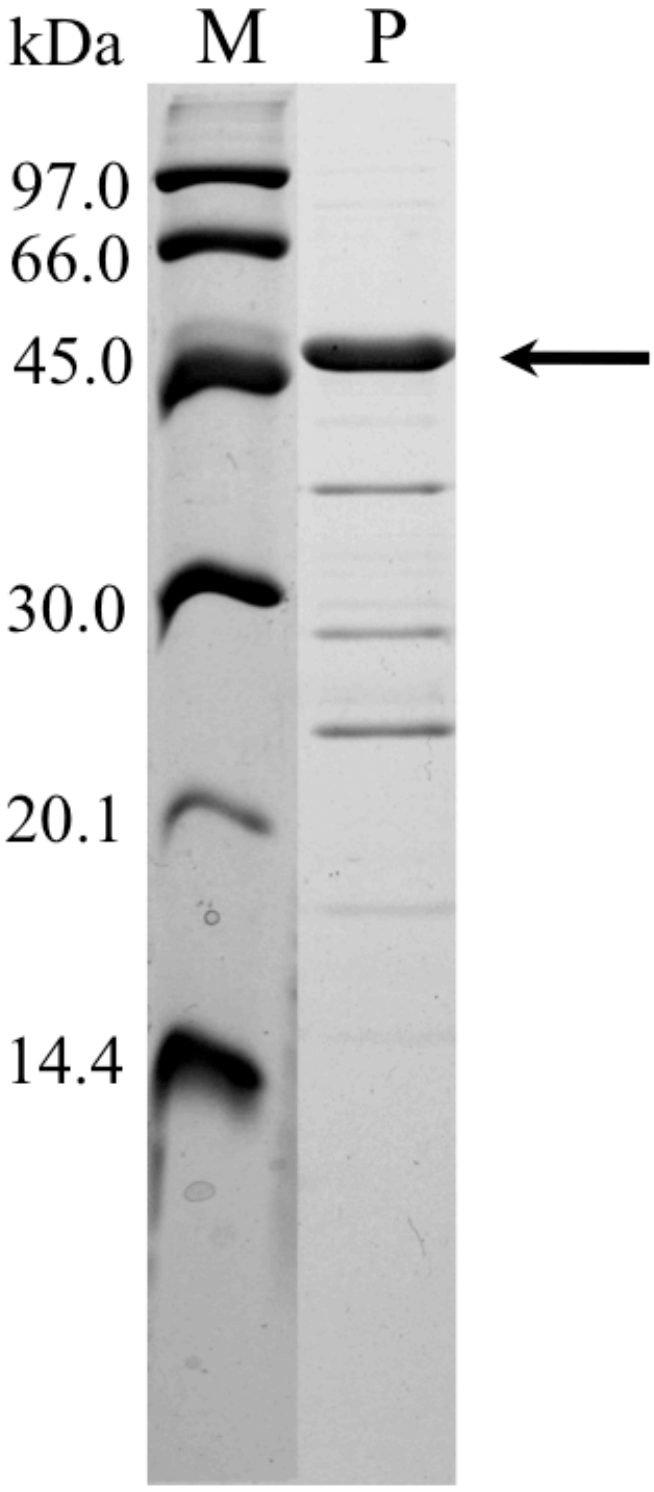

Fig. S1. SDS-PAGE after Sll1558 expression and purification. M, marker; P, purified protein.

The His-tagged Sll1558 protein is indicated by arrow at 45 kDa.

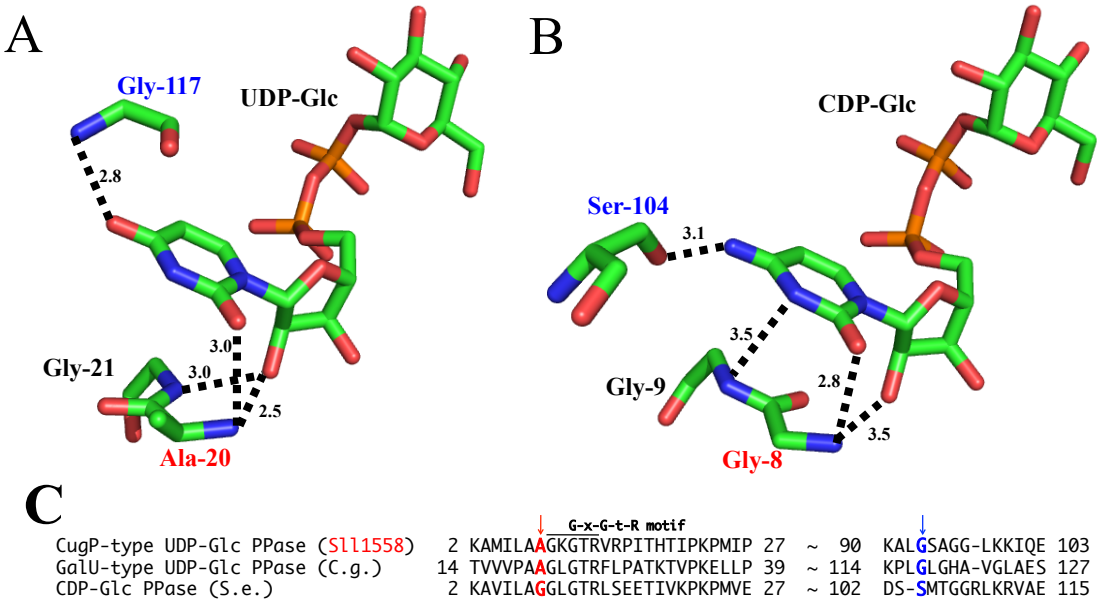

Fig. S2. Key residues in the active sites of two nucleotidyl transferases and alignment of the active-site sequences of these two enzymes with the corresponding Sll1558 sequences. A, Key substrate-binding residues in the active site of the GalU-type UDP-Glc PPase from *Corynebacterium glutamicum* (PDB ID, 2PA4). B, Key substrate-binding residues in the active site of the CDP-Glc PPase from *Salmonella enterica* (PDB ID, 1TZF) (color code: carbon, green; nitrogen, blue; oxygen, red; and phosphorus, orange). The broken lines denote possible hydrogen bonds between transferase residues and the NDP moieties. C, Sequence alignment of Sll1558, the GalU-type UDP-Glc PPase (*C.g.*) and CDP-Glc PPase (*S.e.*). Residues corresponding to Ala8 in Sll1558 are colored red. Residues corresponding to position 93 in Sll1558 are colored blue.

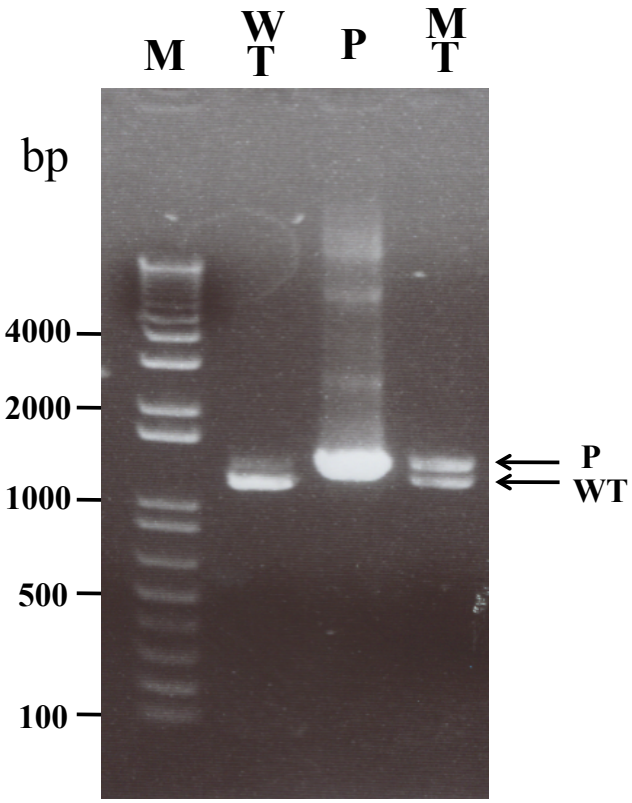

Fig. S3. Agarose gel electrophoresis to check segregation of transformant. M; marker, WT; wild type, P; transformation plasmid, MT; mutant. The band from wild type genome is 1.2 kbp (lower arrow), and that from transformation plasmid is 1.4 kbp (upper arrow).