

**Table S4.** Multiple sequence alignment composition and selected substitution models of cervid satellite sequences.

Satellite sequence	Number of sequences	Alignment length (bp)	Proportion of gaps (%)	Substitution model	$\alpha$
satI	76	934	2.8	GTR + $\Gamma$	2.6
satII	76	690	7.4	K80 + $\Gamma$	3.5
satIII	65	598	1.4	GTR + $\Gamma$	0.7
satIV	64	747	1.3	HKY + $\Gamma$	1.6
<i>mt-cyb</i> gene	18	1140	0	HKY + I	I = 0.61

$\Gamma$  - rate heterogeneity between sites modelled with the  $\Gamma$  distribution,  $\alpha$  - shape parameter of the  $\Gamma$  distribution.