

Child *et al.*, Supplemental Material

Figure. S1. ClustalW2 amino acid sequence alignments of the AcpA, AcpB, AcpC, HapA and HapB orthologs in *F. tularensis* subsp. *tularensis* Schu S4 or FSC033, subsp. *holarctica* FSC200 and subspecies *novicida* U112 strains. The putative Sec-dependent signal peptides identified using SignalP 3.0 are underlined. Sequences in blue and red respectively denote amino acid sequences deduced from the 5' and 3' fragments of interrupted (pseudo)genes in a particular subspecies. For AcpD in FSC200, a 11 amino acid intervening sequence (MCLTKYSRINY) generated at the beginning of the C-terminal fragment by chromosomal rearrangements is not shown for the purpose of alignment. For HapA and HapB, conserved motifs and catalytic histidine residues are highlighted in bold and red, respectively.

AcpA

Schu S4	<u>MKLNKITLGILSLSIATTTFA</u> TDVNNSKPNDYGTLVKIKQKLFNNANTLKTTTPIKHVVI	60
FSC200	-----MNNSKPNDYGTLVKEQKLFNNANTLKTTTPIKHVVI	37
U112	<u>MKLNKITLGILSLSIATTTFA</u> TDVNNSKPNDYGTLVKEQKLFNNANTLKTTTPIKHVVI	60
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Schu S4	IFQENNSFDRYFGMYPNAKNPEGEPKFKVAKENTPNVNGLTQKLENNPNTKNPYRLDRNF	120
FSC200	IFQENNSFDRYFGMYPNAKNPEGEPKFKVAKENTPNVNGLTQKLENNPNTKNPYRLDRNF	97
U112	IFQENNSFDRYFGMYPNAKNPEGEPKFKVAKENTPNVNGLTQKLENNPNTKNPYRLDRNF	120
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Schu S4	QPCSQNHHEYHQEISSFNGLMKNKFVEHGGHDNDTYKQNCQDQVMGYDGNVTALWNYAQ	180
FSC200	QPCSQNHHEYHQEISSFNGLMKNKFVEHGGHDNDTYKQNCQDQVMGYDGNVTALWNYAQ	157
U112	QPCSQNHHEYHQEISSFNGLMKNKFVEHGGHDNDTYKQNCQDQVMGYDGNVTALWNYAQ	180
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Schu S4	NFALNDNTFGTTFGPSTPGALNLVAGANGPAMSPSGNLENIENSYIIDDPNPYYDDCSYG	240
FSC200	NFALNDNTFGTTFGPSTPGALNLVAGANGPAMSPSGNLENIENSYIIDDPNPYYDDCSYG	217
U112	NFALNDNTFGTTFGPSTPGALNLVAGANGPAMSPSGNLENIENSYIIDDPNPYYDDCSYG	240
	*****.*****	
Schu S4	TSKSGDTNTAVAKITDGYNIGHYLTQKGITWGWFGQGFKPTSYSGKTAICDAMSTNKFGI	300
FSC200	TSKSGDTNTAVAKITDGYNIGHYLTQKGITWGWFGQGFKPTSYSGKTAICDAMSTNKFGI	277
U112	TSKSGDTNTAVAKITDGYNIGHYLTQKGITWGWFGQGFKPTSYSGKTAICDAMSTNKFGV	300
	*****:	
Schu S4	KSRDYIPHHEPFNYWKETSNPHELLAPSDDKYIGSNDQANHQYDISEFWKALDQNTMPAVS	360
FSC200	KSRDYIPHHEPFNYWKETSNPHELLAPSDDKYIGSNDQANHQYDISEFWKALDQNNMPAVS	337
U112	KSRDYIPHHEPFNYWKETSNPHELLAPSDDKYIGSNDQANHQYDISEFWKALDQNNMPAVS	360
	*****.*****	
Schu S4	YLKAPGYQDGHGGYSNPLDEQEVLVNTINRIKQSKDWDSTAI IIIYDSDGDYDHVYSPK	420
FSC200	YLKAPGYQDGHGGYSNPLDEQEVLVNTINRIKQSKDWDSTV IIIYDSDGDYDHVYSPK	397
U112	YLKAPGYQDGHGGYSNPLDEQEVLVNTINRIQSKDWDSTAI IIIYDSDGDYDHVYSPK	420
	*****:*****.*****	
Schu S4	SQFSDIKGRQGYGPRLPMLVISPYTKANYIDHSLLNQASVLKFIENWIGSVSKYSNDK	480
FSC200	SQFSDIKGRQGYGPRLPMLVISPYTKANYIDHSLLNQASVLKFIENWIGSVSKYSNDK	457
U112	SQFSDIKGRQGYGPRLPMLVISPYAKANYVDHSLLNQASVLKFIENWIGSVSKYSNDK	480
	*****:***:*****	
Schu S4	YSNNILNMFDFNKKQKTPKLIIDPKTGLVVDKLN	514
FSC200	YSNNILNMFDFNKKQKTPKLIIDPKTGLVVDKLN	491
U112	YSNNILNMFDFNKEQKTLKLIIDPKTGLVMDKLN	514
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AcpB

Schu S4 MTQQQVISYESTAHENEVELILARAKKI IQAQQSLOGNAIVLDIDETALNHYYSLKLAG 60  
 FSC200 MTQQQVISYESTAHENEVELILARAKKI IQAQQSLOGNAIVLDIDETALNHYYSLKLAG 60  
 U112 MTQQQVISYESTAHENEVELILARAKKI IQAQQSLOGNAIVLDIDETALNHYYSLKLAG 60  
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Schu S4 FPQGENHTIWNELLSRTDAYPIKATLDFYLYCLTSGLKVFFISARFAQYLESTKQALRNA 120  
 FSC200 FPQGENHTIWNELLSRTDAYPIKATLDFYLYCLTSGLKVFFISARFAQYLESTKQALRNA 120  
 U112 FPQDENHTIWNELLSRTDAYPIKATLDFYLYCLTSGLKVFFISARFAQYLESTKQALRNA 120  
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Schu S4 GYVNFEDVVFVPENIEQYNSKDFKNFKAERRAYIESLGYKILISIGDQSSDLLGGYTLYT 180  
 FSC200 GYVNFEDVVFVPENIEQYNSKDFKNFKAERRAYIESLGYKILISIGDQSSDLLGGYTLYT 180  
 U112 GYVNFEDVVFVPENIEEYNSKDFKNFKAERRAYIESLGYKILISIGDQSSDLLGGYTLYT 180  
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Schu S4 LQLPNYLYGENSRF 194  
 FSC200 LQLPNYLYGENSRF 194  
 U112 LQLPNYLYGENSRF 194  
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AcpC

Schu S4 --MRQIILIFVIAMQFCFVTAYAATCNSVNI DGVKWYHDSDEKRAIYLEIYNLAVHRIKH 58  
 FSC200 --MRQIILIFVIAMQFCFVTAYAATCNSVNI DGVKWYHDSDEKRAIYLEIYNLAVHRIKH 58  
 U112 MNLRKIVLIFVISIQFCFVTAYAATCNSVNI DGVKWYHDSDEKRAIYLEIYNLAAHRIKH 60  
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Schu S4 QVKEEHLKKGTTWGVILDIDETALDNSWLEYDNYKNYSYSEEKFRQGIIEQKAKGLPGAAG 118  
 FSC200 QVKKNILKK-----AHGVLS----- 72  
 U112 QVKKKEHLKKGTTWGVILDIDETALDNSWLEYDNYKNYSYSEEKFRQGIIEQKAKGLPGAAG 120  
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Schu S4 LTNLVHKLGGYVSFVSNRYGADPEI IKATEENLTKEDIYYDQILFYNEKAKNPKDKNSRF 178  
 FSC200 -----  
 U112 LTNLVHKLGGYVSFVSNRYGGDPEI IKATEENLTKEDIYYDQILFYNEKAKNPKDKNSRF 180

Schu S4 EAVKSGKYTDDIIVTKKLPAAHAVIAFYGDNIQDFPQMTQKNMRNVNDNHKYTIFGEKYYIF 238  
 FSC200 -----MIAYFGDNIQDFPQMTQKNMRNVNDNHKYTIFGEKYYIF 41  
 U112 EAVKSGKYTDDIIVTKKLPAAHAVIAFYGDNIQDFPQMTQKNMRNVNDNHKYTIFGEKYYIF 240  
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Schu S4 PNP MYGSWQ 247  
 FSC200 TNP MYGSWQ 50  
 U112 PNP MYGSWQ 249  
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AcpD

Schu S4 MNKKGSLSTLGFISIFFCYFFVDRQIVWFLYEHNSRQYTIMRFFSDNIISFIKDLVVF 60  
 FSC200 MNKKGSLSNLGVFSIFFCYFFVDRQIVWFLYEHNSRQYTIMRFFSDDIISFIKDLVVF 60  
 U112 MNKKGSLLIILGFISIFFCYFFVDRQIVWFLYEHNSRQYTIMRFFSDDIISFIKDLVVF 60  
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Schu S4 YIYYFIKLILKLVDTDIKILLVANAI IIGHFIKDILKGIFGRYPETFKNPNSLIRDNL 120  
 FSC200 YIYYFIKLILKLVDTDIKILLVANAI IIGYFIKDILKGIFGRYPETFKNPNSLIRDNL 120  
 U112 YVYYFIKLILKLVDDIDTKFLLVANAI IIGQFIKDILKGIFGRYPETFKNPNSLIRDNL 120  
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Schu S4 YGFN-----MWILFPKYRWLWALLAFLVVTQLLQYFHVF 124  
 FSC200 YGFN-----NINNSFSPSGHATFIFSFVSVMWILFPKYRWLWALLAFLVVTQLLQYFHVF 124  
 U112 YGFNWFDNINNSFSPSGHATFIFSFVSVMWILFPKYRWLWALLTFLVVTQLLQYFHFA 180  
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Schu S4 SDLIVGLMLGSIIGYAAQSYTKKSQTI 59  
 FSC200 SDLIVGSMGSIIGYAAQSYTKKSQII 90  
 U112 SDLIAGSMLGSIIGYAAQSYIKKSQTV 208  
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HapA

Schu S4 MRKIFTIGILTIAITPIFAKDSYNINAPQLTNANIVFAADII RHGARTSTQYDPKLEYP 60  
 FSC200 MRKIFTIGILTIAITPIFAKDSYNINAPQLTNANIVFAADII RHGARTSTQYDPKLEYP 60  
 U112 MKKIFTTIGILTIAITPIFAKDSYNINAPQLTNANIVFAADII RHGARTSTQYDPKLEYP 60  
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Schu S4 PLWNVNIPAGQLTQYGFEMERYNGEYFSKEYYKLLGNQYNREDICIVADGTNRDIVSAQ 120  
 FSC200 PLWNVNIPAGQLTQYVFEMERYNGEYFSKEYYKLLGNQYNREDICIVADDTNRDIVSAQ 120  
 U112 PLWNVNIPAGQLTQYGFEMERYNGEYFSKEYYKLLGNQYNREDICIVADGTNRDIVSAQ 120  
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Schu S4 AVLLGMLPHIKNSDVIEIIPKAKDPMLSIHKSIKNINAASGWLDEWRKIGYLSEVLVKHN 180  
 FSC200 AVLLGMLPHIKNSDVIEIIPKAKDPMLSIHKNIKINIAAPGWLDEWRKIGYLSEVLVKHN 180  
 U112 AVLLGMFPHIKNSDVIEIIPKAKDPMLSIHKNIKINIDAAPGWLDEWRKIGYLSEVLVKHN 180  
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Schu S4 YISKDDYCDTKVSTPT----- 196  
 FSC200 YISKDDYCDTKVSTPIQAYKCIQPIAKFAAQLIPLKDYCSKSGCSVFKTYNALTKSDITD 240  
 U112 YISKDDYCDTKVSTPTQAYKCIQPIAKFAAQLIPLKDYCSKSGCSVFKTYNALTKSDITD 240  
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Schu S4 ----- 300  
 FSC200 LIEVFNFNSYSAIPAQSDGFTGFTQDYLQNSINSNGAVVISQIIFDIKQIISNPNNKKY 300  
 U112 LIEVFNFNSYHSAIPAQSDGFTGFTQDYLQNSINSNGAVVISQIIFDIKQIISNPNNKKY 300

Schu S4 ----- 343  
 FSC200 PKYILFVGHDTGIRFNIA YLLSKANKIKITILTNNHGYGADLSFIVNPRVFC----- 343  
 U112 PKYILFVGHDTGIRFNIA YLLSKANKIKITILTNNPGYGADLSFRVYKTNNDYYIRVSYRN 360

Schu S4 ----- 351  
 FSC200 ----- 351  
 U112 SYNSDNNIIIFEDLFSKFEKIYFDNSQLLKQYKNCSSFQLY 402

