Fig S1. Different evolutionary routes of FhuA with other proteins in *Salmonella*.
(a) Maximum likelihood tree of FhuA protein. **(b)** Neighbor-joining tree of *fhuA* gene.
(c)-(e) Neighbor-joining tree of FhuC, FhuD and HrpB protein, respectively. The corresponding ortholog in *E. coli* MG1655 was used as the outgroup for each tree.
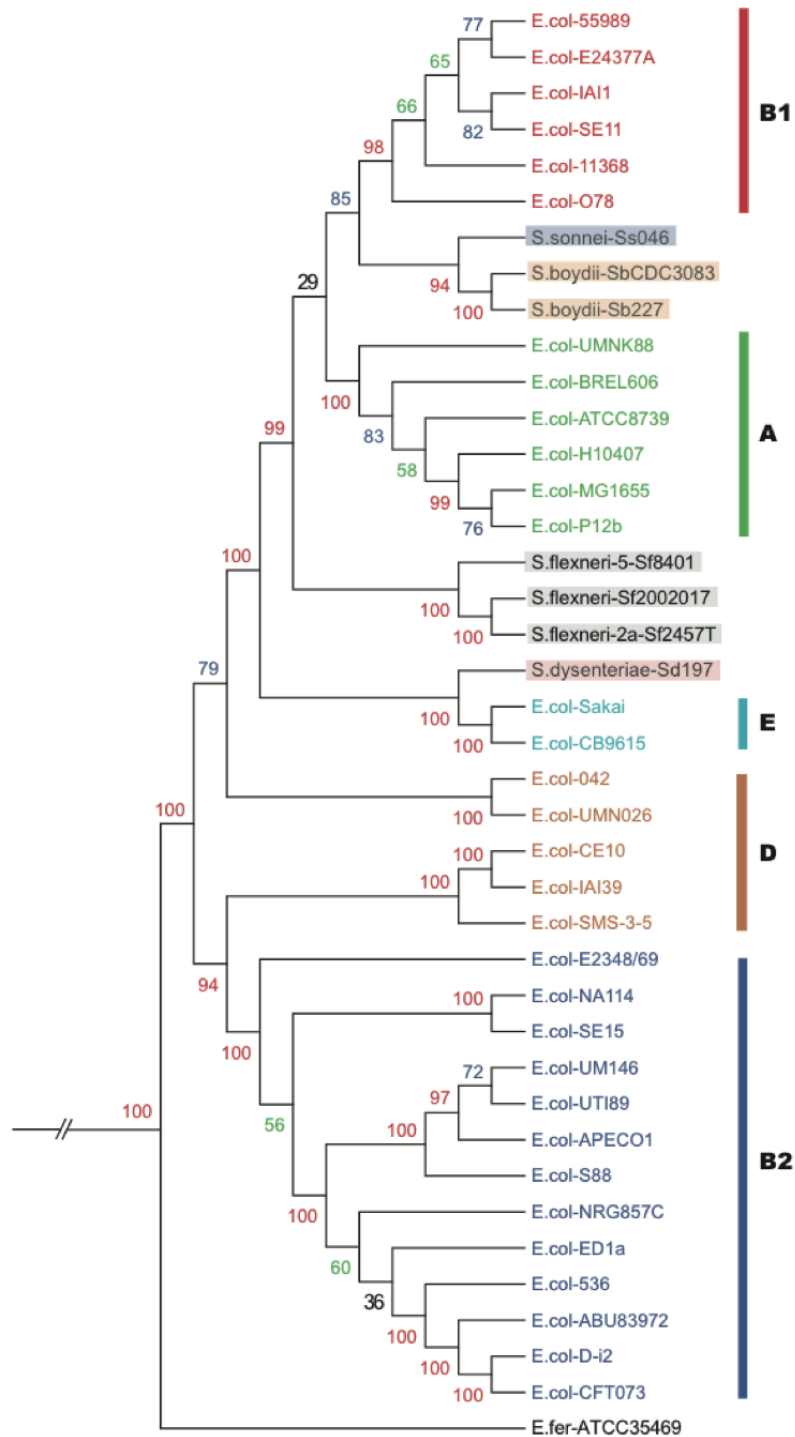
Fig S2. Phylogenomic tree of *E. coli* / *Shigella* complex. The *Enterobacteriaceae* core orthologous proteins were concatenated for each strain and used for neighbor-joining tree building. Different subgroups of *E. coli* / *Shigella* strains were shown in different front or background colors. Percentage scores from 1000 bootstrapping tests are displayed at the nodes of the trees.
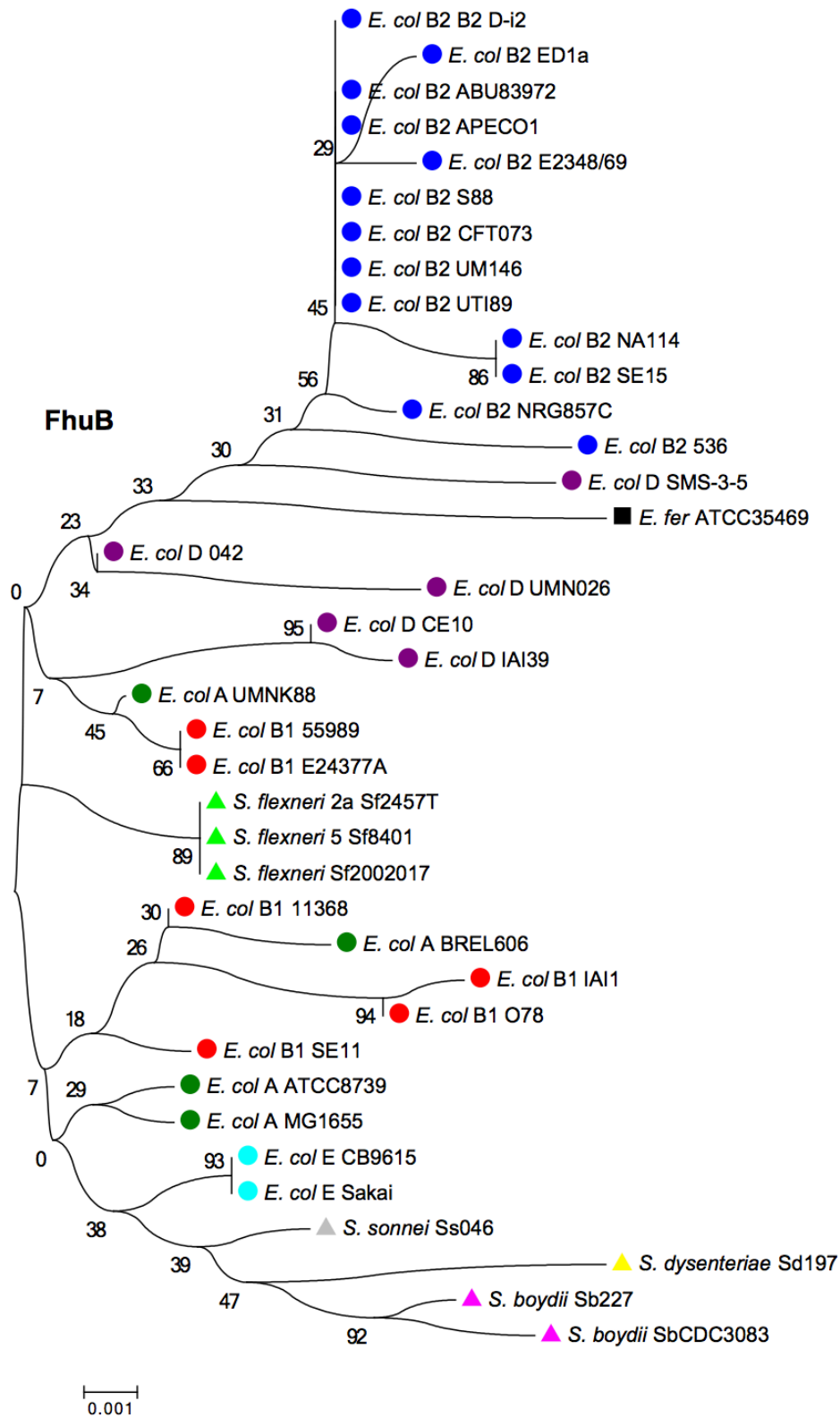
Fig S3. Neighbor-joining tree of FhuB in *E. coli* / *Shigella* complex. Different subgroups of *E. coli* / *Shigella* strains were shown in different colors or shapes. Boostrapping test score was indicated for each node.
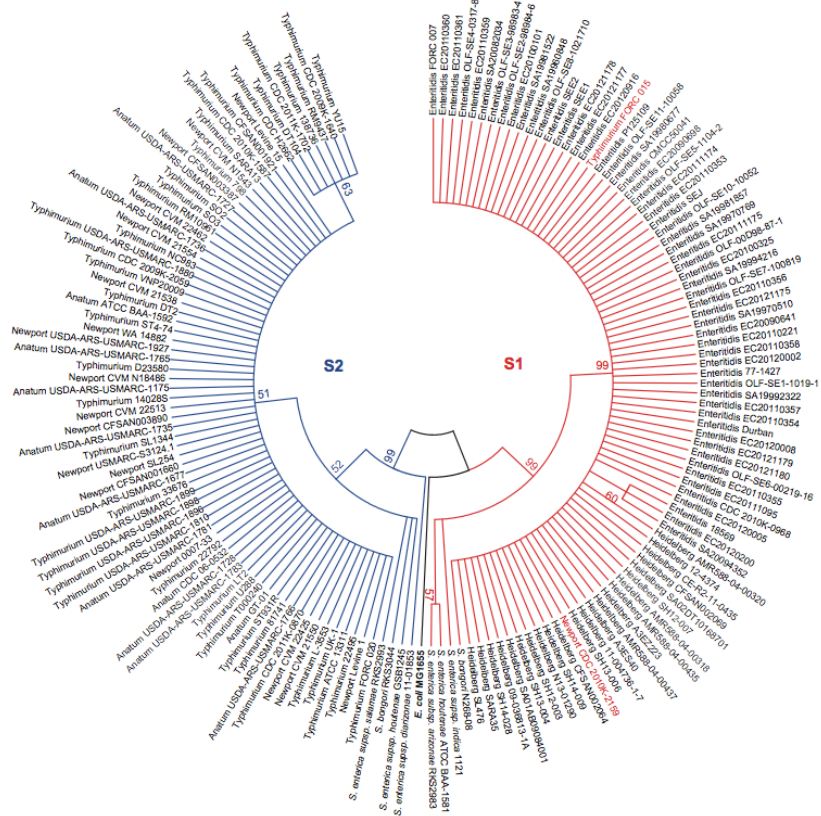
Fig S4. Distribution of FhuA clusters among *Salmonella* serovars. (a) Distribution of FhuA clusters **(a)** among the multiple strains from serovars Enteritidis, Typhimurium, Heidelberg, Newport and Anatum or **(b)** among an enlarged number of serovars.

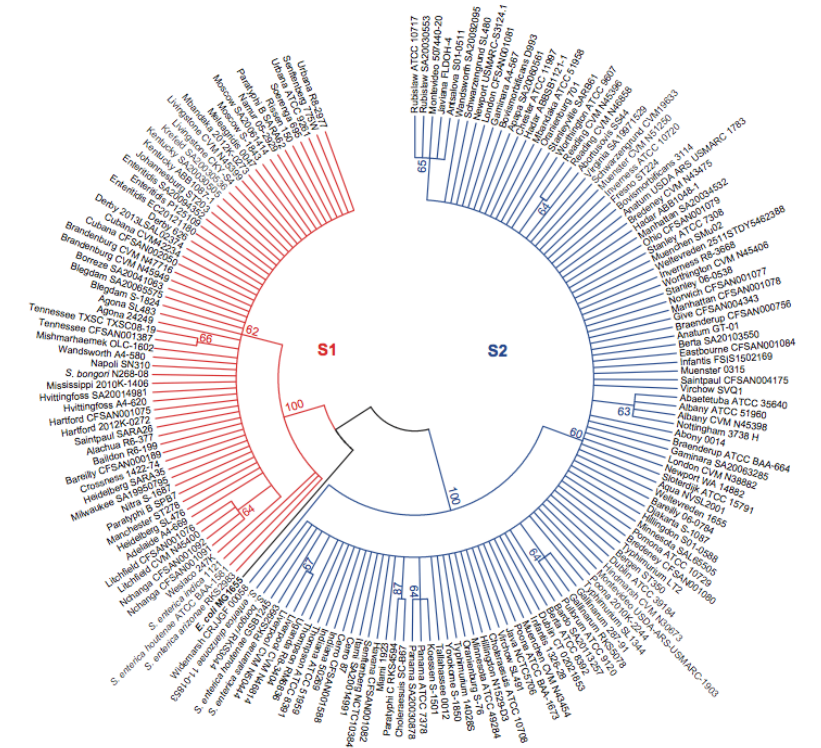| Species/Abbrv	Alignment
1. Cronobacter_sakazaki_ES15	----MARSIHTQIN-TRICRLAVLVATACGGFSASAL-AAD--GQKEHTITVS---AA-AAQESAWGPAPTIAAKRS
2. Cronobacter_turicensis_z3032	----MARSTHTQIN-TRICRLAVVVATACGGFTASAL-AAD--GQKEHTITVS---AA-AAQESAWGPAPTIAAKRS
3. Enterobacter_aerogenes_KCTC2190	----MARLKTAQPN-HSLRKIAVVVATAVSGMSVYAQ-AAE-QPK-EHTIVYT---AAPASQESAWGPAPTIAAKRS
4. Enterobacter_asburiae_LF7a	----MALSNTAQPINTSLRKIAVVVATAVAGMSAYAH-AAE-TPKKEDTITVT---AAPAAQESAWGPAPTIAAKRT
5. Erwinia_billingiae_Eb661	MATLSFDRLSLPVNTSKRR-LALLVAMTIS---------SSAYAANEQTLTVSADANSTAPQESAWGPAPTIAAKHS
6. Enterobacter_cloacae_SCF1	----MARPQTAQPVNTSLRKLAVVVATAISGLPVSAL-AAE--QPAEHTITVT---ATPTAQESAWGPSATIAAKRT
7. Erwinia_pyrifoliae_Ep196	MASTRTISSPFSSINTARCQLSVLIALSLT---------SGSAFAAEQTITLDANASSES-AESAWGPSATIAAKRS
8. Erwinia_tasmaniensis_Et199	MSIMRTISPGNSSIHPVRGRLSFLIALSLG---------CGSAAAAEQTMTVNATASSES-AESAWGPSATIAAKRS
9. Klebsiella_oxytoca_E718	----MARLKTAQPN-HSLRKIAVVVATAVSGMSVYAQ-AAV-EPK-EHTITVT---AAPAPQESAWGPAATIAAKHS
10. Klebsiella_pneumoniae_JM45	----MARPKTAQPN-HSLRKVAAVVATAVSGMSVYAQ-AAE-QPKQEHTITVV---AAPAAQESAWGPAPTIAAKHS
11. Pantoea_ananatis_LMG5342	-MTARTTTFGFPQRLFTRRPLALMIALLSGG--------ASSLAFAEQTVVVSANGGAAVGQENPWGPAATVAAKRS
12. Rahnella_aquatilis_ATCC33071	MVSQCLLSTSVRQGAFRRRTLALTITAALGSAAFYAG-AATPAAAKEDTINVTSQATAEAAPESAWGPAATIAAKHS
13. Raoultella_ornithinolytica_B6	----MARPKTAQPN-HSLRKIAVVVATAVSGMSVYAQ-AAV-EPKQEHTITVI---AAPAAQESAWGPSPTIAAKHS
14. Serratia_liquefaciens_ATCC27592	MSTKRLPS-AAKQSRSHVSGLAMTIAAALGTLAMPAFSADTKSAAKEETLTVVG-SSQSQ-QENAWGPVGTYAAKHS
15. Serratia_marcesens_WW4	MLTKRLSSSAAKQGRLPVNALAITVAAALGTLAMPAFSADAKPAAKEDTITVVGGSNTAQ-QESAWGPVGTYVAAKS
16. Serratia_plymuthica_S13	MLTKRPFSPQAMKGRSPVSGLAITIAAALGTLAMPAFSAEANPVAKEDTLTVVG-SSQPQ-QESAWGPVGTYVAKHS
17. Escherichia_coli_MG1655	----MARSKTAQPK-HSLRKIAVVVATAVSGMSVYAQ-AAV--EPKEDTITVT---AAPAPQESAWGPAATIAARQS
18. Escherichia_coli_BREL606	----MARSKTAQPK-HSLRKIAVVVATAVSGMSVYAQ-AAV--EPKEDTITVT---AAPAPQESAWGPAATIAAKHS
19. Escherichia_coli_11368	----MARSKTAQPK-HSLRKIAVVVATAVSGMSVYAQ-AAV--EPKEDTITVT---VAPAPQESAWGPAATIAARQS
20. Escherichia_coli_O78	----MARSKTAQPK-HSLRKIAVVVATAVSGMSVYAQ-AAV--EPKEDTITVT---AAPAPQESAWGPAATIAAKHS
21. Escherichia_coli_536	----MARSKTAQPK-HSLRKIAVVVATAVSGMSVYAQ-AAV--EPKEDTITVT---AAPAPQESAWGPAATIAARQS
22. Escherichia_coli_ED1a	----MAPSKTAQPK-HSLRKIAVVVATAVSGMSVYAQ-AAV--EPKEDTITVT---AAPAPQESAWGPAATIAARQS
23. Escherichia_coli_E2348-69	----MARSKTAQPK-HSLRKIAVVVATAVSGMSVYAQ-AAV-EPK-EDTITVT---AAPAPQESAWGPAATIAAKHS
24. Escherichia_ferausonii_ATCC35469	----MARSKTAQPK-HSLRKIAVVVATAVSGMSVYAQ-AAV--EPKEDTITVT---AAPAPQESAWGPAATIAAKHS
25. Shigella_boydii_Sb227	----MARSKTAQPK-HSLRKIAVVVATAVSGMSVYAQ-AAV--EPKEDTITVT---AAPAPQESAWGPAATIAARQS
26. Shigella_dysenteriae_Sd197	----MARSKTAQPK-HSLRKIAVVVATAVSGMSVYAQ-AAV--EPKEDTITVT---AAPAPQESAWGPAATIAARQS
27. Shigella_flexneri_2a_Sf2457T	----MARSKTAQPK-HSLRKIAVVVATAVSGMSVYAQ-AAV--EPKEDTITVT---AAPAPQESAWGPAATIAARQS
28. Shigella_sonnei_Ss046	----MARSKTAQPK-HSLRKIAVVVATAVSGMSVYAQ-AAV--EPKEDTITVT---AAPAPQESAWGPAATIAARQS
29. Salmonella_bongori_N268-08	----MARLKTAQPN-SSLRKIAVVVATAVSGMSVYAQ-AAV--QPKEETITVT---AAPAPQESAWGPAATIAAKQS
30. Salmonella_bongori_RKS3044	----MARLKTAQPN-SSLRKIAVVVATAVSGMSVYAQ-AAV--QPKEETITVT---AAPAPQESAWGPAATIAAKRS
31. Salmonella_enterica_LT2	----MARLKTAQPN-SSLRKIAVVVATAVSGMSVYAQ-AAV--QPKEETITVT---AAPAAQESAWGPAPTIAAKRS
32. Salmonella_enterica_SPB7	----MARLKTAQPN-SSLRKIAVVVATAVSGMSVYAQ-AAV--QPKEETITTYT---AAPAAQESAWGPAATIAARQS

Fig S5. Conservation of TonB box in FhuA proteins from *Enterobacteria*. The box was highlighted with grey background in each sequence.