

Unveiling DNA structural properties of promoter regions of prokaryotic transcriptome and their role in gene expression

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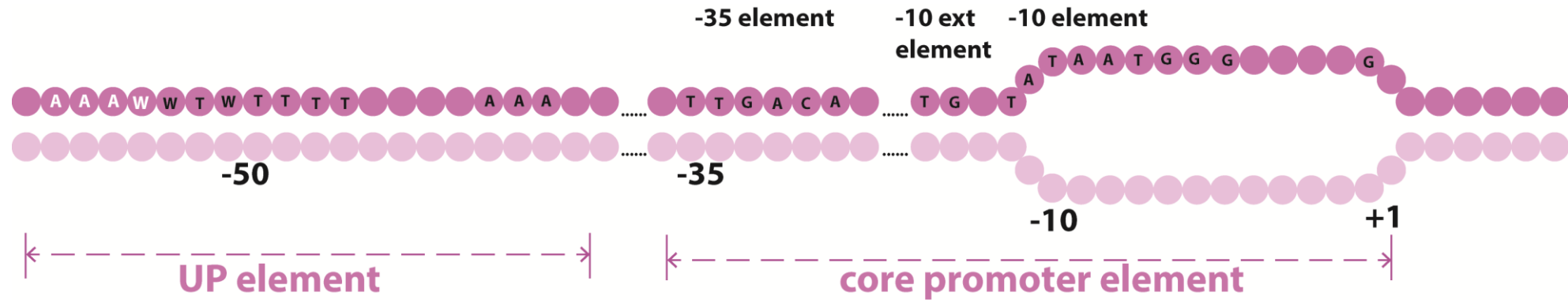
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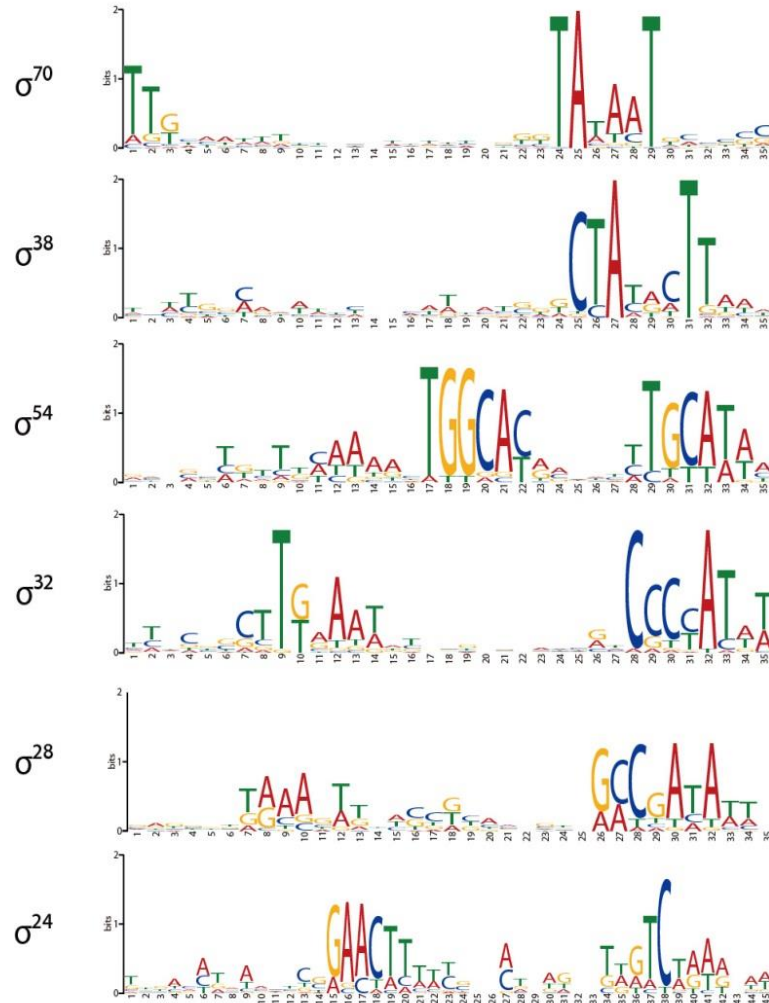
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Prokaryotic promoter elements



- ✓ Core promoter element (-35 and -10) is recognized by σ factor. Specific promoter recognition is done by σ factor.
- ✓ UP element is recognized by α subunit of RNA polymerase. UP elements increase promoter strength and comprised of A- and T- tracts.

Degeneracy of σ -factor binding sites in *E. coli*



σ^{70}	σ^{24}	σ^{19}	σ^{28}	σ^{32}	σ^{54}	σ^{38}	
1643	52	5	42	263	151	805	σ^{70}
	65	0	1	9	7	25	σ^{24}
		7	6	1	1	3	σ^{19}
			51	7	7	28	σ^{28}
				312	26	157	σ^{32}
					180	101	σ^{54}
						903	σ^{38}

Sequence motifs of σ -factors

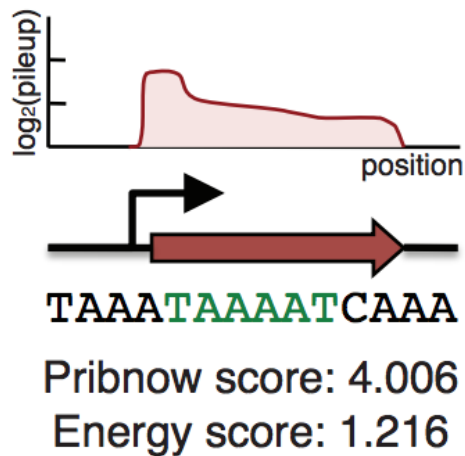
Extensive overlapping between σ -factor binding sites

Structural properties of promoter sequences

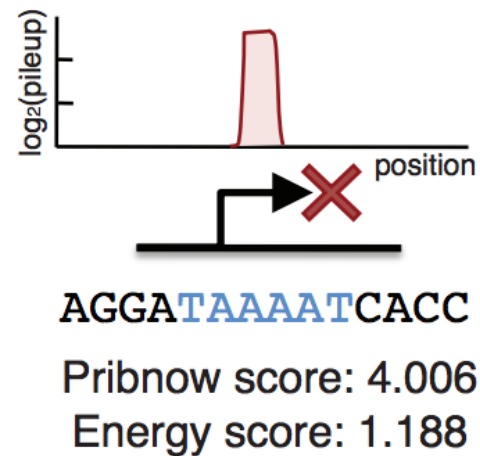
- Experimental evidences suggest that promoter sequences show **unique structural features**:
 - ✓ DNA duplex stability/free energy/melting temp.
 - ✓ Protein induced bendability
 - ✓ Intrinsic curvature
 - ✓ Potential to take up specific non-B structures: A, Z, triplex, quadruplex structures etc.
 - ✓ Non-B DNA motifs (G quadruplex, Z DNA, cruciform etc.) are preferentially present in regulatory regions of operons, in *E. coli*.
- Most importantly these features are present in regulatory regions of organisms from all domains of life

Contribution of different genomic elements to transcription

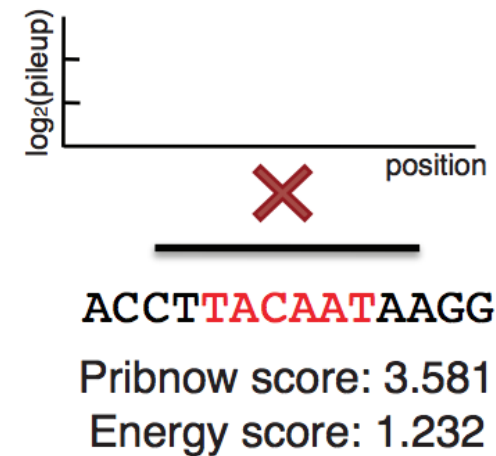
Pribnow and energy scores for individual promoter like sequences



RNA promoter



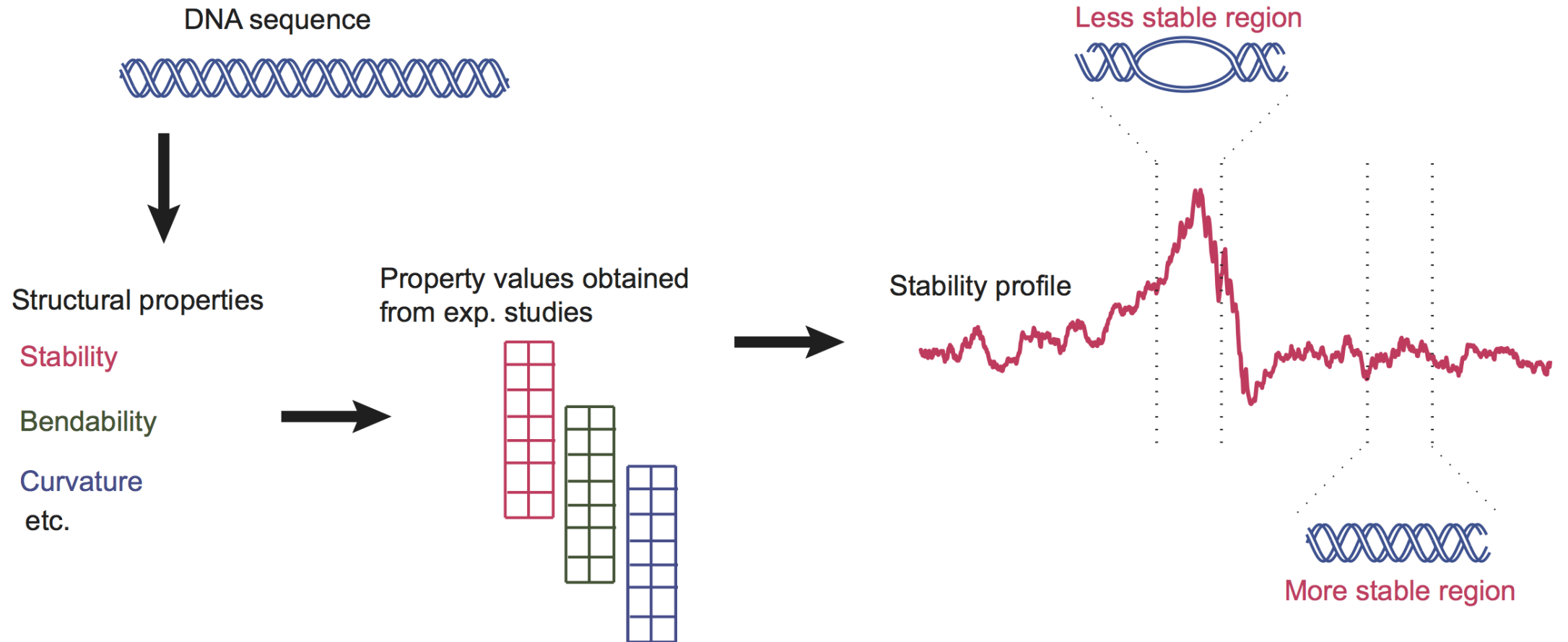
Abortive promoter



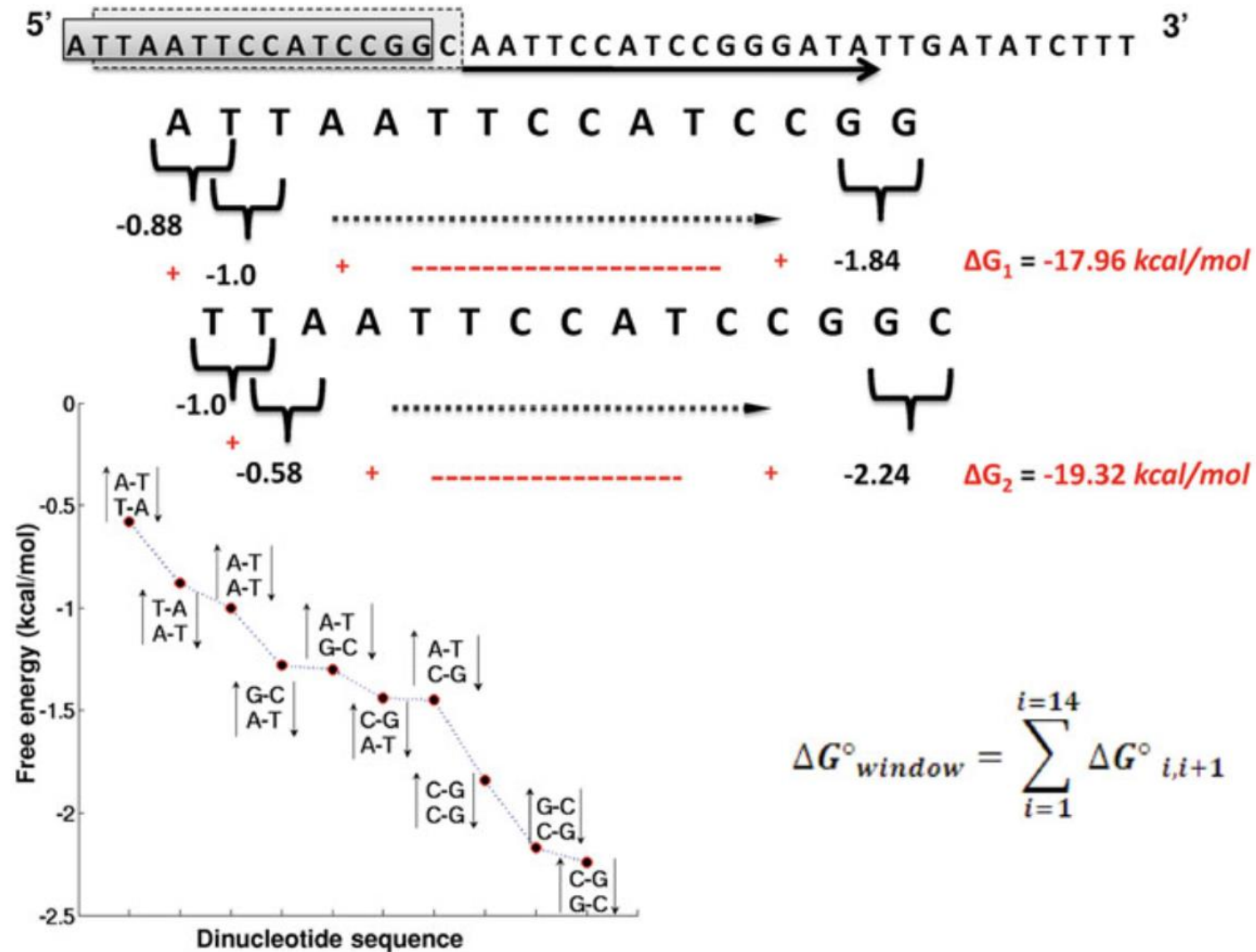
Non-promoter

Adequate structural context is essential for the complete assembly of RNA polymerase complex and for DNA unwinding to initiate transcription initiation

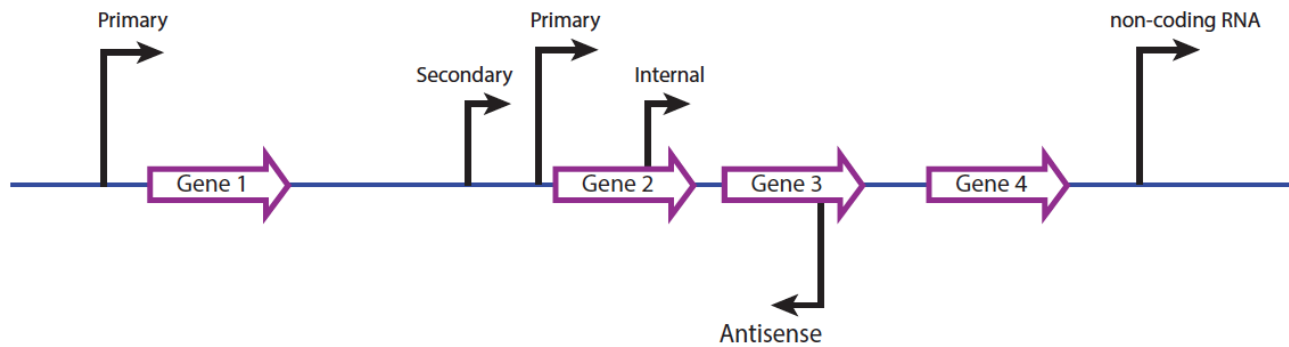
Structural properties profile calculation



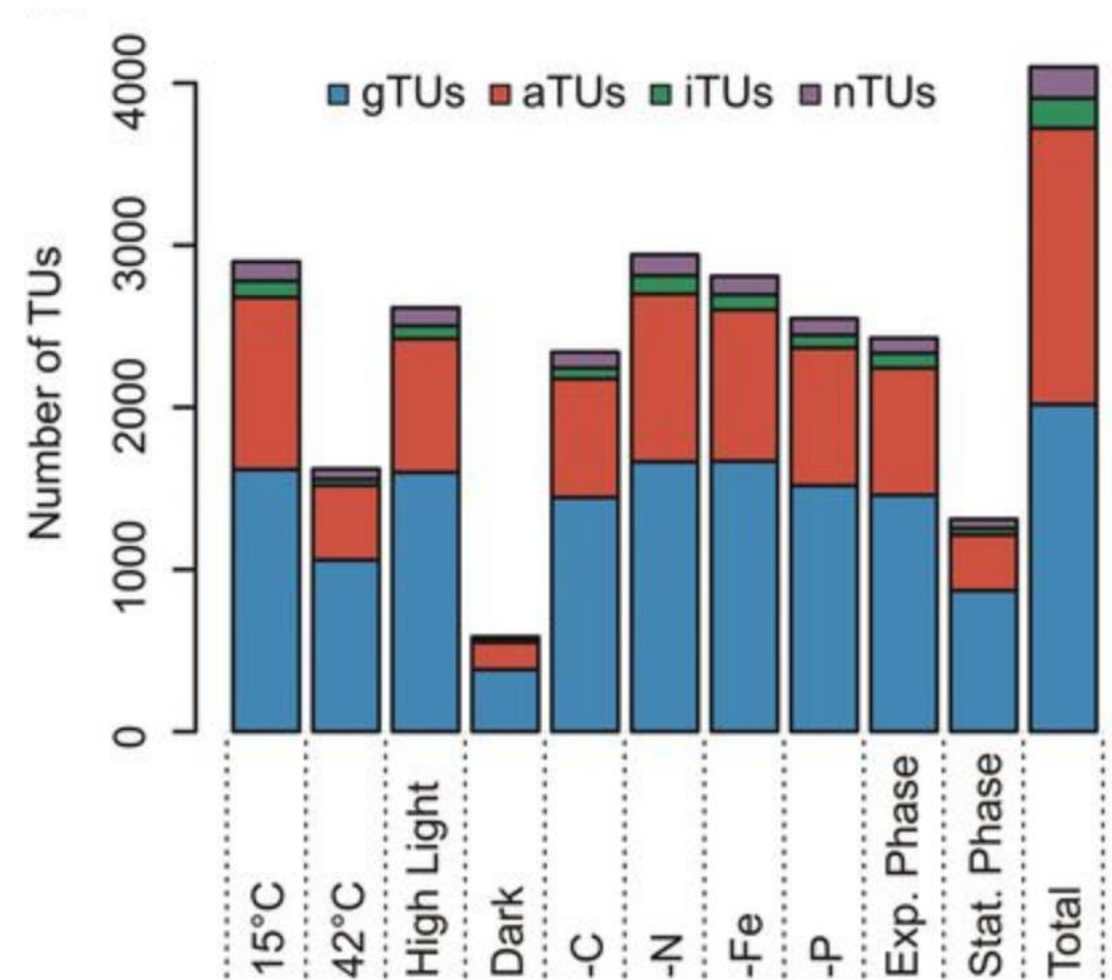
Stability profile calculation of DNA molecule



Prokaryotic transcriptome

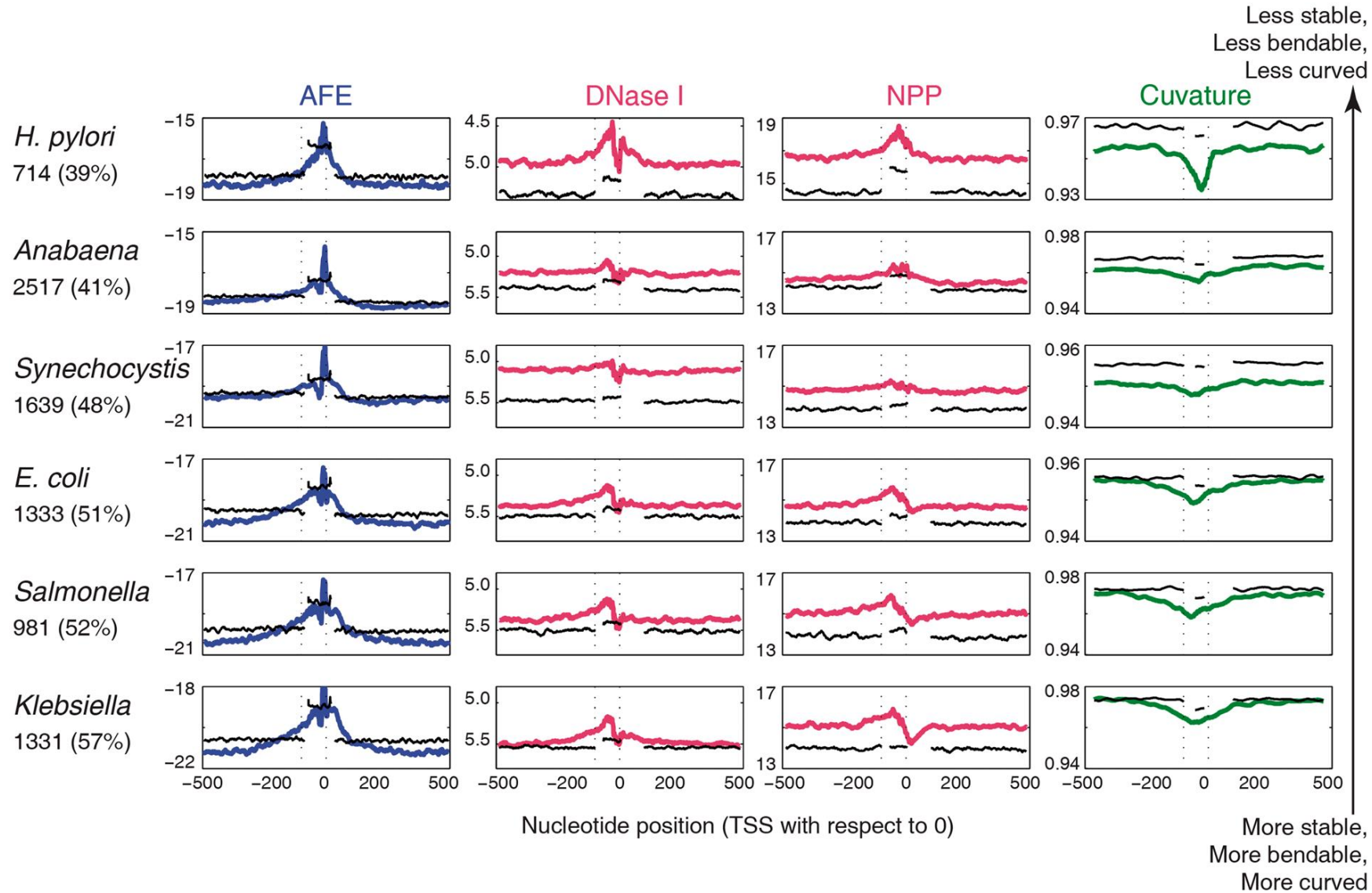


Different category of transcripts present in prokaryotic transcriptome



Transcriptome organization in different conditions

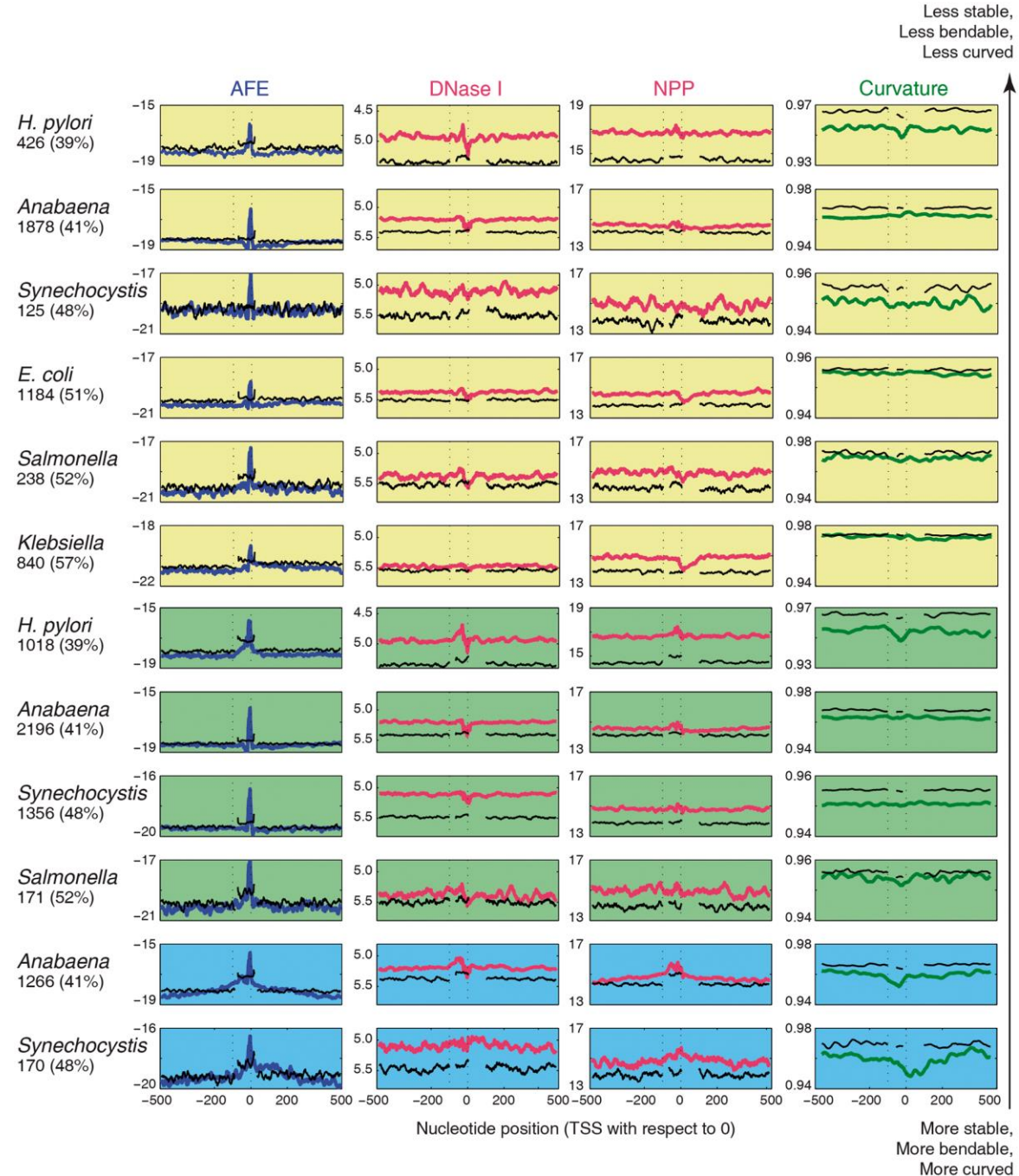
Structural features of primary promoters of prokaryotic transcriptome



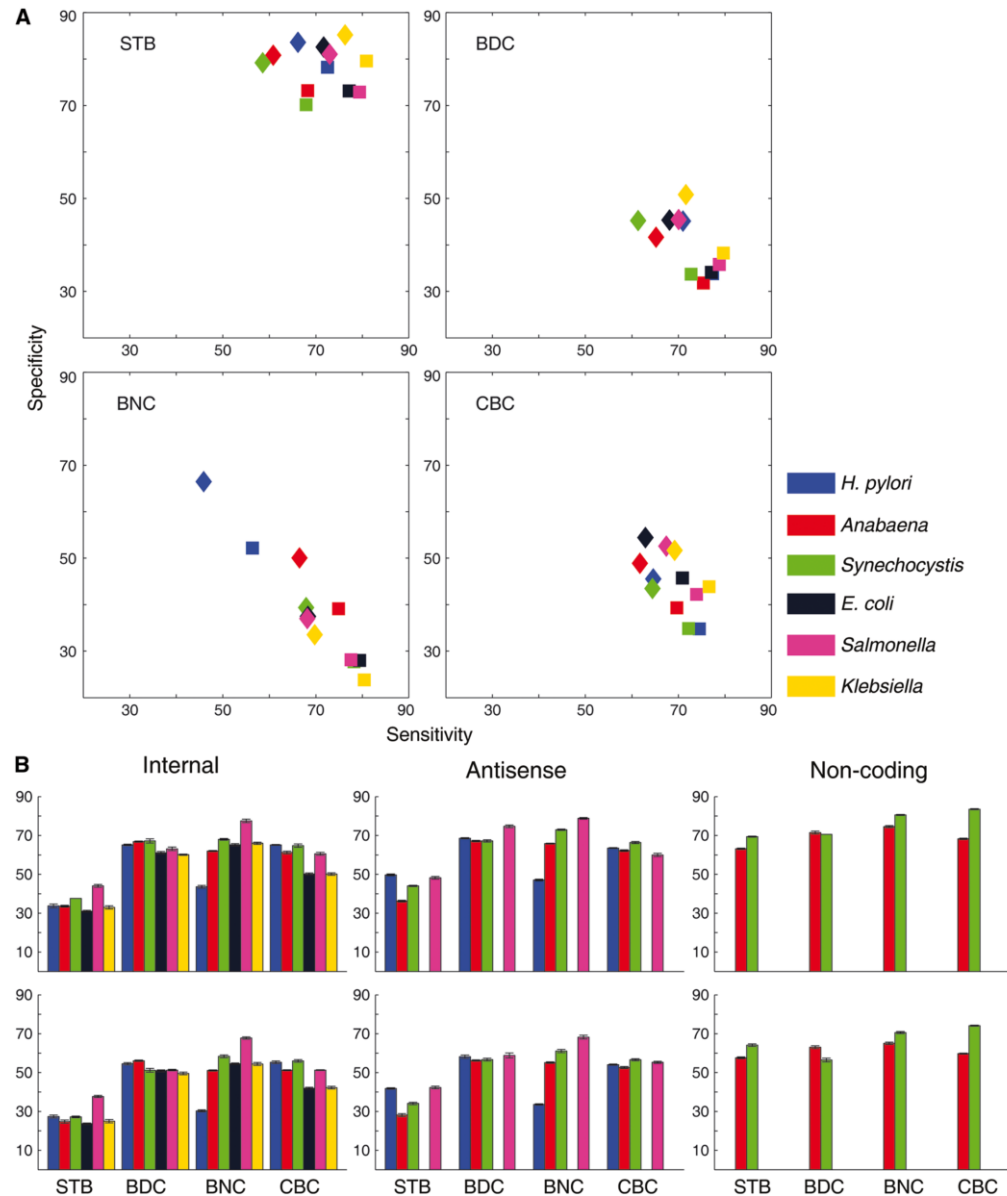
Core promoter regions are less stable, less bendable and more curved.

Structural features
profile for **internal**,
antisense and
non-coding RNA
promoters

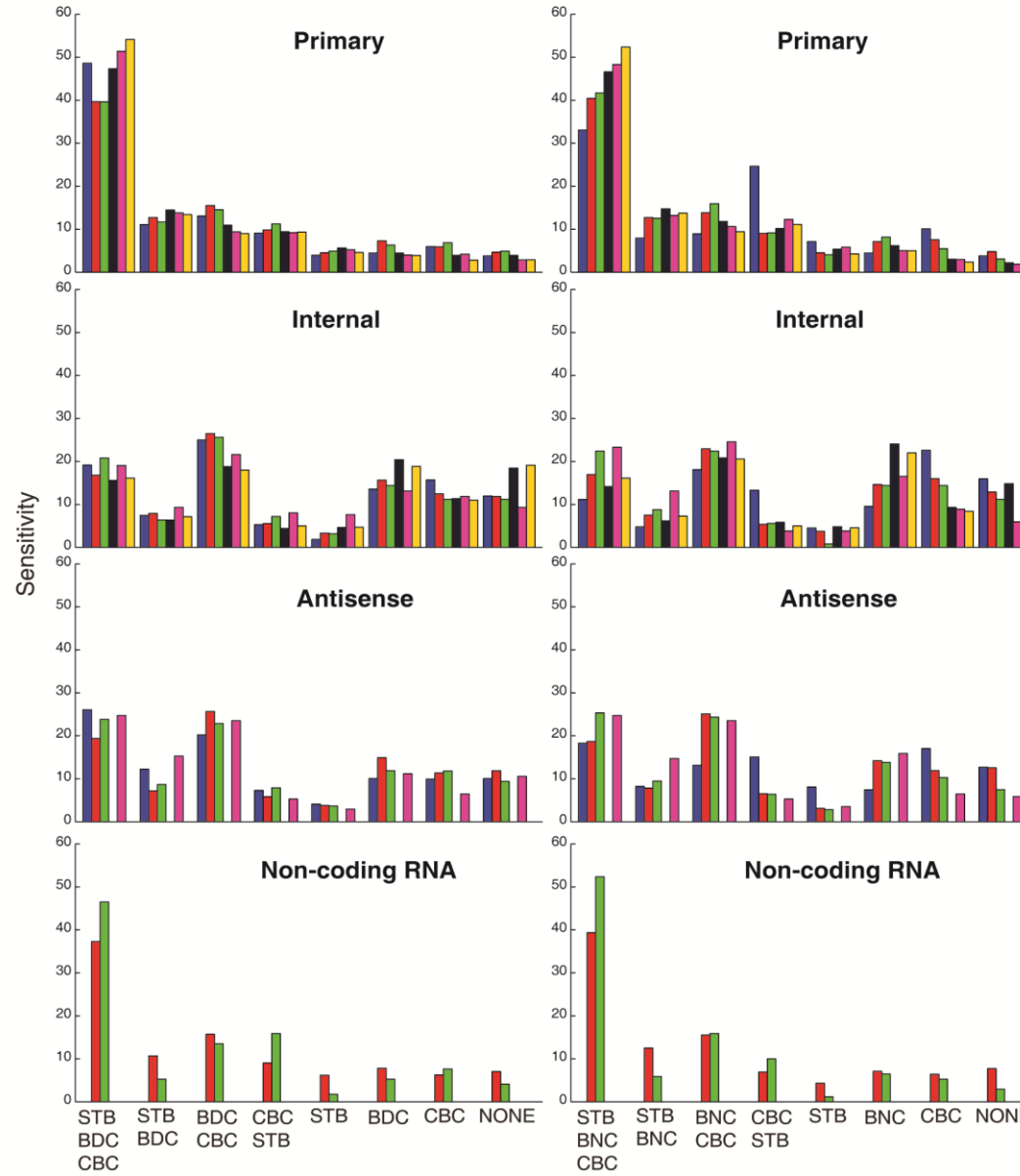
- ✓ Core promoters regions show sharp and narrow stability profiles.
- ✓ Bendability and curvature peaks are less prominent compared to primary promoters.



Performance of promoter prediction algorithm

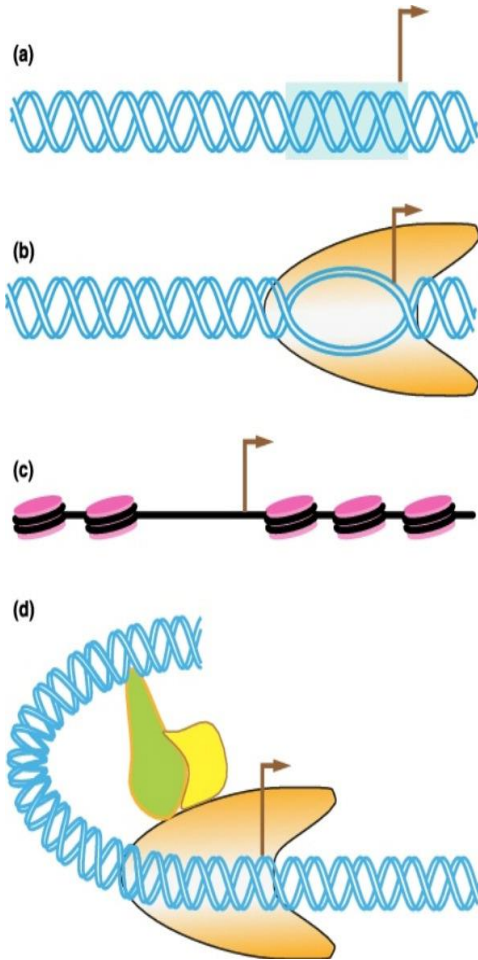


- Square and diamond markers show Cycle I and cycle II of prediction respectively.
- Higher sensitivity was achieved with smaller window size (cycle I) while long widow size (cycle II) was more specific.



Combination of features predicting promoters of different category of transcripts in the prokaryotic transcriptome

Role of sequence dependent structural properties in gene expression



Schematic illustrations showing

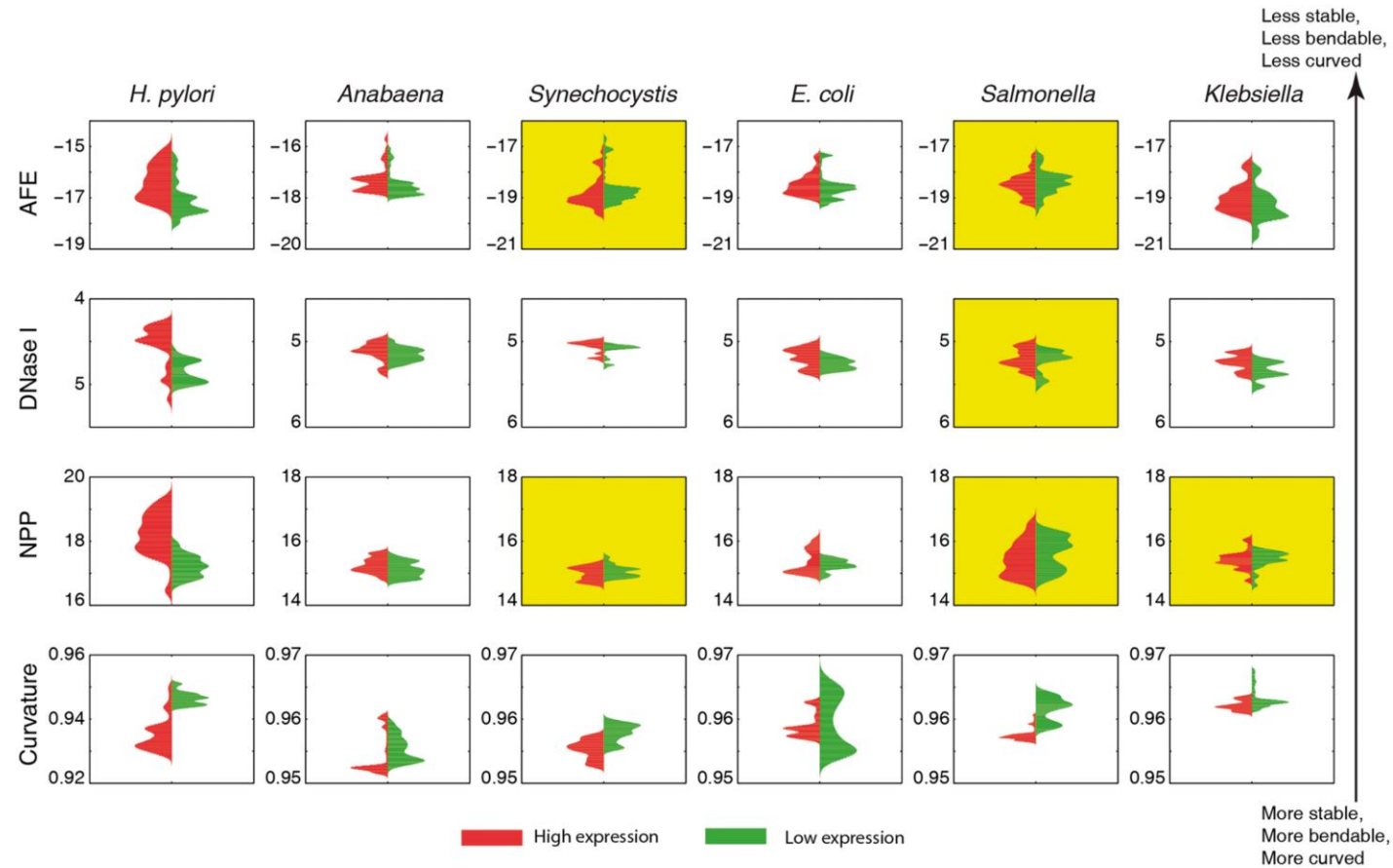
a) canonical B-DNA along with structural elements representing

b) meltable, low stability regions

c) nucleosome depleted/free region (NDR/NFR)

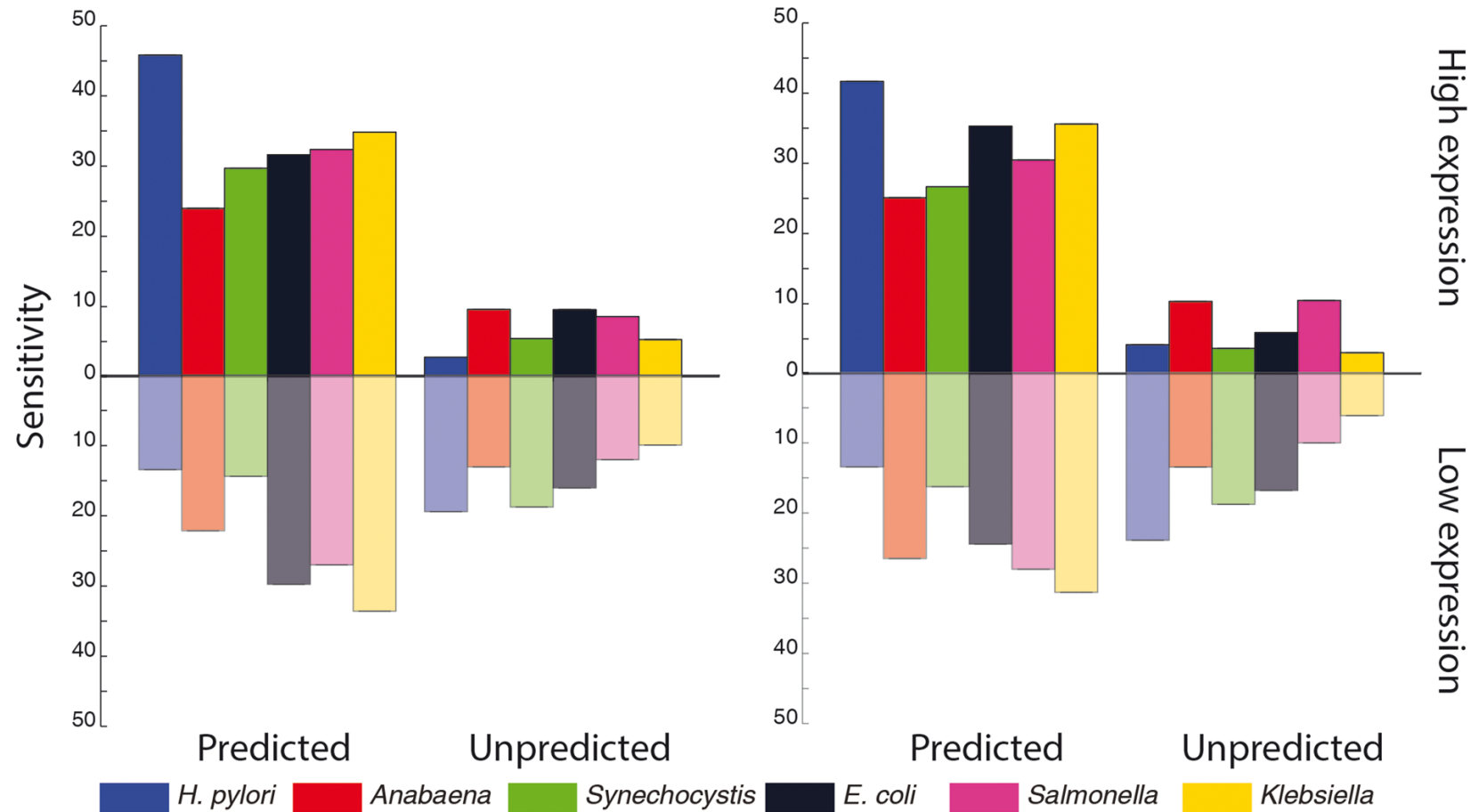
d) curved DNA, that are associated with promoter sequences located upstream of transcription start sites (indicated by brown arrows).

Role of DNA structural features in gene expression

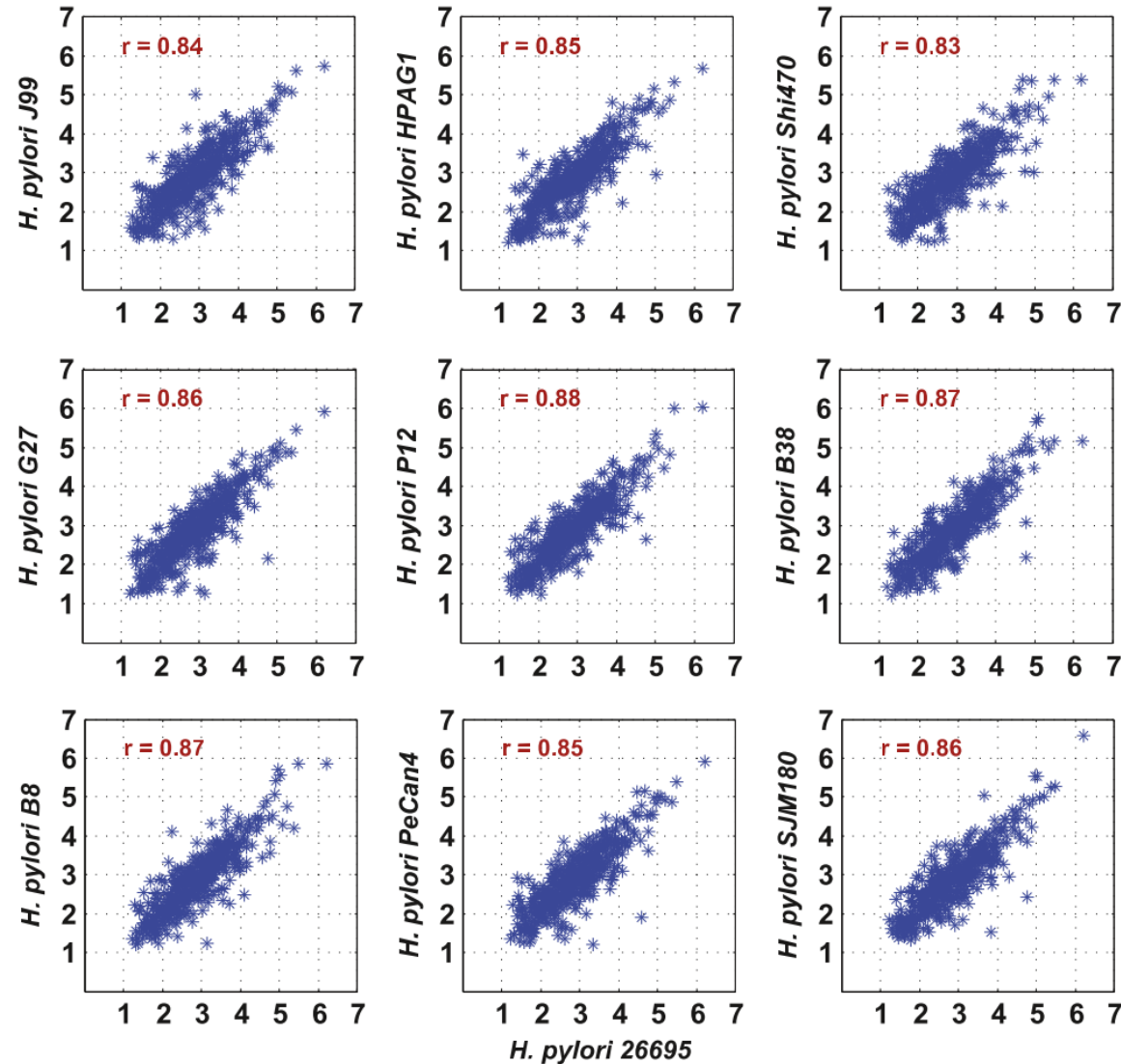


DNA structural properties are more prominent in the promoter regions associated with high gene expression as compare with low gene expression

Promoter annotation for high and low gene expression



Structural properties of promoter regions are conserved



Conclusions

- Promoter regions associated with different category of transcripts of prokaryotic transcriptome show distinct structural properties profile.
- Structural properties of promoter regions are linked to the gene expression of associated gene.
- Promoter regions show conserved DNA structural properties.
- Further we are looking for promoter engineering by altering the DNA structural properties of promoter regions. We are also interested in understanding the gene regulatory networks using structural properties of promoter regions.

Thank you