Table S1. Primers used for RT-qPCR.

Primer name	Primer sequences (5′→3′)
RT- PteuANT1F	TGTATGAAGTGACTGCAGGGG
RT- PteuANT1R	TAGGGTGAGGCTGGTCAGTAA
RT- PteuANT2F	GACATGTTCCTCAATCTGCGC
RT- PteuANT2R	TCTCTCCCTCCACCTGTTTCT
RT- PteuANT3F	TAATGGTATCTTGGGATGTTCG
RT- PteuANT3R	GCAACTGAATCCATACCCTCTC
RT- PtAIL5-1F	ACCGCCTCTGTCATCTCCATAG
RT- PtAIL5-1R	TTGGTTTGTGTTTTTTTGTGCT
RT- PtAIL5-4F	GAACGTGAAAGGCTGGCTAG
RT- PtAIL5-4R	TGTCAGTGAAAAGCAAAAGCA
RT-PtbANT-6F	TCCCTTTCCACTGTCTCTCCT
RT-PtbANT-6R	GCAAGCAAGAGTTGTCAGAGG
RT-euAP2-2F	CTTGGACACACACTCCCTCTC
RT-euAP2-2R	ATGTTTTGGGGAGAGAGAGCG
RT-euAP2-3F	GCTGACGTCTATTTGGTTGCC
RT-euAP2-3R	AGAATCAGCCTCGAACAGTTGT
RT-euAP2-4F	TTACAACAACATTGCAGGCCG
RT-euAP2-4R	GAGACTTGAAGAGCTGCTGGT
PtActin-F	AAACTGTAATGGTCCTCCCTCCG
PtActin-R	GCATCATCACAATCACTCTCCGA
Pt18S-F	GGCATGGAAGGTGATGCAGATC
Pt18S-R	CTGTGTCAAACAAGAACTTGTCC

Table S2. Primers used for amplification *AP2* genes.

Primer name	Primer sequences (5′→3′)
PteuANT1-F3	ATCTGGCTTCTTTTATTTCCTA
PteuANT1-R3	ATTGGGGAACAGATTGAAGGAA
PteuANT2-F1	AGAGAGAGGGGTAGAGTGAAAG
PteuANT2-R1	TCACCCCTCCTTTTCCCTCCTT
PtAIL51-F1	ACGCTCACCGATTACACC
PtAIL51-R1	CGTCAGTCCCAACTCGTCT
PtAIL5-4-F3	TCTTTACTCCCACCATCTCTCT
PtAIL5-4-R1	AGATGAAAGATGACAAAAGG

Table S3. Primers used for the construction of the pYES2 vector.

Primer name	Primer sequences (5′→3′)
pYES2- PtAIL5-1F	ggggtaccATGGATTCTAGTTCTCATCAG
pYES2- PtAIL5-1R	cggaattcTCATTCCATTCCAAAAATG
pYES2- PtAIL5-4F	ggggtaccATGGATTCTACTTCTCATCAG
pYES2- PtAIL5-4R	cggaattcTCATTCCATTCCAAAAATAGG
pYES2- PteuANT1F	ggggtaccATGAAATCGACGGGTGATAAC
pYES2- PteuANT1R	cggaattcTCAGGTGTCATTCCATGCAGCA
PYES2- PteuANT2F	ggggtaccATGAAATCTATGAGTAATAATAAC
pYES2- PteuANT2R	cggaattcTTAGGTATCATTCCATGCAG

Table S4. The PtAP2 gene accession number list.

JGI Gene accession number	Gene Bank accession number
Potri.001G169500	XP_024459631
Potri.003G064700	XP_002304138
Potri.001G018400	XP_002299238
Potri.003G205700	XP_024453004
Potri.006G167700	XP_006381802
Potri.008G076400	XP_024462525
Potri.010G181000	XP_002316179
Potri.018G091600	XP_024445325
Potri.007G011600	XP_024460943
Potri.002G114800	XP_024451945
Potri.005G148400	XP_024456512
Potri.007G007400	XP_006380824
Potri.014G008100	XP_024440363
Potri.014G012200	XP_052303230
Potri.001G041500	XP_002297679
Potri.003G185300	XP_024448435
Potri.006G179900	XP_011018218
Potri.008G011900	XP_002311921
Potri.010G092800	XP_024467077
Potri.010G247200	XP_024465222
Potri.017G078600	XP_011005069
Potri.018G102200	XP_024445391
Potri.T081332	XP_024448435
Potri.005G140700	XP_024456126
Potri.006G132400	XP_006381502
Potri.007G046200	XP_002310715
Potri.008G045300	XP_002312046
Potri.010G216200	XP_024466942
Potri.016G084500	XP_002322849

Table S5. *Ka/ks* analysis in the PtAP2 genes of *P. trichocarpa.*

Sequance1	Sequance2	Ka	Ks	Ka/Ks	EffectiveLen	AverageS-sites	AverageN-sites
PtAIL1-1	*PtAIL1-2*	0.08	0.19	0.43	1623	356.92	1266.08
PtAIL3-1	*PtAIL3-2*	0.03	0.21	0.15	1632	371.25	1260.75
PtAIL5-1	*PtAIL5-4*	0.05	0.25	0.20	1611	374.33	1236.67
PtAIL5-2	*PtAIL5-3*	0.06	0.30	0.21	2139	481.00	1658.00
PteuANT1	*PteuANT3*	0.24	1.25	0.19	1929	438.42	1490.58
PteuANT1	*PteuANT5*	0.25	1.31	0.19	1944	440.00	1504.00
PteuANT3	*PteuANT4*	0.05	0.28	0.19	1602	352.67	1249.33
PtbasalANT1	*PtbasalANT2*	0.05	0.39	0.13	1050	240.83	809.17
PtbasalANT1	*PtbasalANT9*	0.05	0.39	0.13	1050	240.83	809.17
PtbasalANT2	*PtbasalANT8*	0.16	1.61	0.10	1029	237.75	791.25
PtbasalANT2	*PtbasalANT9*	0.00	0.01	0.00	1053	241.83	811.17
PtbasalANT3	*PtbasalANT8*	0.06	0.38	0.16	912	209.33	702.67
PtbasalANT4	*PtbasalANT6*	0.06	0.33	0.18	1062	236.42	825.58
PteuAP2-1	*PteuAP2-3*	0.04	0.30	0.15	1509	337.83	1171.17
PteuAP2-2	*PteuAP2-4*	0.38	1.44	0.27	1446	329.00	1117.00
PteuAP2-2	*PteuAP2-5*	0.38	1.54	0.25	1425	324.92	1100.08
PteuAP2-2	*PteuAP2-6*	0.07	0.20	0.34	1470	340.83	1129.17
PteuAP2-4	*PteuAP2-5*	0.09	0.28	0.31	1506	339.42	1166.58
PteuAP2-4	*PteuAP2-6*	0.38	1.90	0.20	1422	328.42	1093.58
PteuAP2-5	*PteuAP2-6*	0.36	1.81	0.20	1413	324.25	1088.75

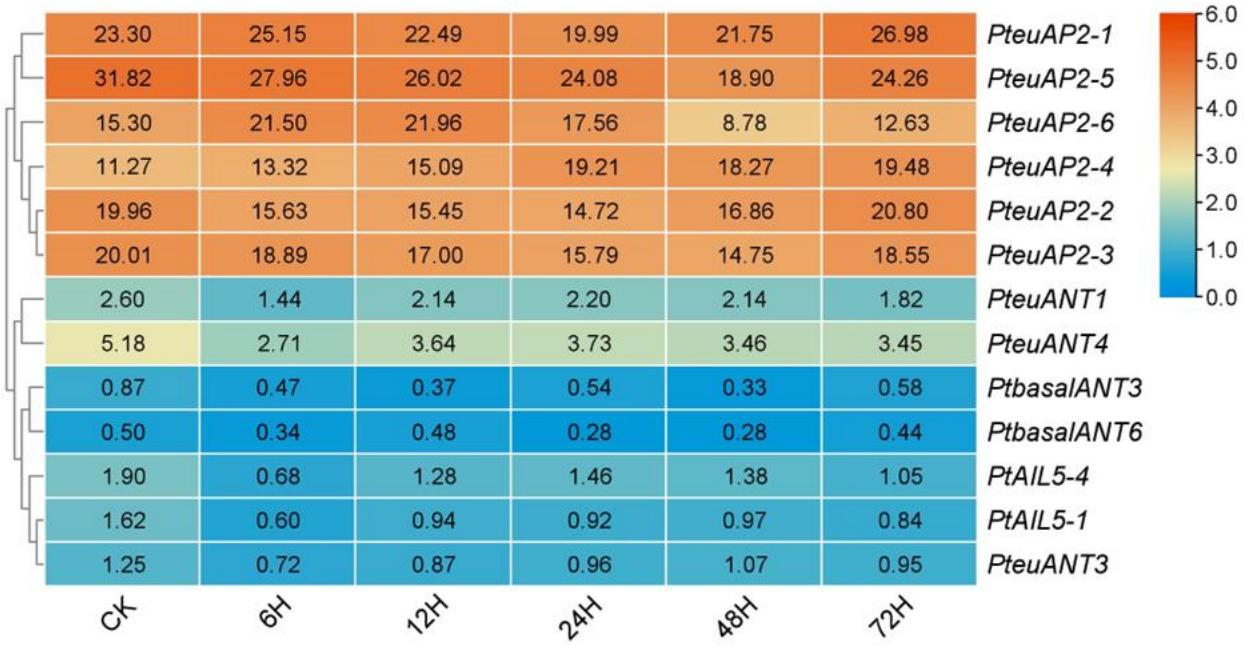


Figure S1. Transcriptome data of *PtAP2* genes under salt stress.

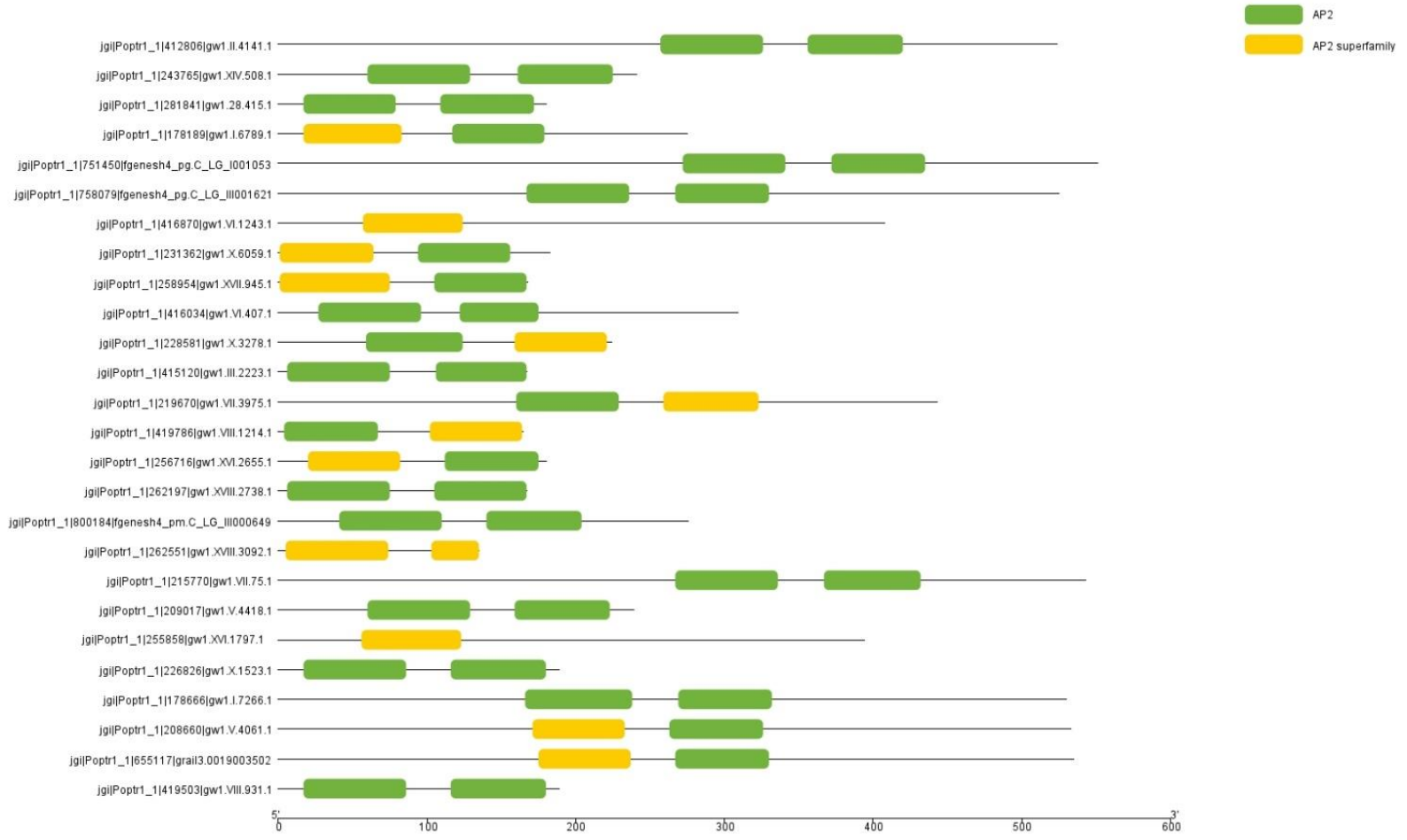


Figure S2. Prediction of protein domain structures of PtAP2 in version 1.1.

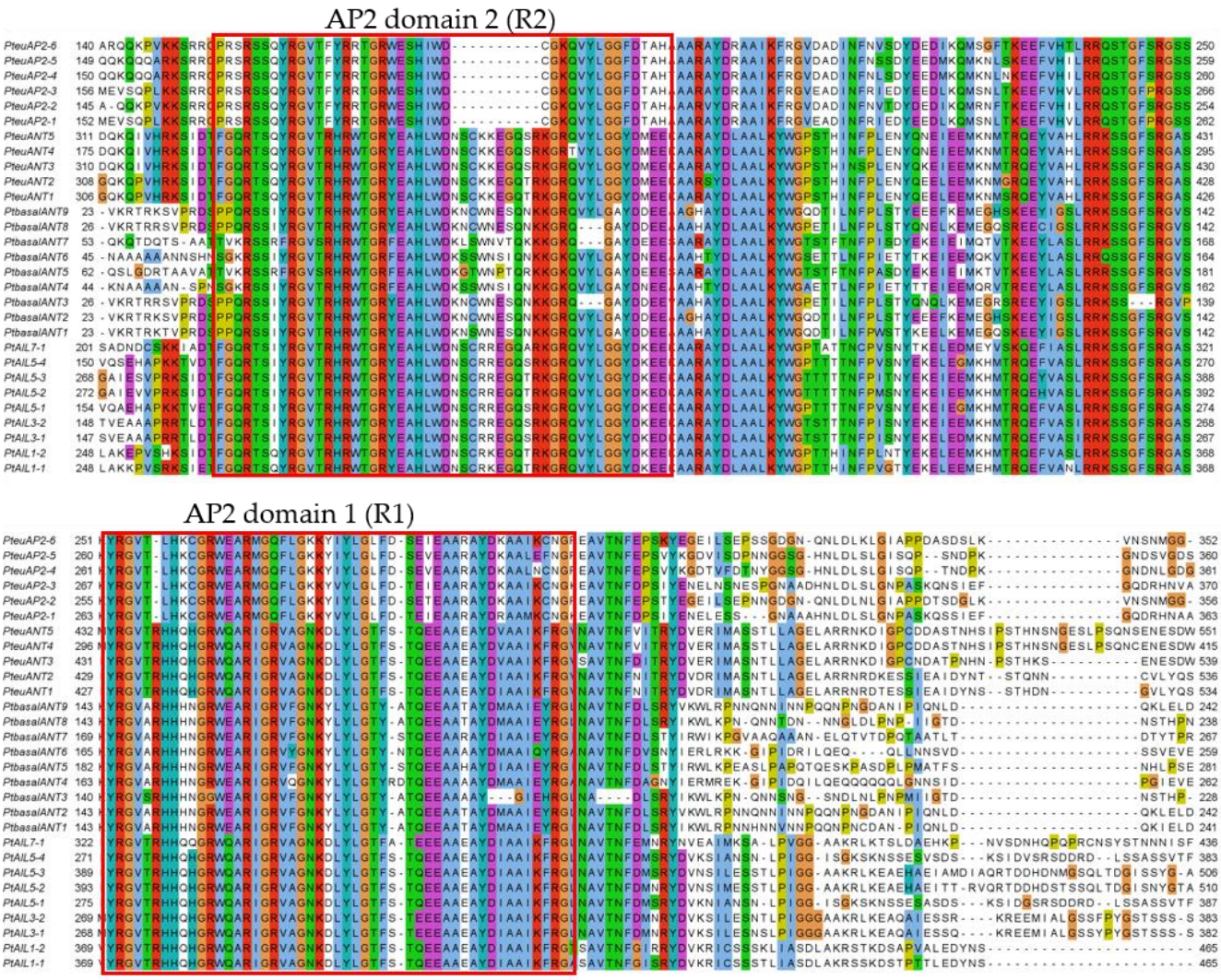


Figure S3. Multiple sequence alignment of all PtAP2 proteins using *ClustalX* 2.1.