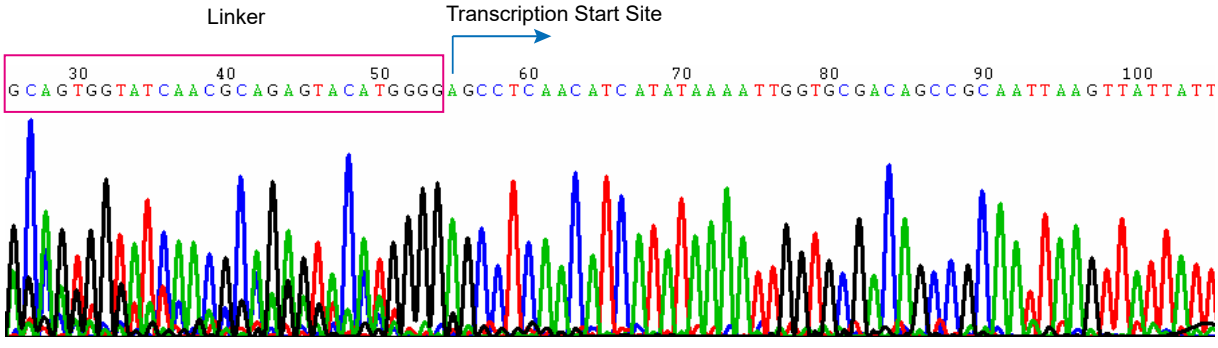
Supplemental_Figure_S1

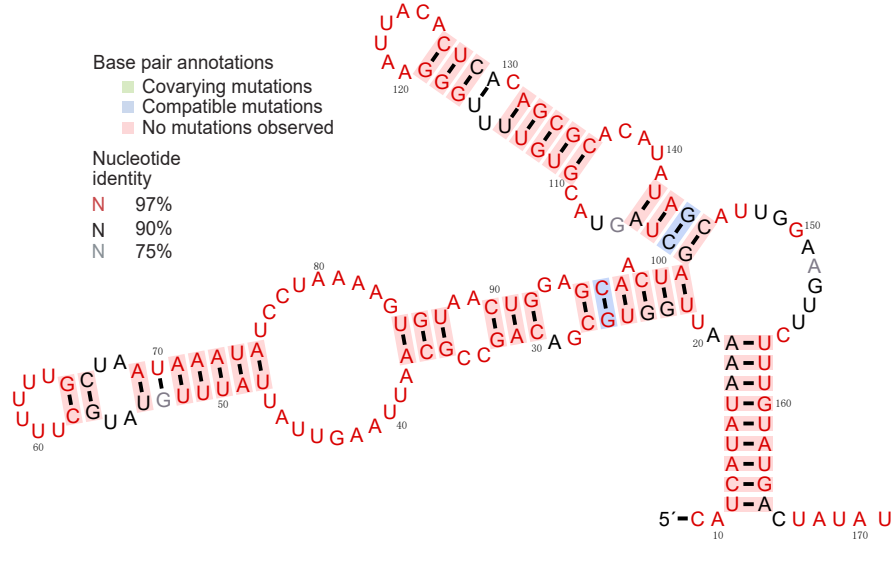
A



B

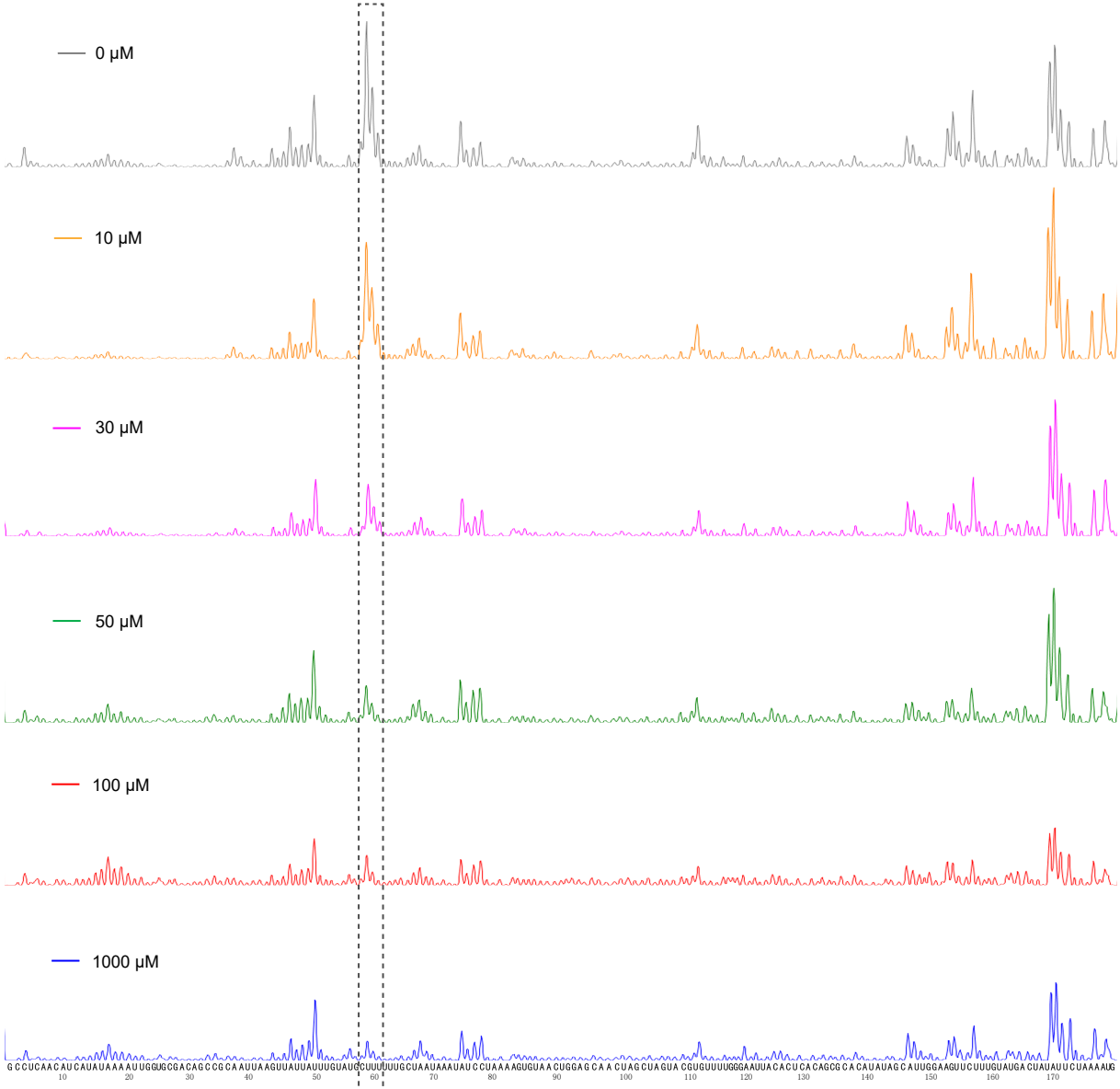
Mutant	Position
WT	
M1	18-20 A-U
M2	29 A-U
M3	36 C-G
M4	45-47 UAU-AUA
M5	53-55 GUA-CAU
M6	55-57 AUG-UAC
M7	53 G-C
M8	67-68 UA-AU
M9	96 C-U
M10	102-103 GC-AU
M11	114-116 UUU-AAA
M12	129-130 CA-GU
M13	131 C-U
M14	136 C-A
M15	142 U-A
M16	144-145 GC-CG
M17	148-149 UG-AC
M18	151-152 AA-UU
M19	152-153 AG-GA
M20	154-155 UU-AA
M21	161 U-C
M22	163 U-C
M23	165-166 AC-UG

C



Supplemental Figure S1 5′ RACE of UTR RNA of *spe2* and mutants used for covariance analysis. **A** Identification of the transcription start site for the *spe2* gene in fission yeast by 5'RACE analysis. **B** Mutant positions are indicated. **C** Secondary structure proposed by covariance model derived from wild-type sequence and the mutation RNA sequences, whose in vivo β-gal expression is close to wild-type construct. Nucleotides present in greater than 97%, 90%, and 75% of the representatives are in red, black, and grey, respectively.

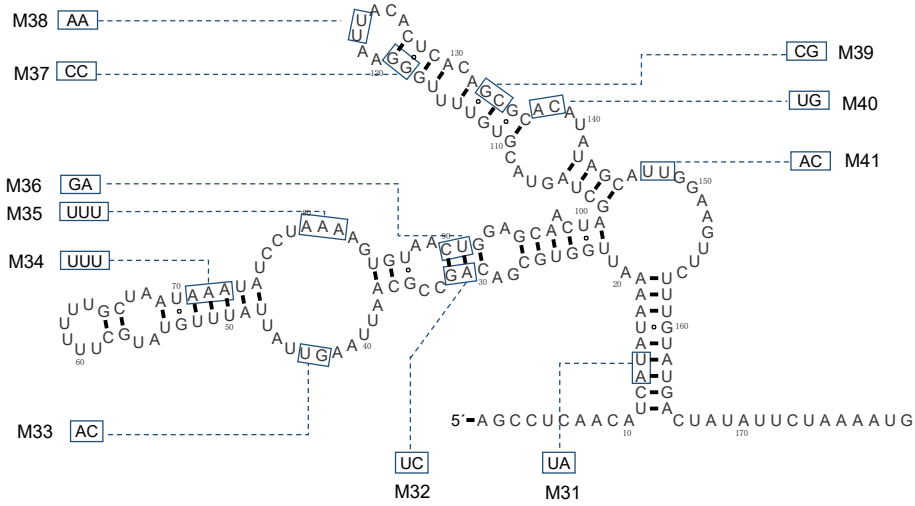
Supplemental_Figure_S2



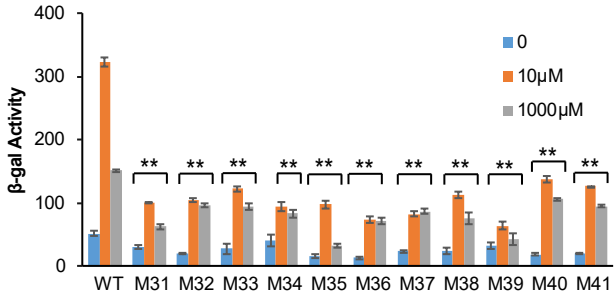
Supplemental Figure S2 Electropherogram of OsO4-modification on full-length *spe2* UTR RNA on spermidine titration.

Supplemental_Figure_S3

A

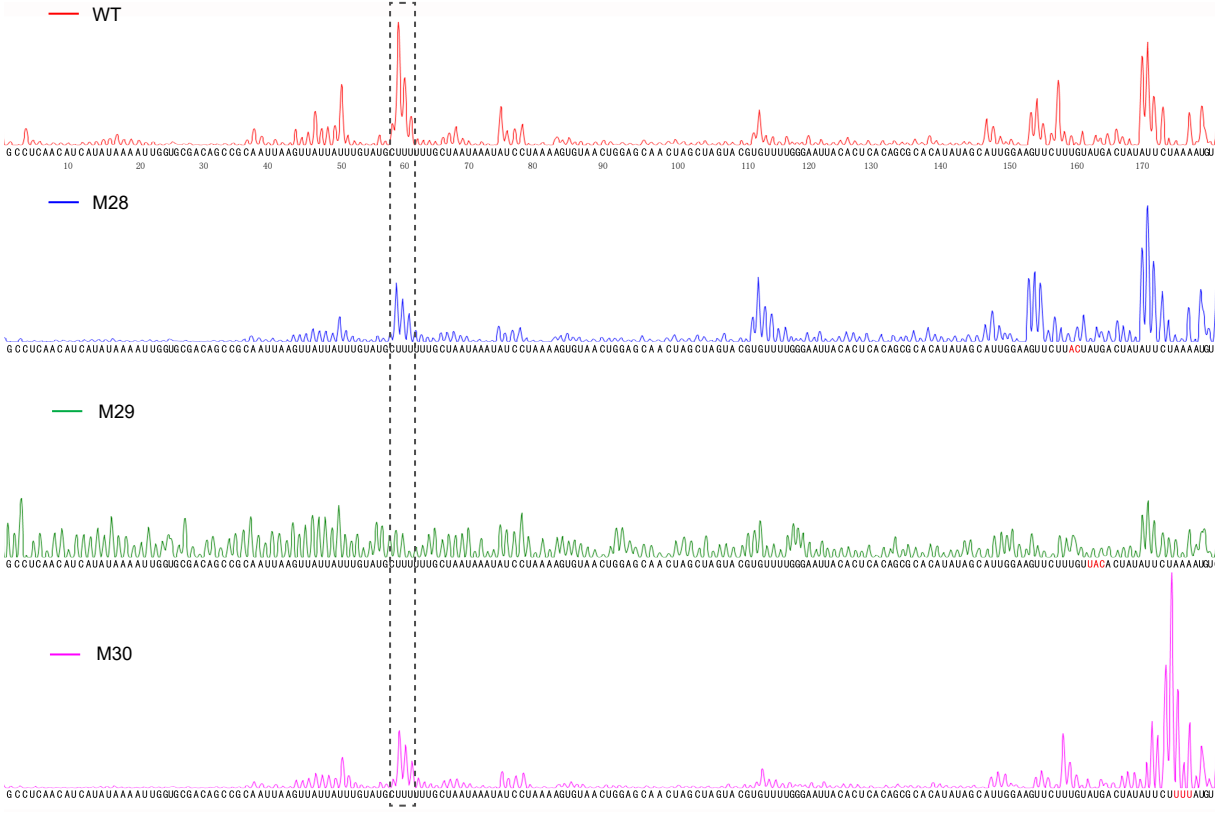


B



Supplemental Figure S3 Reporter gene expression of mutants and real-time PCR analysis of mRNA abundance of the *spe2* UTR RNA. **A** The positions (boxed) and identity of the mutations on the secondary structure of the RNA. **B** Reporter gene expression of inactive RNA mutations (M31-41), responding to 0, 10, and 1,000 μM of Spd. The error bars are the standard deviation of at least 3 independent experiments. Data are presented as mean ± SD from three replicates.Statistical significance was shown compared with WT using Student's t-test, **P<0.01.

Supplemental_Figure_S4



Supplemental Figure S4 Electropherogram of OsO4-modification of the wild type (WT, red trace) and three mutated RNA sequences (M28–30 green, blue, and purple trace, respectively).