

Figure S1. SAM-III riboswitch. A) left: consensus structure of SAM-III riboswitch; A) right: secondary structure of sequence from *Enterococcus sp* which was used to verify with in-line probing. B) In line probing result show structure differences among three different constructs and structure modulation with or without ligand. The ligand concentration is from 0.1 μM to 10 μM . The different colored rectangles show the modulating as the increasing of the ligands for wild and mu2 constructions. The color circles mark structure differences between the three different constructions. The arrows mark the positions which we used to calculate the K_D . The stars mark the mutation position. The black solid lines mark the stem positions of the secondary structure in A. Our experiments did not allow very precise determination of K_{DS} , but there was clear modulation and the K_{DS} could be estimated to be $0.6 \pm 0.5 \mu\text{M}$ for the wild type, and $0.4 \pm 0.5 \mu\text{M}$ for the compatible mutant. However, no K_D could be determined for the disrupted mutant.