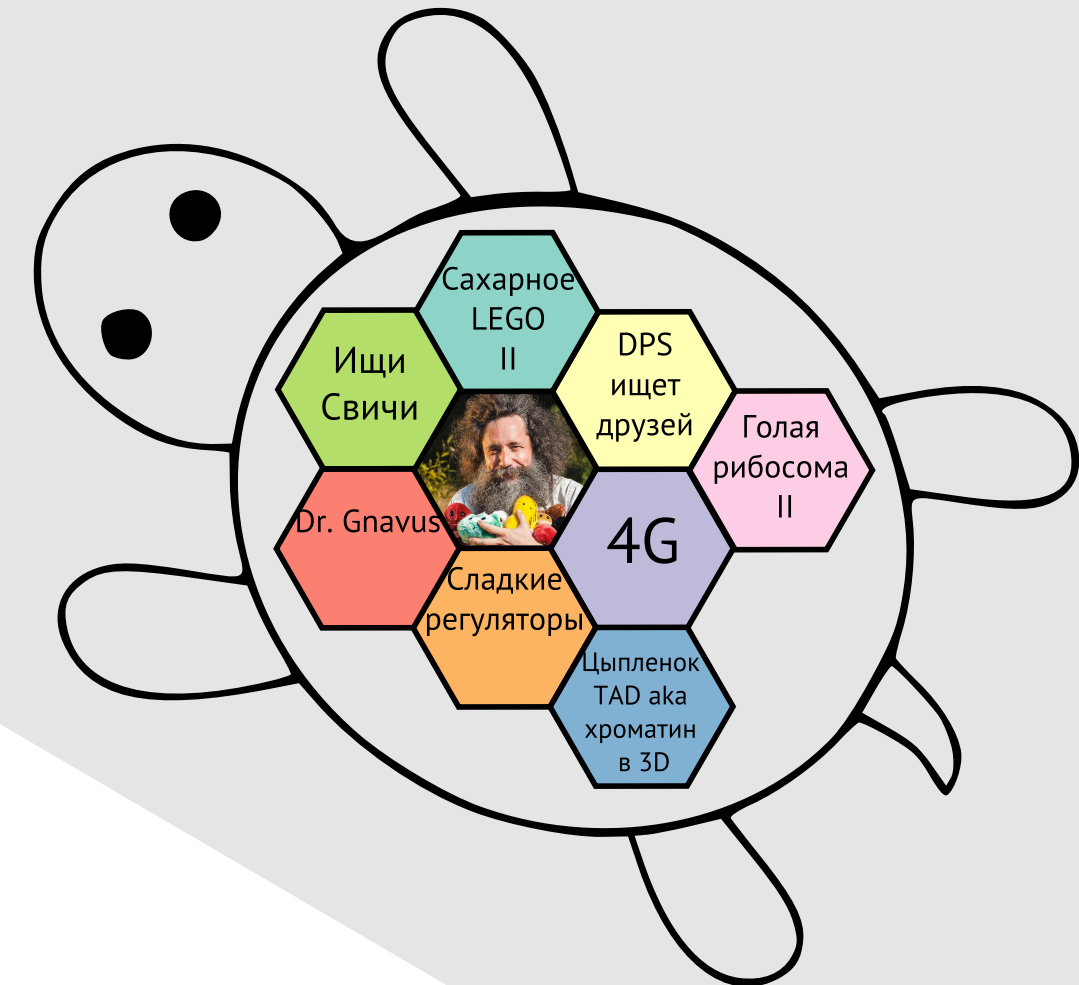




Regulatory RNA structures

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Introduction

Recently several types of non-coding RNAs have been discovered which perform a variety of functions. One of the main common features shared by these RNAs is a stable secondary structure.

The wealth of genomic data produced by state-of-the-art sequencing technologies empower computational approaches to prediction of non-coding RNAs, the latter being an actual problem.

The aim of our project was to investigate the distribution of known non-coding RNA structures and find new cases using a phylogenetical approach. The well-studied phylum Firmicutes was considered (Figure 1).

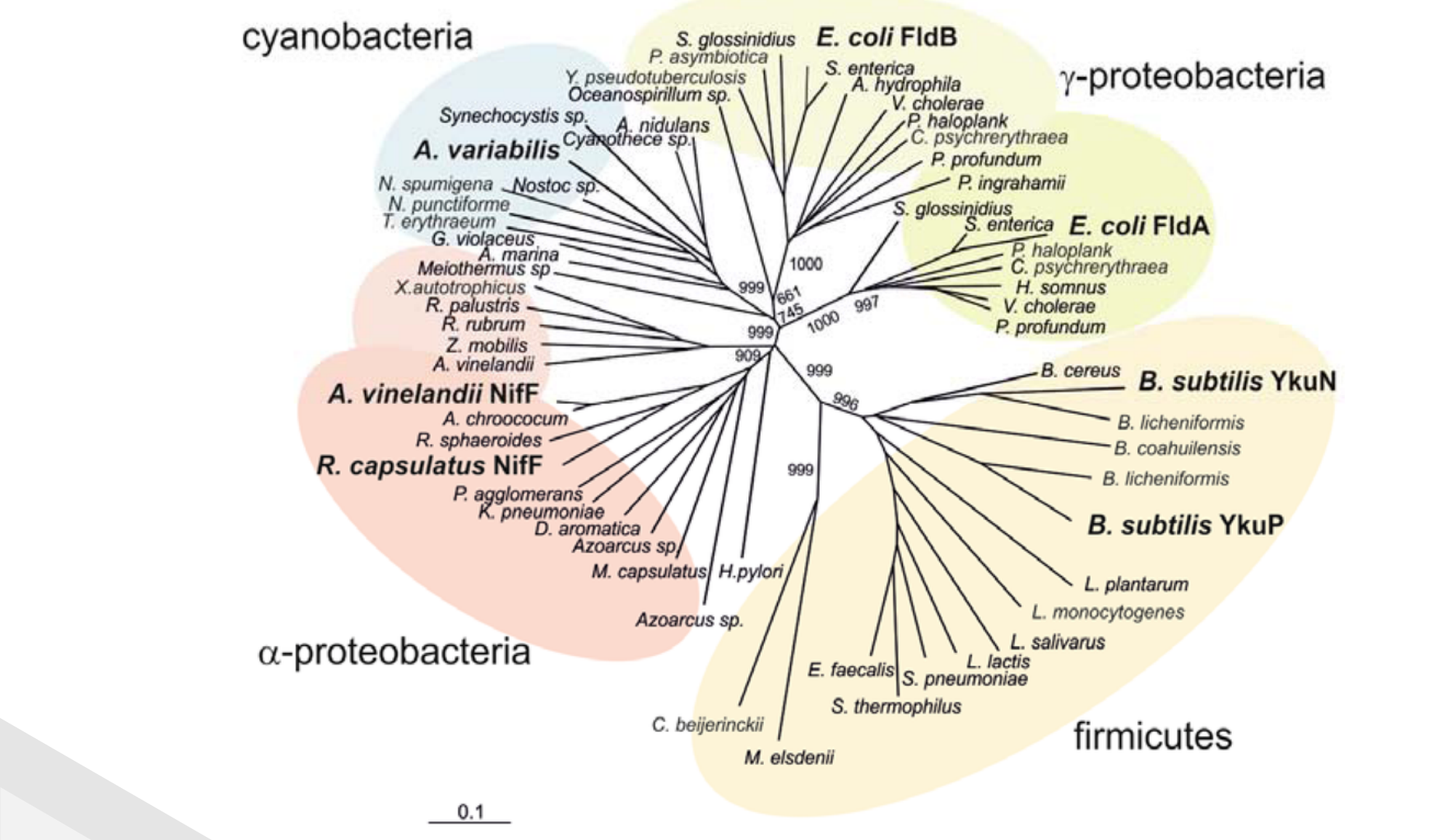


Figure 1. Firmicutes in the phylogenetic tree

Abstract

En es últimes dècades nous tipus de ARN no codificant i les seves funcions han estat descoberts. Una de les característiques principals que els ARN no codificants comparteixen és que presenten una estructura secundària estable. Avui en dia es produeixen moltes dades genòmiques gràcies a les noves tecnologies de seqüenciació. A causa d'aquest fet, els mètodes computacionals per predir ARN no codificant són molt necessaris actualment. En el nostre projecte vam investigar estructures d'ARN no codificants ja conegudes analitzant la seva funció. A més, mitjançant una aproximació filogenètica vam trobar noves estructures de ARN i vam predir potencials elements reguladors en bacteris del filum Firmicutes.

Results

Numerous terminators were identified. Some of them are bidirectional and some are parts of riboswitches (not shown).

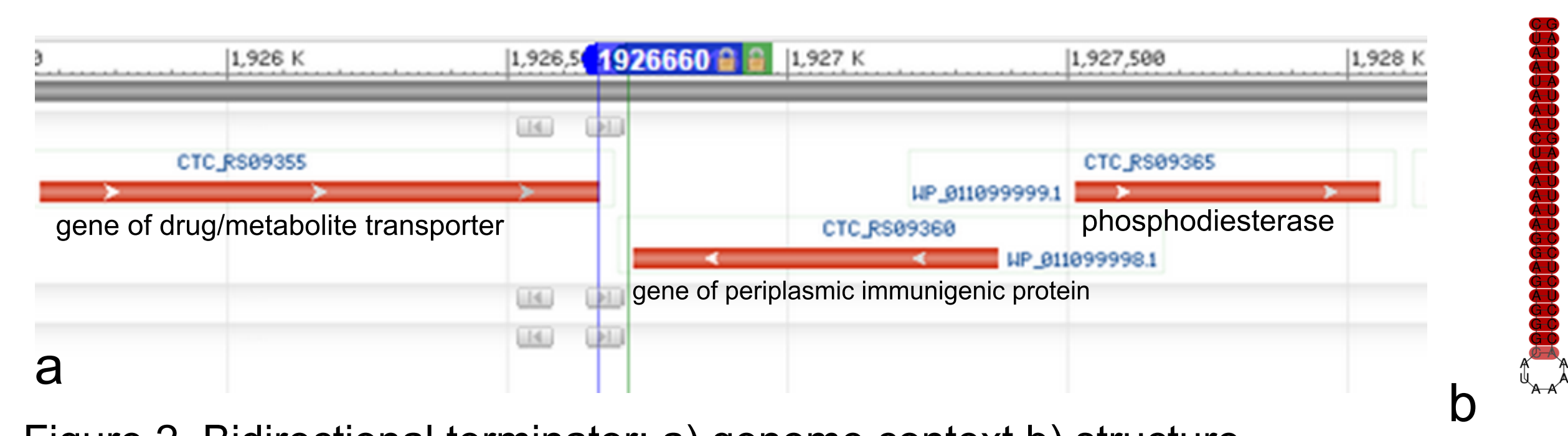


Figure 2. Bidirectional terminator: a) genome context b) structure

RNA regulation may switch between different types in related species (Figure 3).

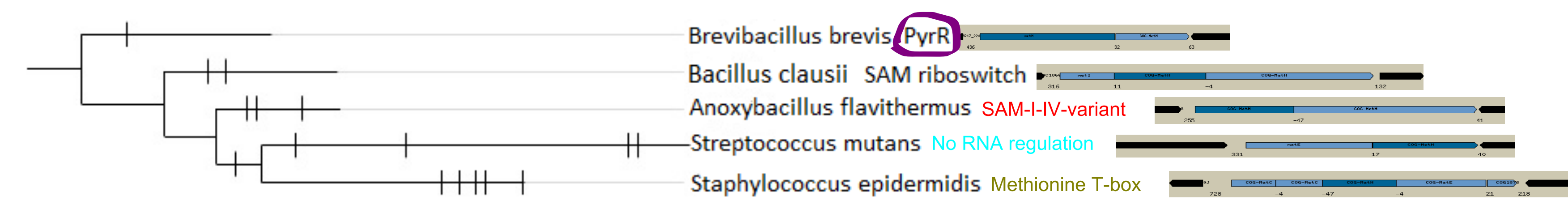
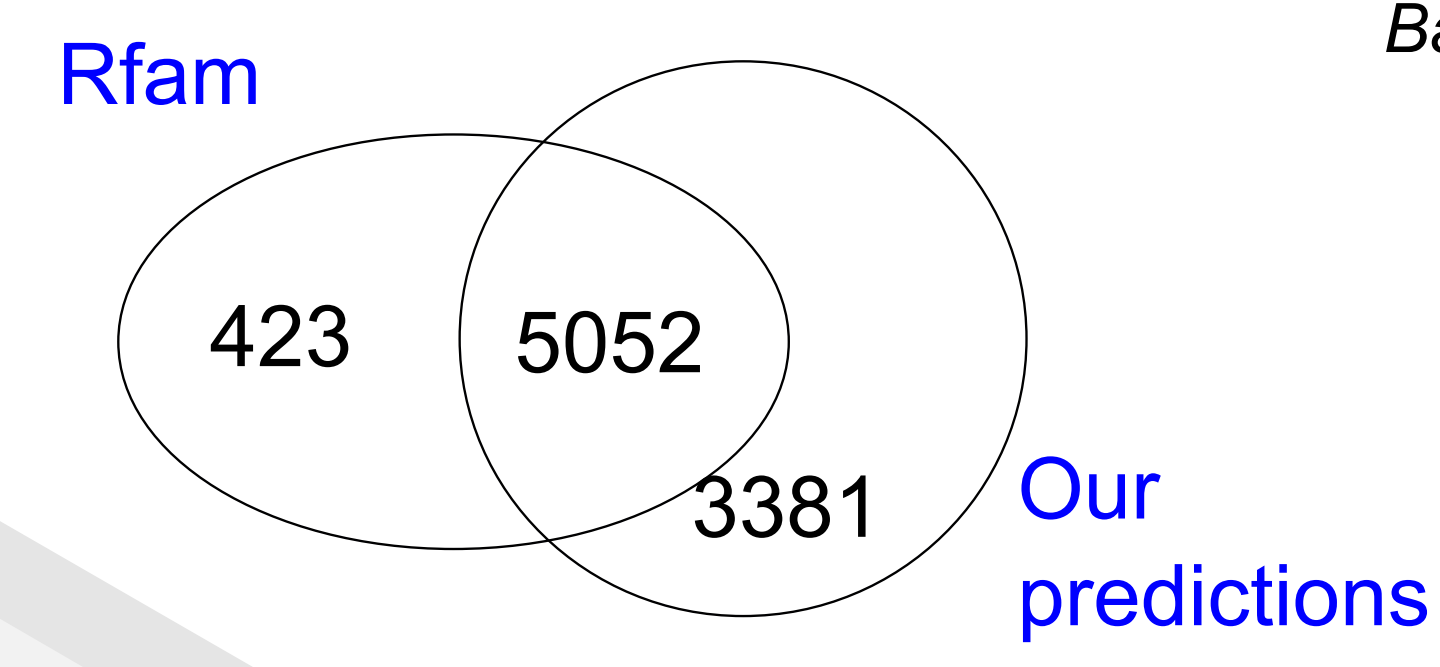
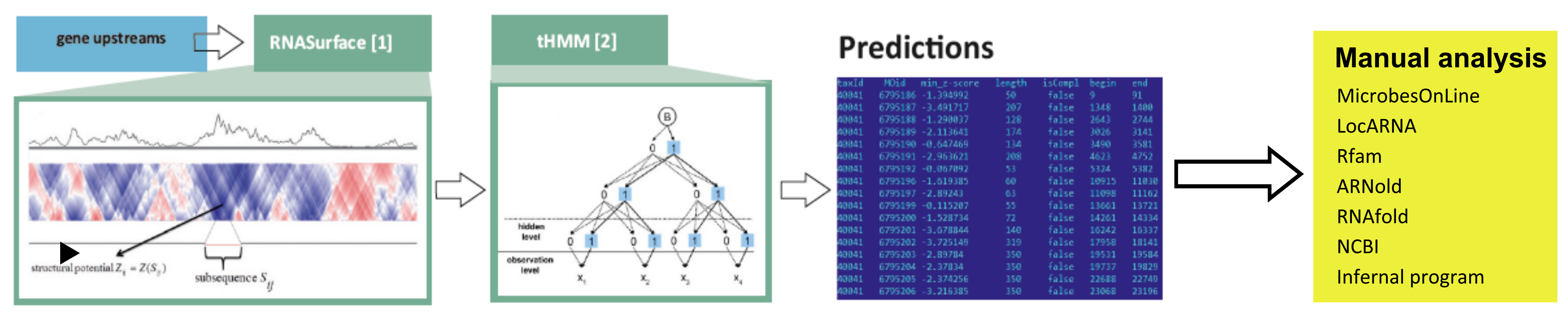


Figure 3. Divergence of methionine-dependent regulatory elements

Statistics



Materials & methods



REFERENCES

- Soldatov RA, Vinogradova SV, Mironov AA (2013) RNASurface: fast and accurate detection of locally optimal potentially structured RNA segments, 30(4):457-63
- Bykova NA, Favorov AV, Mironov AA (2013) Hidden Markov models for evolution and comparative genomics analysis, 8(6):e65012

Missannotation of genes in upstream regions often results in loss of prediction in Rfam. Our approach successfully avoids these problems.

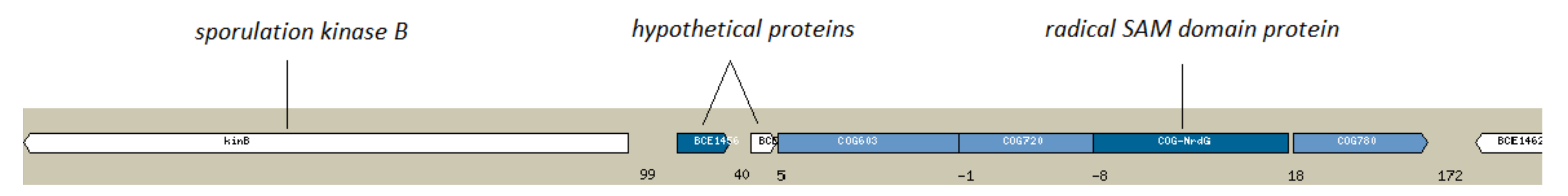


Figure 4. Gene encoding radical SAM domain protein and functionally related genes in *Bacillus cereus* ATCC 10987



Figure 5. Gene encoding radical SAM domain protein and functionally related genes in *Bacillus cereus* G9842

Stable and highly conserved RNA structures have been observed which might lead to new regulatory elements (examples in Figures 6 and 7).

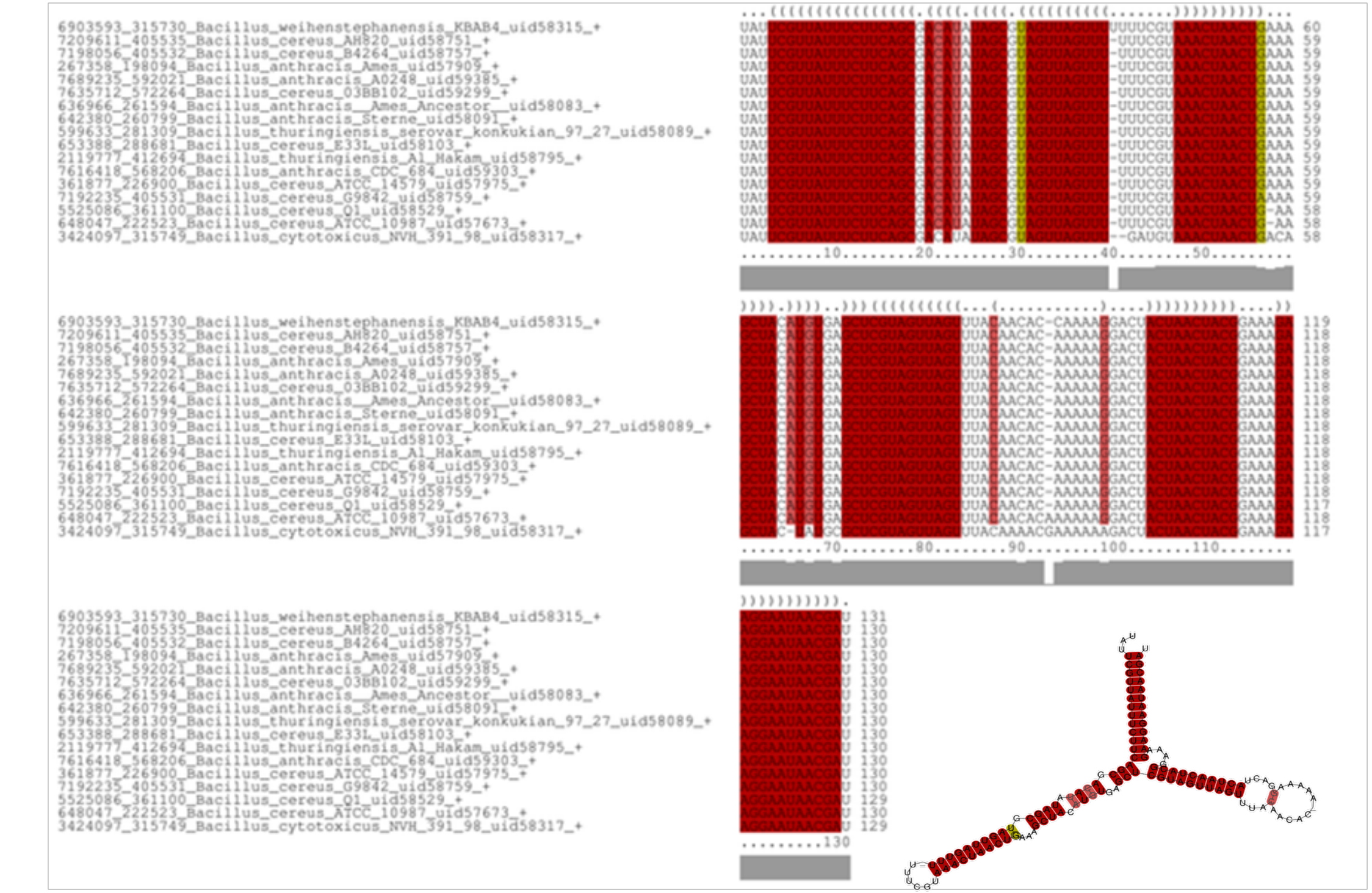


Figure 6. Predicted operon for hypothetical membrane-spanning protein in *Bacillus cereus* ATCC 14579

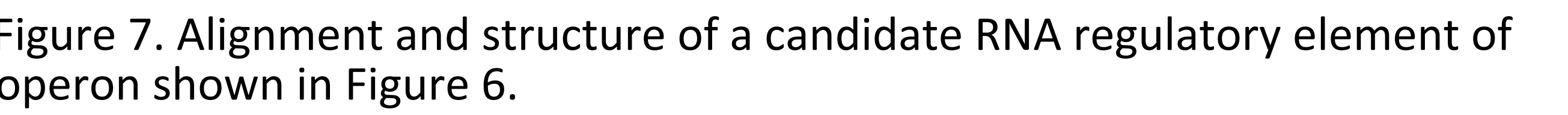


Figure 7. Alignment and structure of a candidate RNA regulatory element of operon shown in Figure 6.