

1 **SUPPLEMENTARY DATA**

2

3 **Figure S1. DksA is required for *S. Typhimurium* growth in minimal medium, but not in**  
4 **rich LB broth. (A)** The growth of the clinical isolates 85982 (containing N88D amino acid  
5 substitution in DksA) and 87541 (harboring a wild-type DksA) and isolate 85982 harboring pWSK29  
6 or pWSK29::*dksA*<sub>87541</sub> was compared in LB minimal medium at 37°C under aerobic growth  
7 conditions. **(B).** *S. Typhimurium* SL1344 (WT), its derivative *dksA* null mutant strain, and the *dksA*  
8 mutant harboring the plasmid pWSK29 or the *dksA* gene (from SL1344) cloned into pWSK29 were  
9 grown in LB for 16 h, washed, diluted 1:100 into M9 and grown at 37°C with aeration. Optical  
10 density (OD<sub>600</sub>) was recorded at the indicated time points. Each time point shows the mean OD<sub>600</sub> of  
11 three independent cultures and the standard error of the mean (SEM) is indicated by the error bars.

12 **Figure S2. DksA is required for *S. Typhimurium* host cells invasion, but not adhesion. *S.***  
13 ***Typhimurium* SL1344 (WT) and its derived *invA* and *dksA* null mutant strains were grown in LB at**  
14 **37°C and used to infect Caco-2 epithelial cell-line (A) and Raw 264.7 macrophage-like cells (B).**  
15 **Adhesion was determined in the presence of cytochalasin D and is shown as the percentage of cell-**  
16 **associated bacteria from the total number of CFU used to infect the cells. Invasion into HeLa cells**  
17 **(C) was determined following mild centrifugation (500 RPM for 5 min) using the gentamycin**  
18 **protection assay and is calculated as the percentage of intracellular bacteria (CFU) recovered at 2 h**  
19 **p.i from the total number of CFU used to infect the cells. Graph bars represent the mean and SEM of**  
20 **four independent infections. ANOVA with Dunnett's Multiple Comparison Test was used to**  
21 **determine differences between data sets. \*\*\*, p<0.0001; ns, not significant.**

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23 **Table S1. Bacterial strains and plasmids used in the study.**

| Strain or plasmid | Genotype and description | Reference or source |
|-------------------|--------------------------|---------------------|
|-------------------|--------------------------|---------------------|

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|  |  |            |
|--|--|------------|
| <i>S. Typhimurium</i> SL1344           | wild type Sm <sup>r</sup> <i>xyl hisG rpsL</i>                                     | SGSC       |
| <i>S. Typhimurium</i> <i>invA</i>      | SL1344 $\Delta$ <i>invA</i>  | (1)        |
| <i>S. Typhimurium</i> <i>dksA</i>      | SL1344 $\Delta$ <i>dksA</i>  | This study |
| <i>S. Typhimurium</i> <i>fliC fljB</i> | SL1344 $\Delta$ <i>fliC</i> $\Delta$ <i>fljB</i>                                   | (2)        |
| <i>S. Typhimurium</i> 85982            | clinical isolate <i>dksA</i> N88D  | This study |
| <i>S. Typhimurium</i> 87541            | clinical isolate   | This study |
| <b>Plasmids</b>                        |  |            |
| pKD3                                   |  | (3)        |
| pKD46                                  |  | (3)        |
| pCP20                                  |  | (3)        |
| pWSK29                                 | Amp <sup>r</sup> low copy number cloning<br>vector                                 | (4)        |
| pWSK129                                | Km <sup>r</sup> low copy number cloning<br>vector                                  | (4)        |
| pCS26                                  | Kan <sup>r</sup> cloning vector for<br><i>luxCDABE</i> fusion                      | (5)        |
| pWSK29:: <i>dksA</i>                   | <i>S. Typhimurium</i> SL1344 <i>dksA</i><br>cloned into pWSK29                     | This study |
| pWSK29:: <i>dksA</i> <sub>87541</sub>  | <i>S. Typhimurium</i> 87541 <i>dksA</i><br>cloned into pWSK29                      | This study |
| pCS26:: <i>PdksA</i>                   | <i>S. Typhimurium</i> SL1344 <i>dksA</i><br>regulatory region cloned into<br>pCS26 | This study |
| pCS26:: <i>PrpoD</i>                   | <i>S. Typhimurium</i> SL1344 <i>rpoD</i><br>regulatory region cloned into<br>pCS26 | (5)        |
| pDE- <i>fliC</i> ::2HA <sub>STM</sub>  | <i>S. Typhimurium</i> SL1344 <i>fliC</i><br>fused to 2HA tag cloned into<br>pWSK29 | (6)        |
| pDE- <i>sopB</i> ::2HA <sub>STM</sub>  | <i>S. Typhimurium</i> SL1344 <i>sipB</i><br>fused to 2HA tag cloned into<br>pWSK29 | (6)        |
| pDE- <i>sopE2</i> ::2HA <sub>STM</sub> | <i>S. Typhimurium</i> SL1344 <i>sopE2</i>  | (6)        |

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fused to 2HA tag cloned into  
pACYC184

24 SGSC – *Salmonella* genetic Stock Center the University of Calgary.

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26 **Table S2. Primers used in the study.**

| Primer            | Sequence 5'-3'*  |
|-------------------|--|
| P1 dksA KO        | CTGCACTCCGCCATTACAC                                      |
| P2 dksA KO cm5'   | GAAGCAGCTCCAGCCTACACATTGCCCTTCTTGCATGTTG<br>CTTCTCC      |
| P3 dksA KO        | CGCTGTGATTGCCATAAGAC                                     |
| P4 dksA KO cm3'   | CTAAGGAGGATATTCATATGCAGATGGCGGGTAAATCCCG<br>TTCGTTTCTACC |
| Clone dskA Fw     | TTTTGAGCTCAACGAACCAGTACCCATAACG                          |
| Clone dskA Rv     | TTTTTCTAGAGGTAGAAACGAACGGGATTAACC                        |
| dksA promoter Fw  | AAA <u>ACTCGAG</u> ATACGCGCAGCTATTGAGCGAG                |
| dksA promoter Rev | AAA <u>AGGATCC</u> CATGTTGCTTCTCCTTAACACGC               |
| rpoD RT-PCR F     | GGTCTGACCATCGAACAGGTG                                    |
| rpoD RT-PCR R     | ATCAGACCGATGTTGCCTTC                                     |
| invF RT-PCR F     | TGTCGCACCAGTATCAGGAG                                     |
| invF RT-PCR R     | ACTCGCAGCGTTTACGATC                                      |
| ssaR RT-PCR F     | ATGTCTTCAGGCCAGGTTTCG                                    |
| ssaR RT-PCR R     | TTCTGGACGTCTGAGTGGG                                      |
| ssrB RT-PCR F     | TGGCCTGGATATCATTCCCTC                                    |
| ssrB RT-PCR R     | TTGCAATGCCGCTAACAGAAC                                    |
| sifA RT-PCR F     | CAACTCCCCAAGGAATACG                                      |
| sifA RT-PCR R     | ATCTCTGTAAGCCGCTCTCG                                     |
| invA RT-PCR F     | TCCACGAATATGCTCCACAAG                                    |
| invA RT-PCR R     | CAGACATGCCACGGTACAAC                                     |
| sopB RT-PCR F     | GAAAATCGGCGCAAAGATATC                                    |
| sopB RT-PCR R     | TCATGATAGGGGGAAAGCAC                                     |
| sipB RT-PCR F     | GTGGGCAAAAATACGGAAG                                      |
| sipB RT-PCR R     | CCCGATACATCCATAATGC                                      |
| sopE2 RT-PCR R    | CCGACTACCCATTTTCATCG                                     |
| sopE2 RT-PCR R    | GCTTCGCATGTCTGACGAGC                                     |
| hilA RT-PCR F     | ATATGCCGTTCTGGTCATCC                                     |
| hilA RT-PCR R     | GCCCTGTCCGTACAGTGTTTC                                    |
| hilD RT-PCR F     | GAGATACCGACGCAACGAC                                      |
| hilD RT-PCR R     | CTGCGCTTTCTCTGTGGG                                       |
| hilE RT-PCR F     | CTGTACGGACAGGGCTATCG                                     |
| hilE RT-PCR R     | CACGCTCAGGCCAAAGG  |
| fliA RT-PCR F     | GATTGAATCGCTGCCGGAAC                                     |

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|               |                           |
|---------------|---------------------------|
| fliA RT-PCR R | ACTATGCAACTGGCTGACCC      |
| fliC RT-PCR F | AAGAGAGGACGTTTTGCGG       |
| fliC RT-PCR R | AGAATCCGCCTTTGTTGG        |
| flhD RT-PCR F | TGTTCCGCCTCGGTATCAAC      |
| flhD RT-PCR R | CGCGAATCCTGAGTCAAACG      |
| csgD Fw RT    | CTGCATAATATTCAACGTTCTCTGG |
| csgD Rev RT   | GCCAGTTTTCAATTTACGGTAG    |
| csgA RT Fw    | CGGCGGCAATAGTTCC          |
| csgA RT Rev   | CCGTTACCATAACCGCTCTG      |
| bcsA RT Fw    | GCTGGTGATGATCTCGTCG       |
| bcsA RT Rev   | GTTGCTAAGATGTCCCAGCTC     |
| bapA RT Fw    | CCATGAAGCAGGCGGC          |
| bapA RT Rev   | GGGATTACCGTCAGGATTGGTG    |

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27 \*The sequence of restriction sites added to the primers is underlined.

## 28 References

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- 30 1. **Galan JE, Curtiss R, 3rd.** 1991. Distribution of the invA, -B, -C, and -D genes of Salmonella  
31 typhimurium among other Salmonella serovars: invA mutants of Salmonella typhi are deficient for  
32 entry into mammalian cells. *Infect Immun* **59**:2901-2908.
- 33 2. **Elhadad D, Desai P, Rahav G, McClelland M, Gal-Mor O.** 2015. Flagellin Is Required for Host Cell  
34 Invasion and Normal Salmonella Pathogenicity Island 1 Expression by Salmonella enterica Serovar  
35 Paratyphi A. *Infect Immun* **83**:3355-3368.
- 36 3. **Datsenko KA, Wanner BL.** 2000. One-step inactivation of chromosomal genes in Escherichia coli K-12  
37 using PCR products. *Proc Natl Acad Sci U S A* **97**:6640-6645.
- 38 4. **Wang RF, Kushner SR.** 1991. Construction of versatile low-copy-number vectors for cloning,  
39 sequencing and gene expression in *Escherichia coli*. *Gene* **100**:195-199.
- 40 5. **Bjarnason J, Southward CM, Surette MG.** 2003. Genomic profiling of iron-responsive genes in  
41 Salmonella enterica serovar typhimurium by high-throughput screening of a random promoter  
42 library. *J Bacteriol* **185**:4973-4982.
- 43 6. **Elhadad D, McClelland M, Rahav G, Gal-Mor O.** 2015. Feverlike Temperature is a Virulence  
44 Regulatory Cue Controlling the Motility and Host Cell Entry of Typhoidal Salmonella. *J Infect Dis*  
45 **212**:147-156.

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