



# Correction for Taniguchi et al., “A Key Enzyme of the NAD<sup>+</sup> Salvage Pathway in *Thermus thermophilus*: Characterization of Nicotinamidase and the Impact of Its Gene Deletion at High Temperatures”

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Volume 199, no. 17, e00359-17, 2017, <https://doi.org/10.1128/JB.00359-17>. Genomic analysis of the  $\Delta$ TTHA0328 deletion strain developed in this study revealed that this strain is a derivative of *Thermus thermophilus* HB27 and not HB8. However, the amino acid sequence of the product of TTHA0328 in the HB8 strain is a perfect match with the homologue of the HB27 strain (locus tag: TTC1655), and all other genes involved in the NAD<sup>+</sup> salvage pathway were also conserved between the two strains. In addition, gene organization and the sequence around the nicotinamidase (NAMase) are similar between the two strains and thus the knockout mutant for TTC1655 was successfully constructed using the primers that were designed based on the HB8 genome sequence.

Therefore, the results and conclusions presented in the original paper, including sequence alignment (Fig. 2) and recombinant protein characteristics (Fig. 3), are valid if the strain and gene names are replaced throughout the text and Fig. 2 and 3 as shown in the table in this correction.

Term relevant to: <sup>a</sup>	Term used in paper	All instances of the term at left should be replaced with:
Strain name	HB8	HB27
Enzyme		
Nicotinamidase (NAMase)	TTHA0328	TTC1655
Nicotinate mononucleotide adenylyltransferase (NaMAT)	TTHA1780	TTC1421
Nicotinate phosphoribosyltransferase (NaPRT)	TTHA0617	TTC0252
ADPR pyrophosphatase (ADPRP)	TTHA0528	TTC0160
Ribose-phosphate pyrophosphokinase (RPK)	TTHA1549	TTC1184
NAD <sup>+</sup> synthase (NADS)	TTHA1900/TTHA1901	TTC1538/TTC1539

<sup>a</sup>All the authors reviewed these facts and agreed to the correction.

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