

“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 S1 - General sequencing information. Bold values (genome size column) were converted from picograms to base pairs using the equation presented in Dolezel et al. (2003).

species	raw reads	clean reads	genome size	coverage
<i>Didelphis albiventris</i>	6.31E+07	5.84E+07	-	-
<i>Didelphis aurita</i>	2.97E+07	2.75E+07	4205400000	0.979 ^a
<i>Didelphis imperfecta</i>	4.17E+07	3.84E+07	-	-
<i>Didelphis marsupialis</i>	4.08E+07	3.77E+07	3.14E+09	1.803 ^b
<i>Didelphis pernigra</i>	6.22E+07	5.74E+07	-	-
<i>Didelphis virginiana</i>	4.22E+07	3.83E+07	4058700000	1.415 ^c
<i>Lutreolina crassicaudata</i>	3.84E+07	3.55E+07	4107600000	1.311 ^a

^aGaragna & Formenti (1981), ^bRedi et al. (2005), ^cTiersch et al. (1989)

References

- Dolezel, J., Bartos, J., Voglmayr, H., & Greilhuber, J. (2003). Nuclear DNA content and genome size of trout and human. *Cytometry*, 51A(2), 127–128. <https://doi.org/10.1002/cyto.a.10013>
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- Redi, C. A., Zacharias, H., Merani, S., Oliveira-Miranda, M., Aguilera, M., Zuccotti, M., Garagna, S., & Capanna, E. (2005). Genome sizes in Afrotheria, Xenarthra, Euarchontoglires, and Laurasiatheria. *Journal of Heredity*, 96(5), 485–493. <https://doi.org/10.1093/jhered/esi080>