

Supplementary Table 1. Nucleotide sequence identities of the kW1 sequence fragments from 8 avian species and 1 crocodilian species with the coding region of the integrase of American alligator *Polinton* DNA transposon (the Polinton-1_AMi sequence)

kW1 sequence fragments	Length of DNA fragment, bp	Nucleotide sequence identity, % ^a
<i>Casuarius casuarius</i> w1-k7 fragment, chromosome Z	286	71.3 (204/286)
<i>Dromaius novaehollandiae</i> w1-k7 fragment, chromosome Z	295	74.2 (219/295)
<i>Pterocnemia pennata</i> w1-k7 fragment, chromosome Z	289	62.6 (181/289)
<i>Struthio camelus</i> w1-k7 fragment, chromosome Z	294	70.7 (208/294)
<i>Apteryx australis manteui</i> kW1 sequence ^b	676	73.1 (494/676)
<i>Eudromia elegans</i> w1-k7 fragment, chromosome W	271	62.0 (168/271)
<i>Bubo blakistoni</i> w1-k7 fragment, chromosome Z	280	65.0 (182/280)
<i>Bubo blakistoni</i> w1-k7 fragment, chromosome W	295	73.6 (217/295)
<i>Nisaetus nipalensis orientalis</i> w1-k7 fragment, chromosome Z	288	67.0 (193/288)
<i>Nisaetus nipalensis orientalis</i> w1-k7 fragment, chromosome W	295	72.2 (213/295)
<i>Crocodylus siamensis</i> w1-k7 fragment	285	90.5 (258/285)

^a The numbers in parentheses indicate identical bases of the integrase of the American alligator *Polinton* DNA transposon/the number of bases of the kW1 sequences. Identities are calculated including nucleotide sequence gaps.

^b Nucleotide sequence was taken from Huynen et al. [2002] (AF308932).