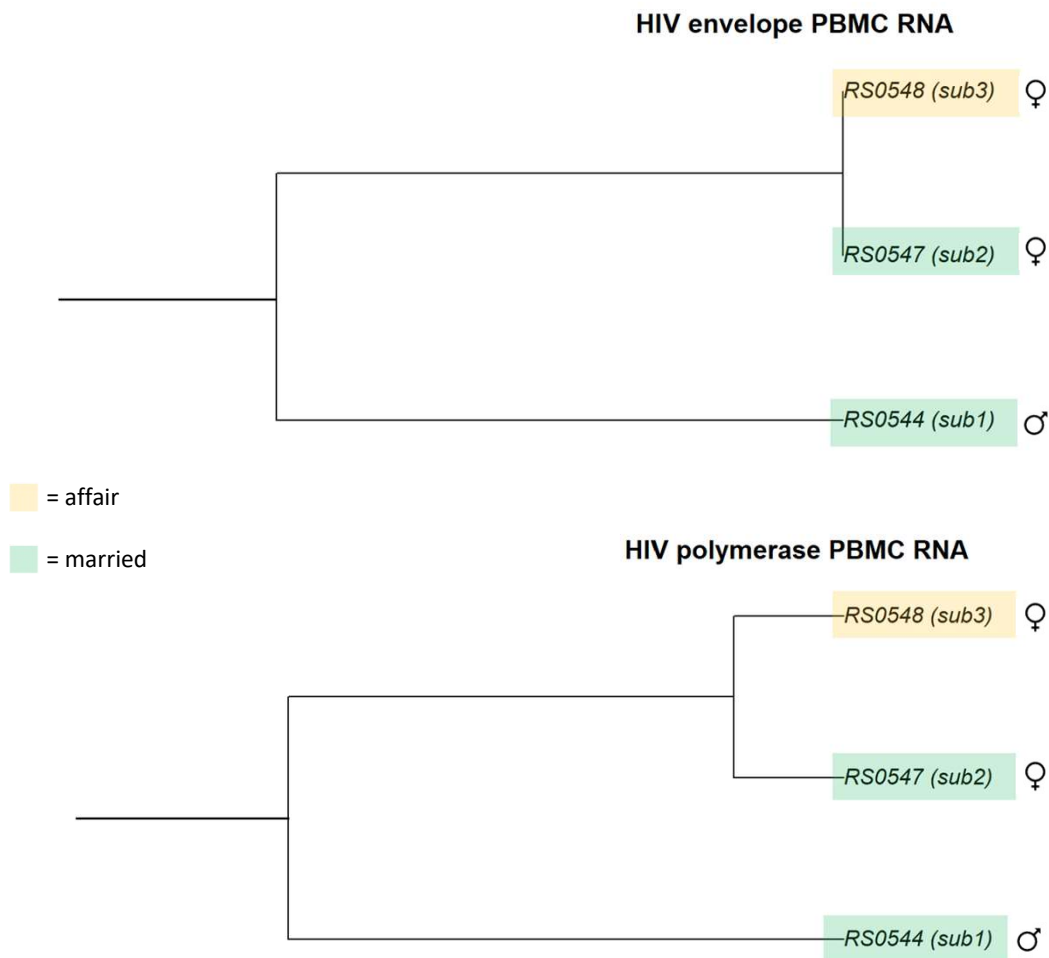


Using phylogenetic analyses to identify potential HIV-transmission crimes



- **Private lawsuit** in Serbia: subject 1 (m; RS0544) accused subject 3 (f; RS0548) of **deliberately/ knowingly infecting** him and his wife (subject 2, f; RS0547) with HIV.

- According to Serbian law, deliberate or inadvertent spread of HIV is **punishable by a 1-15 years sentence**, as in many countries, the spread of HIV can be criminalized .

- A **phylogenetic analysis** of *pol* (polymerase) and *env* (envelope) sequences^[1], extracted from patients PBMCs^[2] was performed to assess the evidence. It showed that the HIV *pol* and *env* of subject 2 and 3 were clustered together when compared to the ones of subject 1. This indicates, that subject 1 infected both subject 3 and subject 3, and therefore **subject 3 is not guilty**.

- These results must be looked at carefully and **are not sufficient** to unambiguously prove direction of transmission.

[1] The *pol* and *env* sequences used for our analysis were taken from NIH Genbank, where Siljic *et al.* deposited their sequence data.

[2] peripheral blood mononuclear cells, e.g. lymphocytes (T-cells, B-cells, NK cells) and monocytes.