Derivation of $R_0{}^T$

The basic reproductive ratio, R_0, is defined as the number of secondary infections from a single infected cell, assuming that virtually all cells are uninfected (i.e. $\dot{T} = \lambda - d\,T \Rightarrow \overline{T} = \frac{\lambda}{d}$).
A simple derivation of R_0 from the basic model of HIV-1 in vivo dynamics is as follows:

R_0 = target cell density × burst size × infection rate constant × average lifetime of the virus

$$= \frac{\lambda}{d} \times n \times k \times \frac{1}{c}$$

For the crHIV-1 gene therapy model we defined a new R_0 for the crHIV-1 virus, $R_0{}^T$, defined as the number of secondary crHIV-1 infections obtained from a single crHIV-1 infection assuming that virtually all cells are uninfected by crHIV-1 but that the system is at steady state for HIV-1 infection (i.e. steady state for the basic model of HIV-1 in vivo dynamics:
$\overline{T} = \frac{c}{k\,n}$, $\overline{V} = \frac{n\,\lambda}{c} - \frac{d}{k}$, $\overline{I} = \frac{\lambda}{\delta} - \frac{c\,d}{\delta\,k\,n}$).

When $R_0{}^T \geq R_0$ crHIV-1 infection will persist, when $R_0{}^T < R_0$ crHIV-1 infection will die.

In order to derive the new $R_0{}^T$ we segment the infection process into 2 components:
1) crHIV-1 infection of T cells
and
2) HIV-1 infection of I_T cells.

The 1st component will yield roughly the density of I_T target cells for the 2nd component.

1)
target cell density for crHIV-1 × crHIV-1 burst size × crHIV-1 infectivity × crHIV-1 lifetime

$$\left(\overline{T} = \frac{c}{k\,n}\right) \times P^2 Dn \times k \times \frac{1}{c}$$

$$= P^2 D\delta'$$

Essentially this is the λ value for the I_T cell population.
This is the I_T "target" cell density except that we have not accounted for the death rate of I_T cells (these cells die at a per cell rate of d). We now acount for the average lifetime of I_T cells to find the actual target cell density:

$$\left(P^2 D\delta' \times \frac{1}{d}\right)$$

2)

I_T "target" cell density $\times$ HIV-1 virus density $\times$ HIV-1 infectivity

$$\left(P^2\, D\delta' \times \frac{1}{d}\right) \times \quad \overline{V} = \frac{n\lambda}{c} - \frac{d}{k} \times \qquad k$$

$$= \quad P^2\, D\left(\frac{n\lambda k}{d\,c} - 1\right)$$

$$= \quad P^2\, D\,(R_0 - 1) \qquad [\zeta]$$

But, in order, for crHIV-1 to persist we require $R_0{}^T \geq R_0$ or $\frac{R_0{}^T}{R_0} \geq 1$.
(This can be explained by considering the predator-prey model of 2 predator species competing for the same prey. Except in special cases, the principle of competitive exclusion applies, the species with the greater R_0 outcompetes or excludes the other predator species. Here, in our crHIV-1 model, if $R_0 > R_0{}^T$ then HIV-1 outcompetes crHIV-1 and excludes crHIV-1. But if the opposite is true $R_0{}^T > R_0$ then crHIV-1 is not excluded but will never outcompete or exclude HIV-1 since crHIV-1 replication depends on HIV-1).

Thus, we divide Eq. ζ above by R_0 and define $R_0{}^T$ as:

$$R_0{}^T = P^2\, D\left(1 - \frac{1}{R_0}\right)$$

When $R_0{}^T \geq 1$ crHIV-1 infection will persist in vivo, otherwise it will die out.
Below $R_0{}^T$ was plotted relative to parameters P and D. The graph is cut-off at 1 on the z-axis, in order to emphasize the transition $R_0{}^T > 1$. The red and blue shading is added in order compare $R_0{}^T$ to regimes where crHIV-1 is either unstable or stable. The red region corresponds to a regime where all eigenvalues of the Jacobian for Eqs.**1-6** are negative for the solution to the Basic Model—thus only HIV-1 is stable (crHIV-1 is unstable and in fact a non-physical solution). The blue region corresponds to a regime where all eigenvalues of the Jacobian for Eqs.**1-6** are negative for the solution to the expanded model—thus crHIV-1 is stable (the Basic Model solution is unstable). The purple spikes are a numerical anomaly and are irrelevant. The transcritical bifurcation (transition from red to blue) corresponds with $R_0{}^T = 1$. The regime where crHIV-1 is stable (blue) corresponds to regime $R_0{}^T > 1$.