SUPPLEMENTAL TEXT

Phylogeographic analysis. The ML phylogeny with branch lengths corrected for recombination was used for ancestral state reconstruction of geographic location of USA300-NAE under parsimony and likelihood. Calculations were done with Mesquite v2.75 (1) and MacClade v4.08 (Sinauer Associates, Sunderland, MA). The two most basal isolates of USA300-NAE in our sample were from Indiana and Mississippi (Fig. 1 circle 3). Mississippi was the most abundant sample of USA300-NAE at 33 isolates and was reconstructed as its origin under parsimony and with 55% likelihood. However, in 100 subsamples where the Mississippi sample was rarefied to 16 isolates (the average of 18 USA300-NAE populations with ≥6 isolates each), Mississippi was the unambiguous origin only 42% of the time under parsimony and with an average of 26% likelihood. Mississippi was especially oversampled among early isolates, accounting for 16 of 36 (44%) isolates collected between 2001-2005, but only 17 of 229 (7.4%) isolates collected between 2007-2011. When only the recent isolates from 2007-2011 were considered, Mississippi was not reconstructed as the origin under parsimony or likelihood. Despite the phylogenomic uncertainty in origin, the distribution of US states and territories on the ML phylogeny was non-random (Slatkin-Maddison test, P<0.001). This signal was likely the result of "microclustering" where two or more isolates from the same US state or territory were adjacent on the phylogeny (Fig. 1 circle 3), as 443 of 515 (86%) unambiguous changes (migrations) and stasis events under parsimony were within US states and territories.

The clade distribution of the international isolates included 20 isolates of USA300-NAE (from Australia, Ireland, Germany and Denmark), all nine isolates of USA300-SAE (from Colombia and Ecuador), one Ecuador isolate of early-branching USA300, and six non-USA300 isolates (from Argentina and Denmark). Among the 20 isolates of USA300-NAE, the three isolates from Germany formed a microcluster, as did two isolates from Ireland, but the 15 remaining isolates were in separate microclusters with US isolates, consistent with prior conclusions of multiple exports of USA300 from the US to the eastern hemisphere (2,3).

Genetic and geographic outliers. Using 2599 biallelic, nonrecombinant SNPs, the average (SD) pairwise Hudson's F_{ST} between the 18 populations with sample size ≥6 isolates was 0.0583 (0.0472). Montana was identified as a genetic outlier population, as its average pairwise F_{ST} was

2.6x higher and it was clearly distinguished in a principal components analysis (Fig. S2). Further sample information was unavailable to assess whether the Montana isolates were from a remote host population(s), but their genetic information indicates that the differentiation was not due to unique recombination events. Puerto Rico was the second most differentiated population (Fig. S2). Hawaii and Puerto Rico were considered to be geographic outliers due to the large bodies of water separating these populations from the nearest continental US populations. For these reasons, the Montana, Hawaii and Puerto Rico populations were excluded from subsequent analysis.

Nonetheless, inclusion of the Montana, Hawaii and Puerto Rico outlier populations did not qualitatively alter our conclusion of an eastern US origin of USA300-NAE though statistical significance was affected. The isolation by distance was weaker when these three populations were included (Mantel test, r= 0.265, P= 0.106, n=153 pairs). When these three populations were included in the test for range expansion and inference of origin, New York was the most likely origin based on decrease in θ_π (Pearson r=-0.510, P=0.015, P_{perm}=0.14, n=18), decrease in tip-to-tip distance (Pearson r=-0.516, P=0.014, P_{perm}=0.15, n=18), and increase in Ψ with linear regression (Pearson r=0.505, P=0.016, P_{perm}=0.17, n=18) (Table S1). The nonlinear regression on Ψ gave the unsampled population of New Hampshire as the best origin (Pearson r=0.535, P_{perm}=0.15, n=18) (Table S1).

References for Supplemental text

1. Maddison WP & Maddison DR (2016) Mesquite: a modular system for evolutionary analysis. Version 3.10 http://mesquiteproject.org
2. Von Dach E*, et al.* (2016) Comparative genomics of community-associated methicillin-resistant *Staphylococcus aureus* shows the emergence of clone ST8-USA300 in Geneva, Switzerland. *J Infect Dis* 213(9):1370-1379.
3. Glaser P*, et al.* (2016) Demography and intercontinental spread of the USA300 community-acquired methicillin-resistant *Staphylococcus aureus* lineage. *MBio* 7(1):e02183-02115.

Figure S1. Time-stamped Bayesian phylogeny of USA300 inferred using BEAST with non-recombinant genome sequences. Branch color indicates posterior probability of tip-ward node. Bars on nodes indicate 95% credibility intervals for node ages. Three colored bars adjacent to the tree indicate the *S. aureus* clade, fluoroquinolone resistance mutation and the geographic source of isolation (see color index).

Clade
- Non-USA300
- USA300-Early Branching
- USA300-South American Epidemic
- USA300-North American Epidemic

Fluoroquinolone resistance mutation
- *gyrA and grlA*
- *grlA* only
- None

Geography

Iowa	Montana
Illinois	Colorado
Indiana	Washington
Ohio	Oregon
Nebraska	California
Missouri	
Georgia	Pennsylvania
South Carolina	New York
Tennessee	Massachusetts
Florida	
Mississippi	Denmark
Texas	Australia
	Ireland
Hawaii	Germany
Puerto Rico	

0   1

Posterior support

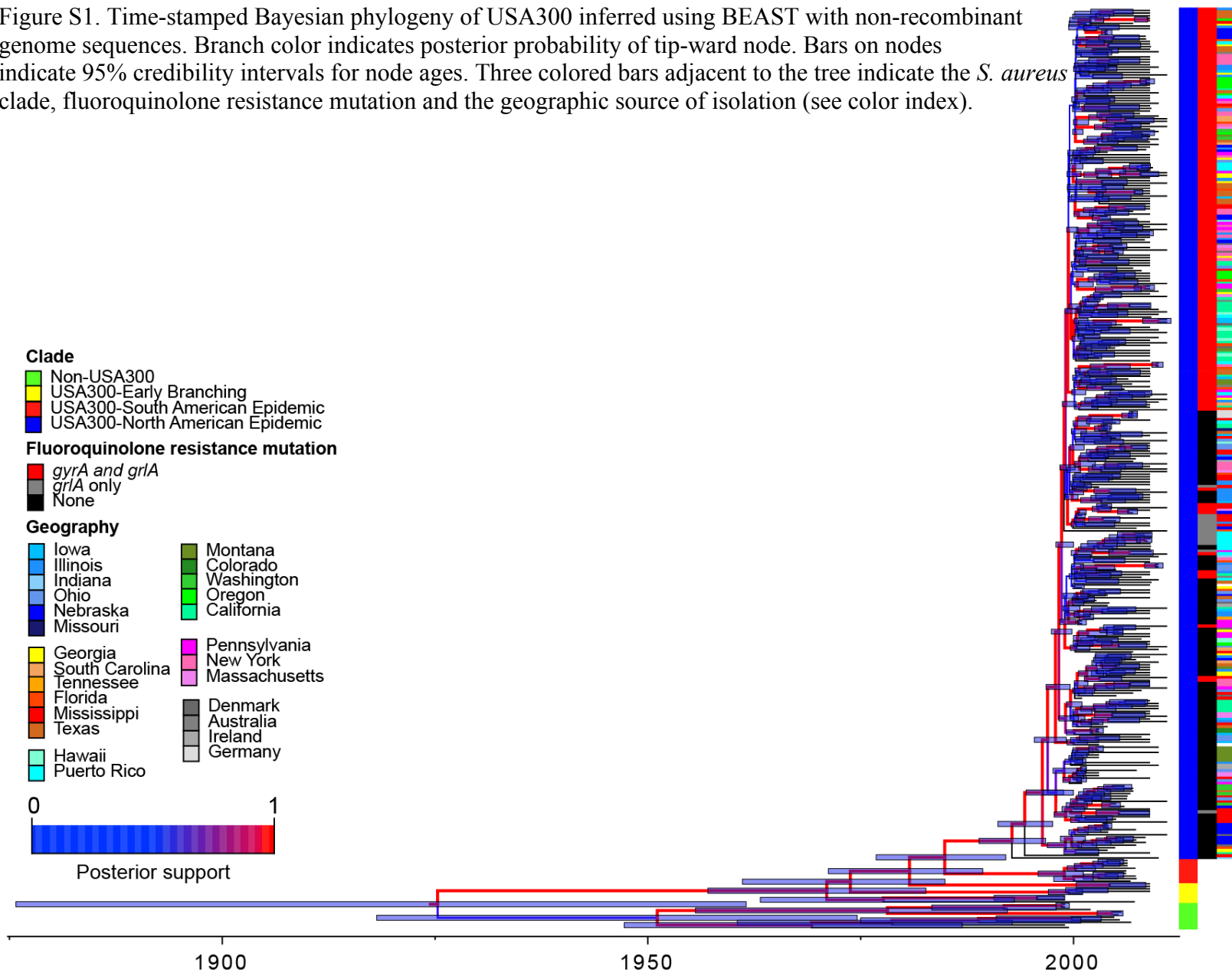1900   1950   2000

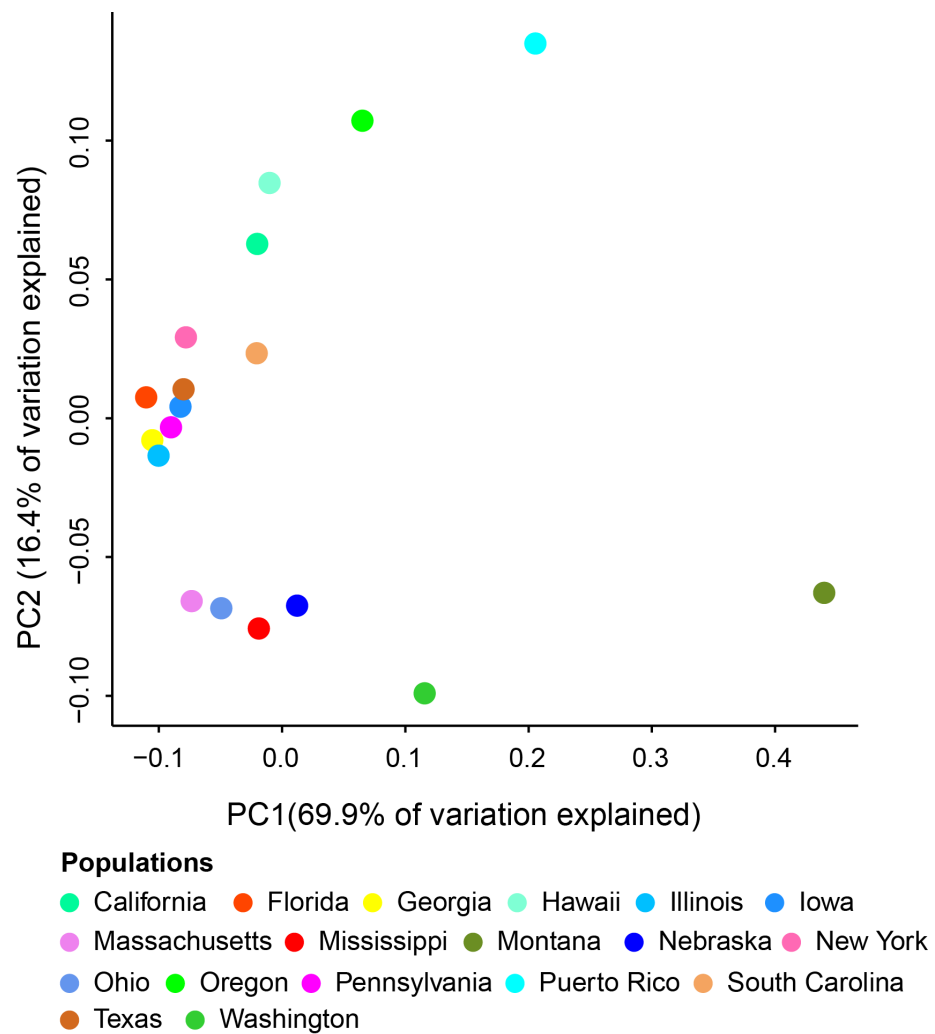Figure S2. Principal components analysis based on the pairwise Hudson's F_{ST} between 18 populations of USA300- NAE.

Table S1. Signatures of range expansion and origin of USA300-NAE with 18 population dataset.

Decrease in genetic diversity (θ_π)				Decrease in genetic diversity (tip-to-tip distance)				Increase in derived allele frequency (Ψ)*			
Origin population	r	P	P_{perm}	Origin population	r	P	P_{perm}	Origin population	r	P	P_{perm}
NY	-0.510	0.0154	0.142	NY	-0.516	0.0142	0.148	NY	0.505	0.0162	0.165
MA	-0.506	0.0160		MA	-0.509	0.0155		MA	0.505	0.0163	
PA	-0.501	0.0171		PA	-0.507	0.0159		PA	0.498	0.0178	
OH	-0.491	0.0193		OH	-0.499	0.0175		OH	0.481	0.0218	
SC	-0.413	0.0443		IL	-0.430	0.0373		SC	0.418	0.0421	
IL	-0.404	0.0482		SC	-0.415	0.0436		GA	0.382	0.0589	
GA	-0.383	0.0583		IA	-0.402	0.0490		IL	0.362	0.0700	
IA	-0.371	0.0648		GA	-0.394	0.0528		PR	0.336	0.0867	
FL	-0.326	0.0935		NE	-0.345	0.0807		FL	0.335	0.0873	
MS	-0.307	0.1080		MS	-0.343	0.0820		IA	0.304	0.1102	
NE	-0.299	0.1137		FL	-0.337	0.0856		MS	0.280	0.1305	
PR	-0.294	0.1178		PR	-0.318	0.0995		NE	0.214	0.1972	
MT	-0.210	0.2019		TX	-0.248	0.1604		TX	0.155	0.2701	
TX	-0.198	0.2161		MT	-0.231	0.1782		MT	0.107	0.3361	
WA	0.036	0.5562		WA	0.034	0.5535		OR	-0.174	0.7549	
OR	0.072	0.6119		OR	0.063	0.5986		WA	-0.194	0.7795	
CA	0.135	0.7028		CA	0.100	0.6536		CA	-0.216	0.8053	
HI	0.381	0.9407		HI	0.395	0.9477		HI	-0.404	0.9519	

*NH (latitude: 43.8836, longitude: -71.9776) was best with nonlinear regression of Ψ (r=0.535, P_{perm}=0.154)

Table S2. Population genomic summary statistics for 15 populations of USA300-NAE (recent isolates).

Population	No. isolates	Average pairwise F_{ST}	θ_π	θ_W	Tajima's D	P (D=0)	Average tip-to-tip distance (x10^{-5})	Sum pairwise Ψ
All 15	229	0.0321	0.0118	0.1440	-2.9377	0.0033	1.2678	-
IL	27	0.0190	0.0104	0.0331	-2.7086	0.0068	1.2196	0.4737
NY	25	0.0254	0.0119	0.0311	-2.4655	0.0137	1.3919	-0.8111
CA	23	0.0465	0.0095	0.0219	-2.2983	0.0215	1.0973	1.0905
TX	19	0.0276	0.0105	0.0239	-2.3636	0.0181	1.2252	0.2931
MS	17	0.0253	0.0112	0.0231	-2.2151	0.0268	1.2836	-0.0732
OH	17	0.0311	0.0151	0.0319	-2.2684	0.0233	1.7133	-2.0332
GA	16	0.0187	0.0134	0.0278	-2.2684	0.0233	1.5136	-1.3311
PA	15	0.0224	0.0137	0.0262	-2.1131	0.0346	1.5356	-1.5834
NE	14	0.0566	0.0121	0.0194	-1.6914	0.0908	1.3468	0.1218
FL	14	0.0175	0.0096	0.0201	-2.3475	0.0189	1.0774	1.1612
IA	11	0.0256	0.0099	0.0156	-1.7511	0.0799	1.0925	0.9153
OR	11	0.0609	0.0095	0.0138	-1.5072	0.1318	1.0406	0.7772
MA	9	0.0248	0.0131	0.0183	-1.4688	0.1419	1.4067	-0.8583
SC	6	0.0381	0.0116	0.0133	-0.8322	0.4053	1.1667	-0.4173
WA	5	0.0417	0.0093	0.0096	-0.2299	0.8182	0.9058	2.2748

Average pairwise F_{ST}, θ_π, θ_W and D was based on 2599 biallelic, non-recombinant SNPs.
Average tip-to-tip distance reflects branch lengths on a ML tree that has been corrected for recombinant sites.
Sum of pairwise Ψ was based on 2595 biallelic, non-recombinant SNPs where ancestral and derived alleles were assigned.

Table S3. Pairwise Hudson's F_{ST} between 15 populations of USA300-NAE using all isolates (lower triangle) and recent isolates (upper triangle).

	CA	FL	GA	IA	IL	MA	MS	NE	NY	OH	OR	PA	SC	TX	WA
CA	0.000	0.029	0.032	0.027	0.039	0.038	0.049	0.093	0.040	0.058	0.070	0.037	0.064	0.046	0.075
FL	0.026	0.000	0.007	0.008	0.001	0.010	0.007	0.053	0.006	0.024	0.036	0.009	0.030	0.006	0.036
GA	0.030	0.007	0.000	0.011	0.002	0.016	0.015	0.043	0.015	0.022	0.055	-0.007	0.019	0.014	0.037
IA	0.025	0.008	0.011	0.000	0.004	0.018	0.019	0.059	0.022	0.022	0.068	0.018	0.038	0.023	0.047
IL	0.036	0.001	0.002	0.004	0.000	0.014	0.005	0.049	0.012	0.016	0.057	0.010	0.026	0.011	0.039
MA	0.034	0.010	0.016	0.018	0.014	0.000	0.011	0.037	0.020	0.010	0.073	0.020	0.045	0.032	0.028
MS	0.070	0.028	0.026	0.032	0.020	0.006	0.000	0.053	0.015	0.022	0.061	0.021	0.037	0.018	0.046
NE	0.074	0.036	0.032	0.046	0.036	0.026	0.023	0.000	0.068	0.033	0.116	0.053	0.078	0.068	0.046
NY	0.038	0.006	0.015	0.022	0.012	0.020	0.045	0.053	0.000	0.038	0.050	0.016	0.011	0.016	0.052
OH	0.054	0.024	0.022	0.022	0.016	0.010	0.010	0.027	0.038	0.000	0.081	0.022	0.046	0.040	0.033
OR	0.071	0.036	0.055	0.068	0.057	0.073	0.102	0.099	0.050	0.081	0.000	0.055	0.072	0.045	0.074
PA	0.039	0.010	-0.005	0.017	0.009	0.020	0.030	0.041	0.019	0.019	0.061	0.000	0.031	0.022	0.029
SC	0.063	0.030	0.019	0.038	0.026	0.045	0.059	0.065	0.011	0.046	0.072	0.032	0.000	0.030	0.043
TX	0.041	0.003	0.010	0.018	0.006	0.026	0.037	0.046	0.015	0.031	0.047	0.019	0.027	0.000	0.041
WA	0.107	0.070	0.060	0.075	0.068	0.039	0.038	0.043	0.088	0.037	0.126	0.058	0.082	0.073	0.000

Pairwise F_{ST} was evaluated with 10,000 permutations. Comparisons that are significant by Bonferroni P-value are highlighted in yellow.

Table S4. Relationships between genetic differentiation (Weir and Cockerham's F_{ST}), geographic distance, and connectivity from all pairwise comparisons of 15 populations of USA300-NAE.

Test	Predictor of genetic distance	All isolates (2001-2011)		Recent isolates (2007-2011)	
		r	P	r	P
Mantel	Geographic distance	0.364	0.0097	0.288	0.066
	Log total airline passengers	-0.379	0.034	-0.345	0.059
	Log total migrants	-0.237	0.113	-0.204	0.161
Partial Mantel	Geographic distance accounting for log total airline passengers	0.334	0.025	0.252	0.146
	Log total airline passengers accounting for geographic distance	-0.351	0.056	-0.318	0.080

Mantel and partial Mantel tests were evaluated with 10,000 permutations.

Table S5. Signatures of range expansion and origin of USA300-NAE with 15 population dataset (all isolates).

Decrease in genetic diversity (θ_π)				Decrease in genetic diversity (tip-to-tip distance)				Increase in derived allele frequency (Ψ)*			
Origin population	r	P	P_{perm}	Origin population	r	P	P_{perm}	Origin population	r	P	P_{perm}
PA	-0.697	0.0019	0.024	PA	-0.684	0.0025	0.031	PA	0.667	0.0033	0.029
MA	-0.696	0.0020		NY	-0.683	0.0025		NY	0.664	0.0035	
NY	-0.695	0.0020		OH	-0.677	0.0028		MA	0.663	0.0035	
OH	-0.684	0.0025		MA	-0.673	0.0030		OH	0.650	0.0043	
SC	-0.558	0.0153		SC	-0.527	0.0218		SC	0.543	0.0182	
GA	-0.490	0.0320		GA	-0.479	0.0355		GA	0.471	0.0382	
IL	-0.432	0.0541		IL	-0.475	0.0367		IL	0.396	0.0718	
FL	-0.403	0.0680		FL	-0.384	0.0786		FL	0.395	0.0725	
MS	-0.262	0.1727		MS	-0.315	0.1265		MS	0.234	0.2008	
IA	-0.240	0.1950		IA	-0.306	0.1338		IA	0.200	0.2374	
NE	0.099	0.6370		NE	-0.013	0.4811		TX	-0.106	0.6461	
TX	0.126	0.6731		TX	0.029	0.5406		NE	-0.140	0.6912	
WA	0.570	0.9868		CA	0.523	0.9772		CA	-0.546	0.9824	
OR	0.578	0.9879		OR	0.555	0.9841		OR	-0.561	0.9852	
CA	0.589	0.9895		WA	0.560	0.9850		WA	-0.593	0.9901	

*NY (latitude: 41.6967, longitude: -73.5591) was best with nonlinear regression of Ψ (r=0. 686, P_{perm}=0.029)

Table S6. Signatures of range expansion and origin of USA300-NAE with 15 population dataset (recent isolates).

Decrease in genetic diversity (θ_π)				Decrease in genetic diversity (tip-to-tip distance)				Increase in derived allele frequency (Ψ)*			
Origin population	r	P	P_{perm}	Origin population	r	P	P_{perm}	Origin population	r	P	P_{perm}
PA	-0.748	0.0007	0.008	PA	-0.732	0.0008	0.010	PA	0.786	0.0003	0.006
OH	-0.731	0.0010		OH	-0.719	0.0008		OH	0.766	0.0004	
NY	-0.730	0.0010		NY	-0.719	0.0013		NY	0.762	0.0005	
MA	-0.727	0.0011		MA	-0.706	0.0017		MA	0.759	0.0005	
SC	-0.596	0.0095		SC	-0.568	0.0106		SC	0.662	0.0036	
GA	-0.536	0.0196		GA	-0.526	0.0164		GA	0.600	0.0090	
IL	-0.469	0.0390		IL	-0.506	0.0230		FL	0.503	0.0279	
FL	-0.435	0.0527		FL	-0.423	0.0434		IL	0.492	0.0313	
MS	-0.363	0.0916		MS	-0.400	0.0549		MS	0.434	0.0533	
IA	-0.258	0.1767		IA	-0.312	0.1271		IA	0.235	0.1993	
NE	0.087	0.6214		NE	0.008	0.4614		TX	-0.032	0.5457	
TX	0.095	0.6321		TX	0.020	0.5303		NE	-0.161	0.7164	
WA	0.577	0.9879		CA	0.565	0.9887		CA	-0.652	0.9958	
OR	0.603	0.9913		WA	0.583	0.9909		OR	-0.656	0.9961	
CA	0.628	0.9939		OR	0.588	0.9912		WA	-0.687	0.9977	

*PA (latitude: 41.2498, longitude: -76.9675) was best with nonlinear regression of Ψ (r=0.795, P_{perm}=0.005)

Table S7. Signatures of range expansion and origin of USA300-NAE with 15 population dataset (non-synonymous SNPs).

Decrease in genetic diversity (θ_π)				Increase in derived allele frequency (Ψ)*			
Origin population	r	P	P_{perm}	Origin population	r	P	P_{perm}
MA	-0.694	0.0020	0.018	MA	0.544	0.0180	0.097
PA	-0.688	0.0023		NY	0.537	0.0194	
NY	-0.687	0.0023		PA	0.530	0.0212	
OH	-0.666	0.0034		OH	0.471	0.0381	
SC	-0.556	0.0158		SC	0.442	0.0493	
GA	-0.492	0.0312		GA	0.391	0.0750	
FL	-0.411	0.0641		IL	0.337	0.1098	
IL	-0.409	0.0650		FL	0.334	0.1118	
MS	-0.266	0.1687		IA	0.245	0.1892	
IA	-0.220	0.2151		MS	0.212	0.2240	
TX	0.094	0.6305		NE	0.091	0.3741	
NE	0.115	0.6588		TX	0.022	0.4692	
WA	0.586	0.9891		CA	-0.429	0.9447	
CA	0.594	0.9903		OR	-0.465	0.9595	
OR	0.597	0.9906		WA	-0.507	0.9732	

*MA (latitude: 42.2787, longitude: -71.58) was best with nonlinear regression of Ψ (r=0.678, P_{perm}=0.036)

Table S8. Signatures of range expansion and origin of USA300-NAE with 15 population dataset (synonymous SNPs).

Decrease in genetic diversity (θ_π)				Increase in derived allele frequency (Ψ)*			
Origin population	r	P	P_{perm}	Origin population	r	P	P_{perm}
OH	-0.636	0.0054	0.073	PA	0.493	0.0309	0.142
PA	-0.618	0.0070		NY	0.492	0.0313	
NY	-0.609	0.0080		MA	0.482	0.0346	
MA	-0.590	0.0103		OH	0.471	0.0383	
SC	-0.477	0.0362		IL	0.373	0.0855	
IL	-0.443	0.0492		SC	0.373	0.0857	
GA	-0.401	0.0690		GA	0.304	0.1353	
FL	-0.312	0.1292		IA	0.273	0.1625	
IA	-0.270	0.1656		FL	0.225	0.2106	
MS	-0.204	0.2328		NE	0.163	0.2810	
NE	0.024	0.5335		MS	0.149	0.2979	
TX	0.222	0.7865		TX	-0.156	0.7099	
OR	0.414	0.9374		OR	-0.302	0.8628	
WA	0.421	0.9410		WA	-0.345	0.8961	
CA	0.474	0.9628		CA	-0.352	0.9007	

*Ontario, Canada (latitude: 44.3365, longitude: -76.9676) was best with nonlinear regression of Ψ (r=0.625, P_{perm}=0.066)

Table S9. Correlation between *gyr*A resistance allele frequency and estimates of outpatient fluoroquinolone (FQ) use in 15 states.

| Estimated FQ use in year * | *gyrA* resistance allele frequency among | | | |
| | All isolates (2001-2011) | | Recent isolates (2007-2011) | |
	r	P	r	P
1999	-0.126	0.6534	-0.106	0.7074
2009	-0.326	0.2357	-0.316	0.2513

Estimates are defined as number of prescriptions per 1000 people
(https://resistancemap.cddep.org/CountryPageSub.php?country=United+States)

Table S10. Signatures of range expansion and origin of USA300-NAE with 15 population dataset (*gyrA* SNP excluded).

Decrease in genetic diversity (θ_π)				Increase in derived allele frequency $(\Psi)^*$			
Origin population	r	P	P_{perm}	Origin population	r	P	P_{perm}
PA	-0.692	0.0021	0.025	MA	0.546	0.0176	0.070
MA	-0.690	0.0022		NY	0.544	0.0180	
NY	-0.690	0.0022		PA	0.538	0.0193	
OH	-0.679	0.0027		OH	0.488	0.0324	
SC	-0.552	0.0164		SC	0.442	0.0495	
GA	-0.484	0.0336		GA	0.385	0.0782	
IL	-0.427	0.0563		IL	0.363	0.0918	
FL	-0.398	0.0707		FL	0.323	0.1204	
MS	-0.259	0.1758		IA	0.273	0.1628	
IA	-0.235	0.1996		MS	0.212	0.2238	
NE	0.100	0.6390		NE	0.121	0.3338	
TX	0.126	0.6731		TX	-0.005	0.5068	
WA	0.565	0.9859		CA	-0.424	0.9425	
OR	0.571	0.9869		OR	-0.442	0.9506	
CA	0.583	0.9887		WA	-0.487	0.9672	

*MA (latitude: 42.2787, longitude: -71.58) was best with nonlinear regression of Ψ (r=0.688, P_{perm}=0.030)

Table S11. Signatures of range expansion and origin of USA300-NAE with 13 population dataset (non-FQ-R Subclade).

Decrease in genetic diversity (θ_π)				Decrease in genetic diversity (tip-to-tip distance)				Increase in derived allele frequency $(\Psi)*$			
Origin population	r	P	P_{perm}	Origin population	r	P	P_{perm}	Origin population	r	P	P_{perm}
OH	-0.632	0.0102	0.103	OH	-0.633	0.0101	0.167	OH	0.635	0.0098	0.069
NY	-0.624	0.0113		PA	-0.586	0.0177		PA	0.637	0.0110	
PA	-0.622	0.0116		NY	-0.582	0.0185		NY	0.623	0.0114	
MA	-0.592	0.0166		MA	-0.546	0.0269		MA	0.603	0.0146	
IL	-0.456	0.0587		IL	-0.534	0.0300		IL	0.490	0.0447	
IA	-0.367	0.1085		IA	-0.451	0.0608		GA	0.400	0.0881	
GA	-0.351	0.1196		GA	-0.365	0.1098		IA	0.397	0.0899	
FL	-0.297	0.1621		MS	-0.332	0.1339		FL	0.350	0.1203	
MS	-0.238	0.2170		FL	-0.283	0.1749		MS	0.313	0.1491	
NE	-0.138	0.3265		NE	-0.261	0.1946		NE	0.125	0.3418	
TX	-0.050	0.4354		TX	-0.150	0.3123		TX	0.083	0.3941	
CA	0.398	0.9107		CA	0.320	0.8569		CA	-0.398	0.9109	
WA	0.510	0.9624		WA	0.462	0.9442		WA	-0.616	0.9875	

*Lake Huron (latitude: 44.3365, longitude: -82.3551) was best with nonlinear regression of Ψ (r=0.629, P_{perm}=0.071)

Note: Two of the 15 sampled populations had isolates <4 in the non-FQ-R subclade, so they were excluded from this analysis.

Table S12. Signatures of range expansion and origin of USA300-NAE with 15 population dataset (BratNextGen recombinations excluded).

Decrease in genetic diversity (θ_π)				Decrease in genetic diversity (tip-to-tip distance)				Increase in derived allele frequency $(\Psi)^*$			
Origin population	r	P	P_{perm}	Origin population	r	P	P_{perm}	Origin population	r	P	P_{perm}
PA	-0.613	0.0076	0.086	OH	-0.599	0.0091	0.088	PA	0.579	0.0118	0.096
NY	-0.610	0.0079		PA	-0.599	0.0092		NY	0.575	0.0124	
MA	-0.606	0.0084		NY	-0.592	0.0100		MA	0.569	0.0134	
OH	-0.598	0.0093		MA	-0.575	0.0124		OH	0.554	0.0160	
SC	-0.457	0.0433		SC	-0.436	0.0521		SC	0.437	0.0519	
GA	-0.391	0.0747		IL	-0.393	0.0737		GA	0.364	0.0911	
IL	-0.348	0.1019		GA	-0.392	0.0743		IL	0.310	0.1300	
FL	-0.300	0.1386		FL	-0.303	0.1364		FL	0.283	0.1531	
IA	-0.178	0.2635		IA	-0.233	0.2020		IA	0.140	0.3096	
MS	-0.165	0.2789		MS	-0.216	0.2200		MS	0.128	0.3243	
NE	0.110	0.6514		NE	0.030	0.5419		NE	-0.149	0.7021	
TX	0.170	0.7271		TX	0.071	0.5989		TX	-0.157	0.7116	
WA	0.464	0.9594		CA	0.445	0.9517		OR	-0.446	0.9522	
OR	0.466	0.9599		OR	0.447	0.9526		CA	-0.450	0.9538	
CA	0.495	0.9696		WA	0.457	0.9568		WA	-0.482	0.9657	

*NY (latitude: 42.4866, longitude: -74.5487) was best with nonlinear regression of Ψ (r=0.599, P_{perm}=0.105)

Table S13. Signatures of range expansion and origin of USA300-NAE with 15 population dataset (all recombinations included).

Decrease in genetic diversity (θ_π)				Decrease in genetic diversity (tip-to-tip distance)				Increase in derived allele frequency (Ψ)*			
Origin population	r	P	P_{perm}	Origin population	r	P	P_{perm}	Origin population	r	P	P_{perm}
FL	-0.737	0.0009	0.013	FL	-0.717	0.0013	0.025	FL	0.760	0.0005	0.04
GA	-0.660	0.0037		GA	-0.644	0.0048		SC	0.704	0.0017	
SC	-0.658	0.0038		SC	-0.629	0.0060		GA	0.695	0.0020	
MS	-0.559	0.0151		MS	-0.578	0.0121		PA	0.583	0.0113	
MA	-0.526	0.0220		PA	-0.507	0.0270		MA	0.582	0.0114	
PA	-0.521	0.0232		MA	-0.503	0.0280		MS	0.567	0.0138	
NY	-0.505	0.0275		NY	-0.490	0.0318		NY	0.556	0.0156	
OH	-0.482	0.0345		OH	-0.477	0.0362		OH	0.538	0.0193	
IL	-0.244	0.1907		IL	-0.268	0.1674		IL	0.282	0.1540	
TX	-0.026	0.4631		TX	-0.081	0.3868		TX	0.030	0.4583	
IA	0.064	0.5891		IA	0.026	0.5359		IA	-0.050	0.5697	
NE	0.408	0.9345		NE	0.349	0.8987		NE	-0.432	0.9462	
CA	0.683	0.9975		CA	0.640	0.9949		CA	-0.716	0.9987	
OR	0.722	0.9988		OR	0.694	0.9980		OR	-0.766	0.9996	
WA	0.742	0.9992		WA	0.720	0.9988		WA	-0.812	0.9999	

*FL (latitude: 27.8744, longitude: -82.3551) was best with nonlinear regression of Ψ (r=0. 749, P_{perm}=0.01)