

(n=1); 3453* this study (n=1), ETH (n=59), SWE (n=2); 3454* this study (n=2); 3455* this study (n=1), CMR (n=1); 3456* this study (n=1), SAU (n=1); 3457* this study (n=1), VEN (n=1); 3458* this study (n=1), BGD (n=1); 3459* this study (n=1), AUT (n=1); 3460* this study (n=1), THA (n=1); 3461* this study (n=2); 3462* this study (n=1), COL (n=1); 3463* this study (n=1), NLD (n=1); 3464* this study (n=1), BGD (n=1); 3465* this study (n=1), FXX (n=1); 3466* this study (n=1), SWE (n=1); 3467* this study (n=1), CMR (n=1); 3468* this study (n=2); 3469* this study (n=1), ESP (n=1); 3470* this study (n=4); 3471* this study (n=4); 3472* this study (n=1), BRA (n=1); 3473* this study (n=2), HTI (n=1); 3474* this study (n=1), HTI (n=1); 3475* this study (n=2), GMB (n=1); 3476* this study (n=1), (n=1); 3477* this study (n=2); 3478* this study (n=1), ESP (n=5), NLD (n=1); 3479* this study (n=3); 3480* this study (n=2); 3481* this study (n=1), AUT (n=1); 3482* this study (n=1), ITA (n=1); 3483* this study (n=2), MYS (n=1); 3484* this study (n=1), MYS (n=1); 3485* this study (n=1), ESP (n=1); 3486* this study (n=1), SWE (n=1); 3487* this study (n=1), JPN (n=1); 3488* this study (n=1), TUR (n=1); 3489* this study (n=1), SWE (n=1); 3490* this study (n=1), BRA (n=1); 3491* this study (n=1), ZAF (n=1); 3492* this study (n=1), USA (n=1); 3493* this study (n=1), ARG (n=1); 3494* this study (n=1), ZAF (n=1); 3495* this study (n=1), BRA (n=1); 3496* this study (n=1), PER (n=1); 3497* this study (n=1), ITA (n=1); 3498* this study (n=1), GNB (n=1); 3499* this study (n=1), ITA (n=1); 3709* this study (n=1), ESP (n=1).

** Lineage designations according to SITVIT2 using revised SpoIDB4 rules; "Unknown" designates patterns with signatures that do not belong to any of the major lineages described in the database.

*** Clustered strains correspond to a similar spoligotype pattern shared by 2 or more strains "within this study"; as opposed to unique strains harboring a spoligotype pattern that does not match with another strain from this study. Unique strains matching a preexisting pattern in the SITVIT2 database are classified as SITs, whereas in case of no match, they are designated as "orphan".