

**Supplemental Table S2.** Description of 433 shared-types (SITs; n=2075) and corresponding spoligotyping defined lineages starting from a total of 2257 strains isolated in Rhône-Alpes region of France.



### Supplemental Table S2, page 3

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\* A total of 368/433 SITs containing 1976 isolates matched a preexisting shared-type in the database, whereas 65/433 SITs (n=99 isolates) were newly created. A total of 198/433 SITs containing 1840 isolates were clustered within this study (2 to 346 isolates per cluster) while 235/433 SITs containing 235 strains were unique (for total unique strains, one should add to this number the 182 orphan strains, which brings the number of unclustered isolates in this study to 417/2257 or 18.48%, and clustered isolates to 1840/2257 or 81.52%). Note that SITs followed by an asterisk indicates "newly created" SITs due to 2 or more strains belonging to an identical new pattern within this study or after a match with an orphan in the database; SIT designations followed by number of strains: 3436\* this study (n=1), MAR (n=1); 3437\* this study (n=2); 3438\* this study (n=2); 3439\* this study (n=1), ETH (n=1); 3440\* this study (n=1), GUF (n=1), USA (n=1); 3441\* this study (n=6); 3442\* this study (n=3), FIN (n=1); 3443\* this study (n=2); 3444\* this study (n=1), MTQ (n=1); 3445\* this study (n=1), ESP (n=1); 3446\* this study (n=1), NLD (n=1); 3447\* this study (n=4); 3448\* this study (n=2), ITA (n=1); 3449\* this study (n=3); 3450\* this study (n=1), ESP (n=1); 3451\* this study (n=3), FXX (n=1); 3452\* this study (n=1), FXX

(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 SpolDB4 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".