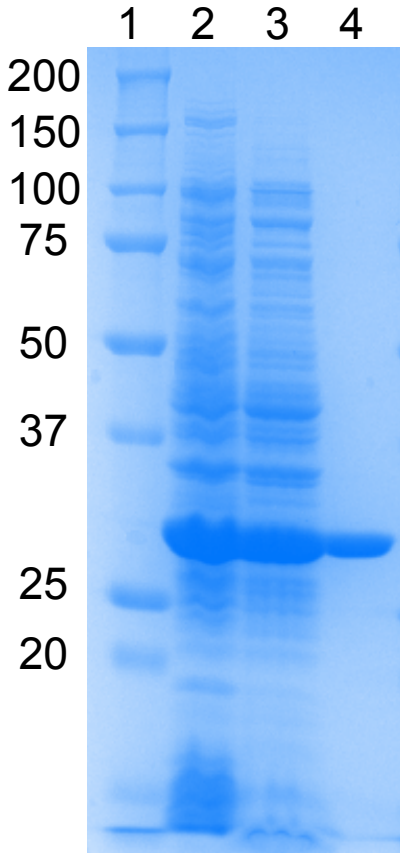

FIG. S1. Overexpression and purification of $TraC_{N292}$ protein. The $TraC_{N292}$ protein was overproduced by IPTG induction of BL21(DE3) cells harboring pET22bN292TraC, and was purified as described in Materials and Methods. Protein fractions were electrophoresed in a 12.5% SDS-polyacrylamide gel and stained with Coomassie brilliant blue. Lane 1, molecular-mass standards; lane 2, total cell fraction; lane 3, crude cell extract; and lane 4, purified fraction after affinity resin treatment. The locations of the molecular mass markers (in kilodaltons) are indicated at the left.

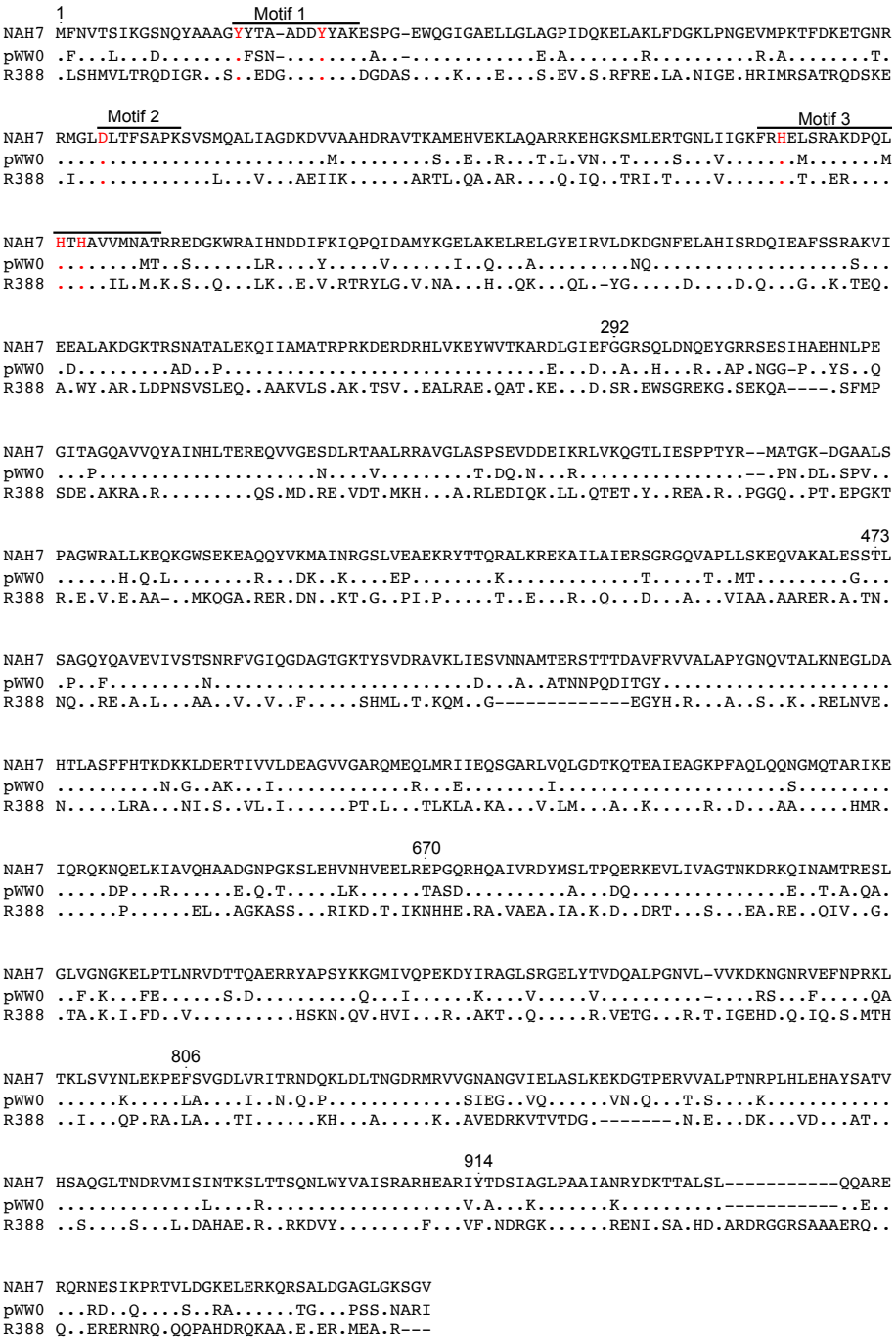

FIG. S2. Comparison of relaxases from NAH7, pWW0 , and R388. These proteins have the relaxase, AAA, and UvrD-like helicase domains, which correspond to the amino-acid positions from 15 to 292, from 473 to 670, and from 806 to 914, respectively, in the NAH7 relaxase. Motifs 1 to 3 are conserved in the relaxase domain of MOB_F-family relaxases (1). The Y18, Y26, D85, H150, H161, and H163 residues in the R388 relaxase have been shown to be important for conjugation (2), and they are depicted in red. dot: amino-acid residue identical to that of NAH7; and hyphen, no amino-acid residue.

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