Figure S1

FarR Cluster Alignments

	1	о.	20	30	40	50	60	70	80	90	100	110	120	130	140	150	160	170	180
FarR-1_SAT0131_02763	MKETDLRVI	KTKKALSSSI	LQLLEQQ	LFQTITVN	QICDNALVH	RTTFYKHFY	DKYDLLEYLF	NQLTKDYFAR	DISDRLNHPF	QTMSDTIN	NKEDLREIAE	EFQEEDAEFNKVI	KNVCIKIMHN.	DIKNNRDRIDI	DSDIPDNLI	FYIYDSLIEGF	IHWIKDEKI	DWPGEDIDNIF	HKVINIKIK
FarR-1a_HMPREF0772_10638	MKETDLRVI	KTKKALSSSI	LQLLEQQ	LFQTITVN	QICDNALVH	RTTFYKHFY	DKYDLLEYLF	NQLTKDYFAR	DISDRLNHPF	QTMSDTIN	NKEDLREIAE	FQEEDAEFNKVI	KNVCIKIMHN	DIKNNRDRIDI	YSDIPDNLI	FYIYDSLIEGF	IHWIKDEKI	DWPGEDIDNIF	HKVINIKIK
FarR-2_BSG37_13870	MKETDLRVI	KTKKALSSSI	LQLLEQQ	LFQTITVN	QICDNALVH	RTTFYKHFY	DKYDLLEYLF	NQLTKDYFAR	DISDRLNHPF	QTMSDTIN	NKEDLREIAE	FQEEDAEFNKVI	KNVCIKIMHN	DIKNNRDRIDI	DSDIPDNLI	FYIYDSLIEGF	IHWIKDEKI	DWPGEDIDNIF	HRLINIKIK
FarR-2a_EFD76_14235	MKETDLRVI	KTKKALSSSI	LQLLEQQ	LFQTITVN	QICDNALVH	RTTFYKHFY	DKYDLLEYLF	NQLTKDYFAR	DISDRLNHPF	QTMSDTIN	NKEDLREIAE	EFQEEDAEFNKVI	KNVCIKIMHN	DIKNNRDRIDI	DSDIPDNLI	FYIYDSLIEGF	I HWIKDGKI	DWP <u>G</u> EDIDNIF	HRLINIKIK
FarR-2b_A5J11_02655	MKETDLRVI	KTKKALSSSI	LQLLEQQ	LFQTITVN	QICDNALVH	RTTFYKHFY	DKYDLLEYLF	NQLTKDYFAR	DISDRLNHPF	QTMSDTIN	NKEDLREIAE	EFQEEDAEFNKVI	KNVCIKIMHN.	DIKNNRDRIDI	DSDIPDNLI	FYIYDSLIEGF	IHWIKDEKI	DWPDEDIDNIF	HRLINIKIK
FarR-2c_SAKG03_25510	MKETDLRVI	KTKKALSSSI	LQLLEQQ	LFQTITVN	QICDNALVH	RTTFYKHFY	DKYDLLEYLF	NQLTKDYFAR	DISDRLNHPF	QTMSDTIN	NKEEDLREI	A E F Q E E D A E F N K	LKNVCIKIMH	NDIKNNRDRIC	DIDSDIPDNL	IFYIYDSLIEG	FIHWIKDEK	IDWPGEDIDNI	FHRLINIKIK
FarR-2d_D9Q92_13255	MKETDLRVI	KTKKALSSSI	LQLLEQQ	LFQTITVN	QICDNALVH	RTTFYKHFY	DKYDLLEYLF	NQLTKDYFAR	DISDRLNHPF	QTMSDTIN	NKEDLREIAE	EFQEEDAEFNKVI	. KNICIKIMHN	DIKNNRDRIDI	DSDIPDNLI	FYIYDSLIEGF	IHWIKDEKI	DWPGEDIDNIF	HRLINIKIK
FarR-2e_E5491_14360	MKETDLRVI	KTKKALSSSI	LQLLEQQ	LFQTITVN	QICDNALVH	RTTFYKHFY	DKYDLLEYLF	NQLTKDYFAR	DISDRLNHPF	QTMSDTIN	NKEDLKEIAE	EFQEEDAEFNKVI	KNVCIKIMHN	DIKNNRDRIDI	DSDIPDNLI	FYIYDSLIEGF	IHWIKDEKI	DWPGEDIDNIF	HRLINIKIK
FarR-2f_ACH32_06180	MKETDLRVI	KTKK <u>A</u> LSSSI	LQLLEQQ	LFQTITVN	QICDNALVH	RTTFYKHFY	DKYDLLEYLF	NQLTKDYFAR	DISDRLNHPF	QTISDTIN	NKEDLREIAE	EFQEEDAEFNKVI	KNVCIKIMHN.	DIKNNRDRIDI	DSDIPDNLI	FYIYDSLIEGF	IHWIKDEKI	DWPGEDIDNIF	HRLINIKIK
FarR-2g_SAI6T6_1018950	MKETDLRVI	KTKKPLSSSI	LQLLEQQ	LFQTITVN	QICDNALVH	RTTFYKHFY	DKYDLLEYLF	NQLTKDYFAR	DISDRLNHPF	QTMSDTINI	NKEDLREIAE	EFQEEDAEFNKVI	KNVCIKIMHN.	DIKNNRDRIDI	DSDIPDNLI	FYIYDSLIEGF	IHWIKDEKI	DWPGEDIDNIF	HRLINIKIK
FarR-2h_CSC57_1845	MKETDLRVI	KTKKALLSSI	LQLLEQQ	LFQTITVN	QICDNALVH	RTTFYKHFY	DKYDLLEYLF	NQLTKDYFAR	D I S D R L N H P F	QTMSDTIN	NKEDLREIAE	EFQEEDAEFNKVI	KNVCIKIMHN	DIKNNRDRIDI	DSDIPDNLI	FYIYDSLIEGF	IHWIKDEKI	DWPGEDIDNIF	HRLINIKIK
FarR-2i_DLJ55_14025	MKETDLRVI	KTKKALSSSI	LQLLEQQ	LFQTITVN	QICDNALVH	RTTFYKHFY	DKYDLLEYLF	NQLTKDYFAR	D I S DHL NH P F	QTMSDTIN	NKEDLREIAE	EFQEEDAEFNKVI	KNVCIKIMHN.	DIKNNRD <u>R</u> IDI	DSDIPDNLI	FYIYDSLIEGF	IHWIKDEKI	DWPGEDIDNIF	HRLINIKIK
FarR-2j_AYM29_14215	MKETDLRVI	KTKKALSSSI	LQLLEQQ	LFQTITVN	QICDNALVH	RTTFYKHFY	DKYDLLEYLF	NQLTKDYFAR	DISDRLNHPF	QTMSDTIN	NKEDLREIAE	EFQEEDAEFNKVI	KNVCIKIMHN.	D I KNNR DH I D I	DSDIPDNLI	FYIYDSLIEGF	IHWIKDEKI	DWPGEDIDNIF	HRLINIKIK
FarR-2k_AYM30_14220	MKETDLRVI	KTKKALSSSI	LQLLEQQ	LFQTITVNO	QICDNALVH	RTTFYKHFY	DKYDLLEYLF	NQLTKDYFAR	D I <u>S</u> DR L NH P F	QTMSDTIN	NKEDLREIAE	EFQEEDAEFNVVI	KNVCIKIMHN.	DIKNNRDRIDI	DSDIPDNLI	FYIYDSLIEGF	THWIKDEKI	DWPGEDIDNIF	HRLINIKIK
FarR-2I_DD547_02586	MKETDLRVI	KTKKALSSSI	LQLLEQQ	LFQTITVNO	QICDNALVH	RTTFYKHFY	DKYDLLEYLF	NQLTKDYFAR	D I GD R L N H P F	QTMSDTIN	NKEDLREIAE	EFQEEDAEFNKVI	. KNVCIKIMHN	DIKNNRDRIDI	DSDIPDNLI	FYIYDSLIEGF	THWIKDEKI	DWPGEDIDNIF	HRLINIKIK
FarR-2m_GZ067_10535	MKETDLRVI	KTKKALSSSI	LQLLEQQ	LFQTITVN	QICDNALVH	RTTFYKHFY	DKYDLLEYLF	NQLTKDYFAR	DISDRITHPF	QTMSDTINI	NKEDLREIAE	EFQEEDAEFNKVI	KNVCIKIMHN.	DIKNNRDRIDI	DSDIPDNLI	FYIYDSLIEGF	IHWIKDEKI	DWPGEDIDNIF	HRLINIKIK
FarR-2n_E3T09_10540	MKETDLRVI	KTKKALSTSI	LQLLEQQ	LFQTITVNO	QICDNALVH	RTTFYKHFY	DKYDLLEYLF	NQLTKDYFAR	DISDRLNHPF	QTMSDTIN	NKEDLREIAE	EFQEEDAEFNKVI	KNVCIKIMH <u>N</u>	DIKNNRDRIDI	DSDIPDNLI	FYIYDSLIEGF	HWIKDEKI	DWPGEDIDNIF	HRLINIKIK
FarR-3_SAA6159_02449	MKETDLRVI	KTKKALSSSI	LQLLEQQ	LFQTITVN	QICDNALVH	RTTFYKHFY	DKYDLLEYLF	NQLTKDYFAR	DISDRLNHPF	QTISDTIN	NKEDLREIAE	EFQEEDIEFNKVI	. KNVCIKIMHD	DIKNNRDRIDI	DSDVPDNLI	FYIYDSLIEGF	MHWIKDEKI	DWPGEDIDNIF	HRLINIKIK
FarR-3a_KUH140087_2018	MKETDLRVI	KTKKALSSSI	LQLLEQQ	LFQTITVN	QICDNALVH	RTTFYKHFY	DKYDLLEYLF	NQLTKDYFAR	DISDRLNHPF	QTISDTINI	NKEDLREIAE	EFQEEDSEFNKVI	. KNVCIKIMHD	DIKNNRDRIDI	DSDVPDNLI	FYIYDSLIEGF	MHWIKDEKI	DWPGEDIDNIF	HRLINIKIK
FarR-4_FIV54_01145	MKETDLRVI	KTKKALSSSI	LQLLEQQ	LFQTITVNO	QICDNALVH	RTTFYKHFY	DKYDLLEYLF	NQLTKDYFAR	DISDRLNHPF	QTISDTINI	NKEDLRDIAE	EFQEEDAEFNKVI	KNVCIKIMHN.	DIKNNRDRIDI	DSDIPDNLI	FYIYDSLIEGF	MHWIKDEKI	DWPGE <u>D</u> ID <u>N</u> IF	H <u>RL</u> INIKIK
FarR-5_FORC26_2261	MKETDLRVI	KTKKALSSSI	LQLLEQQ	LFQTITVN	QICDNALVH	RTTFYKHFY	DKYDLLEYLF	NQLTKDYFAR	DISDRLNHPF	QTISDTIN	NKEDLRDIAE	EFQEEDAEFNKVI	KNVCIKIMHN.	DIKNNRDRIDI	DSDIPDNLI	FYIYDSLIEGF	MHWIKDEKI	DWPGEEIDKIF	HKVINIKIK
FarR-5a_ST398NM01_2603	MKETDLRVI	KTKKALSSSI	LQLLEQQ	LFQTITVN	LICDNALVH	RTTFYKHFY	DKYDLLEYLF	NQLTKDYFAR	DISDRLNHPF	QTISDTINI	NKEDLRDIAE	EFQEEDAEFNKVI	.KNVCIKIMHN	DIKNNRDRIDI	DSDIPDNLI	FYIYDSLIEGF	MHWIKDEKI	DWPGEEIDKIF	HKVINIKIK
FarR-5b_FD482_13120	MKETDLRVI	KTKKALSSSI	LQLLEQQ	LFQTITVN	LICDNALVH	RTTFYKHFY	DKYDLLEYLF	NQLTKDYFAR	DISDRLNHPF	QTISDTINI	NKEDLRDIAE	EFQEEDAEFNKVI	. KNFC I K I MHN	DIKNNRDRIDI	DSDIPDNLI	FYIYDSLIEGF	MHWIKDEKI	DWPGEEIDKIF	HKVINIKIK
FarR-5c_SAEMRSA15_24560	MKETDLRVI	KTKKALSSSI	LQLLEQQ	LFQTITVN	QICDNALVH	RTTFYKHFY	DKYDLLEYLF	NQLTKDYFAR	DISDRLNHPF	QTISDTIN	NKEDLRDIAE	EFQEEDAEFNKVI	KNVCIKIMHN.	DIKNNRDRIDI	DSHIPDNLI	FYIYDSLIEGF	MHWIKDEKI	DWPGEEIDKIF	HKIINIKIK
FarR-5d_C5Y45_13380	MKETDLRVI	KTKKALSSSI	LQLLEQQ	LFQTITVNO	QICDNALVH	RTTFYKHFY	DKYDLLEYLF	NQLTKDYFAR	DISDRLNHPF	QTISDTINI	NKEDLRDIAE	EFQEEDAEFNKVI	KNVCIKIM <u>HN</u>	DIKNNRDRIDI	DSHIPDNLT	FYIYDSLIEGF	MHWIKDEKI	DWP <u>G</u> EEIDKIF	HKIINIKIK
FarR-6_NCTC13552_02618	MKETDLRVI	KTKKALSSSI	LQLLEQH	LFQTITVN	QICHNALVH	RTTFYKHFY	DKYDLLEYLF	NQLTKAYFAT	DISDRLNHPF	QTINDTIN	NKEDLQKVAI	FQQEDAEFNKVI	. KNVCIKIMND	D I K N N S D R I D V	DGD I PNNLL	FYIYDSLIEGF	LHWIKDEKI	DWPSEEIDKIF	HKVINIKIK
FarR-6a_C9J78_07040	MKETDLRVI	KTKKALSSSI	LQLLEQH	LFQTITVN	QICHNALVH	RTTFYKHFY	DKYDLLEYLF	NQLTKAYFAT	D I S D R L N H P F	QTINDTIN	NKEDLQKVAL	FQQEDAEFNKVI	. KNVCIKIMND	DIKNNSDRIDV	DGD I PNNLL	FYIYGSLIEGF	LHWIKDEKI	DWPSEEIDKIF	HKVINIKIK
FarR-6b_SaO17_02469	MKETDLRVI	KTKKALSSSI	LQLLEQH	LFQTITVN	QICHNALVH	RTTFYKHFY	DKYDLLEYLF	NQLTKAYFAT	DISDRLNLPF	QTINDTIN	NKEDLQKVAL	FQQEDAEFNKVI	. KNVCIKIMND	DIKNNSDRIDV	DGD I PNNLL	F Y I Y <mark>G</mark> S L I E G F	LHWIKDEKI	DWPSEEIDKIF	HKVINIKIK
FarR-6c_NCTC7485_02478	MKETDLRVI	KTKKALSSSI	LQLLEQH	LFQTITVN	QICHNALVH	RTTFYKHFY	DKYDLLEYLF	NQLTKAYFAT	DISDRLNHPF	QTINDTIN	NKEDLQKVAI	FQQEDAEFNKVI	KNVCIKIMND.	DIKNNSDRIDV	DGD I PNNLL	FYIYGSLIEGF	LYWIKDEKI	DWPSEEIDKIF	HKVINIKIK
FarR-6d_SAB2427	MKETDLRVI	KTKKALSSSI	LQLLEQH	LFQTITVN	QICHNALVH	RTTFYKHFY	DKYDLLEYLF	NQLTKAYFAT	DISDRLNHPF	QTINDTIN	NKEDLQKVAI	FQQEDAEFNKVI	.KNVCIKIMND	DIKNNCDRIDV	DGD I PNNLL	FYIYGSLIEGF	LHWIKDEKI	DWPSEEIDKIF	HKVINIKIK
FarR-6e_M013TW_2526	MKETDLRVI	KTKKALSSSI	LQLLEQH	LFQTITVN	QICHNALVH	RTTFYKHFY	DKYDLLEYLF	NQLTKAYFAT	DISDRLNHPF	QTINDTIN	NKEDLQKVAI	FQQEDAEFNKVI	.KNVCIKIMND	DIKNNSDRIDV	DGD I PNNLL	FYIYGSLIEGF	MHWIKDEKI	DWPSEEIDKIF	HKVINIKIK

FarB-6d ST707 FarB-6e ST59

Nucleotide Alignment of Representative farR Cluster Genes FarR-1 ST30 FarB-1 ST239 FarB-2 ST5 FarB-2 ST97 ITGAAAGAGGACTGATTTACGAGTTATAAAGACAAAAAAAGCATTGTCGAGTAGCTTGCTACAATTGTTAGAACAGCAATTATTCCAAACGATTACTGTCAAATTTGCGACCACCGCACCACCATTTTATAAAACATTTTTATGATAAAATATGATCTTCTAGAGCAACAGTATTTGTG i f a hard here a transmission of the transmission of trFarR-2 ST25 $\begin{array}{l} {} Atgaaaga creat tacga grant a a a construct co$ FarR-2 ST15 FarR-2 ST8 FarR-2 ST101 FarR-2 ST9 FarR-2I ST45 FarR-2I ST198 FarR-2f ST395 FarR-3 ST93 FarB-4 ST12 FarR-4 ST20 ATGANAGAGACTGATTTACGAGTTATAAAGACAAAAAAAGCATTGTCGAGTAGCTTGCTACAATTGTTAGAACAGCAATTATTCCAAACGATTACTGTCAATCGACACCGCACCACCGCACCACCATTTTATAAACATTTTATGATAAATA FarR-5 ST1 FarR-5 ST188 FarR-5 ST1148 FarR-5a ST398 FarR-5a ST2272 FarR-5b ST22 FarR-6 ST425 FarR-6a ST121 FarR-6b ST133 FarR-6c CC705 FarR-6d ST707 FarR-6e ST59 19 20< FarB-1 ST30 FarB-1 ST239 FarB-2 ST5 FarB-2 ST97 FarR-2 ST25 FarR-2 ST15 FarR-2 ST8 FarR-2 ST101 FarR-2 ST9 FarR-2I ST45 FarR-2I ST198 FarR-2f ST395 FarR-3 ST93 FarB-4 ST12 FarR-4 ST20 FarR-5 ST1 FarR-5 ST188 FarR-5 ST1148 FarR-5a ST398 FarR-5a ST2272 FarR-5b ST22 FarR-6 ST425 FarR-6a ST121 FarR-6b ST133 FarR-6c CC705 FarR-6d ST707 FarR-6e ST59 420 430 440 450 470 490 380 400 410 460 480 500 510 520 силалаталтадададсов то в совется и совется с совета и то совется так и то совется то сов FarB-1 ST30 FarB-1 ST239 FarB-2 ST5 FarR-2 ST97 FarR-2 ST25 FarR-2 ST15 FarR-2 ST8 FarR-2 ST101 FarR-2 ST9 FarR-2l ST45 FarR-2I ST198 $\label{transmission} \label{transmission} \\ \begin{tabular}{label{transmission} \\ \begin{tabular}{label{tr$ FarR-2f ST395 FarR-3 ST93 FarB-4 ST12 FarR-4 ST20 FarR-5 ST1 FarR-5 ST188 FarR-5 ST1148 FarR-5a ST398 FarR-5a ST2272 FarR-5b ST22 FarR-6 ST425 FarR-6a ST121 FarR-6b ST133 FarR-6c CC705

Nucleotide alignment of farR from different clonal complexes, and associated farR variants

	10	00	20	10	sociae ang.		70			100	440	400	100	140	150	100	170	100
D 1 CT20	10	20	30	40	50	60	70	80	90	100	110	120	130	140	150	160	1/0	180
Farn-1 S130	ATGAAAGAGACT	CATTTACGAGIT	ATAAAGACAAAA	AAAGCATIGI	CGAGTAGCT	I GC TACAAT I GI	TAGAACAGCA	ATTATTCCAA	ACGATIACIO	TCAATCAAAT	TTCCCACAA	COLACTOGIAC	ACCOCACA	ACATTTTAL.	AAACACITT	TATGATAAATA	TGATCTICIA	GAGIAITIGII
Fain-2 313	ATCALAGAGACT	CATTTACGAGIT	ATAAAGACAAAA	AAAGCATIGI	COAGTAGET	I GC TACAAT TO I	TAGAACAGCA	ATTATTCCAA	ACGATTACIO	TCAATCAAAI	TTOCGACAA	I GCACTCOTAC	ACCOUNCAL	ACATTTAL.	AAACAIIII	TATGATAAATA	TGATCTICIA	CAGTATITOTT
Farn-2 516	ATGAAAGAGACT	GATTTACGAGIT	ATAAAGACAAAA	AAAGCATIGI	CGAGTAGCT	I GC I ACAAI I GI		ATTATTCCAA	ACGATIACIG	TCAAICAAAI	TTCCCACAA	CCACICGIAC	ACCOLACA	ACATTTTAL.	AAACAIIII	TATGATAAATA	IGAICIICIA	GAGTACTIGTT
Fain-2 3113	ATGAAAGAGACT	GATTTACGAGIT	ATAAAGACAAAA	AAAGCATIGI	CGAGTAGCT		TAGAACAGCA		ACGATIACIO		TTGCGACAA	COCACICOIAC	ACCOCACA	ACATTITAT.	AAACAIIII	TATGATAAATA	TGATCTICIA	GAGTATTIGTT
FarR-2 5197	ATGAAAGAGACT	GATITACGAGIT	ATAAAGACAAAA	AAAGCATIGI	CGAGTAGCT	I GC I ACAAI I GI	TAGAACAGCA	ATTATTCCAA	ACGATIACIG	GICAAICAAAI	TTGCGACAA	COCACICGIAC	ACCGCACA	ACATTTTAL.	AAACAIIII	TAIGAIAAAIA	CATCITCIA	GAGIAIIIGII
Farn-5 STT	ATGAAAGAGACT	CATTTACGAGIT	ATAAAGACAAAA	AAAGCATIGI	I COAGTAGET I	I GC I ACAAI I GI	TAGAACAGCA	ATTATTCCAA	ACGATIACIO	TCAATCAAAT	TTCCCACAA	CCACTCGTAC	ACCGCACA	ACATTTTAL.	AAACAIIII	TATGATAAATA	CATCTICIA	GAGIAITIGII
Parn-50 5122	ATGAAAGAGACT	GATTTACGAGIT	ATAAAGACAAAA	AAAGCATIGI	TCAAGTAGCT	GCIGCAATIGI	TAGAACAGCA	ATTATTCCAA	ACGATTACTO	GICAAICAAAI	TTGCGACAA	COCACTOGIAC	ACCGCACA	ACATTITAT.	AAACAIIII	TAIGAIAAAIA	CATCITCI	GAGIATITATT
511 Fain 11211	ATGAAAGAGACT	GATTTACGAGIT	ATAAAGACAAAA	AAAGCATIGI		I GC I ACAAI I GI	TAGAACAGCA	ATTATICCAA	ACGATTACTO	JICAAICAAAI	TTGCGACAA	GCACICGIAC	ACCGCACA	ACALITIAI.	AAACAIIII	TAIGATAAATA	GATCITCIA	GAGIAITIGIT
CC97 Fark H1211	ATGAAAGAGACT	GATTTACGAGIT	ATAAAGACAAAA	AAAGCATIGI	CGAGTAGCT	IGCIACAAIIGI	TAGAACAGCA	ATTATICCAA	ACGATTACTO	GICAAICAAAI	TTGCGACAA	GCACTCGTAC	ACCGCACA	ACATTITAT.	AAACAIIII	TATGATAAATA	IGAICIICIA	GAGIATIIGII
518 Fark H1211	ATGAAAGAGACT	GATTTACGAGTT	ATAAAGACAAAA	AAAGCATTGI		I GCTACAATTGI	TAGAACAGCA	ATTATTCCAA	ACGATTACTO	GTCAATCAAA1	TTTGCGACAA	CGCACTCGTAC	ACCGUACA	ACATTTTAT.	AAACATTTT	TATGATAAATA	IGATETTETA	GAGTACITGTT
	ATGAAAGAGACT	GATTTACGAGTT	ATAAAGACAAAA	AAAGCATTGI	TCAAGTAGCT	IGCIGCAATIGI	TAGAACAGCA	ATTATTCCAA	ACGATTACTO	GTCAATCAAAI	TTTGCGACAA	GCACTCGTAC	ACCGCACA	ACATTTTAT.	AAACATTTI	TATGATAAATA	IGATCTTCT	GAATATTIATT
SI30 Fark HI21Y	ATGAAAGAGACT	GATTTACGAGTT	ATAAAGACAAAA	AAAGCATTGI	TCGAGTAGCT	IGCTACAATTGT	TAGAACAGCA	AATTATTCCAA	ACGATTACTO	GTCAATCAAAT	TTTGCGACAA	GCACTCGTAC	ACCGCACA	ACATTTTAT.	AAACACITTI	TATGATAAATA	FGATCTTCTA	GAGTATTTGTT
CC1 Fark C116Y	ATGAAAGAGACT	GATTTACGAGTT	ATAAAGACAAAA	AAAGCATTG1	TCGAGTAGCT	I G C T A C A A T T G I	TAGAACAGCA	AATTATTCCAA	ACGATTACTG	GTCAATCAAAT	TTTGCGACAA	CGCACTCGTAC	ACCGCACA	ACATTTTAT.	AAACATTTT	TATGATAAATA	GATCTTCTA	GAGTATTTGTT
SIS Fark CI16Y	ATGAAAGAGACT	GATTTACGAGTT	ATAAAGACAAAA	AAAAGCATTGI	TCGAGTAGCT	FGCTACAATTGT	TAGAACAGCA	AATTATTCCAA	ACGATTACTO	GTCAATCAAAT	TTTGCGACAA	IGCACTCGTAC	ACCGCACA	ACATTTTAT.	AAACATTTT	TATGATAAATA	FGATCTTCTA	GAGTATTTGTT
ST8 Fark C116Y	ATGAAAGAGACT	GATTTACGAGTT	ATAAAGACAAAA	AAAAGCATTG1	TCGAGTAGCT	I G C T A C A A T T G I	TAGAACAGCA	AATTATTCCAA	ACGATTACTG	GTCAATCAAA1	TTTGCGACAA	CGCACTCGTAC	CACCGTACA	ACATTTTAT.	AAACATTTT	TATGATAAATA	FGATCTTCTA	GAGTACTTGTT
ST97 Fark C116Y	ATGAAAGAGACT	GATTTACGAGTT	ATAAAGACAAAA	AAAAGCATTGI	TCGAGTAGCT	FGCTACAATTGT	TAGAACAGCA	AATTATTCCAA	ACGATTACTO	GTCAATCAAAI	TTTGCGACAA	CGCACTCGTAC	ACCGCACA	ACATTTTAT.	AAACATTTT	TATGATAAATA	FGATCTTCTA	GAGTATTTGTT
ST8 FarR G166D USA	ATGAAAGAGACT	GATTTACGAGTT	ATAAAGACAAAA	AAAGCATTGI	TCGAGTAGCT	I G C T A C A A T T G I	FTAGAACAGCA	AATTATTCCAA	ACGATTACTG	GTCAATCAAA1	TTTGCGACAA	CGCACTCGTAC	ACCGTACA	ACATTTTAT.	AAACATTTT	TATGATAAATA	FGATCTTCTA	GAGTACTTGTT
ST8 FarR G166D Norway	ATGAAAGAGACT	GATTTACGAGTT	ATAAAGACAAAA	AAAAGCATTG1	TCGAGTAGCT	FGCTACAATTGT	TAGAACAGCA	AATTATTCCAA	ACGATTACTG	GTCAATCAAAI	TTTGCGACAA	CGCACTCGTAC	ACCGTACA	ACATTTTAT.	AAACATTTT	TATGATAAATA	FGATCTTCTA	GAGTACTTGTT
ST5 FarR G166D USA	ATGAAAGAGACT	GATTTACGAGTT	ATAAAGACAAAA	AAAGCATTGI	CGAGTAGCT	FGCTACAATTGT	T T A G A A C A G C A	AATTATTCCAA	ACGATTACTO	GTCAATCAAA1	TTTGCGACAA	IGCACTCGTAC	ACCGCACA	ACATTTTAT	AAACATTTT	TATGATAAATA	FGATCTTCTA	GAGTATTTGTT
ST5 FarR G166D Denmark	ATGAAAGAGACT	GATTTACGAGTT	ATAAAGACAAAA	AAAGCATTGI	FCGAGTAGCT	FGCTACAATTGI	I TAGAACAGCA	AATTATTCCAA	ACGATTACTG	GTCAATCAAA1	TTGCGACAA	IGCACTCGTAC	CACCGCACA	ACATTTTAT.	AAACATTTT	TATGATAAATA	IGATCTTCTA	GAGTATTTGTT
CC97 FarR G166D	ATGAAAGAGACT	GATTTACGAGTT	ATAAAGACAAAA	AAAAGCATTGT	TCGAGTAGCT	FGCTACAATTGT	F TAGAACAGCA	ATTATTCCAA	ACGATTACTO	GTCAATCAAAT	TTTGCGACAA	CGCACTCGTAC	ACCGCACA	ACATTTTAT.	AAACATTTT	TATGATAAATA	TGATCTTCTA	GAGTATTTGTT
ST15 FarR P165L	ATGAAAGAGACT	GATTTACGAGTT	ATAAAGACAAAA	AAAAGCATTGT	TCGAGTAGCT	FGCTACAATTGT	F TAGAACAGCA	ATTATTCCAA	ACGATTACTO	GTCAATCAAAT	TTGCGACAA	GCACTCGTAC	CACCGCACA	ACATTTTAT.	AAACATTTT	TATGATAAATA	FGATCTTCTA	GAGTATTTGTT
ST5 FarR P165L	ATGAAAGAGACT	GATTTACGAGTT	ATAAAGACAAAA	AAAGCATTGT	TCGAG TAGCT 1	FGCTACAATTGT	Γ TAGAACAGCA	ATTATTCCAA	ACGATTACTG	GTCAATCAAAT	ΓΤΤGCGACAΑ	TGCACTCGTAC	CACCGCACA	ACATTTTAT.	AAACATTT	TATGATAAATA	TGATCTTCTA	GAGTATTTGTT
	190	200 210	0 220	230	240	250	260	270	280	290	300	310	320	330	2	340 350) 36	io 370
FarR-1 ST30	CAATCAATTGAC	TAAAGACTACTT	TGCTAGAGATAT	TCAGTGACCGT	TCTTAATCAT	CCATTCCAAACC	GATGAGTGATA	ACGATTAATAA	TAAAGAGGAT	TTGAGAGAA	ATCGCAGAAT	FCCAAGAAGAA	GACGCTGA	ΑΤΤΤΑΑΤΑΑ.	AGTATTAAA	AAATGTCTGCA	ΓΤΑΑΑΑΤΤΑΤ	GCATAACGATA
FarR-2 ST5	CAATCAATTGAC	TAAAGACTACTT	TGCTAGAGATAT	TCAGTGACCGT	TCTTAATCATC	CCATTCCAAACC	GATGAGTGATA	ACGATTAATAA	TAAAGAGGAT	TTGAGAGAA	ATCGCAGAAT	Г С С А А G A A G A A	GACGCTGA	ATTTAATAA.	AGTATTAAA	AAATGTCTGCA	ΓΤΑΑΑΑΤΤΑΤ	GCATAACGATA
FarR-2 ST8	CAATCAATTGAC	TAAAGACTACTT	TGCTAGAGATAT	FCAGTGACCGT	TCTTAATCATC	CCATTCCAAACC	GATGAGTGATA	ACGATTAATAA	TAAAGAGGAT	TTGAGAGAA	ATCGCAGAAT	FCCAAGAAGAA	GACGCTGA	ATTTAATAA.	AGTATTAAA	AAATGTCTGCA	ΓΤΑΑΑΑΤΤΑΤ	GCATAACGATA
FarR-2 ST15	CAATCAATTGAC	TAAAGACTACTT	TGCTAGAGATAT	TCAGTGACCGT	TCTTAATCATC	CCATTCCAAACO	GATGAGTGATA	ACGATTAATAA	TAAAGAGGAT	TTGAGAGAA	ATCGCAGAAT	T C C A A G A A G A A	GACGCTGA	ΑΤΤΤΑΑΤΑΑ.	AGTATTAAA	AAATGTCTGCA	ΓΤΑΑΑΑΤΤΑΤ	GCATAACGATA
FarR-2 ST97	CAATCAATTGAC	TAAAGACTACTT	TGCTAGAGATAT	FCAGTGACCGT	TCTTAATCAT	CCATTCCAAACO	GATGAGTGATA	ACGATTAATAA	TAAAGAGGAT	TTGAGAGAA	ATCGCAGAAT	ICCAAGAAGAA	GACGCTGA	ATTTAATAA.	AGTATTAAA	AAATGTCTGCA	ΓΤΑΑΑΑΤΤΑΤ	GCATAACGATA
FarR-5 ST1	CAATCAATTGAC	TAAAGACTATTT	TGCCAGAGACAT	TTA GCG ATC GC	CTTAACCAC	CCATTCAAACC	G A T T A G C G A T A	Α CAAT ΤΑ ΑCA Α	TAAAGAAGAT	TTTGCGAGAT /	ATTGCAGAAT	TTCAAGAAGAA	GACGCTGA	ATTTAATAA.	AGTATTAAA	AAATGTCTGCA	ΓΤΑΑΑΑΤΤΑΤ	GCATAACGATA
FarR-5b ST22	TAATCAATTGAC	TAAAGACTATTT	CGCCAGAGACAT	TTA GCG ATC G T	<u>r</u> c t t a a c c a c c	CATTCAAACO	G A T T A G C G A T A	A CAAT TAACAA	TAAAGAAGAT	TTTGCGAGATA	ATTGCAGAAT'	ΓΤϹΑΑGΑΑGΑΑ	GACGCTGA	ΑΤΤΤΑΑΤΑΑ.	AGTATTAAA	AAATGTCTGCA	ΓΤΑΑΑΑΤΤΑΤ	GCATAACGATA
ST1 FarR H121Y	CAATCAATTGAC	TAAAGACTATTT	TGCCAGAGACAT	ГТА GCG ATC GC	CTTAACCAC	CATTCAAACC	G A T T A G C G A T A	ACAATTAACAA	TAAAGAAGAT	TTTGCGAGAT	ATTGCAGAAT	ΓΤCΑΑGΑΑGΑΑ	GACGCTGA	ATTTAATAA.	AGTATTAAA	AAATGTCTGCA	ΓΤΑΑΑΑΤΤΑΤ	GTATAACGATA
CC97 FarR H121Y	CAATCAATTGAC	TAAAGACTACTT	TGCTAGAGATAT	TCAGTGACCGT	TCTTAATCAT	CCATTCCAAACO	GATGAGTGATA	ACGATTAATAA	TAAAGAGGAT	TTGAGAGAA	ATCGCAGAAT	Γ C C A A G A A G A A	GACGCTGA	ATTTAATAA	AGTATTAAA	AAATGTCTGCA	ΓΤΑΑΑΑΤΤΑΤ	GTATAACGATA
ST8 FarR H121Y	CAATCAATTGAC	TAAAGACTACTT	TGCTAGAGATAT	T <u>CAGTGAC</u> CGT	TCTTAA <u>T</u> CA <u>T</u> C	CCATT <u>C</u> CAAACC	GAT <u>G</u> AG <u>T</u> GATA	ACGATTAA <u>T</u> AA	TAAAGAGGAT	TTG <u>A</u> GAGA <u>A</u>	AT <u>C</u> GCAGAAT	T <u>C</u> CAAGAAGAA	GACGCTGA	ATTTAATAA	AGTATTAAA	AAATGTCTGCA	ΓΤΑΑΑΑΤΤΑΤ	GTATAACGATA
CC22 FarR H121Y	TAATCAATTGAC	TAAAGACTATTT	CGCCAGAGACAT	TTA GCG ATC G T	T C T T A A C C A C O	CCATTTCAAACC	J A T T A G C G A T A	A CAAT TAACAA	TAAAGAAGAT	TTGCGAGATA	ATTGCAGAAT	ITCAAGAAGAA	GACGCTGA	ATTTAATAA	AGTATTAAA	AAATGTCTGCA	ΓΤΑΑΑΑΤΤΑΤ	GTATAACGATA
ST30 FarR H121Y	CAATCAATTGAC	TAAAGACTACTT	TGCTAGAGATAT	TCAGTGACCGT	TCTTAATCAT	CCATTCCAAACO	GATGAGTGATA	ACGATTAATAA	TAAAGAGGAT	TTGAGAGAA	ATCGCAGAAT	Г С С А А G A A G A A	GACGCTGA	ΑΤΤΤΑΑΤΑΑ.	AGTATTAAA	AAATGTCTGCA	ГТААААТТАТ	GTATAACGATA
CC1 FarR C116Y	CAATCAATTGAC	TAAAGACTATTT	TGCCAGAGACAT	TTA GCG ATC GC	CTTAACCAC	CATTCAAACO	G A T T A G C G A T A	АСААТ ТААСАА	TAAAGAAGAT	TTGCGAGATA	ATTGCAGAAT	ΓΤСΑΑGΑΑGΑΑ	GACGCTGA	ATTTAATAA	AGTATTAAA	AAATGTCTACA	ΓΤΑΑΑΑΤΤΑΤ	GCATAACGATA
ST5 FarR C116Y	CAATCAATTGAC	TAAAGACTACTT	TGCTAGAGATAT	TCAGTGACCGT	TCTTAATCAT	CCATTCCAAACO	GATGAGTGATA	ACGATTAATAA	TAAAGAGGAT	TTGAGAGAA	ATCGCAGAAT	Г <mark>С</mark> САА <u></u> GAAGAA	GACGCTGA	ΑΤΤΤΑΑΤΑΑ	AGTATTAAA	AAATGTCTACA	ΓΤΑΑΑΑΤΤΑΤ	GCATAACGATA
ST8 FarR C116Y	CAATCAATTGAC	TAAAGACTACTT	TGCTAGAGATAT	TCAGTGACCGT	TCTTAATCATC	CCATTCCAAACO	GATGAGTGATA	ACGATTAATAA	TAAAGAGGAT	TTGAGAGAA	ATCGCAGAAT	FCCAAGAAGAA	GACGCTGA	ΑΤΤΤΑΑΤΑΑ.	AGTATTAAA	AAATGTCTACA	ГТААААТТАТ	GCATAACGATA
ST97 FarR C116Y	CAATCAATTGAC	TAAAGACTACTT	TGCTAGAGATAT	TCAGTGACCGT	TCTTAATCAT	CCATTCCAAACC	GATGAGTGATA	CGATTAATAA	TAAAGAGGAT	TTGAGAGAA	ATCGCAGAAT	T C C A A G A A G A A	GACGCTGA	ATTTAATAA	AGTATTAAA	AAATGTCTACA	ΓΤΑΑΑΑΤΤΑΤ	GCATAACGATA
ST8 FarR G166D USA	CAATCAATTGAC	TAAAGACTACTT	TGCTAGAGATAT	TCAGTGACCGT	TCTTAATCAT	CCATTCCAAACO	GATGAGTGATA	ACGATTAATAA	TAAAGAGGAT	TTGAGAGAA	ATCGCAGAAT	FCCAAGAAGAA	GACGCTGA	ΑΤΤΤΑΑΤΑΑ.	AGTATTAAA	AAATGTCTGCA	ΓΤΑΑΑΑΤΤΑΤ	GCATAACGATA
ST8 FarR G166D Norway	CAATCAATTGAC	TAAAGACTACTT	TGCTAGAGATAT	TCAGTGACCGT	TCTTAATCAT	CCATTCCAAACO	GATGAGTGATA	ACGAT TAATAA	TAAAGAGGAT	TTGAGAGAA	ATCGCAGAAT	T C C A A G A A G A A	GACGCTGA	ATTTAATAA.	AGTATTAAA	AAATGTCTGCA	ΓΤΑΑΑΑΤΤΑΤ	GCATAACGATA
ST5 FarR G166D USA	CAATCAATTGAC	TAAAGACTACTT	TGCTAGAGATAT	TCAGTGACCGT	TCTTAATCAT	CCATTCCAAACC	GATGAGTGATA	CGATTAATAA	TAAAGAGGAT	TTGAGAGAA	ATCGCAGAAT	I C C A A G A A G A A	GACGCTGA	ΑΤΤΤΑΑΤΑΑ	AGTATTAAA	AAATGTCTGCA	ГТААААТТАТ	GCATAACGATA
ST5 FarR G166D Denmark	CAATCAATTGAC	TAAAGACTACTT	TGCTAGAGATAT	TCAGTGACCGT	TCTTAATCATC	CCATTCCAAACO	GATGAGTGATA	ACGAT TAATAA	TAAAGAGGAT	TTGAGAGAA	ATCGCAGAAT	T C C A A G A A G A A	GACGCTGA	ΑΤΤΤΑΑΤΑΑ.	AGTATTAAA	AAATGTCTGCA	ГТААААТТАТ	GCATAACGATA
CC97 FarR G166D	CAATCAATTGAC	TAAAGACTACTT	TGCTAGAGATAT	TCAGTGACCGT	TCTTAATCAT	CCATTCCAAACO	GATGAGTGATA	ACGAT TAATAA	TAAAGAGGAT	TTGAGAGAA	ATCGCAGAAT	T C C A A G A A G A A	GACGCTGA	ATTTAATAA	AGTATTAAA	AAATGTCTGCA	Г ТААААТ ТАТ	GCATAACGATA
ST15 FarR P165L	CAATCAATTGAC	TAAAGACTACTT	TGCTAGAGATAT	TCAGTGACCGT	ГСТТААТСАТС	CCATTCCAAACO	GATGAGTGATA	ACGATTAATAA	TAAAGAGGAT	TTGAGAGAA	ATCGCAGAAT	ГССААБААБАА	GACGCTGA	ΑΤΤΤΑΑΤΑΑ	AGTATTAAA	AAATGTCTGCA	ГТААААТТАТ	GCATAACGATA
ST5 FarR P165L	CAATCAATTGAC	TAAAGACTACTT	TGCTAGAGATAT	TCAGTGACCGT	TCTTAATCAT	CCATTCCAAACC	GATGAGTGATA	ACGAT TAATAA	TAAAGAGGAT	TTGAGAGAA	ATCGCAGAAT	TCCAAGAAGAA	GACGCTGA	ΑΤΤΤΑΑΤΑΑ	AGTATTAAA	AAATGTCTGCA	ГТААААТТАТ	GCATAACGATA
	380	390	400	410	420	430	440	450	460	470	480	490	500	510	520	530	540	
FarR-1 ST30	TCAAAAATAATA	GAGACCGTATCG	ATATTGACAGCG	GACATCCCAGA	ATAATCTCAT	ΑΤΤΤΤΑΤΑΤΤΤΑ	ATGACTCGTTG	GATTGAAGGTT	TTATACATTG	GATAAAAGAT	GAAAAATT	GACTGGCCTGG	GCGAAGATA	TTGATAACA	TTTTCCATA	AGGTCATTAAT	ATTAAGATTA	AATAG
FarR-2 ST5	TCAAAAATAATA	GAGACCGTATCG	ATATTGACAGCG	GACATCCCAGA	ATAATCTCAT	ΑΤΤΤΤΑΤΑΤΤΤΑ	ATGACTCGTTG	GATTGAAGGTT	TTATACATTG	GATAAAAGA1	GAAAAATT	GACTGGCCTGG	GGAAGATA	TTGATAACA	TTTTCCATA	GATTAATCAAT	ATTAAGATTA	AATAG
FarR-2 ST8	ТСАААААТААТА	GAGACCGTATCG	ATATTGACAGCG	GACATCCCAGA	ATAATCTCAT	ATTTTATATT	ATGACTCGTTG	GATTGAAGGTT	TTATACATTG	GATAAAAGAT	GAAAAATT	GATTGGCCTGG	GCGAAGATA	TTGATAACA	TTTTCCATA	GATTAATCAAT	ATTAAGATTA	AATAG
FarR-2 ST15	TCAAAAATAATA	GAGACCGTATCG	ATATTGACAGCG	GACATCCCAGA	ATAATCTCAT	ΑΤΤΤΤΑΤΑΤΤΤΑ	ATGACTCGTTG	GATTGAAGGTT	TTATACATTG	GATAAAAGA1	GAAAAATT	GATTGGCCTGG	GCGAAGATA	TTGATAACA	TTTTCCATA	GATTAATCAAT	ATTAAGATTA	AATAG
FarR-2 ST97	TCAAAAATAATA	GAGACCGTATCG	ATATTGACAGCG	GACATCCCAGA	ATAATCTCAT	ΑΤΤΤΤΑΤΑΤΤΤΑ	ATGACTCGTTG	GATTGAAGGTT	TTATACATTG	GATAAAAGAT	GAAAAATT	GACTGGCCTGG	GGAAGATA	TTGATAACA	TTTTCCATA	GATTAATCAAT	ATTAAGATTA	AATAG
FarR-5 ST1	ТСАААААТААТА	GAGACCGTATCG	ATATTGACAGCG	GACATCCCAGA	ATAATCTCATA	ΑΤΤΤΤΑΤΑΤΤΤΑ	ATGACTCGTTG	GATTGAAGGTT	т татбсатт б	GATAAAAGA1	GAAAAATT	GACTGGCCTGG	GGAAGAAA	ΓΤGΑΤΑΑΑΑ	TTTTCCATA	AGGTAATAAAT	ATTAAGATTA	AATAG
FarR-5b ST22	TCAAAAATAATA	GAGACCGTATCG	ATATTGACAGC	ACATCCCAGA	ATAATCTCAT	ΑΤΤΤΤΑΤΑΤΤΤΑ	ATGACTCGTTG	GATTGAAGGTT	Т Т А Т Б С А Т Т Б	GATAAAAGA1	GAAAAATT	GACTGGCCTGG	TGAAGAAA	TTGATAAAA	TTTTCCATA	AGATAATAAAT	ATTAAGATTA	AATAG
ST1 FarR H121Y	ТСАААААТААТА	GAGACCGTATCG	ATATTGACAGCG	GACATCCCAGA	ATAATCTCAT	ATTTTATATT	ATGACTCGTTG	GATTGAAGGTT	Т Т А Т G С А Т Т G	GATAAAAGAT	GAAAAATT	GACTGGCCTGG	GGAAGAAA	TTGATAAAA	TTTTCCATA	AGGTAATAAAT	ATTAAGATTA	AATAG
CC97 FarR H121Y	ТСАААААТААТА	GAGACCGTATCG	ATATTGACAGCG	GACATCCCAGA	ATAATCTCAT	ΑΤΤΤΤΑΤΑΤΤΤΑ	ATGACTCGTTG	GATTGAAGGTT	TTATACATTG	GATAAAAGAT	GAAAAATT	GACTGGCCTGG	GAAGATA	TTGATAACA	TTTTCCATA	GATTAATCAAT	ATTAAGATTA	AATAG
ST8 FarR H121Y	TCAAAAATAATA	GAGACCGTATCG	ATATTGACAGCG	GACATCCCAGA	ATAATCTCAT	ATTTTATATTTA	ATGACTCGTTG	GATTGAAGGTT	TTATACATTG	GATAAAAGAT	GAAAAATT	GATTGGCCTGG	CGAAGATA	TTGATAACA	TTTTCCATA	GATTAATCAAT	ATTAAGATTA	AATAG
CC22 FarR H121Y	TCAAAAATAATA	GAGACCGTATCG	ATATTGACAGC	ACATCCCAGA	ATAATCTCAT	ATTTTATATTTA	ATGACTCGTTG	GATTGAAGGTT	TTATGCATTO	GATAAAAGAT	GAAAAATTO	GACTGGCCTGG	TGAAGAAA	TTGATAAAA	TTTTCCATA	AGATAATAAAT	ATTAAGATTA	AATAG
ST30 FarR H121Y	TCAAAAATAATA	GAGACCGTATCG	ATATTGACAGCG	GACATCCCAGA	ATAATCTCAT	ATTTTATATT	ATGACTCGTTG	GATTGAAGGTT	TTATACATTO	GATAAAAGAT	GAAAAATT	GACTGGCCTGG	CGAAGATA	TTGATAACA	TTTTCCATA	AGGTCATTAAT	ATTAAGATTA	AATAG
CC1 FarR C116Y	TCAAAAATAATA	GAGACCGTATCG	ATATTGACAGCG	GACATCCCAGA	TAATCTCAT	ATTTTATATTT	ATGACTCGTTG	GATTGAAGGTT	TTATGCATTG	GATAAAAGAT	GAAAAATT	GACTGGCCTGG	GGAAGAAA	TTGATAAAA	TTTTCCATA	AGGTAATAAAT	ATTAAGATTA	AATAG
ST5 FarR C116Y	TCAAAAATAATA	GAGACCGTATCG	ATATTGACAGCG	GACATCCCAGA	TAATCTCAT	ATTTTATATTT	ATGACTCGTTG	GATTGAAGGTT	TTATACATTO	GATAAAAGAT	GAAAAATT	GACTGGCCTGG	CGAAGATA	TTGATAACA	TTTTCCATA	GATTAATCAAT	ATTAAGATTA	AATAG
ST8 FarR C116Y	TCAAAAATAATA	GAGACCGTATCG	ATATTGACAGCO	GACATCCCAGA	TAATCTCAT	ATTTTATATTT	ATGACTCGTTG	GATTGAAGGTT	TTATACATTO	GATAAAAGAT	GAAAAATT	ATTGGCCTGG	CGAAGATA	TTGATAACA	TTTTCCATA	GATTAATCAAT	ATTAAGATTA	AATAG
ST97 FarR C116Y	TCAAAAATAATA	GAGACCGTATCG	ATATTGACAGCG	ACATCCCAGA	TAATCTCAT	ATTTTATATTT	ATGACTCGTTG	TATTGAAGGTT	TTATACATTO	GATAAAAGAT	GAAAAATT	ACTOCCTO	CGAAGATA	TTGATAACA	TTTTCCATA	GATTAATCAAT	ATTAAGATTA	AATAG
ST8 FarR G166D USA	TCAAAAATAATA	GAGACCGTATCG	ATATTGACAGCG	GACATCCCAGA	ATAATCTCAT	ATTTTATATTT	ATGACTCGTTG	GATTGAAGGTT	TTATACATTO	GATAAAAGAT	GAAAAATT	GATTGGCCTCA	CGAAGATA	TTGATAACA	TTTTCCATA	GATTAATCAAT	ATTAAGATTA	AATAG
ST8 FarB G166D Norway	TCAAAAATAATA	GAGACCGTATCG	ATATTGACAGCO	TACATCCCAGA	ATAATCTCAT	ATTTTATATTT	ATGACTCGTTG	GATTGAAGGTT	TTATACATTO	GATAAAAGAT	GAAAAAATT	GATTGGCCTGA	CGAAGATA	TTGATAACA	TTTTCCATA	GATTAATCAAT	ATTAAGATTA	AATAG
ST5 FarB G166D USA	TCAAAAATAATA	GAGACCGTATCG	ATATTGACAGCG	JACATCCCAGA	ATAATCTCAT	ATTTTATATT	ATGACTCGTTG	GATTGAAGGTT	TTATACATTO	GATAAAAGAT	GAAAAAATT	GACTGGCCTGA	CGAAGATA	TTGATAACA	TTTTCCATA	GATTAATCAAT	ATTAAGATTA	AATAG
ST5 FarB G166D Denmark	TCAAAAATAATA	GAGACCGTATCG	ATATTGACAGCG	BACATCCCAGA	ATAATCTCAT	ATTTTATATATT	ATGACTCGTTG	GATTGAAGGTT	TTATACATTO	GATAAAAGAT	GAAAAAATT	3ACTGGCCTGA	CGAAGATA	TTGATAACA	TTTTCCATA	GATTAATCAAT	ATTAAGATTA	AATAG
CC97 FarB G166D	TCAAAAATAATA	GAGACCGTATCG	ATATTGACAGCO	TACATCCCAGA	ATAATCTCAT	ATTTTATATTT	ATGACTCGTTC	TTGAAGGTT	TTATACATTO	GATAAAAGAT	GAAAAAATT	JACTGGCCTCA	CGAAGATA	TTGATAACA	TTTTCCATA	GATTAATCAAT	ATTAAGATTA	AATAG
ST15 FarB P165	TCAAAAATAATA	GAGACCOTATCO	ATATTGACAGOO	BACATCCCACA	ATAATCTCAT	ATTTTATATT	ATGACTCOTTO	GATTGAAGGTT	TTATACATTC	GATAAAAGAI	GAAAAAATT	ATTGGCTTGA	CGAAGATA	TTGATAACA	TTTTCCATA	GATTAATCAAT	ATTAAGATTA	AATAG
ST5 FarB P165I	TCAAAAATAATA	GAGACCGTATCC	ATATTGACACCC	BACATCCCACA	TAATCTCAT		ATGACTCOTTC	ATTGAAGGTT	TTATACATTC	GATAAAGAI	GAAAAAAIIG	ACTOCCTTCC	CGAAGATA	TTGATAACA	TTTTCCATA	GATTAATCAAT	ATTAAGATTA	AATAG
	I CAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	GAGACCUTATCG	ATATIOACAUCU	SACATCCCAGA	ATAATCICAT		ATGACICOTIG	JATTGAAGGII	TATACATIC	JOATAAAAGAI	GAAAAAIII	SACTOOC 1100	COANGATA	IIGAIAACA	LITCCATA	GATIAAICAAI	ALIAAGALIA	AATAO



Figure S4: Phylogenetic detail of cluster 2c (FarR-E93EE) strains.



Fig. S5A: *lysR-leuA* **locus and accumulated pseudogenes in FarR**^{E93EE} **strains.** *lys*R, LysR family transcriptional regulator; *leu*A, putative isopropylmalate synthase; *tsaC*, putative threonylcarbomyladenylate synthase; JH1_0997, membrane associated protein; JH1_0998, putative phospholipid binding protein. The location of single nucleotide polymorphisms that confer pseudogenes in different strains are indicated by arrows; (1), Y6* premature stop codon in SA-1B; (2), frameshift at codon I24 in KUH180129; (3), frameshift at I78 in SH-4, SH-3, SH-2, M19, M153-2, M392, M212, and M209; (4), frameshift at K294 in KUH180129; (5), frameshift at G214 in KUH180129; (6), frameshift at S87 in M1510, M1516, M1523, and M1528.

Fig. S5B: Nucleotide sequence and location of indels at polyA segments in *leuA* (SaurJH1_0995). **Bold underlined** segments represent sites 2, 3 and 4 respectively in S5A, and the *bold italic* segment indicates the site of a frameshift in some FarR^{P165L} strains.



Figure S6. Phenotype of FarR^{E93EE} strain M1516 is consistent with a defect in *uhpT*.

(A), Growth of *S. aureus* strains N315, M182 (FarR^{C116Y}) and M1516 (FarR^{E93EE}) in CDM containing glucose or glucose-6-phosphate (G6P) as carbon source. All data points represent the mean \pm SD from triplicate 3 mL tube cultures after 24h growth. Statistically significant differences (****, P<0.0001; ***, P<0.001; *, P<0.05) compared to *S. aureus* N315 were determined by Tukey's multiple comparison test. (B), Fosfomycin sensi-disc assay. A Fosfomycin sensi-disc (BBL) containing 200 µg fosfomycin was placed on the surface of a TSA plate that had been swabbed with *S. aureus* N315, M182 or M1516. Plates were photographed after incubation at 37°C for 18h.