# Quantifying the impact of nevirapine-based prophylaxis strategies to prevent mother-to-child transmission of HIV-1: A combined pharmacokinetic, pharmaco- and viral dynamic analysis to predict clinical outcomes

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**Running title:** Impact of NVP prophylaxis on vertical transmission of HIV-1

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## Abstract

Nevirapine single dose (sd-NVP) and extended NVP prophylaxis are widely used in resource-constrained settings to prevent vertical HIV-1 transmission.

We assessed the pharmacokinetics of sd-NVP in 62 HIV-1 positive Ugandan pregnant woman and their newborns, taking sd-NVP prophylaxis to prevent mother-to-child HIV-1 transmission. Based on this data we developed a mathematical model system to quantify the impact of different sd-NVP regimens at delivery and extended infant NVP prophylaxis (6, 14, 21, 26, 52, 78, 102 weeks) on the 2 year risk of HIV-1 transmission and development of drug resistance in mothers and their breast-fed infants.

Pharmacokinetic parameter estimates and model-predicted HIV-1 transmission rates were very consistent with other studies. Predicted 2 year HIV-1 transmission risks were 37.5% without prophylaxis, 31.7% for newborn sd-NVP, 20.5% for maternal sd-NVP and 22.3% for maternal/newborn sd-NVP. Maternal sd-NVP reduced newborn infection predominately by trans-placental exchange, providing protective NVP concentrations to the newborn at delivery, than by maternal viral load reduction. Drug resistance was frequently selected in HIV-1 positive mothers after maternal sd-NVP.

Extended newborn NVP prophylaxis further decreased HIV-1 transmission risks but indicated an overall decline in cost-effectiveness for increasing durations of newborn prophylaxis. Additionally, the total number of newborn infections with resistant virus was not increased by extended newborn NVP prophylaxis.

The developed mathematical modeling framework successfully predicted the risk of HIV-1 transmission and resistance development and can be adapted to other drugs/drug combinations to *a priori* assess their potential in reducing vertical HIV-1 transmission and resistance spread.

## Introduction

HIV-1 infection remains a serious health care problem worldwide. In 2009, approximately 370,000 children became infected with HIV-1 (54). Mother-to-child transmission rates of HIV-1 in untreated breastfeeding populations in resource-limited settings ranged from 25% to 48%, accounting for the vast majority of pediatric AIDS (13). Vertical transmission of HIV-1 may occur during pregnancy (5%-10%), during birth (10%-20%), and via breastfeeding (10%-20%) (13).

Intrapartum and newborn single dose nevirapine (NVP) significantly reduce transmission of HIV-1 from the mother to the child (24) and are essential components of HIV-1 prevention strategies in many resource-constrained settings (58-59). However, the exact mechanism of HIV-1 prevention by NVP during intrapartum transmission remains unknown. Furthermore, owing to its long half-life, NVP frequently selects drug resistant viral strains in HIV-infected mothers (18, 23), which can compromise the efficacy of follow-up maternal and newborn antiretroviral treatment (ART) (9, 26, 30, 41).

In many resource-constrained settings, breastfeeding is critical for infant survival (60). Reduction of HIV-1 transmission by short-course antiviral prophylaxis is frequently impaired by subsequent infection during the breastfeeding period (25, 44). Extended newborn NVP prophylaxis has shown to reduce HIV-1 transmission via breastfeeding (3, 7, 28, 40) and current WHO guidelines for the prevention of mother-to-child transmission recommend the use of NVP throughout the entire breastfeeding period (59), which can be as long as 2 years. Clinical trial data on extended prophylactic newborn NVP are currently only available for durations of 6 weeks and 6 months (3, 11, 40). However, to evaluate the effectiveness of extended newborn NVP, a quantification of the HIV-1

transmission risks after different durations of extended NVP prophylaxis in newborns is required.

In the present study, NVP plasma data of 62 Ugandan mothers and newborns who took NVP single dose prophylaxis were simultaneously analyzed in a single integrated population pharmacokinetic model for both populations; the present work extends a previously published pharmacokinetic study, which analyzed woman and newborn NVP concentrations separately (29). The aim of this work was to combine pharmacokinetic and pharmacodynamic analysis by developing a single mathematical modeling framework. The framework should be used to predict the impact of various single and extended NVP-based prophylaxis regimens on the cumulative risk of vertical HIV-1 transmission and on selection of NVP-resistant virus.

## Methods

### *Patient Characteristics and Study Design*

During a program for the prevention of mother-to-child transmission of HIV-1 in western Uganda, 62 HIV-1 positive pregnant women and their newborns were enrolled for pharmacokinetic (PK) analysis after they had given informed consent and delivered at Fort Portal District Hospital (Fort Portal, Kabarole District, western Uganda). Pregnant women received a single 200 mg NVP tablet at onset of labor and newborns received 2 mg/kg NVP syrup orally within 72 h after birth (29). Ethical approval was obtained from the Uganda National Council for Science and Technology.

Median age and body weight of the pregnant women were 26 years and 56 kg [range: 16-39 yrs; 42-84 kg], respectively. Newborns had a median body weight of 3.1 kg [range: 2.0-3.9 kg]. The median time period passed between NVP intake of pregnant women

and birth was 5.1 h [range: 0.3-24.8 h]. The median time interval between birth and NVP administration to the newborn was 0.9 h [range: 0.1-40.6 h] and 8.5 h [range: 1.3-46 h] from NVP intake of the pregnant women until the NVP administration to the newborns (29).

For PK analysis, a total of 113 plasma samples from mothers and newborns were collected over three time periods, i.e. delivery, week 1 and week 2. The geometric mean NVP concentration-time profile was previously presented (29). Here we illustrate the dispersion of the individual plasma concentrations over time for the same population (Figure 1A). NVP concentrations were determined by a validated LC/tandem-mass-spectrometry method according to the criteria set by the FDA (FDA-Guideline, (29, 49)).

### *Pharmacokinetic Analysis*

Based on the previously established pharmacokinetic models and data (29), an integrated population pharmacokinetic model was developed to simultaneously analyze NVP plasma data of mothers and newborns.

For population PK data analysis the nonlinear mixed effects modeling approach implemented in the software program NONMEM$^{TM}$ (Icon development solutions, version VI, 1$^{st}$ update, 2006) was chosen due to sparse data situation. The pharmacokinetic model was parameterized in terms of clearance(s) (CL) and volumes(s) of distribution (V) using the PREDPP subroutines (FOCE with interaction, ADVAN6 TOL5) supplied in NONMEM$^{TM}$. The model building process was guided by changes in the objective function value of nested models provided by NONMEM$^{TM}$, by precision of the PK parameter estimates (relative standard errors, RSE) and by basic goodness of fit (GOF) plots. Model-based simulations for visual predictive checks (VPC) were performed by

NONMEM™ (n=1000 simulations) and the statistics of 5th, median and 95th percentile were calculated using R, version 2.9.

The schematic structure of the final PK model for maternal and newborn data is presented in Figure 1 B. Due to the difference in drug transport processes, solid lines represent those occurring continuously over the whole time and dashed lines only those before delivery except K34 which occurs only after delivery. The NVP absorption rate constants for pregnant women (KA) and newborns (K34) were fixed to 1.34 $h^{-1}$, respectively, due to no available data during the absorption process. Prior published values of absorption rates varied between 0.013 $h^{-1}$ and 3.81 $h^{-1}$ (median: 1.3 $h^{-1}$) (4, 12, 17, 27).

Maternal plasma concentrations were associated to the central compartment with the volume of distribution V2 and fetal/newborn concentrations to the peripheral compartment with the volume of distribution V4. After delivery, but before the NVP administration to newborns, significant NVP concentrations were detected in the plasma of newborns. Considering the placenta-permeability of NVP (37, 39), we implemented a trans-placental exchange of NVP between pregnant woman and fetus (PCL) before the time of delivery (dashed lines in Figure 1 B). The ratio of NVP plasma concentrations between fetus and pregnant women was described by a partition coefficient, PCM. NVP elimination from the central compartment (related to the plasma of mothers) and the peripheral compartment (related to the plasma concentration in the fetus/newborn) were described by the PK parameters CL1 and CL2, respectively.

For the predictive performance of the final PK model a visual predictive check (VPC) is depicted in Figure 1 C-D. The dashed lines represent the 5th and 95th model-simulated percentiles and solid lines represent the model-simulated median of NVP concentrations.

The VPC of mother plasma (Figure 1 C) and newborn plasma data (Figure 1 D) revealed sufficient model predictive performance for the general trend. Overall, the model-predicted variability was sufficient for mothers and newborns and resembled the variability in the observed data.

## *HIV-1 Dynamics Model*

In order to quantify the impact of NVP prophylaxis on virus transmission, we adapted the virus dynamics model presented in (56) by discarding the longer lived cell types (representing macrophages and latently infected T-cells), as they do not impact the observed viral dynamics after short course maternal NVP. The utilized model of HIV-1 dynamics and mother-to-child transmission is depicted in Figure 2 A.

Briefly, the mathematical model of virus dynamics and mutation comprises T-cells $\mathrm{T}$, free virus $\mathrm{V}$, early infected T-cells $\mathrm{T}_1$ (after reverse transcription but before viral genomic integration) and productively infected T-cells $\mathrm{T}_2$ (after viral genomic integration). The average rate of change of the different T-cell species and the number of viruses is given by the following system of ordinary differential equations:

$$\frac{\mathrm{d}}{\mathrm{d}t}\mathrm{T} = \lambda(t) - \mathrm{T}\cdot\delta_{\mathrm{T}} - \sum_i \beta(i,t)\cdot\mathrm{V}(i)\cdot\mathrm{T} + \sum_i \delta_{\mathrm{PIC}}\cdot\mathrm{T}_1(i) \quad (1)$$

$$\frac{\mathrm{d}}{\mathrm{d}t}\mathrm{T}_1(i) = \sum_j p_{j\to i}\cdot\beta(j,t)\cdot\mathrm{V}(j)\cdot\mathrm{T} - \mathrm{T}_1(i)\cdot(\delta_{\mathrm{T1}} + k_{\mathrm{T}} + \delta_{\mathrm{PIC}}) \quad (2)$$

$$\frac{\mathrm{d}}{\mathrm{d}t}\mathrm{T}_2(i) = k_{\mathrm{T}}\cdot\mathrm{T}_1(i) - \mathrm{T}_2(i)\cdot\delta_{\mathrm{T2}} \quad (3)$$

$$\frac{\mathrm{d}}{\mathrm{d}t}\mathrm{V}(i) = \mathrm{N}\cdot\mathrm{T}_2(i) - \mathrm{V}\cdot\mathrm{CL}_{\mathrm{V}}(t) \quad (4)$$

In summary, free virus $V$ of strain $i$ can infect T-cells with infection rate constant $\beta$, which encompasses all steps from target cell binding, fusion, to reverse transcription, resulting in early infected cells $T_1$, which turn into productively infected cells $T_2$ by provirus translocation into the nucleus and integration with rate $k_T$. $T_2$ produce new virus $V$ with the rate constant $N$ (on average 1000 virions/day/cell (47)). Native, early infected and productively infected T-cells are degraded with rate constants $\delta_T, \delta_{T_1}$ and $\delta_{T_2}$, respectively. In early infected cells $T_1$ (prior to proviral integration) essential components of the pre-integration complex can be degraded with rate constant $\delta_{PIC}$, returning the cell to an uninfected stage $T$ (56). Native T-cells are produced with rate constant $\lambda(t)$ and free virus $V$ is cleared with rate $CL_V(t)$ by the immune system. We assumed that the rate constants $\lambda(t)$ and $CL_V(t)$ are constant for the HIV-infected mothers, whereas they were considered time-dependent for the newborn, due to immune system development and growth. A derivation of the parameters $\lambda(t)$ (newborn) and $CL_V(t)$ (newborn) is provided in the supplementary text S1. All model parameters are displayed in Table 1.

Viral Mutation:

HIV can aquire drug resistance by mutation during the process of reverse transcription (comprised in parameter $\beta$ in the model). The probability that a specific mutation occurs during the process of reverse transcription has been quantified *ex vivo* to be $\mu = 2.16 \cdot 10^{-5}$ (per base and reverse transcription process) (31). A single genomic point mutation inducing a change at the protein level, e.g. position Y181 -> 181C (Y181C) will therefore occur with probability $\mu$ during reverse transcription, whereas with probability

$(1-\mu)$ this specific mutation will not occur. In our model, 2 specific sites *L* are regarded to undergo mutation; resulting in the K103N and the Y181C change in the reverse transcriptase enzyme, respectively. As an example, the probability that the wild type virus $wt$ will neither be mutated at one of the 2 sites is $p_{wt\to wt} = (1-\mu)^2$. The probabilities that precicely one mutation occurs is given by $p_{wt\to Y181C} = (1-\mu)\cdot\mu$ and the probability of two specific mutations by $p_{wt\to K103N/Y181C} = \mu^2$. More generally, the probability that a certain transition by mutation from some strain $j$ to some strain $i$ occurs during reverse transcription $p_{j\to i}$, is given by:

$$p_{j\to i} = \mu^{h(i,j)}\cdot(1-\mu)^{L-h(i,j)}, \tag{5}$$

where $h(i,j)$ denotes the hamming distance (the number of differences) between strain $j$ and strain $i$. All mutation probabilities for the utilized model are depicted in Figure 2 B.

Coupling of Viral Dynamics with NVP Pharmacokinetics:

The efficacy of the non-nucleoside reverse transcriptase inhibitor NVP $(1-\eta(i,t))$ at time $t$ against strain $i$ was implemented using the standard $\mathrm{E}_{\max}$-model:

$$(1-\eta(i,t)) = \frac{1}{1+\frac{C(t)}{\mathrm{IC}_{50}(i)}} \tag{6}$$

where $C(t)$ denotes the NVP concentration at time $t$ (derived during PK analysis, see above) and $\mathrm{IC}_{50}(i)$ denotes the strain-specific fifty percent inhibitory concentration (see Figure 2 C). The strain specific infection rate constant under treatment was given by $\beta(i,t) = (1-\eta(i,t))\cdot(1-s(i))\cdot\beta(wt,\phi)\cdot\mathrm{SF(t)}$, where $\beta(wt,\phi)$ denotes the infection rate constant of the wild type $wt$ in the absence of drug $\phi$ (given in Table 1) and $s(i)$,

denotes the fitness loss (e.g., loss in the activity of reverse transcriptase) relative to the wild type (shown in Figure 2 C). The scaling factor $\mathrm{SF(t)}$ corrects the infection rate $\beta$ for the differences in target cell concentration between mother (reference target cell concentration) and uninfected newborn. $\mathrm{SF(t)}$ was considered to be time-dependent for newborns due to immune system development and growth (see Equation S3 and Figure S1 of the supplementary material), whereas it was set to the value of 1 for HIV-1 infected mothers.

## *Deterministic –Stochastic Hybrid Simulation*

The kinetics of biological systems, in which all reactions occur quasi-continuously over time or involve large numbers of reactants are well approximated by continuous-determistic simulations (by numerical solution of the systems' ordinary differential equations). However, the exact kinetics of biological systems which involve rare reaction events with small numbers of reactants are intrinsically stochastic and are therefore only poorly approximated by continuous-determistic simulation (62). In our modelling framework, the process of HIV-1 transmission denotes such an event in which the outcome is intrinsically stochastic: Either the transmitted virus becomes entirely cleared by the immune system before establishing stable infection ($V = 0$), or it suceeds in establishing infection ($V$ approaches its steady state).

In order to fully regard the intrinsic stochasticity of rare events in the utilized model (such as viral challenges) and to allow efficient simulation of quasi-continuous kinetics, we chose the deterministic-stochastic hybrid simulation approach presented in (1).

## *Prediction of HIV-1 Transmission after Intrapartum- and Extended NVP Prophylaxis*

Model simulations were performed starting with the time of the first maternal dose (if no dose was given, with the time of birth) and continued until 2 years postpartum. The number of viruses coming into contact with the newborn during delivery and breastfeeding was modeled as a function of the maternal viral load at the particular time of the respective viral challenge. The intrapartum virus transmission was modeled in terms of a single viral challenge at the time of delivery, while virus transmission via breastfeeding was modeled in terms of repeated viral challenges during the time after delivery until 2 years postpartum. The probability of a viral challenge during breastfeeding was assumed to decrease over time (see Figure S2, supplementary material). Child growth and immune system development were considered simultaneously to the model simulation (see supplementary text S1 and Figure S1, supplementary material). If stable infection of the newborns occurred (defined as total number of viruses $\geq 1 \cdot 10^6$ in the newborn) the respective simulation was stopped and the time between birth and child infection was recorded for subsequent evaluation. The cumulative infection risk 2 years postpartum was assessed by Kaplan-Meier estimates and an intrauterine transmission probability of 5% (13) was added. All model predictions are based on 1000 hybrid deterministic-stochastic simulations to ensure statistic confidence in the results.

We considered four scenarios for sd-NVP: (A: no prophylaxis, B: single postpartum newborn 2 mg/kg NVP dose, C: single intrapartum maternal 200 mg NVP dose and D: intrapartum maternal 200 mg NVP dose plus postpartum newborn 2 mg/kg NVP dose). We took into account the patient characteristics from the Ugandan program for the

prevention of mother-to-child transmission discussed above, in particular the individual time intervals between maternal NVP administration and birth; median 5.1 h [range: 0.3-24.8 h] and the time intervals between birth and newborn NVP administration; median 0.9 h [range: 0.1-40.6 h].

For the *extended* newborn NVP prophylaxis, we first simulated HIV-1 dynamics with maternal intrapartum NVP plus one postpartum newborn NVP dose, as described above, until day 1 after birth, after which we simulated HIV-1 dynamics until 2 years postpartum, following either 6 weeks (SWEN-study (3, 40)), 14-, 21 weeks, 6 months (HPTN 046-study (11)), 52-, 78- or 104 weeks of daily oral 2 mg/kg NVP administration, taking into account the pharmacokinetic characteristics of the population in the program for the prevention of mother-to-child transmission.

## Results

### *Pharmacokinetics of NVP in Pregnant Women/Mothers and Their Newborns*

The estimated PK parameters (using the model in Figure 1 B) are presented in Table 2. Mother and newborn data were best described by combined 1-compartment models with first-order absorption and elimination processes. Since the bioavailability of the oral dose was unknown, the estimated PK parameters have to be reported as relative parameters. The relative volume of distribution of mother data, V2/F was estimated to be 90.9 L and the relative NVP clearance to be 1.22 L/h. Inter-individual variabilities (IIV) were implemented for all structural parameters relating to mother data and estimated to be moderate (34% and 33% coefficient of variation (CV) for V2/F and CL1/F, respectively) but high for KA (160% CV). The placenta clearance PCL/F was estimated to be 111 L/h

suggesting a rapid placental transfer. The partition coefficient between NVP concentrations of fetus and pregnant women (PCM) was quantified to be 1.38. The large volume of distribution and low elimination capacity resulted in a long half-life of 52 h for mothers. The relative volume of distribution V4/F for newborns was estimated to be 20.0 L and the relative clearance CL2/F to be 0.21 L/h. The half-life of NVP in newborns was 66 h.

The residual variability was best described using separate proportional error models for maternal and newborn data, respectively. The proportional error was moderate (27% CV) for mother and higher (49% CV) for newborn data. The precision of the estimated PK parameters was sufficient with RSE < 20.5% for fixed-effects and RSE < 33% for random-effects parameters. The goodness of the final PK model was demonstrated by GOF plots for observed versus model-predicted NVP concentrations. Overall data spread around the line of identity suggesting adequate goodness of the PK model (see supplementary Figure S3).

## *HIV-1 Transmission Risk under various NVP Single Dose Prophylaxis Scenarios*

During the program for prevention of mother-to-child transmission in Uganda (29), NVP was administered once to pregnant women during labor and once to newborns shortly after delivery, with the aim of lowering the transmission probability of HIV-1 from mother-to-child. The results and model-predicted HIV-1 transmission probabilities under the four sd-NVP prophylaxis scenarios are illustrated in Figure 3 (A: no NVP prophylaxis, B: single postpartum newborn NVP dose, C: single intrapartum maternal NVP dose and D: intrapartum maternal NVP dose plus postpartum newborn NVP dose). The model-

predicted transmission risks agreed very well with published data from various trials (3, 20, 28, 36, 40, 50-51, 61). Without prophylaxis, the estimated HIV-1 transmission probability after 2 years was 37.5 ± 2.9% (Figure 3 A). A single postpartum newborn dose reduced the transmission probability to 31.7 ± 2.7% (Figure 3 B) whereas a single intrapartum maternal dose lowered the transmission probability substantially to 20.5 ± 2.3% (Figure 3 C). The combination of maternal and newborn doses reduced the transmission probability to 22.3 ± 2.4% (Figure 3 D), which is insignificantly different from a single maternal dose alone. The intrapartum infection risk (typically assessed 2 weeks after birth) was 17.7 ± 2.4%, 14 ± 2.1%, 2.3 ± 0.9% and 2.4 ± 0.9% for the four investigated regimens. From the shape of the curves in Figure 3 A-D it can also be seen that the subsequent risk of HIV-1 transmission (mainly through breastfeeding) is highest during the first 200 days after birth.

## *Mechanism of Prevention of Intrapartum HIV-1 Transmission by Maternal NVP Prophylaxis*

Our data indicate that maternal NVP single dose alone decreases the transmission risk of HIV-1 substantially compared to newborn NVP dose alone (compare Figure 3B with 3C). Hence, we elucidated the mechanisms by which the maternal NVP dose lowers HIV-1 transmission probabilities.

The dynamics of viral load decay in the HIV-1 infected mother after the maternal NVP dose are shown in Figure 4 A. The viral load declined by less than a factor of two during the first 30 h after single dose NVP. However, the child was born within a range of 0.3-24.8 h, median: 5.1 h (29) (dashed horizontal bar and the open circle in Figure 4 A),

317 indicating that the maternal dose had little or no effect on the number of virions that
318 come in contact with the newborn during intrapartum virus challenge.
319 In Figure 4 B the concentrations of NVP in a representative newborn from the PK
320 investigation are depicted at the time of delivery (intrapartum challenge). Since NVP is
321 known to cross the placenta (37, 39) and this process was quantified by us (PCL, PCM,
322 see above), a fraction of the maternal NVP concentration was present in the newborn at
323 the time of delivery, where it is able to prevent the HI-virus from infecting cells (Figure
324 4B) by lowering the infection rate $\beta$ (see *Methods* section).

325 ## *Predictors for Selection and Persistence of NVP-resistant HIV-1 Strains in*
326 ## *Mothers after NVP Single Dose Administration*

327 Previous studies reported that a single dose of NVP can already select drug resistant
328 viral strains in the HIV-1 infected mothers (18, 23), compromising subsequent maternal
329 treatment success (9, 26, 30) and potentially promoting the transmission of NVP
330 resistant strains to the child during subsequent breastfeeding. We wanted to assess
331 predictors for the selection of drug resistant strains in HIV-1 infected mothers, which
332 might subsequently lead to the transmission of resistant virus to the breastfed child. Our
333 model predictions revealed a strong correlation between the individual half-life of NVP in
334 mothers and the duration in which NVP-resistant strains dominated the viral population
335 in the HIV-1 infected mothers after a single intrapartum maternal NVP dose, see Figure
336 5 A (spearman's rank correlation coefficient $r_S^2 = 0.98$). The model-predicted dynamics of
337 resistance appearance and fading for some representative mothers are shown in Figure
338 5 B-E. Our model predictions indicate that depending on the individual pharmacokinetics
339 of NVP, NVP-resistant strains become selected and might subsequently dominate the

virus population until NVP will be eliminated and resistant virus will be outgrown by the wild type (see Figure 5 B-E) once again. This has important implications on the probability that resistance is transmitted from mother to child and on the success of subsequent extended newborn NVP prophylaxis.

We derived the following equation to clarify the relation between individual NVP concentrations $C$ and resistance selection (derivation is given in supplementary text S2, supplementary material):

$$\textit{resistance selection if :}$$

$$C > \frac{\mathrm{IC}_{50}(\mathrm{wt}) \cdot s(\mathrm{res})}{\left(1\text{-}s(\mathrm{res})\right) - \frac{1}{K_{IC50}}}, \qquad (7)$$

where $\mathrm{IC}_{50}(\mathrm{wt})$, $s(\mathrm{res})$ and $K_{IC50}$ are the fifty percent inhibitory NVP concentration of the wild type, the selective disadvantage of the drug resistant viral strain and the fold increase in the fifty percent inhibitory NVP concentration, respectively. For mutant K103N, Y181C and the double mutant (K103N/Y181C), the minimum NVP concentrations which favor their selection are 3.36 ng/mL, 15.5 ng/mL and 25.5 ng/mL, respectively, based on the phenotypic parameters used in this work ($\mathrm{IC}_{50}(\mathrm{wt})$, $s(\mathrm{res})$ and $K_{IC50}$).

This indicates, that single-point mutations are already selected at concentrations below the $\mathrm{IC}_{50}$ value of the wild type (23 ng/mL (35)), which can persist in the plasma of the mother for several weeks after sd-NVP, depending on the individual pharmacokinetic NVP concentration-time profile. More importantly, if transmission of HIV-1 from mother-to-child occurs during the particular time frame when the resistant virus dominates, it will likely involve resistant virus and therefore lead to resistance spread.

## *Extended NVP Prophylaxis Strategies to Prevent HIV-1 Transmission via Breastfeeding*

We explored the impact of extended newborn NVP prophylaxis on HIV-1 transmission risk in order to evaluate whether these may, similar to pre-exposure viral prophylaxis, decrease the probability that viral challenges lead to infection in breastfed infants. In addition to the maternal dose, we analyzed the impact of 6 weeks (SWEN-study, [17-18]), 14-, 21 weeks, 6 month (HPTN 046-study, [19]), 52-, 78- or 104 weeks of extended newborn NVP 2 mg/kg dosing, on the transmission risk of HIV-1. The predictions for 6 weeks and 6 months extended newborn NVP are displayed in Figure 6 A and Figure 6 B, respectively, together with clinical data from the SWEN-study (3, 40) (6 weeks extended NVP) and the HPTN 046 trial (11) (6 month extended NVP). The agreement between predicted- and observed transmission probabilities was very good. The cumulative HIV-1 transmission risk 2 years postpartum, in the case of 6-, 14-, 21 weeks, 6 month, 52-, 78- or 104 weeks of extended NVP dosing were 18.5% ± 2.1%, 16.1% ± 1.9%, 14.9% ± 1.9%, 14.3% ± 1.8%, 12.5% ± 1.6%, 8.6% ± 1.2% and 7.0% ± 0.9%, respectively (see Figure 6 C): All extended NVP regimen significantly reduced HIV-1 transmission during 2 years postpartum, compared to intrapartum single dose maternal/newborn NVP (cross-tab $\chi^2$ test, $p < 0.05$, respectively). Notably, the 52- and 104 weeks regimens reduced the risk of transmission by further 50% and 70% compared to intrapartum maternal/newborn NVP dose alone. The reduction of HIV-1 transmission per week extended NVP was 0.63%, 0.44%, 0.35%, 0.31%, 0.19%, 0.18% and 0.15% for the 6-, 14-, 21 weeks, 6 months, 52-, 78- or 104 weeks regimens, respectively, indicating a decline in effectiveness of extended NVP regimens.

## *Probability of Transmitting Resistant Virus during Extended NVP Prophylaxis*

The proportion of infections with NVP-resistant virus among the newborns that became infected $P(\text{res.}|\text{inf.})_{0-2y}$ for the entire evaluation period (2 years postpartum) was 19.12%, 15.18%, 24%, 20.21%, 32.89%, 51.35% and 100%, respectively, in the 6-, 14-, 21 weeks, 6 months, 52-, 78- or 104 weeks extended NVP regimens (it was 18.1% in the single dose intrapartum maternal- plus postpartum newborn regimen), neglecting intrauterine infection. The proportion of infections with NVP-resistant virus among the infected newborns during weeks 0-6 and > 6 weeks postpartum were $P(\text{res.}|\text{inf.})_{0-6w} = 100\%$ and $P(\text{res.}|\text{inf.})_{>6w} = 14\%$, respectively in the 6 weeks extended NVP regimen, which is in good agreement with published data from the SWEN study ($P(\text{res.}|\text{inf.})_{0-6w} = 92\%$ and $P(\text{res.}|\text{inf.})_{>6w} = 15\%$, respectively (38)). For a single maternal and newborn NVP dose, the conditional probabilities were $P(\text{res.}|\text{inf.})_{0-6w} = 32\%$ and $P(\text{res.}|\text{inf.})_{>6w} = 13\%$, which is also in good agreement with published data ($P(\text{res.}|\text{inf.})_{0-6w} = 38\%$ and $P(\text{res.}|\text{inf.})_{>6w} = 15\%$, respectively (38)). The total number of infant infected with resistant virus during the breastfeeding period $P(\text{res.}|\text{inf.}) \cdot P(\text{inf.})$ was not significantly different in any extended newborn NVP regimen (2.58%, 1.68%, 2.38%, 1.88%, 2.47%, 1.85% and 2.00%, respectively in the 6-, 14-, 21 weeks, 6 month, 52-, 78- or 104 weeks regimens, neglecting intrauterine infection) and was slightly lower than in the single dose intrapartum maternal- plus postpartum newborn regimen (3.18%). Our results indicated that extended NVP only allows infection with resistant virus during the duration of its administration. Our predictions also indicated that all infections with

406 resistant virus occurred before 200 days postpartum in agreement with resistance
407 domination in the breastfeeding mothers (shown in Figure 5).

## 408 Discussion

409 Short-course NVP prophylaxis is still widely used in resource-constrained settings to
410 prevent mother-to-child transmission of HIV-1. Since pregnant women and their
411 newborns represent particular subpopulations, plasma of mothers and newborns were
412 sampled for PK investigation during a Ugandan program for the prevention of mother-to-
413 child transmission, which comprised sd-NVP to pregnant women and newborns each.
414 For PK analysis of the NVP data, a combined population PK model was developed and
415 subsequently incorporated into pharmacodynamic (PD) investigations.
416 We found, in agreement with similar studies (4, 12, 14, 29), that a one-compartment
417 model with first-order absorption and elimination processes was sufficient to describe
418 the pharmacokinetics of NVP in pregnant women/mothers and newborns. Based on our
419 previously published separated PK models for pregnant women/mothers and newborns
420 (29), we developed a combined PK model in the present work that simultaneously
421 analyzed the NVP concentrations of pregnant women/mothers and newborns. Before
422 delivery, the PK model constituted the structure of a two-compartment model, where the
423 central- and peripheral compartments were linked to the pregnant women/mothers and
424 the fetus, respectively. Utilizing this model structure, we were able to estimate the
425 plasma/placenta transfer of NVP as newborns presented measureable NVP plasma
426 concentrations before receiving their own NVP dose. After delivery the combined PK
427 model for pregnant women/mothers and fetus was separated into two one-compartment
428 models for mothers and newborns, respectively. All PK parameters were precisely

429 estimated as shown by small relative standard errors. The estimated relative volume of
430 distribution in mothers was very high (V2/F = 91 L) and in excellent agreement with
431 previously published values (range: 77-106 L) (4, 14, 27, 39). Maternal NVP elimination
432 capacity was low (CL1/F = 1.22 L/h) and within the range of previously published values
433 (1.23-1.42 L/h) (4, 12, 39). The calculated half-life of NVP in mothers was 52 h, being
434 also within the range of previously published values 43-61 h (4, 12, 39). The half-life in
435 newborns (66 h) was slightly longer than the published value of 47 h (39), but
436 considerably shorter than the value of 110 h, observed in (4). However, in the previous
437 study (4), newborn plasma was only sampled over a very short interval (0-50 h),
438 whereas data in our investigation was sampled over a considerably longer period of time
439 (0-420 h), allowing to more accurately determine the elimination of NVP in newborns.
440 The evaluation of the final combined PK model by GOF plots and VPC demonstrated
441 appropriateness and sufficient predictive performance. Hence, the PK model could be
442 used as an input for further PD investigations. In order to simultaneously analyze the
443 impact of NVP pharmacokinetics on HIV-1 acquisition in the newborn, we developed a
444 PK-coupled stochastic HIV-1 dynamics model. Models for HIV-1 dynamics in
445 asymptomatically infected individuals are rather established (reviewed in (42)). Few *in*
446 *silico* studies have linked viral dynamics to pharmacokinetics (16, 22, 46), modeled the
447 impact of pharmacokinetics on the emergence of drug resistance (55), or considered the
448 dynamics of HIV-1 infection (52-53). However, all these aspects, which concurrently
449 occur *in vivo*, have, to the authors´ knowledge, never been addressed simultaneously by
450 mathematical modeling. In this study, we combined all these aspects in a single model.
451 Furthermore, our model considers many aspects of child growth, immune system
452 development and the characteristics of viral challenge during delivery and breastfeeding,

453 which have been validated with external data (see Figure S1, supplementary material).
454 Although no parameter adjustments for the HIV-1 dynamics model have been performed,
455 model-predicted HIV-1 transmission rates under various NVP-based treatment scenarios
456 were in excellent agreement with data from nine independent studies (see Figure 3 and
457 Figure 6), confirming the validity of the chosen approach.
458 Throughout this work, a reduced virus dynamics model was used, which is suited to
459 accurately predict viral load decay in HIV-1 infected individuals following single dose
460 administration of NVP and to predict the subsequent risk of child infection. In the case of
461 multiple dose maternal drug administration, we recommend to use a model that can
462 capture all phases of viral load decline, e.g. (56). In the present analysis we did not
463 focus on viral load dynamics after the infection of the child, but rather focused on the
464 infection risk (respective simulations were stopped, if newborn infection occurred). For
465 accurately analyzing viral load dynamics in infected children, we also recommend to use
466 more elaborated viral dynamics models, e.g. (56).
467 Our predictions indicated a significant impact of maternal NVP administration on the
468 reduction of HIV-1 transmission to the newborn (see Figure 3 C). An analysis of the HIV-
469 1 dynamics in the pregnant women between the period of NVP administration and
470 delivery indicated that the effect of maternal NVP on intrapartum transmission was not
471 due to a reduction in the number of virus particles potentially coming into contact with
472 the newborn during delivery, since viral load decayed only by less than a factor of two
473 during the first 30 h after NVP administration (see Figure 4A). This model-derived result
474 is confirmed by clinically observed delays in virus load decline for NVP monotherapy
475 (24-48 h (21)). Likewise, delays in the onset of viral decay have been observed in the
476 case of ritonavir monotherapy (~30 h (43)) and under highly active antiretroviral therapy

(HAART) (~18 h (32)). We therefore conclude that a maternal dose, administered at the onset of labor, may hardly have an impact of the number of viruses that come into contact with the newborn during delivery. Instead, the PK analysis coupled to the virus dynamics model, revealed that the main effect of the maternal dose is to provide potentially protective NVP concentrations via *trans-placenta* transport to the newborn at the moment of virus contact during delivery (see Figure 4 B), subsequently preventing HIV-1 infection. These finding were confirmed by rapid NVP exchange through the placenta (as indicated by the exchange parameters PCL, PCM in Table 2 and the almost identical time points of maximum concentrations ($t_{\max}$) values in maternal and newborn plasma and cord blood (4)). This mechanism of HIV-1 transmission prevention provided by the maternal single dosing is highly similar to a pre-exposure prophylaxis, which has recently demonstrated high potential in reducing HIV-1 transmission in the context of sexual HIV-1 transmission (19). This particular mechanism of HIV-1 prevention by maternal sd-NVP has important implications for the timing of the maternal dose: Since trans-placental exchange is rapid (4), the newborn's NVP concentrations during delivery would offer maximal protective effect at $t_{\max}(\text{mother})$ of 3.5 h [range: 3.0-4.1 h] (calculated from individual PK parameter estimates). While NVP is absorbed rapidly (10), HIV-1 prevention by the maternal dose is likely suboptimal before $t_{\max}(\text{mother})$. The protective effect however lasts for relatively long periods of time, since NVP is slowly eliminated (4, 10, 29) (see also Table 2). This indicates that the maternal NVP administration at the onset of labor might be most effective, if feasible.

A single dose of NVP can select drug resistant viral strains in the HIV-infected mothers (18, 23) (see Figure 5) and lead to transmission of NVP resistant strains to the child (e.g. via breastfeeding). Pooled estimates showed that 36% (19–76%) of women have

501 detectable NVP resistance mutations 6–8 weeks after exposure to a single dose of NVP
502 (2). Our model slightly overestimated resistance development in the mothers after
503 receiving a single intrapartum NVP dose (38% and 63% at week 8 if the detection limit
504 for resistance was 50% and 20% respectively). This overestimation can be partially
505 explained by the use of a simplified model of resistance development in our
506 computational study, which ignores the genetic background on which resistance
507 develops; e.g. if resistance develops on some viral strain, which is particularly unfit, then
508 the resistance is less likely to be selected, see parameter $s(\mathrm{res})$ in Equation (7). Instead,
509 in order to reduce the complexity of our mathematical model (and to reduce the
510 computational cost), we assumed that all susceptible viral strains were as fit as the
511 wild type and therefore all viral strains that develop a particular mutation (K103N, Y181C
512 and K103N/Y181C) were only assigned a fitness loss that comes from the resistance
513 mutation and not from the genetic background of the founder strain. In future, more
514 realistic and computationally feasible solutions for this problem should be developed.
515 Nevertheless, our estimates of resistance transmission to the newborns/infants were in
516 good agreement with clinical data from the SWEN study (38).
517 Our model predictions suggested a correlation between the individual half-life of NVP in
518 mothers and the duration in which NVP-resistant strains dominated the viral population
519 in the HIV-1 infected mothers after a single intrapartum maternal NVP dose. Selection of
520 resistant strains could be explained by a simple mathematical formula (see Equation (7)
521 and supplementary material) and minimum concentrations for the selection of NVP-
522 resistant strains were derived. Combining the pharmacokinetic analysis of individual
523 pharmacokinetics with the model of HIV-1 dynamics and transmission, we predicted that
524 transmission of NVP-resistant strains would occur during the first 200 days after single

dose maternal NVP, in line with the time frame in which resistant strains likely dominate the viral population (Figure 5). The observed correlation of NVP half-life and resistance selection suggests that resistance selection and transmission could potentially be reduced if drugs were administered to the mothers, which exhibit a shorter half-life than NVP (e.g. zidovudine) and which can cross the placenta as effectively as NVP. Adding drugs to the maternal sd- NVP is another effective approach to reduce resistance selection in the HIV-1 infected mothers and to further lower intrapartum transmission rates (6, 8, 34), potentially by increasing the genetic barrier to resistance selection. A thorough understanding of the underlying mechanisms, however, is still lacking and mathematical models including combinations of drugs for elucidation remain to be developed in future.

Currently, two main strategies are pursued in order to reduce subsequent HIV-1 transmission via breastfeeding: (i) maternal ART or (ii) extended newborn NVP prophylaxis. Maternal ART has been shown to reduce HIV-1 transmission via breastfeeding, by lowering maternal viral load to less than 400 copies per mL (15, 48), but long-term drug treatment might not be available in resource-limited settings. Extended newborn NVP administration has been suggested to reduce the transmission risk of HIV-1 by postpartum breastfeeding and might be the regimen of choice in extremely resource-limited settings for reasons of cost-effectiveness compared to maternal ART (59). In Figure 6, we analyzed the impact of 6-, 14-, 21 weeks, 6 month, 52-, 78- or 104 weeks extended newborn NVP on the transmission risk of HIV-1. Our data agrees very well with published data from the SWEN-study (3, 40) (6 weeks extended NVP) and the HPTN 049-study (11) (6 month extended NVP). Our results indicate that a significant reduction in the HIV-1 transmission 2 years postpartum could

549 be achieved for all investigated extended NVP regimens, in comparison to single dose
550 intrapartum maternal and newborn NVP dose alone. The cost-effectiveness however
551 decreases with increasing length of extended NVP as reflected by the reduction of HIV-1
552 transmission per week of extended newborn NVP from 0.63% (6 weeks of extended
553 NVP) to 0.15% (104 weeks of NVP). This indicates that although substantial further
554 decrease of HIV-1 transmission could be achieved by extended NVP regimens, shorter
555 periods of extended NVP might be more feasible in (extremely) resource-limited settings
556 with regard to cost-effectiveness. Our estimates of resistance transmission to the
557 newborns were in good agreement with clinical data from the SWEN-study (38). Overall,
558 our results indicated an increase in the *proportion* of infections with resistant virus for
559 longer durations of extended NVP prophylaxis. However, as extended NVP
560 simultaneously minimizes the transmission probability the *total number* of newborns,
561 which become infected with resistant virus was not increased by any of the extended
562 NVP prophylaxis regimens compared to NVP single dose.
563 Summarized, we have developed a coupled *in vitro/in vivo* pharmacokinetic-
564 pharmacodynamic model to assess the effects of distinct NVP prophyalxis regimens on
565 the prevention of mother-to-child transmission of HIV-1 and resistance formation. Our
566 model shows very good predictive performance compared to data from clinical studies.
567 The model may be adapted to predict the outcome of other drug interventions and could
568 therefore be used as a supportive tool to improve HIV-1 prevention, maximize cost-
569 effectiveness and reduce risk of resistance selection when novel studies are planned.

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821

822 ## Legends

823 Figure 1: Final PK model of mother and newborn data. A: Observed NVP concentrations
824 in the plasma of HIV-1 infected pregnant women/mothers (filled diamonds) and in the
825 plasma of newborns (open triangles) sampled over three time periods: delivery, week 1
826 and week 2 after single dose of 200 mg NVP for pregnant women and 2 mg/kg NVP
827 administered to newborns (modified from (29)). B: Schematic structural model for the PK
828 of mothers and newborns. The absorption rate constant for oral dose of mothers and
829 newborns are KA and K34, respectively. V2 describes the central volume of distribution
830 for maternal data. V4 equals the volume of distribution of the peripheral compartment
831 (fetus/newborn compartment). Both compartments were linked by placenta clearance
832 (PCL) term before delivery. All dashed lines highlight time-dependent processes while
833 solid lines present continuous processes over the entire investigational period. The
834 partition coefficient fetus to pregnant women (PCM) denotes the ratio between NVP
835 concentrations in the fetus and maternal NVP concentrations before delivery and at

836 quasi steady state. NVP elimination from the central and the peripheral compartment
837 was described by CL1 and CL2, respectively. C and D: VPC of the observed NVP
838 concentrations in maternal plasma (black diamonds, C) and in newborn plasma (open
839 triangles, D) over time and $5^{th}$ and $95^{th}$ percentiles of model simulations and model-
840 simulated median (dashed- and solid lines).

841 Figure 2: Mathematical model of virus dynamics, mutation and transmission. A: Life-
842 cycle models of HIV-1 in mothers and newborns and their interconnection via
843 intrapartum- and breastfeeding challenge. Free virus can infect T-cells with infection rate
844 constant β, which encompasses all steps from target cell binding, fusion, to reverse
845 transcription. Early infected T-cells (after reverse transcription but prior to pro-virus
846 integration) become transformed into productively infected cells T2, after pro-virus
847 translocation into the nucleus and integration with rate $k_T$. Productively infected T-cells
848 T2 produce new virus V with rate N. Mutation occurs during the process of reverse
849 transcription (embodied in parameter β). NVP inhibits reverse transcription and therefore
850 affects parameter β in our model. All parameter values are listed in Table 1. Intrapartum
851 viral challenge occurs during delivery, whereas breastfeeding viral challenges occur
852 repeatedly after birth until the age of 2 years, according to the breastfeeding frequency
853 (Figure S2, supplementary material). B: Mutational graph showing the transition
854 probabilities $p_{j\to i}$ between the four virus strains (wild type *wt* and 3 mutants *K103N*,
855 *Y181C* and *K103N/Y181C*) considered here. C: Phenotypic attributes of the four
856 mutants. The extension of the bars to the right illustrates their $IC_{50}$ value, whereas the
857 left extension indicates their fitness loss. The $IC_{50}$ values were 23 ng/mL (35) (corrected
858 for protein binding (5)), 1265 ng/mL (45), 3703 ng/mL and >11500 ng/mL (45) for *wt*, the
859 *K103N*, the *Y181C* mutation and the double mutant *K103N/Y181C*, respectively. The

860 selective disadvantage *s* with respect to the wild type was 12.5%, 40% and 52.5% for
861 the *K103N*, the *Y181C* mutation and the double mutant (33).

862 Figure 3: Cumulative HIV-1 transmission risk under various NVP single dose prophylaxis
863 strategies. Solid lines denote the Kaplan-Meier estimates of the model-predicted
864 cumulative probability of infection whereas light-grey areas represent the confidence
865 range for the model predictions. A: no NVP is given (upward- and downward pointing
866 triangles denote data from (61) and (36)); B: a single postpartum NVP dose (2 mg/kg) is
867 given to the newborn within 72 h after birth (squares denote data from (51)); C: a single
868 intrapartum NVP dose (200 mg) is given to the mother at the onset of labor; D: a single
869 intrapartum NVP dose (200 mg) and a single postpartum newborn dose (2 mg/kg) were
870 administered (crosses, open circles, diamonds, filled circles and plus signs denote data
871 from (3, 20, 28, 40, 50)). In all simulations, an intrauterine transmission probability of 5%
872 (13) was assumed.

873 Figure 4: A: Viral load (thick line) during the first 30 h in the plasma of HIV-1 infected
874 pregnant women/mothers after a single intrapartum dose NVP in relation to the time of
875 delivery (open circle denotes the median time of delivery, see *Methods* section and
876 dashed horizontal bar denotes the range). B: NVP concentration in a representative
877 newborn from the PK-investigation before- during- and after birth (solid line). The black
878 square and the black circle indicate the time of birth and the time of the newborn NVP
879 single oral dose in the representative newborn, respectively.

880 Figure 5: Predicted correlation between NVP elimination and persistence of NVP
881 resistance in HIV-1 positive mothers after a single dose of NVP. A: Correlation of
882 individual NVP half-life and predicted duration in which NVP resistance dominated the

883 viral population in mothers. B-E: Examples of resistance appearance and fading in
884 distinct, representative HIV-1 positive mothers after single dose NVP administration at
885 the onset of labor. Solid line: relative wild type abundance, dashed line: relative
886 abundance of NVP resistant strains. The respective half-life of NVP in the distinct
887 representative mothers was 1.3, 2.1, 2.2 and 3.6 days for panels B-E.

888 Figure 6: HIV-1 transmission risk in the case of extended newborn NVP dosing.
889 A: Predicted transmission risk after 6 weeks extended NVP treatment (solid line) and
890 confidence range (light-grey area) together with clinical data from the SWEN-study (3,
891 40) (open circles). B: Predicted transmission risk after 6 month extended NVP treatment
892 (solid line) and confidence range (light-grey area) together with clinical data from the
893 HPTN 046-study (11) (open squares). The intrauterine transmission risk was assumed
894 to be 5% (13). C: Predicted transmission risk after 2 years, in the case of no prophylaxis,
895 a single dose maternal and newborn NVP dose, 6-, 14-, 21 weeks, 6 month, 52-, 78- or
896 104 weeks of extended newborn NVP in addition to a single intrapartum maternal NVP
897 dose.

## Tables

Table 1: Virus dynamics parameters. All units in [1/day], except the point mutation probability $\mu$ in [1/rev. transcr./base], the infection rate constant $\beta(wt,\phi)$ in [1/virions/day] and the T-cell production $\lambda$ [cells/day/kg body weight].

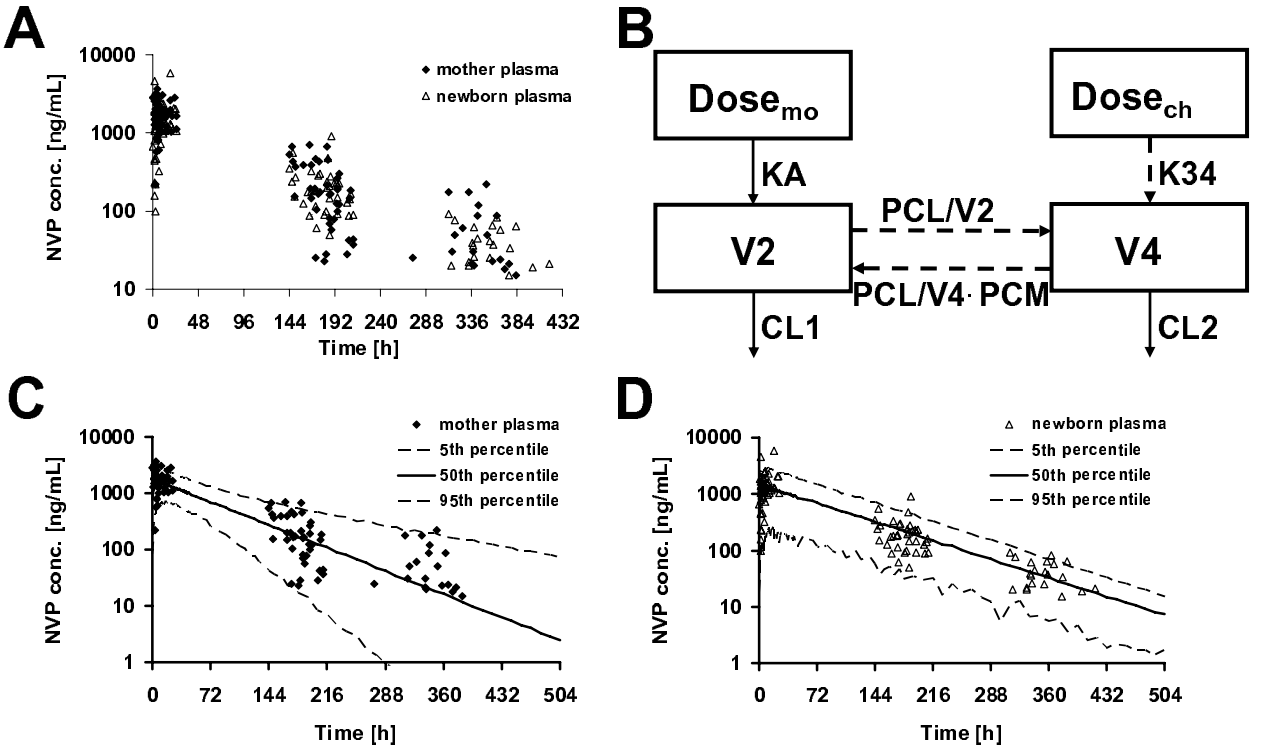
| Parameter | Value | Reference |
|---|---|---|
| $k_T$ | 0.35 | (63) |
| $\delta_{T2}$ | 1 | (32) |
| $N$ | 1000 | (47) |
| $\mu$ | $2.16 \cdot 10^{5}$ | (31) |
| $\delta_T, \delta_{T1}$ | 0.02 | (47) |
| $\beta(wt,\phi)$ | $8 \cdot 10^{-12}$ | (47) |
| $\delta_{\mathrm{PIC}}$ | 0.35 | (56) |
| λ (newborn) | Eq. S2§ | |
| $CL_V$ (newborn) | Eq. S4§ | |
| λ (mother) | $2.86 \cdot 10^{7}$ * | (57) |
| $CL_V$ (mother) | 23 | (32) |

*The maternal zero-order T-cell production of $2 \cdot 10^{9}$ (57) was divided by the weight (70 kg) of the patients in (57), to yield the parameter stated in the table. § see supplementary text S1.

905 Table 2: Population PK estimates of NVP of the final combined PK model for mothers
906 and newborns.

| **Model parameters** | **Units** | **Population estimates** | **RSE[a], %** |
|---|---|---|---|
| *FIXED EFFECTS* | | | |
| KA | [$h^{-1}$] | 1.34 fixed | - |
| V2/F | [L] | 90.9 | 5.85 |
| CL1/F | [$L \cdot h^{-1}$] | 1.22 | 6.33 |
| V4/F | [L] | 20.0 | 18.6 |
| CL2/F | [$L \cdot h^{-1}$] | 0.21 | 16.1 |
| K34 | [$h^{-1}$] | 1.34 fixed | - |
| PCL/F | [$L \cdot h^{-1}$] | 111.0 | 20.5 |
| PCM | | 1.38 | 7.68 |
| *RANDOM EFFECTS* | | | |
| *Interindividual Variability* | | | |
| ωKA | [% CV] | 159.7 | 30.3 |
| ωCL1/F | [% CV] | 32.9 | 25.7 |
| ωV2/F | [% CV] | 34.1 | 33.1 |
| *Residual Variability* | | | |
| σ proportional (mothers) | [% CV] | 27.2 | 10.6 |
| σ proportional (newborns) | [% CV] | 49.1 | 11.0 |

907 [a] Relative standard error (standard error divided by population estimate ·100;
908 for the random effects parameters RSE is related to the corresponding variance scale).

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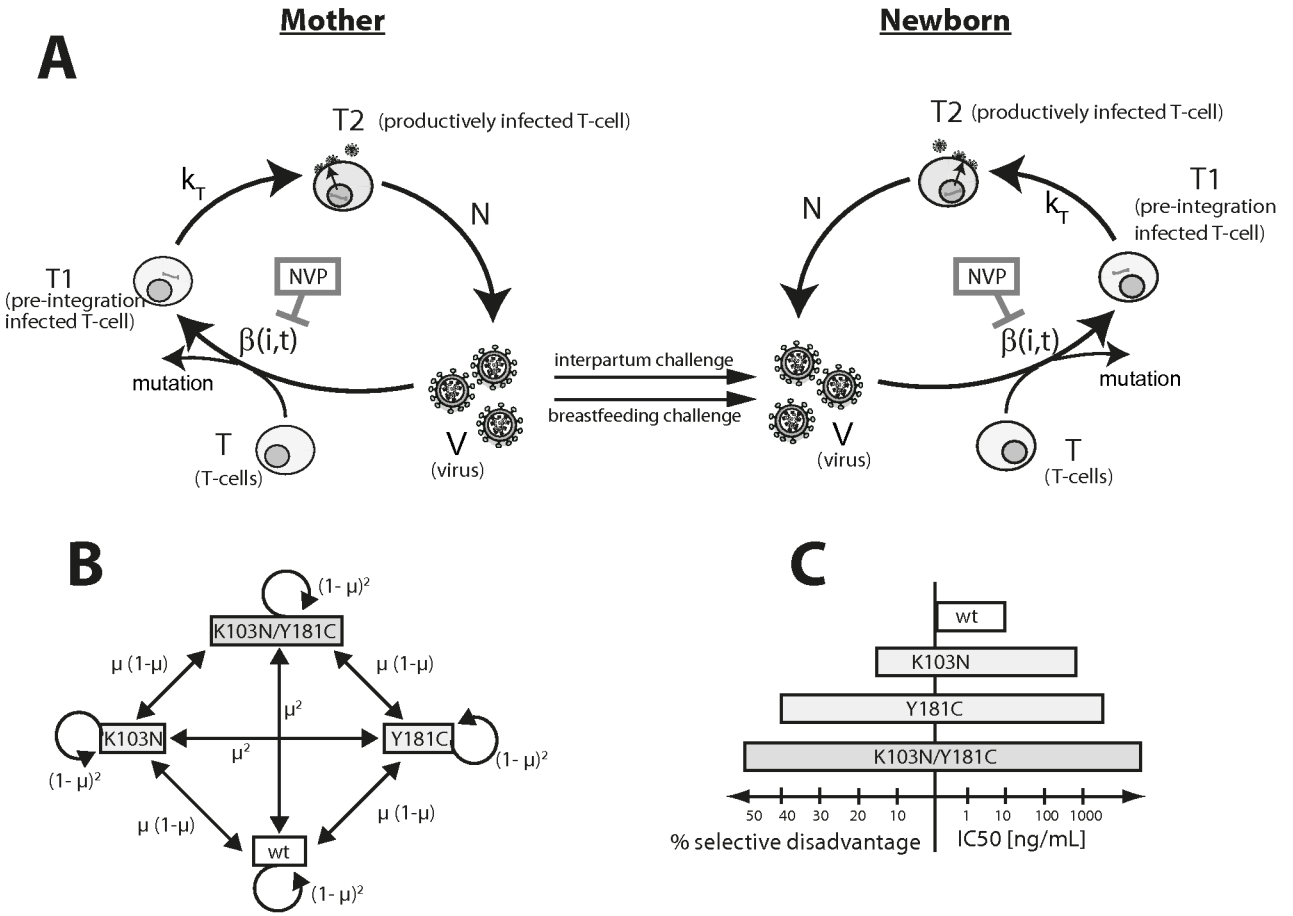


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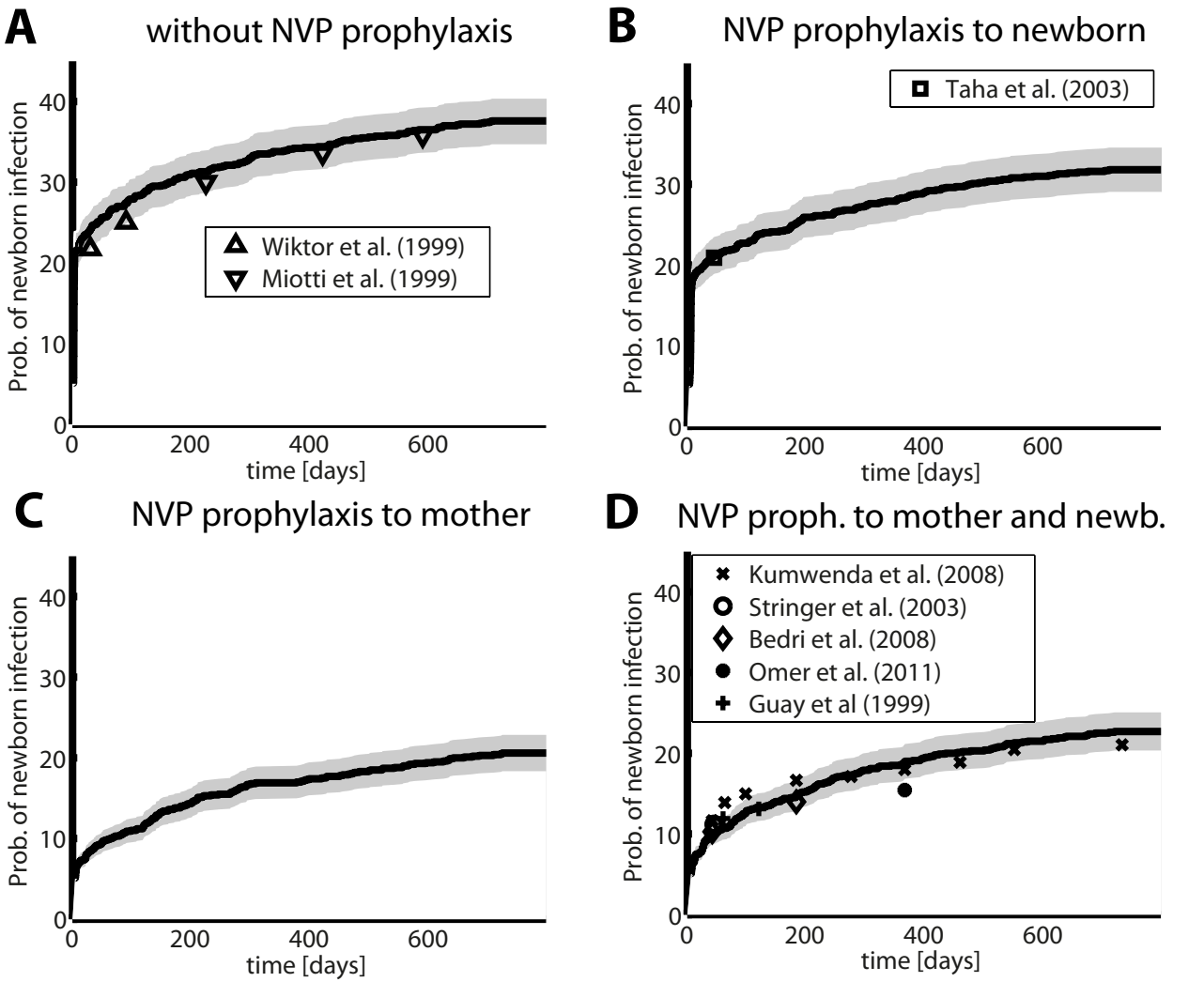


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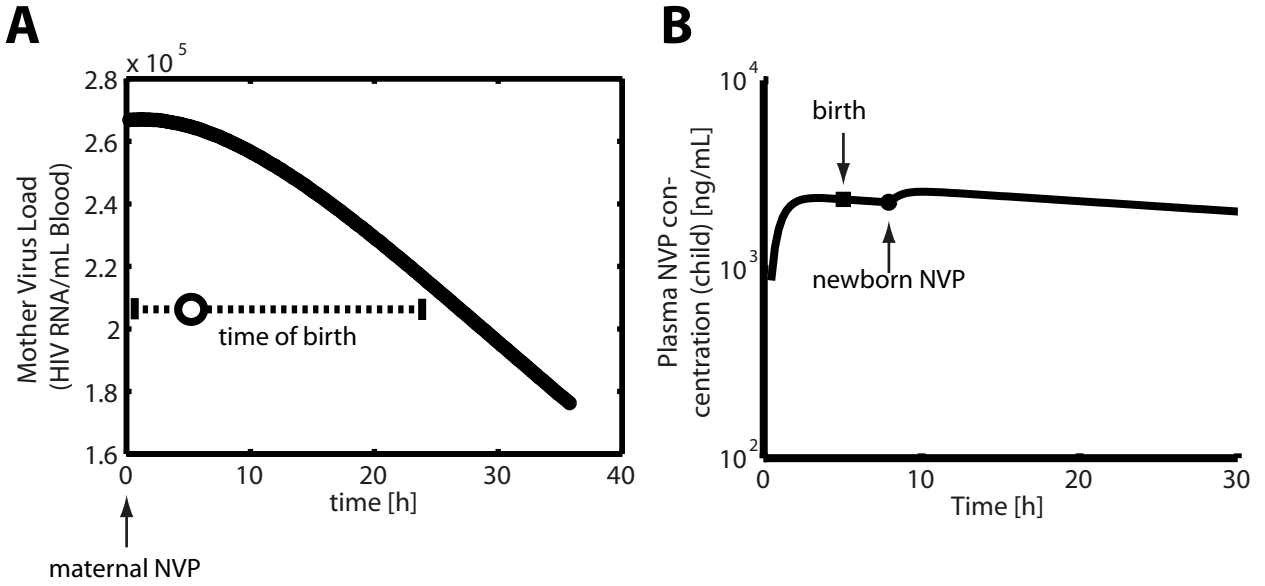


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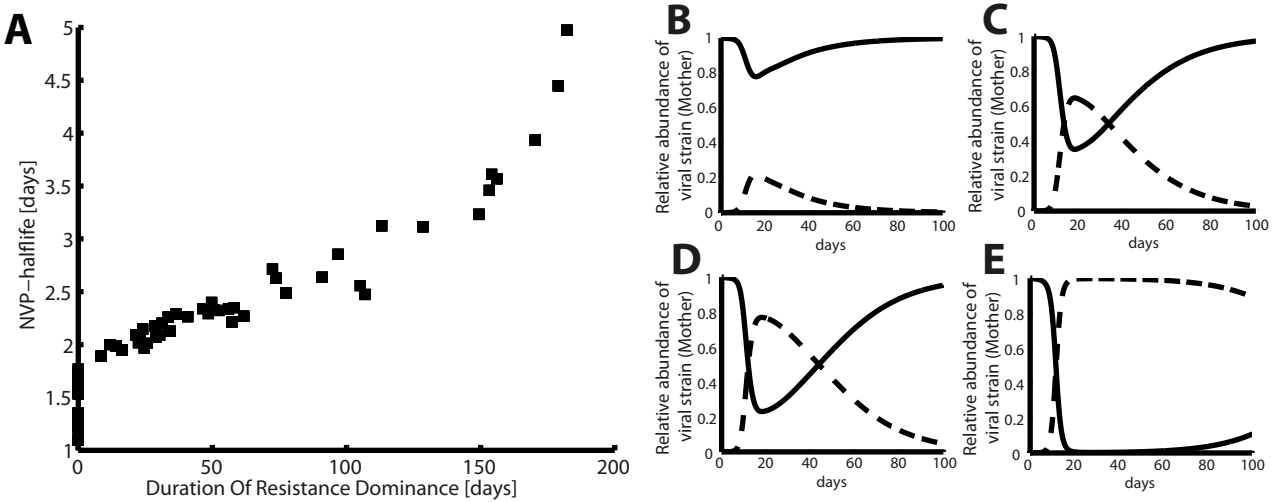


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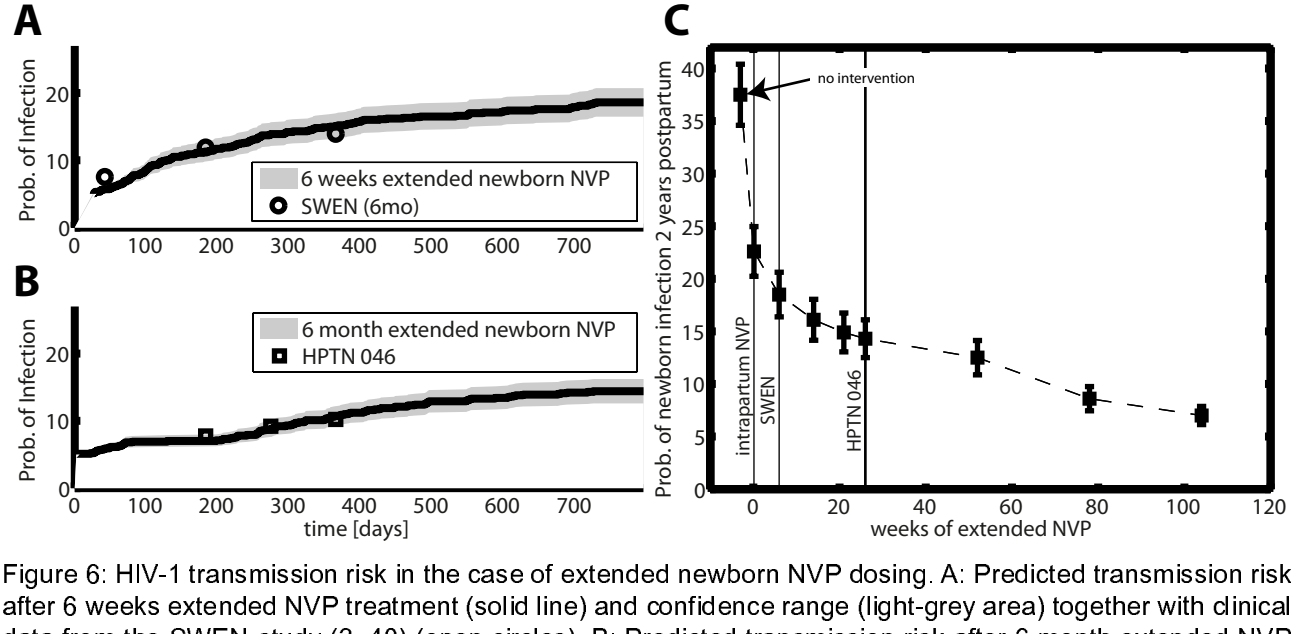


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# Quantifying the impact of nevirapine-based prophylaxis strategies to prevent mother-to-child transmission of HIV: A combined pharmacokinetic, pharmaco- and viral dynamic analysis to predict clinical outcomes

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## S1 Child Growth, CD4$^+$ Proliferation and Immune System Development

For the asymptomatically HIV-infected mother, we considered the rates $\lambda(t)$ and $\mathrm{CL_V}(t)$ to be time-invariant (see Table 2, main article). However, for the child, we considered growth and -immune system development. The body weight $\mathrm{BW_{child}}$ in [kg] of the infants was calculated using the following equation:

$$\mathrm{BW_{child}(age)} \quad = \quad K_{\max} \cdot \frac{\mathrm{age}}{K_{50} + \mathrm{age}} + \mathrm{age} \cdot r + 3.3 \tag{S1}$$

with parameters $K_{\max} = 5.5$ [kg], $K_{50} = 137.2$ [days] and $r = 0.0054$ [kg/day] derived after fitting Eq. (S1) to data from the WHO [1] in Fig. S1 A. The parameter $\lambda_{\mathrm{child}}(t)$, which denotes the children's proliferation of T-cells, was calculated according to

$$\lambda_{\mathrm{child}}(\mathrm{age}) = \frac{\lambda_{\mathrm{adult}}}{\mathrm{BW_{adult}}} \cdot \left(1 + \frac{T_{\max}}{\mathrm{age} + k_{\mathrm{inact}}}\right) \cdot \mathrm{BW_{child}(age)} \tag{S2}$$

with parameters $\lambda_{\mathrm{adult}} = 2 \cdot 10^9$ [cells/day] [2] (and assuming an adult body weight of $\mathrm{BW_{adult}}70$ [kg]), $T_{\max} = 2292$ [days] and $k_{\mathrm{inact}} = 682$ [days]. A comparison of predicted CD4$^+$-counts in uninfected African children born to HIV infected mothers and data from the literature [3] is shown in Figure S1 B.

The scaling factor SF(t), which corrects the infection rate $\beta$ for the differences in target cell density between mother and uninfected child, has been defined as following: $\mathrm{SF(t)} = \frac{\mathrm{T_{child}}(t)}{\mathrm{BW_{child}}(t)} \cdot \frac{\mathrm{BW_{adult}}}{\mathrm{T_{adult}}}$. After substituting Eq. (S2) and approximating $\mathrm{T} = \frac{\lambda}{\delta_{\mathrm{T}}}$, we derive

$$\mathrm{SF(t)} \quad = \quad \left(1 + \frac{T_{\max}}{\mathrm{age} + k_{\mathrm{inact}}}\right). \tag{S3}$$

Finally, we assumed that the child develops an anti-HIV immune response, as a result of immune system maturation and as a result of repeated exposure to HIV during breastfeeding [4]. The HIV-specific response has been modeled in terms of a time-dependent virus clearance $\mathrm{CL_{V\,child}(age)}$:

$$\mathrm{CL_{V\,child}(age)} \quad = \quad \mathrm{age} \cdot \frac{\mathrm{CL_V(infected)} - \mathrm{CL_V(naive)}}{T_{50} + \mathrm{age}} + \mathrm{CL_V(naive)} \tag{S4}$$

with $T_{50} = 100$ [days]. The parameter $\mathrm{CL_V}$(infected) = 23 [1/day] [5] denotes the virus clearance in an asymptomatically infected adult and $\mathrm{CL_V}$(naive) = 2.3 [1/day] [6–8] denotes the virus clearance in a HIV-naive child.

# S2 Minimum NVP Concentration that Selects for Drug Resistance

In this section we will calculate the minimum concentration which selects drug resistance.

The reproductive number [9, 10] $R_0$ denotes the average number of viral particles that are produced from each virus particle in the parent population. In a rapidly reproducing population, like HIV, this quantity is equivalent to the fitness of each virus particle. It can be calculated from the parameters in the presented virus dynamics model (Eq. (1)-(4), main article). In our model, the strain-specific reproductive numbers are given by:

$$R_0(i,t) \quad = \quad \frac{\beta(i,t) \cdot \mathrm{T}(t) \cdot k_T \cdot \mathrm{N}}{\mathrm{CL_V} \cdot (\delta_{\mathrm{PIC}} + k_T + \delta_{\mathrm{T_1}}) \cdot \delta_{\mathrm{T_2}}} \tag{S5}$$

with $\beta(i,t) = (1 - \eta(i,t)) \cdot (1 - s(i)) \cdot \beta(wt, \phi)$. In formula (S5), $i$ denotes the viral strain (wild type, K103N- Y181C- and K103N/Y181C mutant) and $t$ denotes the time. All parameter definitions are provided in the main article.

A drug resistant mutant is selected over the wild type, if its fitness (= reproductive number) is greater than that of the wild type. We therefore derive

$$\text{selection of res. mutant if:} \quad \tfrac{R_0(\mathrm{res},t)}{R_0(\mathrm{wt},t)} \quad > 1. \tag{S6}$$

Inverting Eq. (S6) and substituting Eq. (S5), we derive

$$\text{selection of res. mutant if:} \quad \tfrac{1-\eta(\mathrm{wt},t)}{(1-s(r))\cdot(1-\eta(\mathrm{res},t))} \quad < 1. \tag{S7}$$

After substituting Eq. (6) (main article) and resolving for the concentration of NVP, $C(t)$, we derive

$$\text{selection of res. mutant if:} \quad C(t) \quad > \frac{\mathrm{IC_{50}(wt)} \cdot s(\mathrm{res})}{(1 - s(\mathrm{res})) - \frac{1}{K_{\mathrm{IC_{50}}}}} \tag{S8}$$

where $s$(res) denotes the selective disadvantage of the mutant (relative to the wild type) and $K_{\mathrm{IC_{50}}} = \frac{\mathrm{IC_{50}(res)}}{\mathrm{IC_{50}(wt)}}$ is the fold increase in $\mathrm{IC_{50}}$ of the mutant strain (see e.g. [11]). Using Eq. (S8) with parameters for the K103N, the Y181C and the double mutant [11–14], we derive the threshold values provided in section *Correlation of NVP Elimination and Persistence of NVP Resistance in HIV-1 Infected Mothers after Single Dose Administration* (main article).

# References


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# Supplementary Figures

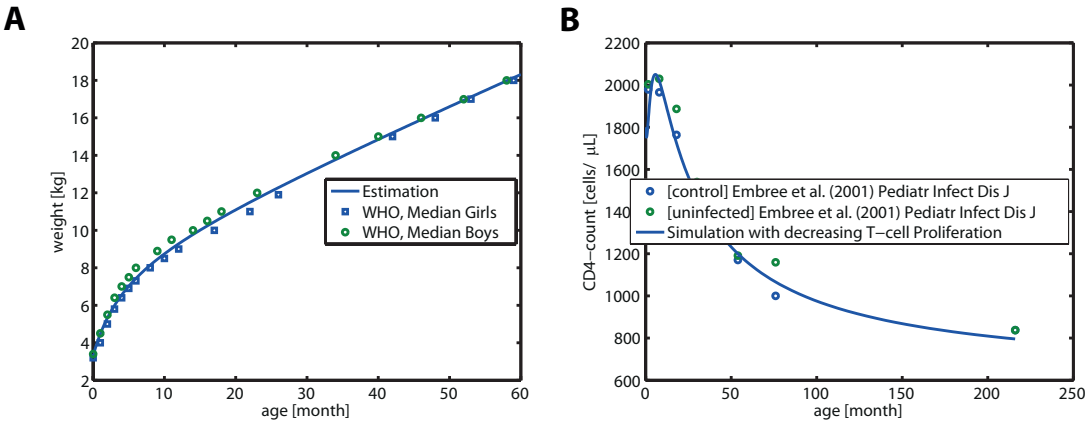


**Figure S1.** A: WHO data [1] (green open circles for boys and blue squares for girls) and prediction using Eq. (S1) (solid blue line) of weight gain for infants during the first 5 years of age. B: Newborn immune system development, exemplified for $CD4^+$ count. Solid line: prediction using Eq. (S2). Green and blue dots: data from [3].

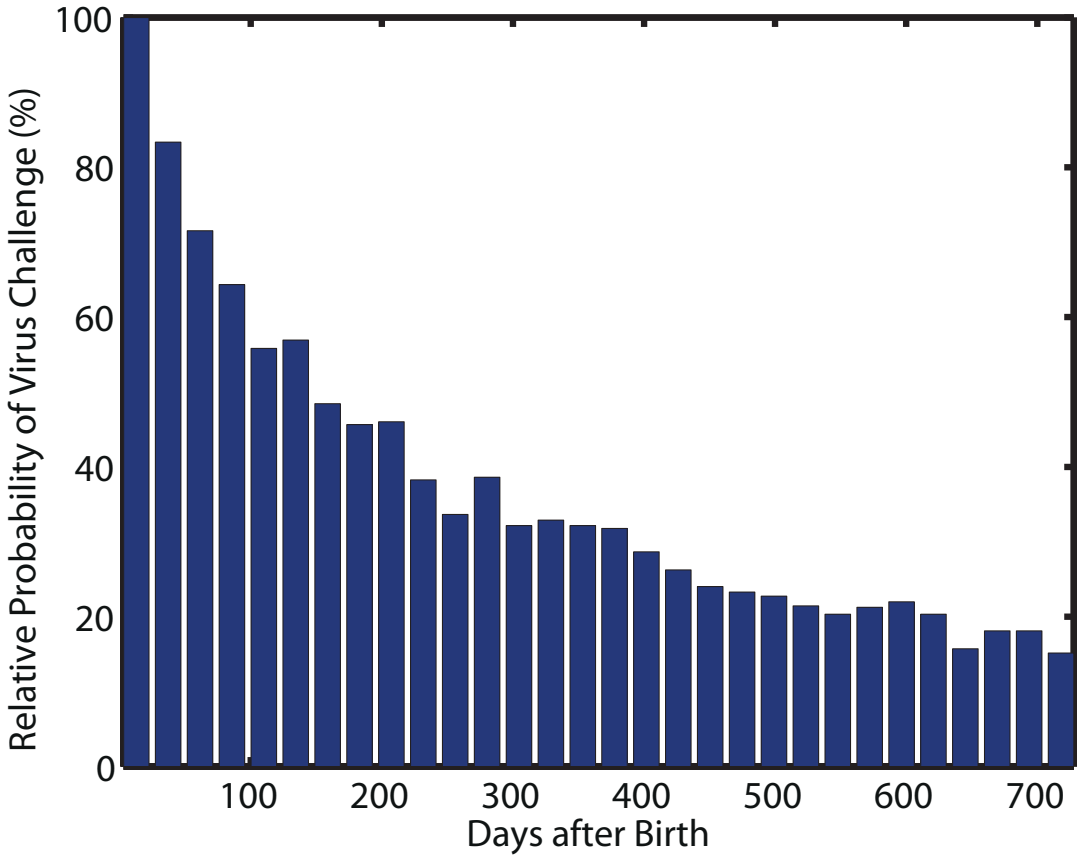


**Figure S2.** The probability of viral challenge through breastfeeding was assumed to decrease with time, as mothers change from exclusive breastfeeding to weaning. Blue bars represent the probability of virus challenge for a given time interval, relative to the first time interval (shortly after birth).

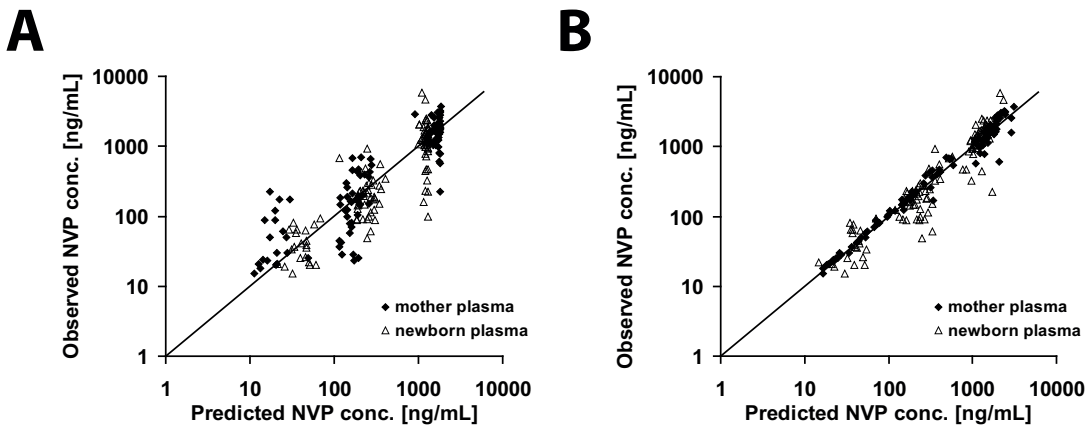


**Figure S3.** Goodness-of-fit Plots. A: Goodness-of-fit for population predicted- versus observed NVP concentrations. B: Goodness-of-fit for individual predicted versus observed NVP concentrations.