

The CMfinder comparative genomics pipeline discovers 22 novel putative RNAs in bacteria
Supplementary Data: diagrams of all motifs

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May 26, 2007

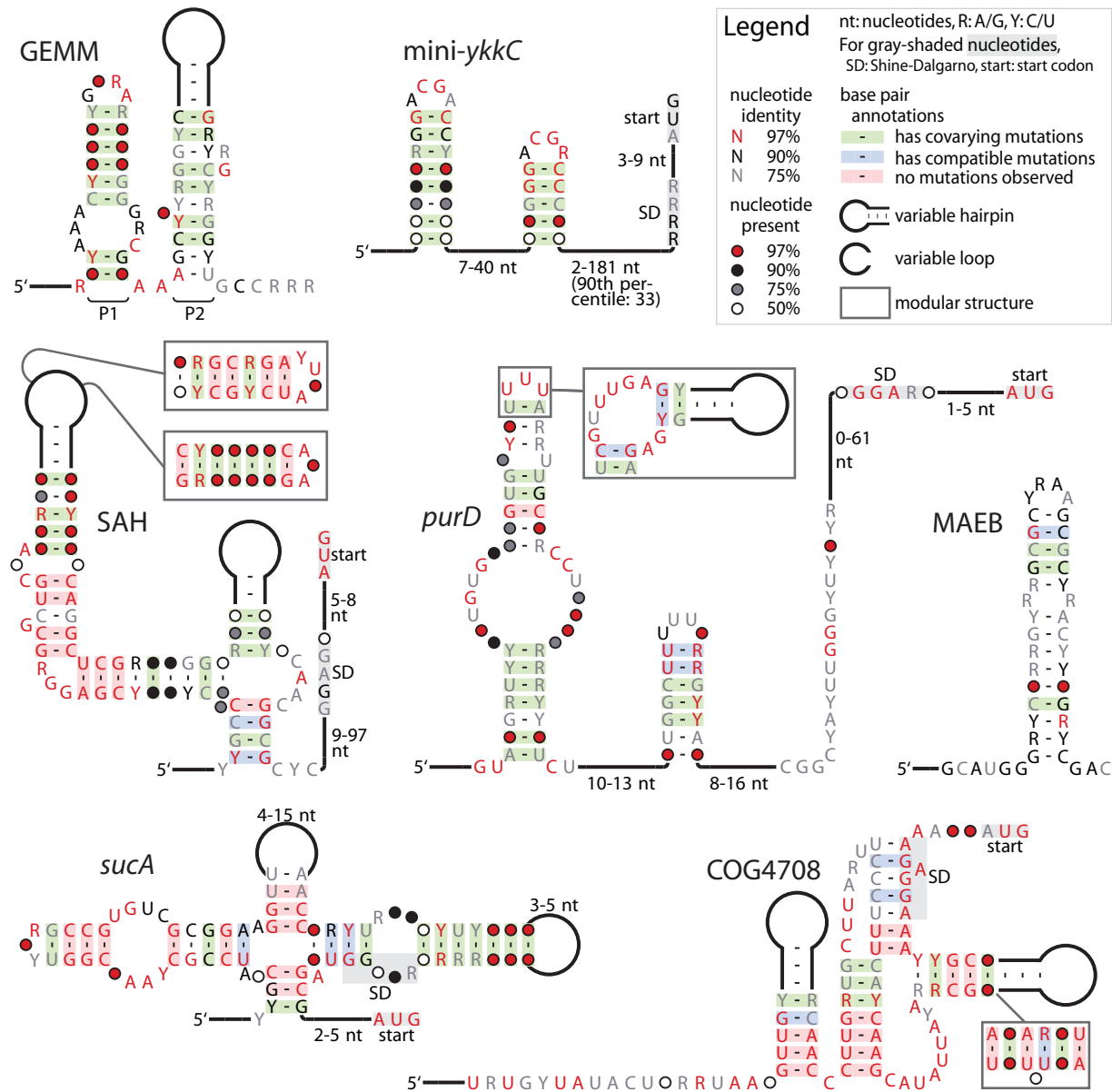
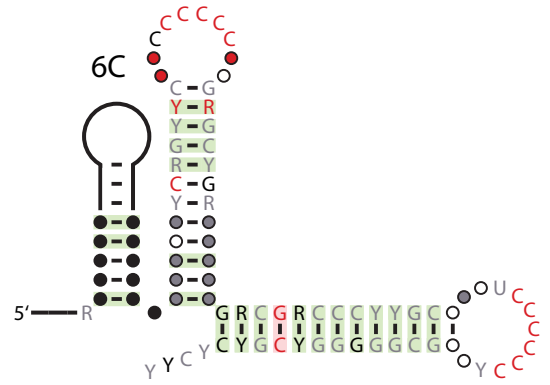
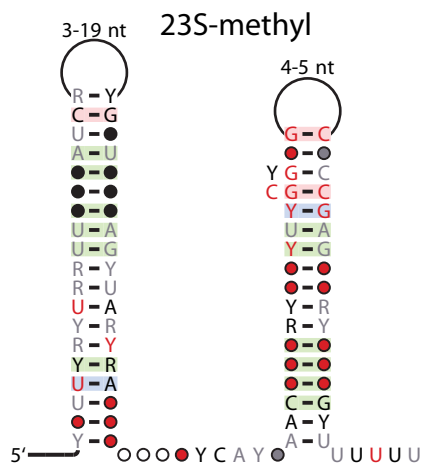


Figure 1: Complete motif consensus diagrams (part 1/4).

This is a duplicate of Figure 1 in the main paper, at high resolution. The remaining 3 pages are of motifs not drawn in the main paper. (Format is the same as Figure 1 in the main paper.)



Legend

nt: nucleotides, SD: Shine-Dalgarno
start: start codon, R: A/G, Y: C/U

nucleotide identity	base pair annotations
N 97%	- has covarying mutations
N 90%	- has compatible mutations
N 75%	- no mutations observed

nucleotide present

- 97%
- 90%
- 75%
- 50%

variable hairpin

variable loop

modular structure

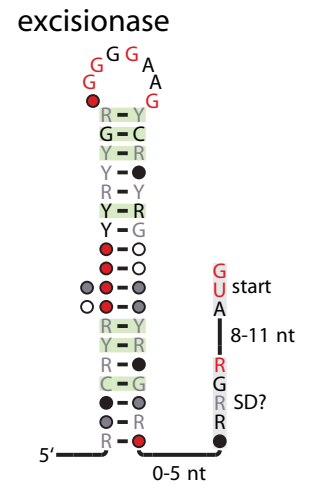
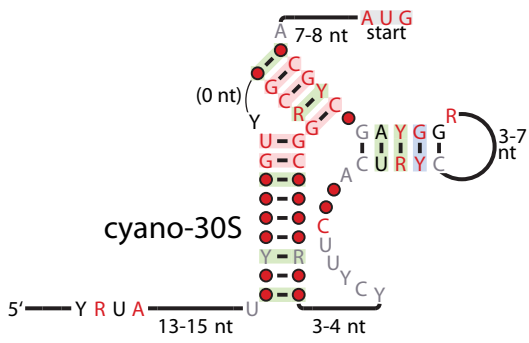
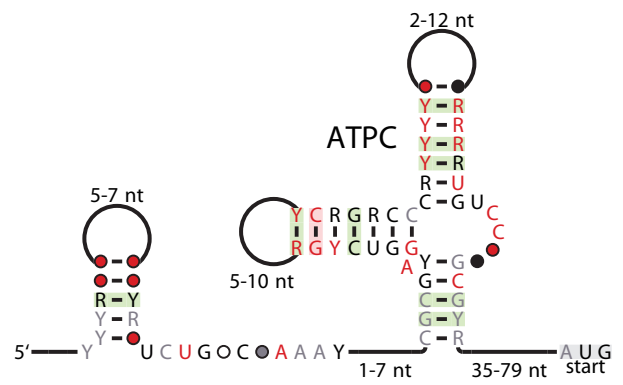


Figure 2: Complete motif consensus diagrams (part 2/4).
(Format is the same as Figure 1 in the main paper.)

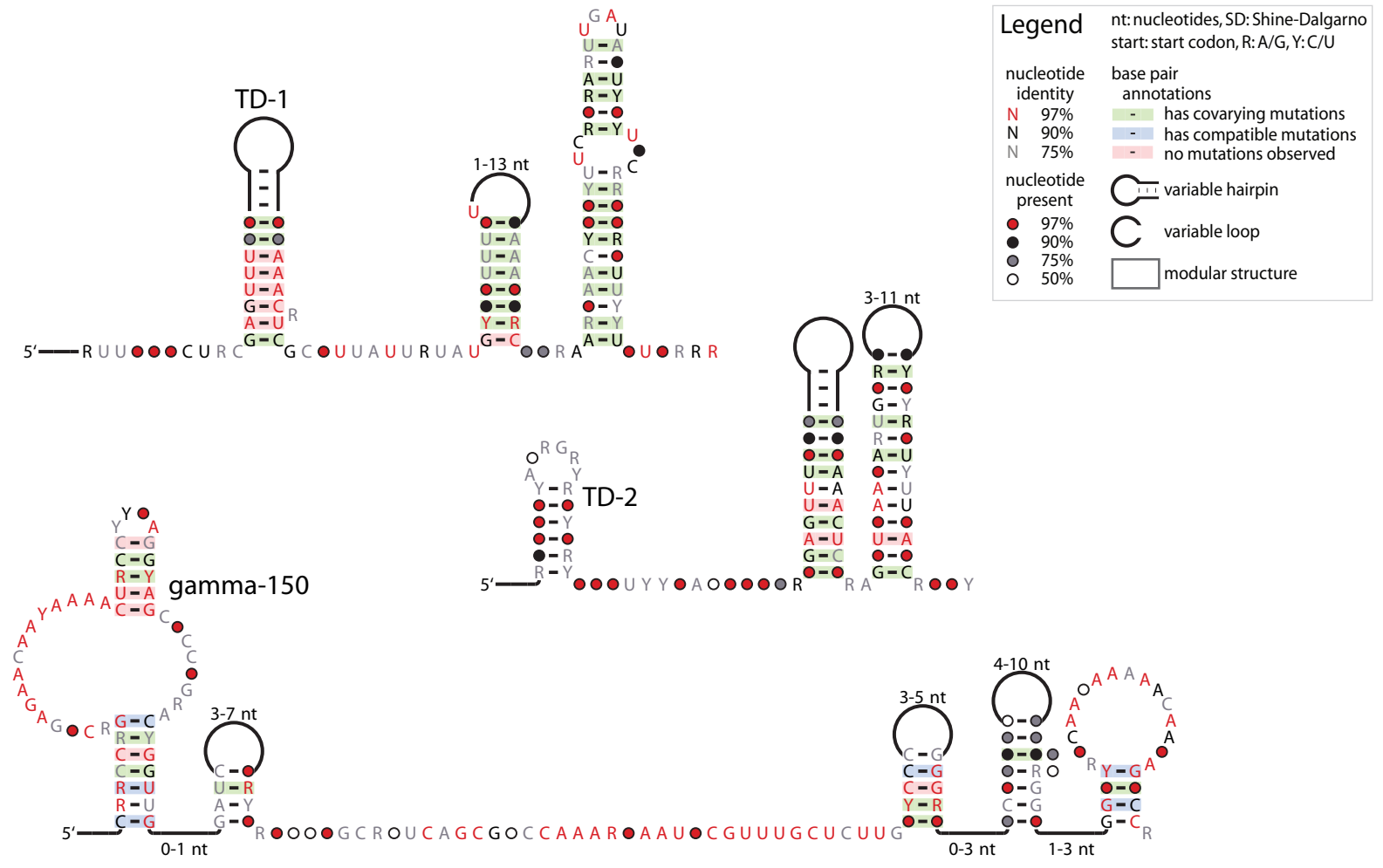


Figure 4: Complete motif consensus diagrams (part 4/4).

(Format is the same as Figure 1 in the main paper.)