Table S1. Substitution models for unphased CG methylation data applicable to clonal populations. Shown are also their matching DNA based substitution models.

DNA substitution model	Are equilibrium frequencies same for all states?	Are relative transition rates always 1?	Q matrix (DNA)	Q matrix (Unphased CpG methylation)
JC69 [1]	Yes	Yes	$\begin{bmatrix} - & \lambda & \lambda & \lambda \\ \lambda & - & \lambda & \lambda \\ \lambda & \lambda & - & \lambda \\ \lambda & \lambda & \lambda & - \end{bmatrix}$	$\begin{bmatrix} - & \lambda & \lambda \\ \lambda & - & \lambda \\ \lambda & \lambda & - \end{bmatrix}$
K80 [2]	Yes	No	$\begin{bmatrix} - & \alpha & \beta & \beta \\ \alpha & - & \beta & \beta \\ \beta & \beta & - & \alpha \\ \beta & \beta & \alpha & - \end{bmatrix}$	$\begin{bmatrix} - & c & d \\ c & - & c \\ d & c & - \end{bmatrix}$
F81 [3]	No	Yes	$\begin{bmatrix} - & \pi_C & \pi_A & \pi_G \\ \pi_T & - & \pi_A & \pi_G \\ \pi_T & \pi_C & - & \pi_G \\ \pi_T & \pi_C & \pi_A & - \end{bmatrix}$	$\begin{bmatrix} - & \pi_2 & \pi_3 \\ \pi_1 & - & \pi_3 \\ \pi_1 & \pi_2 & - \end{bmatrix}$
HKY85 [4-5]	No	No	$\begin{bmatrix} - & \alpha\pi_C & \beta\pi_A & \beta\pi_G \\ \alpha\pi_T & - & \beta\pi_A & \beta\pi_G \\ \beta\pi_T & \beta\pi_C & - & \alpha\pi_G \\ \beta\pi_T & \beta\pi_C & \alpha\pi_A & - \end{bmatrix}$	$\begin{bmatrix} - & c\pi_2 & d\pi_3 \\ c\pi_1 & - & c\pi_3 \\ d\pi_1 & c\pi_2 & - \end{bmatrix}$
GTR [6]	No	No	$\begin{bmatrix} - & a\pi_C & b\pi_A & c\pi_G \\ a\pi_T & - & d\pi_A & e\pi_G \\ b\pi_T & d\pi_C & - & f\pi_G \\ c\pi_T & e\pi_C & f\pi_A & - \end{bmatrix}$	$\begin{bmatrix} - & a\pi_2 & b\pi_3 \\ a\pi_1 & - & c\pi_3 \\ b\pi_1 & c\pi_2 & - \end{bmatrix}$

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