



#### Supplementary Figure S4. Domain structure and disorder predictions for GspD and PulD.

The sequences of GspD from EPEC (YP\_002330719.1) and PulD from *K. oxytoca* (EHT13409.1) were analysed by CDART to position the conserved domain boundaries and DISOPRED2 to calculate probability of intrinsic disorder (Ward *et al.* 2004). The dotted line represents the 5% probability cut-off and all values greater than this are plotted with red bars. The DISOPRED2 calculations are aligned to scale with the amino acid residue numbers in the domain representation of each protein. The intrinsic disorder in the S-domain of PulD has been experimentally verified (Nickerson *et al.* 2011; Tosi *et al.* 2011; Gu *et al.* 2012) and the intrinsic disorder prediction for EPEC GspD is equivalent to that for PulD. Secondary structure predictions were calculated using JPred (Cole *et al.* 2008), red =  $\alpha$ -helix, yellow =  $\beta$ -strand.

#### References

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