

## Supplementary Figures

### Chromosome-encoded IpaH ubiquitin ligases indicate non-human enteroinvasive *Escherichia*

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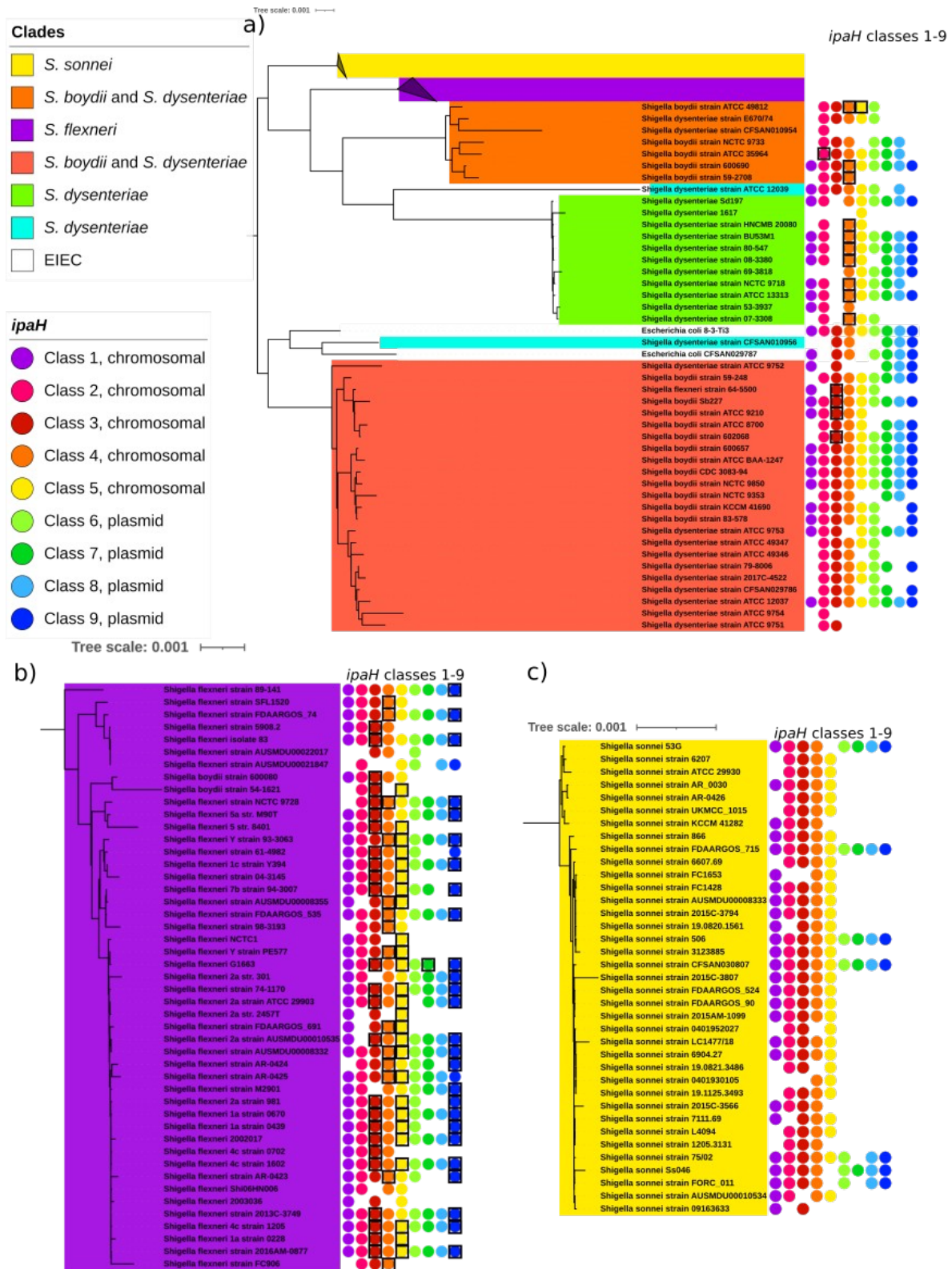
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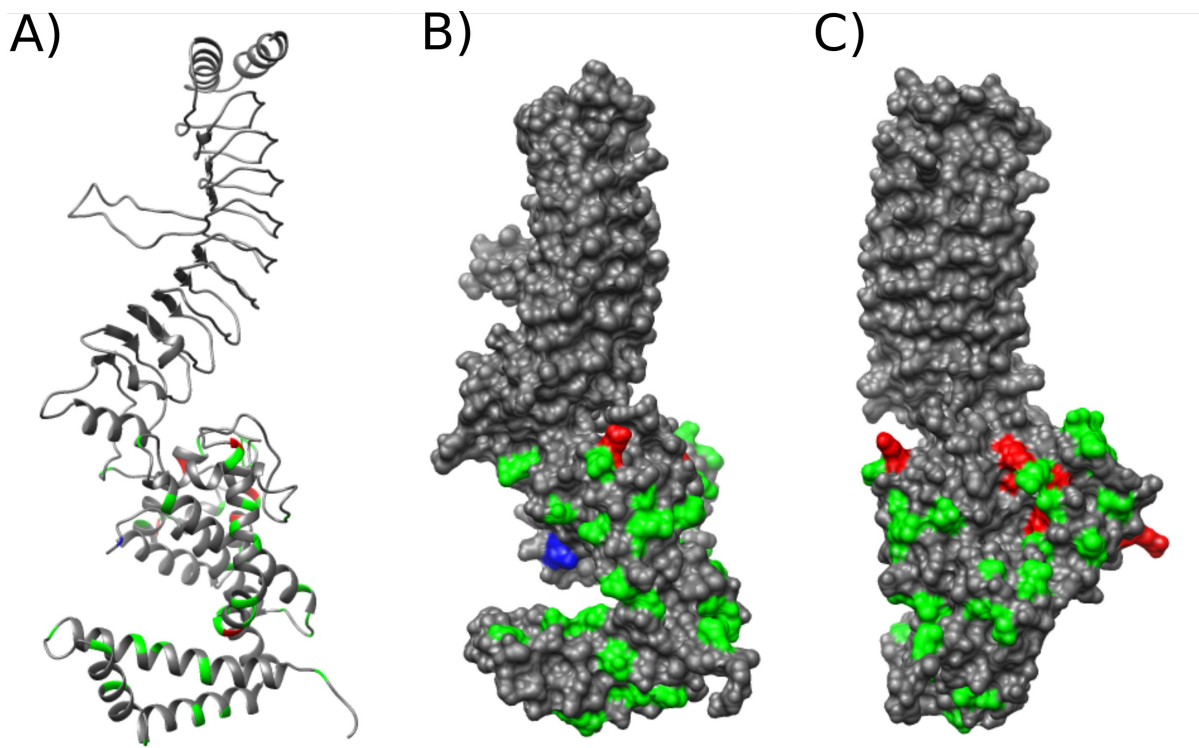
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**Supplementary Figure S2. Abundance of the *ipaH* family members in *Shigella* clades.** The notation as in **Figure 3**. Black frames indicate duplications. Panels (a), (b), and (c) reflect three major tree clades.



**D)**

ShigellaCdomain	GPQIYFSMSDGQNTLHRPLADAVTAWFPENKQSDVSOIWHAFEEEHANTFSAFLDRLS
Non-humanCdomain1	GPQIHFSMSDGQHTSVRPLPEAVAAWFPQNKQSDVSOIWLAFEREHANTFSAFLDRLA
Non-humanCdomain2	GPQIHFSMSDGQHTPVRSLPEAVAAWFPESLRSEVSQRWAAFTDEENAATFSAFLDRLA
ShigellaCdomain	DTV SARNTSGFRQVAWLEKLS TSAELRQQSFAVAADATESCEDRVALTWNLRKTLV
Non-humanCdomain1	DTV ARNAQGFRRQVSALFLEKLS TSAELRQQSFAVAADATESCEDRVALTWNLQKSLV
Non-humanCdomain2	DTV TARNAPGFAQQVSEFLEKLSMSEALRQQCFAVAADATRSCEDRVALTWNLQKTYRV
ShigellaCdomain	HQASEGLFDNDTGALLSLGREMFRLEILEDIARDKVRTLHFVDEIEVYLAFQTMLAEKLG
Non-humanCdomain1	HQASEGLFDNDTGALLSLGREMFRLEILEDIARDKVRTLRFVDEIEVYLAFQTMLAEKLG
Non-humanCdomain2	HQASEGEFDSDLTGALLSLGREMYRLEVLEEIAREKVRTLHFVDEIEVSLAFQTMLAEKLE
ShigellaCdomain	LSTAVKEMRFYGVSGVTANDLRTAEAMVRSRENEFTDWFSLWGPWHAVLKRTEADRWAQ
Non-humanCdomain1	LSTAVKEMRFYGVSGVTENDLRTAEAMVRSRENEFTDWFALWGPWHAVLKRTEADRWAQ
Non-humanCdomain2	LSTAVREMRFYGVSGVTEDDLSSALVRVLSREEREFAEWFARWSPWHAVLKRTEAERWAR
ShigellaCdomain	AEEQKYEMLENEYQPQVADRLKASGLSGDAEREAGAVMRETEQIYRQLTDEVLAIR
Non-humanCdomain1	AEEQKYEMLENEYQPQVADRLKASGLSGDAEREAGAVMRETEQIYRQLTDEVLAIR
Non-humanCdomain2	AEEKKYEMLERKYPQRLAERLSALDLSGDGAEREAGVVRMEEIETIYRQLTTEEVSGER
ShigellaCdomain	RLPENGSRLHHS
Non-humanCdomain1	RLPENGSRLHHS
Non-humanCdomain2	RLAENRAR----

**Supplementary Figure S3. Homology modeling of IpahH from *Escherichia marmotae*.**

The predicted protein structure of *Escherichia marmotae* IpahH class 1 **(A)** as a ribbon representation; **(B)** with surface of the protein as seen from the binding site side; **(C)** with surface of the protein from the side opposite to the binding site. **(D)** Sequence alignment of three variants of the C-terminal domains from *Shigella* spp. and *Escherichia marmotae*. The active site is marked in blue. The

positions strongly shared between two domains from *E. marmotae* but diverse in *Shigella* are marked in red; the positions strongly shared between *Shigella* and *Shigella*-type domain from *E. marmotae* are marked in green.