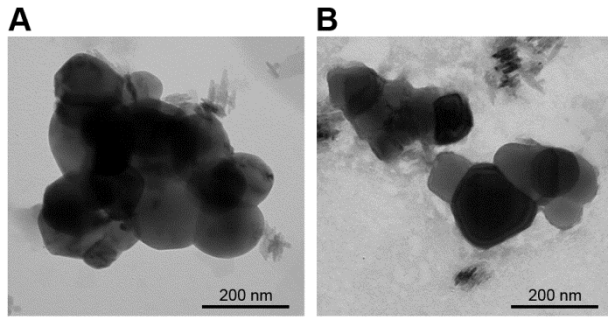
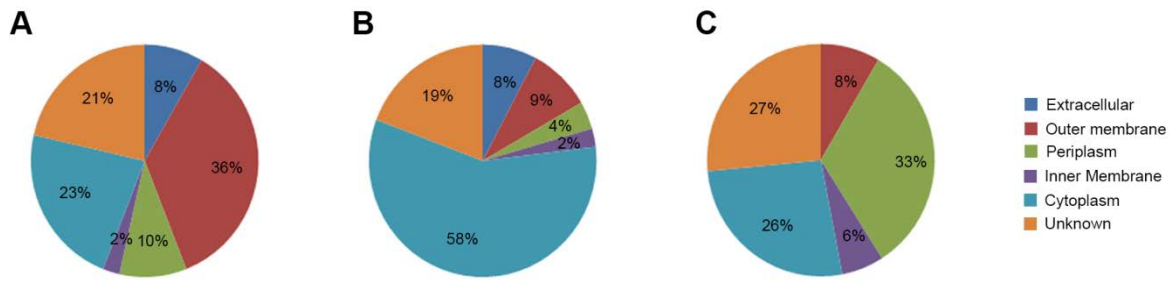


1 **Supplemental Figures and Tables**



3 Fig. S1. TEM analysis of OMVs from two different growth conditions.

4 *Salmonella* OMVs isolated from LB (A) and acidic MgM (B) conditions were mounted onto  
5 carbon-coated copper grids and subjected to negative staining using uranyl acetate. The stained  
6 grids were observed using a LIBRA 120 transmission electron microscope.

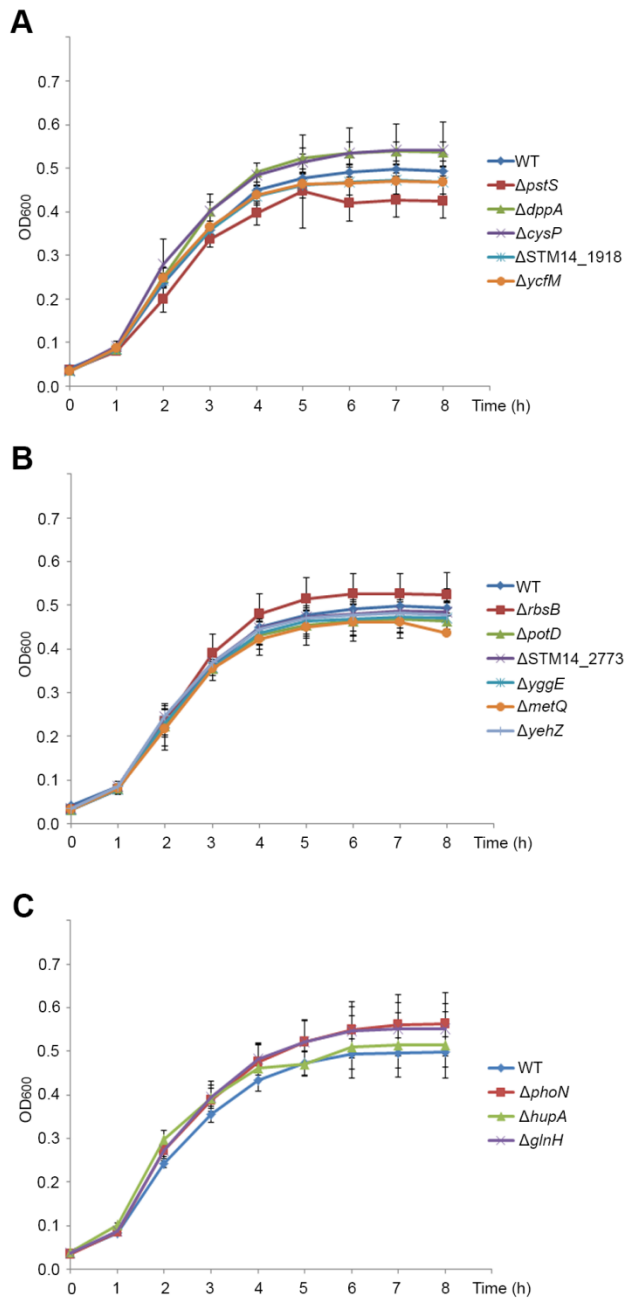


7

8 Fig. S2. Differences in the subcellular distribution of OMV-associated proteins between the two  
 9 growth conditions.

10 The PSORTb prediction was applied to three groups of proteins to determine their subcellular  
 11 locations: 84 OMV proteins found in both growth conditions (A), 78 OMV proteins detected  
 12 only in the LB condition (B), and 83 OMV proteins determined only in the acidic MgM  
 13 condition (C). The percentage of each subcellular location in each protein group is shown.

14



15

16 Fig. S3. *In vitro* growth curves of mutant strains tested in this study.

17 The *Salmonella* mutant strains that showed decrease or increase in intracellular survival were  
 18 grown under acidic MgM conditions to compare their growth *in vitro*: five (A) and six (B)

19 mutant strains that exhibited attenuated and higher intracellular survival, respectively, in Fig. 3A,  
20 and three (C) strains that exhibited impaired survival inside macrophages in Fig. 4B. Their  
21 average growth curves (and standard deviations) from three independent experiments are plotted.  
22 ANOVA was applied for the statistical analysis of the data from each time point, and there was  
23 no significant difference in the growth between the mutants and the wild-type strain ( $P < 0.05$ ).

24

Table S1. Primer sequences used in this study

Gene	Forward (5' to 3')	Reverse (5' to 3')	Purpose
<i>tbpA</i>	TCTCAAGTCCTTTGCCACTCTTAACTGAGGTGCAAAG TGGTGTAGGCTGGAGCTGCTTC	ATTCGCTAATCCATGCCTGGCGTTGTGCTGCCACTTGTT GTTCCGGGGATCCGTCGACCT	Deletion
<i>metQ</i>	GTAAACACAACACAAATACTCATTAAAGGAAATAAGCA TGGTGTAGGCTGGAGCTGCTTC	GGAATCAGCCTAAAACCTACCAGCCTTTCACCGCGCCG CCTTCCGGGGATCCGTCGACCT	Deletion
STM14_0360	ACTTGTCTTTTAGCCCAATATTAAGGCAGGTTCTGAAAT GGTGTAGGCTGGAGCTGCTTC	GTGTTTAAAAGGCGTAAGTAATGCCGAGCATGAAGTCA TTTCCGGGGATCCGTCGACCT	Deletion
<i>foxA</i>	CATCTCTAAAAGGTAATAATTCTTATTTACAATAAAGAT GGTGTAGGCTGGAGCTGCTTC	CGGACGATAAGCGTTATCAAAACGCCCATGACACGCTG CCTTCCGGGGATCCGTCGACCT	Deletion
<i>sfbA</i>	TCCGGCACAGCATCACACTATTTAAAATGGAGAAATTAT GGTGTAGGCTGGAGCTGCTTC	ATGGCCACCGCTGCGATCAGGGTGTGCGGGTCATCCAT TCTTCCGGGGATCCGTCGACCT	Deletion
<i>fepA</i>	TGGCTTATGTGGCTAAAGAAAAGCAGGATATACAATGA ACGTGTAGGCTGGAGCTGCTTC	GGAGGGAAGGTTGCCATCAGAAATGGGTATTAATGCTC ATTTCCGGGGATCCGTCGACCT	Deletion
<i>gltI</i>	CAACATCACAATAGCTATCAATGCGTCGACGGCGCAGA TGGTGTAGGCTGGAGCTGCTTC	TCCCATTTAGTTTTAGTTAGTTAAGCGCTTTATCATTCCG TTCCGGGGATCCGTCGACCT	Deletion
<i>fhuE</i>	TCCTGAACTTACCCCAATAACAAGCAAGGATTTTCAGA TGGTGTAGGCTGGAGCTGCTTC	GCTCTCCGACAGTCTGTCAGAACTGATAATTGGCGGTG AGTTCCGGGGATCCGTCGACCT	Deletion
<i>yefM</i>	GTCAGGCTTTATCTTTATTTGTGAGGAGTGAATTTTGAT GGTGTAGGCTGGAGCTGCTTC	CCGCACCTTTACCTGACCAGATTATCTCGCCAGTTTGCA CTTCCGGGGATCCGTCGACCT	Deletion
<i>potD</i>	CAAGGGCCGATAAGGCCCGTAATTCAGGGGACGTTAAA TGGTGTAGGCTGGAGCTGCTTC	AGGCGCTTTGGCTGAATTAGCGTCCTGCTTTTAGCTTCT GTTCCGGGGATCCGTCGACCT	Deletion
STM14_1918	GAAGCAGCTATACACGTTTTTATCAAAGGGAGTCGTCA TGGTGTAGGCTGGAGCTGCTTC	CCCCTCCATACCCTATTTACAGAGCAATGCGAATAACAT CTTCCGGGGATCCGTCGACCT	Deletion
<i>oppA</i>	AAAAACCAGTAATTATAATGAGTGGAGTACAAACACAA TGGTGTAGGCTGGAGCTGCTTC	GTCCCATGTCTTGCCATTAATGTTTGATAATATATAAGTT TTCCGGGGATCCGTCGACCT	Deletion
<i>fliY</i>	CAGTCTATGGTCATTAACGGCAATATTCGGGGTTACTAT GGTGTAGGCTGGAGCTGCTTC	CGGGCAACGTAGAACATTATTGGGTCACGTCAGCGCCA AATTCCGGGGATCCGTCGACCT	Deletion
<i>yehZ</i>	TCTCTGAAAAAGGCCGTAAGGATGAGGAAAGCATC ATGGTGTAGGCTGGAGCTGCTTC	CAGCATCACTCACAGATTACTTCACCCACCCTTTTTGTC GTTCCGGGGATCCGTCGACCT	Deletion
STM14_2773	GGTTAAAATAACTATTGACATTGAAATGGTGGTGGAG TGGTGTAGGCTGGAGCTGCTTC	TAATTGTTATTCAACTTCAGAAATTATAACTAATTGAAG CTTCCGGGGATCCGTCGACCT	Deletion

<i>cysP</i>	GACCATAAGAAAGTCATTAATTTATAAGGGTGCGCAA TGGTGTAGGCTGGAGCTGCTTC	GCAAGCATTACTTACGCCCCGCCGCCAACAGTTTGTCC AGTTCCGGGGATCCGTCGACCT	Deletion
<i>iroN</i>	TGAGGGCAACAGCGCTACTTTAGACATTATTTAGGGAA TGGTGTAGGCTGGAGCTGCTTC	CGGCGGGCATAATCCATCAAAACGAGGCCGTCACACC GGCTTCCGGGGATCCGTCGACCT	Deletion
<i>sitA</i>	TCGATGATTAATTAACCACATTGTTGCGAGGGATACTAT GGTGTAGGCTGGAGCTGCTTC	GTAATCGCAGATTGACTCATTGTTGACTCCTCAGTCCGT CTTCCGGGGATCCGTCGACCT	Deletion
<i>yggE</i>	TATATCAGGGCAATGACTGCAATATGGAGGAGAGACTG TGGTGTAGGCTGGAGCTGCTTC	CCCAGGCCGGGTGAGATTACTGCGTGCTGGCGGCCGTT GTTTCCGGGGATCCGTCGACCT	Deletion
<i>yrbC</i>	CGCGGGCGAAACGAAATAATCTCAGGAGAATTGAGGC ATGGTGTAGGCTGGAGCTGCTTC	AGTTGCGGCGTCATTACTGTTTCTCGTCCAAAGTAATTT TTTCCGGGGATCCGTCGACCT	Deletion
<i>ugpB</i>	GATATCGCGCATCCCGGCACAAAAGAGAGATAACCGA TGGTGTAGGCTGGAGCTGCTTC	TCCGGCACTTATACACTTAAGATTTGCTCGCTTTCTCAA ATTCCGGGGATCCGTCGACCT	Deletion
<i>dppA</i>	AGGGCAAACAACATACATCACAATTGGAGCAGAAGA ATGGTGTAGGCTGGAGCTGCTTC	CGCAGCGCTCTTTTAATTATTCGACAGAGACGTTTTCGA ATTCCGGGGATCCGTCGACCT	Deletion
<i>pstS</i>	TCAAACAACGATTTACCGAAACCGTGCAGGAGACATTA TGGTGTAGGCTGGAGCTGCTTC	TCCGCCAATTCGTTAATTAATACAGCGCCTTACCGTTGC TTTCCGGGGATCCGTCGACCT	Deletion
<i>rbsB</i>	CAAAAAGCAGTAACAACGACTACAGGACATCTGAAAT ATGGTGTAGGCTGGAGCTGCTTC	TGACCCGTGTCGTTTATTACTGCTTGATGACCAGTTTCA GTTCCGGGGATCCGTCGACCT	Deletion
<i>sbp</i>	CTTTGCTCATCACAACACAACATAAGCGAGTCTGGCGA TGGTGTAGGCTGGAGCTGCTTC	CGCCATTAGCGAAGTGATCTTTTTGCGCCTTCGCCAG CCTTCCGGGGATCCGTCGACCT	Deletion
<i>glnH</i>	AGGGGATCGCCCCGTGGATAGAAAAGGAAATGCTATGA AGGTGTAGGCTGGAGCTGCTTC	CCAACATCAGGTGCTTTTATTTAGGTTCTGTACCGAACC ATTCCGGGGATCCGTCGACCT	Deletion
<i>thpA</i>	CAGGCATGGATTAGCGAATGGCAACGCGCCGTCAGCC GTCTGTCTCTTATACACATCTCA	CGCGGCGGCGCACAGCCCCGGAATCAGCCAGCCGGGA ACTGTCTCTTATACACATCTGGT	CyaA' fusion
<i>metQ</i>	GCAAATAAAGTTTTTAATGGCGGCGCGGTGAAAGGCTG GCTGTCTCTTATACACATCTCA	CCTGAATAATATTACAGATTGTGGAATCAGCCTAAAACC TGTCTCTTATACACATCTGGT	CyaA' fusion
STM14_0360	GCCTCCAATGACTTCATGCTCGGCATTACTTACGCCTTT CTGTCTCTTATACACATCTCA	TCGGGAACCCACAGGACCAGCTATTTTACCGATAGTGT CTGTCTCTTATACACATCTGGT	CyaA' fusion
<i>sfbA</i>	AGCGCCTTCCAGAAACCGGAATGGATGACCGCGACAC CCCTGTCTCTTATACACATCTCA	ATATCACCTCAGAAATTGGGGATGGCCACCGCTGCGA CTGTCTCTTATACACATCTGGT	CyaA' fusion
<i>gltI</i>	AAAGCCCTGTTCAAAGCACCGAATGATAAAGCGCTTAA CCTGTCTCTTATACACATCTCA	AATCGAGAGGACAGGAGTCCCGTCCCATTTAGTTTTAG CTGTCTCTTATACACATCTGGT	CyaA' fusion
<i>wraB</i>	GGGGAATACGTCGCCGGTCTGGCAGTCAAACCTCAACG GCCTGTCTCTTATACACATCTCA	TGCTTCTTGAGTTGGCATTGCAATCCTCCTGTTGAAGA CTGTCTCTTATACACATCTGGT	CyaA' fusion

<i>yefM</i>	GAGATAATCTGGTCAGGTAAAGGTGCGGTCCAACAAC AACTGTCTCTTATACACATCTCA	GAAAATAGCGCGACAGGATCTCGTCGCGCGTTAAGGG ACTGTCTCTTATACACATCTGGT	CyaA' fusion
<i>potD</i>	ATTTATGAAGAGTATTATCAGAAGCTAAAAGCAGGACG CCTGTCTCTTATACACATCTCA	TACGTTTCATCTGTAGGCCCGACAGGCGCTTTGGCTGAA CTGTCTCTTATACACATCTGGT	CyaA' fusion
STM14_1918	GAAGCGACGCAGCCGGATGATGTTATTTCGATTGCTCT GCTGTCTCTTATACACATCTCA	AAGAGATGACTGGAGGGGTTTCCCCCTCCATACCCTAT CTGTCTCTTATACACATCTGGT	CyaA' fusion
<i>oppA</i>	GATAATATTTATGTGAAAACTTATATATTATCAAACATC TGTCTCTTATACACATCTCA	ACACCATGGGACAACCGCAGTTGTCCCATGTCTTGCCA CTGTCTCTTATACACATCTGGT	CyaA' fusion
<i>fliY</i>	GCGCTCTCTGAAAAATGGTTTGGCGCTGACGTGACCCA ACTGTCTCTTATACACATCTCA	TGCCCCGGTGGCGCACTGCCTGCCGGCAACGTAGAAC ACTGTCTCTTATACACATCTGGT	CyaA' fusion
<i>yehZ</i>	GTCGCCGCAGATTACCTCCGACAAAAAGGGTGGGTGA AGCTGTCTCTTATACACATCTCA	CGATTAACCGTGATTTTTTTTGGCAGCATCACTCACAGA CTGTCTCTTATACACATCTGGT	CyaA' fusion
STM14_2773	GGGCATAATTTTGTAGGTGCTTCAATTAGTTATAATTTCC TGTCTCTTATACACATCTCA	ACTCCTTCAGCCAGCAACTCGCTAATTGTTATTCAACTC TGTCTCTTATACACATCTGGT	CyaA' fusion
<i>glpQ</i>	TTCCCCGATAAGGCGGTCATGTTCTGCAAAAAAATGA CCTGTCTCTTATACACATCTCA	GCCCTCATCCGGCGCGTCACTTCGACTATGGCAAACCT CTGTCTCTTATACACATCTGGT	CyaA' fusion
<i>cysP</i>	CACTTTGCCAGCGGGCGGAGCTGGACAAACTGTTGG CGCTGTCTCTTATACACATCTCA	GCGTCGGGAAGAAACGGCAAGCATTACTTACGCCCG CCTGTCTCTTATACACATCTGGT	CyaA' fusion
<i>rpsP</i>	CGCGTTGCGGGCGCTGATCAAAGAAGTAAAAAAGCAG CTCTGTCTCTTATACACATCTCA	GCGGGCAGTTGCTTGCTCATCATGACCACCGTGACAGA CTGTCTCTTATACACATCTGGT	CyaA' fusion
<i>sitA</i>	TTTATTTCCCGCGCGTGGCCAGCGGAGGAAAATCGTC ACTGTCTCTTATACACATCTCA	GAGCATATACTGGTAGCCAAACGGCTCAACAAGCCAGT CTGTCTCTTATACACATCTGGT	CyaA' fusion
<i>yggE</i>	GGAACAGGGCAGACGTCGACAACGGCCGCCAGCACG CAGCTGTCTCTTATACACATCTCA	GAGAAAACGCGCCTGGAAGCGCCCAGGCCGGGTGA GACTGTCTCTTATACACATCTGGT	CyaA' fusion
<i>pgk</i>	CTGCCAGCCGTAGCGATGCTCGAAGAGCGCGCTAAGA AGCTGTCTCTTATACACATCTCA	GCGATAAATCAACGGGCAGGAATCCCTGCCCGTAACGA CTGTCTCTTATACACATCTGGT	CyaA' fusion
<i>yrbC</i>	TCTATCTCTCAACAGAAAATTACTTTGGACGAGAAACA GCTGTCTCTTATACACATCTCA	AGTGTCCGCCTCACGCGTCCAGGTGAGTTGCGGCGTC ACTGTCTCTTATACACATCTGGT	CyaA' fusion
<i>rpmD</i>	ATGGTCAACGCGTTTCCTTCATGGTTAAAGTTGAGGA GCTGTCTCTTATACACATCTCA	GAGCCTTCGGCCGGAGACAGAGTATTTAAACGCATCTC CTGTCTCTTATACACATCTGGT	CyaA' fusion
<i>ugpB</i>	AATCAGTTGCTGCGTCGTTTTGAGAAAGCGAGCAAATC TCTGTCTCTTATACACATCTCA	GGATGGCGGTGCATGCACCTTATCCGGCACTTATACACC TGTCTCTTATACACATCTGGT	CyaA' fusion
<i>pstS</i>	AAGACCAGTATAAAAGACAGCAACGGTAAGGCGCTGT ATCTGTCTCTTATACACATCTCA	AGGGCGGATAAGCGTAGCGCCATCCGCCAATTCGTAA CTGTCTCTTATACACATCTGGT	CyaA' fusion

<i>rbsB</i>	GCCAAATATCCGGTTGACCTGAAACTGGTCATCAAGCA GCTGTCTCTTATACACATCTCA	TCTGTCGCCATCAGGCCATAGTTGACCCGTGTCGTTTAC TGTCTCTTATACACATCTGGT	CyaA' fusion
<i>sbp</i>	TTCGCTAATGGCGGTACGTTTCGACCAAATCAGCAAACG CCTGTCTCTTATACACATCTCA	ACCCGGTAACATAATACGTTACCGGGTTTATAAACGGTC TGTCTCTTATACACATCTGGT	CyaA' fusion
<i>hupA</i>	GCGTTTGTCTCTGGTAAAGCTCTGAAAGACGCAGTTAA GCTGTCTCTTATACACATCTCA	ATGAGCCCCCTTCGATAAAACTGTTACAGTTATGCGTCC TGTCTCTTATACACATCTGGT	CyaA' fusion
<i>phoN</i>	AATTTATTGAGTAAAGAAGATCACCCCAAATTAATTAC CTGTCTCTTATACACATCTCA	TCATTTGCTGTGGCCAGTTTGCGGGAAGACTTTACCT CTGTCTCTTATACACATCTGGT	CyaA' fusion
<i>glnH</i>	AACGAAATCTACAAAAAATGGTTCGGTACAGAACCTAA ACTGTCTCTTATACACATCTCA	GTCCTCACTACCGGGCCACAAGCCAACATCAGGTCGTT CTGTCTCTTATACACATCTGGT	CyaA' fusion
<i>pstS</i>	GAAGACCAGTATAAAAGACAGCAACGGTAAGGCGCTG TATATTCCGGGGATCCGTCGACC	GGGCGGATAAGCGTAGCGCCATCCGCCAATTCGTTAATT AATTGTGTAGGCTGGAGCTGC	2HA fusion
<i>dppA</i>	TCCATTAGGCAAACATCACTTCGAAAACGTCTCTGTGCG AAATTCCGGGGATCCGTCGACC	CCGGCCTACACAACACCGGGGCGCAGCGCTCTTTAAT TAATTGTGTAGGCTGGAGCTGC	2HA fusion
<i>cysP</i>	CGGCGGCGAGCTGGACAAACTGTTGGCGGGCGGGGCGT AAGATTCCGGGGATCCGTCGACC	AAGCCGGGCAGCACGCGTCGGGAAGAAACGGCAAGC ATTAATTGTGTAGGCTGGAGCTGC	2HA fusion
STM14_1918	GGAAGCGACGCAGCCGGATGATGTTATTCGCATTGCTC TGATTCCGGGGATCCGTCGACC	AGAGATGACTGGAGGGGTTTCCCCCTCCATACCCTATTT AATTGTGTAGGCTGGAGCTGC	2HA fusion
<i>ycfM</i>	CGAGATAATCTGGTCAGGTAAAGGTGCGGTCCAACAAC AAATTCCGGGGATCCGTCGACC	AAAATAGCGCGACAGGATCTCGTCGCGGTTAAGGGAT TAATTGTGTAGGCTGGAGCTGC	2HA fusion
<i>rbsB</i>	GGCCAAATATCCGGTTGACCTGAAACTGGTCATCAAGC AGATTCCGGGGATCCGTCGACC	CTGTCGCCATCAGGCCATAGTTGACCCGTGTCGTTTATT AATTGTGTAGGCTGGAGCTGC	2HA fusion
<i>potD</i>	CATTTATGAAGAGTATTATCAGAAGCTAAAAGCAGGAC GCATTCCGGGGATCCGTCGACC	ACGTTTCATCTGTAGGCCCGACAGGCGCTTTGGCTGAAT TAATTGTGTAGGCTGGAGCTGC	2HA fusion
STM14_2773	AGGGCATAATTTTGTAGGTGCTTCAATTAGTTATAATTC ATTCCGGGGATCCGTCGACC	CTCCTTCAGCCAGCAACTCGCTAATTGTTATTCAACTTC AATTGTGTAGGCTGGAGCTGC	2HA fusion
<i>yggE</i>	TGGAACAGGGCAGACGTCGACAACGGCCGCCAGCACG CAGATTCCGGGGATCCGTCGACC	AGAAAACGCGGCCTGGAAGCGCCAGGCCGGGTGAGA TTAATTGTGTAGGCTGGAGCTGC	2HA fusion
<i>metQ</i>	CGCAAATAAAGTTTTTAATGGCGGCGGGTCAAAGGCT GGATTCCGGGGATCCGTCGACC	CTGAATAATATTACAGATTGTGGAATCAGCCTAAAATT AATTGTGTAGGCTGGAGCTGC	2HA fusion
<i>yehZ</i>	AGTCGCCGAGATTACCTCCGACAAAAGGGTGGGTG AAGATTCCGGGGATCCGTCGACC	GATTAACCGTGATTTTTTTGGCAGCATCACTCACAGATT AATTGTGTAGGCTGGAGCTGC	2HA fusion
<i>hupA</i>	GGCGTTTGTCTCTGGTAAAGCTCTGAAAGACGCAGTTA AGATTCCGGGGATCCGTCGACC	TGAGCCCCCTTCGATAAAACTGTTACAGTTATGCGTCTT AATTGTGTAGGCTGGAGCTGC	2HA fusion



<i>glnH</i>	TAACGAAATCTACAAAAAATGGTTCGGTACAGAACCTA AATATCCGTATGTGTTCCCTGATTATGCTAGCCTCTAATGT AGGCTGGAGCTGCTTCG	GCGTCCTCACTACCGGGCCACAAGCCAACATCAGGTC GTTATTCGGGGATCCGTGCGACC	2HA fusion
<i>phoN</i>	TAATTTATTGAGTAAAGAAGATCACCCCAAACCTTAATTA CTATCCGTATGATGTTCCCTGATTATGCTAGCCTCTGATGT AGGCTGGAGCTGCTTCG	TTTCATTTGCTGTGGCCAGTTTGCGGGAAGACTTTTAC CTATTCGGGGATCCGTGCGACC	2HA fusion
<i>tbpA</i>	TTTTAAATCGGCGTGGTTTGCG	AAACGCCTGCCAGAATGAGAAG	Diagnostic PCR
<i>metQ</i>	CGGCTATCAGTACGGTTATATTG	CAGCATTGGTGTAATCCTGAC	Diagnostic PCR
STM14_0360	AATTTGGCGAGGAGATGGATTTC	AAGTTAAGCCCATACCAGAAACG	Diagnostic PCR
<i>foxA</i>	TATCAACATGCCACTAACTTTGCG	TATGGACGAATACAGCGCATTG	Diagnostic PCR
<i>sfbA</i>	GTTGGCGTTAAGACCTCTTATC	GTACCGACAATGCCAAAAATCTC	Diagnostic PCR
<i>fepA</i>	GCCTCTTTCATTATAACCCTGTG	CAGATGTTCAGCTTTACGCTTG	Diagnostic PCR
<i>gltI</i>	ATTCTGGCACGTCTATTGCTTTG	ATACATCTACTCCGAAAAAAAAAGGG	Diagnostic PCR
<i>fhuE</i>	CGAAAAATGACTACATGCTGGAC	TAAAGAGAACATCACTAACCTGG	Diagnostic PCR
<i>ycfM</i>	GAGCCATAACCGTTCATTATC	ATGACGTAAAAAATGGGCTGGTG	Diagnostic PCR
<i>potD</i>	CAGTGAGGTAACGATTTTACGC	ATACGGTGGAAGTGAATCTTGAG	Diagnostic PCR
STM14_1918	AAGCGTATCAACGGAAAACGTG	ACATAGTTGGTTGTACAACCCG	Diagnostic PCR
<i>oppA</i>	GTTGTCAGAAATAACGTGCGAC	ATAAGAATAAACAGCGTCGGAATC	Diagnostic PCR
<i>fliY</i>	CCAGCAATATAAAGCGCATCAG	AAGCGCGTTAAGTGATGTAGTG	Diagnostic PCR
<i>yehZ</i>	GCAAGTTCAACGCTTTTATCGG	TACAAAGCACAGCGTAAACAGC	Diagnostic PCR
STM14_2773	TGAAAATGTGGTCAGAAATGAGTG	TCGCAGCAATAATAAACGTTCTG	Diagnostic PCR
<i>cysP</i>	AACGCAAAACGTCATTGATGGC	CAAACACGCCATTAATAAACGAC	Diagnostic PCR
<i>iroN</i>	ACAGAGAGTCATATTGCAAAATCC	AAAAAGTTCAGGAGACCGTGAG	Diagnostic PCR
<i>sitA</i>	TTTTTCACGAGCGATACGTTTAC	AACGCTTTAAATAACGTAGACTTAC	Diagnostic PCR
<i>yggE</i>	AACGCATTATCAACATTCTGGTTG	GAAGTTCATCACAAAATCATTGCG	Diagnostic PCR
<i>yrbC</i>	AACGTCTATCCTCAAAGATGGG	TTTTTGCCCTGGTTCACAAGGTG	Diagnostic PCR
<i>ugpB</i>	GAGAATAATGTCGTACCTATCCG	GACAAATTGGCTGGAAAAACCAA	Diagnostic PCR
<i>dppA</i>	GACATTCTATTGACAGATTGTAGG	CGGAGAATGAACTGCAACATAAC	Diagnostic PCR
<i>pstS</i>	TTGCGCAAACAGTCTAATTCATC	AACATCAATAGCACAAATCAGCGC	Diagnostic PCR
<i>rbsB</i>	TGATTCTCGGCTTCCTTAATAATG	TAAGGATATGATCGGCATTAATGC	Diagnostic PCR
<i>sbp</i>	TGTACTGATTGTTTTTGCGCGC	ATCACCGCCAGTAAAAAGTAGC	Diagnostic PCR
<i>glnH</i>	CCCTGTATCTCTACTTTGTTATTC	ACTGCATATGTCGTTCCCTGTTAC	Diagnostic PCR
<i>pstS</i>	GCGGGTCTACCGTGAAGTGG	CTTGGCCAGGAGGAGATGATCAAT	Diagnostic PCR

<i>dppA</i>	CGTATGGCGGAAATGATCCAGG	G TTCAGCCAGCAGTTGAGCATGA	Diagnostic PCR
<i>cysP</i>	TTTGCCGAGCGTGGTCTGGG	GAAACCGTTCACTGAGAACAGCG	Diagnostic PCR
STM14_1918	AAGCGCAACGCCTGTACACCAC	GCTTACCCTGAGTTACGATCGTT	Diagnostic PCR
<i>ycfM</i>	CCACTATGACTGGAACGGCG	CCGGATCGCAACACGACCAG	Diagnostic PCR
<i>rbsB</i>	TGCAAGGCATTGCCGGAACATC	CGCCCGTGCAGGCGATAAAC	Diagnostic PCR
<i>potD</i>	ATCCGGCGAATCCGTATATGGAAG	CGAGATGCCGCTTGGCATGGA	Diagnostic PCR
STM14_2773	GGGTATCTCGAAGGATGTGG	ACAATTAGCCTCCCTGTCGC	Diagnostic PCR
<i>yggE</i>	ACGGTAAAAGCATTCTGAAAGGGT	AGCCTCTCTATGAATGCCGGATG	Diagnostic PCR
<i>metQ</i>	CTGGATGAGCTCAAGGACGGTT	GGTTGCGGTGCTTTGAACGGGT	Diagnostic PCR
<i>yehZ</i>	CTCAGCCGTTATCTGAAAGAGGGC	GCCGACTCCCCACAGCATGAC	Diagnostic PCR
<i>hupA</i>	CAAGCGATAAACACATTGTAAGG	TACTTAACTGCGTCTTTCAGAG	Diagnostic PCR
<i>glnH</i>	CTAAATCAGTGCCCCAAAACGGT	GCTAGCATAATCAGGAACATCATA	Diagnostic PCR
<i>phoN</i>	TCGGGGACAAAAGTTAAACAAAATGC	GCTAGCATAATCAGGAACATCATA	Diagnostic PCR
<i>hupA</i>	GAAACGCTGGATCCCGCTATTGA	AAAACGTTCAAGCTTATGCGTCTTAC	Cloning
<i>glnH</i>	TATTGTGCACAGGATCCTTTCACG	CGGGCCACAAGCTTACATCAGGT	Cloning
<i>phoN</i>	ATGACTGATGGATCCTATCGGGGT	AGTTTGCGGGAAGCTTTTCACCTT	Cloning

1 Table S2. OMV-associated SPI-1 and SPI-2 T3SS proteins

2

14028S locus	LT2 locus	Gene name	Description	Location <sup>1</sup>	Signal peptide <sup>2</sup>
SPI-1					
STM14_3472	STM2873	<i>prgI</i>	needle complex major subunit	Unknown	yes
STM14_3484	STM2885	<i>sipB</i>	translocation machinery component	Extracellular	no
STM14_3483	STM2884	<i>sipC</i>	translocation machinery component	Extracellular	yes
STM14_3481	STM2882	<i>sipA</i>	secreted effector protein	Extracellular	yes
STM14_1237	STM1091	<i>sopB</i>	secreted effector protein	Unknown	yes
STM14_2557	STM2066	<i>sopA</i>	secreted effector protein	Unknown	yes
STM14_2244	STM1855	<i>sopE2</i>	secreted effector protein	Extracellular	yes
STM14_3482	STM2883	<i>sipD</i>	translocation machinery component	Extracellular	yes
STM14_3477	STM2878	<i>sptP</i>	protein tyrosine phosphatase, translocated protein antagonizing sopE/E2	Extracellular	yes
STM14_3476	STM2877	<i>iagB</i>	invasion protein precursor	Periplasm	no
SPI-2					
STM14_1696	STM1400	<i>sseC</i>	translocation machinery component	Cytoplasm	no
STM14_3110	STM1398	<i>sseB</i>	translocation machinery component	Unknown	yes
STM14_1697	STM1401	<i>sseD</i>	translocation machinery component	Cytoplasm	no

3

4 <sup>1</sup> Location was predicted using PSORTb ver. 3.0.2 (<http://www.psort.org/psortb/>).

5 <sup>2</sup> Secretion signal peptide was assessed using SecretomeP 2.0 (<http://www.cbs.dtu.dk/services/SecretomeP/>).

6

7 Table S3. Top 48 OMV-associated proteins with unique matches of 4 or more in acidic MgM

14028S locus	LT2 locus	Gene	Description	survival assay <sup>1</sup>	secretion assay <sup>2</sup>
STM14_0127	STM0108	<i>tbpA</i>	thiamine-binding periplasmic protein	yes	yes
STM14_0287	STM0245	<i>metQ</i>	putative outer membrane lipoprotein	yes	yes
STM14_0360	STM0306		homolog of sapA	yes	yes
STM14_0426	STM0364	<i>foxA</i>	ferrioxamine receptor	yes	
STM14_0600	STM0510	<i>sfbA</i>	putative ABC-type transport system ATPase	yes	yes
STM14_0682	STM0585	<i>fepA</i>	outer membrane receptor FepA	yes	
STM14_0773	STM0665	<i>gltI</i>	glutamate/aspartate transporter	yes	yes
STM14_1272	STM1119	<i>wraB</i>	trp-repressor binding protein		yes
STM14_1378	STM1204	<i>fhuE</i>	outer membrane receptor for Fe(III)-coprogen	yes	
STM14_1381	STM1207	<i>ycfM</i>	putative outer membrane lipoprotein	yes	yes
STM14_1397	STM1222	<i>potD</i>	spermidine/putrescine transporter	yes	yes
STM14_1696	STM1400	<i>sseC</i>	secretion system effector		
STM14_1918	STM1586		putative Periplasmic protein	yes	yes
STM14_1936	STM1599	<i>pdgL</i>	periplasmic dipeptidase		
STM14_1977	STM1633		putative Periplasmic binding protein		
STM14_2050	STM1698		putative inner membrane protein		
STM14_2110	STM1746.S	<i>oppA</i>	oligopeptide transport protein	yes	yes
STM14_2116	STM1751	<i>hms</i>	DNA-binding protein HLP-II		
STM14_2372	STM1954	<i>fliY</i>	putative Periplasmic binding transport protein	yes	yes
STM14_2669	STM2165	<i>yehZ</i>	putative ABC superfamily transport protein	yes	yes
STM14_2773	STM2245		putative outer membrane protein	yes	yes
STM14_2817	STM2282	<i>glpQ</i>	glycerophosphodiester phosphodiesterase		yes
STM14_2946	STM2395	<i>pgtE</i>	outer membrane protein E		
STM14_3002	STM2444	<i>cysP</i>	thiosulfate transport protein	yes	yes
STM14_3110	STM1398	<i>sseB</i>	secretion system effector		
STM14_3279	STM2676	<i>rpsP</i>	30S ribosomal subunit protein S16		yes
STM14_3348	STM2777	<i>iroN</i>	outer membrane receptor FepA	yes	
STM14_3458	STM2861	<i>sitA</i>	fur regulated Salmonella iron transporter	yes	yes
STM14_3705	STM3065	<i>yggE</i>	putative Periplasmic immunogenic protein	yes	yes
STM14_3709	STM3069	<i>pgk</i>	phosphoglycerate kinase		yes
STM14_3752	STM3107	<i>yggN</i>	putative Periplasmic protein		
STM14_3998	STM3310	<i>yrbC</i>	putative ABC superfamily transport protein	yes	yes
STM14_4125	STM3422	<i>rpmD</i>	50S ribosomal subunit protein L30		yes
STM14_4128	STM3425	<i>rplF</i>	50S ribosomal subunit protein L6		
STM14_4129	STM3426	<i>rpsH</i>	30S ribosomal subunit protein S8		
STM14_4157	STM3453	<i>fkpA</i>	FKBP-type peptidyl-prolyl cis-trans isomerase		
STM14_4283	STM3557	<i>ugpB</i>	sn-glycerol 3-phosphate transport protein	yes	yes
STM14_4375	STM3630	<i>dppA</i>	dipeptide transport protein	yes	
STM14_4489	STM3727	<i>rpmG</i>	50S ribosomal subunit protein L33		
STM14_4652	STM3857	<i>pstS</i>	high-affinity phosphate transporter	yes	yes
STM14_4681	STM3884	<i>rbsB</i>	D-ribose transport protein	yes	yes
STM14_4887	STM4063	<i>sbp</i>	sulfate transport protein	yes	yes
STM14_4902	STM4077	<i>yneA</i>	putative sugar transport protein		
STM14_5011	STM4170	<i>hupA</i>	transcriptional regulator HU subunit alpha		yes
STM14_5193	STM4319	<i>phoN</i>	non-specific acid phosphatase		yes

STM14_5278	STM4394	<i>rplI</i>	50S ribosomal subunit protein L9		
STM14_964	STM0830	<i>glnH</i>	glutamine high-affinity transporter	yes	yes

8

9 <sup>1</sup> *Salmonella* strains lacking OMV-associated proteins were subjected to macrophage infection to assess their  
10 survival ability.

11 <sup>2</sup> *Salmonella* strains producing CyaA'-tagged proteins were subjected to macrophage infection and the translocation  
12 of CyaA'-tagged proteins into the host cytoplasm was examined.