

“Supplementary Material to “Identification and characterization of repetitive DNA in the genus *Didelphis* Linnaeus, 1758 (*Didelphimorphia*, *Didelphidae*) and the use of satellite DNAs as phylogenetic markers.”

Table S2 - Genome proportion of families of transposable elements with abundance of at least 0.01% in *Didelphis* species and *L. crassicaudata*.

repetitive DNA	Genome proportion (%)						
	<i>D. albiventris</i>	<i>D. aurita</i>	<i>D. imperfecta</i>	<i>L. crassicaudata</i>	<i>D. marsupialis</i>	<i>D. pernigra</i>	<i>D. virginiana</i>
Retrotransposons							
CR1	-	-	-	0.0828	0.0115	-	0.0448
L1	11.1421	12.2224	11.7362	14.7905	12.7786	11.5197	12.7774
RTE	-	0.0122	-	0.0632	0.0180	-	0.0192
SINE	-	-	-	0.0493	0.0220	-	-
LTR							
Endogenous_Retrovirus	1.3136	1.7112	1.4386	1.3728	1.8350	1.3440	1.8862
ERV1	1.1010	1.4512	1.0145	0.9657	1.3810	1.0883	1.6851

Genome proportion (%)							
repetitive DNA	<i>D. albiventris</i>	<i>D. aurita</i>	<i>D. imperfecta</i>	<i>L. crassicaudata</i>	<i>D. marsupialis</i>	<i>D. pernigra</i>	<i>D. virginiana</i>
ERV2	0.0279	0.0637	0.0372	0.0660	0.0486	0.0368	0.0805
Gypsy	-	-	-	-	0.0149	-	-
DNA transposons							
DNANA5_MD	-	-	-	0.0394	-	-	0.0156
Mariner/Tc1	-	0.0134	-	0.0158	0.0168	-	0.0135
hAT	-	0.0234	-	0.0342	0.0220	0.0149	0.0193
Total	13.5845	15.4975	14.2265	17.4795	16.1485	14.0038	16.5414