

Additional file 3, Figure S2. Alignment of NADH oxidase isolated from *Thermus thermophilus* HB27 and its counterpart isolated form *Thermus thermophilus* HB8.

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HB27*      MEATLPVLDAKTAALKRRSIRRYRKDPVPEGLLREILEAALRAPSAWNLQ
HB8         MEATLPVLDAKTAALKRRSIRRYRKDPVPEGLLREILEAALRAPSAWNLQ
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HB27*      PWRIVVVRDPATKRALREAAFGQAHVEEAPVVLVLYADLEDALAHLEVI
HB8         PWRIVVVRDPATKRALREAAFGQAHVEEAPVVLVLYADLEDALAHLEVI
*****

HB27*      HPGVQGERREAQKQAIQRAFAAMGQEARAWASGQSYILLGYLLLLLEAY
HB8         HPGVQGERREAQKQAIQRAFAAMGQEARAWASGQSYILLGYLLLLLEAY
*****

HB27*      GLGSVPMLGFDPERVRAILGLPSRAAIPALVALGYP AEEGYPSEYRLPLER
HB8         GLGSVPMLGFDPERVRAILGLPSRAAIPALVALGYP AEEGYPSEYRLPLER
*****.:*****.:*****.:*****

HB27*      VVLWR
HB8         VVLWR
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Sequence HB27* resulted from cloning and sequencing of PCR product amplified from genomic DNA of *Thermus thermophilus* HB27 that we have at our laboratory. The sequence HB8 was corresponding to gene bank accession number: **CAA42707.1**. Both sequences were aligned using ClustalW algorithm. (*) identical residues. (:) different residues, highlighted in grey.