**S2 Table**. Notation used in models of HTLV-1 within host persistence.

# Notation Description

#### General

i	clone index
S(t)	Expected number of HTLV-1 clones at time t
N(t)	Expected number of HTLV-1 infected cells at time t
Π	Per-capita rate of mitotic spread (infected cell proliferation)
δ	Per-capita rate of infected cell death
r <sub>l</sub>	Per-capita rate of infectious spread (de novo infection)
R	Ratio of infectious to mitotic spread
f	Clone frequency (index)
n <sub>f</sub>	Number of clones of frequency f

### Method 1: Full Simulation Hybrid Model

$x_i(t)$	Expected number of infected cells in clone <i>i</i> at time <i>t</i>
К	Density dependency parameter. Infected cell proliferation rates are half maximal
	when number of infected cells $N(t) = K$
$\pi^{*}(t)$	Density-dependent proliferation rate
с, С	Index and number of possible reactions of system respectively
$ ho_c$	Mapping of reaction c
Vc	Stoichiometric vector of reaction c
α <sub>c</sub>	Propensity function of reaction c
S <sub>max</sub>	Integer chosen to always be larger than $S(t)$ , for all $t$
X(t)	Random variable denoting the state of the entire system (all clones and their
	frequencies) at time t
$X_i(t)$	Random variable denoting the frequency of clone <i>i</i> at time <i>t</i>
У	Potential state of random variable $X(t)$
<b>y</b> 0	Initial state of all clones and their frequencies
Τ	Maximum frequency that stochastically modelled clone allowed to take

F	Threshold frequency above which clones are modelled deterministically and below which clones are modelled stochastically
b(t)	Number of clone births at time t
<i>E(t)</i>	Expected number of clones deaths/extinctions at time t
S <sub>0</sub>	Number of clones at time zero
h	Length of time step in hybrid model
D(t)	State of deterministic part of hybrid model at time t
$\sigma(t)$	State of stochastic part of hybrid model at time t

# Method 2: Upper Bound Approximation

δs	Clone death rate
$\hat{\delta}_{\scriptscriptstyle{small}}$ , $\hat{\delta}_{\scriptscriptstyle{large}}$	Aggregate clone death rate of small and large clones respectively
Γ <sub>I,Supremum</sub>	Estimated supremum of infectious spread rate, assuming cell death rate $\delta$ applies to all clones, irrespective of size
R <sub>Supremum</sub>	Estimated ratio of infectious spread to mitotic spread, assuming cell death rate $\delta$ applies to all clones, irrespective of size
f <sub>max</sub>	Frequency above which clones do not contribute to clone death rate
r <sub>I, fmax</sub>	Estimated upper bound of infectious spread rate, assuming clones above frequency $f_{max}$ do not contribute to clone death rate
R <sub>fmax</sub>	Estimated ratio of infectious spread to mitotic spread, assuming clones above frequency $f_{max}$ do not contribute to clone death rate

# Method 3: Occupancy class model

М	Rate of mitotic events in deterministic clone class model
Ι	Rate of infectious events in deterministic clone class model
Cf	Number of infected cells in class size $n_f$ in deterministic clone class model ( $C_f = fn_f$ )
$R_1$	Ratio of infectious to mitotic spread in terms of proportion of cells that are singletons
R <sub>2</sub>	Ratio of infectious to mitotic spread in terms of species richness