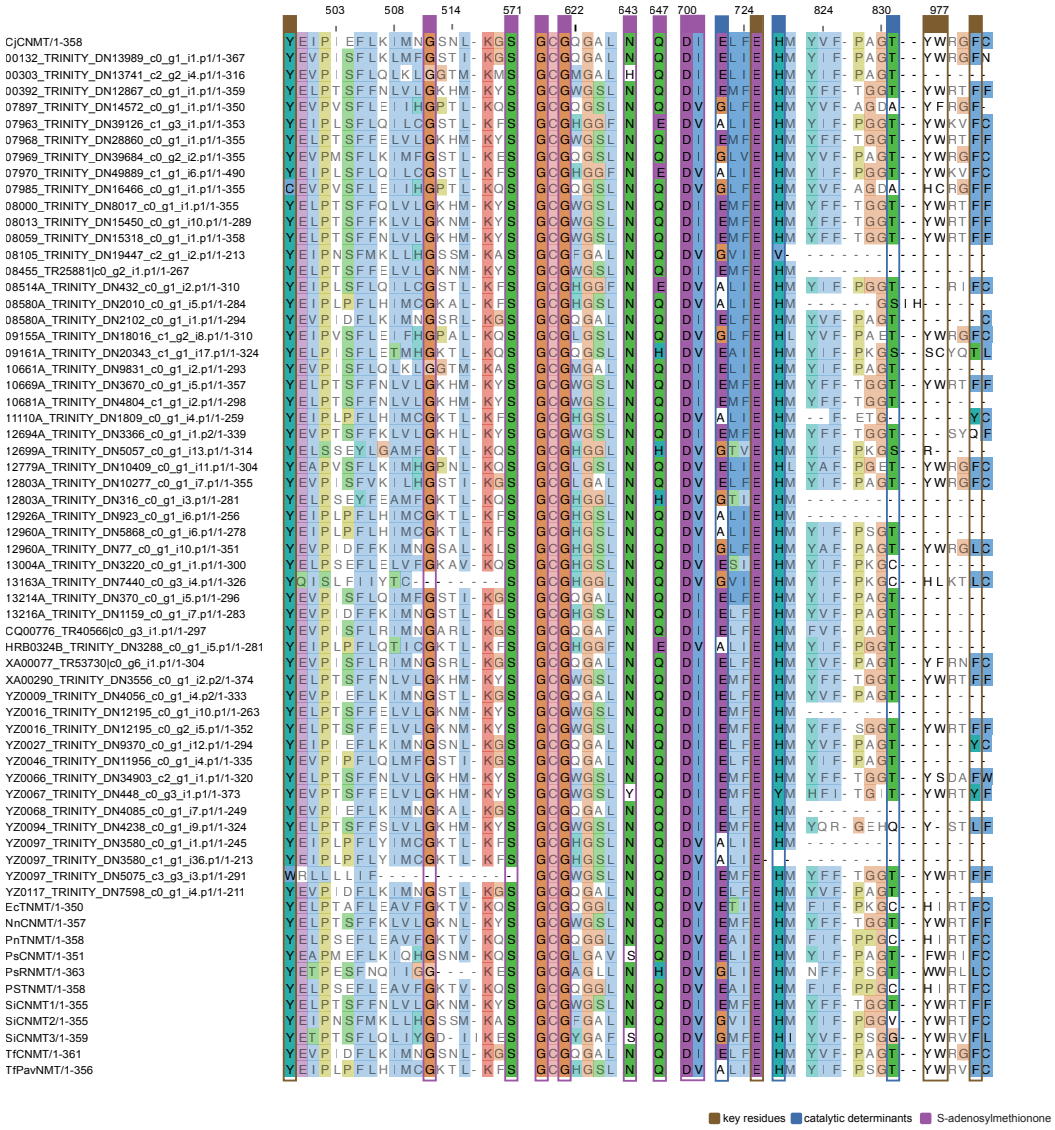

Supplementary Figure 6. Alignment of key amino acid sites in major CNMT gene family sequences. CjCNMT was used as the model, with sequences from eleven other species serving as references. The alignment includes positively selected sequences, where key residues are marked in brown, catalytic determinants in blue, and S-adenosylmethionone in purple.