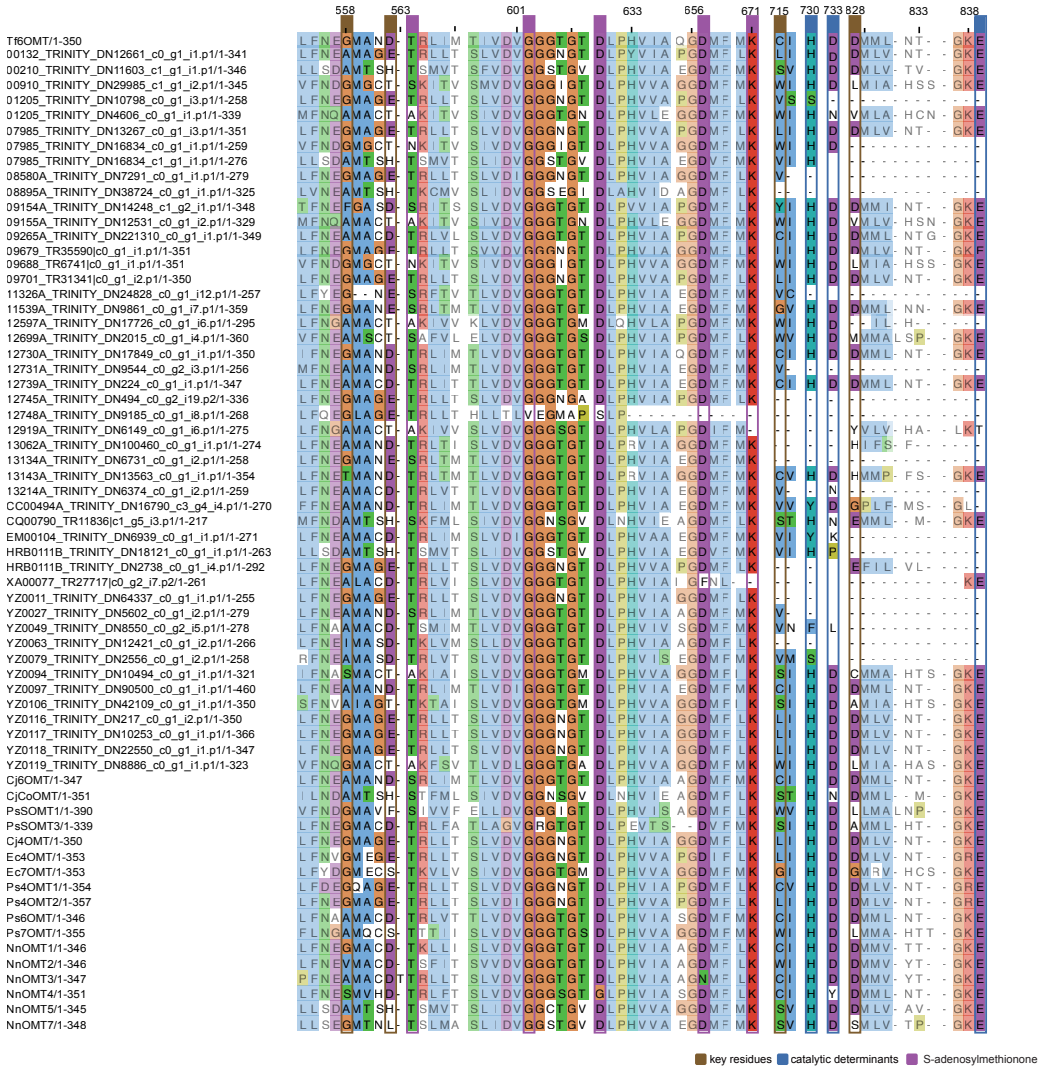

Supplementary Figure 8. Alignment of key amino acid sites in major OMT gene family sequences. TfOMT was used as the model, with sequences from Seventeen other species serving as references. The alignment includes positively selected sequences, where key residues are marked in brown, catalytic determinants in blue, and S-adenosylmethionone in purple**.**