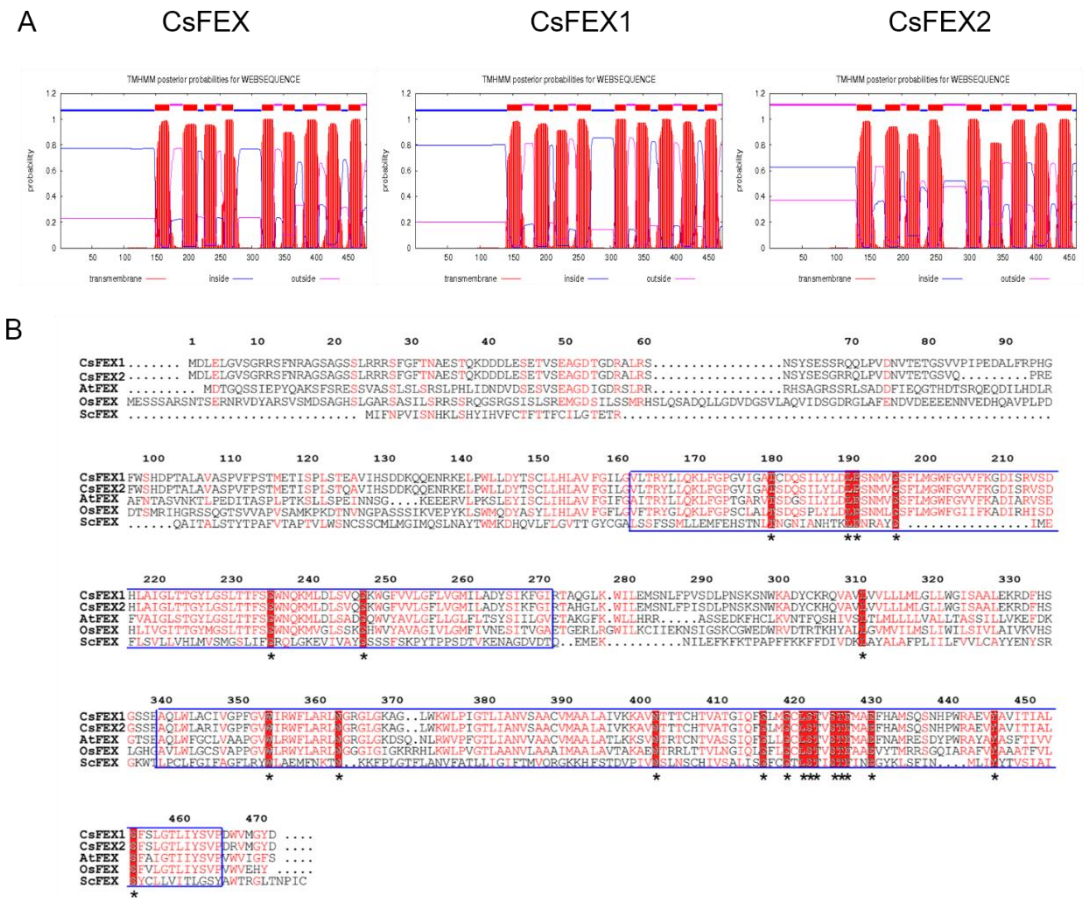

Figure S1. Protein sequence analysis of CsFEX1 and CsFEX2.

(A) Prediction of transmembrane structure of CsFEX, CsFEX1 and CsFEX2 by TMHHM.

(B) Sequence alignment of FEXs from *C.sinensis, A. thaliana, O.sativa,* and *S.cerevisiae.*

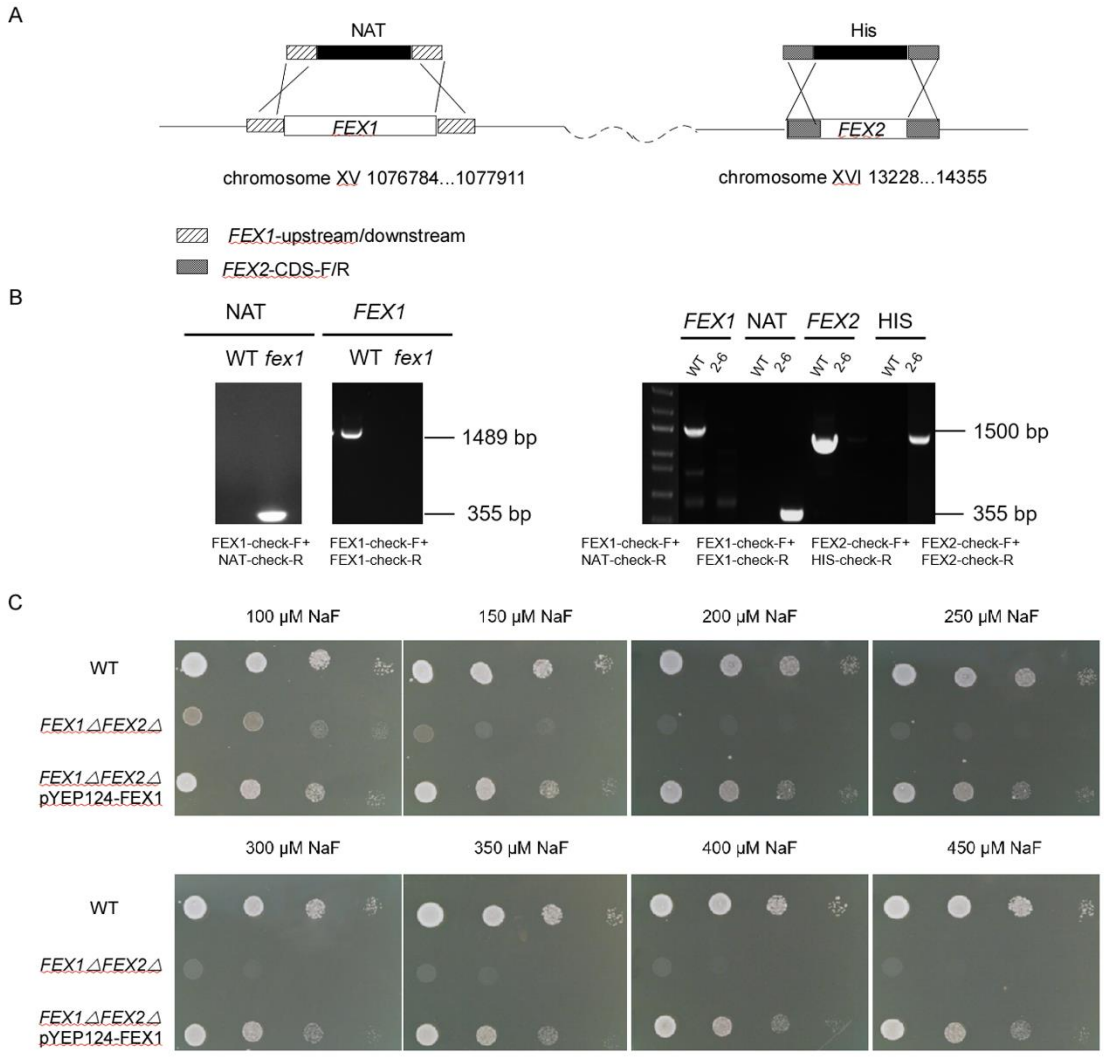

Figure S2. Deletion of FEX1 and FEX2 causes Fluoride Sensitivity in *S.cerevisiae*

(A) Schematic diagram of homologous recombination principle in FEX knock-out.

(B) Identification of the yeast double mutant strains by PCR.

(C) Screening of the minimum concentration of NaF.

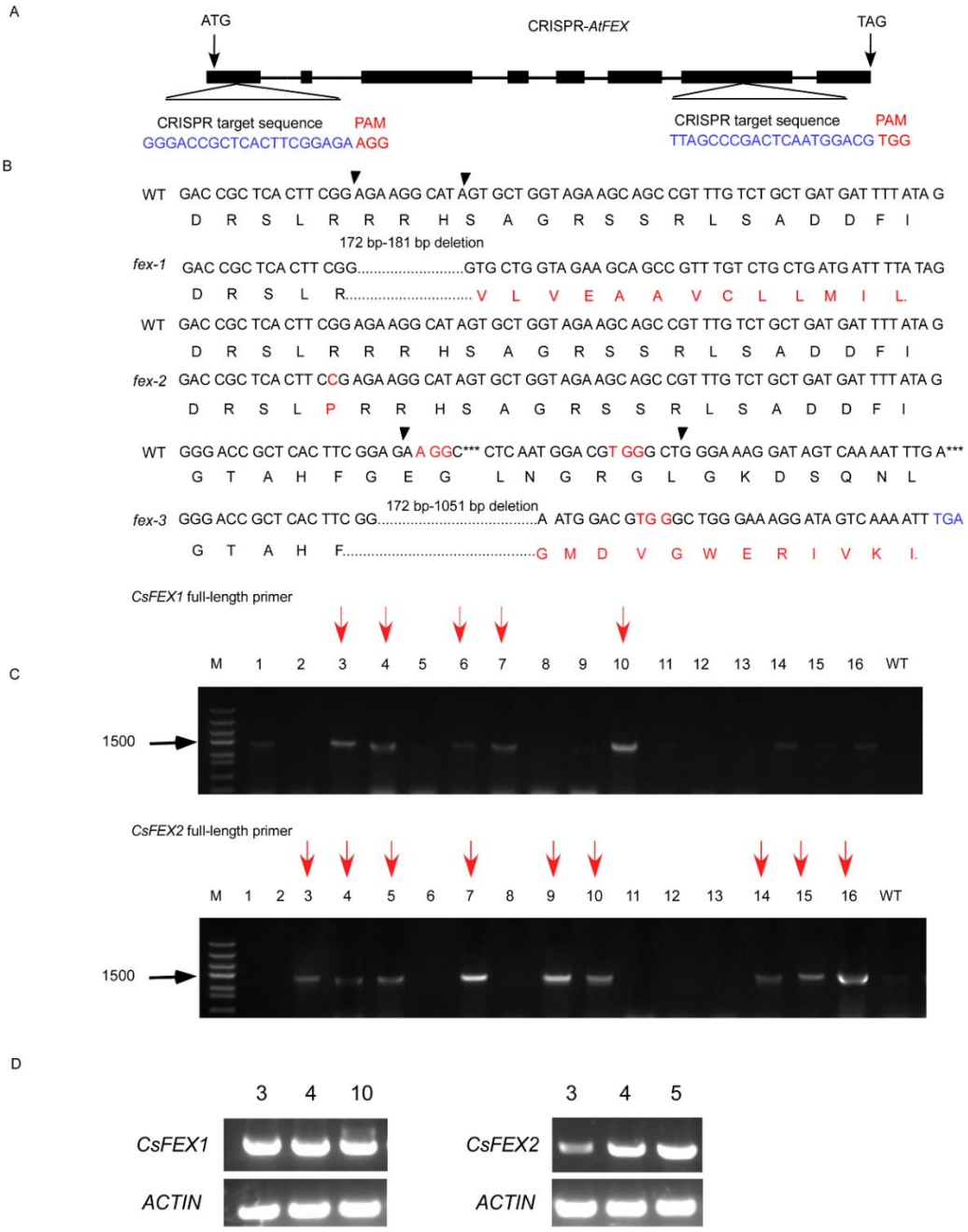

Figure S3. Construction of *AtFEX* mutants and *CsFEXs* complement plants.

(A) Region of *AtFEX* exon 1 and exon 7 were targeted by CRISPR/Cas9. The PAM is in red.

(B) Mutation analysis of *fex-1, fex-2* and *fex-3*.

(C) Identification of *CsFEX1* and *CsFEX2* in transgenic *A. thaliana* lines by PCR.

(D) Expression analysis of *CsFEX1* and *CsFEX2* in transgenic *A. thaliana* lines, with an internal control *AtACTIN2* (AT3G18780).

Table S1. The contents of fluoride in various organs of different tea cultivars.

Tea cultivars	F treatment	Roots /mg•kg^{-1}	Stems /mg•kg^{-1}	Leaves /mg•kg^{-1}	BAF	TF
YunKang 10	0 mM NaF	2.71±1.37	12.28±0.9	110.6±5.9		
	0.3 mM NaF	6.50±1.97	12.2±1.41	210±12.5	16.6	17.1
Fuding Dabaicha	0 mM NaF	3.46±2.55	14.87±1.03	138±10.5		
	0.3 mM NaF	5.50±0.99	15.30±3.0	309±22.8	24.5	29.4
Tie guanyin	0 mM NaF	3.58±1.30	17.13±8.46	267.2±12.8		
	0.3 mM NaF	9.30±1.41	23.6±5.0	631±40.4	50.1	35.1
Pingyang Tezaocha	0 mM NaF	7.80±3.57	18.19±8.8	403.8±18.4		
	0.3 mM NaF	11.8±2.40	21.7±2.56	1009±53.13	80.0	43.6

BAF (bioaccumulation factor) =C_p/C_{so}

C_p is the average fluoride concentrations (mg•kg^{-1}) in the plant and C_{so} is the average fluoride concentrations (mg•kg^{-1}) in the solution.

TF (translocation factor) = C_{s+l}/C_r

C_{s+l} is the average fluoride concentrations (mg•kg^{-1}) in the shoot and leaf and C_r is fluoride concentrations (mg•kg^{-1}) in the root.

Table S2. Strains used in this study.

Name	Description	Reference
S. cerevisiae		
Wild-type	BY4741	1
KO	FEX both alleles deletion *fex1Δfex2Δ*(ura$^-$)	
SpYEP124	empty vector transformed to *fex1Δfex2Δ* yeast strain	
SpYEP124-CsFEX1	pYEP124-CsFEX1 transformed to *fex1Δfex2Δ* yeast strain	
SpYEP124-CsFEX2	pYEP124-CsFEX2 transformed to *fex1Δfex2Δ* yeast strain	
SpYEP124-AtFEX	pYEP124-AtFEX transformed to *fex1Δfex2Δ* yeast strain	

1. Brachmann CB, et al. (1998) Designer deletion strains derived from Saccharomyces cerevisiae S288C: A useful set of strains and plasmids for PCR-mediated gene disruption and other applications. Yeast 14(2):115–132.

Table S3. Plasmids used in this study.

Name	Description
pYEP124	To Express gene in *S. cerevisiae*
pYEP124-GFP	To explore gene subcellular localization in *S. cerevisiae*
pCambia1302	To explore gene subcellular localization in *A. thaliana*
pCAMBIA1300-pYAO-cas9	Engineering CRISPR/Cas9 system
AtU6-26-sgRNA-SK	Engineering CRISPR/Cas9 system

Table S4. Primers Designed in This Study

Primer name	Sequence (5′→ 3′)	Annotation
CsFEX-YEP124-F	ATACCAAGCATACAATCAAGGATGGATCTTGAGCTTGGTGT	construction of the expression vector in *S. cerevisiae*
CsFEX-YEP124-R	CCGGGTACCGAGCTCGAATTCTAATCATAGCCCATGACCC	
CsFEX-YEP124-GFP-F	CTCGAGCTCAAGCTTCGAATTCTGATGGATCTTGAGCTTGGT	
CsFEX-YEP124-GFP-R	GGCAGCGGCAGCAGCCGGATCCCG ATCATAGCCCATGACCC	
CsFEX-1302-F	GAAGATCTGATGGATCTTGAGCTTGGTGT	construction of the expression vector in S. cerevisiae
CsFEX-1302-R	GACTAGTATCATAGCCCATGACCCAAT	
CsFEX1-qRT-F	TGTGCCTATTCCTGAGGATGCTTTATT	qRT-PCR
CsFEX1-qRT-R	GATCGCATGTGGCACCAATTACTCCAG	
CsFEX2-qRT-F	CTGGTAGTGTCCAGCCACGTGAA	
CsFEX2-qRT-R	GATCGCTTGTGGCACCAATTACT	
CsGADPH-qRT-F	GGCAGCACCTTACCAACAGC	internal reference gene in *C. sinensis*
CsGADPH-qRT-R	GTTTGGCGTCGTTGAGGGTC	
AtFEX-CR1-F:	ATTG GGGACCGCTCACTTCGGAGA	construction of the vector for CRISPR-cas9
AtFEX-CR1-R:	AAAC TCTCCGAAGTGAGCGGTCCC	
AtFEX-CR2-F:	ATTGTTAGCCCGACTCAATGGACG	
AtFEX-CR2-R:	AAAC CGTCCATTGAGTCGGGCTAA	