

Supplementary Table S1

List of primers*

a. For cDNA cloning

1. DHR F: 5'-CGTCACGTAACGTCAACATTGCGGGTACGC-3'
R: 5'-TAATTACTTACTAAACGGAATGTATTG-3'
 2. TRPA1 F: 5'-GTCATGACATTTGTGGAACAACGGGCCTA-3'
R: 5'-TCAAGTCGACTTGTAAATGATGCGAGCTCG-3'
-

b. For screening of the $\Delta TRPA1$ mutant

- F: 5'-AGTTTTTTGTACAGGCTGCTGAAAGCGGA-3'
R: 5'-TCTCGGTTGCATGCCAATAAGC-3'
-

*F; Forward primer, R; Reverse primer.

a

BmoDH;	TDMKDESDRGAHSERGALWFGPRL	24
BmaDH;	TDMKDESDRGAHSERGALWFGPRL	24

b

<u>TM1</u>		
BmoDHR;	MNS--ETINDTANASRPVDSTRVPGPQRDTLYIVLPITIIYTIFVSGLGNIFTCIVIV	58
BmaDHR;	MNSLNETLNDTANASRPVDSTRVPGPQRDTLYIVLPITIIYTIFISGLGNIFTCIVIV	60

<u>TM2</u>		
BmoDHR;	RNKNLHTATNNYLFSLAISDLLLVSGMPQEMYSIWSKWPYVFUGHTFCVIRGLAAETSTN	118
BmaDHR;	RNKNLHTATNNYLFSLAISDLLLVSGMPQEMYSIWSKWPYVFUGHTFCVIRGLAAETSTN	120

<u>TM3</u>		
BmoDHR;	ASVLTTITLEFTIERYLAIChPFVSHKMSKLSRAVKHVLLLWVAALALALPQALQFGIRQYQ	178
BmaDHR;	ASVLTTITLEFTIERYLAIChPFVSHKMSKLSRAVKHVLLLWVAALALALPQALQFGIRQYQ	180

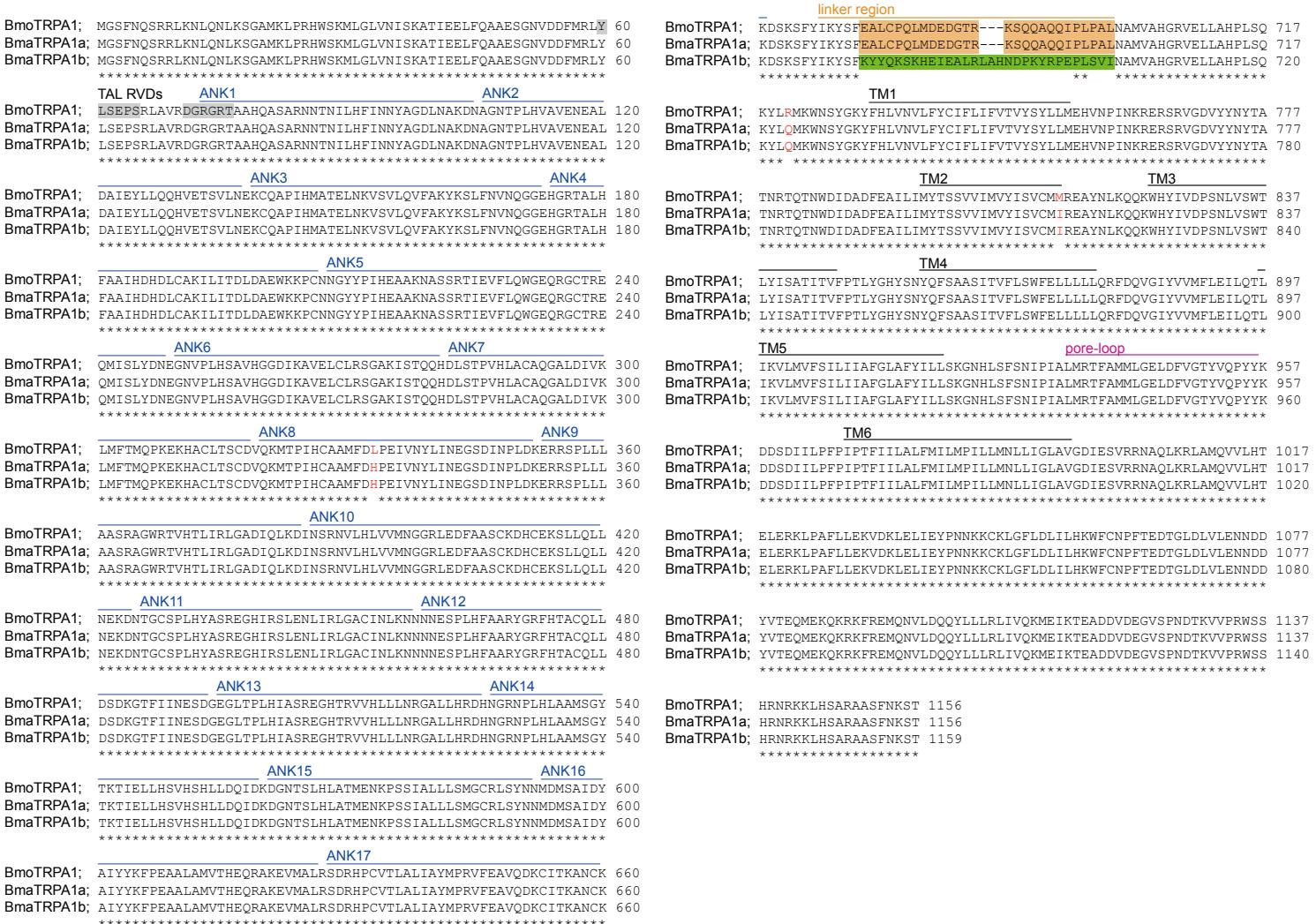
<u>TM4</u>		
BmoDHR;	GVIMCLQTRVIIIEHSFEISTFLFFLAPMVLITVILYFIGLKLREKSNVKEQNQNDFESSI	238
BmaDHR;	GVIMCLQTRVIIIEHSFEISTFVFFLAPMVLITVILYFIGLKLREKSNVKEQNQNDFESSI	240

<u>TM5</u>		
BmoDHR;	RYSHKMCRKPSQSTRRVIKMLVAVVVAFFICWAFPHAQRLVAIYGTNENHLAKSPILFSV	298
BmaDHR;	RYSHKMCRKPSQSTRRVIKMLVAVVVAFFCWAFFHQRLVAIYGTNENHLAKSPILFSV	300

<u>TM6</u>		
BmoDHR;	YLFLTYISGIFYMMSTCINPILYHIMSNKFRDAFKMTLCCCGTRNNDTAVKRSSYTAMAFV	358
BmaDHR;	YLFLTYISGICYMMSTCINPILYHIMSNKFRDAFKMTLCSCGTRNNDTAVKRSSYTAMAFV	360

<u>TM7</u>		
BmoDHR;	RHPTSSGTNSGNSIRNETNLQSCTRRTNGRDKILNDAHCRNGTLSSAAVGKPDSRTNG	418
BmaDHR;	RNPTSSGTNSGNSIRNETNLQSCTRRTNSRDKILNDAHVCNGNTLSSAAVGKPDSRTNG	420
* *****		
BmoDHR;	DRPLDRNLINETYFNTNC	436
BmaDHR;	DRPLDRNLINETYFNTNC	438

Supplementary Figure S1. Alignments of amino acid sequences of diapause hormone (DH) and DH receptor (DHR). The deduced amino acid sequences of *DH-PBAN* (**a**) and *DHR* (Acc. No. LC594680) (**b**) cDNAs in *Bombyx mori* (Bmo) and *B. mandarina* (Bma) were aligned. Identical amino acids are indicated by asterisks. The putative transmembrane domains (TM1~TM7) are indicated.



Supplementary Figure S2. Alignment of amino acid sequences of *Bombyx mori* and *B. mandarina* TRPA1. The deduced amino acid sequences of the TRPA1 cDNA (Acc. Nos. AB703646.1, LC597009.1, and LC597010.1) in *B. mori* (Bmo) and *B. mandarina* (Bma) were aligned. Identical amino acids are indicated by asterisks. The TAL repeat variable diresidues (RVDs), ankyrin repeat (1~17), linker region, transmembrane (1~6), and pore-loop domains are indicated.