Figure S1  ABCC neighbour-joining tree based on Labbé et al. (2011) suggests orthology between Heliotis virescens and Plutella xylostella ABCC2 proteins. Geneious Pro v5.4.5 software produced a protein alignment with MUSCLE and a neighbour-joining consensus tree with the Jukes-Cantor distance model and 5000 bootstrap replicates. *P. xylostella* ABCC2 clusters with 100% bootstrap support with other lepidopteran ABCC2 proteins (red text). Sample names contain species, GenBank accession number and *Drosophila* CG number or description. Dmel, *Drosophila melanogaster*; Bmori, *Bombyx mori*; Px, *Plutella xylostella*; Hvir, *Heliotis virescens*; Hsub, *Heliotis subflexa*; Tni, *Trichoplosia ni*; Hsap, *Homo sapien*. The outgroup is *D. melanogaster* ABCB (NP_648040). A 1268 amino acid *B. mori* ABCC protein sequence (LABBE et al. 2011) was generated by joining BGIBMGA007784-TA and BGIBMGA007785-TA on chromosome 15 (http://silkworm.genomics.org.cn).