(a) SAM/SAH

Base pair annotations
- Covarying mutations
- Compatible mutations
- No mutations observed

Nucleotide present
- 97%
- 90%
- 75%
- 50%
- No mutations observed

Nucleotide identity
- 97%
- 90%
- 75%

R = A or G. Y = C or U. “nt” = nucleotides. “SD” = Shine-Dalgarno (predicted ribosome binding site). “Start” = start codon.

(b) SK209-52 RNA

Cleavage is
- Constant
- Increased by SAM
- Decreased by SAM
- (No data)

(No data)

(c) NR T1 OH SAM

(d) fraction modulated (normalized)

Band
- 23
- 42
- 45

log c (SAM, M)