# Supplementary materials

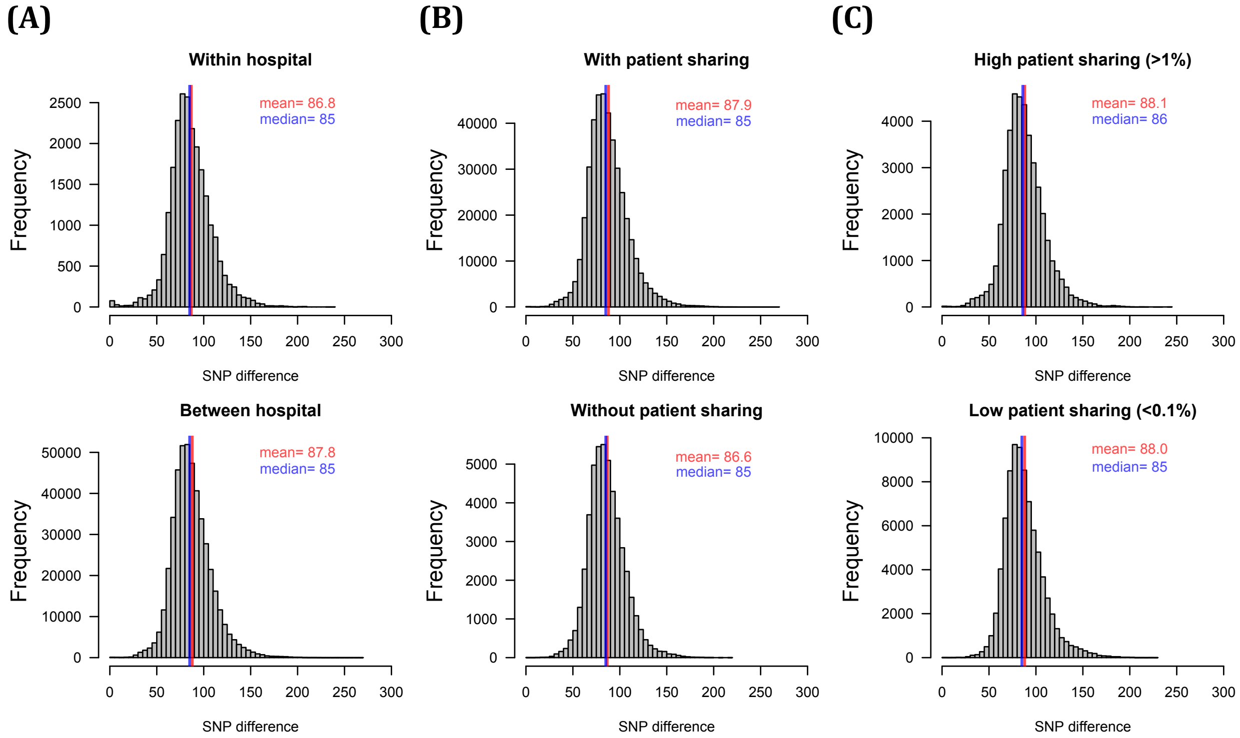


**Figure S1. SNP differences between isolates. (A)** SNP differences between isolates from the same or different hospitals. **(B)** SNP differences between isolates from the hospitals with and without patient sharing. **(C)** SNP differences between isolates from hospitals with high and low patient sharing.

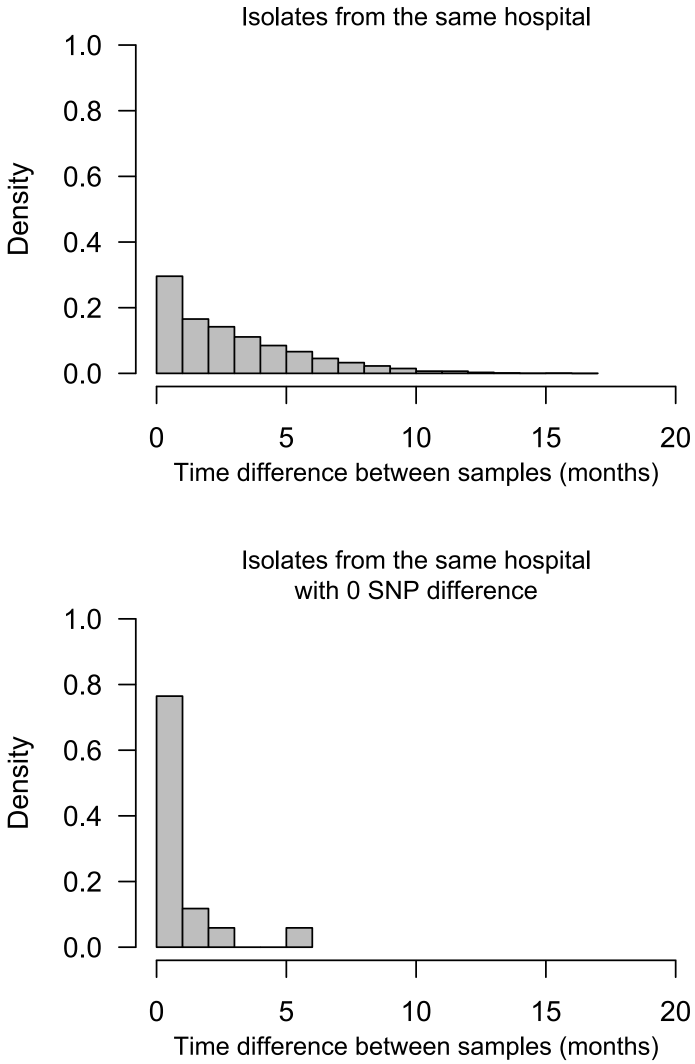


**Figure S2. Time difference between samples.** The difference in the time of collection between isolate pairs from the same hospitals with 0 SNP difference and at least one hospital-onset isolates (bottom) tends to be shorter than that of other isolate pairs.

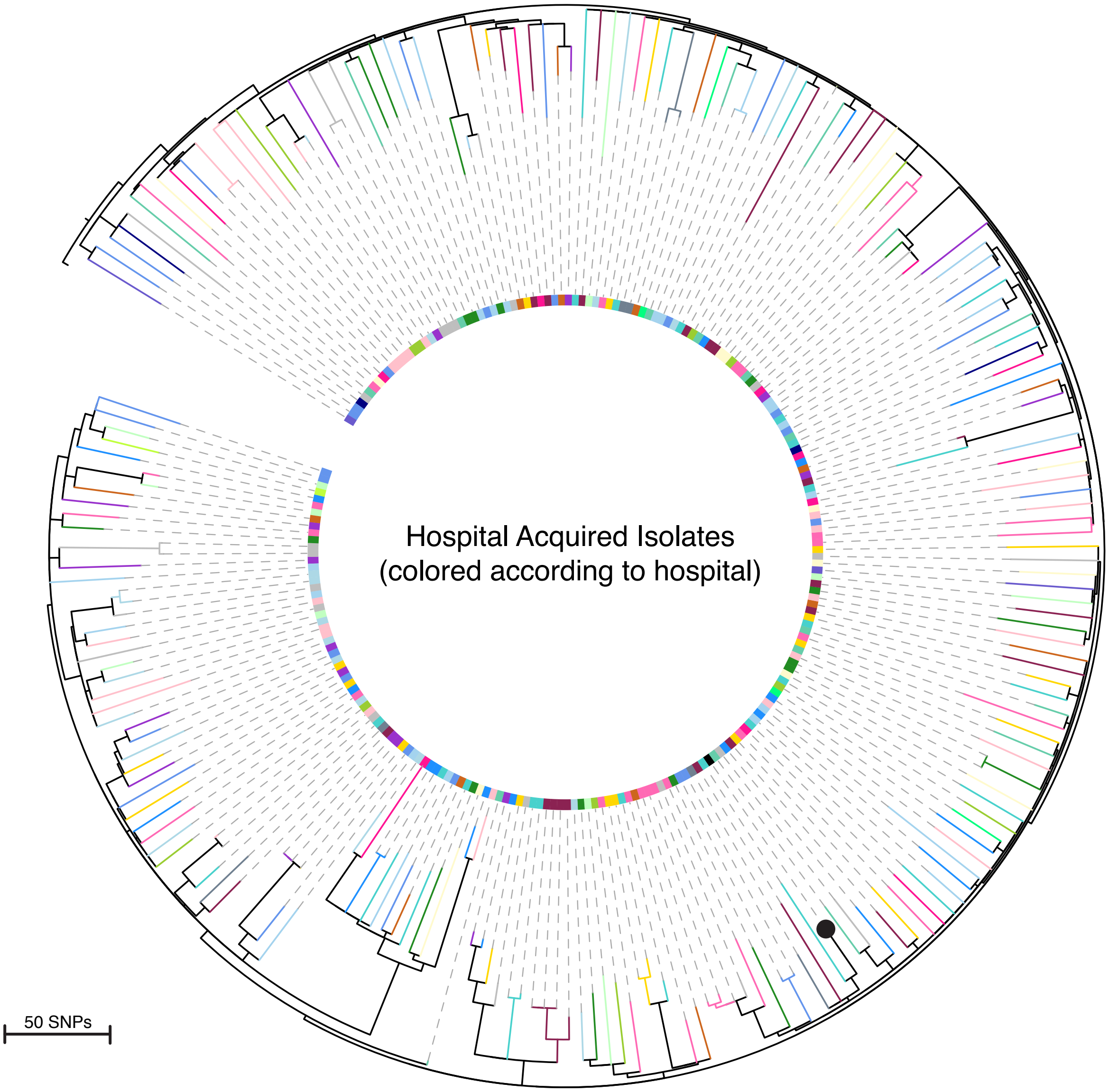


**Figure S3. Rooted phylogenetic tree of hospital-onset isolates.** Branch and inner ring colors represent the hospital origin of any given isolate. The black dot represents the position of the reference genome USA300 FPR 3757 (NC_007793). The tree was rooted using the distant isolate COL (CC8, ST250, accession NC_002951).

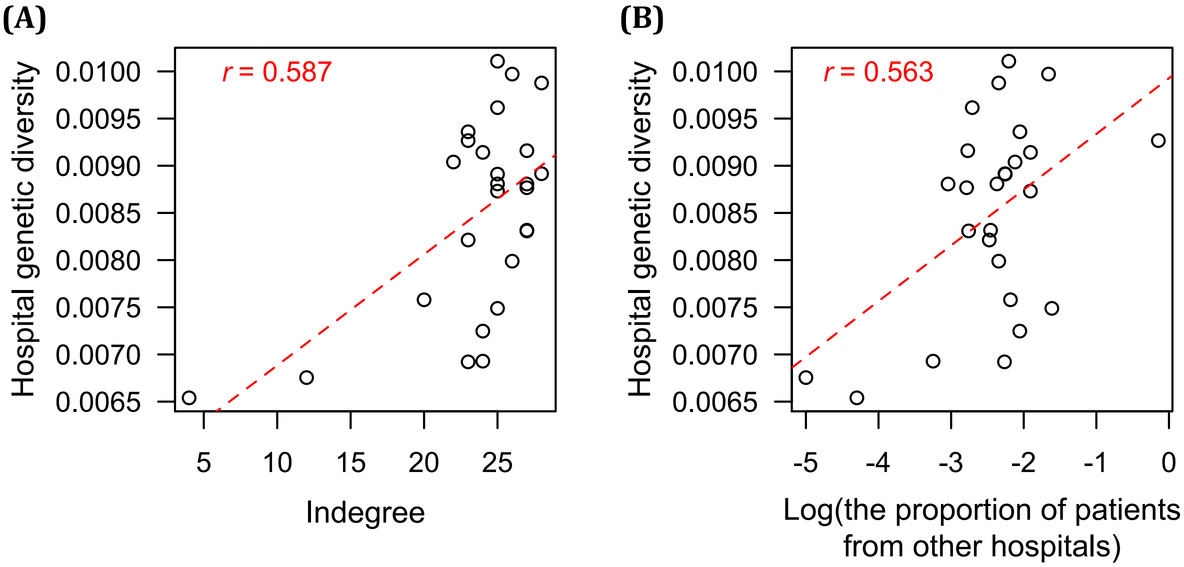


**Figure S4. Within-hospital genetic diversity.** Hospital genetic diversity was associated with **(A)** the number of hospitals a hospital receives patients from and **(B)** the proportion of patients from other hospitals. The correlation coefficient shown here is Pearson partial correlation coefficients when controlling for the sample size.

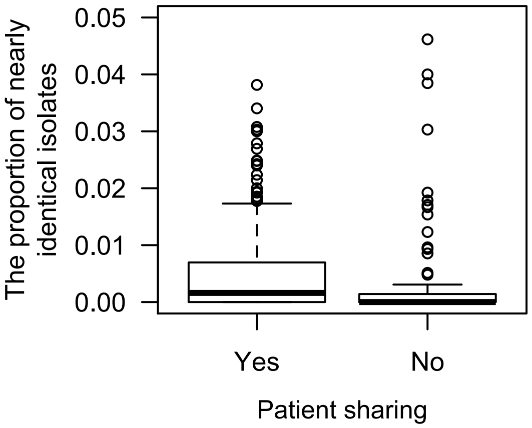


**Figure S5.** The proportion of nearly identical isolates between hospitals with patient sharing was significantly larger than that between hospitals without patient sharing (median= 0.0055 vs. 0; permutation test [*n* = 10000], *p*-value = 0.008).

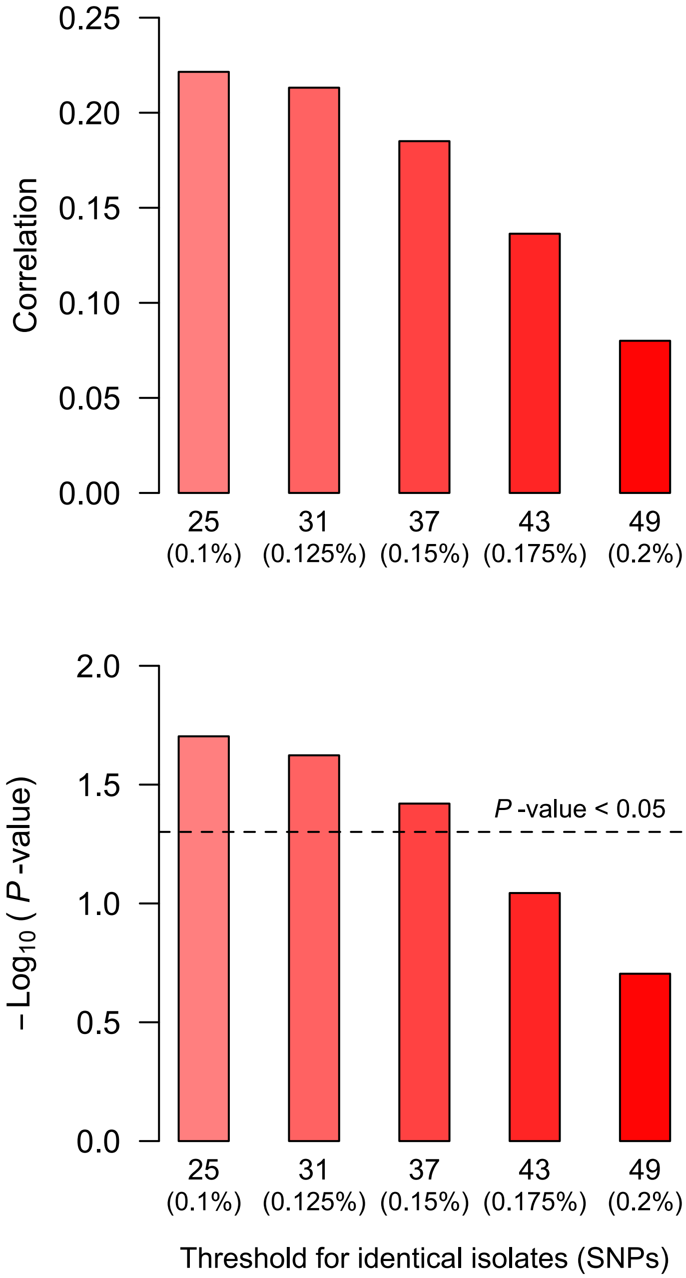
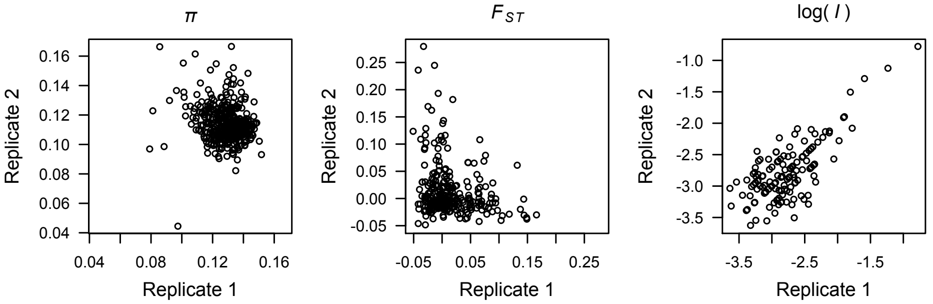
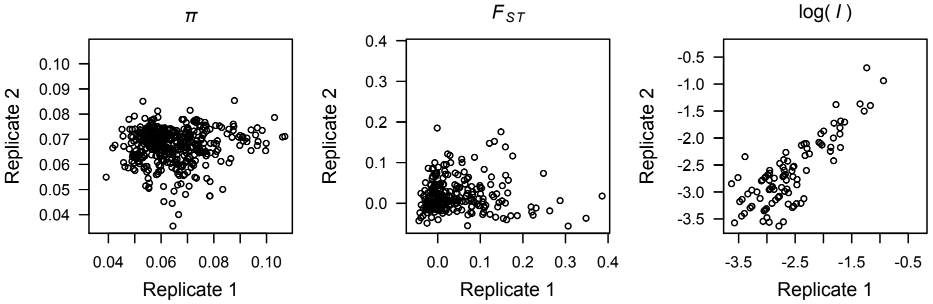


**Figure S6. Correlation coefficients and *p*-values for different threshold values to define nearly identical isolates.** The standard threshold used in this paper is 0.15% (37 SNPs). The results from SNP difference cutoff values different from 37 are similar. Color code corresponds to the different simulated cutoffs in Fig. 3.

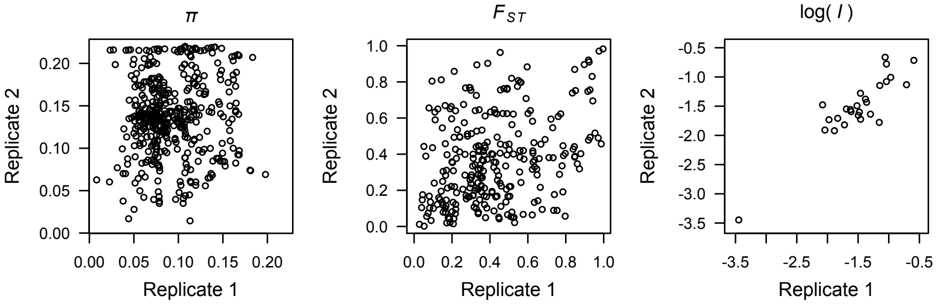
**Model 1**



**Model 2**



**Model 3**



**Model 4**

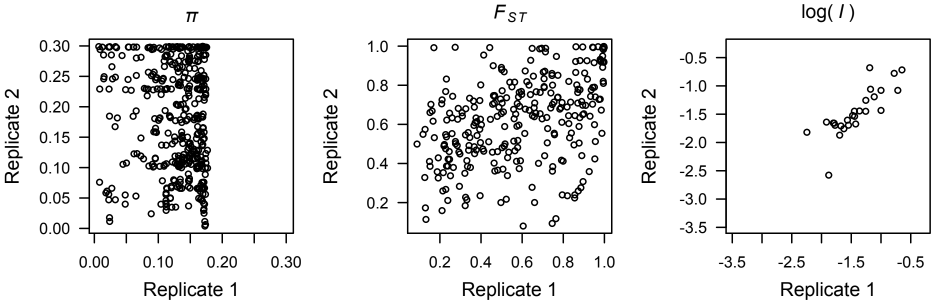


**Figure S7. The stochastic variation of $F_{ST}$ and $\pi$ between simulation runs was higher than that of the proportion of nearly identical isolates (*I*)** (1 SNP difference cutoff was used for nearly identical isolates here).

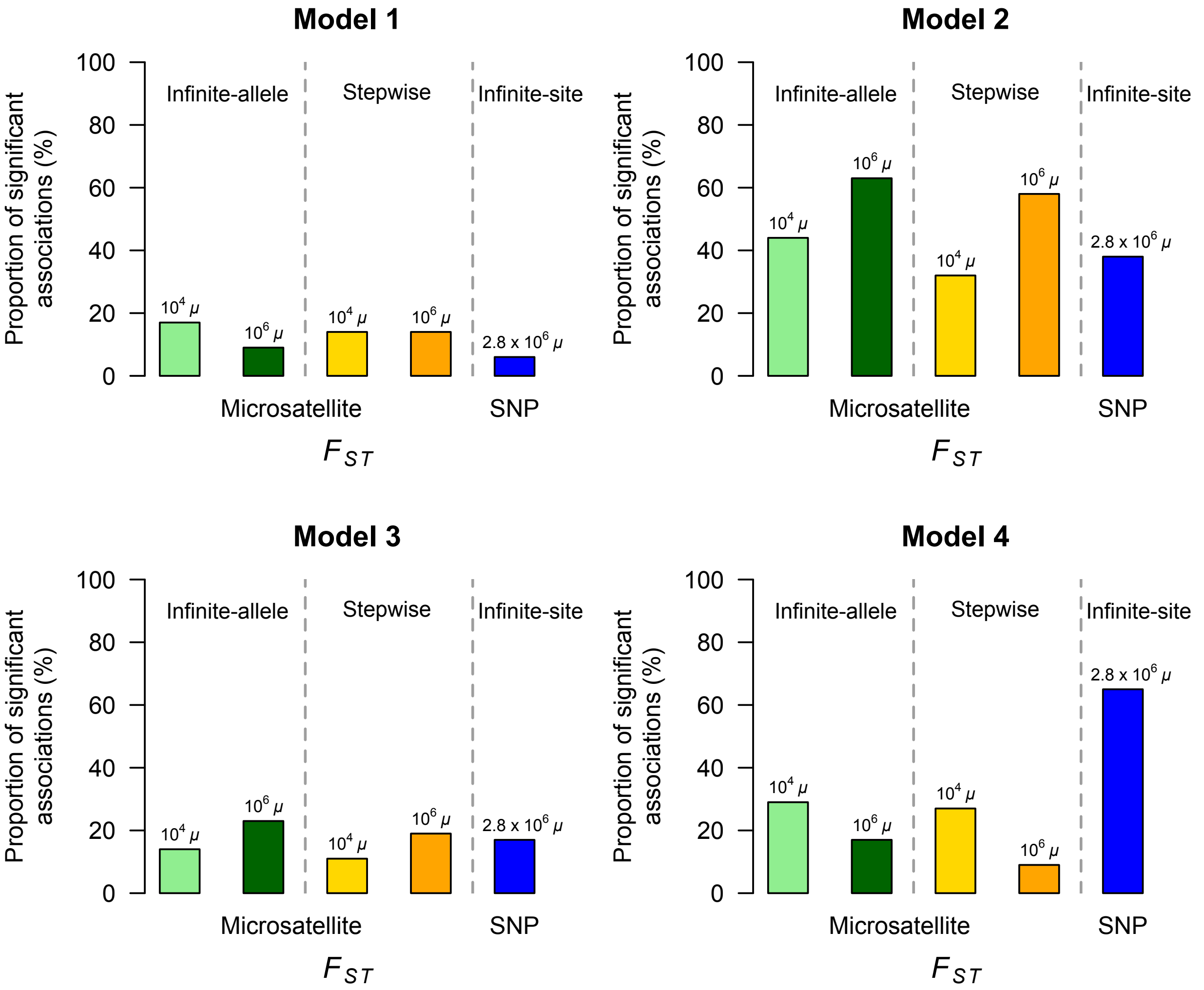


**Figure S8. The power of *$F_{ST}$* calculated from microsatellite markers and genome-wide SNPs.** All patient sharing was shifted by 0.00001 for the purpose of log-transformation. We used two different mutation rates ($10^4\mu$ and $10^6\mu$) in the microsatellite model. The per-site point mutation rate $\mu$= 2.857 × $10^{-6}$ per year; figures above bars denote total mutation rate per site (microsatellite) or per genome (SNP).

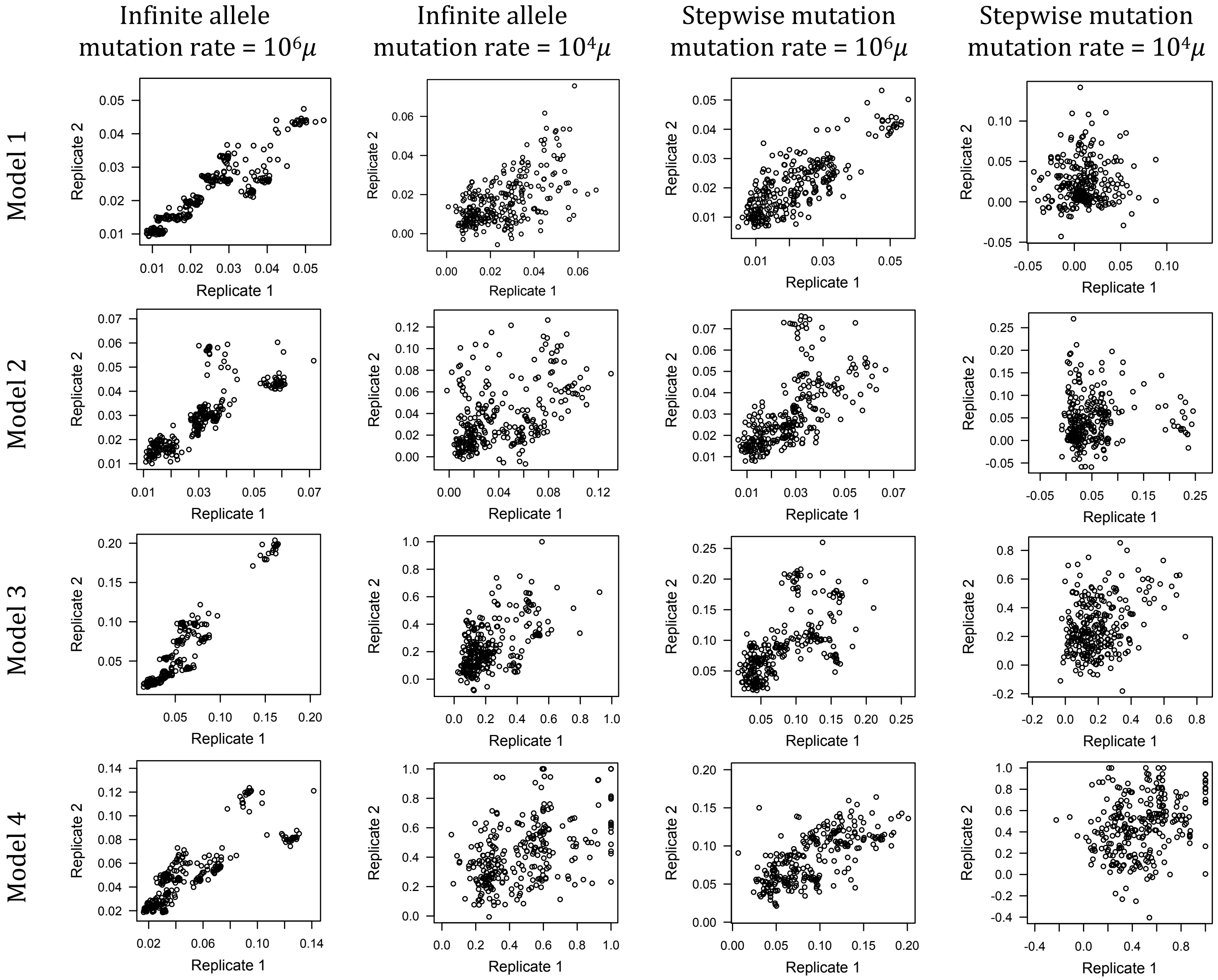


**Figure S9. The stochastic variation of $F_{ST}$ calculated from microsatellite markers was smaller than that calculated from SNPs** (see Figure S6 for comparison).

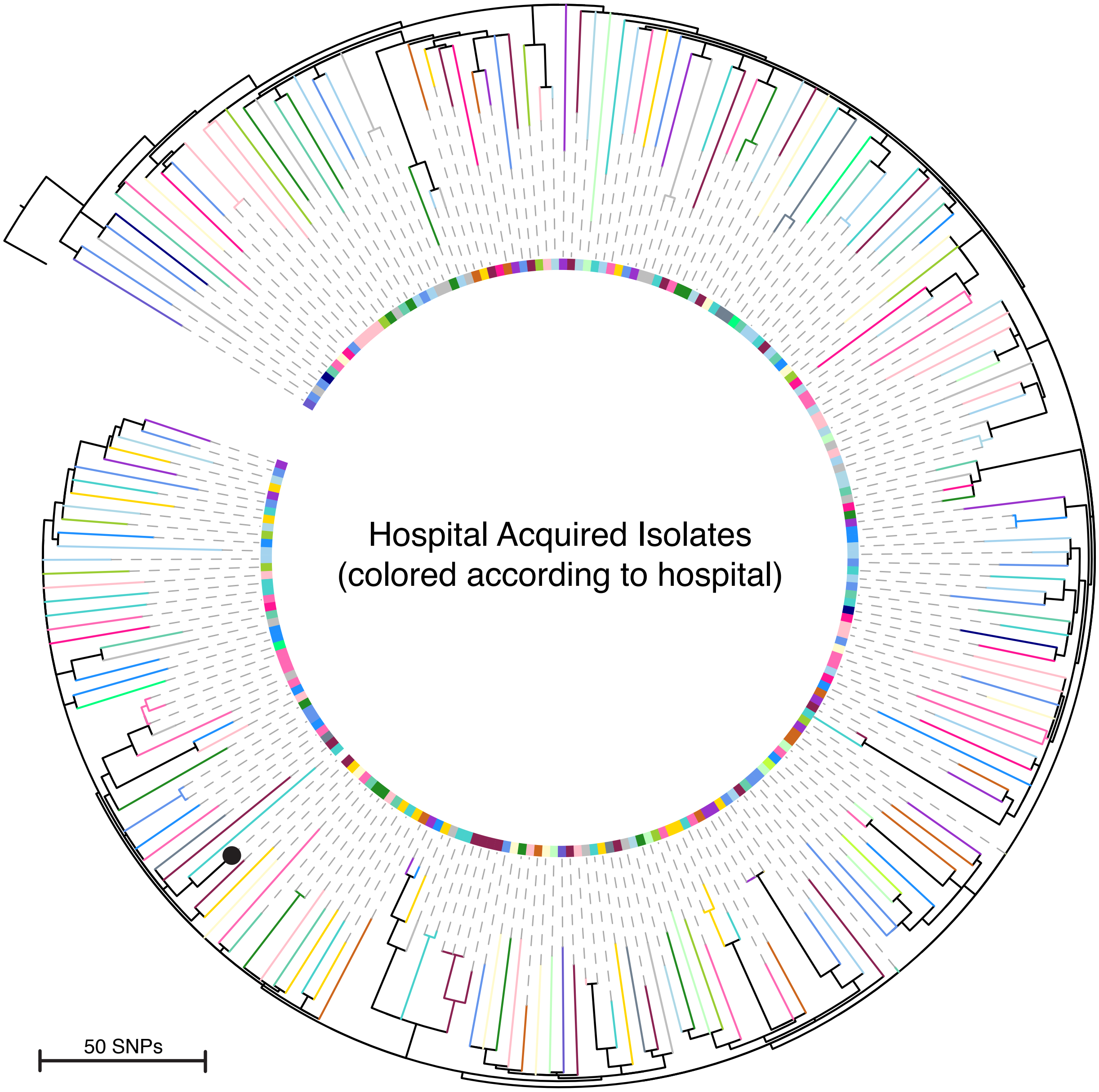


**Figure S10. Phylogenetic tree after removing recombination.**

**Table S1. The sample size and proportion of community-onset isolates in each hospital**

| Hospital | Number of CO | Total sample size | Proportion of CO |
|---|---|---|---|
| 1 | 12 | 16 | 0.75 |
| 2 | 45 | 60 | 0.75 |
| 3 | 18 | 20 | 0.90 |
| 4 | 47 | 64 | 0.73 |
| 5 | 11 | 13 | 0.85 |
| 6 | 57 | 68 | 0.84 |
| 7 | 23 | 23 | 1 |
| 8 | 49 | 65 | 0.75 |
| 9 | 15 | 25 | 0.60 |
| 10 | 14 | 16 | 0.86 |
| 11 | 1 | 1 | 1 |
| 12 | 16 | 28 | 0.57 |
| 13 | 2 | 2 | 1 |
| 14 | 4 | 4 | 1 |
| 15 | 9 | 9 | 1 |
| 16 | 37 | 54 | 0.69 |
| 17 | 29 | 36 | 0.81 |
| 18 | 39 | 50 | 0.78 |
| 19 | 35 | 50 | 0.7 |
| 20 | 20 | 26 | 0.77 |
| 21 | 15 | 16 | 0.94 |
| 22 | 8 | 8 | 1 |
| 23 | 25 | 33 | 0.76 |
| 24 | 39 | 55 | 0.71 |
| 25 | 9 | 16 | 0.56 |
| 26 | 4 | 4 | 1 |
| 27 | 41 | 56 | 0.73 |
| 28 | 26 | 37 | 0.70 |
| 29 | 58 | 65 | 0.89 |
| 30 | 55 | 66 | 0.83 |

**Table S3. Analysis before and after removing recombination**

| | **All SNPs** | | **Removing recombination** | |
|---|---|---|---|---|
| Within-hospital pairwise difference | | | | |
| | 87bp | 0.353% | 83bp | 0.335% |
| Between-hospital pairwise difference | | | | |
| | 88bp | 0.357% | 85bp | 0.340% |
| The correlation between indegree and within-hospital genetic diversity | | | | |
| | *r* | *p*-value | *r* | *p*-value |
| | 0.583 | 0.0018 | 0.636 | $7.78\times10^{-5}$ |
| The correlation between the proportion of patients from other hospitals and within-hospital genetic diversity | | | | |
| | *r* | *p*-value | *r* | *p*-value |
| | 0.501 | 0.0092 | 0.594 | 0.0004 |
| The association between log($I$) and log($M$) | | | | |
| | *r* | *p*-value | *r* | *p*-value |
| | 0.185 | 0.038 | 0.175 | 0.044 |
| The association between $F_{ST}$ and log($M$) | | | | |
| | *r* | *p*-value | *r* | *p*-value |
| | -0.112 | 0.11 | -0.146 | 0.061 |
| The association between $\pi$ and log($M$) | | | | |
| | *r* | *p*-value | *r* | *p*-value |
| | 0.085 | 0.20 | 0.101 | 0.15 |

1. Croucher NJ, Page AJ, Connor TR, Delaney AJ, Keane JA, Bentley SD, Parkhill J, Harris SR: **Rapid phylogenetic analysis of large samples of recombinant bacterial whole genome sequences using Gubbins.** *Nucleic Acids Res* 2015, **43:**e15.