Supplemental Figure

Figure S1: Screening of the MGD::kan library in C2BBe1 epithelial cells. Caco-2 C2BBe1 cells were seeded in 48-well plates and infected with *S*. Typhimurium 14028s wild type (WT) or MGD::kan strain (genetic regions deleted in each MGD mutant are indicated). The MOI was 100, except where indicated by #, in which case the MOI was 1000. * indicates strains that were non-invasive or very poorly invasive. These bacteria were added to monolayers at an MOI of 100, followed by centrifugation at 600 xg for 5 min. The proportion of cytosolic:vacuolar bacteria at 7 h p.i. was determined by the CHQ resistance assay (CHQ-resistant CFU/(Total CFU-CHQ-resistant CFU)). Each data point is the average of duplicate wells from 1-5 independent experiments. The shaded area indicates 14028s wild type mean ± 2SD. Arrows indicate MGD mutants that were the focus of this study.

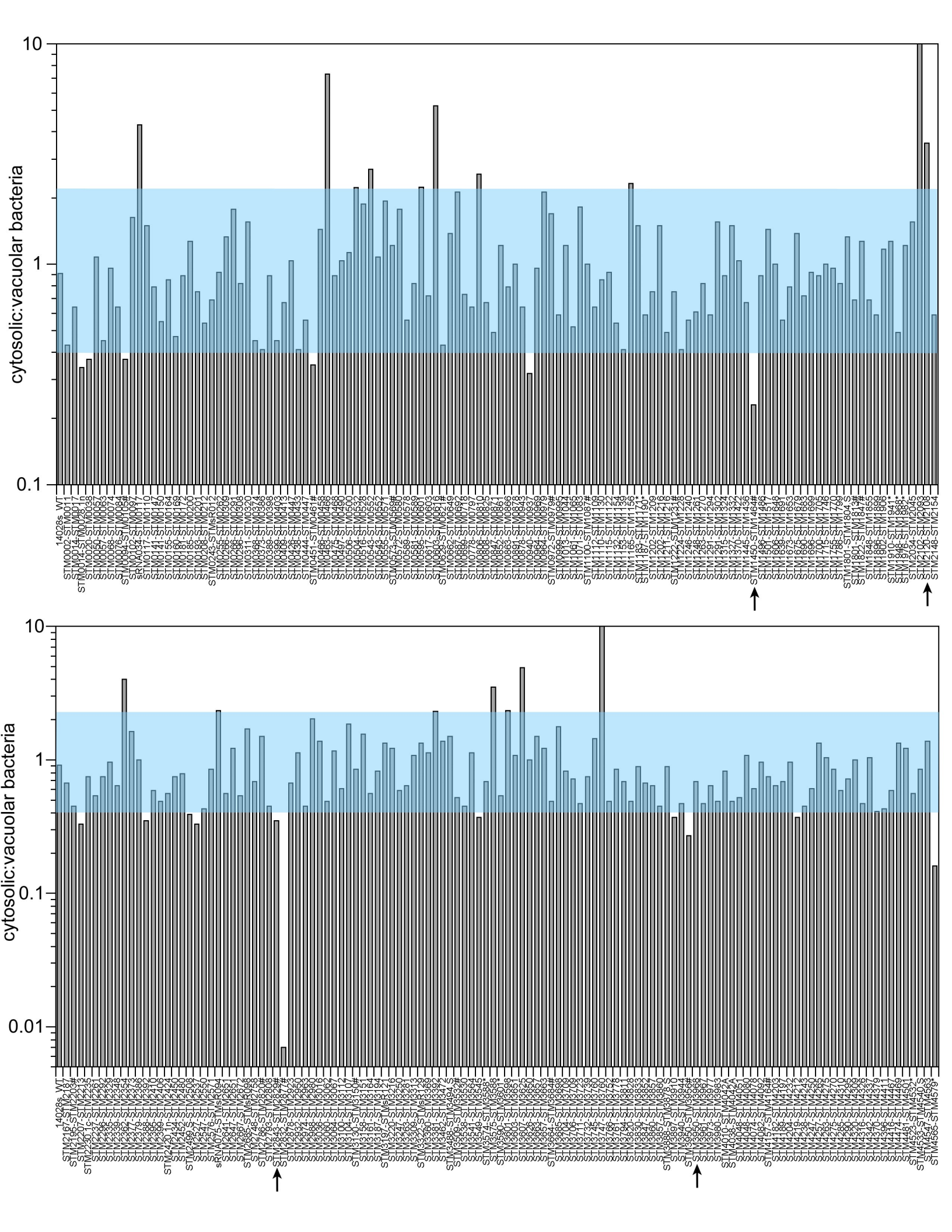
cytosolic:vacuolar bacteria
10
1
0.1
cytosolic:vacuolar bacteria
10
1
0.1
0.01

Table S1: Oligonucleotides used in this study

Oligonucleotide name	Sequence (5'-3')	For construction of
asmA F2	GGCTCTGCCCTTTGGCCAAAAA**CTACAT**GCTACCCTCAATGGACCGGCAG	Δ*asmA*
asmA R1	CTGCCGGTCCATTGAGGGTAGC**ATGTAG**TTTTTGGCCAAAGGGCAGAGCC	Δ*asmA*
asmA-XbaF1	GCTCTAGAACTGACCGACGCGCGTTTG	Δ*asmA*
asmA-XmaR2	TCCCCCCGGGGCCGTTTTCTTTCCGCTAAC	Δ*asmA*
corA OL-F	CCGGTC**ATG**CTGAGCTGGCTG**TAA**GACATTAAGGCCAGGGTG	Δ*corA*
corA OL-R	AATGTC**TTA**CAGCCAGCTCAG**CAT**GACCGGGACTCCCAATG	Δ*corA*
Xma corA	CCCCCCGGGCCATGCAGAAACTGACGCTAAC	Δ*corA*
Kpn corA new	GGGGTACCATATTGTCATGCTAACGACG	Δ*corA*
Hha OL-F	GAATTT**ATG**TCTGATATTCGT**TAA**TCACGCTACATTACTTTTTAG	Δ*hha*
Hha OL-R	GCGTG**ATT**AACGAATATCAGA**CAT**AAATTCTACCTATGATTG	Δ*hha*
XmaI hha	CCCCCCGGGCTGTTATCGCGTTTTTCACGG	Δ*hha*
KpnI hha	GGGGTACCATCCTTACTGCGTTAAAGGC	Δ*hha*
recA F2	CCGCCCCACCATCACCTGATGA**TTACAT**TATTACTCCTGTCATGCAACTT	Δ*recA*
recA R1	AAGTTGCATGACAGGAGTAATA**ATGTAA**TCATCAGGTGATGGTGGGGCGG	Δ*recA*
recA-XmaF1	TCCCCCCGGGATTGGTAAACAACAGAGTG	Δ*recA*
recA-XbaR2	GCTCTAGACTATATCCCAGACATCCC	Δ*recA*
recA-BamHIF	CCACCGGGATCCACAGCCGTAGTTGACAGG	pWSK29-*recA*
recA-KpnIR	CTTGGGGGTACCTTAACGTTTTGCTGAATGG	pWSK29-*recA*
srlR F2	ATAAGTCAGGGTAATCACGCCT**ATGTGA**TGCACTACTAAACGCGGGCCGT	Δ*srlR*
srlR R1	ACGGCCCGCGTTTAGTAGTGCA**TCACAT**AGGCGTGATTACCCTGACTTAT	Δ*srlR*
srlR-Kpn2R2	GGGGTACCGACGCCTTTCACAACATG	Δ*srlR*
srlR-Xba2F1	GCTCTAGACTGGGCATTAAGCCC	Δ*srlR*
ydgT F2	TTGATGTTAAACGCTACTTTCT**TTACAT**ATTAAATATAATGCCAACGGAG	Δ*ydgT*
ydgT R1	CTCCGTTGGCATTATATTTAAT**ATGTAA**AGAAAGTAGCGTTTAACATCAA	Δ*ydgT*
ydgT-KpnF1	GGGGTACCCCCAGAACCGCACAGTTAG	Δ*ydgT*
ydgT-XbaR2	GCTCTAGACGCGCCTGTGACAGTGTCAC	Δ*ydgT*
ydgT-KpnIF	CGGGGTACCTTGTGGAAGACGGAAAGTACC	pWSK29-*ydgT* (1)
ydgT-SacIR	CCGAGCTCAACGCTACTTTCTTTATTGCACA	pWSK29-*ydgT* (1)

Start and stop codons are in bold. Engineered restriction sites are underlined.

1. **Coombes BK, Wickham ME, Lowden MJ, Brown NF, Finlay BB.** 2005. Negative regulation of *Salmonella* pathogenicity island 2 is required for contextual control of virulence during typhoid. Proc Natl Acad Sci USA **102**:17460-17465.