Figure S4. Expression of a possible antitoxin for the *yonT* type I toxin. Recently, several putative type I toxins were identified in the *B. subtilis* genome (Fozo *et al.*, 2010), including the *yonT* gene. Our analysis of the Hfq coIP data revealed that four examples of previously identified type I antitoxins appeared to exhibit preferential enrichment by Hfq. Inspection of the putative *yonT* toxin gene revealed an Hfq-associated peak located in the region where an antitoxin transcript would be most likely to occur. Therefore, we speculate that the Hfq-associated peak that overlaps *yonT* might correspond to an antitoxin transcript.