

Supplementary Materials

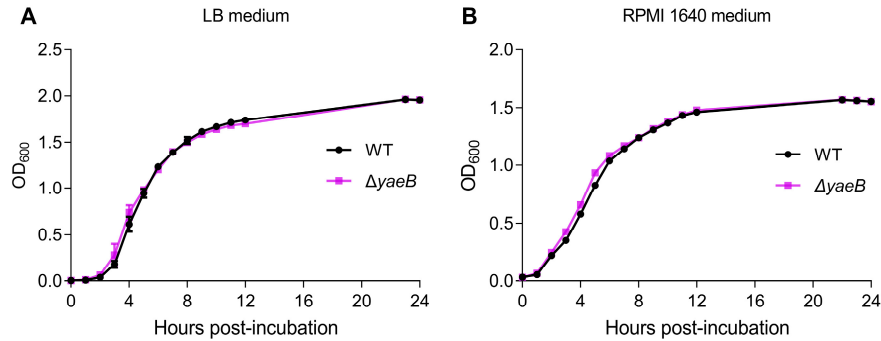


Figure S1. Deletion of *yaeB* did not influence *S. Typhimurium* growth in LB medium and RPMI-1640 medium. Overnight cultures of the WT strain and the *yaeB* mutant were subcultured 1:100 into fresh LB medium (A) or RPMI-1640 medium (B) and cultured for an additional 24 h at 37 °C with shaking at 200 rpm. The optical density at 600 nm (OD₆₀₀) of 1 ml aliquots of culture was measured regularly over this period.

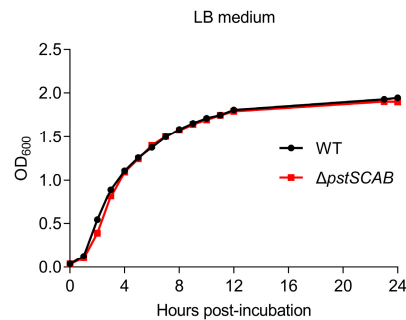


Figure S2. Deletion of *pst* genes did not influence *S. Typhimurium* growth in LB medium. Overnight cultures of the WT strain and the *pstSCAB* mutant were subcultured 1:100 into fresh LB medium and cultured for an additional 24 h at 37 °C with shaking at 200 rpm. The optical density at 600 nm (OD₆₀₀) of 1 ml aliquots of culture was measured regularly over this period.

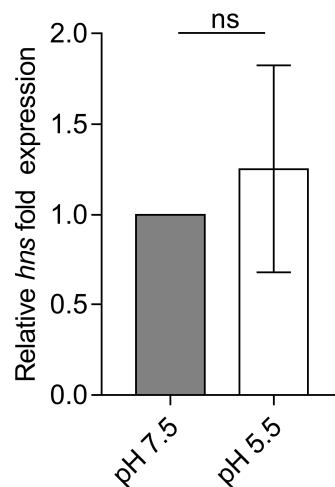


Figure S3. *hns* transcription was not induced by acidic pH. *S. Typhimurium* WT strain were cultured in N-minimal medium at pH 5.5 or pH 7.5 to the stationary phase. Fold changes of *hns* expression at pH 5.5 relative to their expression at pH 7.5 are presented. ns, not significant.

CLUSTAL 0(1.2.4) multiple sequence alignment		
WT_rpos	-----TAGCACGGCACCAGCTCTACACGCTTGCAATTTGAAATTCGTTAC	46
hns_mutant_rpos	ATCGCTACTATGGGTAGCACGGCACCAGCTCTACACGCTTGCAATTTGAAATTCGTTAC	60
14028S_genome_rpos		0
WT_rpos	AAGGGGAATCCGTAACCCGCTGCGTTATTACCGCAGCGATAAAGCGCGGAACACGG	106
hns_mutant_rpos	AAGGGGAATCCGTAACCCGCTGCGTTATTACCGCAGCGATAAAGCGCGGAACACGG	120
14028S_genome_rpos		0
WT_rpos	CTTTGACTTGTAGTTCGCTCAGGGATCAGGGTAGGAGCCACCTTATGAGTCAGAATA	166
hns_mutant_rpos	CTTTGACTTGTAGTTCGCTCAGGGATCAGGGTAGGAGCCACCTTATGAGTCAGAATA	180
14028S_genome_rpos	ATGAGTCAGAATA	13

WT_rpos	CGCTGAAGTTTCATGATTTAATGAGACGGGAATTTGATGAGACGGAGTAGAGGCTT	226
hns_mutant_rpos	CGCTGAAGTTTCATGATTTAATGAGACGGGAATTTGATGAGACGGAGTAGAGGCTT	240
14028S_genome_rpos	CGCTGAAGTTTCATGATTTAATGAGACGGGAATTTGATGAGACGGAGTAGAGGCTT	73

WT_rpos	TTGACGAAAAAGCCTTGAGTGAAGAGGAACCCAGTGATAACGACCTGGCTGAAGAAGGC	286
hns_mutant_rpos	TTGACGAAAAAGCCTTGAGTGAAGAGGAACCCAGTGATAACGACCTGGCTGAAGAAGGC	300
14028S_genome_rpos	TTGACGAAAAAGCCTTGAGTGAAGAGGAACCCAGTGATAACGACCTGGCTGAAGAAGGC	133

WT_rpos	TGTTATCGCAAGGGCCACACAGCGTGTGTGGAACGCACTCAGCTTACCTTGGTGAGA	346
hns_mutant_rpos	TGTTATCGCAAGGGCCACACAGCGTGTGTGGAACGCACTCAGCTTACCTTGGTGAGA	360
14028S_genome_rpos	TGTTATCGCAAGGGCCACACAGCGTGTGTGGAACGCACTCAGCTTACCTTGGTGAGA	193

WT_rpos	TTGGGTATTACACACTGTTAACACCGGAAGAAGTCTATTTCGGCGTCGCGCACTGC	406
hns_mutant_rpos	TTGGGTATTACACACTGTTAACACCGGAAGAAGTCTATTTCGGCGTCGCGCACTGC	420
14028S_genome_rpos	TTGGGTATTACACACTGTTAACACCGGAAGAAGTCTATTTCGGCGTCGCGCACTGC	253

WT_rpos	GTGGAGATGTGGCTTCTCGCGTCGCATGATTGAGAGTAACCTGGCTCTGGTGTAAAAA	466
hns_mutant_rpos	GTGGAGATGTGGCTTCTCGCGTCGCATGATTGAGAGTAACCTGGCTCTGGTGTAAAAA	480
14028S_genome_rpos	GTGGAGATGTGGCTTCTCGCGTCGCATGATTGAGAGTAACCTGGCTCTGGTGTAAAAA	313

WT_rpos	TTGCCCGCGTTATGGCAATCGTGGACTGGCGTTGCTGGACCTGATTGAAGAGGGCAACC	526
hns_mutant_rpos	TTGCCCGCGTTATGGCAATCGTGGACTGGCGTTGCTGGACCTGATTGAAGAGGGCAACC	540
14028S_genome_rpos	TTGCCCGCGTTATGGCAATCGTGGACTGGCGTTGCTGGACCTGATTGAAGAGGGCAACC	373

WT_rpos	TGGGGCTTATCCGTCGAGTCGAGAAGTTTGACCGGAACGGGGTTCCGCTTCTCAACAT	586
hns_mutant_rpos	TGGGGCTTATCCGTCGAGTCGAGAAGTTTGACCGGAACGGGGTTCCGCTTCTCAACAT	600
14028S_genome_rpos	TGGGGCTTATCCGTCGAGTCGAGAAGTTTGACCGGAACGGGGTTCCGCTTCTCAACAT	433

WT_rpos	ACGCAACCTGGTGATTGCGCAGACAATCGAAGCGGGGATCATGAACCAACCCGTACGA	646
hns_mutant_rpos	ACGCAACCTGGTGATTGCGCAGACAATCGAAGCGGGGATCATGAACCAACCCGTACGA	660
14028S_genome_rpos	ACGCAACCTGGTGATTGCGCAGACAATCGAAGCGGGGATCATGAACCAACCCGTACGA	493

WT_rpos	TTGCGTTGCCGATTACATTTGTTAAAGAGCTGAAGTATACCTGGCAGCCGACGTGAGT	706
hns_mutant_rpos	TTGCGTTGCCGATTACATTTGTTAAAGAGCTGAAGTATACCTGGCAGCCGACGTGAGT	720
14028S_genome_rpos	TTGCGTTGCCGATTACATTTGTTAAAGAGCTGAAGTATACCTGGCAGCCGACGTGAGT	553

WT_rpos	TGTCGCATAAAGTGGACACGAACCGAGTGGCGAAGAAATTCAGAGCAACTGGATAAAC	766
hns_mutant_rpos	TGTCGCATAAAGTGGACACGAACCGAGTGGCGAAGAAATTCAGAGCAACTGGATAAAC	780
14028S_genome_rpos	TGTCGCATAAAGTGGACACGAACCGAGTGGCGAAGAAATTCAGAGCAACTGGATAAAC	613

WT_rpos	CGGTTGATGACGTCAGCGGTATGCTTCTGCTCAACGAGCGGATTACCTGGTAGACACCC	826
hns_mutant_rpos	CGGTTGATGACGTCAGCGGTATGCTTCTGCTCAACGAGCGGATTACCTGGTAGACACCC	840
14028S_genome_rpos	CGGTTGATGACGTCAGCGGTATGCTTCTGCTCAACGAGCGGATTACCTGGTAGACACCC	673

WT_rpos	CGCTGGGCGGTGATTCCGAAAAAGCGTTGCTGGACATCTGGCCGATGAAAAAGAGAAGC	886
hns_mutant_rpos	CGCTGGGCGGTGATTCCGAAAAAGCGTTGCTGGACATCTGGCCGATGAAAAAGAGAAGC	900
14028S_genome_rpos	CGCTGGGCGGTGATTCCGAAAAAGCGTTGCTGGACATCTGGCCGATGAAAAAGAGAAGC	733

WT_rpos	GTCCGGAAGACACCAAGATGACGATATGAACAGAGCATGCTCAATGGTTGTTGCTG	946
hns_mutant_rpos	GTCCGGAAGACACCAAGATGACGATATGAACAGAGCATGCTCAATGGTTGTTGCTG	960
14028S_genome_rpos	GTCCGGAAGACACCAAGATGACGATATGAACAGAGCATGCTCAATGGTTGTTGCTG	793

WT_rpos	AAGTGAACGCCAACAGCGTGAAGTGTGGCGCCCGTTTCGGTCTGCTGGGATATGAAG	1006
hns_mutant_rpos	AAGTGAACGCCAACAGCGTGAAGTGTGGCGCCCGTTTCGGTCTGCTGGGATATGAAG	1020
14028S_genome_rpos	AAGTGAACGCCAACAGCGTGAAGTGTGGCGCCCGTTTCGGTCTGCTGGGATATGAAG	853

WT_rpos	CTGGCAGACTGGAAGATGTAGCCGCTGAATCGGCTTACGCGTCAAGCTGTTCTGCAGA	1066
hns_mutant_rpos	CTGGCAGACTGGAAGATGTAGCCGCTGAATCGGCTTACGCGTCAAGCTGTTCTGCAGA	1080
14028S_genome_rpos	CTGGCAGACTGGAAGATGTAGCCGCTGAATCGGCTTACGCGTCAAGCTGTTCTGCAGA	913

WT_rpos	TTCAAGTTGAAGGCTTCGCCCTCTCGCGAAATTCGACAGCAGGGGCTGAATATCG	1126
hns_mutant_rpos	TTCAAGTTGAAGGCTTCGCCCTCTCGCGAAATTCGACAGCAGGGGCTGAATATCG	1140
14028S_genome_rpos	TTCAAGTTGAAGGCTTCGCCCTCTCGCGAAATTCGACAGCAGGGGCTGAATATCG	973

WT_rpos	AAGCGCTGTTCGCGAGTAAGTACCCTTGTCAAAAAAGGCCAGTCTGTGACTGGCCTT	1186
hns_mutant_rpos	AAGCGCTGTTCGCGAGTAAGTACCCTTGTCAAAAAAGGCCAGTCTGTGACTGGCCTT	1200
14028S_genome_rpos	AAGCGCTGTTCGCGAGTAA-----	993

WT_rpos	TTTTTTACCGTTTGTCTTCTGCGACAGCGGGGGATACGCGACCATTTGGCGGTCAT	1246
hns_mutant_rpos	TTTTTTACCGTTTGTCTTCTGCGACAGCGGGGGATACGCGACCATTTGGCGGTCAT	1260
14028S_genome_rpos	-----	993
WT_rpos	CAATATCTTTTGGCTCATGCGAAACGCTTGTGATAGTGTTCGGCGCTGGTACGGCGTA	1306
hns_mutant_rpos	CAATATCTTTTGGCTCATGCGAAACGCTTGTGATAGTGTTCGGCGCTGGTACGGCGTA	1320
14028S_genome_rpos	-----	993
WT_rpos	ACGGTTCGGTATCGGCCAGGTATACAGACAATGCTGACACTGATATACGCTCCAGACTC	1366
hns_mutant_rpos	ACGGTTCGGTATCGGCCAGGTATACAGACAATGCTGACACTGATATACGCTCCAGACTC	1380
14028S_genome_rpos	-----	993
WT_rpos	CTTTTACCGCGGAAGTCGCC	1386
hns_mutant_rpos	CTTTTACCGCGGAAGTCGCC	1400
14028S_genome_rpos	-----	993

Figure S7. Mutation was not occurred in *rpoS* loci in the *hns* mutant strain. Sequence alignment of *rpoS* gene of the *hns* mutant, WT strain and *S. Typhimurium* ATCC 14028s strain genome using Clustal Omega (<https://www.ebi.ac.uk/Tools/msa/clustalo/>). Bases with * are strictly conserved.

CLUSTAL O(1.2.4) multiple sequence alignment

WT_phop	GCCATGACGCGGCAAATTATATCGGTGCGGCTGTGACTCTGGTCGACGAACCTTAATAA	60
hns_mutant_phop	-----ATATCGGTGCGGCTGTGACTCTGGTCGACGAACCTTAATAA	41
14028S_genome_phop	-----	0
WT_phop	TGCCTGCCTACCCTCTTTTCTTCAGAAAGAGGGTGACTATTGTCTGGTTTATTAACGT	120
hns_mutant_phop	TGCCTGCCTACCCTCTTTTCTTCAGAAAGAGGGTGACTATTGTCTGGTTTATTAACGT	101
14028S_genome_phop	-----	0
WT_phop	TTTATCCCAAAGCACCATAATCAACGCTAGACTGTTCTTATTGTTAACACAAGGAGAA	180
hns_mutant_phop	TTTATCCCAAAGCACCATAATCAACGCTAGACTGTTCTTATTGTTAACACAAGGAGAA	161
14028S_genome_phop	-----	0
WT_phop	GAGATGATGCGCGTACTGGTTGTAGAGGATAATGCATTATTACGCCACCACTGAAGGTT	240
hns_mutant_phop	GAGATGATGCGCGTACTGGTTGTAGAGGATAATGCATTATTACGCCACCACTGAAGGTT	221
14028S_genome_phop	----ATGATGCGCGTACTGGTTGTAGAGGATAATGCATTATTACGCCACCACTGAAGGTT	57

WT_phop	CAGCTCCAGGATTACAGTACCAGGTCGATGCCGAGAAAGATGCCAGGGAAGCTGATTAC	300
hns_mutant_phop	CAGCTCCAGGATTACAGTACCAGGTCGATGCCGAGAAAGATGCCAGGGAAGCTGATTAC	281
14028S_genome_phop	CAGCTCCAGGATTACAGTACCAGGTCGATGCCGAGAAAGATGCCAGGGAAGCTGATTAC	117

WT_phop	TACCTTAATGAACACCTTCCGGATATCGCTATTGTCGATTAGGTCTGCCGGATGAAGAC	360
hns_mutant_phop	TACCTTAATGAACACCTTCCGGATATCGCTATTGTCGATTAGGTCTGCCGGATGAAGAC	341
14028S_genome_phop	TACCTTAATGAACACCTTCCGGATATCGCTATTGTCGATTAGGTCTGCCGGATGAAGAC	177

WT_phop	GGCCTTTCCTTAATACGCGCTGGCGCAGCAGTGATGTTTCACTGCCGTTCTGGTGTTA	420
hns_mutant_phop	GGCCTTTCCTTAATACGCGCTGGCGCAGCAGTGATGTTTCACTGCCGTTCTGGTGTTA	401
14028S_genome_phop	GGCCTTTCCTTAATACGCGCTGGCGCAGCAGTGATGTTTCACTGCCGTTCTGGTGTTA	237

WT_phop	ACCGCGCGGAAGGCTGGCAGGATAAAGTCGAGGTTCTCAGTCCGGGGCCGATGACTAC	480
hns_mutant_phop	ACCGCGCGGAAGGCTGGCAGGATAAAGTCGAGGTTCTCAGTCCGGGGCCGATGACTAC	461
14028S_genome_phop	ACCGCGCGGAAGGCTGGCAGGATAAAGTCGAGGTTCTCAGTCCGGGGCCGATGACTAC	297

WT_phop	GTGACGAAGCCATTCCACATCGAAGAGGTAATGGCGGTATGCAGGCGTTAATGCGCGT	540
hns_mutant_phop	GTGACGAAGCCATTCCACATCGAAGAGGTAATGGCGGTATGCAGGCGTTAATGCGCGT	521
14028S_genome_phop	GTGACGAAGCCATTCCACATCGAAGAGGTAATGGCGGTATGCAGGCGTTAATGCGCGT	357

WT_phop	AATAGCGGTCTGGCTCCCAGGTGATCAACATCCGCGCTTCCAGGTGGATCTCTCAGC	600
hns_mutant_phop	AATAGCGGTCTGGCTCCCAGGTGATCAACATCCGCGCTTCCAGGTGGATCTCTCAGC	581
14028S_genome_phop	AATAGCGGTCTGGCTCCCAGGTGATCAACATCCGCGCTTCCAGGTGGATCTCTCAGC	417

WT_phop	CGGGAATTATCCGTCATGAAGAGGTATCAAACTACGGCGTTCGAATACACCATATG	660
hns_mutant_phop	CGGGAATTATCCGTCATGAAGAGGTATCAAACTACGGCGTTCGAATACACCATATG	641
14028S_genome_phop	CGGGAATTATCCGTCATGAAGAGGTATCAAACTACGGCGTTCGAATACACCATATG	477

WT_phop	GAAACGCTTATCCGTAACAACGTTAAAGTGCTCAGCAAGATTGCTGATGCTTCAGCTG	720
hns_mutant_phop	GAAACGCTTATCCGTAACAACGTTAAAGTGCTCAGCAAGATTGCTGATGCTTCAGCTG	701
14028S_genome_phop	GAAACGCTTATCCGTAACAACGTTAAAGTGCTCAGCAAGATTGCTGATGCTTCAGCTG	537

WT_phop	TATCGGATGCGGAAGTACGCGAAAGTCATACCATTTGATGTTCTCATGGGCGTCTGCGG	780
hns_mutant_phop	TATCGGATGCGGAAGTACGCGAAAGTCATACCATTTGATGTTCTCATGGGCGTCTGCGG	761
14028S_genome_phop	TATCGGATGCGGAAGTACGCGAAAGTCATACCATTTGATGTTCTCATGGGCGTCTGCGG	597

WT_phop	AAAAAATACAGGCCAGTATCCGACGATGTCATTACCACCGTACGCGGACAAGGATAT	840
hns_mutant_phop	AAAAAATACAGGCCAGTATCCGACGATGTCATTACCACCGTACGCGGACAAGGATAT	821
14028S_genome_phop	AAAAAATACAGGCCAGTATCCGACGATGTCATTACCACCGTACGCGGACAAGGATAT	657

WT_phop	CTTTTGAATTGCGCTAATGAATAAATTTGCTCGCCATTTTCTGCCGCTGCTGCGGG	900
hns_mutant_phop	CTTTTGAATTGCGCTAATGAATAAATTTGCTCGCCATTTTCTGCCGCTGCTGCGGG	881
14028S_genome_phop	CTTTTGAATTGCGCTAATGAATAAATTTGCTCGCCATTTTCTGCCGCTGCTGCGGG	675

WT_phop	TTGTTTTTTGCTGGCGACAGCCGGCTGCTGCTGCTTCTTTGGCATATGGCATAG	960
hns_mutant_phop	TTGTTTTTTGCTGGCGACAGCCGGCTGCTGCTGCTTCTTTGGCATATGGCATAG	941
14028S_genome_phop	TTGTTTTTTGCTGGCGACAGCCGGCTGCTGCTGCTTCTTTGGCATATGGCATAG	675

WT_phop	TGGCGTGCTGCGCTATAGCGTAAGTTTTGATAAAACCACTTTCGTTTGTGCGCGCGG	1020
hns_mutant_phop	TGGCGTGCTGCGCTATAGCGTAAGTTTTGATAAAACCACTTTCGTTTGTGCGCGCGG	1001
14028S_genome_phop	-----	675

WT_phop	AAAGCAACCTGTTTTATACCTCGCCAAATGGGAAAAATAAAAAATCAGCGTTGAGCTGC	1080
hns_mutant_phop	AAAGCAACCTGTTTTATACCTCGCCAAATGGGAAAAATAAAAAATCAGCGTTGAGCTGC	1061
14028S_genome_phop	-----	675

Figure S8. Mutation was not occurred in *phoP* loci in the *hns* mutant strain. Sequence alignment of *phoP* gene of the *hns* mutant, WT strain and *S. Typhimurium* ATCC 14028s strain genome using Clustal Omega (<https://www.ebi.ac.uk/Tools/msa/clustalo/>). Bases with * are strictly conserved.