

Table S1. Primer sequences for qRT-PCR.

Gene	Forward primer	Reverse primer
<i>MrActin</i>	AATGGAACTGGAATGGTCAAGGC	TGCCAGATCTTCTCCATGTCATCCCA
<i>MrPR1</i>	AGAGGTGGGTGTTGGACCTA	GCTGCTCCATGCGATGTTTT
<i>MrPR2</i>	GCTCAGAGGGAGCTGCAAA	CACTCCCCACCAATACACGA
<i>MrPR5</i>	GGAGTTCTCTCCGGAAACGG	CCACAATCACCGGTAAGGCA
<i>MrPR10</i>	CGGATGGTTCACCTCCTACGG	ATTGACCGGGATCGCAGAA
<i>MrBAK1</i>	ATGGCACCAGAATCGCTGTT	ATGCACCCTCAACGCAGTAT
<i>MrBRI1</i>	GGTCAACCTCTGCATACCGT	CCAGCAATCTCCTCGACTCC
<i>MrBZR1</i>	AGTGGGCAAGTTCCATGCTT	GAGCTACACAAGCCATTGCG
<i>MrBES1</i>	TGGCTCCTGAGTTGTTCTACA	AGTTTGGCTTGAATGGTCTGC

Table S2. Sequence reads of the transcriptome and their alignment with the reference genome.

Sample	Obtained Reads (M)	Obtained Bases(Gb)	Q20(%)	Q30(%)	GC(%)
Mock-1	21.31	6.35	98.38	95.43	46.63
Mock-2	20.45	6.12	98.19	94.85	46.46
Mock-3	21.41	6.41	97.45	93.06	46.75
XJ27-1	19.89	5.95	97.61	93.29	46.26
XJ27-2	19.53	5.85	97.72	93.56	46.32
XJ27-3	21.93	6.57	98.05	94.31	46.26
BL+XJ27-1	20.76	6.21	98.22	94.94	46.49
BL+XJ27-2	20.57	6.16	98.29	95.08	46.47
BL+XJ27-3	19.41	5.81	97.04	92.09	46.9