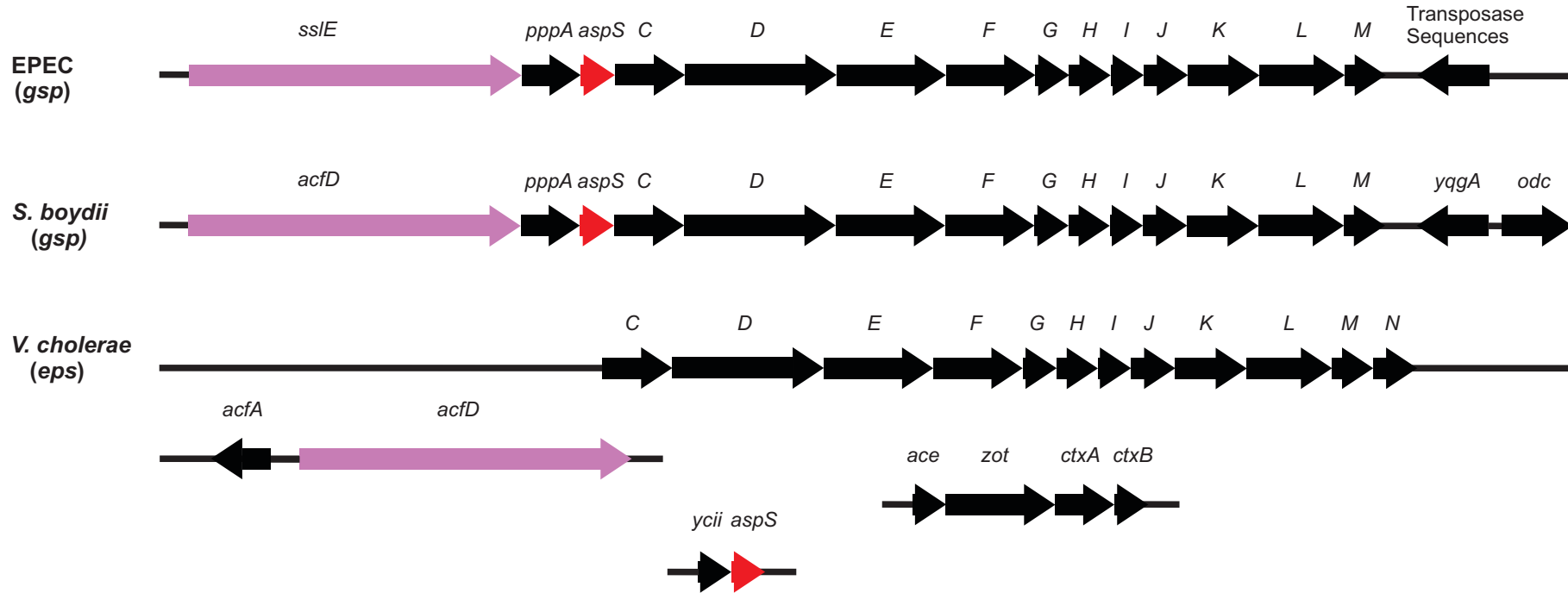


A.

EPEC CAS----HNENASLLAKKQAQNISQNLPIKSAGYTLVLAQSSGTTVKMTIISEAGAQTTPDAFLTSYQROMCADPTVKLMI^{*}TEGINYSITINDTRTGNQYQRKLDRTTCGIVKA
S.boydii CAS----HNENASLLAKKQAQNISQNLPIKSAGYTLVLAQSSGTTVKMTIISEAGTQTTPDAFLTSYQROMCADPTVKLMI^{*}TEGINYSITINDTRTGNQYQRKLDRTTCGIVKA
V.cholerae CSSGSAEKQRNLELLAGNRASLLSTELPLEFGLNLRATAKGSTVELMMVYNTDANNAKPTEQVLQSAVSSFCANKDIRSNLDVGI^{*}SYRIQMRNTRGQLMADQLVTKESCKQG
 : :.* .*** :*. :* :***: . :.* :***: :. :.:.:.:.:.: :.* * :***: :. :. :.*** * :.*** :. :. :.*

B.



Supplementary Figure S1. Gene detection, characteristics and synteny for the T2SS in EPEC, *Shigella* and *Vibrio cholerae*.

(A) Multiple sequence alignment of AspS homologs, aligned from the cysteine residue predicted to be at +1 and acylated after the signal peptidase cleavage, (*) indicates sequence identity (:) indicates highly conserved (.) indicates some degree of conservation. Disulfide-linked cysteine residues are underlined. (B) The Comprehensive Microbial Resource (CMR) was used to detect sequence relationships in the genomes of EPEC (i.e. enteropathogenic *E. coli* O127:H6 str. E2348/69), *Shigella boydii* D9 and *Vibrio cholerae*. The genes are coloured for the pilotin AspS (red) and the substrate SslE/AcfD (pink), and neighbouring genes are depicted in black and drawn to scale according to their length.