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Superinfection with drug-resistant HIV is rare and does not contribute substantially to therapy failure in a large European cohort

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Preliminary analysis

4425 patients' routinely collected *pol* sequences analyzed with RAxML
100 randomly initialized ML tree built on 13816 sequences

303 positive cases

100 negative cases

MrBayes+BLAST

MrBayes+BLAST

3 confirmed
(3% false negative rate)

Calibration to Final analysis Comparing RAxML+BLAST vs MrBayes+BLAST on **170** patients and calibrating size of background sequence set

Final analysis

RAxML+BLAST

107 putative superinfection cases

94 closely related non monophyletic cases

Validation by sequencing

Fresh sample amplification and sequencing of *pol* and *env* genes in **14 putative superinfection** cases

2 confirmed superinfection cases
9 sample mixups
2 monophyletic trees based on *env* only
1 cluster of closely related sequences