

Gene Name	TAIR Gene ID	Protein length (aa)	G+C nucleotide content (%)	Codon Adaptation Index value		Kozak related features Nucleotide sequence surrounding mRNA AUG	Growth characteristics of AtPIP expressing yeast			
				<i>in Arabidopsis thaliana</i>	<i>in Saccharomyces cerevisiae</i>		Lag time (λ) (mins)	Max. growth rate (μ) $\text{Ln}(\text{Corr. OD}_t / \text{Corr. OD}_i) \text{ h}^{-1}$	Carrying capacity (κ) $\text{Ln}(\text{Corr. OD}_t / \text{Corr. OD}_i)$	Max.
<i>AtPIP1;1</i>	AT3G61430	286	50	0.80	0.72	AGA <u>ACC</u> AUG <u>GAA</u>	259 ± 24 ^{b,c,d}	0.189 ± 0.006 ^{b,c}	2.40 ± 0.05 ^{a,b,c}	
<i>AtPIP1;2</i>	AT2G45960	286	50	0.80	0.71	AGA <u>ACC</u> AUG <u>GAA</u>	251 ± 14 ^{b,c,d}	0.184 ± 0.002 ^{b,c}	2.40 ± 0.06 ^{a,b,c}	
<i>AtPIP1;3</i>	AT1G01620	286	52	0.76	0.69	AGA <u>ACC</u> AUG <u>GAA</u>	262 ± 15 ^{a,b,c,d}	0.195 ± 0.010 ^{a,b,c}	2.29 ± 0.05 ^{c,d}	
<i>AtPIP1;4</i>	AT4G00430	287	51	0.78	0.70	AGA <u>ACC</u> AUG <u>GAA</u>	250 ± 16 ^{b,c,d}	0.177 ± 0.003 ^{c,d}	2.22 ± 0.03 ^d	
<i>AtPIP1;5</i>	AT4G23400	287	49	0.79	0.72	AGA <u>ACC</u> AUG <u>GAA</u>	250 ± 19 ^{b,c,d}	0.178 ± 0.002 ^{c,d}	2.36 ± 0.05 ^{b,c,d}	
<i>AtPIP2;1</i>	AT3G53420	287	50	0.76	0.71	AGA <u>ACC</u> AUG <u>GCA</u>	265 ± 12 ^{a,b,c,d}	0.183 ± 0.005 ^{b,c}	2.47 ± 0.06 ^{a,b}	
<i>AtPIP2;2</i>	AT2G37170	285	51	0.73	0.68	AGA <u>ACC</u> AUG <u>GCC</u>	240 ± 13 ^{c,d}	0.199 ± 0.012 ^{a,b}	2.53 ± 0.08 ^a	
<i>AtPIP2;3</i>	AT2G37180	285	51	0.73	0.67	AGA <u>ACC</u> AUG <u>GCT</u>	225 ± 14 ^d	0.181 ± 0.007 ^{b,c,d}	2.49 ± 0.07 ^{a,b}	
<i>AtPIP2;4</i>	AT5G60660	291	51	0.73	0.69	AGA <u>ACC</u> AUG <u>GCA</u>	257 ± 24 ^{b,c,d}	0.164 ± 0.005 ^d	2.36 ± 0.07 ^{a,b,c,d}	
<i>AtPIP2;5</i>	AT3G54820	286	52	0.76	0.70	AGA <u>ACC</u> AUG <u>ACG</u>	228 ± 31 ^{c,d}	0.140 ± 0.008 ^e	2.01 ± 0.07 ^e	
<i>AtPIP2;6</i>	AT2G39010	289	51	0.74	0.68	AGA <u>ACC</u> AUG <u>ACG</u>	308 ± 34 ^{a,b}	0.187 ± 0.005 ^{b,c}	2.53 ± 0.07 ^a	
<i>AtPIP2;7</i>	AT4G35100	280	50	0.81	0.74	AGA <u>ACC</u> AUG <u>TCG</u>	315 ± 24 ^a	0.212 ± 0.008 ^a	2.49 ± 0.05 ^{a,b}	
<i>AtPIP2;8</i>	AT2G16850	278	49	0.78	0.73	AGA <u>ACC</u> AUG <u>TCA</u>	291 ± 25 ^{a,b,c}	0.201 ± 0.012 ^{a,b}	2.41 ± 0.07 ^{a,b,c}	
empty vector	-	-	-	-	-	-	279 ± 20 ^{a,b,c,d}	0.195 ± 0.006 ^{a,b}	2.51 ± 0.05 ^{a,b}	

Supplemental Table S1. *AtPIP* codon compatibility for heterologous expression in yeast and growth characteristics of *AtPIP* expressing yeast lines.

The *AtPIP*s have similar good codon compatibility (CAI values and GC contents) for heterologous expression in yeast, with yeast CAI values similar to native yeast *AQP* genes (*AQY1*: 0.71 CAI and 51% G+C; *AQY2*: 0.79 CAI and 46% G+C). The upstream Kozak region (red nucleotides) were engineered as part of the vector construction. *AtPIP* expressing yeast cultured in standard selection medium (no treatment) show slight differences in growth characteristics between each other and empty vector control. Superscript letters denote statistical groupings, ANOVA with Tukey's test ($P < 0.05$). $N \geq 10$ for each line.

