



Supplementary Figure S2 – Analysis of FIO1 methyltransferase domain mutants based on homology model.

The three mutants were mapped to the homology model of FIO1 (see Materials and Methods). The *fio1-1* mutation involved the loss of five amino acids highlighted in pink, including the loss of a potential hydrogen bond between the threonine and asparagine. The *sum8* mutation changes the serine (orange), which normally hydrogen bonds to a tryptophan, into an asparagine. The resulting larger side-chain of asparagine is unlikely to be accommodated in the constrained protein interior, leading to changes in the protein structure and loss of function. The *fio1-5* mutation involves a large deletion (orange) and missense mutations (light cyan) in a partially buried alpha helix, which are very likely to disrupt protein folding and function.