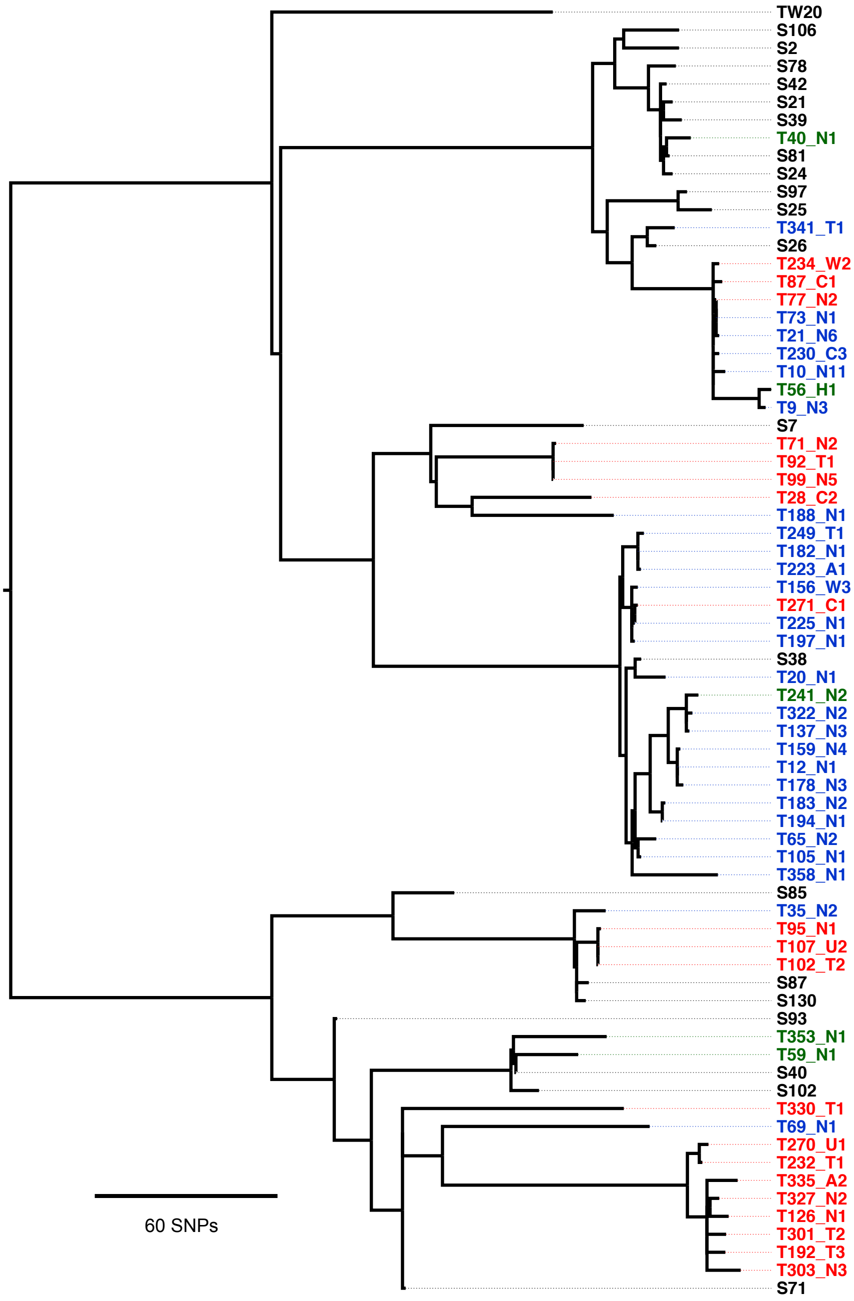

Figure S1. Genetic diversity of MRSA ST 239 in a single hospital

Maximum likelihood phylogenetic tree based on core genome SNPs of the first isolate from 46 patients (prefix T, red label – surgical ICU; blue label – pediatric ICU), 5 healthcare workers (prefix T, green label), 20 MRSA ST 239 isolates recovered from patients in the same hospital between Oct 2006 and Apr 2007 (black; prefix S), and the reference ST 239 (TW20). The first number assigned to each case represents the study number. The second letter/number combination (where present) refers to the type/site of sample from which the MRSA isolate was cultured (N, nasal swab; T, throat swab; A, axillae swab; W, wound swab; U, urine; C, tracheal suction), followed by the sample number from that particular site. For example, T178-N3 refers to the third nasal swab taken from case T178.

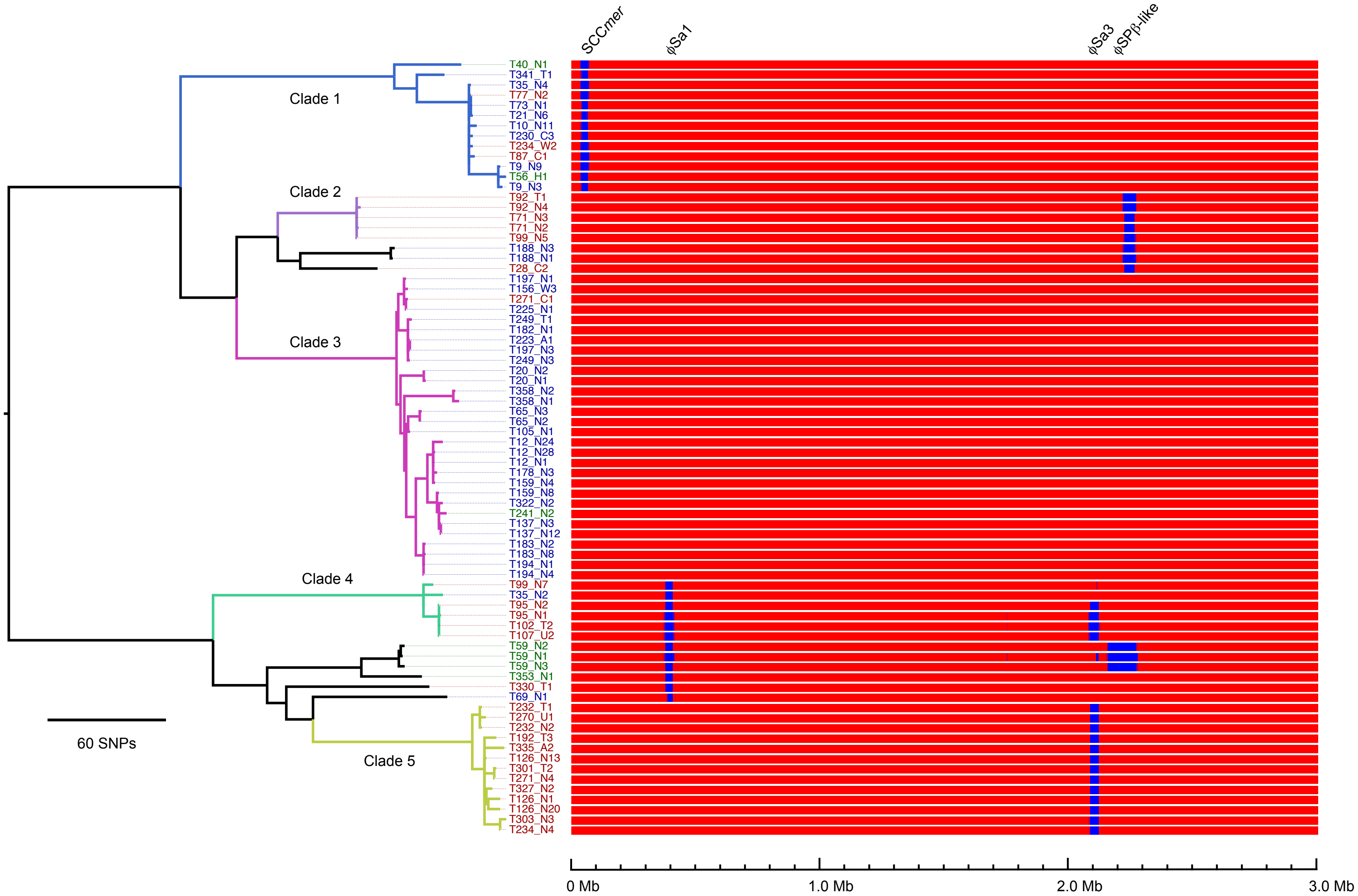

Figure S2. Large-scale genomic deletions defined from mapping against the TW20 reference chromosome

Red denotes presence of reference sequence; blue denotes absence of reference sequence. Mobile genetic elements in the TW20 reference that are variably present are indicated at the top of the mapping block, and a scale at the bottom indicates the size of the chromosome and relative positions of the mobile genetic elements.

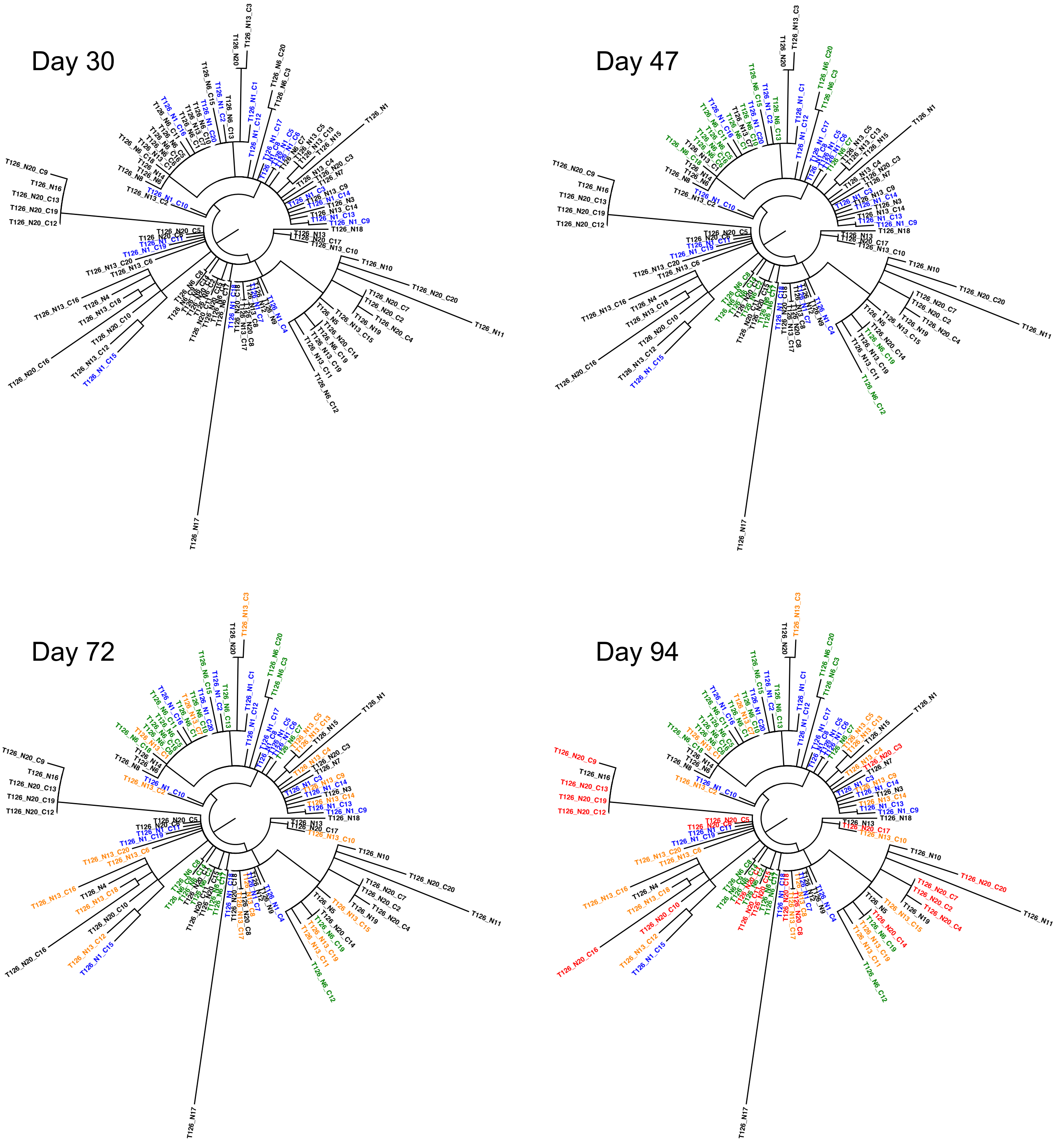

Figure S3. Intra-host diversity of MRSA isolates cultured from a single patient over time
Circular maximum likelihood phylogenetic tree based on core genome SNPs for 99 MRSA ST 239 clade 5 isolates from patient T126. Sequences from 21 colonies at each of four time points (days 30, 47, 72, 94) are highlighted in blue, green, orange and red, respectively, and are displayed as four sequential trees.

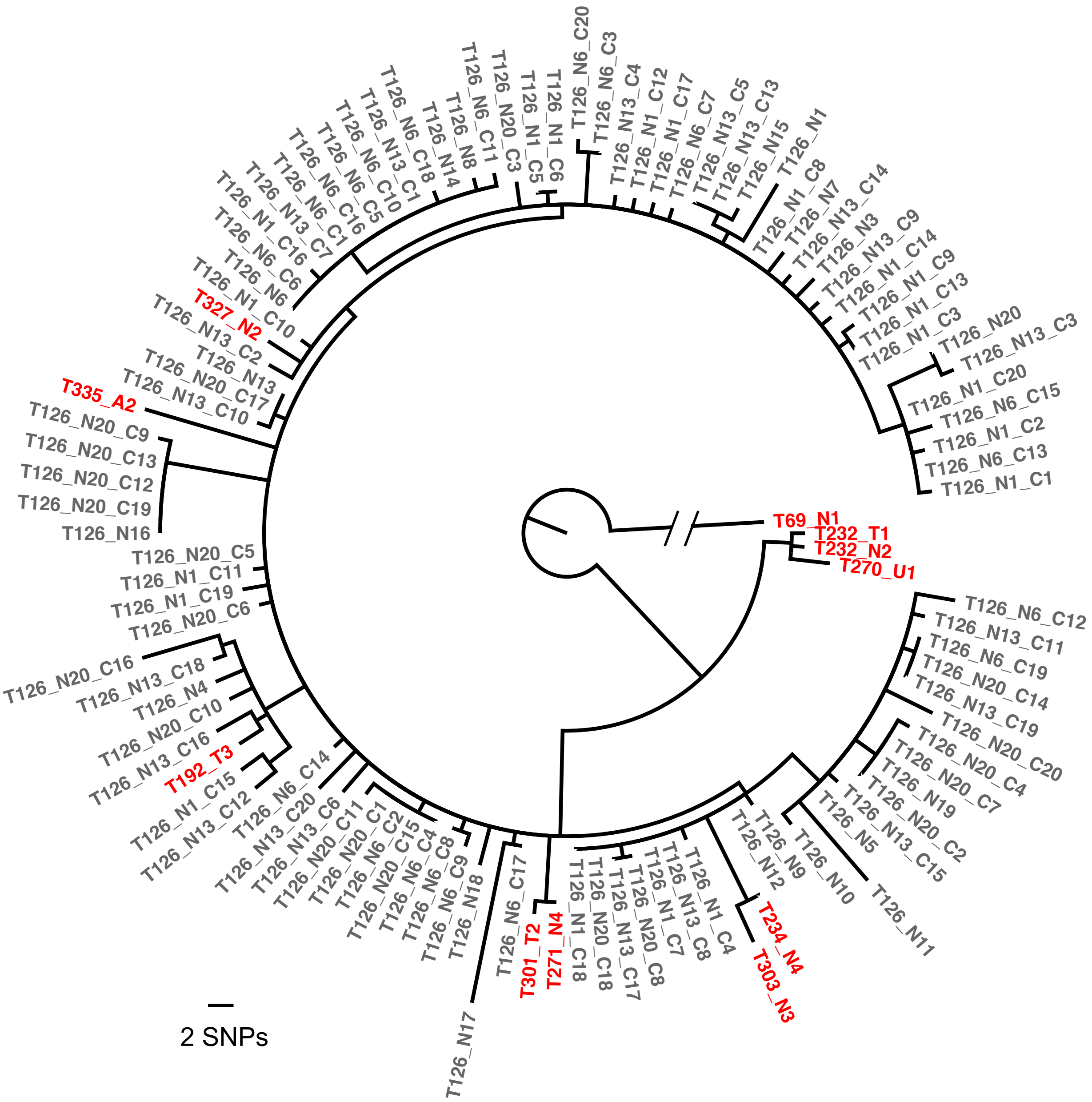

Figure S4. Intra- and inter-host diversity for isolates belonging to MRSA ST 239 clade 5
Circular maximum likelihood phylogenetic tree based on core genome SNPs for 99 isolates from patient T126 and other clade 5 isolates concurrently isolated on the adult ICU (rooted using patient T69 isolate). Isolates from patient T126 are in grey and isolates from other patients are in red. The first T number assigned to each represents the case study number. The second letter/number combination refers to the type of sample (N, nasal swab; T, throat swab; A, axillae swab; U, urine), and the sample number from that particular site. The third letter/number (when present) combination refers to samples from which more than one primary plate colony was picked and gives the colony study number. For example, T126_N20_N10 refers to patient T126, the 20th nasal swab taken, and the 10th colony picked.