

Characterization of promoters in archaeal genomes based on DNA structural parameters

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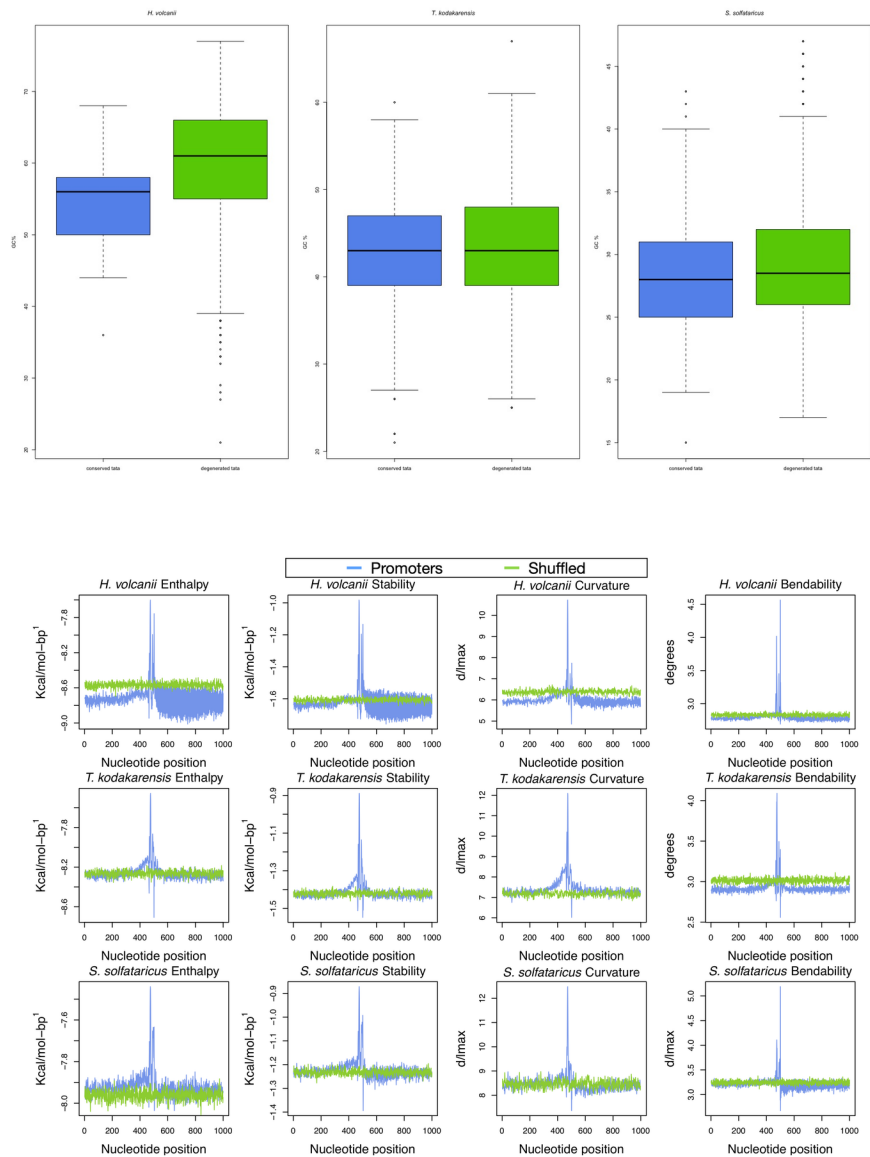
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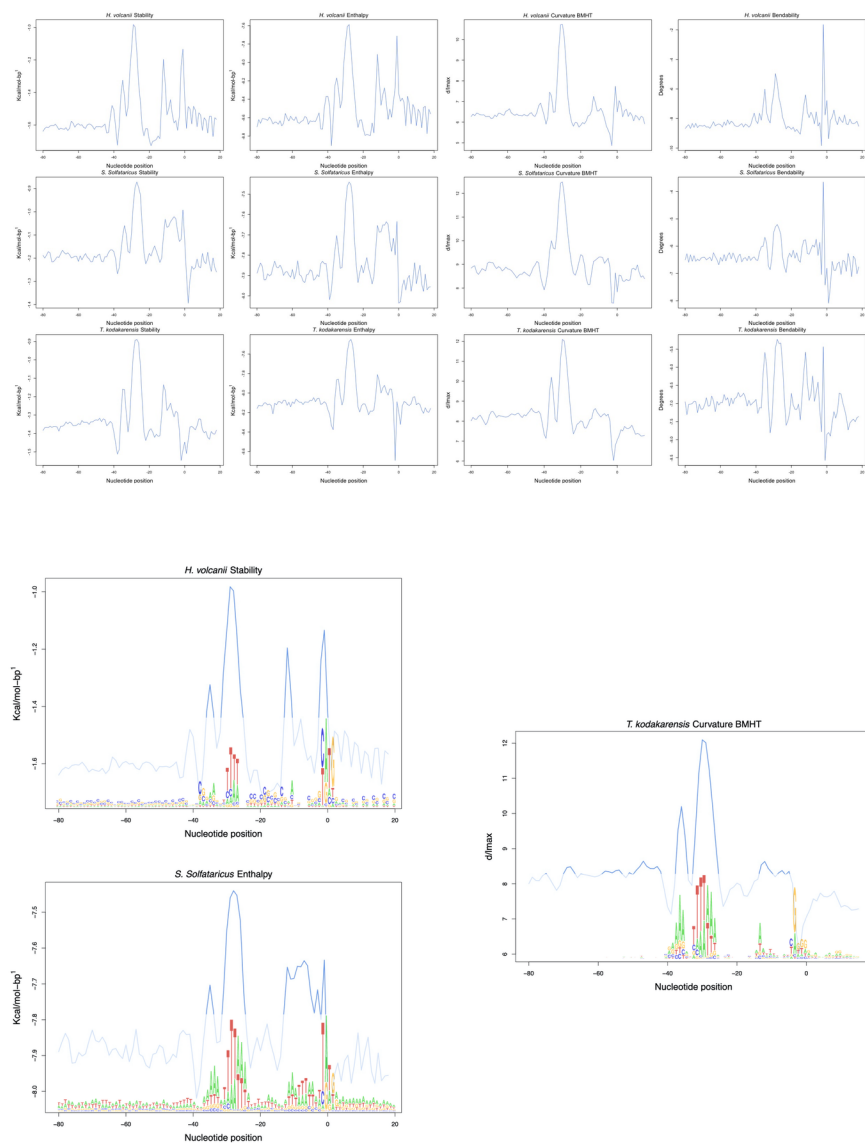
Abstract

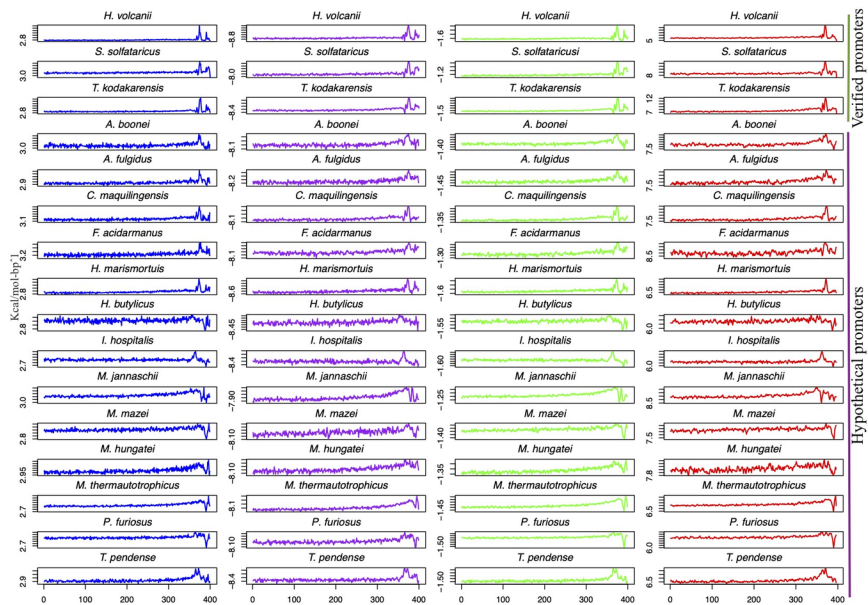
The transcription machinery of archaea can be roughly classified as a simplified version of eukaryotic organisms. The basal transcription factor machinery binds to the TATA-box found around 28 nucleotides upstream of the transcription start site; however, some transcription units lack a clear TATA-box and still have TBP/TFB binding over them. This apparent absence of conserved sequences could be a consequence of sequence divergence associated with the upstream region, operonic and gene organization. Furthermore, earlier studies have found that a structural analysis gains more information compared to a simple sequence inspection. In this work, we evaluated and coded 3630 archaeal promoter sequences of three organisms, *Haloferax volcanii*, *Thermococcus kodakarensis*, and *Sulfolobus solfataricus* into DNA duplex stability, enthalpy, curvature, and bendability parameters. We also split our dataset into conserved TATA and degenerated TATA promoters in order to identify differences among these two classes of promoters. The structural analysis reveals variations in archaeal promoters' architecture, i.e., a distinctive signal is observed in the TFB, TBP, and TFE binding sites independently of these being TATA-conserved or TATA-degenerated. In addition, the promoter encountering method was validated with upstream regions of 13 other archaea, suggesting that there might be promoter sequences among them. Therefore, we suggest a novel method for locating promoters within the genome of archaea based on energetic/structural features.

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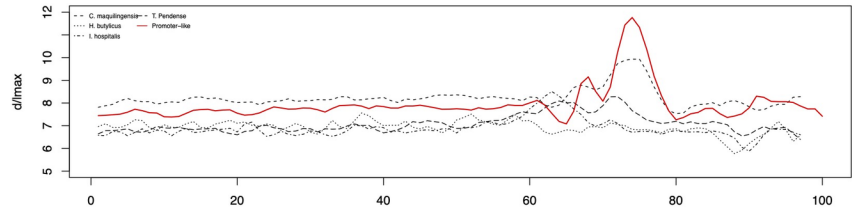
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TACK archaea – BMHT curvature



Euryarchaea – BMHT curvature

