Supplementary figure 3 A. Multiple sequence alignment of Q8GAJ8 from *P. nicotinovorans* pAO1 with an integrase from *Mycobacterium gordonae*, Cre recombinase and a Tn554A transposase. The alignment was performed with Cobalt and visualized with Jalview. The residues are highlighted based on the identity levels and catalytic site residues are marked with red. Alignments were performed with Cobalt and visualized with Jalview.
Supplementary figure 3 B. Multiple sequence alignment of Q8GAJ7 from *P. nicotinovorans* pAO1 with the corresponding A0A1D9FFG5 of pZXY21, Tn554, Tyrosine recombinase XerD from *E. coli* and an integrase from *Mycobacterium gordonae*. The residues are highlighted based on the identity levels and catalytic site residues are marked with red. Alignments were performed with Cobalt and visualized with Jalview.
Supplementary figure 3 C. Multiple sequence alignment of Q8GAJ5 from *P. nicotinovorans* pAO1 with the corresponding A0A1D9FFQ7 of pZXY21, a Tn554-related transposase C of *Paenarthrobacter aurescens* TC1 and a transposase from *Mycobacterium gordonae*. The proteins show a conserved leucine (L) zipper motif. Alignments were performed with Cobalt and visualized with Jalview. The residues are highlighted based on the identity levels.