Table S2. Detection of recombination within lineages I and II at MvLST and MLST genes

		θ		ρ		r/μ	
	locus	lineage I	lineage II	lineage I	lineage II	lineage I	lineage II
MvLST	*actA*	0.016	0.016	0.05	4.925 *	0.007	0.681
	clpP	0.006	0.001	0.151	2.044	0.057	4.517
	dal	0.020	0.025	0	2.613 *	0	0.244
	inlA	0.009	0.010	0.276	18.791 *	0.013	0.758
	inlB	0.016	0.006	0.729	0	0.106	0
	inlC	0.005	0.002	0	9.146	0	10.108
	lisR	0.002	0.018	0.427	0.603	0.425	0.076
	prfA	0.008	0.001	0	1.800	0	3.993
	Concat[b]	0.010	0.010	0	0.151 *	0	0.003
MLST	*abcZ*	0.008	0.010	0	1.131	0	0.204
	bglA	0.007	0.006	3.317	3.543	1.256	1.552
	cat	0.002	0.005	16.759	6.181	16.659	2.718
	dapE	0.003	0.005	3.411 *	9.121 *	2.421	3.739
	dat	0.002	0.002	1.706	4.673	1.701	5.167
	ldh	0.005	0.012	0	0.377	0	0.071
	lhkA	0.002	0.002	74.916	2.714	93.458	2.396
	Concat[b]	0.004	0.006	22.626 *	6.814 *	1.699	0.343

Values for rho were obtained by dividing the per-locus recombination rate estimate from LDhat by the sequence length.

a, Significant estimates (at the 5% level).

b, Concat., concatenated data set with no indels.