAGATGAAGTATATAAAG
3C5m-R	TCGAGTTTATACTAGTTCATCTTTTATACTAGTTCATCTTTTATACTAGTTCATCA
pabai-c-F	CAAGGAAACCGAAATCAAA
pabai-c-R	CATACAGAGCACATGCCTCG
P1F	GTTATGTTAGTTGCACGCAGC
P1R	GGAATGGATCGGATACGATGC
P1_LUC_ARM-F	gggccccccctcgaggtcgacGTTATGTTAGTTGCACGCAGC
P1_LUC_ARM-R	cgctctagaactagtgatccGGAATGGATCGGATACGATGC
P2F	CTAGACAAGAGTTCAGTTCAG
P2_LUC_ARM-F	gggccccccctcgaggtcgacCTAGACAAGAGTTCAGTTCAG
P3_LUC_ARM-R	cgctctagaactagtgatccCTACTGAACTCTTGTCTAG
P4_LUC_ARM-R	cgctctagaactagtgatccCATAGCTGCCATCATCAGATC
62SK-F	cgcaagacccttcctc
62SK-R	aaccctaatttccttatcgg
62SK_NF-YA8_ARM-F	cgctctagaactagtgatccATGTGCCTTTTACGGGAAATG
62SK_NF-YA8_ARM-R	ggtaccgggccccccctcgagTCACCTTATGGTGAAACACGC
Zm-PER1-ChIP-F	GCAATGAACTTTAGCCAATTGTG
Zm-PER1-ChIP-R	CAGTAACTAATTAGTCGTCATGC
Zm-GH3-ChIP-F	GTTCTGGACCCAGATTGGTCAGG
Zm-GH3-ChIP-R	AGGTAGCCAGGTCCACTGC
Nt_actin_F	TCCATGCTCAATGGGATACT
Nt_actin_R	TTCAACCCCTTGCTGTGTAT