Figure S3. Maximum likelihood (ML) phylogenetic tree of the Cytydiltransferase domain as obtained by RAxML (WAG + Γ + I). The tree is rooted using the midpoint-rooted tree option. Statistical support was obtained by RAxML 100-bootstrap replicates (BV) and Bayesian Posterior Probabilities (PP). Both values are shown on key branches. A black dot in a node indicates BV > 95% and PP > 0.95. Eukaryotes are shown in bold. "A_" indicates Archaeal sequences. Characteristic domain architecture shown in key taxa.