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Correction: Cloning and analysis of a bifunctional methyltransferase/restriction endonuclease TspGWI, the prototype of a *Thermus* sp. enzyme family

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Correction

The TspGWI restriction endonuclease, which originates from thermophilic *Thermus* sp. GW, was cloned previously [1] in *Escherichia coli* (*E. coli*) using a method employing aa sequencing of proteolytic fragments N-termini, followed by a combination of sequencing of degenerated, inverse and standard PCR products and clones containing the *tspGWIRM* gene. A combination of these methods yielded a sequence of 3688 bp, comprising an entire TspGWI Open Reading Frame (ORF: 3291 bp) and flanking sequences [GenBank: EF095488, ABO26710]. However, more recent resequencing of the *tspGWIRM* gene with the use of genomic *Thermus* sp. GW DNA as a template in PCR, obtained with primers external to ORF, has revealed a sequencing error. This resulted in a frameshift of 233 aa, starting at aa 740 and returning to the original ORF at aa 973. The frameshift was located within the 3′-terminal portion of the gene, coding for a Target Recognition Domain (TRD). The nt sequence of the *tspGWIRM* gene was corrected at 2217 bp (C insertion) and further downstream at 2915 nt (C deletion), restoring the ORF (Additional file one (Additional file 1 here) and Figure five (Figure 1 here) corrected).

New figures have been prepared using the corrected DNA and aa sequences (Figure five (Figure 1 here) and Additional file one (Additional file 1 here)). Data concerning corrected nt and aa TspGWI sequence have been deposited in GenBank [GenBank: KJ730526].

The correction was located within a variable TRD segment, thus the conclusions of the bioinformatics sequence analysis must be slightly modified compared to our originally published results [1]. The corrected sequence of TspGWI shows similarity to the TaqII sequence and residues 660–960 in TspGWI that were originally (in the previous version) predicted to be intrinsically disordered, were predicted to be precisely ordered in the corrected version of the sequence (data not shown).

The DNA sequence and the predicted amino acid sequence of the 120.2 kDa TspGWI protein is indicated in capital letters. DNA sequences of flanking regions are indicated in italics. The ATG start codon and TGA stop codon are emboldened and underlined. Potential TspGWI Ribosome Binding Sites (RBS) are emboldened, underlined italics.

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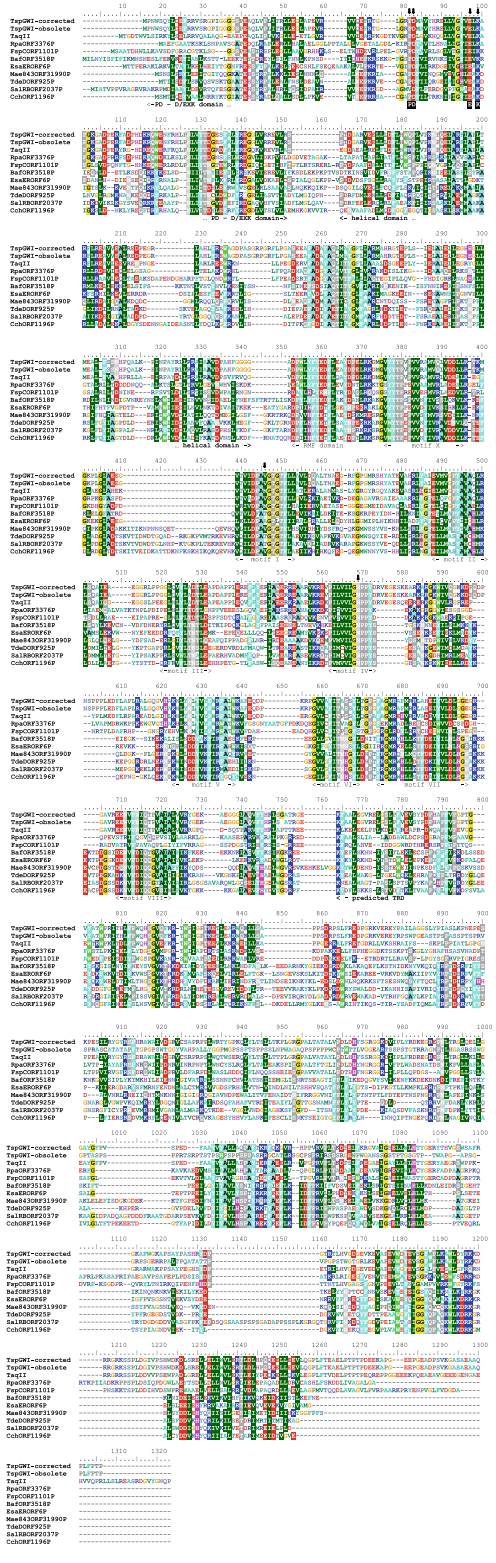

Figure 1 Sequence alignment between TspGWI and its close homologues in REBASE.

Additional file

Additional file 1: *tspGWIRM* gene and its flanking regions.

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Reference

1. Żylicz-Stachula A, Bujnicki JM, Skowron PM: **Cloning and analysis of bifunctional DNA methyltransferase/nuclease TspGWI, the prototype of a Thermus sp. family.** *BMC Mol Biol* 2009, **10**:52.

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