**S2 Fig**



S2 Fig. Structure and polymorphisms in SmtB. Panel A shows the sequence alignment of SmtBhomologs. The locations of the α5 metal-binding sites are highlighted in blue and pink. In red is the mutated sequence of SmtB. Panel B shows the structure of the CzrA dimer from *Sthaphylococcus aureus*. Zn, in orange, binds at the interface between the two monomers. Panel C shows a model of the effect of the mutation in ML0825 on the dimer, which compromises the binding of Zn ions. The mutated part is represented in red lines. The protein was modeled using the homology modeling webserver SWISS-MODEL7 and the structure of the transcriptional repressor CzrA from *Staphyloccocus aureus* (PDB code 1R1V) as template.

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