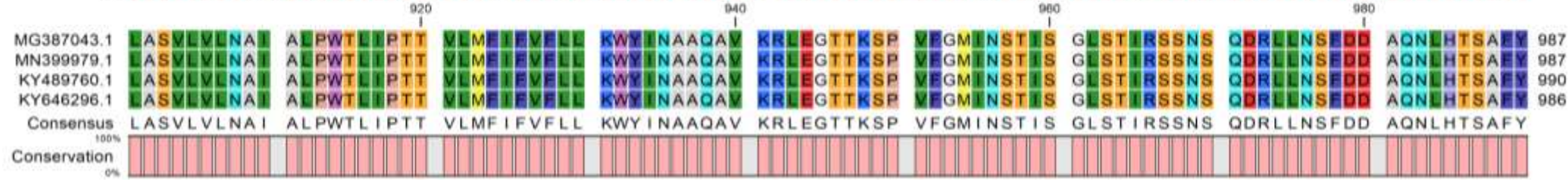
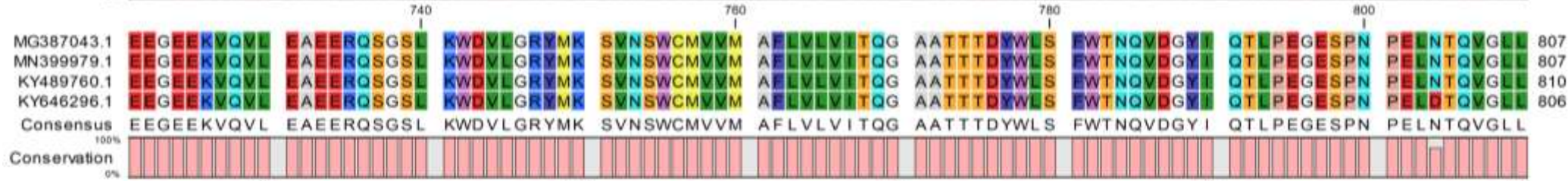
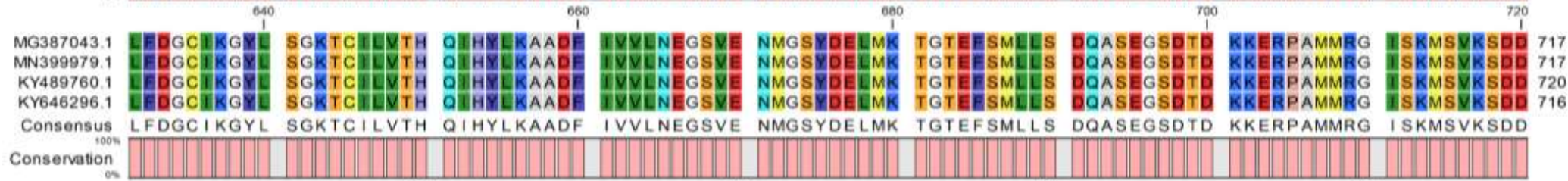
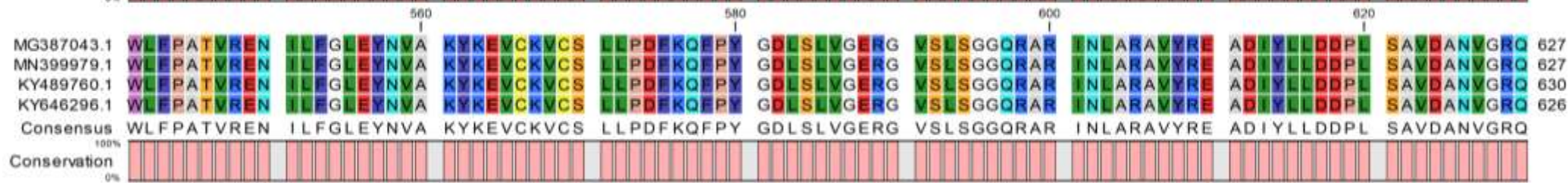
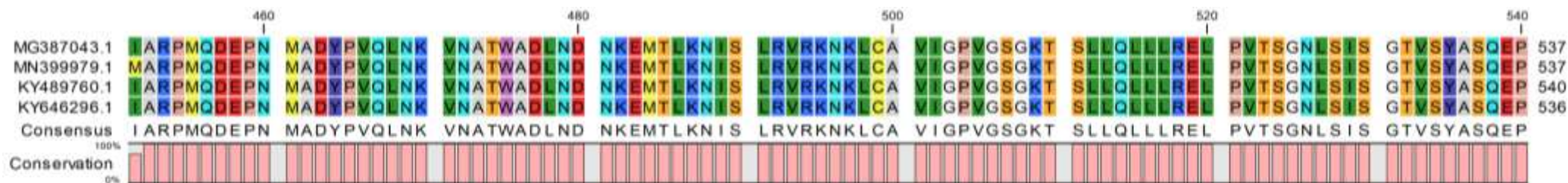


Figure S1- Representative overview (sample PRS_7 shown) of intron (blue) and exon (green) sequence coverage of the *SfABCC2* gene from the *S. frugiperda* corn v6.0 genome from LepidoDB when using overlapping TILING primers developed against an earlier gene model from genome assembly v3.1. Regions of the *SfABCC2* gene model with no sequence coverage are primarily intronic. The largest section with no coverage corresponds to the 1.9 Kbp of intron 13, which joined scaffolds 11087 and 7154 in the v3.1 genome version and was not available when the study was initiated. Other regions with no sequence coverage include exon 1 (218 bp), introns 1 and 2, and small sections (ranging from 32-322 bp) of introns 18, 21 and 23. In total, 23 of the 25 exons were covered by the TILING amplicons (~90%). This graphical overview was produced using CLC Genomics Workbench 9.5.3 with mapping at default parameters and sequence coverage was too deep to show the individual sequences (e.g. exon 2 had 19X coverage whereas other sites had >1,000X).





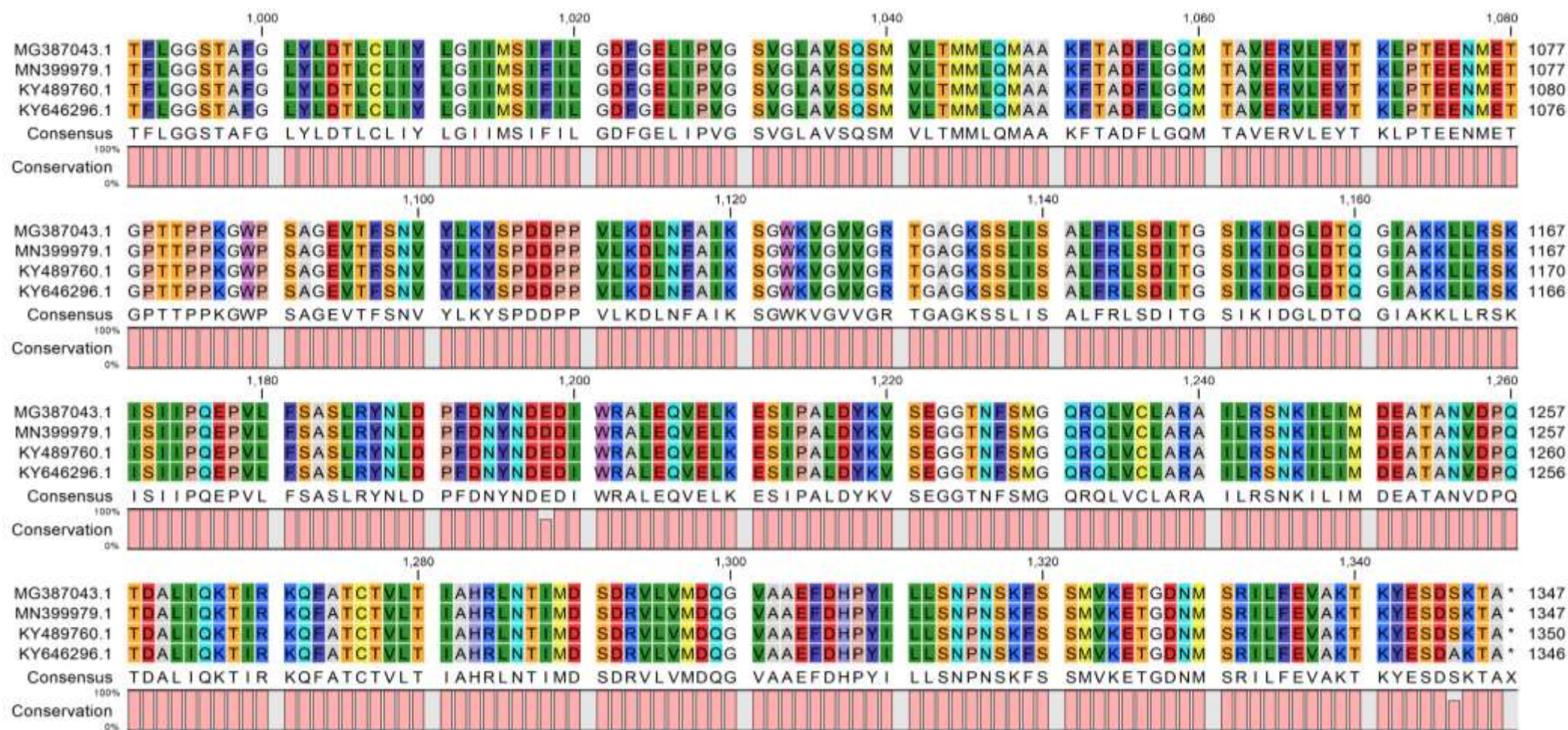


Figure S2- Alignment of *SfABCC2* cDNAs from NCBI (GenBank accession numbers MG387043.1, MN399979.1, KY489760.1 and KY646296.1) to obtain a consensus *SfABCC2* protein sequence used as a reference to locate mutations. Sequence alignment and consensus determination was performed in CLC Genomics Workbench 21.0.4. Residue coloring represents Rasmol colors indicating traditional amino acid properties.