Integrated Population Pharmacokinetic/Viral Dynamic Modeling of Lopinavir/Ritonavir in HIV-1 Treatment Naïve Patients

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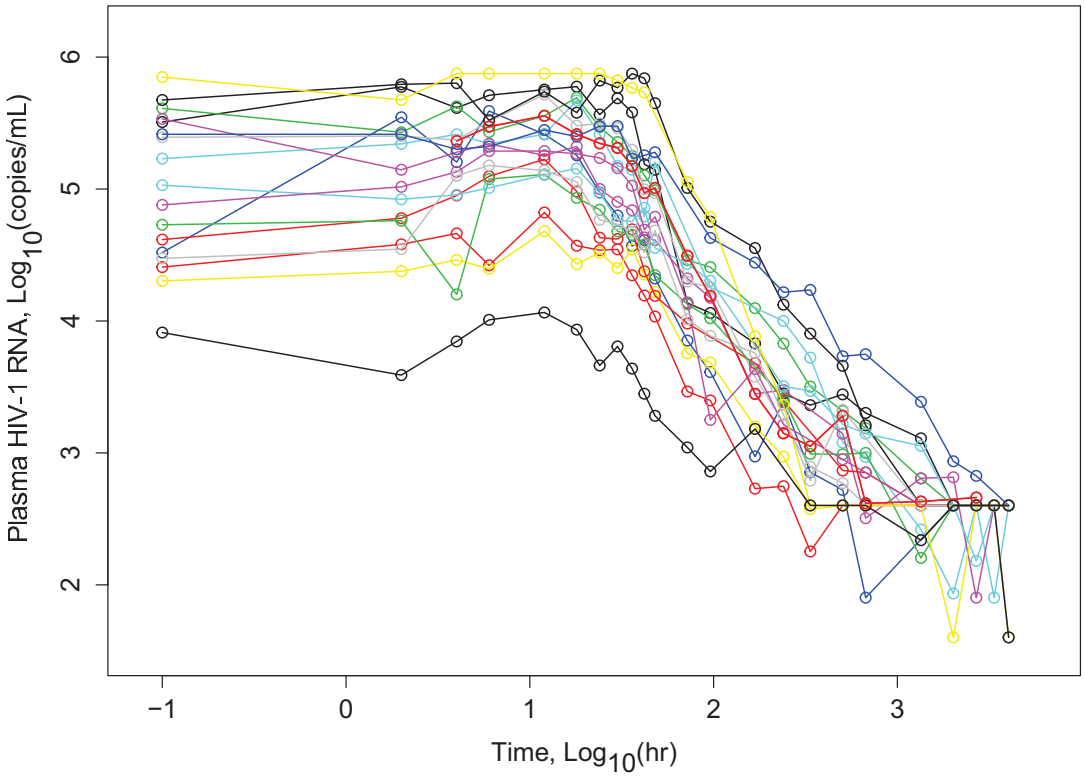
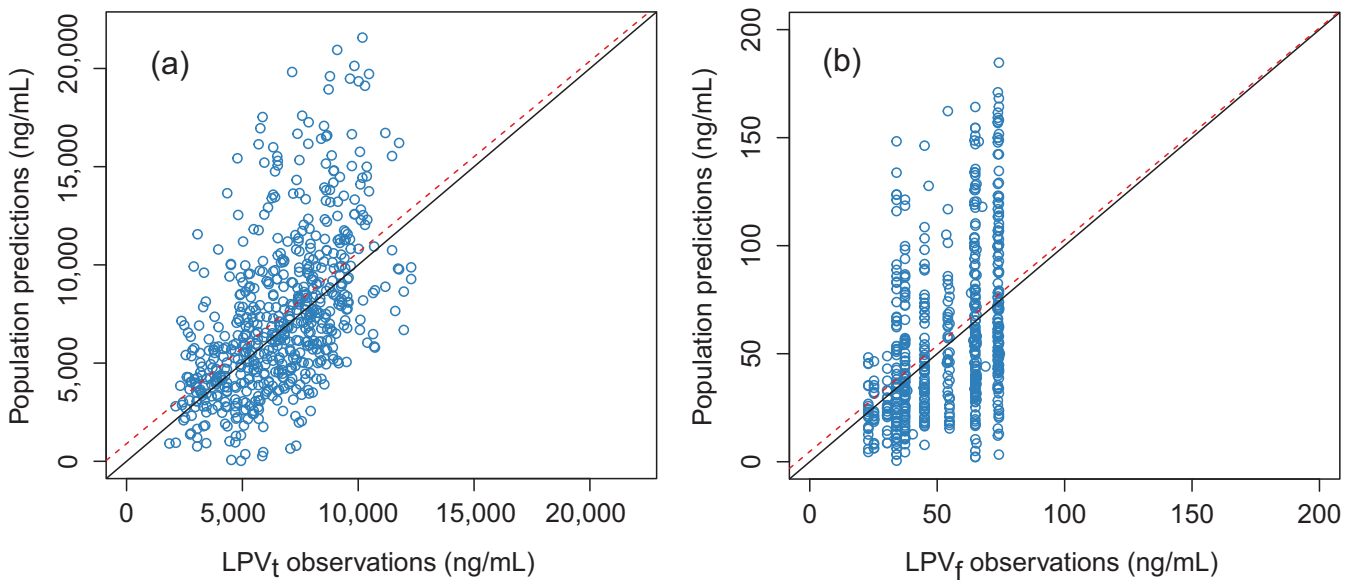
Supplemental Digital Content

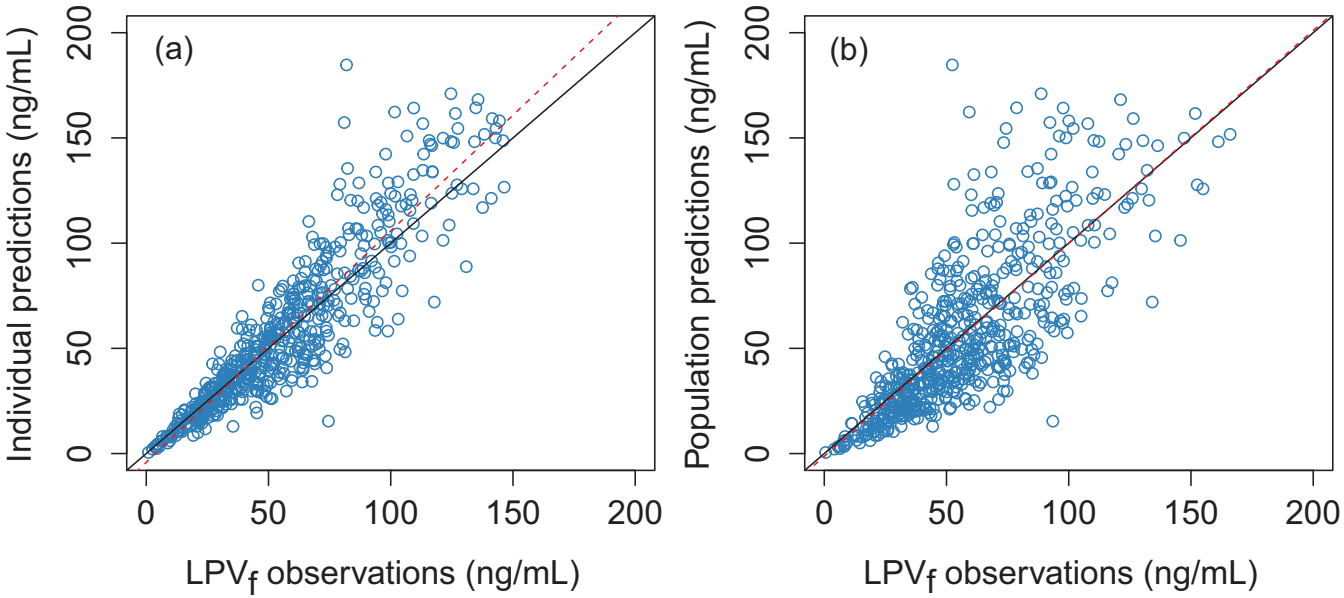
These figures are the Supplemental Digital Content referred to in the full version of this article, which published at Clinical Pharmacokinetics



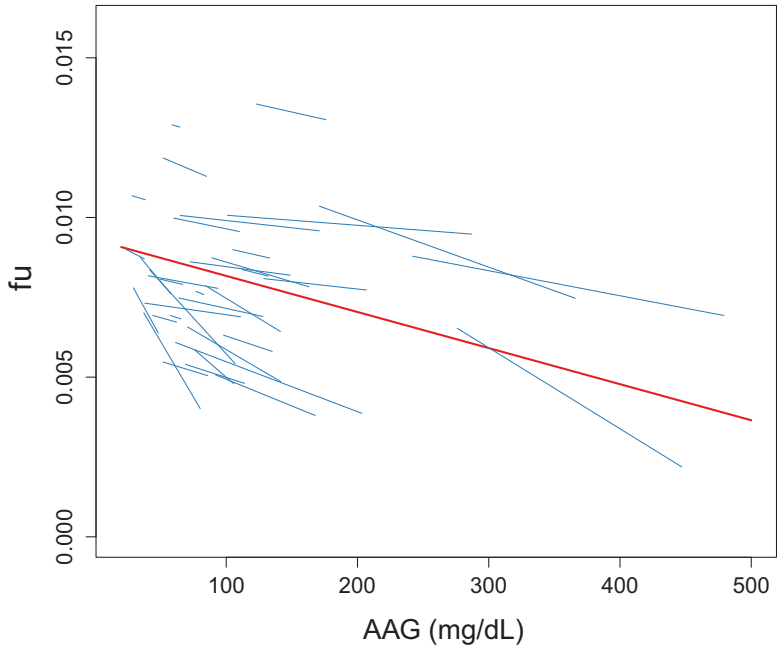
Supplementary Fig. 1. Plasma HIV-1 RNA change over time. Measurements above the limit of quantitation were set to 750,000 copies/mL.



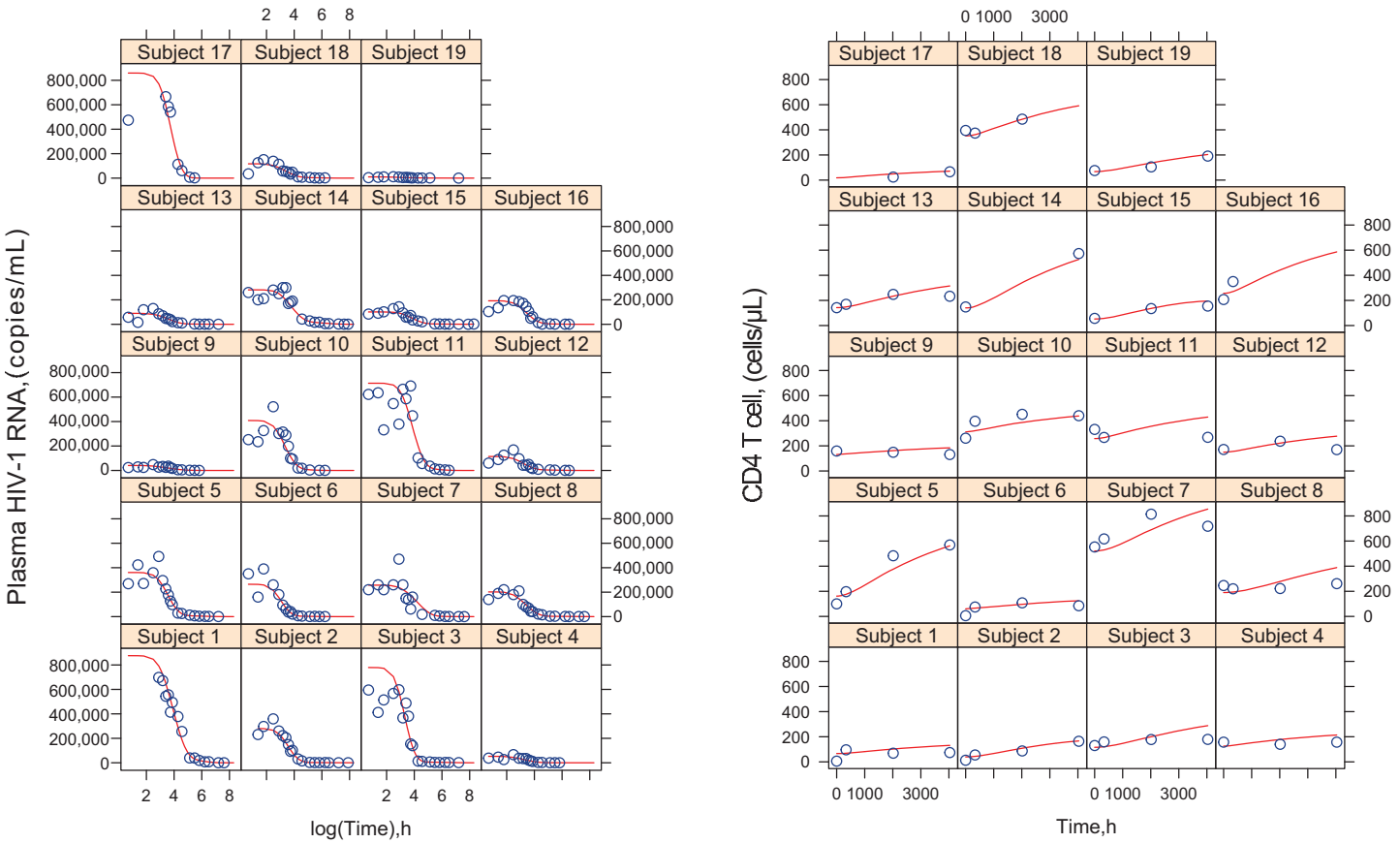
Supplementary Fig.2. Population prediction goodness of fit plots for the combined total lopinavir/ritonavir (LPV_t/RTV) model (a) and the free lopinavir (LPV_f) model (b). Symbols are observed data. Red dashed lines are the linear regression fit. Solid lines are the lines of unity.



Supplementary Fig.3. Goodness of fit plots for alpha-1-acid glycoprotein - free lopinavir (AAG-LPV$_f$) model (individual - (a) ; population - (b)). Symbols are the observed data. Red dashed lines are the linear regression. Solid black lines are the lines of unity.



Supplementary Fig.4. Simulated fu (fraction of unbound lopinavir) as a function of AAG (alpha-1-acid glycoprotein) for each individual. Red line is the population prediction. The blue lines are individual predictions over the AAG range measured in each subject.



Supplementary Fig.5. Individual plots of plasma HIV-1 RNA (left panel) and CD4 T cell count (right panel). Symbols are observed data. Solid red lines are the individual predictions.