

SUPPORTING INFORMATION

Genome-Wide Analysis of *Nuclear factor-YC* Genes in the Tea Plant (*Camellia sinensis*) and Functional Identification of *CsNF-YC6*

Supporting Tables

Table S1. The primers used in the tests.

Primer name	Primer sequence (5' to 3')	Used
<i>CsNF-YC1</i>	F: ATGGATCAGCACGGACAAC R: TCAGAAAGCGGGCACAG	Cloning
<i>CsNF-YC2</i>	F: ATGTTCTGGACGTACCAACGC R: TTAAAATCTCTGCCTCCTAAATGTG	Cloning
<i>CsNF-YC3</i>	F: ATGGATCAGCAAGGGC R: TTAAGAATCTGCAGGTGGTT	Cloning
<i>CsNF-YC4</i>	F: ATGGATCAACAAGGGCA R: CTAATTTAGCAGATCACATCTG	Cloning
<i>CsNF-YC6</i>	F: ATGGATCAGCAAGGGCAT R: TTAAGAATCTGCAGGTGGTTGC	Cloning
<i>CsNF-YC7</i>	F: ATGAGGCAAGCAAGAAC R: TCACATTTGGCCACC	Cloning
<i>CsNF-YC8</i>	F: ATGAGACAAGCAGGAACATATTCAG R: TCAAGTCCCATAAGCCTTACCA	Cloning
<i>CsNF-YC9</i>	F: ATGGAGAACAACCAACAACA R: TCACTTGGTAATGAGGTGC	Cloning
<i>CsNF-YC6-OE</i>	F: gagaacacggggacgagctcATGGATCAGCAAGGGCATGG R: gcccttgctcaccatgtcgacAGAATCTGCAGGTGGTTGCTG	Cloning
<i>CsGAPDH</i> -qPCR	F: GATAGTGTTACGGTCAATGGA R: GCAGCAGCCTTATCCTTATCAG	Internal reference
<i>CsNF-YC1</i> -qPCR	F: GCTTGCCTATCAACATATCCA R: TGTTTTCTCAGTATGATTCCA	Expressing
<i>CsNF-YC2</i> -qPCR	F: ATCTCCGCCGAAGCC R: GCCCACAATCTCTACCCCT	Expressing
<i>CsNF-YC3</i> -qPCR	F: AACCATAGCCTTCCATTAGC R: GATTCCAAGACCGTAGCG	Expressing
<i>CsNF-YC4</i> -qPCR	F: AGGAAAACAAAAGGAGGACA R: AGGCGAATGCTGAGGTG	Expressing
<i>CsNF-YC5</i> -qPCR	F: AAGAGATGAGTTGAAAGAAGAGGG R: TGGGGGGCTGAGGTTGT	Expressing

Primer name	Primer sequence (5' to 3')	Used
<i>CsNF-YC6</i> -qPCR	F: CAGTTACGGGGGTGATGG R: GCTGCTGGTGGATGTGCT	Expressing
<i>CsNF-YC7</i> -qPCR	F: TCTGCTGTTGTAGCCACTGAT R: CTATGACTCCCACACCCCA	Expressing
<i>CsNF-YC8</i> -qPCR	F: GCCGCTGGCGAGGA R: TCATCAGAGTTAGCAGAATCAGAA	Expressing
<i>CsNF-YC9</i> -qPCR	F: CATCACTCGCACTGACATTTTC R: GCTCCCTCCGCTGGC	Expressing
<i>AtActin2</i> -qPCR	F: CTTGCACCAAGCAGCATGAA R: CCGATCCAGACACTGTACTTCCTT	Internal reference
<i>AtFLC</i> -qPCR	F: CCTAATTTGATCCTCAGGTTTGGG R: CCGACGAAGAAAAAGTAGATAGGCAC	Expressing
<i>AtSOC1</i> -qPCR	F: GCTCTCAGTGCTTTGTGATGC R: AAGAACGTACTTGGAGCTGGC	Expressing
<i>AtCO</i> -qPCR	F: CCGGGTCTGCGAGTCATG R: GGCATCATCTGCCTCACACA	Expressing
<i>AtFD</i> -qPCR	F: GCGCTAGGAAACAGGAATGCTTATACAAA R: AGCTGTGGAAGACCGTTGAAGTGTG	Expressing
<i>AtFT</i> -qPCR	F: GAGACCCTCTTATAGTAAGCAGAGTTG R: GGGAGTTCAAGTGAAAGAACCAAAGT	Expressing
<i>AtLFY</i> -qPCR	F: TTGGTGGTTTAGAGGGACTATTCG R: GCCGTAAAACCTAACTCCGCTA	Expressing
<i>AtAPI</i> -qPCR	F: AACCAAGGCCACAATATGCC R: CGGGTTCAAGAGTCAGTTCG	Expressing
<i>AtDREB2A</i> -qPCR	F: TGACCTAAATGGCGACGATGT R: TCCAAGTAACTCAAGTCGTGC	Expressing
<i>AtNCED3</i> -qPCR	F: CAGCTTGTAGCTTTTGGGCTGTA R: TAACAGAAACCAGCTGAGCTCGA	Expressing
<i>AtRD29A</i> -qPCR	F: GTTACTGATCCCACCAAAGAAGA R: GGAGACTCATCAGTCACTTCCA	Expressing
<i>AtABI1</i> -qPCR	F: AGAGTGTGCCTTTGTATGGTTTTA R: CATCCTCTCTCTACAATAGTTCGCT	Expressing
<i>AtABI5</i> -qPCR	F: CAATAAGAGAGGGATAGCGAACGAG R: CGTCCATTGCTGTCTCCTCCA	Expressing
P1300	F: TCATTGCGATAAAGGAAAGGC R: GCCACGATTTGACACATTTTTAC	Identification
<i>CZCsNF-YC6</i>	F: ACGCACAATCCCACTATCCTTC R: CGTTTACGTCGCCGTCCAG	Identification
hyg(280)	F: ACGGTGTCGTCCATCACAGTTTGCC R: ttccGGAAGTGCTTGACATTGGGGA	Identification

Table S2. Tea plant *NF-YC* family members predict

Gene name	Sequence ID	Chromosome number	Chromosome location (bp)	HMM length	E value	AA	Molecular weight (KDa)	Isoelectric
CsNF-YC1	GWHPACFB011961	2	107147531-107148430	64	3.70E-21	260	29.32	5.85
CsNF-YC2	GWHPACFB013851	3	104792750-104795981	64	1.6E-20	177	19.96	5.38
CsNF-YC3	GWHPACFB026946	ChaUn10827 (TEA022201.1: chr4)	13103-13882	64	1.00E-21	228	25.41	5.77
CsNF-YC4	GWHPACFB020260	6	107576981-107578654	64	3.40E-21	247	27.59	6.05
CsNF-YC5	GWHPACFB024733	8	152348395-152350737	64	6.80E-21	309	34.58	5.45
CsNF-YC6	GWHPACFB033498	ChaUn9861 (TEA002102.1: chr10)	29812-42002	64	3.50E-21	480	52.95	6.01
CsNF-YC7	GWHPACFB005786	12	8344610-8345166	65	3.20E-21	153	16.43	10.01
CsNF-YC8	GWHPACFB009167	14	54319197-54320242	65	5E-21	126	13.67	9.3
CsNF-YC9	GWHPACFB031341	ChaUn5166 (TEA008802.1: chr15)	28410-29461	64	1.60E-20	230	25.51	5.33

Table S3. Basic information of all identified *CsNF-YCs* genes in tea plant.

Gene name	Identities	ORF (bp)	AA	pI	Molecular weight (KDa)	Instability Index	Aliphatic Index	GRAVY	SignalP	TMHs
<i>CsNF-YC1</i>	95.60%	747	248	5.85	27.98	71.06	68.87	-0.668	NO	0
<i>CsNF-YC2</i>	98.80%	501	166	5.04	18.54	51.09	83.43	-0.316	NO	0
<i>CsNF-YC3</i>	87.82%	780	259	5.88	28.74	71.24	64.48	-0.605	NO	0
<i>CsNF-YC4</i>	86.71%	1011	336	7.21	37.82	65.80	68.01	-0.619	NO	0
<i>CsNF-YC6</i>	99.86%	726	241	5.81	27.12	72.33	66.06	-0.648	NO	0
<i>CsNF-YC7</i>	94.34%	372	123	9.77	13.28	62.03	72.11	-0.341	NO	0
<i>CsNF-YC8</i>	98.60%	357	118	7.85	12.92	46.71	88.47	-0.226	NO	0
<i>CsNF-YC9</i>	97.69%	729	242	5.06	26.83	67.18	75.83	-0.378	NO	0

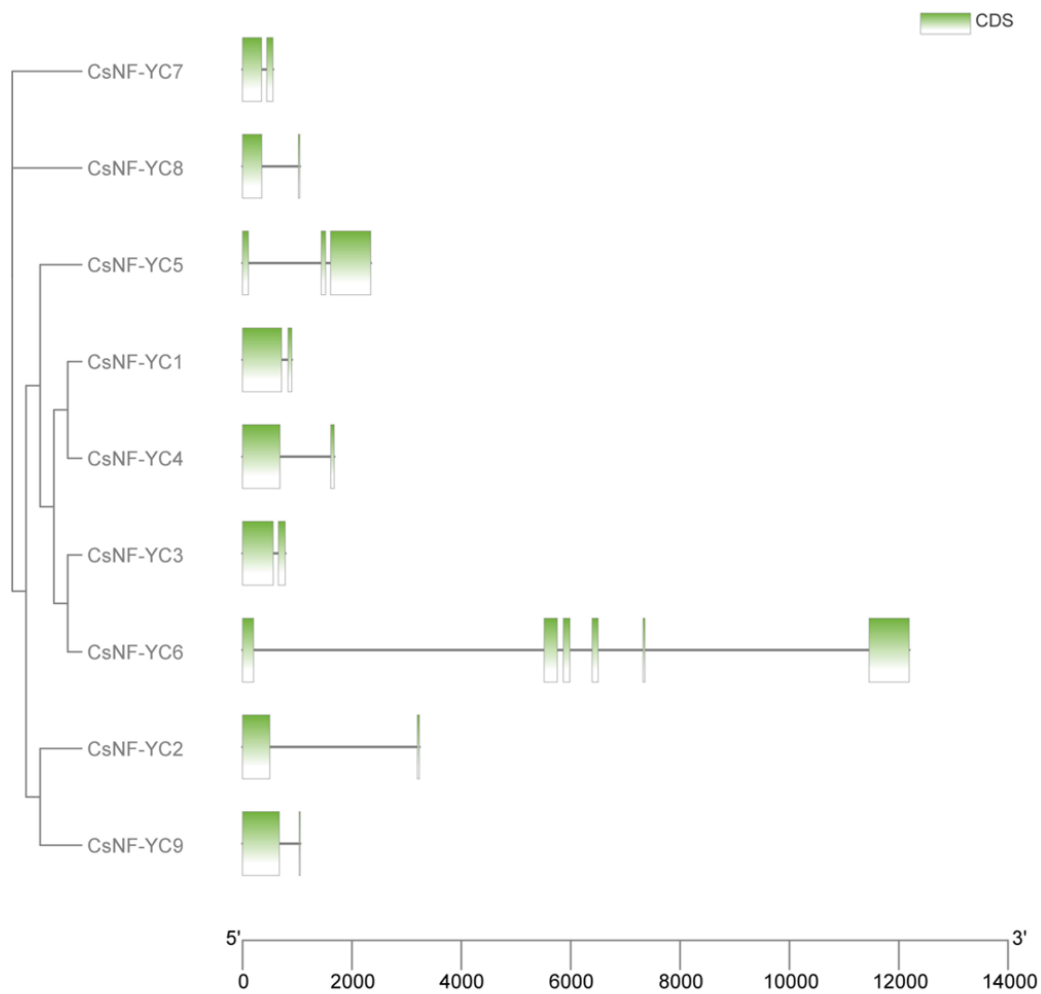


Figure S1. Exon-intron structure of *CsNF-YCs* genes.

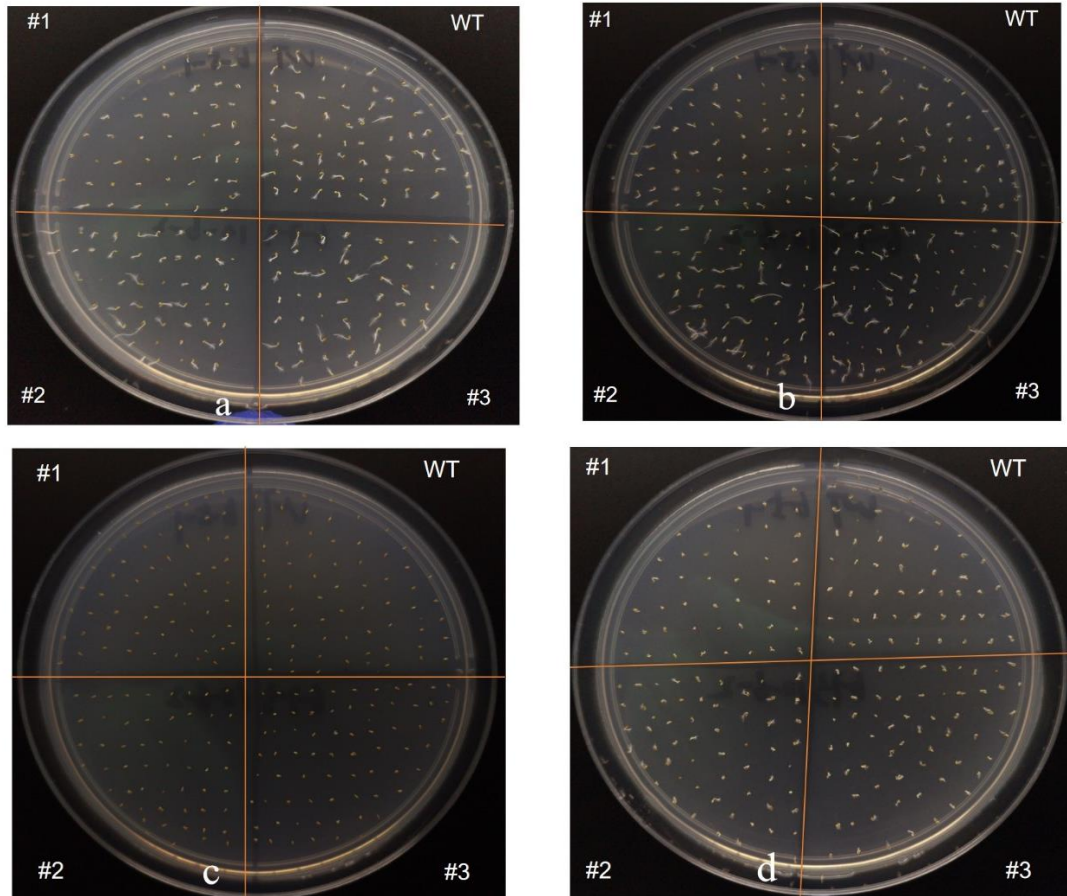


Figure S2. The phenotype of WT and three lines grown in 1/2 MS (a), 0.5 μ M GA (b), 0.5 μ M ABA (c) and 150 mM NaCl (d) medium for 4 days

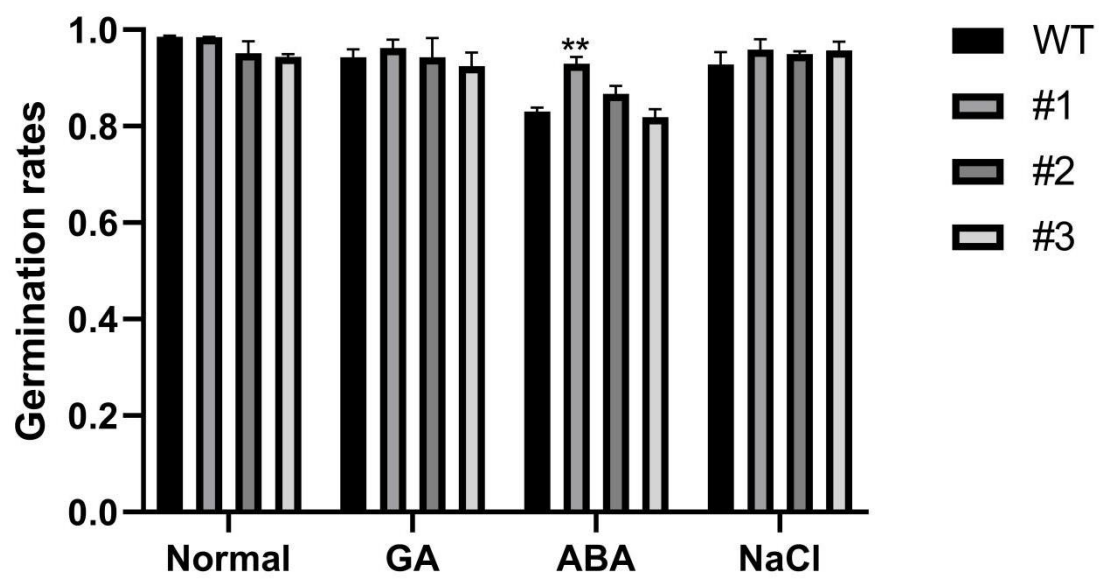


Figure S3. Germination rates of *CsNF-YC6-OE* Arabidopsis lines under different stress condition

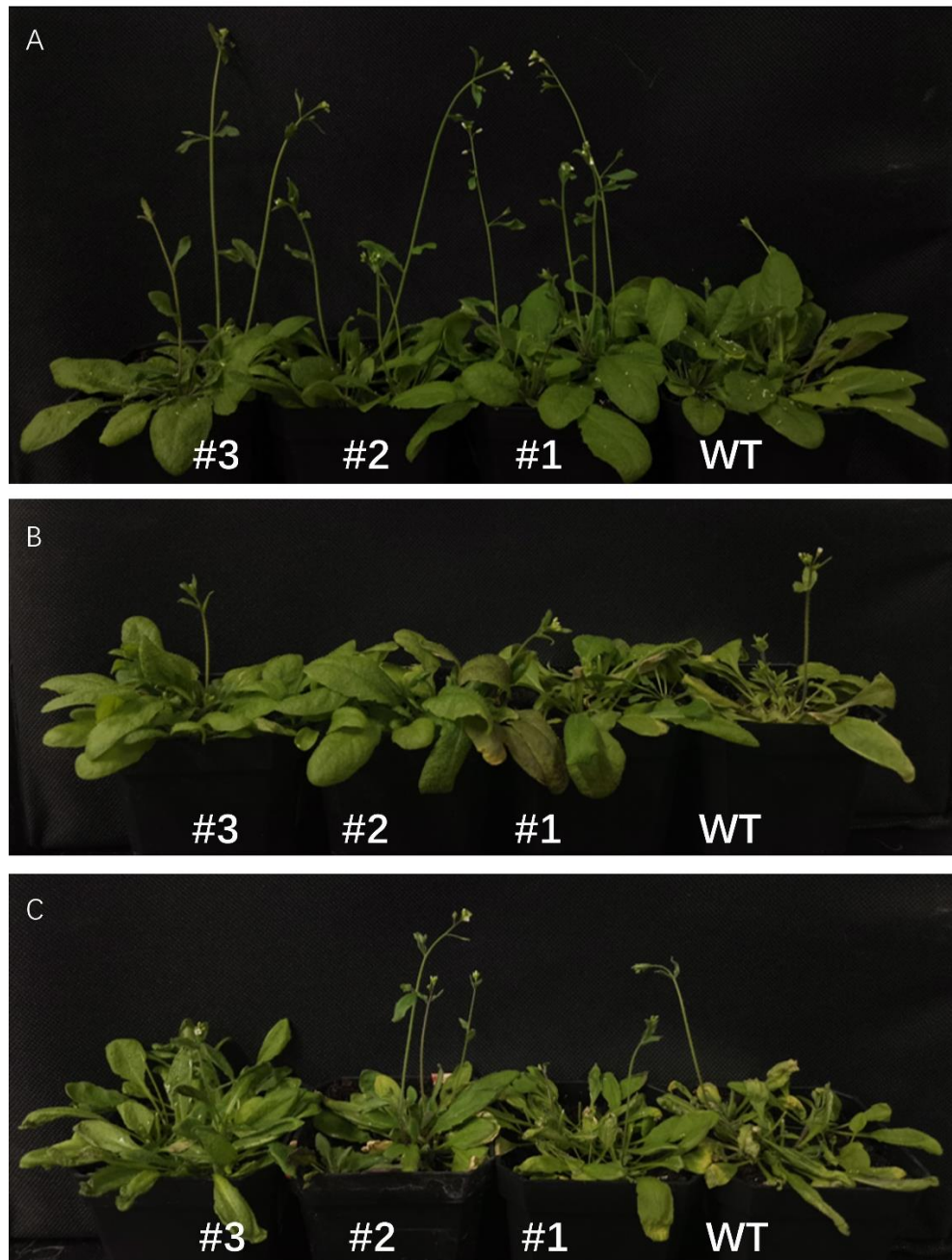


Figure S4. Phenotypic analysis of CsNF-YC6- overexpressed *Arabidopsis thaliana* lines and wild-type under different stresses: normal culture conditions (A), 200 mM NaCl treatment (B) and 15% PEG treatment (C).

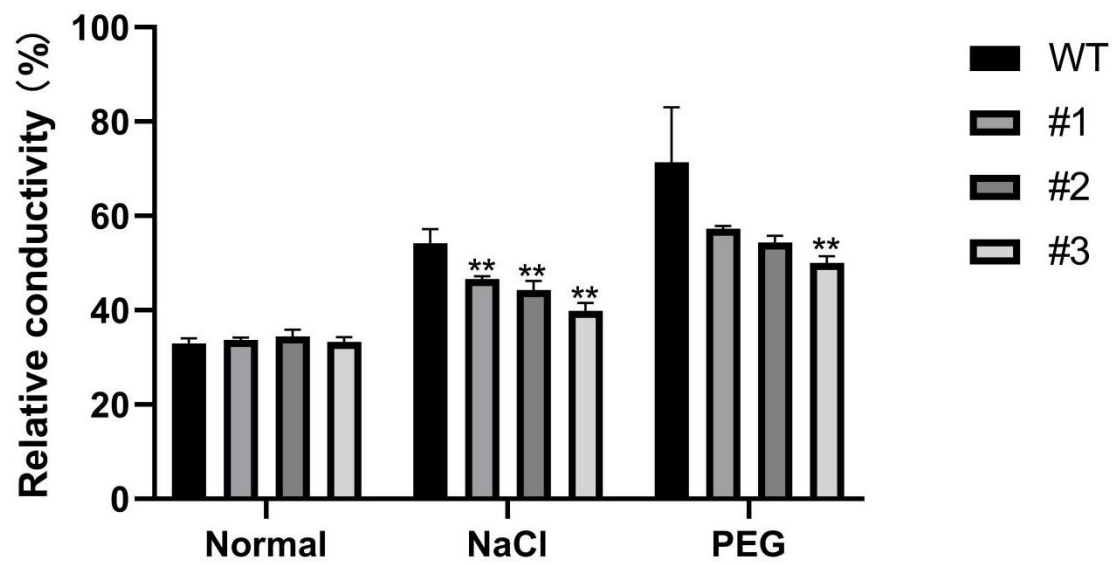


Figure S5. The relative conductivity of wild type and *CsNF-YC6-OE* Arabidopsis under stress.

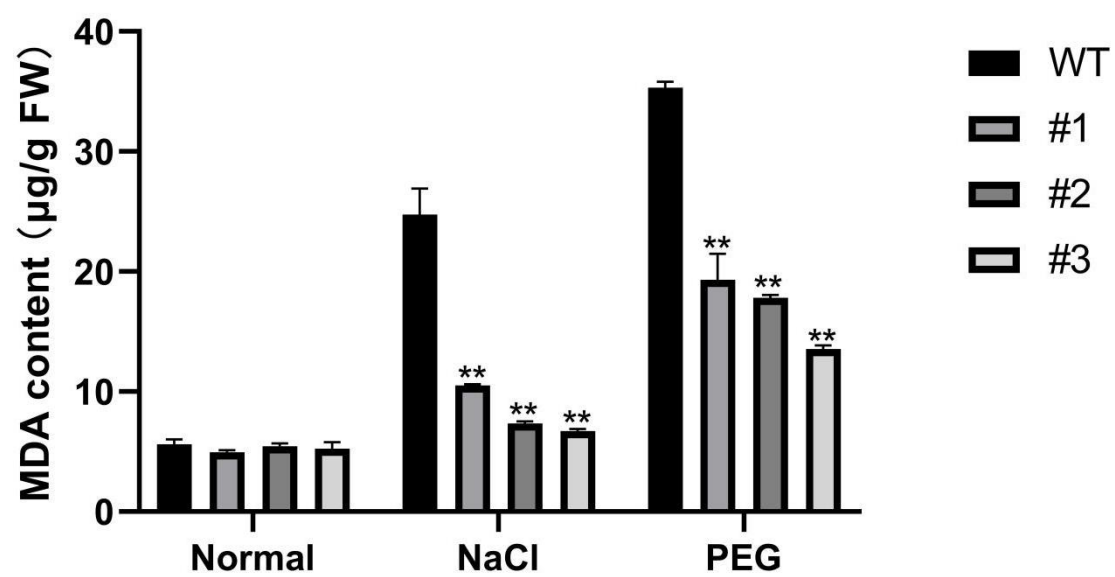


Figure S6. The MDA content of wild type and *CsNF-YC6-OE* Arabidopsis under stress.

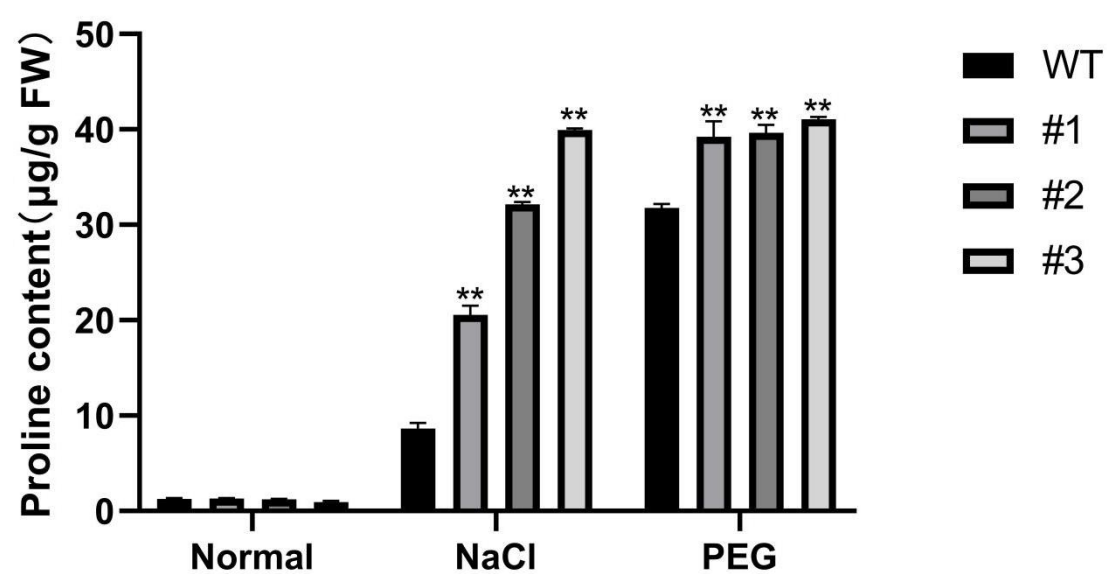


Figure S7. The proline content of wild type and *CsNF-YC6-OE* Arabidopsis under stress.

