Additional file 6. Molecular evolutionary analysis of OryzaTPS1 using the species tree

Model	**Parameters estimated**					**LnL**	**Significant?**	**Positively selected sites**[a]
Branch models								
1ω	ω_0= 0.6397					-2831.9384		
$2\omega_D$	ω_0= 0.5732; ω_D= 999.0000					-2829.4825	Yes ($P<0.05$)	
Branch-site models								
Null (M1a)	ω_0= 0; ω_1= 1					-2822.1200		
Null (neutral)	Site class	0	1	2a	2b	-2822.1200		
	ω_B[b]	0	1	0	1			
	ω_A	0	1	0.4000	0.4000			
Positive selection	Site class	0	1	2a	2b	-2819.2042	Yes (vs neutral) ($P<0.05$)	**32R (0.977*)** **318L (0.976*)** **429G (0.978*)** **433I (0.955*)** **486P (0.977*)**
	ω_B[b]	0	1	0	1			
	ω_A	0	1	753.2913	753.2913			

- [a] the amino acids and their positions refer to those of OrTPS1M.
- [b] for Background, , ω_A for foreground(OrTPS1M);
- *denotes posterior probabilities by Bayes Empirical Bayes analysis.