

Table A2: List of *S. aureus* reference genomes used for evaluation and extension of the *in silico* typing scheme. Table **A)** depicts all NCBI RefSeq genomes available on Dec 18th, 2014, which were used to establish the allele libraries. Table **B)** depicts the representative genomes of diverse MLST ST that were used to extend the allele libraries.

| A) | | | | | | B) | |
|-----|----------------|---------------|-----------------------------------------------------------|---------------|------|----------------------------|-----------|
| No. | Strain | Accession Nr. | Characteristics (according to GenBank entry) | PMID | ST | ENA Accession Nr. | ST |
| 1 | N315 | NC_002745 | human MRSA | 11418146 | 5 | ERR033388 | 12 |
| 2 | Mu50 | NC_002758 | human MRSA | 11418146 | 5 | ERR114897 | 121 |
| 3 | COL | NC_002951 | early human MRSA | 15774886 | 250 | ERR211639 | 130 |
| 4 | MRSA252 | NC_002952 | hospital-acquired EMRSA-16 MRSA, gen. diverse | 15213324 | 36 | ERR211687 | 133 |
| 5 | MSSA476 | NC_002953 | invasive, community-acquired, susceptible | 15213324 | 1 | ERR084616 | 151 |
| 6 | MW2 | NC_003923 | CA-MRSA, highly virulent | 12044378 | 1 | ERR172063 | 20 |
| 7 | RF122 | NC_007622 | bovine mastitis, Ireland | 17971880 | 151 | ERR072252 | 22 |
| 8 | USA300_FPR3757 | NC_007793 | CA-MRSA, virulent (USA300), ACME | 16517273 | 8 | SRR016396 | 30 |
| 9 | NCTC8325 | NC_007795 | early MSSA | vgl. 16559089 | 8 | SRR445031 | 398 |
| 10 | JH9 | NC_009487 | vancomycin resistant MRSA, evolved isolate | 14645269 | 105 | ERR108050 | 45 |
| 11 | JH1 | NC_009632 | vancomycin susceptible MRSA, parental isolate | 14645269 | 105 | ERR086060 | 5 |
| 12 | Newman | NC_009641 | MSSA, human infection, < virulence than MW2 | 17951380 | 254 | ERR204157 | 59 |
| 13 | Mu3 | NC_009782 | variable vancomycin-resistance, MRSA, pneumonia, Japan | 9400512 | 5 | ERR109588 | 7 |
| 14 | USA300_TCH1516 | NC_010079 | MRSA, virulent (USA300), pediatric | 17986343 | 8 | ERR111110 | 80 |
| 15 | ED98 | NC_013450 | chicken pathogen, MSSA?? | 19884497 | 5 | ERR048356 | 239 |
| 16 | VC40 | NC_016912 | vancomycin- and daptomycin-resistant MRSA | 22461548 | 8 | ERR070041 | 1 |
| 17 | M013 | NC_016928 | CA-MRSA, pvl-Positive, ST59-SCCmec V, pus/wound, Taiwan | 22328755 | 59 | ERR127444 | 15 |
| 18* | MSHR1132 | NC_016941 | early-branching, CC75, small access. genome, Australia | 21813488 | 1850 | ERR175883 | 97 |
| 19 | TW20 | NC_017331 | highly transmissible, MRSA, MDR, antiseptics-res., ST239 | 19948800 | 239 | ERR212215 | 247 |
| 20 | ST398 | NC_017333 | livestock-acquired MRSA (pigs, calves) | 20546576 | 398 | ERR234846 | 25 |
| 21 | ED133 | NC_017337 | ruminant (Wiederkäuer) pathogen | 20624747 | 133 | ERR246635 | 352 |
| 22 | JKD6159 | NC_017338 | Australian CA-MRSA | 20729356 | 93 | SRR016154 | 8 |
| 23 | 04-02981 | NC_017340 | human MRSA, European clone, ST225 | 20386717 | 225 | ERR033380 | 101 |
| 24 | JKD6008 | NC_017341 | human MRSA, ST239, interm. vancomycin res., New Zealand | 20802046 | 239 | ERR127412 | 88 |
| 25 | TCH60 | NC_017342 | human MRSA | Unpublished | 30 | NCBI GenBank | ST |
| 26 | ECT-R2 | NC_017343 | MR-MRSA, human wound, Sweden, SCCmec remnant | 21590357 | 5 | CP010941.1, strain SA17_S6 | 152 |
| 27 | T0131 | NC_017347 | human ST239-MRSA-SCCmec Type III, China | 21551295 | 239 | | |
| 28 | LGA251 | NC_017349 | human and bovine, type-XI SCCmec, prevalent in Europe | 21641281 | 425 | | |
| 29 | 11819-97 | NC_017351 | European CA-MRSA, ST80-IV | 22374956 | 80 | | |
| 30 | 71193 | NC_017673 | animal-independent ST398 MSSA | 22375071 | 398 | | |
| 31 | HO 5096 0412 | NC_017763 | EMRSA15, neonatal outbreak | 23299977 | 22 | | |
| 32 | 08BA02176 | NC_018608 | LA-MRSA, ST398, Canada | 23144384 | 398 | | |
| 33 | ST228-01 | NC_020529 | South German Clone ST228-MRSA-I | 22720005 | 228 | | |
| 34 | ST228-02 | NC_020532 | | 22720005 | 228 | | |
| 35 | ST228-03 | NC_020533 | | 22720005 | 228 | | |
| 36 | ST228-04 | NC_020536 | - microevolution study - | 22720005 | 228 | | |
| 37 | ST228-05 | NC_020537 | hospital in Lausanne, Switzerland | 22720005 | 228 | | |
| 38 | ST228-06 | NC_020564 | 2001 - 2008 | 22720005 | 228 | | |
| 39 | ST228-07 | NC_020566 | | 22720005 | 228 | | |
| 40 | ST228-08 | NC_020568 | | 22720005 | 228 | | |
| 41 | M1 | NC_021059 | MRSA, t024-ST8-IVa, Denmark | 23792746 | 8 | | |
| 42 | CA-347 | NC_021554 | MRSA (USA600), CC45, nasal colonisation / sepsis | 23887918 | 45 | | |
| 43 | Bmb9393 | NC_021670.1 | human MRSA, biofilm formation, ST239, prevalent in Brazil | 23929475 | 239 | | |
| 44 | 55/2053 | NC_022113.1 | none | Unpublished | 30 | | |
| 45 | CN1 | NC_022226.1 | CA-MRSA, PVL-negative, ST72, Korea | 23977354 | 72 | | |
| 46 | SA957 | NC_022442.1 | CA-MRSA, ST59, "Taiwan Clone", PVL-positive, virulent | 24039691 | 59 | | |
| 47 | SA40 | NC_022443.1 | CA-MRSA, ST59, "Asian-Pacific Clone", colonizer | 24039691 | 59 | | |
| 48 | Z172 | NC_022604 | HA-MRSA, ST239-SCCmec type III, interm.-VRSA, Taiwan | 24309740 | 239 | | |

excluded for typing comparison - high similarity to ST228-01

* The alleles of strain MSHR 1132 were retroactively excluded from the allele libraries due to high diversity to other alleles