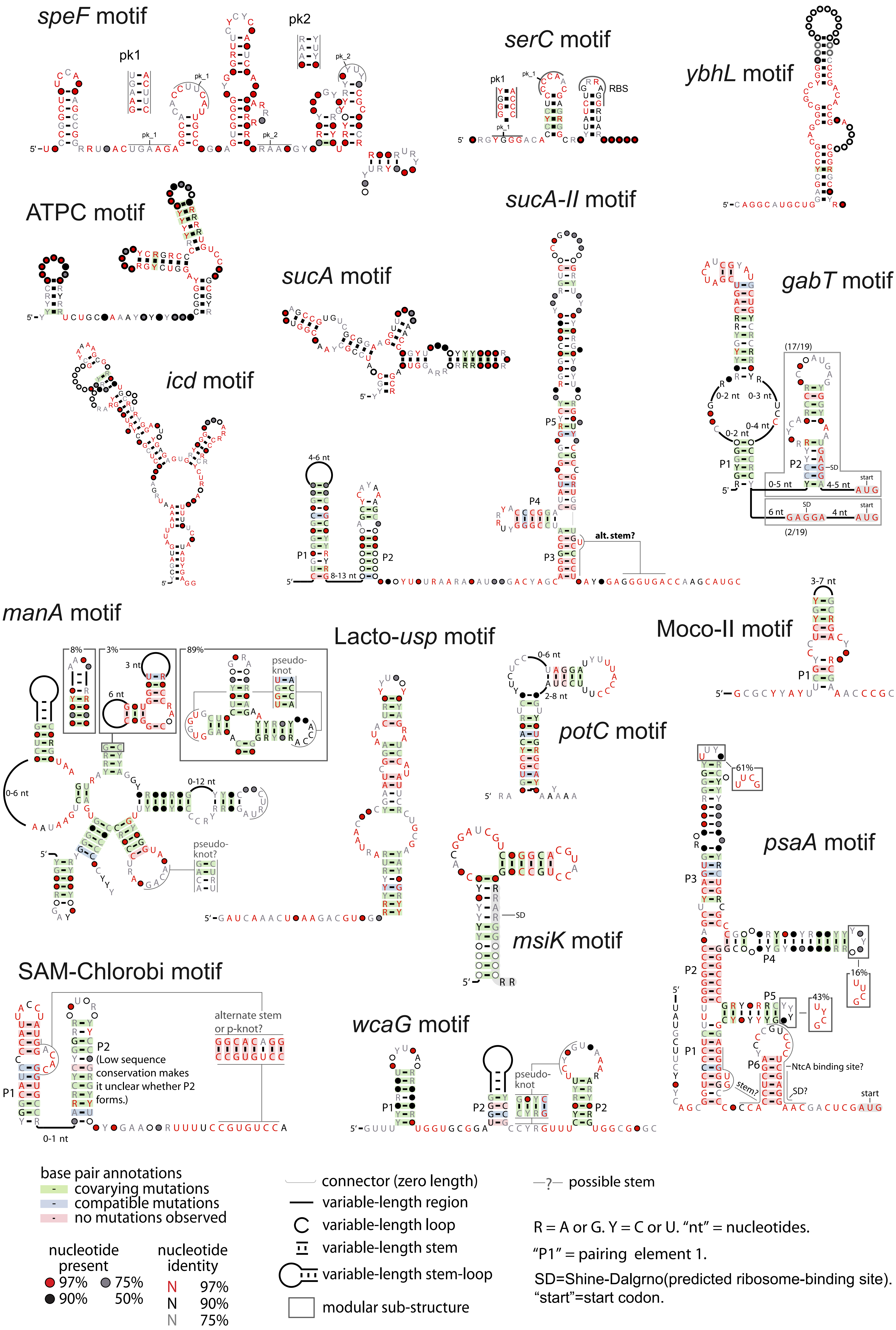speF motif
pk1
pk2
pk_1
pk_2
5'-U
serC motif
RBS
5'-RGYGGACA
ybhL motif
5'-CAGGCAUGCUG
ATPC motif
5'-Y
sucA motif
5'-Y
sucA-II motif
P5
P4
P3
alt. stem?
4-6 nt
8-13 nt
P1
P2
5'
YUURAARAAUGACYAGC
AY GAGGGUGACCAAGCAUGC
gabT motif
(17/19)
(2/19)
0-2 nt
0-3 nt
0-4 nt
0-5 nt
4-5 nt
6 nt
4 nt
SD
start
AUG
GAGGA
icd motif
manA motif
8%
3%
89%
3 nt
6 nt
0-6 nt
0-12 nt
pseudo-knot
pseudo-knot?
Lacto-usp motif
5'-GAUCAAACUAAGACGUG
Moco-II motif
3-7 nt
5'-GCGCYYAYU
AACCCGC
potC motif
0-6 nt
2-8 nt
5' RA
AAAAA
msiK motif
SD
5'
RR
psaA motif
61%
16%
43%
P6
NtcA binding site?
SD?
stem?
start
AACGACUCGAUG
SAM-Chlorobi motif
P2 (Low sequence conservation makes it unclear whether P2 forms.)
alternate stem or p-knot?
GGCACAGG
CCGUGUCC
0-1 nt
YGAA RUUUUCCGUGUCCA
wcaG motif
pseudo-knot
5'-GUUU
UGGUGCGGA
CCYRGUUU
UGGCGGC
base pair annotations
covarying mutations
compatible mutations
no mutations observed
nucleotide present
97%
75%
90%
50%
nucleotide identity
N 97%
N 90%
N 75%
connector (zero length)
variable-length region
variable-length loop
variable-length stem
variable-length stem-loop
modular sub-structure
—?— possible stem
R = A or G. Y = C or U. "nt" = nucleotides.
"P1" = pairing element 1.
SD=Shine-Dalgrno(predicted ribosome-binding site).
"start"=start codon.