

Figure S1. Distribution and variability of virulence factors in 130 *L. monocytogenes* ST155 strains.

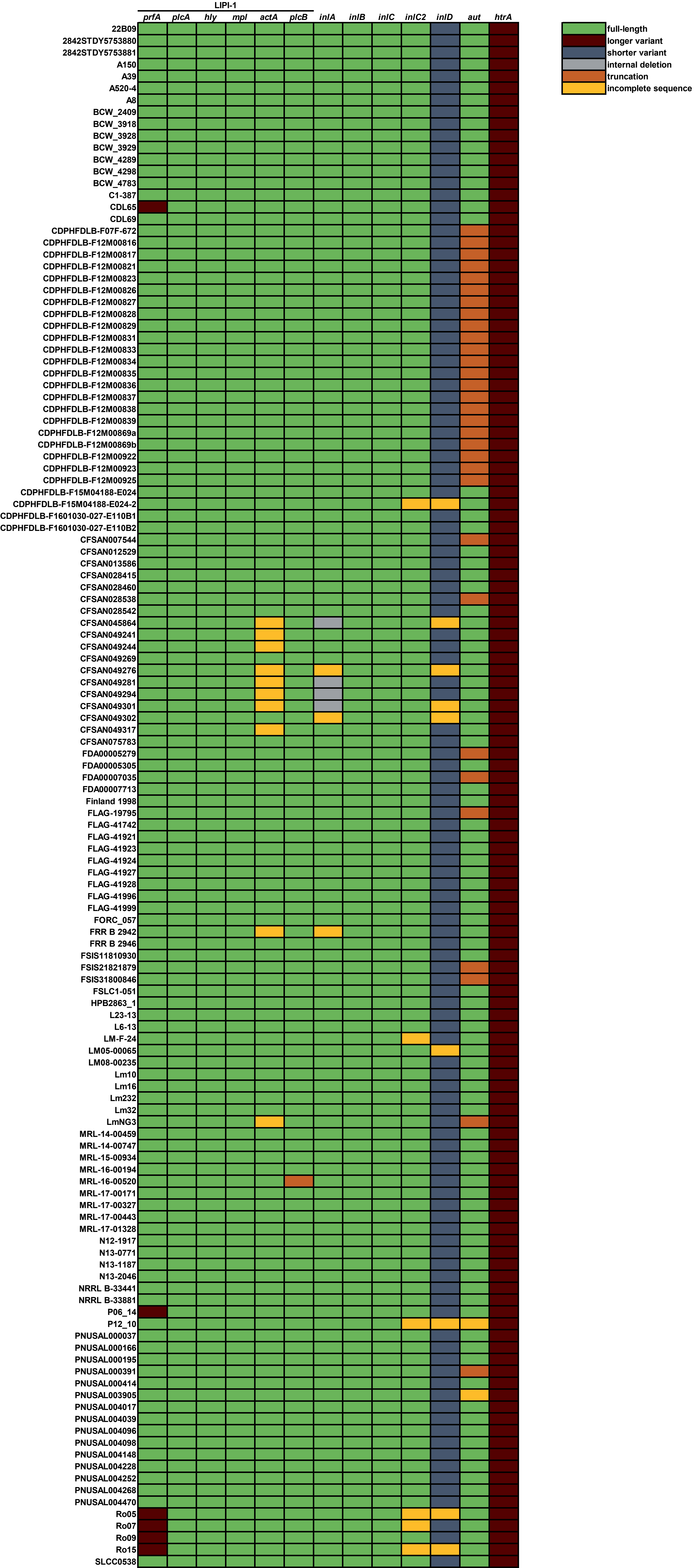


Figure S2A. Alignment of *inlA* nucleotide sequences

ScottA_ST2	1	GTGAGAA[AAAAACGATATGTATGGTTGAAAAGTATACTAGTAGCAATATTAGTATTTGGCAGTGGAGTAT
EGD-e_ST35	1	GTGAGAAAAAAACGATATGTATGGTTGAAAAGTATACTAGTAGCAATATTAGTATTTGGCAG[GGAGTAT
10403S_ST85	1	GTGAGAAAAAAACGATATGTATGGTTGAAAAGTATACTAGTAGCAATATTAGTATTTGGCAGTGGAGTAT
F2365_ST1	1	GTGAGAA[AAAAACGATATGTATGGTTGAAAAGTATACTAGTAGCAATATTAGTATTTGGCAGTGGAGTAT
L6-13	1	GTGAGAAAAAAACGATATGTATGGTTGAAAAGTATACTAGTAGCAATATTAGTATTTGGCAGTGGAGTAT
MRL-14-00459	1	GTGAGAAAAAAACGATATGTATGGTTGAAAAGTATACTAGTAGCAATATTAGTATTTGGCAGTGGAGTAT
CFSAN045864	1	GTGAGAAAAAAACGATATGTATGGTTGAAAAGTATACTAGTAGCAATATTAGTATTTGGCAGTGGAGTAT
CFSAN049281	1	GTGAGAAAAAAACGATATGTATGGTTGAAAAGTATACTAGTAGCAATATTAGTATTTGGCAGTGGAGTAT
CFSAN049294	1	GTGAGAAAAAAACGATATGTATGGTTGAAAAGTATACTAGTAGCAATATTAGTATTTGGCAGTGGAGTAT
CFSAN049301	1	GTGAGAAAAAAACGATATGTATGGTTGAAAAGTATACTAGTAGCAATATTAGTATTTGGCAGTGGAGTAT
ScottA_ST2	71	GGATTAACACGAGT[TAACGGGACAAATGCTCAGGCAGCTACAATTACACAAGATACTCCTATTAATCAGAT
EGD-e_ST35	71	GGATTAACACGAGT[TAACGGGACAAATGCTCAGGCAGCTACAATTACACAAGATACTCCTATTAATCAGAT
10403S_ST85	71	GGATTAACACGAGCAACGGGACAAATGCTCAGGCAGCTACAATTACACAAGATACTCCTATTAATCAGAT
F2365_ST1	71	GGATTAACACGAGT[TAACGGGACAAATGCTCAGGCAGCTACAATTACACAAGATACTCCTATTAATCAGAT
L6-13	71	GGATTAACACGAGCAACGGGACAAATGCTCAGGCAGCTACAATTACACAAGATACTCCTATTAATCAGAT
MRL-14-00459	71	GGATTAACACGAGCAACGGGACAAATGCTCAGGCAGCTACAATTACACAAGATACTCCTATTAATCAGAT
CFSAN045864	71	GGATTAACACGAGCAACGGGACAAATGCTCAGGCAGCTACAATTACACAAGATACTCCTATTAATCAGAT
CFSAN049281	71	GGATTAACACGAGCAACGGGACAAATGCTCAGGCAGCTACAATTACACAAGATACTCCTATTAATCAGAT
CFSAN049294	71	GGATTAACACGAGCAACGGGACAAATGCTCAGGCAGCTACAATTACACAAGATACTCCTATTAATCAGAT
CFSAN049301	71	GGATTAACACGAGCAACGGGACAAATGCTCAGGCAGCTACAATTACACAAGATACTCCTATTAATCAGAT
ScottA_ST2	141	TTTACAGAT[TCAGCTCTAGCGGAAAAAATGAAGACGGTCTTAGGAAAAACGAATGTAACAGACACGGTC
EGD-e_ST35	141	TTTACAGAT[TCAGCTCTAGCGGAAAAAATGAAGACGGTCTTAGGAAAAACGAATGTAACAGACACGGTC
10403S_ST85	141	TTTACAGACGCAGCTCTAGCGGAAAAAATGAAGACGGTCTTAGGAAAAACGAATGTAACAGACACGGTC
F2365_ST1	141	TTTACAGAT[TCAGCTCTAGCGGAAAAAATGAAGACGGTCTTAGGAAAAACGAATGTAACAGACACGGTC
L6-13	141	TTTACAGACGCAGCTCTAGCGGAAAAAATGAAGACGGTCTTAGGAAAAACGAATGTAACAGACACGGTC
MRL-14-00459	141	TTTACAGACGCAGCTCTAGCGGAAAAAATGAAGACGGTCTTAGGAAAAACGAATGTAACAGACACGGTC
CFSAN045864	141	TTTACAGACGCAGCTCTAGCGGAAAAAATGAAGACGGTCTTAGGAAAAACGAATGTAACAGACACGGTC
CFSAN049281	141	TTTACAGACGCAGCTCTAGCGGAAAAAATGAAGACGGTCTTAGGAAAAACGAATGTAACAGACACGGTC
CFSAN049294	141	TTTACAGACGCAGCTCTAGCGGAAAAAATGAAGACGGTCTTAGGAAAAACGAATGTAACAGACACGGTC
CFSAN049301	141	TTTACAGACGCAGCTCTAGCGGAAAAAATGAAGACGGTCTTAGGAAAAACGAATGTAACAGACACGGTC
ScottA_ST2	211	TC[CAAAACAGATCTAGACCAAGTTACGACGCTTCAGGCGGATAG[TTAGGGATAAAATCTATCGATGGAT
EGD-e_ST35	211	TCACAAACAGATCTAGACCAAGTTAC[ACGCTTCAGGCGGATAG[TTAGGGATAAAATCTATCGATGGAG
10403S_ST85	211	TC[CAAAACAGATCTAGACCAAGTTAC[ACGCTTCAGGCGGATAG[TTAGGGATAAAATCTATCGATGGAT
F2365_ST1	211	TC[CAAAACAGATCTAGACCAAGTTACGACGCTTCAGGCGGATAG[TTAGGGATAAAATCTATCGATGGAT
L6-13	211	TCACAAACAGATCTAGACCAAGTTACGACGCTTCAGGCGGATAGGTTAGGGATAAAATCTATCGATGGAG
MRL-14-00459	211	TCACAAACAGATCTAGACCAAGTTACGACGCTTCAGGCGGATAGGTTAGGGATAAAATCTATCGATGGAG
CFSAN045864	211	TCACAAACAGATCTAGACCAAGTTACGACGCTTCAGGCGGATAGGTTAGGGATAAAATCTATCGATGGAG
CFSAN049281	211	TCACAAACAGATCTAGACCAAGTTACGACGCTTCAGGCGGATAGGTTAGGGATAAAATCTATCGATGGAG
CFSAN049294	211	TCACAAACAGATCTAGACCAAGTTACGACGCTTCAGGCGGATAGGTTAGGGATAAAATCTATCGATGGAG
CFSAN049301	211	TCACAAACAGATCTAGACCAAGTTACGACGCTTCAGGCGGATAGGTTAGGGATAAAATCTATCGATGGAG
ScottA_ST2	281	TGGAATACTTGAACAATTTAACACAAATAAAATTTTCAGCAATAATCAACTTACGGACATAAC[CCACTTAA
EGD-e_ST35	281	TGGAATACTTGAACAATTTAACACAAATAAAATTTTCAGCAATAATCAACTTACGGACATAACGCCACTTAA
10403S_ST85	281	TGGAATACTTGAACAATTTAACACAAATAAAATTTTCAGCAATAATCAACTTACGG[ATAACGCCACTTAA
F2365_ST1	281	TGGAATACTTGAACAATTTAACACAAATAAAATTTTCAGCAATAATCAACTTACGGACATAAC[CCACTTAA
L6-13	281	TGGAATACTTGAACAATTTAACACAAATAAAATTTTCAGCAATAATCAACTTACGGACATAACGCCACTTAA
MRL-14-00459	281	TGGAATACTTGAACAATTTAACACAAATAAAATTTTCAGCAATAATCAACTTACGGACATAACGCCACTTAA
CFSAN045864	281	TGGAATACTTGAACAATTTAACACAAATAAAATTTTCAGCAATAATCAACTTACGGACATAACGCCACTTAA
CFSAN049281	281	TGGAATACTTGAACAATTTAACACAAATAAAATTTTCAGCAATAATCAACTTACGGACATAACGCCACTTAA
CFSAN049294	281	TGGAATACTTGAACAATTTAACACAAATAAAATTTTCAGCAATAATCAACTTACGGACATAACGCCACTTAA
CFSAN049301	281	TGGAATACTTGAACAATTTAACACAAATAAAATTTTCAGCAATAATCAACTTACGGACATAACGCCACTTAA
ScottA_ST2	351	A[ATTTAACTAAGTTAGTTGATATTTTGATGAATAATAATCAAAATAGCAGATATAACTCCGCTAGCTAAT
EGD-e_ST35	351	AAATTTAACTAAGTTAGTTGATATTTTGATGAATAATAATCAAAATAGCAGATATAACTCCGCTAGCTAAT
10403S_ST85	351	A[ATTTAACTAAGTTAGTTGATATTTTGATGAATAATAATCAAAATAGCAGATATAACTCCGCTAGCTAAT
F2365_ST1	351	A[ATTTAACTAAGTTAGTTGATATTTTGATGAATAATAATCAAAATAGCAGATATAACTCCGCTAGCTAAT
L6-13	351	AAATTTAACTAAGTTAGTTGATATTTTGATGAATAATAATCAAAATAGCAGATATAACTCCGCTAGCTAAT
MRL-14-00459	351	AAATTTAACTAAGTTAGTTGATATTTTGATGAATAATAATCAAAATAGCAGATATAACTCCGCTAGCTAAT
CFSAN045864	351	AAATTTAACTAAGTTAGTTGATATTTTGATGAATAATAATCAAAATAGCAGATATAACTCCGCTAGCTAAT
CFSAN049281	351	AAATTTAACTAAGTTAGTTGATATTTTGATGAATAATAATCAAAATAGCAGATATAACTCCGCTAGCTAAT
CFSAN049294	351	AAATTTAACTAAGTTAGTTGATATTTTGATGAATAATAATCAAAATAGCAGATATAACTCCGCTAGCTAAT
CFSAN049301	351	AAATTTAACTAAGTTAGTTGATATTTTGATGAATAATAATCAAAATAGCAGATATAACTCCGCTAGCTAAT
ScottA_ST2	421	TTG[CGAATCTAAGTTGGTTTGACTTTGTTCAACAATCAGATAACGGAT[ATAGACCCGCTTAAAAATCTAA
EGD-e_ST35	421	TTGACGAATCTAAGTTGGTTTGACTTTGTTCAACAATCAGATAACGGAT[ATAGACCCGCTTAAAAATCTAA
10403S_ST85	421	TTGACGAATCTAAGTTGGTTTGACTTTGTTCAACAATCAGATAAC[AGATATAGACCCGCTTAAAAATCTAA
F2365_ST1	421	TTG[CGAATCTAAGTTGGTTTGACTTTGTTCAACAATCAGATAACGGAT[ATAGACCCGCTTAAAAATCTAA
L6-13	421	TTGACGAATCTAAGTTGGTTTGACTTTGTTCAACAATCAGATAACGGATCTAGACCCGCTTAAAAATCTAA
MRL-14-00459	421	TTGACGAATCTAAGTTGGTTTGACTTTGTTCAACAATCAGATAACGGATCTAGACCCGCTTAAAAATCTAA
CFSAN045864	421	TTGACGAATCTAAGTTGGTTTGACTTTGTTCAACAATCAGATAACGGATCTAGACCCGCTTAAAAATCTAA
CFSAN049281	421	TTGACGAATCTAAGTTGGTTTGACTTTGTTCAACAATCAGATAACGGATCTAGACCCGCTTAAAAATCTAA

CFSAN049294	421	TTGACGAATCTAACTGGTTTGACTTTGTTCAACAATCAGATAACGGATCTAGACCCGCTTAAAAATCTAA
CFSAN049301	421	TTGACGAATCTAACTGGTTTGACTTTGTTCAACAATCAGATAACGGATCTAGACCCGCTTAAAAATCTAA
ScottA ST2	491	CAAATTTAAATCGGCTAGAACTATCTAGTAACACGATTAGTGATATTAGTGCGCTTTCAGGTTTAACTAG
EGD-e ST35	491	CAAATTTAAATCGGCTAGAACTATCAGTAACACGATTAGTGATATTAGTGCGCTTTCAGGTTTAACTAG
10403S ST85	491	CAAATTTAAATCGGCTAGAACTATCTAGTAACACGATTAGTGATATTAGTGCGCTTTCAGGTTTAACTA
F2365 ST1	491	CAAATTTAAATCGGCTAGAACTATCTAGTAACACGATTAGTGATATTAGTGCGCTTTCAGGTTTAACTAG
L6-13	491	CAAATTTAAATCGGCTAGAACTATCTAGTAACACGATTAGTGATATTAGTGCGCTTTCAGGTTTAACTAG
MRL-14-00459	491	CAAATTTAAATCGGCTAGAACTATCTAGTAACACGATTAGTGATATTAGTGCGCTTTCAGGTTTAACTAG
CFSAN045864	491	CAAATTTAAATCGGCTAGAACTATCTAGTAACACGATTAGTGATATTAGTGCGCTTTCAGGTTTAACTAG
CFSAN049281	491	CAAATTTAAATCGGCTAGAACTATCTAGTAACACGATTAGTGATATTAGTGCGCTTTCAGGTTTAACTAG
CFSAN049294	491	CAAATTTAAATCGGCTAGAACTATCTAGTAACACGATTAGTGATATTAGTGCGCTTTCAGGTTTAACTAG
CFSAN049301	491	CAAATTTAAATCGGCTAGAACTATCTAGTAACACGATTAGTGATATTAGTGCGCTTTCAGGTTTAACTAG
ScottA ST2	561	TCTACAGCAATTATCTTTTGGTAATCAAGTGACAGATTTAAAACCATTAGCTAATTTAACACACTAGAA
EGD-e ST35	561	TCTACAGCAATTATCTTTTGGTAATCAAGTGACAGATTTAAAACCATTAGCTAATTTAACACACTAGAA
10403S ST85	561	TCTACAGCAATTATCTTTTGGTAATCAAGTGACAGATTTAAAACCATTAGCTAATTTAACACACTAGAA
F2365 ST1	561	TCTACAGCAATTATCTTTTGGTAATCAAGTGACAGATTTAAAACCATTAGCTAATTTAACACACTAGAA
L6-13	561	TCTACAGCAATTATCTTTTGGTAATCAAGTGACAGATTTAAAACCATTAGCTAATTTAACACACTAGAA
MRL-14-00459	561	TCTACAGCAATTATCTTTTGGTAATCAAGTGACAGATTTAAAACCATTAGCTAATTTAACACACTAGAA
CFSAN045864	561	TCTACAGCAATTATCTTTTGGTAATCAAGTGACAGATTTAAAACCATTAGCTAATTTAACACACTAGAA
CFSAN049281	561	TCTACAGCAATTATCTTTTGGTAATCAAGTGACAGATTTAAAACCATTAGCTAATTTAACACACTAGAA
CFSAN049294	561	TCTACAGCAATTATCTTTTGGTAATCAAGTGACAGATTTAAAACCATTAGCTAATTTAACACACTAGAA
CFSAN049301	561	TCTACAGCAATTATCTTTTGGTAATCAAGTGACAGATTTAAAACCATTAGCTAATTTAACACACTAGAA
ScottA ST2	631	CGACTAGATATTTCAAGTAATAAGGTGTCGGATATTAGTGTTCTGGCTAAATTAACCAATTTAGAAAAGTC
EGD-e ST35	631	CGACTAGATATTTCAAGTAATAAGGTGTCGGATATTAGTGTTCTGGCTAAATTAACCAATTTAGAAAAGTC
10403S ST85	631	CGACTAGATATTTCAAGTAATAAGGTGTCGGATATTAGTGTTCTGGCTAAATTAACCAATTTAGAAAAGTC
F2365 ST1	631	CGACTAGATATTTCAAGTAATAAGGTGTCGGATATTAGTGTTCTGGCTAAATTAACCAATTTAGAAAAGTC
L6-13	631	CGACTAGATATTTCAAGTAATAAGGTGTCGGATATTAGTGTTCTGGCTAAATTAACCAATTTAGAAAAGTC
MRL-14-00459	631	CGACTAGATATTTCAAGTAATAAGGTGTCGGATATTAGTGTTCTGGCTAAATTAACCAATTTAGAAAAGTC
CFSAN045864	631	CGACTAGATATTTCAAGTAATAAGGTGTCGGATATTAGTGTTCTGGCTAAATTAACCAATTTAGAAAAGTC
CFSAN049281	631	CGACTAGATATTTCAAGTAATAAGGTGTCGGATATTAGTGTTCTGGCTAAATTAACCAATTTAGAAAAGTC
CFSAN049294	631	CGACTAGATATTTCAAGTAATAAGGTGTCGGATATTAGTGTTCTGGCTAAATTAACCAATTTAGAAAAGTC
CFSAN049301	631	CGACTAGATATTTCAAGTAATAAGGTGTCGGATATTAGTGTTCTGGCTAAATTAACCAATTTAGAAAAGTC
ScottA ST2	701	TTATCGCTACTAACAACCAAAATAAGTGATATAACTCCACTTGGGATTTTAAACAAATTTGGACGAATTATC
EGD-e ST35	701	TTATCGCTACTAACAACCAAAATAAGTGATATAACTCCACTTGGGATTTTAAACAAATTTGGACGAATTATC
10403S ST85	701	TTATCGCTACTAACAACCAAAATAAGTGATATAACTCCACTTGGGATTTTAAACAAATTTGGACGAATTATC
F2365 ST1	701	TTATCGCTACTAACAACCAAAATAAGTGATATAACTCCACTTGGGATTTTAAACAAATTTGGACGAATTATC
L6-13	701	TTATCGCTACTAACAACCAAAATAAGTGATATAACTCCACTTGGGATTTTAAACAAATTTGGACGAATTATC
MRL-14-00459	701	TTATCGCTACTAACAACCAAAATAAGTGATATAACTCCACTTGGGATTTTAAACAAATTTGGACGAATTATC
CFSAN045864	701	TTATCGCTACTAACAACCAAAATAAGTGATATAACTCCACTTGGGATTTTAAACAAATTTGGACGAATTATC
CFSAN049281	701	TTATCGCTACTAACAACCAAAATAAGTGATATAACTCCACTTGGGATTTTAAACAAATTTGGACGAATTATC
CFSAN049294	701	TTATCGCTACTAACAACCAAAATAAGTGATATAACTCCACTTGGGATTTTAAACAAATTTGGACGAATTATC
CFSAN049301	701	TTATCGCTACTAACAACCAAAATAAGTGATATAACTCCACTTGGGATTTTAAACAAATTTGGACGAATTATC
ScottA ST2	771	CTTAAATGGTAACCAAGTTAAAAGATATAGGCACATTGGCGAGTTTAAACAAACCTTACAGATTTAGATTTA
EGD-e ST35	771	CTTAAATGGTAACCAAGTTAAAAGATATAGGCACATTGGCGAGTTTAAACAAACCTTACAGATTTAGATTTA
10403S ST85	771	CTTAAATGGTAACCAAGTTAAAAGATATAGGCACATTGGCGAGTTTAAACAAACCTTACAGATTTAGATTTA
F2365 ST1	771	CTTAAATGGTAACCAAGTTAAAAGATATAGGCACATTGGCGAGTTTAAACAAACCTTACAGATTTAGATTTA
L6-13	771	CTTAAATGGTAACCAAGTTAAAAGATATAGGCACATTGGCGAGTTTAAACAAACCTTACAGATTTAGATTTA
MRL-14-00459	771	CTTAAATGGTAACCAAGTTAAAAGATATAGGCACATTGGCGAGTTTAAACAAACCTTACAGATTTAGATTTA
CFSAN045864	771	CTTAAATGGTAACCAAGTTAAAAGATATAGGCACATTGGCGAGTTTAAACAAACCTTACAGATTTAGATTTA
CFSAN049281	771	CTTAAATGGTAACCAAGTTAAAAGATATAGGCACATTGGCGAGTTTAAACAAACCTTACAGATTTAGATTTA
CFSAN049294	771	CTTAAATGGTAACCAAGTTAAAAGATATAGGCACATTGGCGAGTTTAAACAAACCTTACAGATTTAGATTTA
CFSAN049301	771	CTTAAATGGTAACCAAGTTAAAAGATATAGGCACATTGGCGAGTTTAAACAAACCTTACAGATTTAGATTTA
ScottA ST2	841	GCAAATAACCAAAATTAGTAATCTAGCACCAGTGTGCGGTCTAACAAAACCTAAGTAACTGAGTTAAAACCTGGAG
EGD-e ST35	841	GCAAATAACCAAAATTAGTAATCTAGCACCAGTGTGCGGTCTAACAAAACCTAAGTAACTGAGTTAAAACCTGGAG
10403S ST85	841	GCAAATAACCAAAATTAGTAATCTAGCACCAGTGTGCGGTCTAACAAAACCTAAGTAACTGAGTTAAAACCTGGAG
F2365 ST1	841	GCAAATAACCAAAATTAGTAATCTAGCACCAGTGTGCGGTCTAACAAAACCTAAGTAACTGAGTTAAAACCTGGAG
L6-13	841	GCAAATAACCAAAATTAGTAATCTAGCACCAGTGTGCGGTCTAACAAAACCTAAGTAACTGAGTTAAAACCTGGAG
MRL-14-00459	841	GCAAATAACCAAAATTAGTAATCTAGCACCAGTGTGCGGTCTAACAAAACCTAAGTAACTGAGTTAAAACCTGGAG
CFSAN045864	841	GCAAATAACCAAAATTAGTAATCTAGCACCAGTGTGCGGTCTAACAAAACCTAAGTAACTGAGTTAAAACCTGGAG
CFSAN049281	841	GCAAATAACCAAAATTAGTAATCTAGCACCAGTGTGCGGTCTAACAAAACCTAAGTAACTGAGTTAAAACCTGGAG
CFSAN049294	841	GCAAATAACCAAAATTAGTAATCTAGCACCAGTGTGCGGTCTAACAAAACCTAAGTAACTGAGTTAAAACCTGGAG
CFSAN049301	841	GCAAATAACCAAAATTAGTAATCTAGCACCAGTGTGCGGTCTAACAAAACCTAAGTAACTGAGTTAAAACCTGGAG
ScottA ST2	911	CTAACCAAAATAAGTAACATCAGTCCCCTAGCAGGTCTAACCGCACTCACTAAGTAACTGAGCTTAATGAAAA
EGD-e ST35	911	CTAACCAAAATAAGTAACATCAGTCCCCTAGCAGGTCTAACCGCACTCACTAAGTAACTGAGCTTAATGAAAA
10403S ST85	911	CTAACCAAAATAAGTAACATCAGTCCCCTAGCAGGTCTAACCGCACTCACTAAGTAACTGAGCTTAATGAAAA
F2365 ST1	911	CTAACCAAAATAAGTAACATCAGTCCCCTAGCAGGTCTAACCGCACTCACTAAGTAACTGAGCTTAATGAAAA
L6-13	911	CTAACCAAAATAAGTAACATCAGTCCCCTAGCAGGTCTAACCGCACTCACTAAGTAACTGAGCTTAATGAAAA
MRL-14-00459	911	CTAACCAAAATAAGTAACATCAGTCCCCTAGCAGGTCTAACCGCACTCACTAAGTAACTGAGCTTAATGAAAA

CFSAN045864	911	CTAACCAAATAAGTAACATCAGTCCCCTAGCAGGTTTAAACCGCACTCCTAACTTAGAGCTTAATGAAA
CFSAN049281	911	CTAACCAAATAAGTAACATCAGTCCCCTAGCAGGTTTAAACCGCACTCCTAACTTAGAGCTTAATGAAA
CFSAN049294	911	CTAACCAAATAAGTAACATCAGTCCCCTAGCAGGTTTAAACCGCACTCCTAACTTAGAGCTTAATGAAA
CFSAN049301	911	CTAACCAAATAAGTAACATCAGTCCCCTAGCAGGTTTAAACCGCACTCCTAACTTAGAGCTTAATGAAA
ScottA_ST2	981	TCAGTTGAAGATATTAGCCCAATTTCTAACCTGAAAAATCTCACATATTTAACCTTGTTACTTTAATAAT
EGD-e_ST35	981	TCAGCTGGAAGATATTAGCCCAATTTCTAACCTGAAAAATCTCACATATTTAACCTTGTTACTTTAATAAT
10403S_ST85	981	TCAGCTGGAAGATATTAGCCCAATTTCTAACCTGAAAAATCTCACATATTTAACCTTGTTACTTTAATAAT
F2365_ST1	981	TCAGTTGAAGATATTAGCCCAATTTCTAACCTGAAAAATCTCACATATTTAACCTTGTTACTTTAATAAT
L6-13	981	TCAGCTGGAAGATATTAGCCCAATTTCTAACCTGAAAAATCTCACATATTTAACCTTGTTACTTTAATAAT
MRL-14-00459	981	TCAGCTGGAAGATATTAGCCCAATTTCTAACCTGAAAAATCTCACATATTTAACCTTGTTACTTTAATAAT
CFSAN045864	981	TCAGCTGGAAGATATTAGCCCAATTTCTAACCTGAAAAATCTCACATATTTAACCTTGTTACTTTAATAAT
CFSAN049281	981	TCAGCTGGAAGATATTAGCCCAATTTCTAACCTGAAAAATCTCACATATTTAACCTTGTTACTTTAATAAT
CFSAN049294	981	TCAGCTGGAAGATATTAGCCCAATTTCTAACCTGAAAAATCTCACATATTTAACCTTGTTACTTTAATAAT
CFSAN049301	981	TCAGCTGGAAGATATTAGCCCAATTTCTAACCTGAAAAATCTCACATATTTAACCTTGTTACTTTAATAAT
ScottA_ST2	1051	ATAAGTGATATAAGCCCAGTTTCTAGTTTAAACAAAGCTTCAAAGATTATTTTCTATAATAACAAGGTAA
EGD-e_ST35	1051	ATAAGTGATATAAGCCCAGTTTCTAGTTTAAACAAAGCTTCAAAGATTATTTTCTATAATAACAAGGTAA
10403S_ST85	1051	ATAAGTGATATAAGCCCAGTTTCTAGTTTAAACAAAGCTTCAAAGATTATTTTCTATAATAACAAGGTAA
F2365_ST1	1051	ATAAGTGATATAAGCCCAGTTTCTAGTTTAAACAAAGCTTCAAAGATTATTTTCTATAATAACAAGGTAA
L6-13	1051	ATAAGTGATATAAGCCCAGTTTCTAGTTTAAACAAAGCTTCAAAGATTATTTTCTATAATAACAAGGTAA
MRL-14-00459	1051	ATAAGTGATATAAGCCCAGTTTCTAGTTTAAACAAAGCTTCAAAGATTATTTTCTATAATAACAAGGTAA
CFSAN045864	1051	ATAAGTGATATAAGCCCAGTTTCTAGTTTAAACAAAGCTTCAAAGATTATTTTCTATAATAACAAGGTAA
CFSAN049281	1051	ATAAGTGATATAAGCCCAGTTTCTAGTTTAAACAAAGCTTCAAAGATTATTTTCTATAATAACAAGGTAA
CFSAN049294	1051	ATAAGTGATATAAGCCCAGTTTCTAGTTTAAACAAAGCTTCAAAGATTATTTTCTATAATAACAAGGTAA
CFSAN049301	1051	ATAAGTGATATAAGCCCAGTTTCTAGTTTAAACAAAGCTTCAAAGATTATTTTCTATAATAACAAGGTAA
ScottA_ST2	1121	GTGACGTAAGCTCACTTGCGAACTTAACCAATTAATTAATTGGCTTTCGCTGGGCATAACCAAATTAGCGA
EGD-e_ST35	1121	GTGACGTAAGCTCACTTGCGAACTTAACCAATTAATTAATTGGCTTTCAGCTGGGCATAACCAAATTAGCGA
10403S_ST85	1121	GTGACGTAAGCTCACTTGCGAACTTAACCAATTAATTAATTGGCTTTCAGCTGGGCATAACCAAATTAGCGA
F2365_ST1	1121	GTGACGTAAGCTCACTTGCGAACTTAACCAATTAATTAATTGGCTTTCGCTGGGCATAACCAAATTAGCGA
L6-13	1121	GTGACGTAAGCTCACTTGCGAACTTAACCAATTAATTAATTGGCTTTCAGCTGGGCATAACCAAATTAGCGA
MRL-14-00459	1121	GTGACGTAAGCTCACTTGCGAACTTAACCAATTAATTAATTGGCTTTCAGCTGGGCATAACCAAATTAGCGA
CFSAN045864	1121	GTGACGTAAGCTCACTTGCGAACTTAACCAATTAATTAATTGGCTTTCAGCTGGGCATAACCAAATTAGCGA
CFSAN049281	1121	GTGACGTAAGCTCACTTGCGAACTTAACCAATTAATTAATTGGCTTTCAGCTGGGCATAACCAAATTAGCGA
CFSAN049294	1121	GTGACGTAAGCTCACTTGCGAACTTAACCAATTAATTAATTGGCTTTCAGCTGGGCATAACCAAATTAGCGA
CFSAN049301	1121	GTGACGTAAGCTCACTTGCGAACTTAACCAATTAATTAATTGGCTTTCAGCTGGGCATAACCAAATTAGCGA
ScottA_ST2	1191	TCTTACACCATTGGCTAATTTAAACAAGAACTACCCAATTAGGTTGAATGACCAAGAAATGGACAAATCCA
EGD-e_ST35	1191	TCTTACACCATTGGCTAATTTAAACAAGAACTACCCAACCTAGGGTTGAATGATCAAGCATGGACAAATGCA
10403S_ST85	1191	TCTTACACCATTGGCTAATTTAAACAAGAACTACCCAACCTAGGGTTGAATGATCAAGCATGGACAAATGCA
F2365_ST1	1191	TCTTACACCATTGGCTAATTTAAACAAGAACTACCCAATTAGGTTGAATGACCAAGAAATGGACAAATCCA
L6-13	1191	TCTTACACCATTGGCTAATTTAAACAAGAACTACCCAACCTAGGGTTGAATGATCAAGCATGGACAAATGCA
MRL-14-00459	1191	TCTTACACCATTGGCTAATTTAAACAAGAACTACCCAACCTAGGGTTGAATGATCAAGCATGGACAAATGCA
CFSAN045864	1191	TCTTACACCATTGGCTAATTTAAACAAGAACTACCCAACCTAGGGTTGAATGATCAAGCATGGACAAATGCA
CFSAN049281	1191	TCTTACACCATTGGCTAATTTAAACAAGAACTACCCAACCTAGGGTTGAATGATCAAGCATGGACAAATGCA
CFSAN049294	1191	TCTTACACCATTGGCTAATTTAAACAAGAACTACCCAACCTAGGGTTGAATGATCAAGCATGGACAAATGCA
CFSAN049301	1191	TCTTACACCATTGGCTAATTTAAACAAGAACTACCCAACCTAGGGTTGAATGATCAAGCATGGACAAATGCA
ScottA_ST2	1261	CCAGTAACTACAAAGCAAATGTATCCATTCCAAACACGGTGAAAAATGTGACGGCGCTTTAATTGCAC
EGD-e_ST35	1261	CCAGTAACTACAAAGCAAATGTATCCATTCCAAACACGGTGAAAAATGTGACTGGCGCTTTAATTGCAC
10403S_ST85	1261	CCAGTAACTACAAAGCAAATGTATCCATTCCAAACACGGTGAAAAATGTGACTGGCGCTTTAATTGCAC
F2365_ST1	1261	CCAGTAACTACAAAGCAAATGTATCCATTCCAAACACGGTGAAAAATGTGACGGCGCTTTAATTGCAC
L6-13	1261	CCAGTAACTACAAAGCAAATGTATCCATTCCAAACACGGTGAAAAATGTGACTGGCGCTTTAATTGCAC
MRL-14-00459	1261	CCAGTAACTACAAAGCAAATGTATCCATTCCAAACACGGTGAAAAATGTGACTGGCGCTTTAATTGCAC
CFSAN045864	1261	CCAGTAACTACAAAGCAAATGTATCCATTCCAAACACGGTGAAAAATGTGACTGGCGCTTTAATTGCAC
CFSAN049281	1261	CCAGTAACTACAAAGCAAATGTATCCATTCCAAACACGGTGAAAAATGTGACTGGCGCTTTAATTGCAC
CFSAN049294	1261	CCAGTAACTACAAAGCAAATGTATCCATTCCAAACACGGTGAAAAATGTGACTGGCGCTTTAATTGCAC
CFSAN049301	1261	CCAGTAACTACAAAGCAAATGTATCCATTCCAAACACGGTGAAAAATGTGACTGGCGCTTTAATTGCAC
ScottA_ST2	1331	CAGCTACTATTAGCGATGGTGGTAGTTATCAGACCTGATATAACATGGAATTACCTAGTTATACAA
EGD-e_ST35	1331	CAGCTACTATTAGCGATGGCGGTAGTTACACAGAGCCTGATATAACATGGAACCTACCTAGTTATACAAA
10403S_ST85	1331	CAGCTACTATTAGCGATGGCGGTAGTTACACAGAGCCTGATATAACATGGAACCTACCTAGTTATACAAA
F2365_ST1	1331	CAGCTACTATTAGCGATGGTGGTAGTTATCAGACCTGATATAACATGGAATTACCTAGTTATACAA
L6-13	1331	CAGCTACTATTAGCGATGGCGGTAGTTACACAGAGCCTGATATAACATGGAACCTACCTAGTTATACAAA
MRL-14-00459	1331	CAGCTACTATTAGCGATGGCGGTAGTTACACAGAGCCTGATATAACATGGAACCTACCTAGTTATACAAA
CFSAN045864	1331	CAGCTACTATTAGCGATGGCGGTAGTTACACAGAGCCTGATATAACATGGAACCTACCTAGTTATACAAA
CFSAN049281	1331	CAGCTACTATTAGCGATGGCGGTAGTTACACAGAGCCTGATATAACATGGAACCTACCTAGTTATACAAA
CFSAN049294	1331	CAGCTACTATTAGCGATGGCGGTAGTTACACAGAGCCTGATATAACATGGAACCTACCTAGTTATACAAA
CFSAN049301	1331	CAGCTACTATTAGCGATGGCGGTAGTTACACAGAGCCTGATATAACATGGAACCTACCTAGTTATACAAA
ScottA_ST2	1401	TGAAGTAAGTTATACCTTTTAACTCTGTACCATTTGGAAAAGGAACGACAACATTTAGTGGAACCTGTG
EGD-e_ST35	1401	TGAAGTAAGCTATACCTTTAGCCAACCTGTCACTATTGGAAAAGGAACGACAACATTTAGTGGAACCGTG
10403S_ST85	1401	TGAAGTAAGCTATACCTTTAGCCAACCTGTCACTATTGGAAAAGGAACGACAACATTTAGTGGAACCGTG
F2365_ST1	1401	TGAAGTAAGTTATACCTTTTAACTCTGTACCATTTGGAAAAGGAACGACAACATTTAGTGGAACCTGTG

L6-13	1401	TGAAGTAAGCTATACCTTTAGCCAACCTGTCACCTATTGGAAAAGGAACGACAACATTTAGTGGAACCGTG
MRL-14-00459	1401	TGAAGTAAGCTATACCTTTAGCCAACCTGTCACCTATTGGAAAAGGAACGACAACATTTAGTGGAACCGTG
CFSAN045864	1401	TGAAGTAAGCTATACCTTTAGCCAACCTGTCACCTATTGGAAAAGGAACGACAACATTTAGTGGAACCGTG
CFSAN049281	1401	TGAAGTAAGCTATACCTTTAGCCAACCTGTCACCTATTGGAAAAGGAACGACAACATTTAGTGGAACCGTG
CFSAN049294	1401	TGAAGTAAGCTATACCTTTAGCCAACCTGTCACCTATTGGAAAAGGAACGACAACATTTAGTGGAACCGTG
CFSAN049301	1401	TGAAGTAAGCTATACCTTTAGCCAACCTGTCACCTATTGGAAAAGGAACGACAACATTTAGTGGAACCGTG

ScottA_ST2	1471	ACGCAGCCACTTAAGGCAATTTTTTAATGCTAAGTTTCATGTGGACGGCAAAGAAACAACCAAAGAAGTGG
EGD-e_ST35	1471	ACGCAGCCACTTAAGGCAATTTTTTAATGCTAAGTTTCATGTGGACGGCAAAGAAACAACCAAAGAAGTGG
10403S_ST85	1471	ACGCAGCCACTTAAGGCAATTTTTTAATGCTAAGTTTCATGTGGACGGCAAAGAAACAACCAAAGAAGTGG
F2365_ST1	1471	ACGCAGCCACTTAAGGCAATTTTTTAATGCTAAGTTTCATGTGGACGGCAAAGAAACAACCAAAGAAGTGG
L6-13	1471	ACGCAGCCACTTAAGGCAATTTTTTAATGCTAAGTTTCATGTGGACGGCAAAGAAACAACCAAAGAAGTGG
MRL-14-00459	1471	ACGCAGCCACTTAAGGCAATTTTTTAATGCTAAGTTTCATGTGGACGGCAAAGAAACAACCAAAGAAGTGG
CFSAN045864	1471	ACGCAGCCACTTAAGGCAATTTTTTAATGCTAAGTTTCATGTGGACGGCAAAGAAACAACCAAAGAAGTGG
CFSAN049281	1471	ACGCAGCCACTTAAGGCAATTTTTTAATGCTAAGTTTCATGTGGACGGCAAAGAAACAACCAAAGAAGTGG
CFSAN049294	1471	ACGCAGCCACTTAAGGCAATTTTTTAATGCTAAGTTTCATGTGGACGGCAAAGAAACAACCAAAGAAGTGG
CFSAN049301	1471	ACGCAGCCACTTAAGGCAATTTTTTAATGCTAAGTTTCATGTGGACGGCAAAGAAACAACCAAAGAAGTGG

ScottA_ST2	1541	AAGCTGGGAATTTATTGACTGAACCAGCTAAGCCGTGTAAGAAAGAGGTCTATACATTTGTTGGCTGGTTTGA
EGD-e_ST35	1541	AAGCTGGGAATTTATTGACTGAACCAGCTAAGCCCGTAAAGAAAGGTTCACACATTTGTTGGTTGGTTTGA
10403S_ST85	1541	AAGCTGGGAATTTATTGACTGAACCAGCTAAGCCCGTAAAGAAAGGTTCACACATTTGTTGGTTGGTTTGA
F2365_ST1	1541	AAGCTGGGAATTTATTGACTGAACCAGCTAAGCCGTGTAAGAAAGAGGTCTATACATTTGTTGGCTGGTTTGA
L6-13	1541	AAGCTGGGAATTTATTGACTGAACCAGCTAAGCCCGTAAAGAAAGGTTCACACATTTGTTGGTTGGTTTGA
MRL-14-00459	1541	AAGCTGGGAATTTATTGACTGAACCAGCTAAGCCCGTAAAGAAAGGTTCACACATTTGTTGGTTGGTTTGA
CFSAN045864	1541	AAGCTGGGAATTTATTGACTGAACCAGCTAAGCCCGTAAAGAAAGGTTCACACATTTGTTGGTTGGTTTGA
CFSAN049281	1541	AAGCTGGGAATTTATTGACTGAACCAGCTAAGCCCGTAAAGAAAGGTTCACACATTTGTTGGTTGGTTTGA
CFSAN049294	1541	AAGCTGGGAATTTATTGACTGAACCAGCTAAGCCCGTAAAGAAAGGTTCACACATTTGTTGGTTGGTTTGA
CFSAN049301	1541	AAGCTGGGAATTTATTGACTGAACCAGCTAAGCCCGTAAAGAAAGGTTCACACATTTGTTGGTTGGTTTGA

ScottA_ST2	1611	TGCCCAAACCGGCGGAACCTAAATGGGATTTTCAGTACGGGATAAAATGCCGACAAATGACATCGATTATAT
EGD-e_ST35	1611	TGCCCAAACAGGCGGAACCTAAATGGGATTTTCAGTACGGGATAAAATGCCGACAAATGACATCAATTATAT
10403S_ST85	1611	TGCCCAAACAGGCGGAACCTAAATGGGATTTTCAGTACGGGATAAAATGCCGACAAATGACATCAATTATAT
F2365_ST1	1611	TGCCCAAACCGGCGGAACCTAAATGGGATTTTCAGTACGGGATAAAATGCCGACAAATGACATCGATTATAT
L6-13	1611	TGCCCAAACAGGCGGAACCTAAATGGGATTTTCAGTACGGGATAAAATGCCGACAAACGACATCGATTATAT
MRL-14-00459	1611	TGCCCAAACAGGCGGAACCTAAATGGGATTTTCAGTACGGGATAAAATGCCGACAAACGACATCGATTATAT
CFSAN045864	1611	TGCCCAAACAGGCGGAACCTAAATGGGATTTTCAGTACGGGATAAAATGCCGACAAACGACATCGATTATAT
CFSAN049281	1611	TGCCCAAACAGGCGGAACCTAAATGGGATTTTCAGTACGGGATAAAATGCCGACAAACGACATCGATTATAT
CFSAN049294	1611	TGCCCAAACAGGCGGAACCTAAATGGGATTTTCAGTACGGGATAAAATGCCGACAAACGACATCGATTATAT
CFSAN049301	1611	TGCCCAAACAGGCGGAACCTAAATGGGATTTTCAGTACGGGATAAAATGCCGACAAACGACATCGATTATAT

ScottA_ST2	1681	GCACAATTTAGTATTAACAGCTACACAGCAACGTTTGATAATGACGGGTGAACAACATCTCAAACAGTAG
EGD-e_ST35	1681	GCACAATTTAGTATTAACAGCTACACAGCAACCTTTTGATAATGACGGGTGAACAACATCTCAAACAGTAG
10403S_ST85	1681	GCACAATTTAGTATTAACAGCTACACAGCAACCTTTTGATAATGACGGGTGAACAACATCTCAAACAGTAG
F2365_ST1	1681	GCACAATTTAGTATTAACAGCTACACAGCAACGTTTGATAATGACGGGTGAACAACATCTCAAACAGTAG
L6-13	1681	GCACAATTTAGTATTAACAGCTACACAGCAACGTTTGATAATGACGGGTGAACAACATCTCAAACAGTAG
MRL-14-00459	1681	GCACAATTTAGTATTAACAGCTACACAGCAACGTTTGATAATGACGGGTGAACAACATCTCAAACAGTAG
CFSAN045864	1681	GCACAATTTAGTATTAACAGCTACACAGCAACGTTTGATAATGACGGGTGAACAACATCTCAAACAGTAG
CFSAN049281	1681	GCACAATTTAGTATTAACAGCTACACAGCAACGTTTGATAATGACGGGTGAACAACATCTCAAACAGTAG
CFSAN049294	1681	GCACAATTTAGTATTAACAGCTACACAGCAACGTTTGATAATGACGGGTGAACAACATCTCAAACAGTAG
CFSAN049301	1681	GCACAATTTAGTATTAACAGCTACACAGCAACGTTTGATAATGACGGGTGAACAACATCTCAAACAGTAG

ScottA_ST2	1751	ATTATCAAGGCTTGCTACAAGAACCTACGGCACCAACAAAAGAAGGTTATACCTTTCAAAGGCTGGTATGA
EGD-e_ST35	1751	ATTATCAAGGCTTGCTACAAGAACCTACGGCACCAACAAAAGAAGGTTATACCTTTCAAAGGCTGGTATGA
10403S_ST85	1751	ATTATCAAGGCTTGCTACAAGAACCTACGGCACCAACAAAAGAAGGTTATACCTTTCAAAGGCTGGTATGA
F2365_ST1	1751	ATTATCAAGGCTTGCTACAAGAACCTACGGCACCAACAAAAGAAGGTTATACCTTTCAAAGGCTGGTATGA
L6-13	1751	ATTATCAAGGCTTGCTACAAGAACCTACGGCACCAACAAAAGAAGGTTATACCTTTCAAAGGCTGGTATGA
MRL-14-00459	1751	ATTATCAAGGCTTGCTACAAGAACCTACGGCACCAACAAAAGAAGGTTATACCTTTCAAAGGCTGGTATGA
CFSAN045864	1751	ATTATCAAGGCTTGCTACAAGAACCTACGGCACCAACAAAAGAAGG-----
CFSAN049281	1751	ATTATCAAGGCTTGCTACAAGAACCTACGGCACCAACAAAAGAAGG-----
CFSAN049294	1751	ATTATCAAGGCTTGCTACAAGAACCTACGGCACCAACAAAAGAAGG-----
CFSAN049301	1751	ATTATCAAGGCTTGCTACAAGAACCTACGGCACCAACAAAAGAAGG-----

ScottA_ST2	1821	CGCAAAAACCTGGTGGTGACAAGTGGGATTTTCGCAACTAGCAAAATGCCTGCTAAAAACATCACCTTATAT
EGD-e_ST35	1821	CGCAAAAACCTGGTGGTGACAAGTGGGATTTTCGCAACTAGCAAAATGCCTGCTAAAAACATCACCTTATAT
10403S_ST85	1821	CGCAAAAACCTGGTGGTGACAAGTGGGATTTTCGCAACTAGCAAAATGCCTGCTAAAAACATCACCTTATAT
F2365_ST1	1821	CGCAAAAACCTGGTGGTGACAAGTGGGATTTTCGCAACTAGCAAAATGCCTGCTAAAAACATCACCTTATAT
L6-13	1821	CGCAAAAACCTGGTGGTGACAAGTGGGATTTTCGCAACTAGCAAAATGCCTGCTAAAAACATCACCTTATAT
MRL-14-00459	1821	CGCAAAAACCTGGTGGTGACAAGTGGGATTTTCGCAACTAGCAAAATGCCTGCTAAAAACATCACCTTATAT
CFSAN045864	1797	-----
CFSAN049281	1797	-----
CFSAN049294	1797	-----
CFSAN049301	1797	-----

ScottA_ST2	1891	GCTCAATATAGCGCCAATAGCTATACAGCAACCTTTGATCTTGATGGAAAAACAACGACTCAACAGTAG
EGD-e_ST35	1891	GCTCAATATAGCGCCAATAGCTATACAGCAACCTTTGATCTTGATGGAAAAACAACGACTCAACAGTAG

10403S_ST85	1891	GC	CAATATAGCGCCAATAGCTATACAGCAACG	TTGAT	TTGATGGA	AAATCAACGACTCAAG	CAGTAG
F2365_ST1	1891	GCT	CAATATAGCGCCAATAGCTATACAGCAACCT	TTGAT	TTGATGGA	AAATCAACGACTCAAG	CAGTAG
L6-13	1891	GC	CAATATAGCGCCAATAGCTATACAGCAACG	TTGAT	TTGATGGA	AAATCAACGACTCAAG	CAGTAG
MRL-14-00459	1891	GC	CAATATAGCGCCAATAGCTATACAGCAACG	TTGAT	TTGATGGA	AAATCAACGACTCAAG	CAGTAG
CFSAN045864	1797	-----	-----	-----	-----	-----	-----
CFSAN049281	1797	-----	-----	-----	-----	-----	-----
CFSAN049294	1797	-----	-----	-----	-----	-----	-----
CFSAN049301	1797	-----	-----	-----	-----	-----	-----

ScottA_ST2	1961	ACTATCAAGGACTTCTAAAAGAACCAAAAGC	CCAAC	AAAGCCGGATATACTTTCAAAGG	TGGTATGA
EGD-e_ST35	1961	ACTATCAAGGACTTCTAAAAGAACCAAAAGC	CCAAC	AAAGCCGGATATACTTTCAAAGGCTGGTATGA	
10403S_ST85	1961	ACTATCAAGGACTTCTAAAAGAACCAAAAGC	CCAAC	AAAGCCGGATATACTTTCAAAGGCTGGTATGA	
F2365_ST1	1961	ACTATCAAGGACTTCTAAAAGAACCAAAAGC	CCAAC	AAAGCCGGATATACTTTCAAAGG	TGGTATGA
L6-13	1961	ACTATCAAGGACTTCTAAAAGAACCAAAAGC	CCAAC	AAAGCCGGATATACTTTCAAAGGCTGGTATGA	
MRL-14-00459	1961	ACTATCAAGGACTTCTAAAAGAACCAAAAGC	CCAAC	AAAGCCGGATATACTTTCAAAGGCTGGTATGA	
CFSAN045864	1797	-----	-----	TTATACTTTCAAAGGCTGGTATGA	
CFSAN049281	1797	-----	-----	TTATACTTTCAAAGGCTGGTATGA	
CFSAN049294	1797	-----	-----	TTATACTTTCAAAGGCTGGTATGA	
CFSAN049301	1797	-----	-----	ATATACTTTCAAAGGCTGGTATGA	

ScottA_ST2	2031	CGAAAAAACAGATGG	TAAAAAATGGGATTTTGCGAC	GATAAAATGCCAGCAAATGA	TATTACGCTGTAC
EGD-e_ST35	2031	CGAAAAAACAGATGGGAAAAAATGGGATTTTGCGACGGATAAAATGCCAGCAAATGACATTACGCTGTAC			
10403S_ST85	2031	CGAAAAAACAGATGGGAAAAAATGGGATTTTGCGACGGATAAAATGCCAGCAAATGACATTACGCTGTAC			
F2365_ST1	2031	CGAAAAAACAGATGG	TAAAAAATGGGATTTTGCGAC	GATAAAATGCCAGCAAATGA	TATTACGCTGTAC
L6-13	2031	CGAAAAAACAGATGGGAAAAAATGGGATTTTGCGACGGATAAAATGCCAGCAAATGACATTACGCTGTAC			
MRL-14-00459	2031	CGAAAAAACAGATGGGAAAAAATGGGATTTTGCGACGGATAAAATGCCAGCAAATGACATTACGCTGTAC			
CFSAN045864	1821	CGAAAAAACAGATGGGAAAAAATGGGATTTTGCGACGGATAAAATGCCAGCAAATGACATTACGCTGTAC			
CFSAN049281	1821	CGAAAAAACAGATGGGAAAAAATGGGATTTTGCGACGGATAAAATGCCAGCAAATGACATTACGCTGTAC			
CFSAN049294	1821	CGAAAAAACAGATGGGAAAAAATGGGATTTTGCGACGGATAAAATGCCAGCAAATGACATTACGCTGTAC			
CFSAN049301	1821	CGAAAAAACAGATGGGAAAAAATGGGATTTTGCGACGGATAAAATGCCAGCAAATGACATTACGCTGTAC			

ScottA_ST2	2101	GCTCAATT	CACGAAAAATCCTGTGGCACCACCAACAAC	TGGAGGGAACAC	TCCGCC	GACT	ACAAAAA	TAACG
EGD-e_ST35	2101	GCTCAATTTACGAAAAATCCTGTGGCACCACCAACAAC	TGGAGGGAACACACCGCCTACAA	CAAA	TAACG			
10403S_ST85	2101	GCTCAATTTACGAAAAATCCTGTGGCACCACCAACAAC	TGGAGGGAACACACCGCCTACAA	CAAA	TAACG			
F2365_ST1	2101	GCTCAATT	CACGAAAAATCCTGTGGCACCACCAACAAC	TGGAGGGAACAC	TCCGCC	GACT	ACAAAAA	TAACG
L6-13	2101	GCTCAATTTACGAAAAATCCTGTGGCACCACCAACAAC	TGGAGGGAACACACCGCCTACAA	CAAA	TAACG			
MRL-14-00459	2101	GCTCAATTTACGAAAAATCCTGTGGCACCACCAACAAC	TGGAGGGAACACACCGCCTACAA	CAAA	TAACG			
CFSAN045864	1891	GCTCAATTTACGAAAAATCCTGTGGCACCACCAACAAC	TGGAGGGAACACACCGCCTACAA	CAAA	TAACG			
CFSAN049281	1891	GCTCAATTTACGAAAAATCCTGTGGCACCACCAACAAC	TGGAGGGAACACACCGCCTACAA	CAAA	TAACG			
CFSAN049294	1891	GCTCAATTTACGAAAAATCCTGTGGCACCACCAACAAC	TGGAGGGAACACACCGCCTACAA	CAAA	TAACG			
CFSAN049301	1891	GCTCAATTTACGAAAAATCCTGTGGCACCACCAACAAC	TGGAGGGAACACACCGCCTACAA	CAAA	TAACG			

ScottA_ST2	2171	GA	GGGAAC	ACTACACCACCTTCCGCAAATATACCTGGAAGC	ACACATCTAACACATCAACTGGGAATTC
EGD-e_ST35	2171	GCGGGAATACTACACCACCTTCCGCAAATATACCTGGAAGCGACACATCTAACACATCAACTGGGAATTC			
10403S_ST85	2171	GCGGGAATACTACACCACCTTCCGCAAATATACCTGGAAGCGACACATCTAACACATCAACTGGGAATTC			
F2365_ST1	2171	GA	GGGAAC	ACTACACCACCTTCCGCAAATATACCTGGAAGC	ACACATCTAACACATCAACTGGGAATTC
L6-13	2171	GCGGGAATACTACACCACCTTCCGCAAATATACCTGGAAGCGACACATCTAACACATCAACTGGGAATTC			
MRL-14-00459	2171	GCGGGAATACTACACCACCTTCCGCAAATATACCTGGAAGCGACACATCTAACACATCAACTGGGAATTC			
CFSAN045864	1961	GCGGGAATACTACACCACCTTCCGCAAATATACCTGGAAGCGACACATCTAACACATCAACTGGGAATTC			
CFSAN049281	1961	GCGGGAATACTACACCACCTTCCGCAAATATACCTGGAAGCGACACATCTAACACATCAACTGGGAATTC			
CFSAN049294	1961	GCGGGAATACTACACCACCTTCCGCAAATATACCTGGAAGCGACACATCTAACACATCAACTGGGAATTC			
CFSAN049301	1961	GCGGGAATACTACACCACCTTCCGCAAATATACCTGGAAGCGACACATCTAACACATCAACTGGGAATTC			

ScottA_ST2	2241	AGC	TAGCACAACAAGTACAATGAACGCTTATGACCCCTTATAATTCAAAGAAGCTTC	ACTCCCTACA	AACT
EGD-e_ST35	2241	AGCCAGCACAACAAGTACAATGAACGCTTATGACCCCTTATAATTCAAAGAAGCTTC	ACTCCCTACA	AACT	
10403S_ST85	2241	AGCCAGCACAACAAGTACAATGAACGCTTATGACCCCTTATAATTCAAAGAAGCTTC	ACTCCCTACA	AACT	
F2365_ST1	2241	AGC	TAGCACAACAAGTACAATGAACGCTTATGACCCCTTATAATTCAAAGAAGCTTC	ACTCCCTACA	AACT
L6-13	2241	AGCCAGCACAACAAGTACAATGAACGCTTATGACCCCTTATAATTCAAAGAAGCTTC	ACTCCCTACA	AACT	
MRL-14-00459	2241	AGCCAGCACAACAAGTACAATGAACGCTTATGACCCCTTATAATTCAAAGAAGCTTC	ACTCCCTACA	AACT	
CFSAN045864	2031	AGCCAGCACAACAAGTACAATGAACGCTTATGACCCCTTATAATTCAAAGAAGCTTC	ACTCCCTACA	AACT	
CFSAN049281	2031	AGCCAGCACAACAAGTACAATGAACGCTTATGACCCCTTATAATTCAAAGAAGCTTC	ACTCCCTACA	AACT	
CFSAN049294	2031	AGCCAGCACAACAAGTACAATGAACGCTTATGACCCCTTATAATTCAAAGAAGCTTC	ACTCCCTACA	AACT	
CFSAN049301	2031	AGCCAGCACAACAAGTACAATGAACGCTTATGACCCCTTATAATTCAAAGAAGCTTC	ACTCCCTACA	AACT	

ScottA_ST2	2311	GC	TGATAGCGATAATGCGCTCTACCT	CTTTG	TATAGG	TT	TTAGCAGTAGGA	AACTGCA	TGGCTC	TTACTA
EGD-e_ST35	2311	GCGGATAGCGATAATGCGCTCTACCTTTTGT	TAGGGTTATTAGCAGTAGGA	AACTGCA	ATGGCTC	TTACTA				
10403S_ST85	2311	GCGGATAGCGATAATGCGCTCTACCTTTTGT	TAGGGTTATTAGCAGTAGGA	AACTGCA	ATGGCTC	TTACTA				
F2365_ST1	2311	GC	TGATAGCGATAATGCGCTCTACCT	CTTTG	TATAGG	TT	TTAGCAGTAGGA	AACTGCA	TGGCTC	TTACTA
L6-13	2311	GCGGATAGCGATAATGCGCTCTACCTTTTGT	TAGGGTTATTAGCAGTAGGA	AACTGCA	ATGGCTC	TTACTA				
MRL-14-00459	2311	GCGGATAGCGATAATGCGCTCTACCTTTTGT	TAGGGTTATTAGCAGTAGGA	AACTGCA	ATGGCTC	TTACTA				
CFSAN045864	2101	GCGGATAGCGATAATGCGCTCTACCTTTTGT	TAGGGTTATTAGCAGTAGGA	AACTGCA	ATGGCTC	TTACTA				
CFSAN049281	2101	GCGGATAGCGATAATGCGCTCTACCTTTTGT	TAGGGTTATTAGCAGTAGGA	AACTGCA	ATGGCTC	TTACTA				
CFSAN049294	2101	GCGGATAGCGATAATGCGCTCTACCTTTTGT	TAGGGTTATTAGCAGTAGGA	AACTGCA	ATGGCTC	TTACTA				
CFSAN049301	2101	GCGGATAGCGATAATGCGCTCTACCTTTTGT	TAGGGTTATTAGCAGTAGGA	AACTGCA	ATGGCTC	TTACTA				

ScottA ST2	2381	AAAAAGCACGTGCTAGTAAATAG
EGD-e ST35	2381	AAAAAGCACGTGCTAGTAAATAG
10403S ST85	2381	AAAAAGCACGTGCTAGTAAATAG
F2365_ST1	2381	AAAAAGCACGTGCTAGTAAATAG
L6-13	2381	AAAAAGCACGTGCTAGTAAATAG
MRL-14-00459	2381	AAAAAGCACGTGCTAGTAAATAG
CFSAN045864	2171	AAAAAGCACGTGCTAGTAAATAG
CFSAN049281	2171	AAAAAGCACGTGCTAGTAAATAG
CFSAN049294	2171	AAAAAGCACGTGCTAGTAAATAG
CFSAN049301	2171	AAAAAGCACGTGCTAGTAAATAG

Figure S2B. Alignment of InlA protein sequences

ScottA_ST2	1	VRKKRYVWLKSI	VAILVFGSGVWINTSNGTNAQAATITQDTPINQIF	TDALAEKMKTVL	GKTNVTDTV	
EGD-e_ST35	1	VRKKRYVWLKSI	VAILVFGSGVWINTSNGTNAQAATITQDTPINQIF	TDALAEKMKTVL	GKTNVTDTV	
10403S_ST85	1	VRKKRYVWLKSI	VAILVFGSGVWINTSNGTNAQAATITQDTPINQIF	TDALAEKMKTVL	GKTNVTDTV	
F2365_ST1	1	VRKKRYVWLKSI	VAILVFGSGVWINTSNGTNAQAATITQDTPINQIF	TDALAEKMKTVL	GKTNVTDTV	
L6-13	1	VRKKRYVWLKSI	VAILVFGSGVWINTSNGTNAQAATITQDTPINQIF	TDALAEKMKTVL	GKTNVTDTV	
MRL-14-00459	1	VRKKRYVWLKSI	VAILVFGSGVWINTSNGTNAQAATITQDTPINQIF	TDALAEKMKTVL	GKTNVTDTV	
CFSAN045864	1	VRKKRYVWLKSI	VAILVFGSGVWINTSNGTNAQAATITQDTPINQIF	TDALAEKMKTVL	GKTNVTDTV	
CFSAN049281	1	VRKKRYVWLKSI	VAILVFGSGVWINTSNGTNAQAATITQDTPINQIF	TDALAEKMKTVL	GKTNVTDTV	
CFSAN049294	1	VRKKRYVWLKSI	VAILVFGSGVWINTSNGTNAQAATITQDTPINQIF	TDALAEKMKTVL	GKTNVTDTV	
CFSAN049301	1	VRKKRYVWLKSI	VAILVFGSGVWINTSNGTNAQAATITQDTPINQIF	TDALAEKMKTVL	GKTNVTDTV	
ScottA_ST2	71	SQTDLDQVTTLQ	ADRLGIKSIDGEYLN	NLTQINF	SNNQLTDITPLKDLTKLVDILMNNNQIADITPLAN	
EGD-e_ST35	71	SQTDLDQVTTLQ	ADRLGIKSIDGEYLN	NLTQINF	SNNQLTDITPLKDLTKLVDILMNNNQIADITPLAN	
10403S_ST85	71	SQTDLDQVTTLQ	ADRLGIKSIDGEYLN	NLTQINF	SNNQLTDITPLKDLTKLVDILMNNNQIADITPLAN	
F2365_ST1	71	SQTDLDQVTTLQ	ADRLGIKSIDGEYLN	NLTQINF	SNNQLTDITPLKDLTKLVDILMNNNQIADITPLAN	
L6-13	71	SQTDLDQVTTLQ	ADRLGIKSIDGEYLN	NLTQINF	SNNQLTDITPLKDLTKLVDILMNNNQIADITPLAN	
MRL-14-00459	71	SQTDLDQVTTLQ	ADRLGIKSIDGEYLN	NLTQINF	SNNQLTDITPLKDLTKLVDILMNNNQIADITPLAN	
CFSAN045864	71	SQTDLDQVTTLQ	ADRLGIKSIDGEYLN	NLTQINF	SNNQLTDITPLKDLTKLVDILMNNNQIADITPLAN	
CFSAN049281	71	SQTDLDQVTTLQ	ADRLGIKSIDGEYLN	NLTQINF	SNNQLTDITPLKDLTKLVDILMNNNQIADITPLAN	
CFSAN049294	71	SQTDLDQVTTLQ	ADRLGIKSIDGEYLN	NLTQINF	SNNQLTDITPLKDLTKLVDILMNNNQIADITPLAN	
CFSAN049301	71	SQTDLDQVTTLQ	ADRLGIKSIDGEYLN	NLTQINF	SNNQLTDITPLKDLTKLVDILMNNNQIADITPLAN	
ScottA_ST2	141	LTNLTGTLFNNQITD	LPLK	NLTNLRLE	SSNTISDISALSGLTSLQQLSFGNQVTDL	KPLANLTTLE
EGD-e_ST35	141	LTNLTGTLFNNQITD	LPLK	NLTNLRLE	SSNTISDISALSGLTSLQQLSFGNQVTDL	KPLANLTTLE
10403S_ST85	141	LTNLTGTLFNNQITD	LPLK	NLTNLRLE	SSNTISDISALSGLTSLQQLSFGNQVTDL	KPLANLTTLE
F2365_ST1	141	LTNLTGTLFNNQITD	LPLK	NLTNLRLE	SSNTISDISALSGLTSLQQLSFGNQVTDL	KPLANLTTLE
L6-13	141	LTNLTGTLFNNQITD	LPLK	NLTNLRLE	SSNTISDISALSGLTSLQQLSFGNQVTDL	KPLANLTTLE
MRL-14-00459	141	LTNLTGTLFNNQITD	LPLK	NLTNLRLE	SSNTISDISALSGLTSLQQLSFGNQVTDL	KPLANLTTLE
CFSAN045864	141	LTNLTGTLFNNQITD	LPLK	NLTNLRLE	SSNTISDISALSGLTSLQQLSFGNQVTDL	KPLANLTTLE
CFSAN049281	141	LTNLTGTLFNNQITD	LPLK	NLTNLRLE	SSNTISDISALSGLTSLQQLSFGNQVTDL	KPLANLTTLE
CFSAN049294	141	LTNLTGTLFNNQITD	LPLK	NLTNLRLE	SSNTISDISALSGLTSLQQLSFGNQVTDL	KPLANLTTLE
CFSAN049301	141	LTNLTGTLFNNQITD	LPLK	NLTNLRLE	SSNTISDISALSGLTSLQQLSFGNQVTDL	KPLANLTTLE
ScottA_ST2	211	RLDISSNKVSDISV	LAKLTNLES	LIATNNQISDITPLG	ILTNLDEL	SLNGNQLKDIGTLASLTNLTDLDL
EGD-e_ST35	211	RLDISSNKVSDISV	LAKLTNLES	LIATNNQISDITPLG	ILTNLDEL	SLNGNQLKDIGTLASLTNLTDLDL
10403S_ST85	211	RLDISSNKVSDISV	LAKLTNLES	LIATNNQISDITPLG	ILTNLDEL	SLNGNQLKDIGTLASLTNLTDLDL
F2365_ST1	211	RLDISSNKVSDISV	LAKLTNLES	LIATNNQISDITPLG	ILTNLDEL	SLNGNQLKDIGTLASLTNLTDLDL
L6-13	211	RLDISSNKVSDISV	LAKLTNLES	LIATNNQISDITPLG	ILTNLDEL	SLNGNQLKDIGTLASLTNLTDLDL
MRL-14-00459	211	RLDISSNKVSDISV	LAKLTNLES	LIATNNQISDITPLG	ILTNLDEL	SLNGNQLKDIGTLASLTNLTDLDL
CFSAN045864	211	RLDISSNKVSDISV	LAKLTNLES	LIATNNQISDITPLG	ILTNLDEL	SLNGNQLKDIGTLASLTNLTDLDL
CFSAN049281	211	RLDISSNKVSDISV	LAKLTNLES	LIATNNQISDITPLG	ILTNLDEL	SLNGNQLKDIGTLASLTNLTDLDL
CFSAN049294	211	RLDISSNKVSDISV	LAKLTNLES	LIATNNQISDITPLG	ILTNLDEL	SLNGNQLKDIGTLASLTNLTDLDL
CFSAN049301	211	RLDISSNKVSDISV	LAKLTNLES	LIATNNQISDITPLG	ILTNLDEL	SLNGNQLKDIGTLASLTNLTDLDL
ScottA_ST2	281	ANNQISNLAPLSGL	TKLTELKLGANQIS	NISPLAGLTALT	NLELNENQLEDISPISNLK	NLTYLTYLFNN
EGD-e_ST35	281	ANNQISNLAPLSGL	TKLTELKLGANQIS	NISPLAGLTALT	NLELNENQLEDISPISNLK	NLTYLTYLFNN
10403S_ST85	281	ANNQISNLAPLSGL	TKLTELKLGANQIS	NISPLAGLTALT	NLELNENQLEDISPISNLK	NLTYLTYLFNN
F2365_ST1	281	ANNQISNLAPLSGL	TKLTELKLGANQIS	NISPLAGLTALT	NLELNENQLEDISPISNLK	NLTYLTYLFNN
L6-13	281	ANNQISNLAPLSGL	TKLTELKLGANQIS	NISPLAGLTALT	NLELNENQLEDISPISNLK	NLTYLTYLFNN
MRL-14-00459	281	ANNQISNLAPLSGL	TKLTELKLGANQIS	NISPLAGLTALT	NLELNENQLEDISPISNLK	NLTYLTYLFNN
CFSAN045864	281	ANNQISNLAPLSGL	TKLTELKLGANQIS	NISPLAGLTALT	NLELNENQLEDISPISNLK	NLTYLTYLFNN
CFSAN049281	281	ANNQISNLAPLSGL	TKLTELKLGANQIS	NISPLAGLTALT	NLELNENQLEDISPISNLK	NLTYLTYLFNN
CFSAN049294	281	ANNQISNLAPLSGL	TKLTELKLGANQIS	NISPLAGLTALT	NLELNENQLEDISPISNLK	NLTYLTYLFNN
CFSAN049301	281	ANNQISNLAPLSGL	TKLTELKLGANQIS	NISPLAGLTALT	NLELNENQLEDISPISNLK	NLTYLTYLFNN
ScottA_ST2	351	ISDISPVSSLTKL	QRLFFYNNKVS	DVSSLANLT	NINWLSAGHNQISDLTPLANL	TRITQLGLNDQAWTNP
EGD-e_ST35	351	ISDISPVSSLTKL	QRLFFYNNKVS	DVSSLANLT	NINWLSAGHNQISDLTPLANL	TRITQLGLNDQAWTNA
10403S_ST85	351	ISDISPVSSLTKL	QRLFFYNNKVS	DVSSLANLT	NINWLSAGHNQISDLTPLANL	TRITQLGLNDQAWTNA
F2365_ST1	351	ISDISPVSSLTKL	QRLFFYNNKVS	DVSSLANLT	NINWLSAGHNQISDLTPLANL	TRITQLGLNDQAWTNP
L6-13	351	ISDISPVSSLTKL	QRLFFYNNKVS	DVSSLANLT	NINWLSAGHNQISDLTPLANL	TRITQLGLNDQAWTNA
MRL-14-00459	351	ISDISPVSSLTKL	QRLFFYNNKVS	DVSSLANLT	NINWLSAGHNQISDLTPLANL	TRITQLGLNDQAWTNA
CFSAN045864	351	ISDISPVSSLTKL	QRLFFYNNKVS	DVSSLANLT	NINWLSAGHNQISDLTPLANL	TRITQLGLNDQAWTNA
CFSAN049281	351	ISDISPVSSLTKL	QRLFFYNNKVS	DVSSLANLT	NINWLSAGHNQISDLTPLANL	TRITQLGLNDQAWTNA
CFSAN049294	351	ISDISPVSSLTKL	QRLFFYNNKVS	DVSSLANLT	NINWLSAGHNQISDLTPLANL	TRITQLGLNDQAWTNA
CFSAN049301	351	ISDISPVSSLTKL	QRLFFYNNKVS	DVSSLANLT	NINWLSAGHNQISDLTPLANL	TRITQLGLNDQAWTNA
ScottA_ST2	421	PVNYKANVSIP	NTVK	NVTGAL	IAPATISDGGSYTEPDITWN	LPSYTNEVSYTFSQVPTIGKGTTFSGTV
EGD-e_ST35	421	PVNYKANVSIP	NTVK	NVTGAL	IAPATISDGGSYTEPDITWN	LPSYTNEVSYTFSQVPTIGKGTTFSGTV
10403S_ST85	421	PVNYKANVSIP	NTVK	NVTGAL	IAPATISDGGSYTEPDITWN	LPSYTNEVSYTFSQVPTIGKGTTFSGTV
F2365_ST1	421	PVNYKANVSIP	NTVK	NVTGAL	IAPATISDGGSYTEPDITWN	LPSYTNEVSYTFSQVPTIGKGTTFSGTV
L6-13	421	PVNYKANVSIP	NTVK	NVTGAL	IAPATISDGGSYTEPDITWN	LPSYTNEVSYTFSQVPTIGKGTTFSGTV
MRL-14-00459	421	PVNYKANVSIP	NTVK	NVTGAL	IAPATISDGGSYTEPDITWN	LPSYTNEVSYTFSQVPTIGKGTTFSGTV
CFSAN045864	421	PVNYKANVSIP	NTVK	NVTGAL	IAPATISDGGSYTEPDITWN	LPSYTNEVSYTFSQVPTIGKGTTFSGTV

CFSAN049281	421	PVNYKANVSIPNTVKNVTGALIAPATISDGGSYTEPDITWNLPSTNEVSYTFSQPVTIGKGTTFSGTV
CFSAN049294	421	PVNYKANVSIPNTVKNVTGALIAPATISDGGSYTEPDITWNLPSTNEVSYTFSQPVTIGKGTTFSGTV
CFSAN049301	421	PVNYKANVSIPNTVKNVTGALIAPATISDGGSYTEPDITWNLPSTNEVSYTFSQPVTIGKGTTFSGTV

ScottA ST2	491	TQPLKAIFNAKFHVDGKETTTKEVEAGNLLTEPAKPVKEGHTFVGWFDAQTGGTKWNFESTDKMPTNDIDL
EGD-e ST35	491	TQPLKAIFNVKFHVDGKETTTKEVEAGNLLTEPAKPVKEGHTFVGWFDAQTGGTKWNFESTDKMPTNDINLY
10403S ST85	491	TQPLKAIFNAKFHVDGKETTTKEVEAGNLLTEPAKPVKEGHTFVGWFDAQTGGTKWNFESTDKMPTNDINLY
F2365 ST1	491	TQPLKAIFNAKFHVDGKETTTKEVEAGNLLTEPAKPVKEGHTFVGWFDAQTGGTKWNFESTDKMPTNDIDL
L6-13	491	TQPLKAIFNVKFHVDGKETTTKEVEAGNLLTEPAKPVKEGHTFVGWFDAQTGGTKWDFSTDKMPTNDIDL
MRL-14-00459	491	TQPLKAIFNVKFHVDGKETTTKEVEAGNLLTEPAKPVKEGHTFVGWFDAQTGGTKWDFSTDKMPTNDIDL
CFSAN045864	491	TQPLKAIFNVKFHVDGKETTTKEVEAGNLLTEPAKPVKEGHTFVGWFDAQTGGTKWDFSTDKMPTNDIDL
CFSAN049281	491	TQPLKAIFNVKFHVDGKETTTKEVEAGNLLTEPAKPVKEGHTFVGWFDAQTGGTKWDFSTDKMPTNDIDL
CFSAN049294	491	TQPLKAIFNVKFHVDGKETTTKEVEAGNLLTEPAKPVKEGHTFVGWFDAQTGGTKWDFSTDKMPTNDIDL
CFSAN049301	491	TQPLKAIFNVKFHVDGKETTTKEVEAGNLLTEPAKPVKEGHTFVGWFDAQTGGTKWDFSTDKMPTNDIDL

ScottA ST2	561	AQFSINSYATATFDNDGVTTSTQTVDYQGLLQEPAPTKEGYTFKGWYDAKTGGDKWDFATSKMPAKNITLY
EGD-e ST35	561	AQFSINSYATATFDNDGVTTSTQTVDYQGLLQEPAPTKEGYTFKGWYDAKTGGDKWDFATSKMPAKNITLY
10403S ST85	561	AQFSINSYATATFDNDGVTTSTQTVDYQGLLQEPAPTKEGYTFKGWYDAKTGGDKWDFATSKMPAKNITLY
F2365 ST1	561	AQFSINSYATATFDNDGVTTSTQTVDYQGLLQEPAPTKEGYTFKGWYDAKTGGDKWDFATSKMPAKNITLY
L6-13	561	AQFSINSYATATFDNDGVTTSTQTVDYQGLLQEPAPTKEGYTFKGWYDAKTGGDKWDFATSKMPAKNITLY
MRL-14-00459	561	AQFSINSYATATFDNDGVTTSTQTVDYQGLLQEPAPTKEGYTFKGWYDAKTGGDKWDFATSKMPAKNITLY
CFSAN045864	561	AQFSINSYATATFDNDGVTTSTQTVDYQGLLQEPAPT-----
CFSAN049281	561	AQFSINSYATATFDNDGVTTSTQTVDYQGLLQEPAPT-----
CFSAN049294	561	AQFSINSYATATFDNDGVTTSTQTVDYQGLLQEPAPT-----
CFSAN049301	561	AQFSINSYATATFDNDGVTTSTQTVDYQGLLQEPAPT-----

ScottA ST2	631	AQYSANSYATATFDNDGKSTTQAVDYQGLLKEPKAPTPTKAGYTFKGWYDEKTDGKKWDFATDKMPANDITLY
EGD-e ST35	631	AQYSANSYATATFDNDGKSTTQAVDYQGLLKEPKAPTPTKAGYTFKGWYDEKTDGKKWDFATDKMPANDITLY
10403S ST85	631	AQYSANSYATATFDNDGKSTTQAVDYQGLLKEPKAPTPTKAGYTFKGWYDEKTDGKKWDFATDKMPANDITLY
F2365 ST1	631	AQYSANSYATATFDNDGKSTTQAVDYQGLLKEPKAPTPTKAGYTFKGWYDEKTDGKKWDFATDKMPANDITLY
L6-13	631	AQYSANSYATATFDNDGKSTTQAVDYQGLLKEPKAPTPTKAGYTFKGWYDEKTDGKKWDFATDKMPANDITLY
MRL-14-00459	631	AQYSANSYATATFDNDGKSTTQAVDYQGLLKEPKAPTPTKAGYTFKGWYDEKTDGKKWDFATDKMPANDITLY
CFSAN045864	595	-----PTKAGYTFKGWYDEKTDGKKWDFATDKMPANDITLY
CFSAN049281	595	-----PTKAGYTFKGWYDEKTDGKKWDFATDKMPANDITLY
CFSAN049294	595	-----PTKAGYTFKGWYDEKTDGKKWDFATDKMPANDITLY
CFSAN049301	595	-----PTKAGYTFKGWYDEKTDGKKWDFATDKMPANDITLY

ScottA ST2	701	AQFTKNPVAPPTTGGNTPTPTTNNGGNTTTPPSANIPGSDTNTSTGNSASTTSTMNAYDPYNSKEASLPPT
EGD-e ST35	701	AQFTKNPVAPPTTGGNTPTPTTNNGGNTTTPPSANIPGSDTNTSTGNSASTTSTMNAYDPYNSKEASLPPT
10403S ST85	701	AQFTKNPVAPPTTGGNTPTPTTNNGGNTTTPPSANIPGSDTNTSTGNSASTTSTMNAYDPYNSKEASLPPT
F2365 ST1	701	AQFTKNPVAPPTTGGNTPTPTTNNGGNTTTPPSANIPGSDTNTSTGNSASTTSTMNAYDPYNSKEASLPPT
L6-13	701	AQFTKNPVAPPTTGGNTPTPTTNNGGNTTTPPSANIPGSDTNTSTGNSASTTSTMNAYDPYNSKEASLPPT
MRL-14-00459	701	AQFTKNPVAPPTTGGNTPTPTTNNGGNTTTPPSANIPGSDTNTSTGNSASTTSTMNAYDPYNSKEASLPPT
CFSAN045864	631	AQFTKNPVAPPTTGGNTPTPTTNNGGNTTTPPSANIPGSDTNTSTGNSASTTSTMNAYDPYNSKEASLPPT
CFSAN049281	631	AQFTKNPVAPPTTGGNTPTPTTNNGGNTTTPPSANIPGSDTNTSTGNSASTTSTMNAYDPYNSKEASLPPT
CFSAN049294	631	AQFTKNPVAPPTTGGNTPTPTTNNGGNTTTPPSANIPGSDTNTSTGNSASTTSTMNAYDPYNSKEASLPPT
CFSAN049301	631	AQFTKNPVAPPTTGGNTPTPTTNNGGNTTTPPSANIPGSDTNTSTGNSASTTSTMNAYDPYNSKEASLPPT

ScottA ST2	771	GDSDNALYLLGLLAVGTAMALTKKARASK
EGD-e ST35	771	GDSDNALYLLGLLAVGTAMALTKKARASK
10403S ST85	771	GDSDNALYLLGLLAVGTAMALTKKARASK
F2365 ST1	771	GDSDNALYLLGLLAVGTAMALTKKARASK
L6-13	771	GDSDNALYLLGLLAVGTAMALTKKARASK
MRL-14-00459	771	GDSDNALYLLGLLAVGTAMALTKKARASK
CFSAN045864	701	GDSDNALYLLGLLAVGTAMALTKKARASK
CFSAN049281	701	GDSDNALYLLGLLAVGTAMALTKKARASK
CFSAN049294	701	GDSDNALYLLGLLAVGTAMALTKKARASK
CFSAN049301	701	GDSDNALYLLGLLAVGTAMALTKKARASK

Figure S3A. Alignment of *htrA* nucleotide sequences

ScottA_ST2	1	ATGGACGAGAAAGAAAAGAATTTAAATGAAAACAGCGAGAATGAAAGCACGCC	AAAAGAGAGGTCGAGG
EGD-e_ST35	1	ATGGACGAGAAAGAAAAGAATTTAAATGAAAACAGCGAGAATGAAAGCACGCCG	AAAAGAGAGGTCGAGG
10403S_ST85	1	ATGGACGAGAAAGAAAAGAATTTAAATGAAAACAGCGAGAATGAAAGCACGCCG	AAAAGAGAGGTCGAGG
F2365_ST1	1	ATGGACGAGAAAGAAAAGAATTTAAATGAAAACAGCGAGAATGAAAGCACGCC	AAAAGAGAGGTCGAGG
P12_10_ST155	1	ATGGACGAGAAAGAAAAGAATTTAAATGAAAACAGCGAGAATGAAAGCACGCCG	AAAAGAGAGGTCGAGG
ScottA_ST2	71	ATACTTTACATACACCGGAGAGCGCGCAACCAGTCCAAGAACTCCTATTGTAGAAAGGCGTGACCCCA	G
EGD-e_ST35	71	ATACTTTACATACACCGGAGAGCGCGCAACCAGTCCAAGAACTCCTATTGTAGAAAGGCGTGACCCCA	G
10403S_ST85	71	ATACTTTACATACACCGGAGAGCGCGCAACCAGTCCAAGAACTCCTATTGTAGAAAGGCGTGACCCCA	G
F2365_ST1	71	ATACTTTACATACACCGGAGAGCGCGCAACCAGTCCAAGAACTCCTATTGTAGAAAGGCGTGACCCCA	G
P12_10_ST155	71	ATACTTTACATACACCGGAGAGCGCGCAACCAGTCCAAGAACTCCTATTGTAGAAAGGCGTGACCCCA	G
ScottA_ST2	141	AGGGGAGAAATTTGCCGGAGCGACAGAAGATGCAGCCGAGGCGAGTTCTACAAATGCATTTTTTGAAGAA	
EGD-e_ST35	141	AGGGGAGAAATTTGCCGGAGCGACAGAAGATGCAGCCGAGGCGAGTTCTACAAATGCATTTTTTGAAGAA	
10403S_ST85	141	AGGGGAGAAATTTGCCGGAGCGACAGAAGATGCAGCCGAGGCGAGTTCTACAAATGCATTTTTTGAAGAA	
F2365_ST1	141	AGGGGAGAAATTTGCCGGAGCGACAGAAGATGCAGCCGAGGCGAGTTCTACAAATGCATTTTTTGAAGAA	
P12_10_ST155	141	AGGGGAGAAATTTGCCGGAGCGACAGAAGATGCAGCCGAGGCGAGTTCTACAAATGCATTTTTTGAAGAA	
ScottA_ST2	211	GCAAGTAATAAAGAAC	CAGAACCTGCTAGACCGGCTCCAGGGCCAAGACGCGCTGGTACAACCTGGTGGCG
EGD-e_ST35	211	GCAAGTAATAAAGAAC	CAGAACCTGCTAGACCGGCTCCAGGGCCAAGACGCGCTGGTACAACCTGGTGGCG
10403S_ST85	211	GCAAGTAATAAAGAAC	CAGAACCTGCTAGACCGGCTCCAGGGCCAAGACGCGCTGGTACAACCTGGTGGCG
F2365_ST1	211	GCAAGTAATAAAGAAC	CAGAACCTGCTAGACCGGCTCCAGGGCCAAGACGCGCTGGTACAACCTGGTGGCG
P12_10_ST155	211	GCAAGTAATAAAGAAC	CAGAACCTGCTAGACCGGCTCCAGGGCCAAGACGCGCTGGTACAACCTGGTGGCG
ScottA_ST2	281	GGGCAGTTCAC	CTAATAGAGTGAATAATGGCGGAAGTGGTAACGGGAATGGTGAACCACCGAAACG
EGD-e_ST35	281	GGGCAGTTCAC	CTAATAGAGTGAATAATGGCGGAAGTGGTAACGGGAATGGTGAACCACCGAAACG
10403S_ST85	281	GGGCAGTTCAC	CTAATAGAGTGAATAATGGCGGAAGTGGTAACGGGAATGGTGAACCACCGAAACG
F2365_ST1	281	GGGCAGTTCAC	CTAATAGAGTGAATAATGGCGGAAGTGGTAACGGGAATGGTGAACCACCGAAACG
P12_10_ST155	281	GGGCAGTTCAC	CTAATAGAGTGAATAATGGCGGAAGTGGTAACGGGAATGGTGAACCACCGAAACG
ScottA_ST2	348	CGGCAAAACACTTTAT	CGGTACTTTTTTAACAGCACTTATTGGTGTATTATCGGAGGACTTATTATTTTC
EGD-e_ST35	348	CGGCAAAACACTTTAT	CGGTACTTTTTTAACAGCACTTATTGGTGTATTATCGGAGGACTTATTATTTTC
10403S_ST85	351	CGGCAAAACACTTTAT	CGGTACTTTTTTAACAGCACTTATTGGTGTATTATCGGAGGACTTATTATTTTC
F2365_ST1	348	CGGCAAAACACTTTAT	CGGTACTTTTTTAACAGCACTTATTGGTGTATTATCGGAGGACTTATTATTTTC
P12_10_ST155	351	CGGCAAAACACTTTAT	CGGTACTTTTTTAACAGCACTTATTGGTGTATTATCGGAGGACTTATTATTTTC
ScottA_ST2	418	TTTGTGCGTTGGGATAATGGT	GA
EGD-e_ST35	418	TTTGTGCGTTGGGATAATGGC	GATAACAACCTCAAACCTCAAATAATAAAGCTACCAAAGTAG
10403S_ST85	421	TTTGTGCGTTGGGATAATGGC	GATAACAACCTCAAACCTCAAATAATAAAGCTACCAAAGTAG
F2365_ST1	418	TTTGTGCGTTGGGATAATGGT	GA
P12_10_ST155	421	TTTGTGCGTTGGGATAATGGC	GATAACAACCTCAAACCTCAAATAATAAAGCTACCAAAGTAG
ScottA_ST2	488	AAAAAGTTTC	GTAGATACAACATCAGATGTAACAAAAGCAGTAGACAAAGT
EGD-e_ST35	488	AAAAAGTTTC	GTAGATACAACATCAGATGTAACAAAAGCAGTAGACAAAGT
10403S_ST85	491	AAAAAGTTTC	GTAGATACAACATCAGATGTAACAAAAGCAGTAGACAAAGT
F2365_ST1	488	AAAAAGTTTC	GTAGATACAACATCAGATGTAACAAAAGCAGTAGACAAAGT
P12_10_ST155	491	AAAAAGTTTC	GTAGATACAACATCAGATGTAACAAAAGCAGTAGACAAAGT
ScottA_ST2	558	TGT	CTAAATTACCAATCATCTTCATCCCTTGATGGAACAACGACTTCTGAACAAGAAGCTTCCTCAGGA
EGD-e_ST35	558	TGT	CTAAATTACCAATCATCTTCATCCCTTGATGGAACAACGACTTCTGAACAAGAAGCTTCCTCAGGA
10403S_ST85	561	TGT	CTAAATTACCAATCATCTTCATCCCTTGATGGAACAACGACTTCTGAACAAGAAGCTTCCTCAGGA
F2365_ST1	558	TGT	CTAAATTACCAATCATCTTCATCCCTTGATGGAACAACGACTTCTGAACAAGAAGCTTCCTCAGGA
P12_10_ST155	561	TGT	CTAAATTACCAATCATCTTCATCCCTTGATGGAACAACGACTTCTGAACAAGAAGCTTCCTCAGGA
ScottA_ST2	628	TCTGGTGTATT	TATAAAAAGGCAAAATGGAAGCCTACATCGTAACAAATAATCACGTTGTTGCTGATG
EGD-e_ST35	628	TCTGGTGTATT	TATAAAAAGGCAAAATGGAAGCCTACATCGTAACAAATAATCACGTTGTTGCTGATG
10403S_ST85	631	TCTGGTGTATT	TATAAAAAGGCAAAATGGAAGCCTACATCGTAACAAATAATCACGTTGTTGCTGATG
F2365_ST1	628	TCTGGTGTATT	TATAAAAAGGCAAAATGGAAGCCTACATCGTAACAAATAATCACGTTGTTGCTGATG
P12_10_ST155	631	TCTGGTGTATT	TATAAAAAGGCAAAATGGAAGCCTACATCGTAACAAATAATCACGTTGTTGCTGATG
ScottA_ST2	698	CAATAAATTAGAAGTA	AACTTTTACAACCGGTAAAAAATCCGAAGCAAAATTACT
EGD-e_ST35	698	CAATAAATTAGAAGTA	AACTTTTACAACCGGTAAAAAATCCGAAGCAAAATTACT
10403S_ST85	701	CAATAAATTAGAAGTA	AACTTTTACAACCGGTAAAAAATCCGAAGCAAAATTACT
F2365_ST1	698	CAATAAATTAGAAGTA	AACTTTTACAACCGGTAAAAAATCCGAAGCAAAATTACT
P12_10_ST155	701	CAATAAATTAGAAGTA	AACTTTTACAACCGGTAAAAAATCCGAAGCAAAATTACT
ScottA_ST2	768	GAACGATTTAGCTGT	TCTTGAAATTGATGATAAAAATGTTACTACAGTCGCTGCATTTCGGCGATTTCAGAT
EGD-e_ST35	768	GAACGATTTAGCTGT	TCTTGAAATTGATGATAAAAATGTTACTACAGTCGCTGCATTTCGGCGATTTCAGAT
10403S_ST85	771	GAACGATTTAGCTGT	TCTTGAAATTGATGATAAAAATGTTACTACAGTCGCTGCATTTCGGCGATTTCAGAT

F2365 ST1	768	GAACGATTAGCTGTTCTTGAAATTGATGATAAAAAATGTTACTACAGTCGCTGCATTTCGGCGATTTCAGAT
P12_10_ST155	771	GAACGATTAGCTGTTCTTGAAATTGATGATAAAAAATGTTACTACAGTCGCTGCATTTCGGCGATTTCAGAT
ScottA ST2	838	TCATTAAAACTTGGTGAACCAGCAATTGCAATTGGTAGCCCACTAGGAACGAATTTCCGGTTCTGTAA
EGD-e ST35	838	TCATTAAAACTTGGTGAACCAGCAATTGCAATTGGTAGCCCACTAGGAACGGAATTTCCGGTTCTGTAA
10403S ST85	841	TCATTAAAACTTGGTGAACCAGCAATTGCAATTGGTAGCCCACTAGGAACGGAATTTCCGGTTCTGTAA
F2365 ST1	838	TCATTAAAACTTGGTGAACCAGCAATTGCAATTGGTAGCCCACTGGAACGAATTTCCGGTTCTGTAA
P12_10_ST155	841	TCATTAAAACTTGGTGAACCAGCAATTGCAATTGGTAGCCCACTAGGAACGGAATTTCCGGTTCTGTAA
ScottA ST2	908	CACAAGGTATTATTCTGGTCTAAACCGTGCAGTACCAGTTGATACAAATGGCGACGGAACAGAAGACTG
EGD-e ST35	908	CACAAGGTATTATTCTGGTCTAAACCGTGCAGTACCAGTTGATACAAATGGCGACGGAACAGAAGACTG
10403S ST85	911	CACAAGGTATTATTCTGGTCTAAACCGTGCAGTACCAGTTGATACAAATGGCGACGGAACAGAAGACTG
F2365 ST1	908	CACAAGGTATTATTCTGGTCTAAACCGTGCAGTACCAGTTGATACAAATGGCGACGGAACAGAAGACTG
P12_10_ST155	911	CACAAGGTATTATTCTGGTCTAAACCGTGCAGTACCAGTTGATACAAATGGCGACGGAACAGAAGACTG
ScottA ST2	978	GGAAGCAGATGTTATCCAAACAGATGCAGCAATTAACCCGGTAACAGTGGTGGAGCTTTAATTAATTAATT
EGD-e ST35	978	GGAAGCAGATGTTATCCAAACAGATGCAGCAATCAATCCAGGTAAACAGTGGTGGAGCTTTAATTAACATT
10403S ST85	981	GGAAGCAGATGTTATCCAAACAGATGCAGCAATCAATCCAGGTAAACAGTGGTGGAGCTTTAATTAACATT
F2365 ST1	978	GGAAGCAGATGTTATCCAAACAGATGCAGCAATTAACCCGGTAACAGTGGTGGAGCTTTAATTAATTAATT
P12_10_ST155	981	GGAAGCAGATGTTATCCAAACAGATGCAGCAATCAATCCAGGTAAACAGTGGTGGAGCTTTAATTAACATT
ScottA ST2	1048	GAAGGCCAAGTAATGGTATTAACTCAATGAAAATTTTCGATGGAAAATGTAGAAGGTATTAGCTTTGC
EGD-e ST35	1048	GAAGGCCAAGTAATCGGTATTAACTCAATGAAAATTTTCGATGGAAAATGTAGAAGGTATTAGCTTTGC
10403S ST85	1051	GAAGGCCAAGTAATCGGTATCACTCAATGAAAATTTTCGATGGAAAATGTAGAAGGTATTAGCTTTGC
F2365 ST1	1048	GAAGGCCAAGTAATGGTATTAACTCAATGAAAATTTTCGATGGAAAATGTAGAAGGTATTAGCTTTGC
P12_10_ST155	1051	GAAGGCCAAGTAATCGGTATTAACTCAATGAAAATTTTCGATGGAAAATGTAGAAGGTATTAGCTTTGC
ScottA ST2	1118	TTCCAAGTAACACAGTAGAACCAATCATCGAACAACTAGAAACAAAAGGCGAAGTAGAACGTCCATCTCT
EGD-e ST35	1118	TTCCAAGTAACACAGTAGAACCAATATCGAACAACTAGAAACAAAAGGCGAAGTAGAACGTCCATCTCT
10403S ST85	1121	TTCCAAGTAACACAGTAGAACCAATCATCGAACAACTAGAAACAAAAGGCGAAGTAGAACGTCCATCTCT
F2365 ST1	1118	TTCCAAGTAACACAGTAGAACCAATCATCGAACAACTAGAAACAAAAGGCGAAGTAGAACGTCCATCTCT
P12_10_ST155	1121	TTCCAAGTAACACAGTAGAACCAATATCGAACAACTAGAAACAAAAGGCGAAGTAGAACGTCCATCTCT
ScottA ST2	1188	AGGCGTATCCTTACGTGATGGTTGATACAATTCCAGAAACACAACAAAAAATATCTTGAAATTACCTGAT
EGD-e ST35	1188	AGGTGTATCCTTACGTGACGTTGATACAATTCCAGAAACACAACAAAAAATATCTTGAAATTACCTGAT
10403S ST85	1191	AGGTGTATCCTTACGTGACGTTGATACAATTCCAGAAACACAACAAAAAATATCTTGAAATTACCTGAT
F2365 ST1	1188	AGGCGTATCCTTACGTGATGGTTGATACAATTCCAGAAACACAACAAAAAATATCTTGAAATTACCTGAT
P12_10_ST155	1191	AGGTGTATCCTTACGTGACGTTGATACAATTCCAGAAACACAACAAAAAATATCTTGAAATTACCTGAT
ScottA ST2	1258	AGCGTAGATTACGGCGCAATGGTACAACAAGTAGTATCCGGTTCTGCAGCAGACAAAGCAGGCTTGAAAC
EGD-e ST35	1258	AGCGTAGATTACGGCGCAATGGTACAACAAGTAGTATCCGGTTCTGCAGCAGACAAAGCAGGCTTGAAAC
10403S ST85	1261	AGCGTAGATTACGGCGCAATGGTACAACAAGTAGTATCCGGTTCTGCAGCAGACAAAGCAGGCTTGAAAC
F2365 ST1	1258	AGCGTAGATTACGGCGCAATGGTACAACAAGTAGTATCCGGTTCTGCAGCAGACAAAGCAGGCTTGAAAC
P12_10_ST155	1261	AGCGTAGATTACGGCGCAATGGTACAACAAGTAGTATCGGTTCTGCAGCAGACAAAGCAGGCTTGAAAC
ScottA ST2	1328	AATACGATGTTATTGTTGAACTAAACGGCCAAAAAGTAACAAACTCCATGACATTACGCAAAATTCCTATA
EGD-e ST35	1328	AATACGATGTTATTGTTGAACTAAACGGCCAAAAAGTAACAAACTCCATGACATTACGCAAAATTCCTATA
10403S ST85	1331	AATACGATGTTATTGTTGAACTAAACGGCCAAAAAGTAACAAACTCCATGACATTACGCAAAATTCCTATA
F2365 ST1	1328	AATACGATGTTATTGTTGAACTAAACGGCCAAAAAGTAACAAACTCCATGACATTACGCAAAATTCCTATA
P12_10_ST155	1331	AATACGATGTAATTGTTGAACTAAACGGCCAAAAAGTAACAAACTCTATGACATTACGCAAAATTCCTATA
ScottA ST2	1398	CGGTAACGACGTGAAAATTGGCGATAAAGTCAAAGTAAATACTATCGTGACGGTAAAGAAAAATCCACA
EGD-e ST35	1398	CGGTAACGACGTGAAAATTGGCGATAAAGTCAAAGTAAATACTATCGTGACGGTAAAGAAAAATCCACA
10403S ST85	1401	CGGTAACGACGTGAAAATTGGCGATAAAGTCAAAGTAAATACTATCGTGACGGTAAAGAAAAATCCACA
F2365 ST1	1398	CGGTAACGACGTGAAAATTGGCGATAAAGTCAAAGTAAATACTATCGTGACGGTAAAGAAAAATCCACA
P12_10_ST155	1401	CGGTAACGACGTGAAAATTGGCGATAAAGTCAAAGTAAATACTATCGTGACGGTAAAGAAAAATCCACA
ScottA ST2	1468	GATATTAAATTAGAAGCAGCAAAAACAACTACATGA
EGD-e ST35	1468	GATATTAAATTAGAAGCAGCAAAAACAACTACATGA
10403S ST85	1471	GATATTAAATTAGAAGCAGCAAAAACAACTACATGA
F2365 ST1	1468	GATATTAAATTAGAAGCAGCAAAAACAACTACATGA
P12_10_ST155	1471	GATATTAAATTAGAAGCAGCAAAAACAACTACATGA

Figure S3B. Alignment of HtrA protein sequences

ScottA_ST2	1	MDEKEKNLNENSENESTPKREVEDTLHTPESAQPVQETPIVEGVTPERGEKFAGATEDAAEASSTNAFFEE
EGD-e_ST35	1	MDEKEKNLNENSENESTPKREVEDTLHTPESAQPVQETPIVEGVTPERGEKFAGATEDAAEASSTNAFFEE
10403S_ST85	1	MDEKEKNLNENSENESTPKREVEDTLHTPESAQPVQETPIVEGVTPERGEKFAGATEDAAEASSTNAFFEE
F2365_ST1	1	MDEKEKNLNENSENESTPKREVEDTLHTPESAQPVQETPIVEGVTPERGEKFAGATEDAAEASSTNAFFEE
P12_10_ST155	1	MDEKEKNLNENSENESTPKREVEDTLHTPESAQPVQETPIVEGVTPERGEKFAGATEDAAEASSTNAFFEE
ScottA_ST2	71	ASNKEPEPARPAPGPRRAGTTGGGAVPP-NRVNNGSGSGNGEPPKRGKHFIGYFLTALIGVIIIGGLIIF
EGD-e_ST35	71	ASNKESEPARPAPGPRRAGTTGGGAVPP-NRVNNGSGSGNGEPPKRGKHFIGYFLTALIGVIIIGGLIIF
10403S_ST85	71	ASNKESEPARPAPGPRRAGTTGGGAVPP-NRVNNGSGSGNGEPPKRGKHFIGYFLTALIGVIIIGGLIIF
F2365_ST1	71	ASNKEPEPARPAPGPRRAGTTGGGAVPP-NRVNNGSGSGNGEPPKRGKHFIGYFLTALIGVIIIGGLIIF
P12_10_ST155	71	ASNKESEPARPAPGPRRAGTTGGGAVPP-NRVNNGSGSGNGEPPKRGKHFIGYFLTALIGVIIIGGLIIF
ScottA_ST2	140	FVAWDNGDNADTTNSNNKATKVEKVSVDTTSDVTKAVDKVQDAVSVLNYQSSSSLDGTTTSEQEASSG
EGD-e_ST35	140	FVAWDNGDNADTTNSNNKATKVEKVSVDTTSDVTKAVDKVQDAVSVLNYQSSSSLDGTTTSEQEASSG
10403S_ST85	141	FVAWDNGDNADTTNSNNKATKVEKVSVDTTSDVTKAVDKVQDAVSVLNYQSSSSLDGTTTSEQEASSG
F2365_ST1	140	FVAWDNGDNADTTNSNNKATKVEKVSVDTTSDVTKAVDKVQDAVSVLNYQSSSSLDGTTTSEQEASSG
P12_10_ST155	141	FVAWDNGDNADTTNSNNKATKVEKVSVDTTSDVTKAVDKVQDAVSVLNYQSSSSLDGTTTSEQEASSG
ScottA_ST2	210	SGVIYKKANGKAYIVTNNHVADANKLEVFTNGKKSEAKLLGTDEWNDLAVLEIDDKNVTVAAFGDS
EGD-e_ST35	210	SGVIYKKANGKAYIVTNNHVADANKLEVFTNGKKSEAKLLGTDEWNDLAVLEIDDKNVTVAAFGDS
10403S_ST85	211	SGVIYKKANGKAYIVTNNHVADANKLEVFTNGKKSEAKLLGTDEWNDLAVLEIDDKNVTVAAFGDS
F2365_ST1	210	SGVIYKKANGKAYIVTNNHVADANKLEVFTNGKKSEAKLLGTDEWNDLAVLEIDDKNVTVAAFGDS
P12_10_ST155	211	SGVIYKKANGKAYIVTNNHVADANKLEVFTNGKKSEAKLLGTDEWNDLAVLEIDDKNVTVAAFGDS
ScottA_ST2	280	SLKLGEPAIAIGSPLGTEFSGSVTQGIISGLNRAVPVDTNGDGTEDWEADVQTDAAINPGNSGGALINI
EGD-e_ST35	280	SLKLGEPAIAIGSPLGTEFSGSVTQGIISGLNRAVPVDTNGDGTEDWEADVQTDAAINPGNSGGALINI
10403S_ST85	281	SLKLGEPAIAIGSPLGTEFSGSVTQGIISGLNRAVPVDTNGDGTEDWEADVQTDAAINPGNSGGALINI
F2365_ST1	280	SLKLGEPAIAIGSPLGTEFSGSVTQGIISGLNRAVPVDTNGDGTEDWEADVQTDAAINPGNSGGALINI
P12_10_ST155	281	SLKLGEPAIAIGSPLGTEFSGSVTQGIISGLNRAVPVDTNGDGTEDWEADVQTDAAINPGNSGGALINI
ScottA_ST2	350	EGQVIGINSMKISMENVEGISFAIPSNVTEPIIEQLETKGEVERPSLGVSLRDVDTIPETQQKNILKLPD
EGD-e_ST35	350	EGQVIGINSMKISMENVEGISFAIPSNVTEPIIEQLETKGEVERPSLGVSLRDVDTIPETQQKNILKLPD
10403S_ST85	351	EGQVIGINSMKISMENVEGISFAIPSNVTEPIIEQLETKGEVERPSLGVSLRDVDTIPETQQKNILKLPD
F2365_ST1	350	EGQVIGINSMKISMENVEGISFAIPSNVTEPIIEQLETKGEVERPSLGVSLRDVDTIPETQQKNILKLPD
P12_10_ST155	351	EGQVIGINSMKISMENVEGISFAIPSNVTEPIIEQLETKGEVERPSLGVSLRDVDTIPETQQKNILKLPD
ScottA_ST2	420	SVDYGAMVQQVVS GS AADKAGLKQYDVIVELNGQKVTNSMTLRKILYGN DVKIGDKVKVKYYRDGKEKST
EGD-e_ST35	420	SVDYGAMVQQVVS GS AADKAGLKQYDVIVELNGQKVTNSMTLRKILYGN DVKIGDKVKVKYYRDGKEKST
10403S_ST85	421	SVDYGAMVQQVVS GS AADKAGLKQYDVIVELNGQKVTNSMTLRKILYGN DVKIGDKVKVKYYRDGKEKST
F2365_ST1	420	SVDYGAMVQQVVS GS AADKAGLKQYDVIVELNGQKVTNSMTLRKILYGN DVKIGDKVKVKYYRDGKEKST
P12_10_ST155	421	SVDYGAMVQQVVS GS AADKAGLKQYDVIVELNGQKVTNSMTLRKILYGN DVKIGDKVKVKYYRDGKEKST
ScottA_ST2	490	DIKLEAAKTTT
EGD-e_ST35	490	DIKLEAAKTTT
10403S_ST85	491	DIKLEAAKTTT
F2365_ST1	490	DIKLEAAKTTT
P12_10_ST155	491	DIKLEAAKTTT

Figure S4A. Alignment of aut nucleotide sequences

ScottA ST2	1	ATGATAAAATAAAAA-TGGATGAAAAATTGTAATGATTCCGATGCTA-TTGT-----
EGD-e ST35	1	ATGAT---TAAAAAAGTTTTTCATTTTATACTTGTACTGATGTTA-CTGTAAGTATAATA
10403S ST85	1	ATGAT---TAAAAAAGTTTTTCATTTTATACTTGTACTGATGTTA-CTGTAAGTATAATA
F2365 ST1	1	ATGATAAAATAAAAA-TGGATGAAAAATTGTAATGATTCCGATGCTA-TTGT-----
L6-13 ST155	1	ATGAT---TAAAAAAGTTTTTCATTTTATACTTGTACTGATGTTA-CTGTAAGTATAATA
MRL-14-00459 ST	1	ATGAT---TAAAAAAGTTTTTCATTTTATACTTGTACTGATGTTA-CTGTAAGTATAATA
LmNG3_ST155	1	ATGAT---TAAAAAAGTTTTTCATTTTATACTTGTACTGATGTTA-CTGTAAGTATAATA

ScottA ST2	51	--TCCAATGTACGGTTTGACAACTG-----TTGGCG
EGD-e ST35	58	CCTCTATTCCATGCTAAAGCAGCTGAAACAATAATGGAGTAGATAGTAGTGAACAGGAA
10403S ST85	58	CCTCTATTCCATGCTAAAGCAGCTGAAACAATAATGGAGTAGATAGTAGTGAACAGGAA
F2365 ST1	51	--TCCAATGTACGGTTTGACAACTG-----TTGGCG
L6-13 ST155	58	CCTCTATTCCATGCTAAAGCAGCTGAAACAATAATGGAGTAGATAGTAGTGAACAGGAA
MRL-14-00459 ST	58	CCTCTATTCCATGCTAAAGCAGCTGAAACAATAATGGAGTAGATAGTAGTGAACAGGAA
LmNG3_ST155	58	CCTCTATTCCATGCTAAAGCAGCTGAAACAATAATGGAGTAGATAGTAGTGAACAGGAA

ScottA ST2	80	GACAATTACAGATT-----
EGD-e ST35	118	GATAATACCAAGTTGCGCGTGAAGAAATGCCTCCAGAGTCTGAGGAACCAAGTATTCTCG
10403S ST85	118	GATAATACCAAGTTGCGCGTGAAGAAATGCCTCCAGAGTCTGAGGAACCAAGTATTCTCG
F2365 ST1	80	GACAATTACAGATT-----
L6-13 ST155	118	GATAATACCAAGTTGCGCGTGAAGAAATGCCTCCAGAGTCTGAGGAACCAAGTATTCTCG
MRL-14-00459 ST	118	GATAATACCAAGTTGCGCGTGAAGAAATGCCTCCAGAGTCTGAGGAACCAAGTATTCTCG
LmNG3_ST155	118	GATAATACCAAGTTGCGCGTGAAGAAATGCCTCCAGAGTCTGAGGAACCAAGTATTCTCG

ScottA ST2	95	-----CATTAACCTGAGAGAAAT
EGD-e ST35	178	CTTGAACAAAATAGAGATGATGCTATGGCTGCTTTAGTCGTGCCTCAAACCTAGAAATAGT
10403S ST85	178	CTTGAACAAAATAGAGATGATGCTATGGCTGCTTTAGTCGTGCCTCAAACCTAGAAATAGT
F2365 ST1	95	-----CATTAACCTGAGAGAAAT
L6-13 ST155	178	CTTGAACAAAATAGAGATGATGCTATGGCTGCTTTAGTCGTGCCTCAAACCTAGAAATAGT
MRL-14-00459 ST	178	CTTGAACAAAATAGAGATGATGCTATGGCTGCTTTAGTCGTGCCTCAAACCTAGAAATAGT
LmNG3_ST155	178	CTTGAACAAAATAGAGATGATGCTATGGCTGCTTTAGTCGTGCCTCAAACCTAGAAATAGT

ScottA ST2	112	TCCTTTGTGTTAAAGAGTTTGAAGCTCAACGACAGCATCGCAACAACCATTTATCGACAAA
EGD-e ST35	238	TTTTTT-----GAGAGCAGCTAGTACTCCGACATTTCAACAACCATTTATAAATTCC
10403S ST85	238	TTTTTT-----GAGAGCAGCTAGTACTCCGACATTTCAACAACCATTTATAAATTCC
F2365 ST1	112	TCCTTTGTGTTAAAGAGTTTGAAGCTCAACGACAGCATCGCAACAACCATTTATCGACAAA
L6-13 ST155	238	TTTTTT-----GAGAGCAGCTAGTACTCCGACATTTCAACAACCATTTATAAATTCC
MRL-14-00459 ST	238	TTTTTT-----GAGAGCAGCTAGTACTCCGACATTTCAACAACCATTTATAAATTCC
LmNG3_ST155	238	TTTTTT-----GAGAGCAGCTAGTACTCCGACATTTCAACAACCATTTATAAATTCC

ScottA ST2	172	ATAGCACCTGCTGCCAGGCATCTCTACAAAAATATCATCTCTTATCTAGTTTAACTTTA
EGD-e ST35	289	ATTTTCACGCAAGCAATGGATTTATCTAAAAAGTACAATTTTATCCATCTCTAATGATT
10403S ST85	289	ATTTTCACGCAAGCAATGGATTTATCTAAAAAGTACAATTTTATCCATCTCTAATGATT
F2365 ST1	172	ATAGCACCTGCTGCCAGGCATCTCTACAAAAATATCATCTCTTATCTAGTTTAACTTTA
L6-13 ST155	289	ATTTTCACGCAAGCAATGGATTTATCTAAAAAGTACAATTTTATCCATCTCTAATGATT
MRL-14-00459 ST	289	ATTTTCACGCAAGCAATGGATTTATCTAAAAAGTACAATTTTATCCATCTCTAATGATT
LmNG3_ST155	289	ATTTTCACGCAAGCAATGGATTTATCTAAAAAGTACAATTTTATCCATCTCTAATGATT

ScottA ST2	232	GCTCAAGCAATTCTAGAAATCTGGTTGGGGAAAGAGTGAATTAGGGAGGGCCCTAATTAC
EGD-e ST35	349	GCTCAAGCGGCTCTTGAGAGTAACTGGGGAAAGAGTGAATTAGGGAGGGCCCTAATTAC
10403S ST85	349	GCTCAAGCGGCTCTTGAGAGTAACTGGGGAAAGAGTGAATTAGGGAGGGCCCTAATTAC
F2365 ST1	232	GCTCAAGCAATTCTAGAAATCTGGTTGGGGAAAGAGTGAATTAGGGAGGGCCCTAATTAC
L6-13 ST155	349	GCTCAAGCGGCTCTTGAGAGTAACTGGGGAAAGAGTGAATTAGGGAGGGCCCTAATTAC
MRL-14-00459 ST	349	GCTCAAGCGGCTCTTGAGAGTAACTGGGGAAAGAGTGAATTAGGGAGGGCCCTAATTAC
LmNG3_ST155	349	GCTCAAGCGGCTCTTGAGAGTAACTGGGGAAAGAGTGAATTAGGGAGGGCCCTAATTAC

ScottA ST2	289	AATTTTTTTGGTATAAAAGGCAATATAATGGACAAATCAGTTATCATGACAACTTCTGAA
EGD-e ST35	409	AACTTCTTTTGGAAATAAAAGGATCATATAATGGCAAAAGTGTAACAATGAAAACCTTGGGAA
10403S ST85	409	AACTTCTTTTGGAAATAAAAGGATCATATAATGGCAAAAGTGTAACAATGAAAACCTTGGGAA
F2365 ST1	289	AATTTTTTTGGTATAAAAGGCAATATAATGGACAAATCAGTTATCATGACAACTTCTGAA
L6-13 ST155	409	AACTTCTTTTGGAAATAAAAGGATCATATAATGGCAAAAGTGTAACAATGAAAACCTTGGGAA
MRL-14-00459 ST	409	AACTTCTTTTGGAAATAAAAGGATCATATAATGGCAAAAGTGTAACAATGAAAACCTTGGGAA
LmNG3_ST155	409	AACTTCTTTTGGAAATAAAAGGATCATATAATGGCAAAAGTGTAACAATGAAAACCTTGGGAA

ScottA ST2	349	TATGTGAA---CGGTGAGTGGATTAAATTCATGCTGAATTCGCGAAATACCCTAGCTGG
EGD-e ST35	469	TATGTGATTCCAAAGGTTGGTATCAAATCACGCAAACTTTGCCAAATACCCATCACAC
10403S ST85	469	TATGTGATTCCAAAGGTTGGTATCAAATCACGCAAACTTTGCCAAATACCCATCACAC
F2365 ST1	349	TATGTGAA---CGGTGAGTGGATTAAATTCATGCTGAATTCGCGAAATACCCTAGCTGG
L6-13 ST155	469	TATGTGATTCCAAAGGTTGGTATCAAATCACGCAAACTTTGCCAAATACCCATCACAC
MRL-14-00459 ST	469	TATGTGATTCCAAAGGTTGGTATCAAATCACGCAAACTTTGCCAAATACCCATCACAC
LmNG3 ST155	469	TATGTGATTCCAAAGGTTGGTATCAAATCACGCAAACTTTGCCAAATACCCATCACAC

ScottA ST2	406	AATGAATCTCTCACTGACCATCTCTTTTATTAGTGAACGGAACTTCTGGATATAAAGAC
EGD-e ST35	529	AAAGAATCTTTAGAAAGACAATCGGAAAAAACTTAGAAATGGCCCAAGTTGGTACTCTAGT
10403S ST85	529	AAAGAATCTTTAGAAAGACAATCGGAAAAAACTTAGAAATGGCCCAAGTTGGTACTCTAGT
F2365 ST1	406	AATGAATCTCTCACTGACCATCTCTTTTATTAGTGAACGGAACTTCTGGATATAAAGAC
L6-13 ST155	529	AAAGAATCTTTAGAAAGACAATCGGAAAAAACTTAGAAATGGCCCAAGTTGGTACTCTAGT
MRL-14-00459 ST	529	AAAGAATCTTTAGAAAGACAATCGGAAAAAACTTAGAAATGGCCCAAGTTGGTACTCTAGT
LmNG3 ST155	529	AAAGAATCTTTAGAAAGACAATCGGAAAAAACTTAGAAATGGCCCAAGTTGGTACTCTAGT

ScottA ST2	466	TTATATAAGAAAGT-----TGTCGACGCAACGGATTATAAAGTAGCTGCAATGGAGCTT
EGD-e ST35	589	TATTACAAAGGTGCATGGCGCGAGATGCAAAAACATACAAAGATGCGACTGCATGCTTA
10403S ST85	589	TATTACAAAGGTGCATGGCGCGAGATGCAAAAACATACAAAGATGCGACTGCATGCTTA
F2365 ST1	466	TTATATAAGAAAGT-----TGTCGACGCAACGGATTATAAAGTAGCTGCAATGGAGCTT
L6-13 ST155	589	TATTACAAAGGTGCATGGCGCGAGATGCAAAAACATACAAAGATGCGACTGCATGCTTA
MRL-14-00459 ST	589	TATTACAAAGGTGCATGGCGCGAGATGCAAAAACATACAAAGATGCGACTGCATGCTTA
LmNG3 ST155	589	TATTACAAAGGTGCATGGCGCGAGATGCAAAAACATACAAAGATGCGACTGCATGCTTA

ScottA ST2	520	CAAAAAGCTGCGATATGCAACCTCTCCTACATATGGTCTTAAATTCAGTAATTGAG
EGD-e ST35	649	CAGGGA---CGTTATGCAACGGACAACACATATGCTTCTAGCTAAATACCTAATTTCT
10403S ST85	649	CAGGGA---CGTTATGCAACGGACAACACATATGCTTCTAGCTAAATACCTAATTTCT
F2365 ST1	520	CAAAAAGCTGCGATATGCAACCTCTCCTACATATGGTCTTAAATTCAGTAATTGAG
L6-13 ST155	649	CAGGGA---CGTTATGCAACGGACAACACATATGCTTCTAGCTAAATACCTAATTTCT
MRL-14-00459 ST	649	CAGGGA---CGTTATGCAACGGACAACACATATGCTTCTAGCTAAATACCTAATTTCT
LmNG3 ST155	649	CAGGGA---CGTTATGCAACGGACAACACATATGCTTCTAGCTAAATACCTAATTTCT

ScottA ST2	580	AATTATGATTAGCCAAATATGATGTTTTATACGACAAAATCTTACTCAAAAATCCACT
EGD-e ST35	706	TCATATAATTTGACTGCAATATGATACTCTGTACGATACGATTAAACAACAAAAAATGTT
10403S ST85	706	TCATATAATTTGACTGCAATATGATACTCTGTACGATACGATTAAACAACAAAAAATGTT
F2365 ST1	580	AATTATGATTAGCCAAATATGATGTTTTATACGACAAAATCTTACTCAAAAATCCACT
L6-13 ST155	706	TCATATAATTTGACTGCAATATGATACTCTGTACGATACGATTAAACAACAAAAAATGTT
MRL-14-00459 ST	706	TCATATAATTTGACTGCAATATGATACTCTGTACGATACGATTAAACAACAAAAAATGTT
LmNG3 ST155	706	TCATATAATTTGACTGCAATATGATACTCTGTACGATACGATTAAACAACAAAAAATGTT

ScottA ST2	640	TCCGGAAAAGCAACTGTTACAAGTCCGACTGGAAATGGTGTATGGACTTTACCGTATAAA
EGD-e ST35	766	TCTGAAGATGCTAAAGTAGTTAAAGCAGATGGGCATGGTGTATAGTGGAATTTACAAT
10403S ST85	766	TCTGAAGATGCTAAAGTAGTTAAAGCAGATGGGCATGGTGTATAGTGGAATTTACAAT
F2365 ST1	640	TCCGGAAAAGCAACTGTTACAAGTCCGACTGGAAATGGTGTATGGACTTTACCGTATAAA
L6-13 ST155	766	TCTGAAGATGCTAAAGTAGTTAAAGCAGATGGGCATGGTGTATAGTGGAATTTACAAT
MRL-14-00459 ST	766	TCTGAAGATGCTAAAGTAGTTAAAGCAGATGGGCATGGTGTATAGTGGAATTTACAAT
LmNG3 ST155	724	-----

ScottA ST2	700	GTAAAAGGAGTGCAATCTGTTAGTCCAGCTAGCA-----CATACGCTAACAGGATATC
EGD-e ST35	826	ACGTCTGCAGCCAGTGCAGAAAAGTTATCTACTGGAGCGCCTTACAACAATAAAGATGTA
10403S ST85	826	ACGTCTGCAGCCAGTGCAGAAAAGTTATCTACTGGAGCGCCTTACAACAATAAAGATGTA
F2365 ST1	700	GTAAAAGGAGTGCAATCTGTTAGTCCAGCTAGCA-----CATACGCTAACAGGATATC
L6-13 ST155	826	ACGTCTGCAGCCAGTGCAGAAAAGTTATCTACTGGAGCGCCTTACAACAATAAAGATGTA
MRL-14-00459 ST	826	ACGTCTGCAGCCAGTGCAGAAAAGTTATCTACTGGAGCGCCTTACAACAATAAAGATGTA
LmNG3 ST155	724	-----

ScottA ST2	754	GATTTAGTATCTGTTGCTACAACAAGAGAGGTACGTACTATCAATTTAAATATAATGGT
EGD-e ST35	886	AAAATTTTAAAGAAGGCACTACAAGCAGAGGAACGTGGGTCCAATTTCTCTCAATAAT
10403S ST85	886	AAAATTTTAAAGAAGGCACTACAAGCAGAGGAACGTGGGTCCAATTTCTCTCAATAAT
F2365 ST1	754	GATTTAGTATCTGTTGCTACAACAAGAGAGGTACGTACTATCAATTTAAATATAATGGT
L6-13 ST155	886	AAAATTTTAAAGAAGGCACTACAAGCAGAGGAACGTGGGTCCAATTTCTCTCAATAAT
MRL-14-00459 ST	886	AAAATTTTAAAGAAGGCACTACAAGCAGAGGAACGTGGGTCCAATTTCTCTCAATAAT
LmNG3 ST155	724	-----

ScottA ST2	814	AAAGTAGTTGGTTGGGTAGATGGCAAAGCATTAAC TATTTATGATAGTGTC AATTATGAT
EGD-e ST35	946	AAAGTAATCGGCTGGATGGATAAACGCGCATTTGTCTATTATCCAAAAGCAACAAATGTA
10403S ST85	946	AAAGTAATCGGCTGGATGGATAAACGCGCATTTGTCTATTATCCAAAAGCAACAAATGTA
F2365 ST1	814	AAAGTAGTTGGTTGGGTAGATGGCAAAGCATTAAC TATTTATGATAGTGTC AATTATGAT
L6-13 ST155	946	AAAGTAATCGGCTGGATGGATAAACGCGCATTTGTCTATTATCCAAAAGCAACAAATGTA
MRL-14-00459 ST	946	AAAGTAATCGGCTGGATGGATAAACGCGCATTTGTCTATTATCCAAAAGCAACAAATGTA
LmNG3 ST155	724	-----
ScottA ST2	874	AAAGTAAATGTCGGACGTGCTAAAATTACTAGCCCAGTAAGTAACGGTATCTGGTCTAAA
EGD-e ST35	1006	AAAACGCTTAACCTAACAGGTAAAATCACTGCTGGATCTACTAATGGTTTATGGTCTGAG
10403S ST85	1006	AAAACGCTTAACCTAACAGGTAAAATCACTGCTGGATCTACTAATGGTTTATGGTCTGAG
F2365 ST1	874	AAAGTAAATGTCGGACGTGCTAAAATTACTAGCCCAGTAAGTAACGGTATCTGGTCTAAA
L6-13 ST155	1006	AAAACGCTTAACCTAACAGGTAAAATCACTGCTGGATCTACTAATGGTTTATGGTCTGAG
MRL-14-00459 ST	1006	AAAACGCTTAACCTAACAGGTAAAATCACTGCTGGATCTACTAATGGTTTATGGTCTGAG
LmNG3 ST155	724	-----
ScottA ST2	934	---CCATACAATGTTTATGGAAGAGAATTTGTTACGAATGCAACAACCTTACGCACAACAA
EGD-e ST35	1066	GTTCCAGGTACAGTGAATGCGAAAAAATTAGCTACAACAGCTGGTGCTTACCAAAATAAA
10403S ST85	1066	GTTCCAGGTACAGTGAATGCGAAAAAATTAGCTACAACAGCTGGTGCTTACCAAAATAAA
F2365 ST1	934	---CCATACAATGTTTATGGAAGAGAATTTGTTACGAATGCAACAACCTTACGCACAACAA
L6-13 ST155	1066	GTTCCAGGTACAGTGAATGCGAAAAAATTAGCTACAACAGCTGGTGCTTACCAAAATAAA
MRL-14-00459 ST	1066	GTTCCAGGTACAGTGAATGCGAAAAAATTAGCTACAACAGCTGGTGCTTACCAAAATAAA
LmNG3 ST155	724	-----
ScottA ST2	991	GAAATTAAACTTTTACGCGAAGCACAAACTGCTAAAGGTACTTATTACCAATTTAGCATA
EGD-e ST35	1126	GATGCTAAAAATTATTAAGCAAGGTCAAATTAGTGGCCGAACCTACTATCAATTTCCAAGTA
10403S ST85	1126	GATGCTAAAAATTATTAAGCAAGGTCAAATTAGTGGCCGAACCTACTATCAATTTCCAAGTA
F2365 ST1	991	GAAATTAAACTTTTACGCGAAGCACAAACTGCTAAAGGTACTTATTACCAATTTAGCATA
L6-13 ST155	1126	GATGCTAAAAATTATTAAGCAAGGTCAAATTAGTGGCCGAACCTACTATCAATTTCCAAGTA
MRL-14-00459 ST	1126	GATGCTAAAAATTATTAAGCAAGGTCAAATTAGTGGCCGAACCTACTATCAATTTCCAAGTA
LmNG3 ST155	724	-----
ScottA ST2	1051	AATAATAAAACTATTGGTTGGATTGATAAACGAGCTCTCACTATCTATCCGTATGATTCC
EGD-e ST35	1186	GGCGGTAAAAACAATTGGTTGGTTGGACGCTCGTGCAATTTTCATGTTTATGATAAAATCCAA
10403S ST85	1186	GGCGGTAAAAACAATTGGTTGGTTGGACGCTCGTGCAATTTTCATGTTTATGATAAAATCCAA
F2365 ST1	1051	AATAATAAGACTATTGGTTGGATTGATAAACGAGCTCTCACTATCTATCCGTATGATTCC
L6-13 ST155	1186	GGCGGTAAAAACAATTGGTTGGTTGGACGCTCGTGCAATTTTCATGTTTATGATAAAATCCAA
MRL-14-00459 ST	1186	GGCGGTAAAAACAATTGGTTGGTTGGACGCTCGTGCAATTTTCATGTTTATGATAAAATCCAA
LmNG3 ST155	724	-----
ScottA ST2	1111	ATTATTTCAAGTAAAAATGTGAACCTTGACGGACAAATTACTAAT----CCAACCGGAAA
EGD-e ST35	1246	AGCCAGTCAAATGTAAATTGGAATCGAACTATTTTAAATGCCGATAAGCACGGTGTGTAC
10403S ST85	1246	AGCCAGTCAAATGTAAATTGGAATCGAACTATTTTAAATGCCGATAAGCACGGTGTGTAC
F2365 ST1	1111	ATTATTTCAAGTAAAAATGTGAACCTTGACGGACAAATTACTAAT----CCAACCGGAAA
L6-13 ST155	1246	AGCCAGTCAAATGTAAATTGGAATCGAACTATTTTAAATGCCGATAAGCACGGTGTGTAC
MRL-14-00459 ST	1246	AGCCAGTCAAATGTAAATTGGAATCGAACTATTTTAAATGCCGATAAGCACGGTGTGTAC
LmNG3 ST155	724	-----
ScottA ST2	1167	TGGTATTTGGACTAAAGCGTACAAACTTGAAGGAACAACCTTCTGTGGCGCAGGCTACGAA
EGD-e ST35	1306	TCGGGTGTTTATAATACTTTCATCAAGTAGTATGAATAAACTAAGTA----CAGGTCGC
10403S ST85	1306	TCGGGTGTTTATAATACTTTCATCAAGTAGTATGAATAAACTAAGTA----CAGGTCGC
F2365 ST1	1167	TGGTATTTGGACTAAAGCGTACAAACTTGAAGGAACAACCTTCTGTGGCGCAGGCTACGAA
L6-13 ST155	1306	TCGGGTGTTTATAATACTTTCATCAAGTAGTATGAATAAACTAAGTA----CAGGTCGC
MRL-14-00459 ST	1306	TCGGGTGTTTATAATACTTTCATCAAGTAGTATGAATAAACTAAGTA----CAGGTCGC
LmNG3 ST155	724	-----
ScottA ST2	1227	ATATGCAATAAAGATGTGAAAAATCAGCCAACAAATCGAACTCAACATGGTACTTATTA
EGD-e ST35	1362	ATATAATAATAAAAAAGTAAAAGTTATTAAGCAAGCCAAGACCGCGCTGGAACCTGGTA
10403S ST85	1362	ATATAATAATAAAAAAGTAAAAGTTATTAAGCAAGCCAAGACCGCGCTGGAACCTGGTA
F2365 ST1	1227	ATATGCAATAAAGATGTGAAAAATCAGCCAACAAATCGAACTCAACATGGTACTTATTA
L6-13 ST155	1362	ATATAATAATAAAAAAGTAAAAGTTATTAAGCAAGCCAAGACCGCGCTGGAACCTGGTA
MRL-14-00459 ST	1362	ATATAATAATAAAAAAGTAAAAGTTATTAAGCAAGCCAAGACCGCGCTGGAACCTGGTA
LmNG3 ST155	724	-----

ScottA ST2	1287	CAATATCAGTATCGATGGGAAAGCAATTGGTTGGTTAGATAGAAACGCTATTACACTGTA
EGD-e ST35	1422	TCAATTCCAAGTAAATGGCAAAACAGTTGGTTGGATGGATTA-----TCGTGCATTCTT
10403S ST85	1422	TCAATTCCAAGTAAATGGCAAAACAGTTGGTTGGATGGATTA-----TCGTGCATTCTT
F2365 ST1	1287	CAATATCAGTATCGATGGGAAAGCAATTGGTTGGTTAGATAGAAACGCTATTACACTGTA
L6-13 ST155	1422	TCAATTCCAAGTAAATGGCAAAACAGTTGGTTGGATGGATTA-----TCGTGCATTCTT
MRL-14-00459 ST	1422	TCAATTCCAAGTAAATGGCAAAACAGTTGGTTGGATGGATTA-----TCGTGCATTCTT
LmNG3 ST155	724	-----

ScottA ST2	1347	TGATCAAGAGGAATACAATAAAACAGTTGCTATTGACGCAGTAGTAAAAATGTGAAGGG
EGD-e ST35	1476	TGACACAATTACCTCCCAAAAAACAATGAATAAAACAGTTACTGTGGGTAATGCCACGAA
10403S ST85	1476	TGACACAATTACCTCCCAAAAAACAATGAATAAAACAGTTACTGTGGGTAATGCCACGAA
F2365 ST1	1347	TGATCAAGAGGAATACAATAAAACAGTTGCTATTGACGCAGTAGTAAAAATGTGAAGGG
L6-13 ST155	1476	TGACACAATTACCTCCCAAAAAACAATGAATAAAACAGTTACTGTGGGTAATGCCACGAA
MRL-14-00459 ST	1476	TGACACAATTACCTCCCAAAAAACAATGAATAAAACAGTTACTGTGGGTAATGCCACGAA
LmNG3 ST155	724	-----

ScottA ST2	1407	TAATGCTGTATGGACAGAACCTTACCGTA---CAGTTGGTACAAAATTAATCGGACCAGC
EGD-e ST35	1536	TCATGGCGTTTTTGATGGGGTTTATCGAACCTCGCCAACGGTAAAAACGAATTTCTTTGGG
10403S ST85	1536	TCATGGCGTTTTTGATGGAGTTTATCGAACCTCGCCAACGGTAAAAACGAATTTCTTTGGG
F2365 ST1	1407	TAATGCTGTATGGACAGAACCTTACCGTA---CAGTTGGTACAAAATTAATCGGACCAGC
L6-13 ST155	1536	TCATGGCGTTTTTGATGGGGTTTATCGAACCTCGCCAACGGTAAAAACGAATTTCTTTGGG
MRL-14-00459 ST	1536	TCATGGCGTTTTTGATGGGGTTTATCGAACCTCGCCAACGGTAAAAACGAATTTCTTTGGG
LmNG3 ST155	724	-----

ScottA ST2	1464	GAAACTTACTTGAATAAAGAAGTGGAAGTCGTCCGTGAAGCAAAAACGCCAAAAGGAAC
EGD-e ST35	1596	GAAACCATACAATAATAAAAAAGTAAAAGTGCTCAAAGAAGCTGTAACAGACCATGCCAC
10403S ST85	1596	GAAACCATACAATAATAAAAAAGTAAAAGTGCTCAAAGAAGCTGTAACAGACCATGCCAC
F2365 ST1	1464	GAAACTTACTTGAATAAAGAAGTGGAAGTCGTCCGTGAAGCAAAAACGCCAAAAGGAAC
L6-13 ST155	1596	GAAACCATACAATAATAAAAAAGTAAAAGTGCTCAAAGAAGCTGTAACAGACCATGCCAC
MRL-14-00459 ST	1596	GAAACCATACAATAATAAAAAAGTAAAAGTGCTCAAAGAAGCTGTAACAGACCATGCCAC
LmNG3 ST155	724	-----

ScottA ST2	1524	TTACTACCAATTTAAATCTGGTGGCAAAGTAATCGGCTGGTTAGATAAAAAAGCTTTTCGA
EGD-e ST35	1656	ATGGGTTCAATTTAAATACGGTAACA---CAACTGCATGGATGGACAAAAAGCATTTAA
10403S ST85	1656	ATGGGTTCAATTTAAATACGGTAACA---CAACTGCATGGATGGACAAAAAGCATTTAA
F2365 ST1	1524	TTACTACCAATTTAAATCTGGTGGCAAAGTAATCGGCTGGTTAGATAAAAAAGCTTTTCGA
L6-13 ST155	1656	ATGGGTTCAATTTAAATACGGTAACA---CAACTGCATGGATGGACAAAAAGCATTTAA
MRL-14-00459 ST	1656	ATGGGTTCAATTTAAATACGGTAACA---CAACTGCATGGATGGACAAAAAGCATTTAA
LmNG3 ST155	724	-----

ScottA ST2	1584	TGTATATGACAAATAATTACAAACAAAGCGGTTAATTTAGATGCTGTAGTGGAAAATGT
EGD-e ST35	1713	-----ATAATTAA-----
10403S ST85	1713	-----ATAATTAA-----
F2365 ST1	1584	TGTATATGACAAATAATTACAAACAAAGCGGTTAATTTAGATGCTGTAGTGGAAAATGT
L6-13 ST155	1713	-----ATAATTAA-----
MRL-14-00459 ST	1713	-----ATAATTAA-----
LmNG3 ST155	724	-----ATA-----

ScottA ST2	1644	GACAGGTAATGCAGTTTGGACGGCTCCTTATAAGAGTAAAGGTGTTAACTTGTTACTTC
EGD-e ST35		-----
10403S ST85		-----
F2365 ST1	1644	GACAGGTAATGCAGTTTGGACGGCTCCTTATAAGAGTAAAGGTGTTAACTTGTTACTTC
L6-13 ST155		-----
MRL-14-00459 ST		-----
LmNG3 ST155		-----

ScottA ST2	1704	AGCAGCAACCTATAAAGGCAAGGCAACAAAAATAACTCGTGAAGCGCAACAAGTAGAGG
EGD-e ST35		-----
10403S ST85		-----
F2365 ST1	1704	AGCAGCAACCTATAAAGGCAAGGCAACAAAAATAACTCGTGAAGCGCAACAAGTAGAGG
L6-13 ST155		-----
MRL-14-00459 ST		-----
LmNG3 ST155		-----

ScottA ST2	1764	AACATATTACGAGTTTAGTGTTGATGGTAAAGTCATTGGCTGGTTAGATAAAAAAGCTTT
EGD-e ST35		-----
10403S ST85		-----
F2365 ST1	1764	AACATATTACGAGTTTAGTGTTGATGGTAAAGTCATTGGCTGGTTAGATAAAAAAGCTTT
L6-13 ST155		-----
MRL-14-00459 ST		-----
LmNG3 ST155		-----
ScottA ST2	1824	CGATGTATATGACAATATTAATTACAACAAAGCGGTAACTTAGATGCTGTAGTGAAAA
EGD-e ST35		-----
10403S ST85		-----
F2365 ST1	1824	CGATGTATATGACAATATTAATTACAACAAAGCGGTAACTTAGATGCTGTAGTGAAAA
L6-13 ST155		-----
MRL-14-00459 ST		-----
LmNG3 ST155		-----
ScottA ST2	1884	TGTGACAGGCAACGCAGTTTGGACTGCTCCATATAAGAGTAAGGGTGTTAAATTAGTTAC
EGD-e ST35		-----
10403S ST85		-----
F2365 ST1	1884	TGTGACAGGCAACGCAGTTTGGACTGCTCCATATAAGAGTAAGGGTGTTAAATTAGTTAC
L6-13 ST155		-----
MRL-14-00459 ST		-----
LmNG3 ST155		-----
ScottA ST2	1944	TTCAGCAGCCACATATAAAGATAAAGCAACTAAAATAACTCGAGAAGCGCAAACAAGTAG
EGD-e ST35		-----
10403S ST85		-----
F2365 ST1	1944	TTCAGCAGCCACATATAAAGATAAAGCAACTAAAATAACTCGAGAAGCGCAAACAAGTAG
L6-13 ST155		-----
MRL-14-00459 ST		-----
LmNG3 ST155		-----
ScottA ST2	2004	AGGAACTTACTACGAATTTAGCGTAAACGGCAAAGTAATCGGTTGGTTAGATAAAAAAGC
EGD-e ST35		-----
10403S ST85		-----
F2365 ST1	2004	AGGAACTTACTACGAATTTAGCGTAAACGGCAAAGTAATCGGTTGGTTAGATAAAAAAGC
L6-13 ST155		-----
MRL-14-00459 ST		-----
LmNG3 ST155		-----
ScottA ST2	2064	TTTTGATGTATATGATTCTATTGAGTACAATAAAGCGATTAATATGACTGGATTACTTAG
EGD-e ST35		-----
10403S ST85		-----
F2365 ST1	2064	TTTTGATGTATATGATTCTATTGAGTACAATAAAGCGATTAATATGACTGGATTACTTAG
L6-13 ST155		-----
MRL-14-00459 ST		-----
LmNG3 ST155		-----
ScottA ST2	2124	CAACGCGCCAGGTAATGGCATTTGGACAGAGCCGTATAGAGTTATTGGCACAAAAAATGT
EGD-e ST35		-----
10403S ST85		-----
F2365 ST1	2124	CAACGCGCCAGGTAATGGCATTTGGACAGAGCCGTATAGAGTTATTGGCACAAAAAATGT
L6-13 ST155		-----
MRL-14-00459 ST		-----
LmNG3 ST155		-----
ScottA ST2	2184	AGGACAAGCAACTGCTTATGCTAACAAGACAGTACAGTTGATACGCGAGGCTAAGACTAC
EGD-e ST35		-----
10403S ST85		-----
F2365 ST1	2184	AGGACAAGCAACTGCTTATGCTAACAAGACAGTACAGTTGATACGCGAGGCTAAGACTAC
L6-13 ST155		-----
MRL-14-00459 ST		-----
LmNG3 ST155		-----

ScottA ST2	2244	ACGTGCAACTTACTATCAAATGAGTGTAATGGTAAAATAGTTGGTTGGGTAGATAAACG
EGD-e ST35		-----
10403S ST85		-----
F2365 ST1	2244	ACGTGCAACTTACTATCAAATGAGTGTAATGGTAAAATAGTTGGTTGGGTAGATAAACG
L6-13 ST155		-----
MRL-14-00459 ST		-----
LmNG3 ST155		-----

ScottA ST2	2304	AGCTTTTACAAACGTTAAATAG
EGD-e ST35		-----
10403S ST85		-----
F2365 ST1	2304	AGCTTTTACAAACGTTAAATAG
L6-13 ST155		-----
MRL-14-00459 ST		-----
LmNG3 ST155		-----

Figure S4B. Alignment of Aut protein sequences

ScottA_ST2	1	MI-----NKKWMI VMI PMLVVP MYGLITTVGGQLQDS
EGD-e_ST35	1	MIKKVFHFILVLMLSVSIIPLFHAKAAETNGVDSSEQEDNTEVAE EEMPP ESEEP VFSLEQNRDDAMAA
10403S_ST85	1	MIKKVFHFILVLMLSVSIIPLFHAKAAETNGVDSSEQEDNTEVAE EEMPP ESEEP VFSLEQNRDDAMAA
F2365_ST1	1	MI-----NKKWMI VMI PMLVVP MYGLITTVGGQLQDS
L6-13_ST155	1	MIKKVFHFILVLMLSVSIIPLFHAKAAETNGVDSSEQEDNTEVAE EEMPP ESEEP VFSLEQNRDDAMAA
MRL-14-00459_ST	1	MIKKVFHFILVLMLSVSIIPLFHAKAAETNGVDSSEQEDNTEVAE EEMPP ESEEP VFSLEQNRDDAMAA
LmNG3_ST155	1	MIKKVFHFILVLMLSVSIIPLFHAKAAETNGVDSSEQEDNTEVAE EEMPP ESEEP VFSLEQNRDDAMAA
ScottA_ST2	33	IT---GENSFVKEVEAATTASQQAFFIDKIAPAAQASQEKYHLLSSITAAQALLESQGWKSGLA--TQGYNL
EGD-e_ST35	71	LVVPQTRNSFLR--AASTPTFOOTFINSISTQAMDLCCKYNYLPSVMTAAQALESNWGRSELCKAPNYNL
10403S_ST85	71	LVVPQTRNSFLR--AASTPTFOOTFINSISTQAMDLCCKYNYLPSVMTAAQALESNWGRSELCKAPNYNL
F2365_ST1	33	IT---GENSFVKEVEAATTASQQAFFIDKIAPAAQASQEKYHLLSSITAAQALLESQGWKSGLA--TQGYNL
L6-13_ST155	71	LVVPQTRNSFLR--AASTPTFOOTFINSISTQAMDLCCKYNYLPSVMTAAQALESNWGRSELCKAPNYNL
MRL-14-00459_ST	71	LVVPQTRNSFLR--AASTPTFOOTFINSISTQAMDLCCKYNYLPSVMTAAQALESNWGRSELCKAPNYNL
LmNG3_ST155	71	LVVPQTRNSFLR--AASTPTFOOTFINSISTQAMDLCCKYNYLPSVMTAAQALESNWGRSELCKAPNYNL
ScottA_ST2	99	FGIKGSYNGKSVTMTWEYSDSKGWYQINANEAKYPSHKESLEDNAKKLRNGPSWDSSYYKGAWRENAKT
EGD-e_ST35	139	FGIKGSYNGKSVTMTWEYSDSKGWYQINANEAKYPSHKESLEDNAKKLRNGPSWDSSYYKGAWRENAKT
10403S_ST85	139	FGIKGSYNGKSVTMTWEYSDSKGWYQINANEAKYPSHKESLEDNAKKLRNGPSWDSSYYKGAWRENAKT
F2365_ST1	99	FGIKGSYNGKSVTMTWEYSDSKGWYQINANEAKYPSHKESLEDNAKKLRNGPSWDSSYYKGAWRENAKT
L6-13_ST155	139	FGIKGSYNGKSVTMTWEYSDSKGWYQINANEAKYPSHKESLEDNAKKLRNGPSWDSSYYKGAWRENAKT
MRL-14-00459_ST	139	FGIKGSYNGKSVTMTWEYSDSKGWYQINANEAKYPSHKESLEDNAKKLRNGPSWDSSYYKGAWRENAKT
LmNG3_ST155	139	FGIKGSYNGKSVTMTWEYSDSKGWYQINANEAKYPSHKESLEDNAKKLRNGPSWDSSYYKGAWRENAKT
ScottA_ST2	166	YKVAAMELQKAGYATSPITYASLIQVIENYDLAKYDVLYDKILTQKSTSGKATVTSTPTGNGVWTLPLYKVK
EGD-e_ST35	209	YKDATAWLQ--CRYATDNTY--SKLNTLISSYNLTQYDTLYDTIKQQKNVSEDAKVVKADGHGVYSGIYNTS
10403S_ST85	209	YKDATAWLQ--CRYATDNTY--SKLNTLISSYNLTQYDTLYDTIKQQKNVSEDAKVVKADGHGVYSGIYNTS
F2365_ST1	166	YKVAAMELQKAGYATSPITYASLIQVIENYDLAKYDVLYDKILTQKSTSGKATVTSTPTGNGVWTLPLYKVK
L6-13_ST155	209	YKDATAWLQ--CRYATDNTY--SKLNTLISSYNLTQYDTLYDTIKQQKNVSEDAKVVKADGHGVYSGIYNTS
MRL-14-00459_ST	209	YKDATAWLQ--CRYATDNTY--SKLNTLISSYNLTQYDTLYDTIKQQKNVSEDAKVVKADGHGVYSGIYNTS
LmNG3_ST155	209	YKDATAWLQ--CRYATDNTY--SKLNTLISSYNLTQI-----
ScottA_ST2	236	G--VQSVSPASTYANKDIDLVSVAATTKRGTYQFQKYNQKVVGVWDGKALTIYDSVNYDKVNVGRAKITSP
EGD-e_ST35	278	AASAKKLSTGAPYNNKDVKILKEGTTSRGTWVQFSLNNKVIWMDKRAFFVYYPKATNVKTLNLTGKITAG
10403S_ST85	278	AASAKKLSTGAPYNNKDVKILKEGTTSRGTWVQFSLNNKVIWMDKRAFFVYYPKATNVKTLNLTGKITAG
F2365_ST1	236	G--VQSVSPASTYANKDIDLVSVAATTKRGTYQFQKYNQKVVGVWDGKALTIYDSVNYDKVNVGRAKITSP
L6-13_ST155	278	AASAKKLSTGAPYNNKDVKILKEGTTSRGTWVQFSLNNKVIWMDKRAFFVYYPKATNVKTLNLTGKITAG
MRL-14-00459_ST	278	AASAKKLSTGAPYNNKDVKILKEGTTSRGTWVQFSLNNKVIWMDKRAFFVYYPKATNVKTLNLTGKITAG
LmNG3_ST155		-----
ScottA_ST2	304	VSNGIWSK-PYNVYGREFVTNATTYAQQEIKLLREAQTAKGTTYQFSINNKTIGWIDKRALTIYPYDSII
EGD-e_ST35	348	STNGLWSEVPGTVNAKKLATTAGAYQNKDAKIIKQGQISGRTTYQFQVGGKTIGWLDARAFHV--YDKIQ
10403S_ST85	348	STNGLWSEVPGTVNAKKLATTAGAYQNKDAKIIKQGQISGRTTYQFQVGGKTIGWLDARAFHV--YDKIQ
F2365_ST1	304	VSNGIWSK-PYNVYGREFVTNATTYAQQEIKLLREAQTAKGTTYQFSINNKTIGWIDKRALTIYPYDSII
L6-13_ST155	348	STNGLWSEVPGTVNAKKLATTAGAYQNKDAKIIKQGQISGRTTYQFQVGGKTIGWLDARAFHV--YDKIQ
MRL-14-00459_ST	348	STNGLWSEVPGTVNAKKLATTAGAYQNKDAKIIKQGQISGRTTYQFQVGGKTIGWLDARAFHV--YDKIQ
LmNG3_ST155		-----
ScottA_ST2	373	SSKNVNLDGQITNPTNGGIWTKAYKLEGTT--SVAQATKYANKDVKISQQIETQHGTYYNISIDGKAIGW
EGD-e_ST35	416	SQSNVNNWRTILNADKHGVYSGVYNTSSSSMNKLSTGAKYNNKKVVKVIQAKTARGTWYQFQVNGKTVGW
10403S_ST85	416	SQSNVNNWRTILNADKHGVYSGVYNTSSSSMNKLSTGAKYNNKKVVKVIQAKTARGTWYQFQVNGKTVGW
F2365_ST1	373	SSKNVNLDGQITNPTNGGIWTKAYKLEGTT--SVAQATKYANKDVKISQQIETQHGTYYNISIDGKAIGW
L6-13_ST155	416	SQSNVNNWRTILNADKHGVYSGVYNTSSSSMNKLSTGAKYNNKKVVKVIQAKTARGTWYQFQVNGKTVGW
MRL-14-00459_ST	416	SQSNVNNWRTILNADKHGVYSGVYNTSSSSMNKLSTGAKYNNKKVVKVIQAKTARGTWYQFQVNGKTVGW
LmNG3_ST155		-----
ScottA_ST2	441	LDRNAI--TLYDQEEYNKTVDAIDAVKVNKGNVWTEPYRTVGT-KLIGPAETYLNKEVEVVEAKTPKG
EGD-e_ST35	486	MDYRAFFDITTSQKTMNKTVT----VGNATNHGVFDGVYRTSPTVKRISLGKPYNNKKVKVLKEAVTDHA
10403S_ST85	486	MDYRAFFDITTSQKTMNKTVT----VGNATNHGVFDGVYRTSPTVKRISLGKPYNNKKVKVLKEAVTDHA
F2365_ST1	441	LDRNAI--TLYDQEEYNKTVDAIDAVKVNKGNVWTEPYRTVGT-KLIGPAETYLNKEVEVVEAKTPKG
L6-13_ST155	486	MDYRAFFDITTSQKTMNKTVT----VGNATNHGVFDGVYRTSPTVKRISLGKPYNNKKVKVLKEAVTDHA
MRL-14-00459_ST	486	MDYRAFFDITTSQKTMNKTVT----VGNATNHGVFDGVYRTSPTVKRISLGKPYNNKKVKVLKEAVTDHA
LmNG3_ST155		-----
ScottA_ST2	508	TTYQFKSGGKVIWGLDKKAFDVEDYDNINYNKAVNLDVAVENVTGNAVWTAAPYKSGVKLVTSAAATYK GKAT
EGD-e_ST35	552	TWVQFKY-GNTTAWMDKKAFKY-----
10403S_ST85	552	TWVQFKY-GNTTAWMDKKAFKY-----
F2365_ST1	508	TTYQFKSGGKVIWGLDKKAFDVEDYDNINYNKAVNLDVAVENVTGNAVWTAAPYKSGVKLVTSAAATYK GKAT
L6-13_ST155	552	TWVQFKY-GNTTAWMDKKAFKY-----
MRL-14-00459_ST	552	TWVQFKY-GNTTAWMDKKAFKY-----
LmNG3_ST155		-----
ScottA_ST2	578	KITREAQTSRGTYEFSVDGKVIWGLDKKAFDVEDYDNINYNKAVNLDVAVENVTGNAVWTAAPYKSGVKLV

EGD-e ST35		-----
10403S ST85		-----
F2365 ST1	578	KITREAQTSRGTYEFSVDGKVGWLDKKAFDVYDNINYNKAVNLDAVVENVTGNAVWTAPYKSGVKLV
L6-13 ST155		-----
MRL-14-00459 ST		-----
LmNG3_ST155		-----

ScottA ST2	648	TSAATYKDKATKITREAQTSRGTYEFSVNGKVGWLDKKAFDVYDSIEYNKAINMTGLLSNAPGNGIWT
EGD-e ST35		-----
10403S ST85		-----
F2365 ST1	648	TSAATYKDKATKITREAQTSRGTYEFSVNGKVGWLDKKAFDVYDSIEYNKAINMTGLLSNAPGNGIWT
L6-13 ST155		-----
MRL-14-00459 ST		-----
LmNG3_ST155		-----

ScottA ST2	718	EPYRVIGTKNVGQATAYANKTVQLIREAKTTRATYYQMSVNGKIVGWVDKRAFTNVK
EGD-e ST35		-----
10403S ST85		-----
F2365 ST1	718	EPYRVIGTKNVGQATAYANKTVQLIREAKTTRATYYQMSVNGKIVGWVDKRAFTNVK
L6-13 ST155		-----
MRL-14-00459 ST		-----
LmNG3_ST155		-----

Figure S5A. Alignment of *prfA* nucleotide sequences .
red: stop codon, yellow: sequence downstream of *prfA*

ScottA ST2	1	ATGAACGCTCAAGCAGAAGAATTCAAAAAATATTTAGAACTAACGGGATAAAACCAAAACAATTCATAAAAAAGAACT
EGD-e ST35	1	ATGAACGCTCAAGCAGAAGAATTCAAAAAATATTTAGAACTAACGGGATAAAACCAAAACAATTCATAAAAAAGAACT
10403S ST85	1	ATGAACGCTCAAGCAGAAGAATTCAAAAAATATTTAGAACTAACGGGATAAAACCAAAACAATTCATAAAAAAGAACT
F2365 ST1	1	ATGAACGCTCAAGCAGAAGAATTCAAAAAATATTTAGAACTAACGGGATAAAACCAAAACAATTCATAAAAAAGAACT
CDL65 ST155	1	ATGAACGCTCAAGCAGAAGAATTCAAAAAATATTTAGAACTAACGGGATAAAACCAAAACAATTCATAAAAAAGAACT
P06_14 ST155	1	ATGAACGCTCAAGCAGAAGAATTCAAAAAATATTTAGAACTAACGGGATAAAACCAAAACAATTCATAAAAAAGAACT
Ro05 ST155	1	ATGAACGCTCAAGCAGAAGAATTCAAAAAATATTTAGAACTAACGGGATAAAACCAAAACAATTCATAAAAAAGAACT
Ro09 ST155	1	ATGAACGCTCAAGCAGAAGAATTCAAAAAATATTTAGAACTAACGGGATAAAACCAAAACAATTCATAAAAAAGAACT
Ro15 ST155	1	ATGAACGCTCAAGCAGAAGAATTCAAAAAATATTTAGAACTAACGGGATAAAACCAAAACAATTCATAAAAAAGAACT

ScottA ST2	81	TATTTTTAACCAATGGGATCCACAAGAATATTGTATTTTCTATATGATGGTATTACAAAGCTTACAGTATTAGTGAGA
EGD-e ST35	81	TATTTTTAACCAATGGGATCCACAAGAATATTGTATTTTCTATATGATGGTATTACAAAGCTCAGAGTATTAGCGAGA
10403S ST85	81	TATTTTTAACCAATGGGATCCACAAGAATATTGTATTTTCTATATGATGGTATTACAAAGCTCAGAGTATTAGCGAGA
F2365 ST1	81	TATTTTTAACCAATGGGATCCACAAGAATATTGTATTTTCTATATGATGGTATTACAAAGCTTACAGTATTAGCGAGA
CDL65 ST155	81	TATTTTTAACCAATGGGATCCACAAGAATATTGTATTTTCTATATGATGGTATTACAAAGCTCAGAGTATTAGCGAGA
P06_14 ST155	81	TATTTTTAACCAATGGGATCCACAAGAATATTGTATTTTCTATATGATGGTATTACAAAGCTCAGAGTATTAGCGAGA
Ro05 ST155	81	TATTTTTAACCAATGGGATCCACAAGAATATTGTATTTTCTATATGATGGTATTACAAAGCTCAGAGTATTAGCGAGA
Ro09 ST155	81	TATTTTTAACCAATGGGATCCACAAGAATATTGTATTTTCTATATGATGGTATTACAAAGCTCAGAGTATTAGCGAGA
Ro15 ST155	81	TATTTTTAACCAATGGGATCCACAAGAATATTGTATTTTCTATATGATGGTATTACAAAGCTCAGAGTATTAGCGAGA

ScottA ST2	161	ACGGGACCATCATGAATTTACAATACTATAAAGCTGGCTTCGTTATAATGTCTGGCTTTATCGATACAGAAACATCGGTT
EGD-e ST35	161	ACGGGACCATCATGAATTTACAATACTACAAAGGGGCTTCGTTATAATGTCTGGCTTTATCGATACAGAAACATCGGTT
10403S ST85	161	ACGGGACCATCATGAATTTACAATACTACAAAGGGGCTTCGTTATAATGTCTGGCTTTATCGATACAGAAACATCGGTT
F2365 ST1	161	ACGGGACCATCATGAATTTACAATACTATAAAGCTGGCTTCGTTATAATGTCTGGCTTTATCGATACAGAAACATCGGTT
CDL65 ST155	161	ACGGGACCATCATGAATTTACAATACTACAAAGGGGCTTCGTTATAATGTCTGGCTTTATCGATACAGAAACATCGGTT
P06_14 ST155	161	ACGGGACCATCATGAATTTACAATACTACAAAGGGGCTTCGTTATAATGTCTGGCTTTATCGATACAGAAACATCGGTT
Ro05 ST155	161	ACGGGACCATCATGAATTTACAATACTACAAAGGGGCTTCGTTATAATGTCTGGCTTTATCGATACAGAAACATCGGTT
Ro09 ST155	161	ACGGGACCATCATGAATTTACAATACTACAAAGGGGCTTCGTTATAATGTCTGGCTTTATCGATACAGAAACATCGGTT
Ro15 ST155	161	ACGGGACCATCATGAATTTACAATACTACAAAGGGGCTTCGTTATAATGTCTGGCTTTATCGATACAGAAACATCGGTT

ScottA ST2	241	GGCTATTATAAATTTAGAAGTCATTAGCGAGCAGGCTACCGCATACGTTATCAAAATAAACGAACATAAAAGAACTACTGAG
EGD-e ST35	241	GGCTATTATAAATTTAGAAGTCATTAGCGAGCAGGCTACCGCATACGTTATCAAAATAAACGAACATAAAAGAACTACTGAG
10403S ST85	241	GGCTATTATAAATTTAGAAGTCATTAGCGAGCAGGCTACCGCATACGTTATCAAAATAAACGAACATAAAAGAACTACTGAG
F2365 ST1	241	GGCTATTATAAATTTAGAAGTCATTAGCGAGCAGGCTACCGCATACGTTATCAAAATAAACGAACATAAAAGAACTACTGAG
CDL65 ST155	241	GGCTATTATAAATTTAGAAGTCATTAGCGAGCAGGCTACCGCATACGTTATCAAAATAAACGAACATAAAAGAACTACTGAG
P06_14 ST155	241	GGCTATTATAAATTTAGAAGTCATTAGCGAGCAGGCTACCGCATACGTTATCAAAATAAACGAACATAAAAGAACTACTGAG
Ro05 ST155	241	GGCTATTATAAATTTAGAAGTCATTAGCGAGCAGGCTACCGCATACGTTATCAAAATAAACGAACATAAAAGAACTACTGAG
Ro09 ST155	241	GGCTATTATAAATTTAGAAGTCATTAGCGAGCAGGCTACCGCATACGTTATCAAAATAAACGAACATAAAAGAACTACTGAG
Ro15 ST155	241	GGCTATTATAAATTTAGAAGTCATTAGCGAGCAGGCTACCGCATACGTTATCAAAATAAACGAACATAAAAGAACTACTGAG

ScottA ST2	321	CAAAATCTTACGCACTTTTCTATGTTTTCCAAACCCTACAAAACAAGTTTCATACAGCTCTAGCTAAATTTAATGATT
EGD-e ST35	321	CAAAATCTTACGCACTTTTCTATGTTTTCCAAACCCTACAAAACAAGTTTCATACAGCTCTAGCTAAATTTAATGATT
10403S ST85	321	CAAAATCTTACGCACTTTTCTATGTTTTCCAAACCCTACAAAACAAGTTTCATACAGCTCTAGCTAAATTTAATGATT
F2365 ST1	321	CAAAATCTTACGCACTTTTCTATGTTTTCCAAACCCTACAAAACAAGTTTCATACAGCTCTAGCTAAATTTAATGATT
CDL65 ST155	321	CAAAATCTTACGCACTTTTCTATGTTTTCCAAACCCTACAAAACAAGTTTCATACAGCTCTAGCTAAATTTAATGATT
P06_14 ST155	321	CAAAATCTTACGCACTTTTCTATGTTTTCCAAACCCTACAAAACAAGTTTCATACAGCTCTAGCTAAATTTAATGATT
Ro05 ST155	321	CAAAATCTTACGCACTTTTCTATGTTTTCCAAACCCTACAAAACAAGTTTCATACAGCTCTAGCTAAATTTAATGATT
Ro09 ST155	321	CAAAATCTTACGCACTTTTCTATGTTTTCCAAACCCTACAAAACAAGTTTCATACAGCTCTAGCTAAATTTAATGATT
Ro15 ST155	321	CAAAATCTTACGCACTTTTCTATGTTTTCCAAACCCTACAAAACAAGTTTCATACAGCTCTAGCTAAATTTAATGATT

ScottA ST2	401	TTTCGATTAACGGGAAGCTGGGCTCTATTGCGGTCAACTTTTAATCCTGACCTATGTGTATGGTAAAGAACTCCTGAT
EGD-e ST35	401	TTTCGATTAACGGGAAGCTGGGCTCTATTGCGGTCAACTTTTAATCCTGACCTATGTGTATGGTAAAGAACTCCTGAT
10403S ST85	401	TTTCGATTAACGGGAAGCTGGGCTCTATTGCGGTCAACTTTTAATCCTGACCTATGTGTATGGTAAAGAACTCCTGAT
F2365 ST1	401	TTTCGATTAACGGGAAGCTGGGCTCTATTGCGGTCAACTTTTAATCCTGACCTATGTGTATGGTAAAGAACTCCTGAT
CDL65 ST155	401	TTTCGATTAACGGGAAGCTGGGCTCTATTGCGGTCAACTTTTAATCCTGACCTATGTGTATGGTAAAGAACTCCTGAT
P06_14 ST155	401	TTTCGATTAACGGGAAGCTGGGCTCTATTGCGGTCAACTTTTAATCCTGACCTATGTGTATGGTAAAGAACTCCTGAT
Ro05 ST155	401	TTTCGATTAACGGGAAGCTGGGCTCTATTGCGGTCAACTTTTAATCCTGACCTATGTGTATGGTAAAGAACTCCTGAT
Ro09 ST155	401	TTTCGATTAACGGGAAGCTGGGCTCTATTGCGGTCAACTTTTAATCCTGACCTATGTGTATGGTAAAGAACTCCTGAT
Ro15 ST155	401	TTTCGATTAACGGGAAGCTGGGCTCTATTGCGGTCAACTTTTAATCCTGACCTATGTGTATGGTAAAGAACTCCTGAT

ScottA ST2	481	GGCATCAAGATTACACTGGATAATTTAACAATGCAGGAGTTAGGATATTCAAGCGGTATCGCACATAGCTCAGCTGTTAG
EGD-e ST35	481	GGCATCAAGATTACACTGGATAATTTAACAATGCAGGAGTTAGGATATTCAAGTGGCATCGCACATAGCTCAGCTGTTAG
10403S ST85	481	GGCATCAAGATTACACTGGATAATTTAACAATGCAGGAGTTAGGATATTCAAGTGGCATCGCACATAGCTCAGCTGTTAG
F2365 ST1	481	GGCATCAAGATTACACTGGATAATTTAACAATGCAGGAGTTAGGATATTCAAGCGGTATCGCACATAGCTCAGCTGTTAG
CDL65 ST155	481	GGCATCAAGATTACACTGGATAATTTAACAATGCAGGAGTTAGGATATTCAAGTGGCATCGCACATAGCTCAGCTGTTAG
P06_14 ST155	481	GGCATCAAGATTACACTGGATAATTTAACAATGCAGGAGTTAGGATATTCAAGTGGCATCGCACATAGCTCAGCTGTTAG
Ro05 ST155	481	GGCATCAAGATTACACTGGATAATTTAACAATGCAGGAGTTAGGATATTCAAGTGGCATCGCACATAGCTCAGCTGTTAG
Ro09 ST155	481	GGCATCAAGATTACACTGGATAATTTAACAATGCAGGAGTTAGGATATTCAAGTGGCATCGCACATAGCTCAGCTGTTAG
Ro15 ST155	481	GGCATCAAGATTACACTGGATAATTTAACAATGCAGGAGTTAGGATATTCAAGTGGCATCGCACATAGCTCAGCTGTTAG

ScottA ST2	561	CAGAATTATTTCTAAATTAAAGCAAGAGAAAGTTATCGTGTATAAAAAATTCATGCTTTTATGTACAAAATCTTGATTATC
EGD-e ST35	561	CAGAATTATTTCCAAATTAAAGCAAGAGAAAGTTATCGTGTATAAAAAATTCATGCTTTTATGTACAAAATCTTGATTATC
10403S ST85	561	CAGAATTATTTCCAAATTAAAGCAAGAGAAAGTTATCGTGTATAAAAAATTCATGCTTTTATGTACAAAATCTTGATTATC
F2365 ST1	561	CAGAATTATTTCTAAATTAAAGCAAGAGAAAGTTATCGTGTATAAAAAATTCATGCTTTTATGTACAAAATCTTGATTATC
CDL65 ST155	561	CAGAATTATTTCCAAATTAAAGCAAGAGAAAGTTATCGTGTATAAAAAATTCATGCTTTTATGTACAAAATCTTGATTATC
P06 14 ST155	561	CAGAATTATTTCCAAATTAAAGCAAGAGAAAGTTATCGTGTATAAAAAATTCATGCTTTTATGTACAAAATCTTGATTATC
Ro05 ST155	561	CAGAATTATTTCCAAATTAAAGCAAGAGAAAGTTATCGTGTATAAAAAATTCATGCTTTTATGTACAAAATCTTGATTATC
Ro09 ST155	561	CAGAATTATTTCCAAATTAAAGCAAGAGAAAGTTATCGTGTATAAAAAATTCATGCTTTTATGTACAAAATCTTGATTATC
Ro15 ST155	561	CAGAATTATTTCCAAATTAAAGCAAGAGAAAGTTATCGTGTATAAAAAATTCATGCTTTTATGTACAAAATCTTGATTATC

ScottA ST2	641	TCAAAAGATATGCTCCTAAATTAGATGAATGGTTTTATTTAGCATGTCCTGCTACTTGGGGAAAAATTAATTAATCAAA
EGD-e ST35	641	TCAAAAGATATGCCCCTAAATTAGATGAATGGTTTTATTTAGCATGTCCTGCTACTTGGGGAAAAATTAATTAATC-AA
10403S ST85	641	TCAAAAGATATGCCCCTAAATTAGATGAATGGTTTTATTTAGCATGTCCTGCTACTTGGGGAAAAATTAATTAATC-AA
F2365 ST1	641	TCAAAAGATATGCTCCTAAATTAGATGAATGGTTTTATTTAGCATGTCCTGCTACTTGGGGAAAAATTAATTAATCAAA
CDL65 ST155	641	TCAAAAGATATGCCCCTAAATTAGATGAATGGTTTTATTTAGCATGTCCTGCTACTTGGGGAAAAATTT----AAATC-AA
P06 14 ST155	641	TCAAAAGATATGCCCCTAAATTAGATGAATGGTTTTATTTAGCATGTCCTGCTACTTGGGGAAAAATTT----AAATC-AA
Ro05 ST155	641	TCAAAAGATATGCCCCTAAATTAGATGAATGGTTTTATTTAGCATGTCCTGCTACTTGGGGAAAAATTT----AAATC-AA
Ro09 ST155	641	TCAAAAGATATGCCCCTAAATTAGATGAATGGTTTTATTTAGCATGTCCTGCTACTTGGGGAAAAATTT----AAATC-AA
Ro15 ST155	641	TCAAAAGATATGCCCCTAAATTAGATGAATGGTTTTATTTAGCATGTCCTGCTACTTGGGGAAAAATTT----AAATC-AA

ScottA ST2	721	AAACAGGATGTCTCAATGAGGCATCCTGTTTTATATTTTATTTCG-----
EGD-e ST35	720	AAACAGTATTCCTCAATGAGGAATACTGTTTTATATTTTATTTCG-----
10403S ST85	720	AAACAGTATTCCTCAATGAGGAATACTGTTTTATATTTTATTTCG-----
F2365 ST1	721	AAACAGGATGTCTCAATGAGGCATCCTGTTTTATATTTTATTTCG-----
CDL65 ST155	715	AAACAGTATTCCTCAATGAGGAATACTGTTTTATATTTTATTTCGAATAAAGAAGCTTACAGAAGCATTTTCATGAACGCGT
P06 14 ST155	715	AAACAGTATTCCTCAATGAGGAATACTGTTTTATATTTTATTTCGAATAAAGAAGCTTACAGAAGCATTTTCATGAACGCGT
Ro05 ST155	715	AAACAGTATTCCTCAATGAGGAATACTGTTTTATATTTTATTTCGAATAAAGAAGCTTACAGAAGCATTTTCATGAACGCGT
Ro09 ST155	715	AAACAGTATTCCTCAATGAGGAATACTGTTTTATATTTTATTTCGAATAAAGAAGCTTACAGAAGCATTTTCATGAACGCGT
Ro15 ST155	715	AAACAGTATTCCTCAATGAGGAATACTGTTTTATATTTTATTTCGAATAAAGAAGCTTACAGAAGCATTTTCATGAACGCGT

ScottA ST2		-----
EGD-e ST35		-----
10403S ST85		-----
F2365 ST1	801	-----
CDL65 ST155	795	ACGATTGCTTCACCAAGAAGAGCTGCAACAGATAGTTGTTCCATTTTGTCAATCCATTTTCTTCTGGAAGAGCGATGGA
P06 14 ST155	795	ACGATTGCTTCACCAAGAAGAGCTGCAACAGATAGTTGTTCCATTTTGTCAATCCATTTTCTTCTGGAAGAGCGATGGA
Ro05 ST155	795	ACGATTGCTTCACCAAGAAGAGCTGCAACAGATAGTTGTTCCATTTTGTCAATCCATTTTCTTCTGGAAGAGCGATGGA
Ro09 ST155	795	ACGATTGCTTCACCAAGAAGAGCTGCAACAGATAGTTGTTCCATTTTGTCAATCCATTTTCTTCTGGAAGAGCGATGGA
Ro15 ST155	795	ACGATTGCTTCACCAAGAAGAGCTGCAACAGATAGTTGTTCCATTTTGTCAATCCATTTTCTTCTGGAAGAGCGATGGA

ScottA ST2	-----
EGD-e ST35	-----
10403S ST85	-----
F2365 ST1	-----
CDL65 ST155	875 GTTTGTA
P06 14 ST155	875 GTTTGTA
Ro05 ST155	875 GTTTGTA
Ro09 ST155	875 GTTTGTA
Ro15 ST155	875 GTTTGTA

Figure S5B. Alignment of *prfA* amino acid sequences.

ScottA_ST2	1	MNAQAEEFKKYLETNGIKPKQFHKKELIFNQWDPQEYCIFLYDGITKLTISENGTIMNLQYYKGAFVIM
EGD-e_ST35	1	MNAQAEEFKKYLETNGIKPKQFHKKELIFNQWDPQEYCIFLYDGITKLTISENGTIMNLQYYKGAFVIM
10403S_ST85	1	MNAQAEEFKKYLETNGIKPKQFHKKELIFNQWDPQEYCIFLYDGITKLTISENGTIMNLQYYKGAFVIM
F2365_ST1	1	MNAQAEEFKKYLETNGIKPKQFHKKELIFNQWDPQEYCIFLYDGITKLTISENGTIMNLQYYKGAFVIM
CDL65_ST155	1	MNAQAEEFKKYLETNGIKPKQFHKKELIFNQWDPQEYCIFLYDGITKLTISENGTIMNLQYYKGAFVIM
P06_14_ST155	1	MNAQAEEFKKYLETNGIKPKQFHKKELIFNQWDPQEYCIFLYDGITKLTISENGTIMNLQYYKGAFVIM
Ro05_ST155	1	MNAQAEEFKKYLETNGIKPKQFHKKELIFNQWDPQEYCIFLYDGITKLTISENGTIMNLQYYKGAFVIM
Ro09_ST155	1	MNAQAEEFKKYLETNGIKPKQFHKKELIFNQWDPQEYCIFLYDGITKLTISENGTIMNLQYYKGAFVIM
Ro15_ST155	1	MNAQAEEFKKYLETNGIKPKQFHKKELIFNQWDPQEYCIFLYDGITKLTISENGTIMNLQYYKGAFVIM

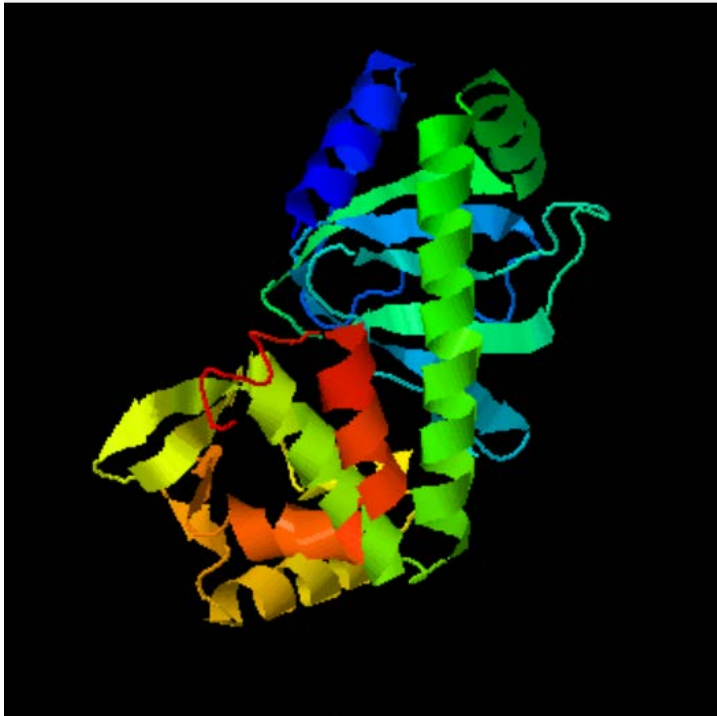
ScottA_ST2	71	SGFIDTETSVGYNLEVISEQATAYVIKINELKELLSKNLTHFFYVFQTLQKQVSYSYSLAKFNDFSINGKL
EGD-e_ST35	71	SGFIDTETSVGYNLEVISEQATAYVIKINELKELLSKNLTHFFYVFQTLQKQVSYSYSLAKFNDFSINGKL
10403S_ST85	71	SGFIDTETSVGYNLEVISEQATAYVIKINELKELLSKNLTHFFYVFQTLQKQVSYSYSLAKFNDFSINGKL
F2365_ST1	71	SGFIDTETSVGYNLEVISEQATAYVIKINELKELLSKNLTHFFYVFQTLQKQVSYSYSLAKFNDFSINGKL
CDL65_ST155	71	SGFIDTETSVGYNLEVISEQATAYVIKINELKELLSKNLTHFFYVFQTLQKQVSYSYSLAKFNDFSINGKL
P06_14_ST155	71	SGFIDTETSVGYNLEVISEQATAYVIKINELKELLSKNLTHFFYVFQTLQKQVSYSYSLAKFNDFSINGKL
Ro05_ST155	71	SGFIDTETSVGYNLEVISEQATAYVIKINELKELLSKNLTHFFYVFQTLQKQVSYSYSLAKFNDFSINGKL
Ro09_ST155	71	SGFIDTETSVGYNLEVISEQATAYVIKINELKELLSKNLTHFFYVFQTLQKQVSYSYSLAKFNDFSINGKL
Ro15_ST155	71	SGFIDTETSVGYNLEVISEQATAYVIKINELKELLSKNLTHFFYVFQTLQKQVSYSYSLAKFNDFSINGKL

ScottA_ST2	141	GSICGQLLILTYVYGKETPDGIKITLDNLTMQELGYSSGIAHSSAVSRIISKLKQEKVIVYKNSCFYVQN
EGD-e_ST35	141	GSICGQLLILTYVYGKETPDGIKITLDNLTMQELGYSSGIAHSSAVSRIISKLKQEKVIVYKNSCFYVQN
10403S_ST85	141	GSICGQLLILTYVYGKETPDGIKITLDNLTMQELGYSSGIAHSSAVSRIISKLKQEKVIVYKNSCFYVQN
F2365_ST1	141	GSICGQLLILTYVYGKETPDGIKITLDNLTMQELGYSSGIAHSSAVSRIISKLKQEKVIVYKNSCFYVQN
CDL65_ST155	141	GSICGQLLILTYVYGKETPDGIKITLDNLTMQELGYSSGIAHSSAVSRIISKLKQEKVIVYKNSCFYVQN
P06_14_ST155	141	GSICGQLLILTYVYGKETPDGIKITLDNLTMQELGYSSGIAHSSAVSRIISKLKQEKVIVYKNSCFYVQN
Ro05_ST155	141	GSICGQLLILTYVYGKETPDGIKITLDNLTMQELGYSSGIAHSSAVSRIISKLKQEKVIVYKNSCFYVQN
Ro09_ST155	141	GSICGQLLILTYVYGKETPDGIKITLDNLTMQELGYSSGIAHSSAVSRIISKLKQEKVIVYKNSCFYVQN
Ro15_ST155	141	GSICGQLLILTYVYGKETPDGIKITLDNLTMQELGYSSGIAHSSAVSRIISKLKQEKVIVYKNSCFYVQN

ScottA_ST2	211	LDYLKRYAPKLDEWFYLA	CPATWGKLN-----
EGD-e_ST35	211	LDYLKRYAPKLDEWFYLA	CPATWGKLN-----
10403S_ST85	211	LDYLKRYAPKLDEWFYLA	CPATWGKLN-----
F2365_ST1	211	LDYLKRYAPKLDEWFYLA	CPATWGKLN-----
CDL65_ST155	211	LDYLKRYAPKLDEWFYLA	CPATWGKLNQKQYSSMRNTVLYFIRIKNLQKHFH
P06_14_ST155	211	LDYLKRYAPKLDEWFYLA	CPATWGKLNQKQYSSMRNTVLYFIRIKNLQKHFH
Ro05_ST155	211	LDYLKRYAPKLDEWFYLA	CPATWGKLNQKQYSSMRNTVLYFIRIKNLQKHFH
Ro09_ST155	211	LDYLKRYAPKLDEWFYLA	CPATWGKLNQKQYSSMRNTVLYFIRIKNLQKHFH
Ro15_ST155	211	LDYLKRYAPKLDEWFYLA	CPATWGKLNQKQYSSMRNTVLYFIRIKNLQKHFH

ScottA_ST2	-----	
EGD-e_ST35	-----	
10403S_ST85	-----	
F2365_ST1	-----	
CDL65_ST155	281	CQSIFLLEERWSL
P06_14_ST155	281	CQSIFLLEERWSL
Ro05_ST155	281	CQSIFLLEERWSL
Ro09_ST155	281	CQSIFLLEERWSL
Ro15_ST155	281	CQSIFLLEERWSL

Figure S5: Predicted 3D protein structure of PrfA using I-TASSER



PrfA_EGDe
C-score= 1.07



PrfA_CDL65 (ST155)
C-score= -1.62

C-score is calculated based on the significance of threading template alignments and the convergence parameters of the structure assembly simulations. C-score is typically in the range of $[-5, 2]$, where a C-score of a higher value signifies a model with a higher confidence and vice-versa.

Figure S7. Distribution and variability of stress-associated factors among 130 *L. monocytogenes* ST155 strains.

