Supplemental Table 6: SNP diversity of isolates in subclade IVa, associated with the 2012 Burkina Faso epidemic.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|   | Burkina Faso 2011 | Burkina Faso 2012 | Burkina Faso 2012 | Burkina Faso 2012 | Burkina Faso 2012 | Mali 2012 |
|  | Entire country | Entire country | CHU-SS | CHUP-CDG | Centre Muraz | Entire country |
| Burkina Faso 2011 |   |   |   |   |   |   |
|  Entire country | 1-67 |  |  |  |  |  |
| Burkina Faso 2012 |   |   |   |   |   |   |
|  Entire country | 6-456 | 0-684 |  |  |  |  |
|  CHU-SS | 21-91 | 0-437 | 0-26 |  |  |  |
|  CHUP-CDG | 6-456 | 0-684 | 8-437 | 0-684 |  |  |
|  Centre Muraz | 19-315 | 2-633 | 8-298 | 2-633 | 3-287 |  |
| Mali 2012 |   |   |   |   |   |   |
|  Entire country | 21-337 | 1-657 | 10-301 | 8-657 | 1-423 | 0-445 |
|  |  |  |

Minimum and maximum counts of hqSNPs distinguishing isolates in groups are presented on the diagonal and below. Isolate counts for each sampling period are: Burkina Faso 2011 (n=12), Burkina Faso 2012 (n=21), CHU-SS (n=7), CHUP-CDG (n=8), Centre Muraz (n=6), Mali 20012 (n=22). The maximum sequence similarity in each comparison exceeds 99.99%.