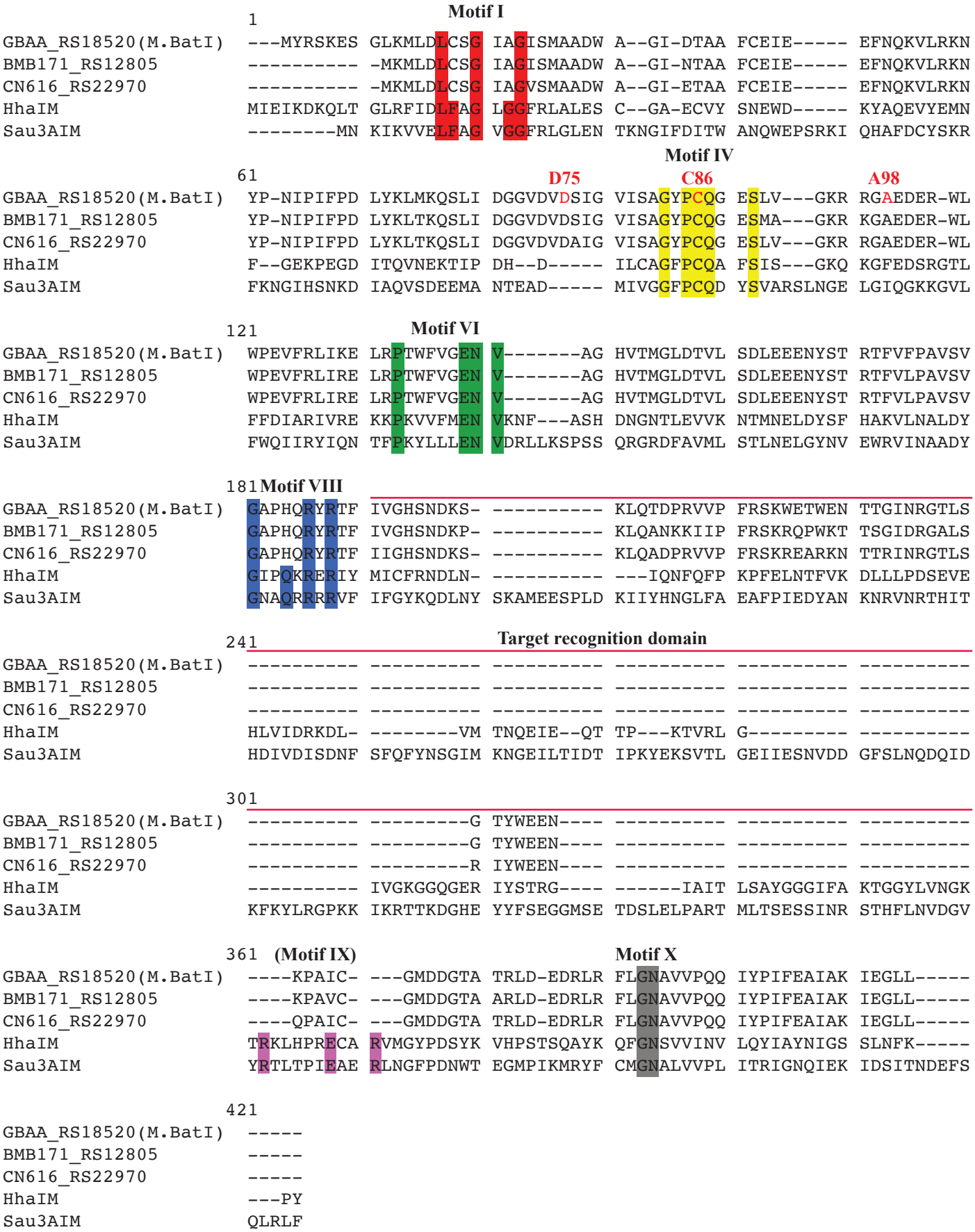

S2 Fig. Alignment of M.BatI and its homologs together with other representative cytosine methyltransferase. Conserved motifs of cytosine methyltransferase were colored. The region corresponding to target recognition domain were indicated with red line above the alignment. In M.BatI sequence, letters of residues of variants we constructed were colored in red.