

FIG 3 B anti-PhoQ Left

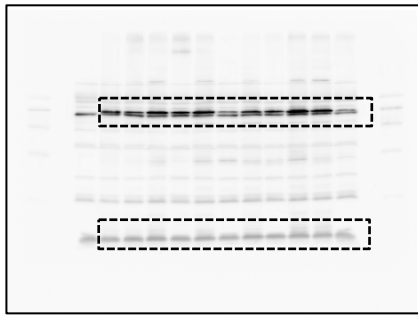


FIG 3 B anti-PhoQ Right

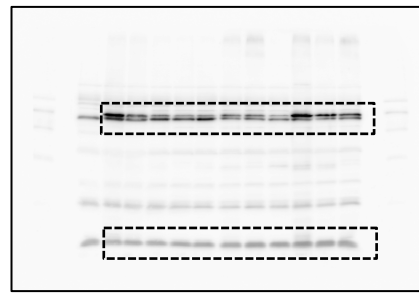


FIG 3 B anti-HA Left

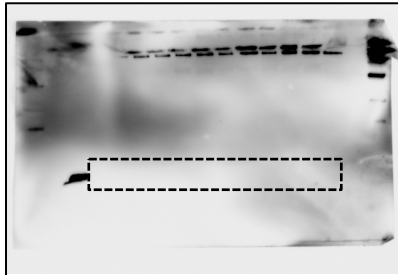


FIG 3 B anti-HA Right

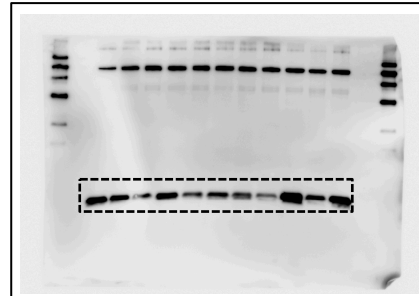


FIG 4 B anti-PhoQ Left(S43A-S158A)

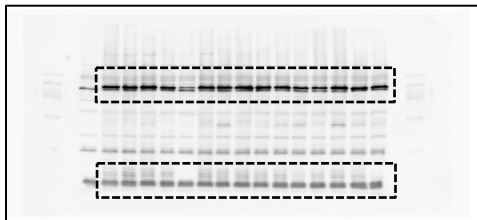


FIG 4 B anti-PhoQ Left
(D179A-S187A)

FIG 4 B anti-PhoQ Right
(Wild-T48A)

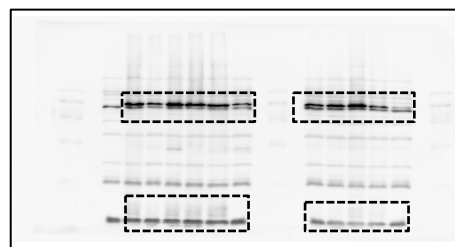


FIG 4 B anti-PhoQ Right
(L51A-S187A)

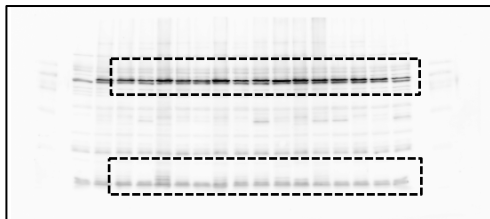


FIG 4 B anti-HA Left(S43A-S158A)

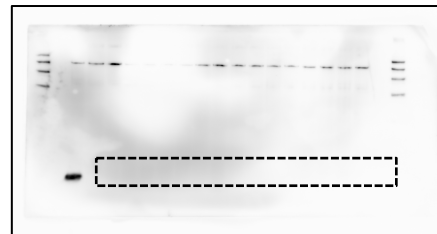


FIG 4 B anti-HA Left
(D179A-S187A)

FIG 4 B anti-HA Right
(Wild-T48A)

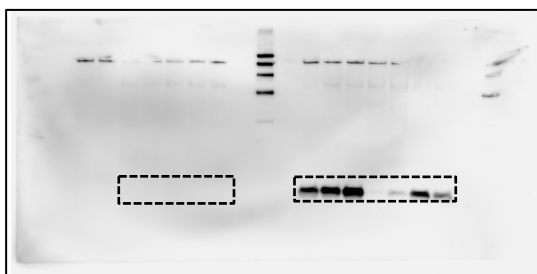


FIG 4 B anti-HARight
(L51A-S187A)

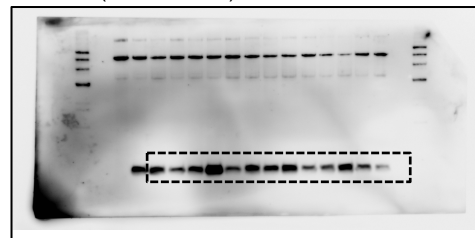


Figure S1. Complete scanned gels for western blots shown in Figures 3 and 4. Blocks in dashed line are the cropped region shown in the respective figures.

Salmonella PhoQ –SD structure (1YAX)

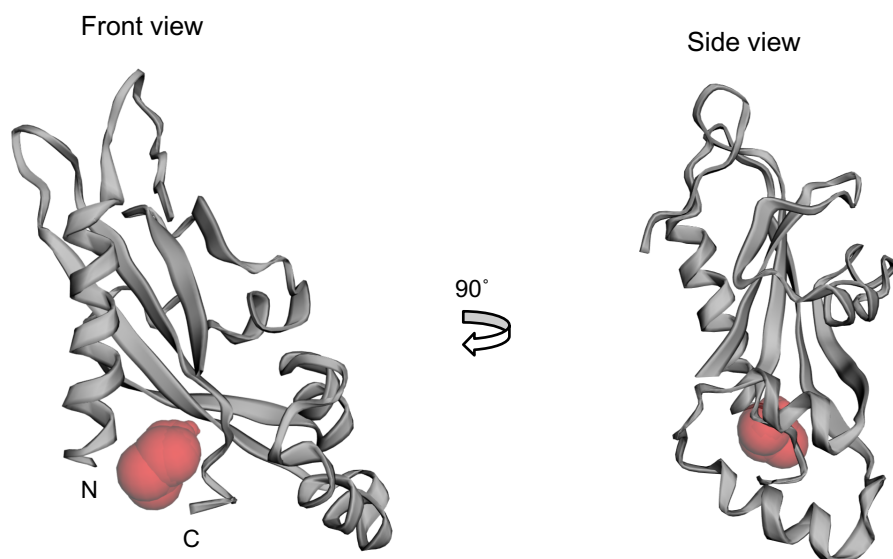


Figure S2. SD pocket in *Salmonella* PhoQ (PDB code: 1YAX) [26], estimated by CASTp program [34]. The location and volume of the pocket are shown with red balls (39.5 Å³).

TABLE S1 Primer used in this study

Primer	Sequence
pBAD F	5'-ATGCCATAGCATTTTTATCC-3'
pBAD R	5'-TCATTTAATCTGTATCAGGC-3'
pBAD F2	5'-GCTTTCGCTTGCCTACGGAA-3'
QS43AF	ATCGGTTATAGCGTCGCTTTCGATAAAACTACG-3'
QS43AR	5'-CGTAGTTTTATCGAAAGCGACGCTATAACCGAT-3'
QF44AF	5'-GGTTATAGCGTCAGTGCCGATAAAACTACGTTT-3'
QF44AR	5'-AAACGTAGTTTTATCGGCACTGACGCTATAACC-3'
QD45AF	5'-TATAGCGTCAGTTTTCGCTAAAACTACGTTTCGG-3'
QD45AR	5'-CCGAAACGTAGTTTTAGCGAAACTGACGCTATA-3'
T48A F	5'-TAAAACTGCATTTTCGGCTGT-3'
T48A R	5'-ACAGCCGAAATGCAGTTTTTA-3'
L51A F	5'-AAAACCTACGTTTCGGGCGTTACGTGGCGAGAGC-3'
L51A R	5'-GCTCTCGCCACGTAACGCCCGAAACGTAGTTTT-3'
L52A F	5'-TTTCGGCTGGCACGTGGCGA-3'
L52A R	5'-TCGCCACGTGCCAGCCGAAA-3'
QG54AF	5'-TTTCGGCTGTTACGTGCCGAGAGCAATCTGTTC-3'
QG54AR	5'-GAACAGATTGCTCTCGGCACGTAACAGCCGAAA-3'
E55A F	5'-CAGATTGCTCTCGCCAGCTAACAGCCGAAACGT-3'
E55A R	5'-ATAGAACAGATTGCTCGCGCCACGTAACAGCCG-3'
QS82AF	5'-AATATCGACAAGCAAGCCCCCACCATGACGCTA-3'
QS82AR	5'-TAGCGTCATGGTGGGGGCTTGCTTGTCGATATT-3'
QP83AF	5'-ATCGACAAGCAAAGCGCCACCATGACGCTAATT-3'
QP83AR	5'-AATTAGCGTCATGGTGGCGCTTTGCTTGTCGAT-3'
QT84AF	5'-GACAAGCAAAGCCCCGCCATGACGCTAATTTAT-3'
QT84AR	5'-ATAAATTAGCGTCATGGCGGGGCTTTGCTTGTC-3'
QF119AF	5'-CTGAAATCGAATGGTGCTCATGAAATTGAAGCG-3'
QF119AR	5'-CGCTTCAATTTTCATGAGCACCATTCGATTTTCAG-3'
E121A F	5'-AATGGTTTTTCATGCAATTGAAGCGGAT-3'
E121A R	5'-ATCCGCTTCAATTGCATGAAAACCATT-3'

TABLE S1

Primer	Sequence
QS158AF	5'-GCGGAGATGACCCACGCCGTGGCAGTAAACGTC-3'
QS158AR	5'-GACGTTTACTGCCACGGCGTGGGTCATCTCCGC-3'
D179A F	5'-ATTGTGGTGGTGCGGACCATTCCGGT-3'
D179A R	5'-ACCGGAATGGTCCGCACCACCACAAT-3'
I181A F	5'-GTGGATACCGCTCCGGTGGAG-3'
I181A R	5'-CTCCACCGGAGCGGTATCCAC-3'
V183A F	5'-GTGGATACCATTCGGCGGAGCTAAAAAGTTCC-3'
V183A R	5'-GGAACCTTTTAGCTCCGCCGGAATGGTATCCAC-3'
K186A F	5'-CCGGTGGAGCTAGCAAGTTCCTATATG-3'
K186A R	5'-CATATAGGAACTTGCTAGCTCCACCGG-3'
S187A F	5'-GTGGAGCTAAAAAGTGCCTATATGGTCTGGAGC-3'
S187A R	5'-GCTCCAGACCATATAGGCACTTTTATAGCTCCAC-3'
D179R F	5'-AAATTAACCATTGTGGTGGTGGACACCATTCCGGTGGAGCTAAAA-3'
D179R R	5'-TTTATAGCTCCACCGGAATGGTGTCCACCACCACAATGGTTAATTT-3'
D179G F	5'-ACCATTGTGGTGGTGGGTACCATTCCGGTGGAG-3'
D179G R	5'-CTCCACCGGAATGGTACCCACCACCACAATGGT-3'
D179Q F	5'-ACCATTGTGGTGGTCAATACCATTCCGGTGGAG-3'
D179Q R	5'-CTCCACCGGAATGGTATTGACCACCACAATGGT-3'
D179E F	5'-ACCATTGTGGTGGTGGAAACCATTCCGGTGGAG-3'
D179E R	5'-CTCCACCGGAATGGTTTCCACCACCACAATGGT-3'
D179N F	5'-ACCATTGTGGTGGTGAACACCATTCCGGTGGAG-3'
D179N R	5'-CTCCACCGGAATGGTGTTCACCACCACAATGGT-3'
D179L F	5'-ACCATTGTGGTGGTGCTTACCATTCCGGTGGAG-3'
D179L R	5'-CTCCACCGGAATGGTAAGCACCACCACAATGGT-3'
D179P F	5'-ACCATTGTGGTGGTGCCTACCATTCCGGTGGAG-3'
D179P R	5'-CTCCACCGGAATGGTAGGCACCACCACAATGGT-3'
D179K F	5'-ACCATTGTGGTGGTGAAAACCATTCCGGTGGAG-3'
D179K R	5'-CTCCACCGGAATGGTTTTTCACCACCACAATGGT-3'
D179W F	5'-ACCATTGTGGTGGTGTGGACCATTCCGGTGGAG-3'
D179W R	5'-CTCCACCGGAATGGTCCACACCACCACAATGGT-3'
ha-safA F	5'- CCACCACTAACCATGTATCCATATGATGTTCCAGATTATGCCGGCCATG CGACCACA-3'
ha-SafA R	5'- TGTGGTCGCATGGCCGGCATAATCTGGAACATCATATGGATACATGGTT AGTGGTGG-3'
HindIII-HA-safA	5'-AAAAAAAGCTTAAGGAGGTTTAAATTATGTATCCATATGAT-3'
safA-BamH1	5'-TTTTTGGATCCTCAGCCTTGCAAACCTATTGATA-3'