

**Table S1.** Results of a two-way ANOVA (family, drought and family x drought) for root:shoot, stomatal conductance, net photosynthesis, water use efficiency, and changes in height and diameter of eight *Pinus contorta* families displaying source of variation, F-value and *p*-value. Significant sources of variation are highlighted in bold.

Source of Variation	F-value	<i>p</i> -value
<b>Root:Shoot</b>		
Family	2.520	<b>0.023</b>
Drought	0.760	0.388
Family x Drought	0.550	0.788
<b>Stomatal conductance (gs)</b>		
Family	0.490	0.823
Drought	39.180	<b>&lt;0.001</b>
Family x Drought	1.360	0.314
<b>Net photosynthesis (Pn)</b>		
Family	0.820	0.569
Drought	22.120	<b>&lt;0.001</b>
Family x Drought	0.780	0.605
<b>Water use efficiency (iWUE)</b>		
Family	0.660	0.703
Drought	70.320	<b>&lt;0.001</b>
Family x Drought	1.360	0.226
<b>Changes in height</b>		
Family	2.220	0.049
Drought	0.080	0.775
Family x Drought	2.030	0.070
<b>Changes in diameter</b>		
Family	1.49	0.194
Drought	9.73	<b>0.003</b>
Family x Drought	1.30	0.269

**Table S2.** Results of two-way ANOVA (family, drought and family x drought) for relative gene expression of five aquaporin genes (*PiconPIP1;2*, *PiconPIP2;1*, *PiconPIP2;2*, *PiconPIP2;3*, and *PiconTIP1;1*) from eight families of *Pinus contorta* displaying source of variation, F-value and p-value. Significant sources of variation highlighted in bold.

Source of Variation	F-value	p-value
<b><i>PiconPIP1;2</i></b>		
Family	27.45	<b>&lt;0.001</b>
Drought	30.05	<b>&lt;0.001</b>
Family x Drought	1.30	0.283
<b><i>PiconPIP2;1</i></b>		
Family	25.23	<b>&lt;0.001</b>
Drought	4.47	<b>0.042</b>
Family x Drought	10.05	<b>&lt;0.001</b>
<b><i>PiconPIP2;2</i></b>		
Family	22.70	<b>&lt;0.001</b>
Drought	2.42	0.129
Family x Drought	12.45	<b>&lt;0.001</b>
<b><i>PiconPIP2;3</i></b>		
Family	52.29	<b>&lt;0.001</b>
Drought	0.28	0.603
Family x Drought	6.27	<b>&lt;0.001</b>
<b><i>PiconTIP1;1</i></b>		
Family	9.08	<b>&lt;0.001</b>
Drought	0.01	0.921
Family x Drought	6.70	<b>&lt;0.001</b>

**Table S3.** Primer name and sequences for quantitative real-time PCR analysis of five aquaporins and two internal control genes.

Primer name	Primer sequences
<i>Pine_ACT7</i>	For: 5'- CCTTCCATCGTCCACAGAAA -3' Rev: 5'- CCACCATCATCTCAAGCAAAC -3'
<i>Pine_EF-1a</i>	For: 5' - CTGCGGTCAAGAAGGGTAAA -3' Rev: 5' - CTCGTGCATCAGAACATCAGACA -3'
<i>PinePIP1;2_qPCR</i>	For: 5' - GGACTGGTAACACACCTGTATTG -3' Rev: 5' - CAGATGGCTTTGGCCTAAAT -3'
<i>PinePIP2;2_qPCR</i>	For: 5' - GTCAGTGTCTCAAGTCTGTAGG -3' Rev: 5' - ATTCTCCTCACTGTTGCTACTT -3'
<i>PinePIP2;1_qPCR</i>	For: 5' - AAAGTCCAGGGTATGATGAG -3' Rev: 5' - CTGCTGCTACTGTGACTACAA -3'
<i>PinePIP2;3_qPCR</i>	For: 5' - CAGGTGGACTTGTCTGTATC -3' Rev: 5' - TTCTCTTCACCGGTTCTCATC -3'
<i>PineTIP1;1_qPCR</i>	For: 5' - GGC GTTATCTACGAGCTGTTA -3' Rev: 5' - GCCCTGTAAGAAGCCACTTTA -3'

**Table S4.** Aquaporin gene and primer sequences for cloning five aquaporin genes.

Gene	Primer sequences
<i>PiconPIP1;2</i>	For: 5' - ATGGCGACTTCTTGTTCTTT -3' Rev: 5' - CTAGGAGCGAGTTGAAGGG -3'
<i>PiconPIP2;1</i>	For: 5' - ATGACAAAGGAAGAAAGGAAGGA -3' Rev: 5' - TTACACATTGCGTTGCTTCG -3'
<i>PiconPIP2;2</i>	For: 5' - ATGGCTAAGGAAGGTGGCAA -3' Rev: 5' - GGTTGCTGCCGAAGGAT -3'
<i>PiconPIP2;3</i>	For: 5' - ATGATAAAATGAAGAAGGAGCTGTATCGG -3' Rev: 5' - TTACGCATTAACGTTGCCTCGAAC -3'
<i>PiconTIP1;1</i>	For: 5' - ATGCCGTTCGGAGGAATTGC -3' Rev: 5' - TCAGTACTCGTCGAGGGCAAC -3'

**Table S5.** Primer name and sequences for 3' rapid amplification of cDNA ends (RACE).

Primer name	Primer sequences
3'-RACE-Q0	5' - CCAGTGAGCAGAGTGACG -3'
3'-RACE-Q1	5' - GAGGACTCGAGCTCAAGC -3'
3'-RACE-QT	5' - CCAGTGAGCAGAGTGACGAGGACTCG AGCTCAAGCTTTTTTTTTTTTTTT -3'
<i>PiconPIP2;3-GSP1</i>	5' - CTGCCGCTGATCTCATTGAC -3'
<i>PiconPIP2;3-GSP2</i>	5' - TTGGTTTACTGCACTGCTGG -3'
<i>PiconPIP2;1-GSP1</i>	5' - AGAAGTTGAGCAGCAGGGAT -3'
<i>PiconPIP2;1-GSP2</i>	5' - ATGTGGCCAAGGACTACACA -3'

<i>PiconPIP2;2-GSP1</i>	5'- GAAGGAATTGGAGCAGCAGG -3'
<i>PiconPIP2;2-GSP2</i>	5'- GGGCATATCAATCCTGCTGT -3'
<i>PiconPIP1;2-GSP1</i>	5'- AGATGTTAACCTCGGTGCGA -3'
<i>PiconPIP1;2-GSP2</i>	5'- CACAGTCATGGGTGTCAAGG -3'
<i>PiconTIP1;1-GSP1</i>	5'- GCCATGGCTTCGACAAACT -3'
<i>PiconTIP1;1-GSP2</i>	5'- GCCACATCACGCTTCTAAGG -3'

PiconPIP2;1	MAKEGGKEVEQQGYVAKDYTDPPPAALFDVGEFKLWAFYR <b>AVIAEFTIATLLFLYITVATV</b>	60
PiconPIP2;2	MTKEERKELEQQGFP SKD YTDPPPAALIETSEFKLWSFYR <b>ALIAEFTATLLFLYITIATV</b>	60
PiconPIP2;3	MINEEGAVSEQRGFVGKDYTDPPA ADLIDTNEFKLWSFYR <b>ALIAEFTATLLFLYITVATV</b>	60
PiconPIP2;1	<b>I</b> GHKRNQ TACGSV <b>GLLGIAWA FGGMIFV L VYCTAGISGGHINPA</b> VTFGLFLARKVSLPRA	120
PiconPIP2;2	<b>I</b> GHSRNSTNCGSV <b>GVLGIAWS FGGMIFV L VYCTAGISGGHINPA</b> VTFGLFLARKVSLPRA	120
PiconPIP2;3	<b>I</b> GYARTSTD CGSV <b>GVLGIAWS FGGMIFIL VYCTAGISGGHINPA</b> VTFGLFLARKVSLPRA	120
PiconPIP2;1	<b>VLYMVAQCLGAICGCGLVKA</b> FQKSYYDEYGGGANSVAHGYT <b>KGVGLSAEII GTFVLVYTV</b>	180
PiconPIP2;2	<b>ILYMIAQCLGAICGTGLVKA</b> FQKSFYDRYGGGANYVHHGYT <b>KGVGLAAEII GTFVLVYTV</b>	180
PiconPIP2;3	<b>VLYMIAQCLGAICGTGLVKA</b> FQKSFYDKYGGGANYVHPGYT <b>KGVGLAAEII GTFVLVYTV</b>	180
PiconPIP2;1	<b>FSAT</b> DPKR NARDS <b>HIPVLA PLPIGF AVFMV H LATI P ITG TG INP ARSF GAA VIY GH QK SW</b>	240
PiconPIP2;2	<b>FSAT</b> DPKR SARD <b>S HVPVLA PLPIGF AVFMV H LATI P ITG TG INP ARSF GAA VIY GR KQ PW</b>	240
PiconPIP2;3	<b>FSAT</b> DPKR SARD <b>S HVPVLA PLPIGF SVFMV H LATI P ITG TG INP ARSF GAA V TFGH KQ SW</b>	240
PiconPIP2;1	DDQ <b>WIFWVGPFLGAAGAAAYHQYIL</b> RAGAIKALGSFRSNPHV	282
PiconPIP2;2	NDQ <b>WIFWVGPFLGAALASAYHQYIL</b> RAAIKALGSFRSNANV	282
PiconPIP2;3	DDH <b>WIFWVGPFLGAALAAAYHQYIL</b> RAAIKALGSFRGNVNA	282

(a)

PiconPIP1;2	MEGKEEDVNLGANKYSERQPLGTAAQTQE K DYTEPGPAPLFEPEGEFVWSFYRAGIAE <b>FM</b>	60
PiconPIP1;2	<b>A</b> TFLFLYITIILTVMGVKD ATDICNGS VGIQ <b>GIAWA FGGMIFCLVYCTAGISGGHINPA</b> VT	120
PiconPIP1;2	FGLFLARKLSSLPR <b>ALLYMICQCLGAMCGAGVVKGFGPSQ</b> YE FN GGGANTVAHGYTKGD <b>GL</b>	180
PiconPIP1;2	<b>GAEIVGTFVLVYTVFSAT</b> DAKRSARDSHVP <b>ILAPLPIGF AVFLVH LATI P ITG TG INP AR</b>	240
PiconPIP1;2	<b>SLGAAI</b> VF DSSHAWHDQ <b>WIFWVGPFIGAALAAFYHVIVI</b> RAIPFKSRH 288	

(b)

PiconTIP1;1	<b>MPFGGIAVGRPEEATHPEALK</b> <b>A A LAEGISTL IFV FAGEGSGMA</b> F DKLTS DASTTPA <b>GLVA</b>	60
PiconTIP1;1	<b>VALAHALGLFVAVAVGANISGGHV</b> NPAVTFGAFVGGHI <b>TLLRGILYWFAQLIGATVACLL</b>	120
PiconTIP1;1	<b>LKFTTGGLSTS AF</b> <b>SLSSGVGVGN</b> AVVFEIVMTFGLVYTVYATAVDPKKGNL <b>GTIAPICIG</b>	180
PiconTIP1;1	<b>FIVGANILAGGA</b> FDG <b>ASMNPARA</b> FGPA LVSWT WENH <b>WIYWVGPLLGGGLAGVIYELFMIS</b>	240
PiconTIP1;1	PEPTHQPLPSNEY 253	

(c)

**Figure S1.** Protein sequence alignment of (a) PiconPIP2;1, PiconPIP2;2 and PiconPIP2;3; (b) PiconPIP1;2; and (c) PiconTIP1;1 sequence showing conserved six membrane-spanning helices (H1-H6): highlighted and italicized and five connecting loops (LA-LE). Amino acids at NPA domains: green; ar/R selectivity filters: red; Froger's P1-P5 residues: turquoise.