# Supplementary material for "Core promoter information content correlates with optimal growth temperature"

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## ABSTRACT

The subtle mechanisms by which protein-DNA interactions remain functional across a wide range of temperatures are largely unknown. In this work, we manually curated available information relating fully sequenced archaeal genomes with organism growth temperatures. We built a motif that represents the core promoter of each species and calculated its information content. We then studied the relation between optimal growth temperature (OGT) and information content (IC) in the promoter region.We found a positive correlation between G+C content and OGT in tRNA regions and not in overall genome. Furthermore, we found that there is a positive correlation between information content and optimal growth temperatures in Archaea. This can't be explained by an increased C+G composition nor by other obvious mechanisms. These findings suggest that increased information content could produce a positive fitness in organisms living at high temperatures. We suggest that molecular information theory may need to be adapted for hyperthermophiles.

## Supplementary Material

We originally considered for this study all NCBI's reference archaeal genomes. We later on excluded Methane generating Archaea, as there are some doubts about the mechanism of transcription initiation in these groups[1]. The taxa, that have a TBP, but are excluded for this reason are the following: NC 000909, NC 014222, NC 014253, NC 014002, NC 017034, NC 014658, NC 009515 , NC 015416 , NC 013665 , NC 009464 , NC 014122 , NC 003901 , NC 014408 , NC 009051 , NC 015636 , NC 015562 , NC 017527 , NC 007355 , NC 013790 , NC 013407 , NC 018876 ,NC 005791.

We show that the G+C content of 16s rRNA but not whole genome sequences correlates with OGT in Figure S 1. This might help to explain why the usual perception states that G+C content correltates with OGT.

We show that OGT deacreses with increasing genome size in Figure S 2 and that the number of ORFs correlates with genome size on the inset in the same Figure S 2.

We show that most of the sites are within 100 bp shown in Figure S 3 and that running a similar analysis to the one performed in Fig 3 but using only 500 bp yields similar results in Figure S 4.

We show in Figure S 5 that in the region surrounding the transcription start sites (TSS) a negative correlation between G+C % and IC is visible.

We also include a figure about the number of tRNA in the different genomes considered in Figure S 6 and show it is quite evenly distributed along the optimal temperature range.

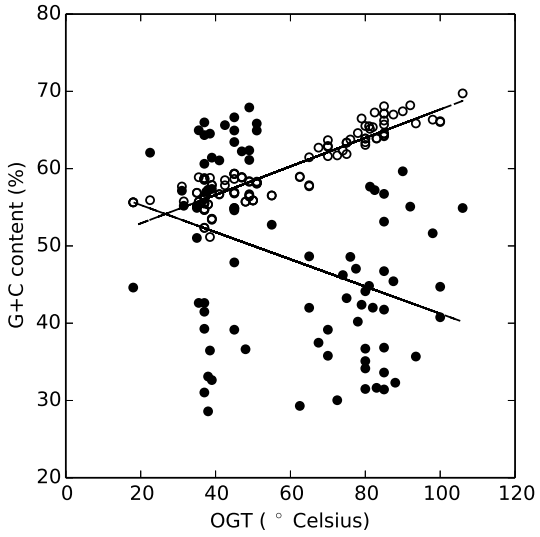
We show in Figure S 7 that using a more restrictive threshold for the score of the motifs, does not change the tendency.

As most of our results derive on putative motifs identified by MEME and to avoid biases produced by that tool, we have obtained putative binding sequences in a MEME independent way. We have directly recovered and aligned the regions between 50 to 20 bp upstream of TSS of each tRNA for the 39 Archaea genomes included in Fig 3. For the alignment we used Clustalw under the parameters -type=DNA -pwgapopen=500, and then calculated Rseq applying small sample correction (using exact method[2] ). As seen on figure S8, the source of the motifs does not change the observed tendency in Figure 3.

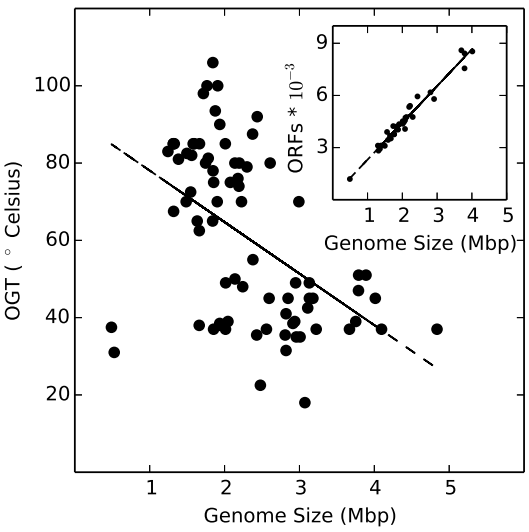
We then analysed if the motif divergency clusters maps neatly onto a phylogenic tree, shown in Figure S 9 or if they are related to the temperature clusters shown in Figure S 10. Although not an exhaustive analysis, at least it shows that the motifs found are not grouped by temperature range or phylogenetic groups.

We show that applying small sample correction (using exact method[2]) does not change the observed tendency, in Figure S 11.

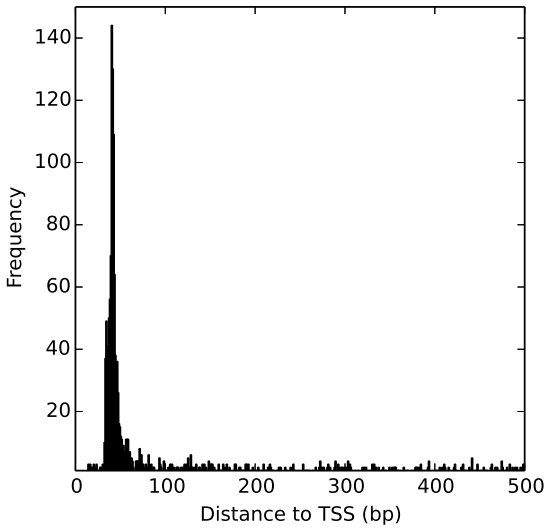
We include motifs instances as supplementary .fasta file, where each sequence name includes the NC code, version, starting position, and orientation of the sequence.



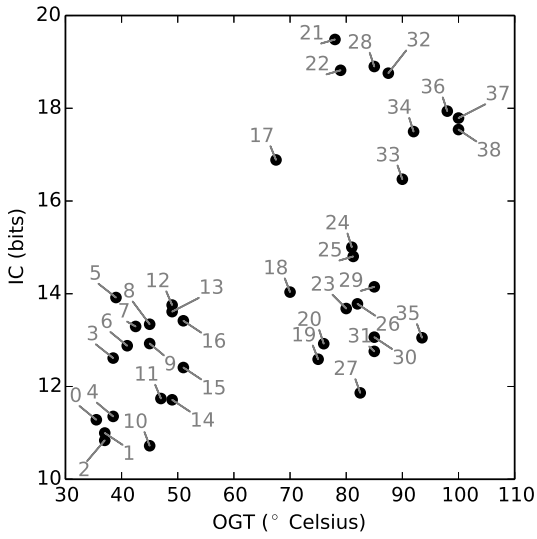

**Supplementary Figure 1.** 16S rRNA but not full genome composition increases its G+C content as a function of temperature. All archaeal genomes in our dataset were analyzed in terms of base compositions considering full genome (filled circles) or 16S rRNA (empty circles) and plotted against OGT. No correlation was found for full genome composition obtaining (R =$-0.21$, p =$2 \times 10^{-4}$) while a clear correlation was found for 16S rRNA (R =0.91, p = $9.8 \times 10^{-49}$).



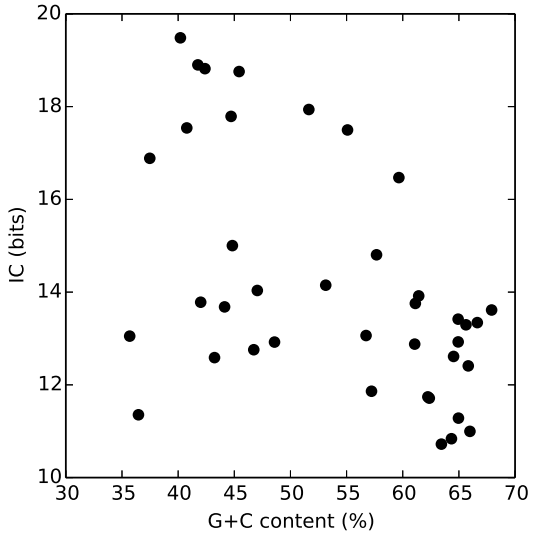

**Supplementary Figure 2.** Genome size (Eq.1 $\omega$) and number of ORFs (Eq.1 $\gamma$) decrease at higher temperatures. Optimal growth temperature for our set of organisms was compared to its corresponding genome's size presenting a negative slope ($R = -0.5$, $p = 4.6 \times 10^{-6}$). Inset: The amount of ORFs were correlated with genome size ($R = 0.968$, $p = 4.2 \times 10^{-27}$).



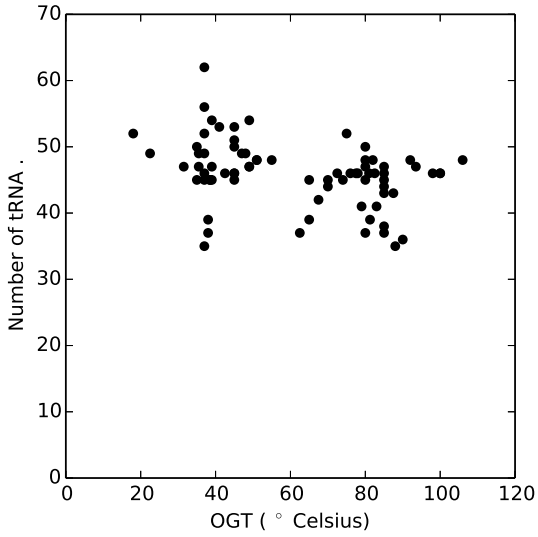

**Supplementary Figure 3.** Histogram of the distances from each of the TATA motif to the beginning of its corresponding TSS. Combined data from all the species is shown. Mode is -40 bp, consistent with what was expected for core promoter region.



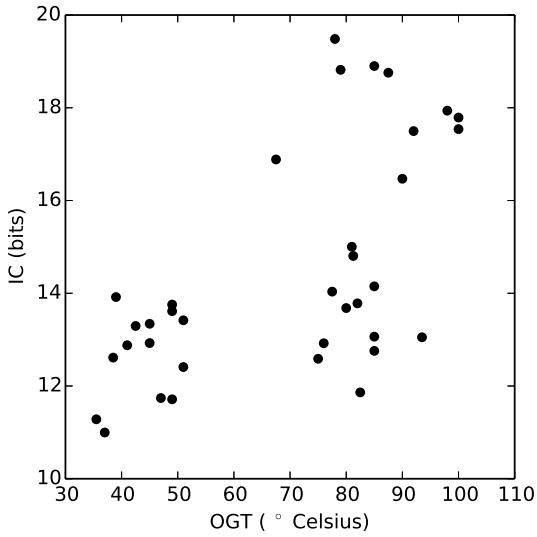

**Supplementary Figure 4.** Information content correlates with optimal growth temperature. Information content of the TBS for 39 archaeal genomes is plotted against optimal growth temperature. Each dot represents one species average IC calculated upon the motifs obtained with a 500 bp window instead of a 100 bp window as is shown in the main text.



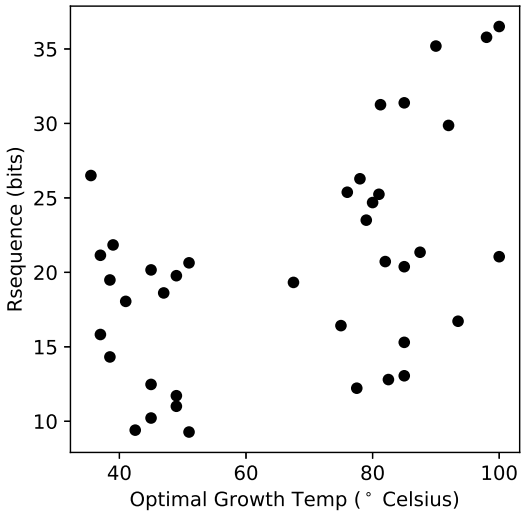

**Supplementary Figure 5.** Information content does not increase with genome G+C content. G+C % and information content were calculated for each genome and plotted. Variance in information content seems to be negatively correlated to G+C composition, with a correlation coefficient of -0.67 and a p-value of $7 \times 10^{-5}$



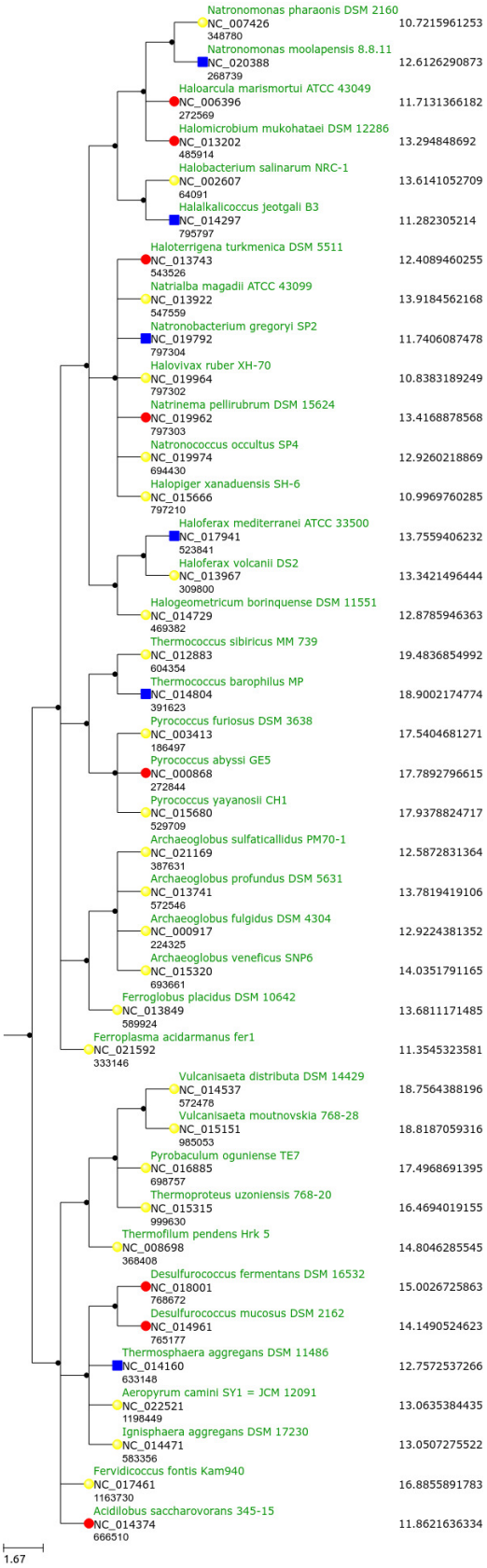

**Supplementary Figure 6.** For all Archeal genomes the number of tRNA for an organism, is relatively uniform with varying OGT in our dataset. This accounts only for annotated tRNA.



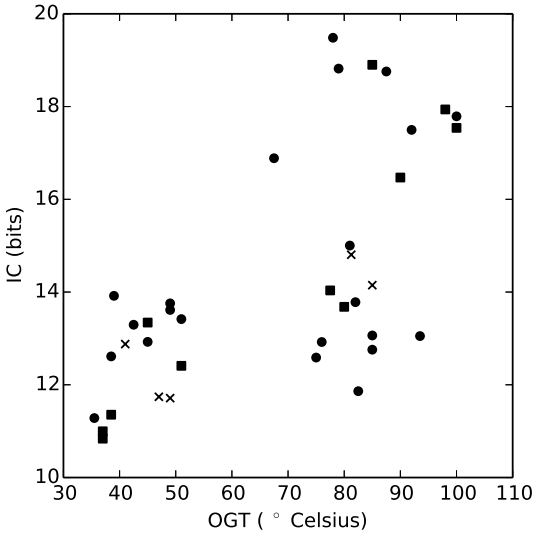

**Supplementary Figure 7.** Information content correlates with optimal growth temperature. Information content of the TBS for 36 archaeal genomes is plotted against optimal growth temperature. We changed the e-value threshold to $10^{-10}$. In the main text we perform a similar analysis with an e-value cutoff of $10^{-3}$), being more restrictive does not change the trend in the results.(But excludes 3 genomes and therefore the number of datapoints is 36 not 39)



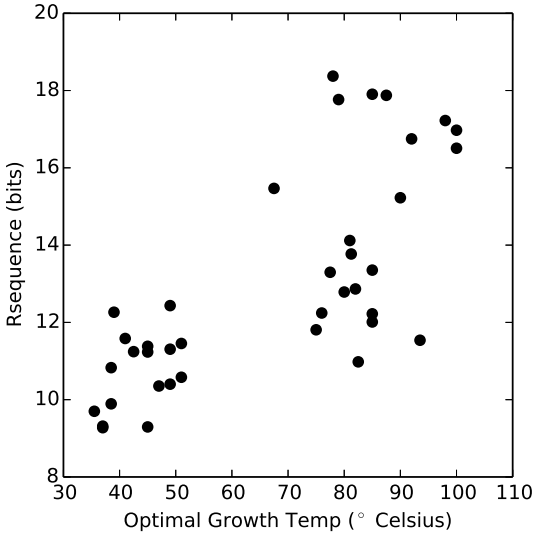

**Supplementary Figure 8.** Rsequence vs OGT of the regions between 50 to 20 upstream of TSS of each tRNA for each of the 39 Archaea genomes included in Fig 3. We aligned sequences using Clustalw under the parameters -type=DNA -pwgapopen=500, and then calculate Rseq applying small sample correction (using exact method[2]). Correlation coefficient ( $R = 0.5 p = 0.001$ ).




**Supplementary Figure 9.** NCBI's phylogenetic tree of the 39 Archea genomes included in Fig 3. The symbols on the left of each NC code denote they belong to a certain cluster. Clusters where generated using a k-medoids algorithm with n=3, using as distance between motifs TOM-TOM e-values.




**Supplementary Figure 10.** Information content plotted against optimal growth temperature for the 39 archeal genomes in Fig 3, but each symbol (square, circle, cross) represents a cluster formed with the same clustering method as in Figure S 9.




**Supplementary Figure 11.** Rsequence correlates with optimal growth temperature. We calculated Rseq considering small sample correction.[2].

**Supplementary Table 1.** Optimal Growth Temperature for all reference completed archaeal genomes.

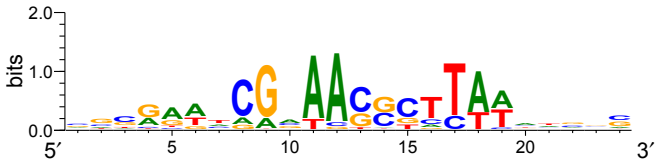
| Species | Opt. Growth Temp (°C) |
|---|---|
| *Acidianus hospitalis* | 80[3] |
| *Acidilobus saccharovorans* | 82[4] |
| *Aciduliprofundum boonei* | 70[5] |
| *Aeropyrum camini* | 85[6] |
| *Archaeoglobus fulgidus* | 76[7] |
| *Archaeoglobus profundus* | 82[8] |
| *Archaeoglobus sulfaticallidus* | 75[9] |
| *Archaeoglobus veneficus* | 77[10] |
| *Caldisphaera lagunensis* | 72[11] |
| *Caldivirga maquilingensis* | 85[12] |
| *Cenarchaeum symbiosum* | 10[13] |
| *Desulfurococcus fermentans* | 81[14] |
| *Desulfurococcus mucosus* | 85[15] |
| *Ferroglobus placidus* | 80[16] |
| *Ferroplasma acidarmanus* | 38[17] |
| *Fervidicoccus fontis* | 67[18] |
| *Halalkalicoccus jeotgali* | 35[19] |
| *Haloarcula hispanica* | 37[20] |
| *Haloarcula marismortui* | 49[21] |
| *Halobacterium salinarum* | 49[21] |
| *Haloferax mediterranei* | 49[21] |
| *Haloferax volcanii* | 45[21] |
| *Halogeometricum borinquense* | 41[21] |
| *Halomicrobium mukohataei* | 42[22] |
| *Halopiger xanaduensis* | 37[23] |
| *Haloquadratum walsbyi* | 45[24] |
| *Halorubrum lacusprofundi* | 34[25] |
| *Haloterrigena turkmenica* | 51[21] |
| *Halovivax ruber* | 37[26] |
| *Ignicoccus hospitalis* | 86[27] |
| *Ignisphaera aggregans* | 93[28] |
| *Metallosphaera cuprina* | 65[29] |
| *Metallosphaera sedula* | 74[30] |
| *Methanobrevibacter ruminantium* | 39[31] |
| *Methanobrevibacter smithii* | 37[32] |
| *Methanocaldococcus infernus* | 85[33] |
| *Methanocaldococcus jannaschii* | 85[34] |
| *Methanocaldococcus vulcanius* | 80[35] |
| *Methanocella arvoryzae* | 45[36] |
| *Methanocella conradii* | 55[37] |
| *Methanocella paludicola* | 35[38] |
| *Methanococcus maripaludis* | 38[39] |
| *Methanococcus voltae* | 38[40] |
| *Methanoculleus marisnigri* | 22[41] |
| *Methanohalobium evestigatum* | 48[42] |
| *Methanohalophilus mahii* | 37[43] |
| *Methanolobus psychrophilus* | 18[44] |
| *Methanomethylovorans hollandica* | 35[45] |
| *Methanoregula formicica* | 31[46] |
| *Methanosaeta concilii* | 35[47] |
| *Methanosaeta harundinacea* | 37[48] |
| *Methanosalsum zhilinae* | 45[49] |
| *Methanosarcina barkeri* | 37[50] |
| *Methanosarcina mazei* | 37[51] |
| *Methanothermobacter marburgensis* | 65[52] |
| *Methanothermococcus okinawensis* | 62[53] |
| *Methanothermus fervidus* | 83[54] |
| *Methanotorris igneus* | 88[55] |
| *Natrialba magadii* | 39[42] |
| *Natrinema pellirubrum* | 51[21] |
| *Natronobacterium gregoryi* | 37[42] |
| *Natronococcus occultus* | 45[21] |
| *Natronomonas moolapensis* | 38[56] |
| *Natronomonas pharaonis* | 45[21] |
| *Pyrobaculum aerophilum* | 100[57] |
| *Pyrobaculum arsenaticum* | 84[58] |
| *Pyrobaculum oguniense* | 92[59] |
| *Pyrococcus abyssi* | 96[60] |
| *Pyrococcus furiosus* | 100[61] |
| *Pyrococcus yayanosii* | 98[62] |
| *Pyrolobus fumarii* | 106[63] |
| *Staphylothermus hellenicus* | 85[64] |
| * *Sulfolobus acidocaldarius* | 80[65] |
| *Sulfolobus islandicus* | 80[66] |
| *Sulfolobus solfataricus* | 80[67] |
| *Thermococcus barophilus* | 85[68] |
| *Thermococcus gammatolerans* | 88[69] |
| *Thermococcus kodakarensis* | 95[70] |
| *Thermococcus onnurineus* | 80[71] |
| *Thermococcus sibiricus* | 78[72] |
| *Thermofilum pendens* | 87[73] |
| *Thermogladius cellulolyticus* | 84[74] |
| *Thermoplasmatales archaeon* | 40 *[31] |
| *Thermoproteus uzoniensis* | 90[75] |
| *Thermosphaera aggregans* | 85[76] |
| *Vulcanisaeta distributa* | 87[77] |
| *Vulcanisaeta moutnovskia* | 79[78] |

* Isolated from cow rumen, at 40 °C[31]

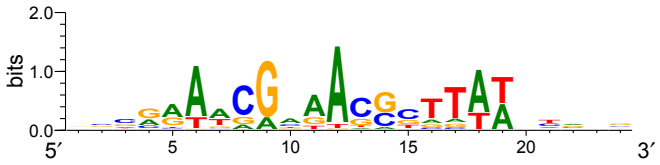
**Supplementary Table 2.** Average information content by position, it shows that some positions might be more relevant than others. For each position the Pearson's correlation coefficient of IC vs OGT, and its two tailed p-value are shown.

| Position | Average IC | Pearson R | P value |
|---|---|---|---|
| 1 | 1 | -0.187 | 0.254 |
| 2 | 1.15 | -0.421 | 0.00762 |
| 3 | 1.01 | -0.0835 | 0.613 |
| 4 | 1.15 | 0.367 | 0.0214 |
| 5 | 1.07 | 0.296 | 0.0677 |
| 6 | 0.786 | -0.0718 | 0.664 |
| 7 | 0.934 | -0.16 | 0.329 |
| 8 | 1.16 | 0.157 | 0.341 |
| 9 | 1.26 | 0.677 | **2.17e-06** |
| 10 | 1.08 | 0.395 | 0.0127 |
| 11 | 1.12 | 0.254 | 0.119 |
| 12 | 1.02 | 0.262 | 0.107 |
| 13 | 1.13 | 0.0185 | 0.911 |
| 14 | 1.07 | -0.139 | 0.399 |

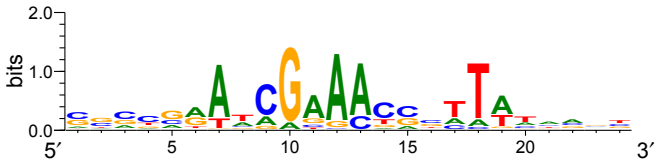
IC: Average IC for all motifs; R: Pearson's correlation value between IC and OGT; P: two tailed p-value calculated for each position. Positions are relative to the logo shown on Fig 2



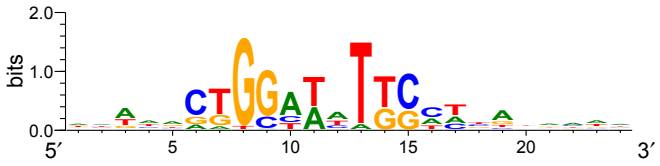

Panel 0



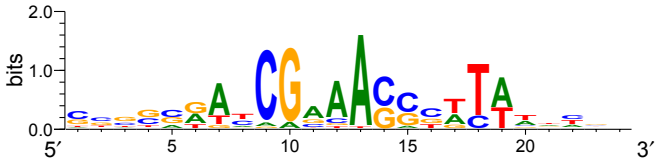

Panel 1



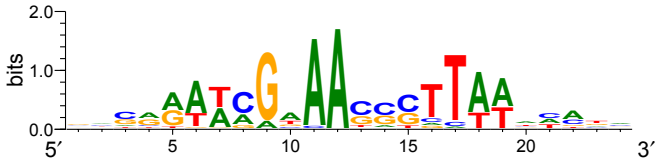

Panel 2



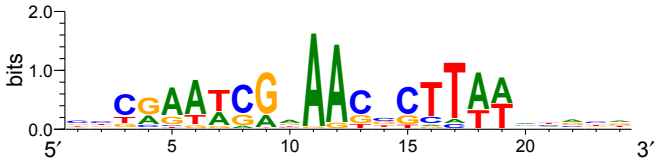

Panel 3



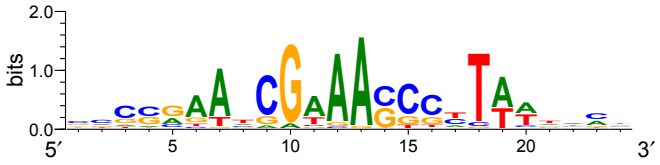

Panel 4



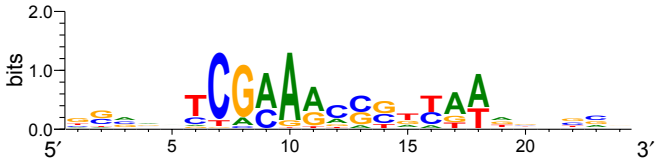

Panel 5



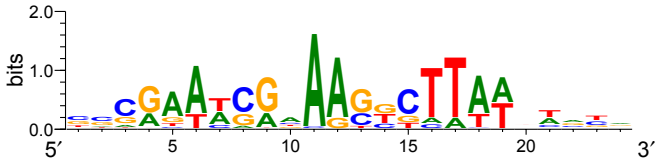

Panel 6



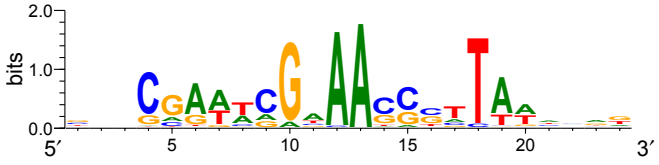

Panel 7



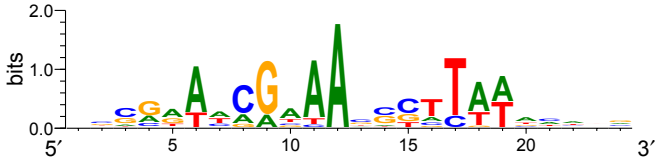

Panel 8




Panel 9

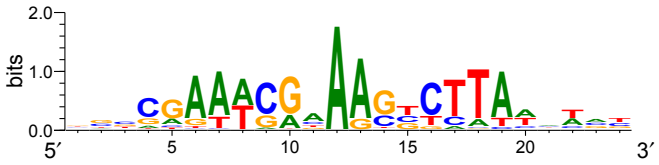



Panel 10

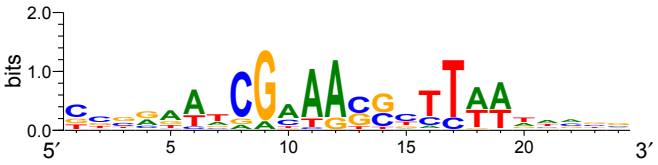



Panel 11

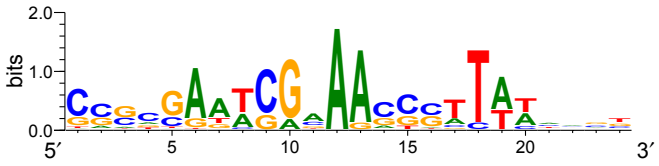
**Supplementary Figure 12.** Core promoter Motifs for all studied archaea. Numbering corresponds to Figure 3 and Table 1 .



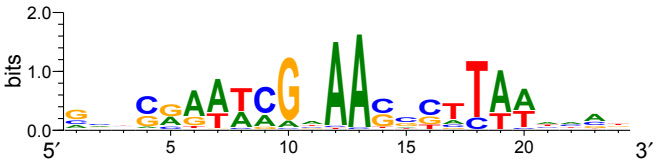

Panel 12



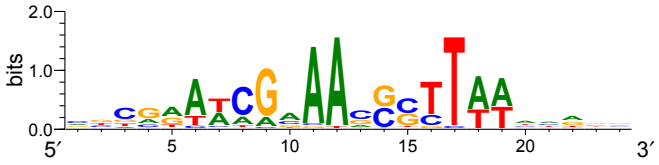

Panel 13



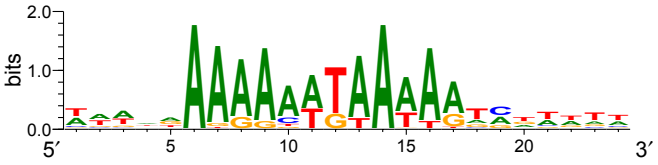

Panel 14



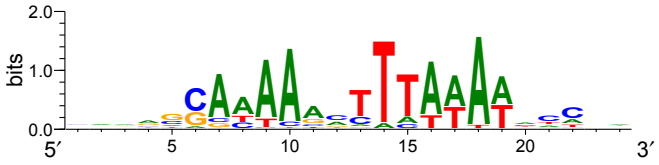

Panel 15



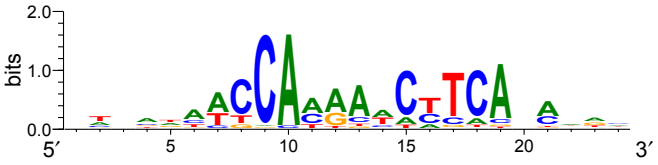

Panel 16



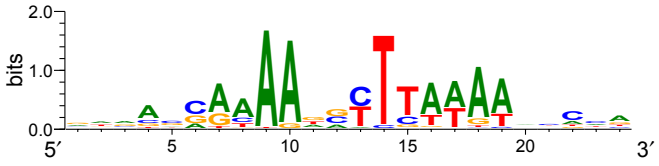

Panel 17



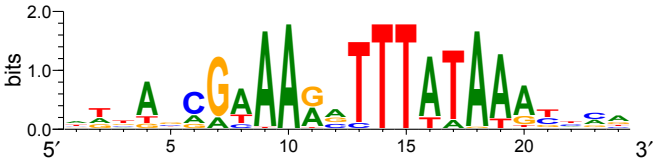

Panel 18



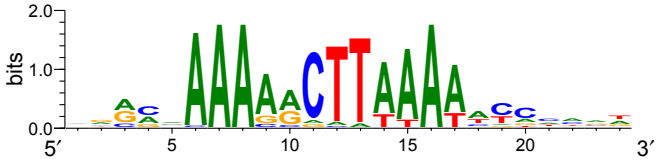

Panel 19



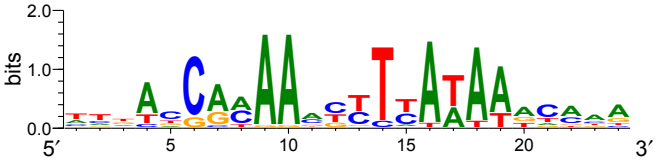

Panel 20




Panel 21

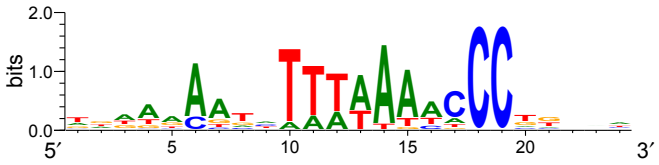



Panel 22

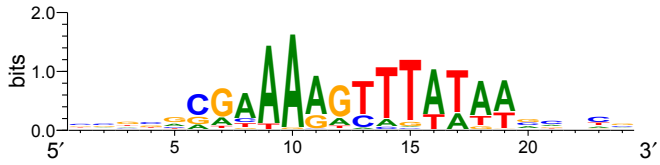



Panel 23

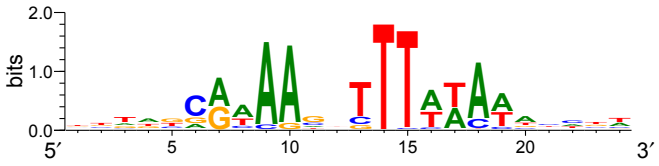
**Supplementary Figure 12.** Core promoter Motifs for all studied archaea. Numbering corresponds to Figure 3 and Table 1 .



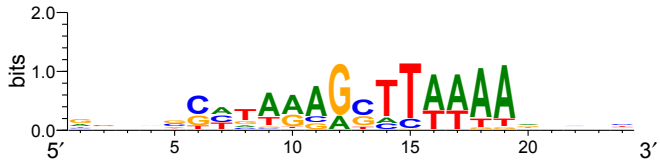

Panel 24



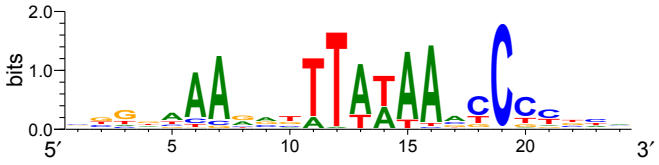

Panel 25



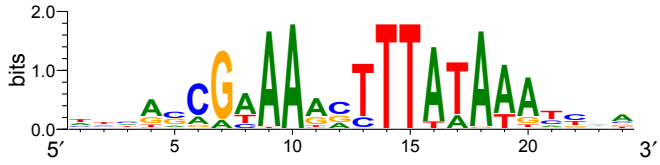

Panel 26



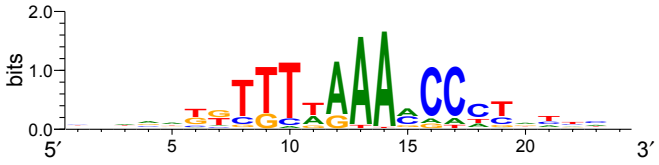

Panel 27



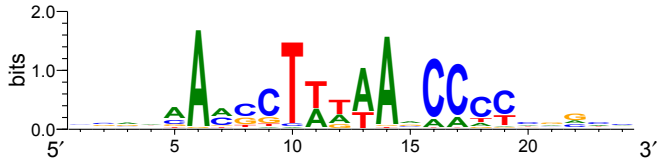

Panel 28



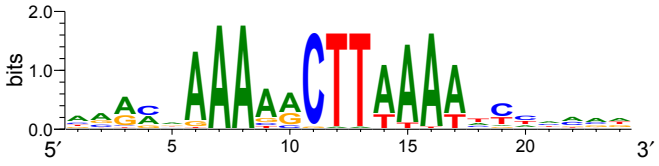

Panel 29



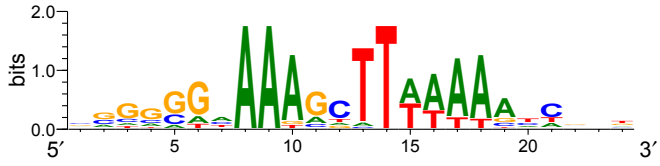

Panel 30



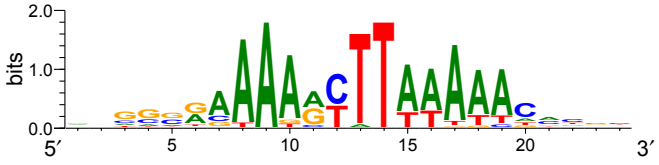

Panel 31



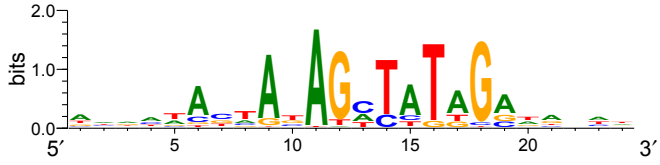

Panel 32




Panel 33

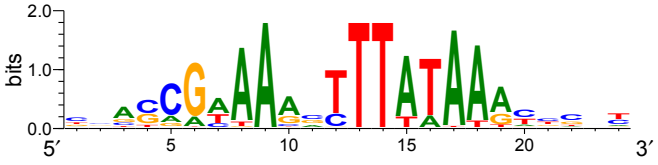



Panel 34

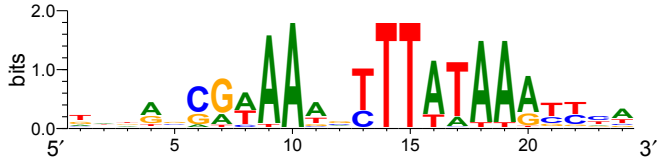



Panel 35

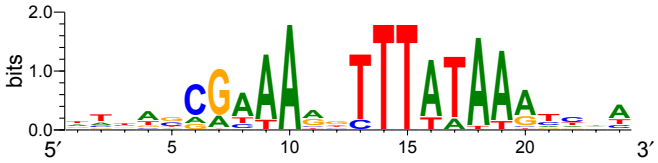
**Supplementary Figure 12.** Core promoter Motifs for all studied archaea. Numbering corresponds to Figure 3 and Table 1 .




Panel 36




Panel 37




Panel 38

**Supplementary Figure 12.** Core promoter Motifs for all studied archaea. Numbering corresponds to Figure 3 and Table 1 .

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