*Appendix: Inverse probability of treatment and censoring weights*

To control for confounding of the relationship between chronic HCV and detectable HIV RNA, we used stabilized time-fixed inverse probability-of-exposure weights denoted as:

These weights create a pseudo-population in which chronic HCV is no longer associated with measured covariates, assuming no statistical model misspecification [33,34]. The numerator of the exposure weight represents the probability of having the exposure that participant *i* factually had; the denominator is the probability of having the exposure that participant *i* factually had conditional on . is a vector of covariate values at baseline for participant *i*, assumed to be sufficient to control for confounding. Logistic regression was used to estimate the denominator of the exposure weight.

Time-varying inverse probability-of-censoring weights are denoted as:

These weights account for selection bias due to right-censoring from loss to follow-up and death [35]. We fit separate weight models for right-censoring due to death and loss to follow-up to allow the parameter estimates to differ for each censoring mechanism [36]. The numerator of the censoring weights represent the probability of remaining in the study at visit *k*, conditional on exposure and . The denominators of the censoring weight are the conditional probability of remaining free from censoring, where is a vector of time-fixed and time-varying covariate histories measured up to visit *k*-1*.* Pooled logistic regression models were used to estimate the censoring weights.

The log binomial regression models were weighted by the product of the treatment and censoring weights (. The average of the estimated weights was 1.05 (standard deviation: 1.78) and they ranged from 0.20 to 25.57. We obtained 95% confidence intervals (CIs) for the weighted ratio measures using a nonparametric bootstrap with 200 resamples with replacement. The estimated weights in the 200 samples ranged from 0.06 to 535.95. We trimmed the weights at the 0.5th and 99.5th percentile to reduce the variability of the estimated effect of chronic HCV on detectable HIV RNA.