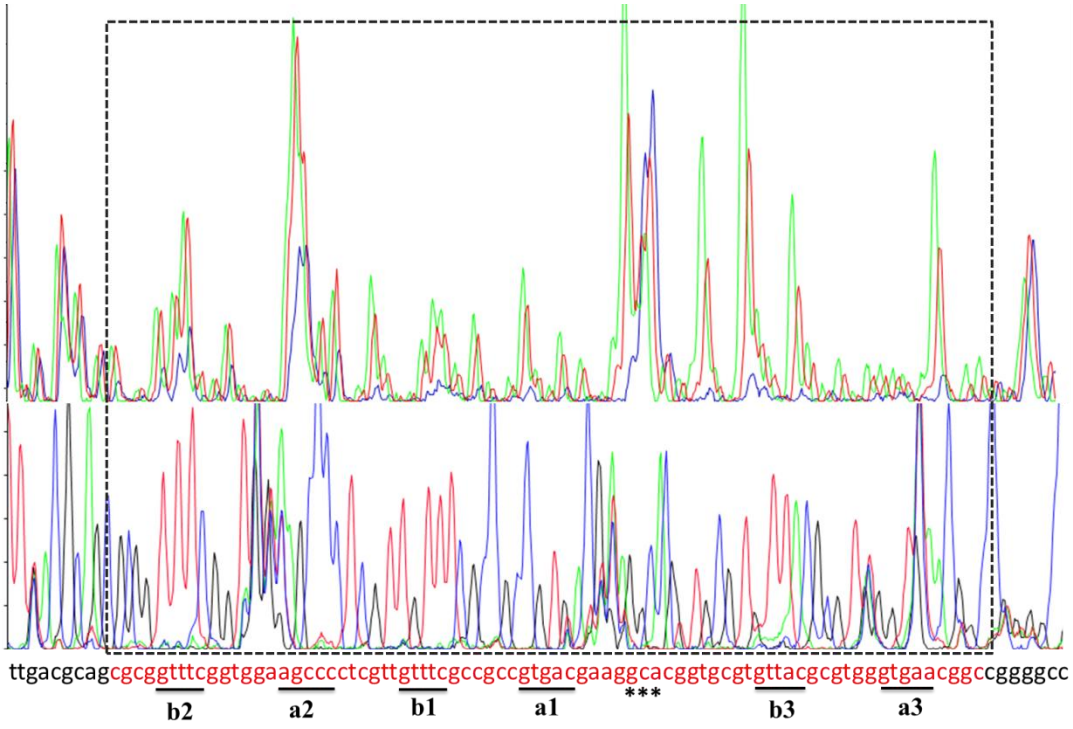


**Fig. S1. Identification of the GlnR protected *cis*-elements in non-coding strand of the *amtB* promoter region.** The DNA sequences of the non-coding strand that were protected by GlnR from DNase I cleavage were shown. The colored lines stood for different concentrations of GlnR used: green line, 0 μg; red line, 0.2 μg and blue line, 0.4 μg. The GlnR binding boxes were boxed and the DNase I-hypersensitive sites ("GCA", next to the hypersensitive site "ggt" in the coding strand) were denoted with asterisks. The protected patterns remained the same even when GlnR was increased up to 2.4 μg (data not shown). The fmol DNA Cylce Sequencing System (Promega) was used for DNA sequencing reactions. The sequencing products together with the digestions products were analyzed with ABI 3130xl DNA Analyzer and Peak Scanner software v1.0 (Applied Biosystems). The four sequencing results (G, A, T and C) were marked with 4 different colors separately and then merged together. The overlapping peaks were probably caused by secondary structures within the promoter region. The electropherograms were aligned together with the usage of standards.