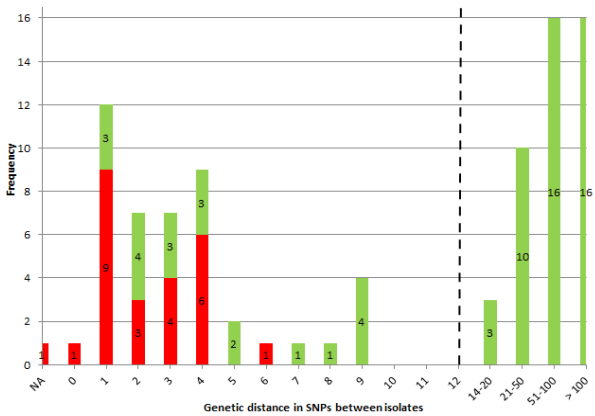
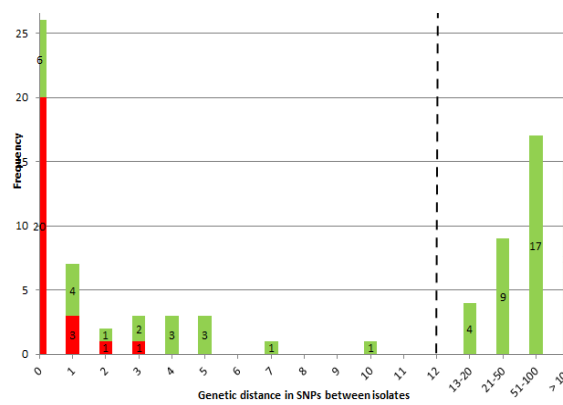


International validation WGS analysis pipeline; 535 *M. tuberculosis* complex sequences re-analysed in reference centers

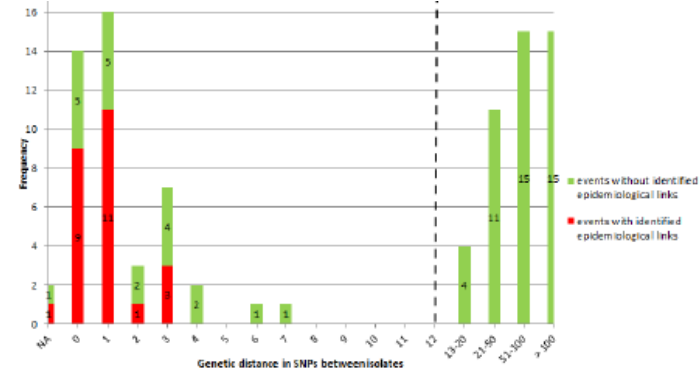
National Institute Public Health - RIVM SNP pipeline – The Netherlands



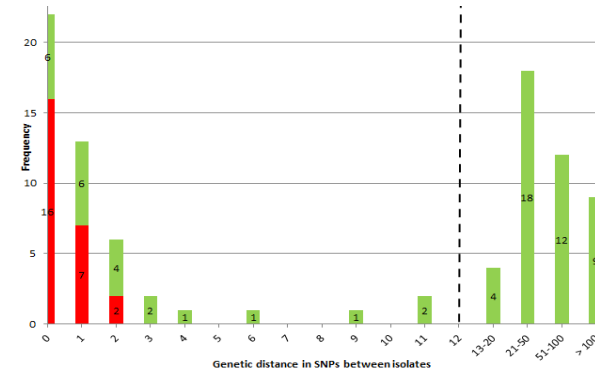
Public Health England Oxford SNP



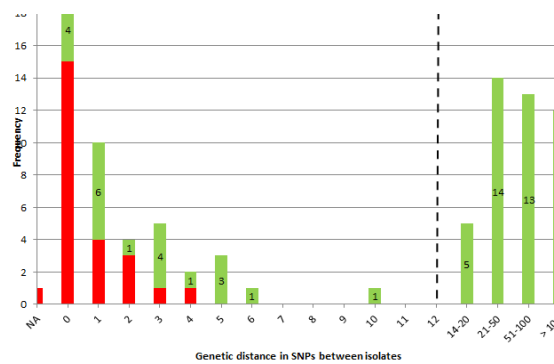
Borstel, German National Reference Center SNP



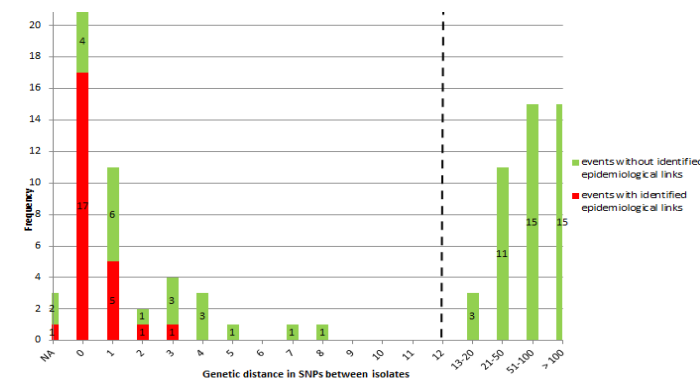
Borstel National Reference Center cgMLST



Statens Serum Institut – Denmark - SNP



IBV-CSIC Valencia SNP



Jajou R, Kohl TA, Walker T, Norman A, Cirillo DM, Tagliani E, Niemann S, de Neeling A, Lillebaek T, Anthony RM, van Soolingen D. Towards standardization: comparison of five whole genome sequencing (WGS) analysis pipelines for detection of epidemiologically linked tuberculosis cases. Eurosurveillance. 2019. (in press)

Clustering of cases with (n=41) and without (n=93) an epidemiological link in 7 pipelines

| | Cases clustered by WGS (≤ 12 SNPs) | | Mean SNP distance epi-linked cases |
|----------------|---|-------------|------------------------------------|
| | Epi-link yes | Epi-link no | |
| RIVM SNP | 39* | 34 | 2.4 |
| PHE SNP | 41 | 34 | 0.3 |
| Borstel SNP | 39* | 32* | 0.9 |
| Borstel cgMLST | 41 | 39 | 0.4 |
| Denmark SNP | 39* | 34 | 0.7 |
| Valencia SNP | 39* | 33** | 0.4 |

*One paired isolate was excluded due to low coverage
**Two paired isolates were excluded