

**S2 Table. Expression of 15 BIP1-regulated genes during initial stages of rice infection (16hpi).**

<b>Class</b>	<b>Gene</b>	<b>Name</b>	<b>Ratio <math>\Delta bip1/P1.2</math> *</b>
SSPs	<i>MGG_11610</i>	<i>BAS3</i>	0
	<i>MGG_09693</i>	<i>BAS2</i>	0
	<i>MGG_00751</i>	-	0
	<i>MGG_12655</i>	<i>AVR-Pi9</i>	0
	<i>MGG_17425</i>	-	0,002 #
	<i>MGG_06666</i>	-	0,016 #
	<i>MGG_05638</i>	-	0,15 #
	<i>MGG_03504</i>	-	0,22
	<i>MGG_08428</i>	-	0,38
	<i>MGG_07934</i>	-	0,45
Enzymes	<i>MGG_02201</i>	endopeptidase	0,003 #
	<i>MGG_08480</i>	lipase/esterase	0,13 #
	<i>MGG_11966</i>	cutinase	0,58
ACE1 Cluster	<i>MGG_12447</i>	<i>ACE1</i>	0
	<i>MGG_08381</i>	<i>ORF3</i>	0
Control genes	<i>MGG_05344</i>	snodprot 1	0,58
	<i>MGG_03245</i>	aldose 1-epimerase	0,76

\*Expression was determined by qRT-PCR. The ratio of expression between the  $\Delta bip1$  mutant and the wild-type control was calculated using the formula  $2^{-\Delta Ct \Delta bip1} / 2^{-\Delta Ct \text{ wild type}}$ . "0" indicates expressed in WT but not expressed in  $\Delta bip1$ . # indicates significantly different at  $p > 0,05$  according to t-test using expression values from three biological replicate samples. Similar results were obtained in two other independent experiments.