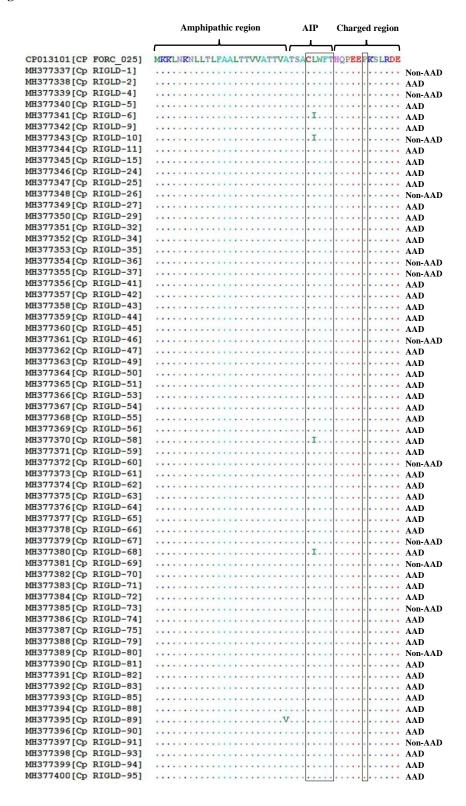
Prevalence and characterization of *Clostridium perfringens* toxinotypes among patients with antibiotic-associated diarrhea in Iran

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Supplementary information

Supplementary Figure 1:



Supplementary Figure 1. Complete amino acid sequence alignment of AgrD from 64 *C. perfringens* isolates from patients in antibiotic-associated diarrhea (AAD) group and non-AAD group. The AgrD amino acid sequence of *C. perfringens* strain FORC_025 (CP013101.1) as the reference strain is shown on the top line. The peptides are split into three regions representing the N-terminal amphipathic region, the autoinducing peptide (AIP) encoding region and the C-terminal charged region. The putative amino acid motif to form the thiolactone/lactone ring structure of the mature AIP and a highly conserved proline residue found in all AgrD peptides are surrounded in boxes.