

The Description of Additional Supplementary Files

Supplementary Data 1: Raw count data, log2 fold change values and adjusted p-values generated during transcriptomic analysis within this study as well as transcriptomic data specifically used for generating the heatmap (Fig. 1) and the overview of *A. dehalogenans* methyltransferase systems (Supplementary Figure 3)

Supplementary Data 2: CdmB homologues used to compute the conservation score for CdmB displayed in Fig. 3 and to generate the AlphaFold 3 models shown in Supplementary Fig. 10.

Supplementary Data 3: BLASTp queries and data used for Cdm system completeness prediction for Fig. 5 and Supplementary Fig. 12.