

**S6 Appendix. Bootstrap 50% majority-rule consensus tree reconstructed from the MRP matrix of the SuperTRI analysis**

**Evolutionary history of Carnivora (Mammalia, Laurasiatheria) inferred from mitochondrial genomes**

Alexandre Hassanin<sup>1\*</sup>, Géraldine Veron<sup>1</sup>, Anne Ropiquet<sup>2</sup>, Bettine Jansen van Vuuren<sup>3</sup>, Alexis Lécuyer<sup>4</sup>, Steven M. Goodman<sup>5</sup>, Jibril Haider<sup>1,6,7</sup>, Trung Thanh Nguyen<sup>1</sup>

<sup>1</sup> Institut de Systématique, Évolution, Biodiversité (ISYEB), Sorbonne Université, MNHN, CNRS, EPHE, UA, Paris.

<sup>2</sup> Department of Natural Sciences, Faculty of Science and Technology, Middlesex University, United Kingdom.

<sup>3</sup> Centre for Ecological Genomics and Wildlife Conservation, Department of Zoology, University of Johannesburg, South Africa.

<sup>4</sup> Parc zoologique de Paris, Muséum national d'Histoire naturelle, Paris.

<sup>5</sup> Field Museum of Natural History, Chicago, IL, USA.

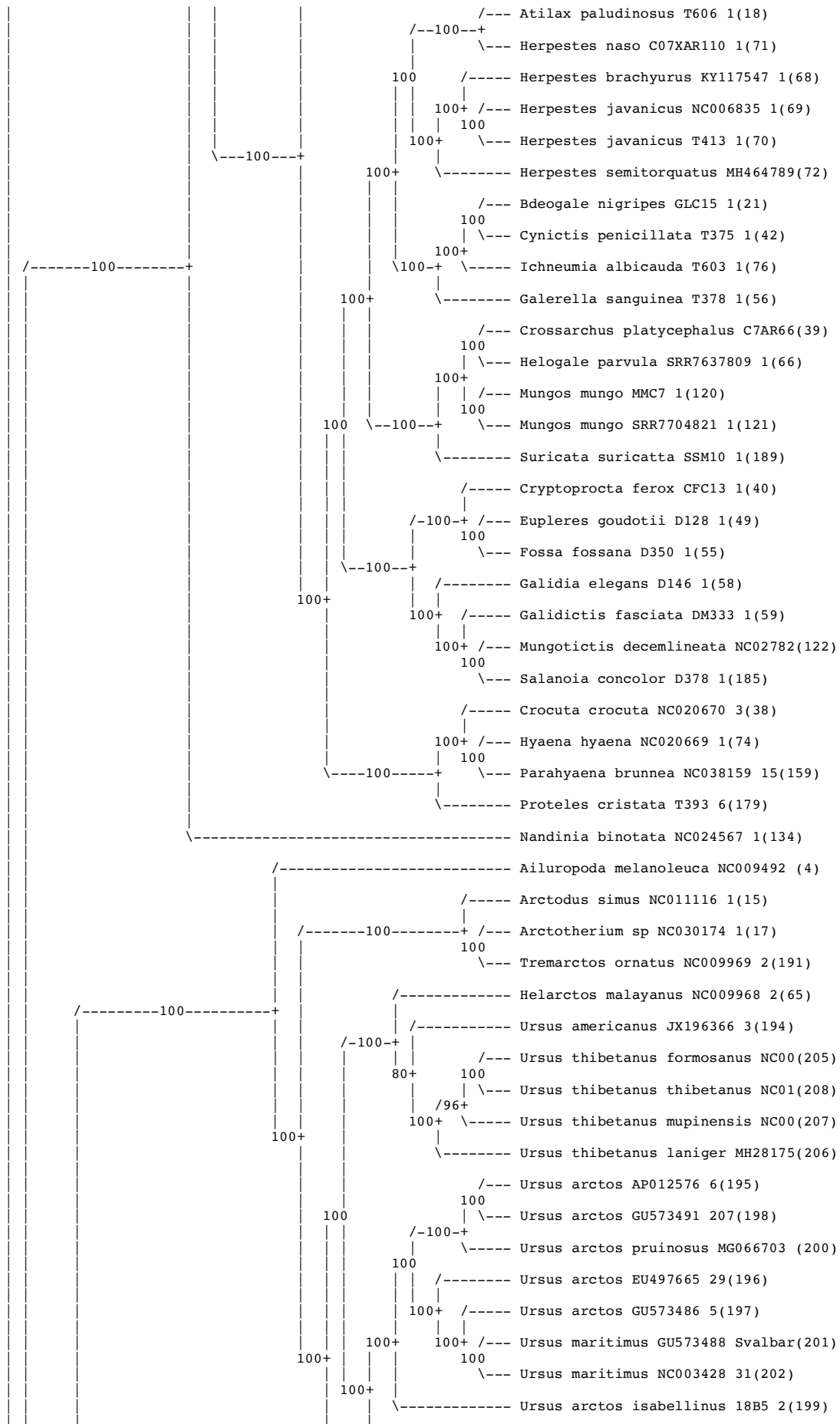
<sup>6</sup> Department of Wildlife Management, Pir Mehr Ali Shah, Arid Agriculture University Rawalpindi, Pakistan.

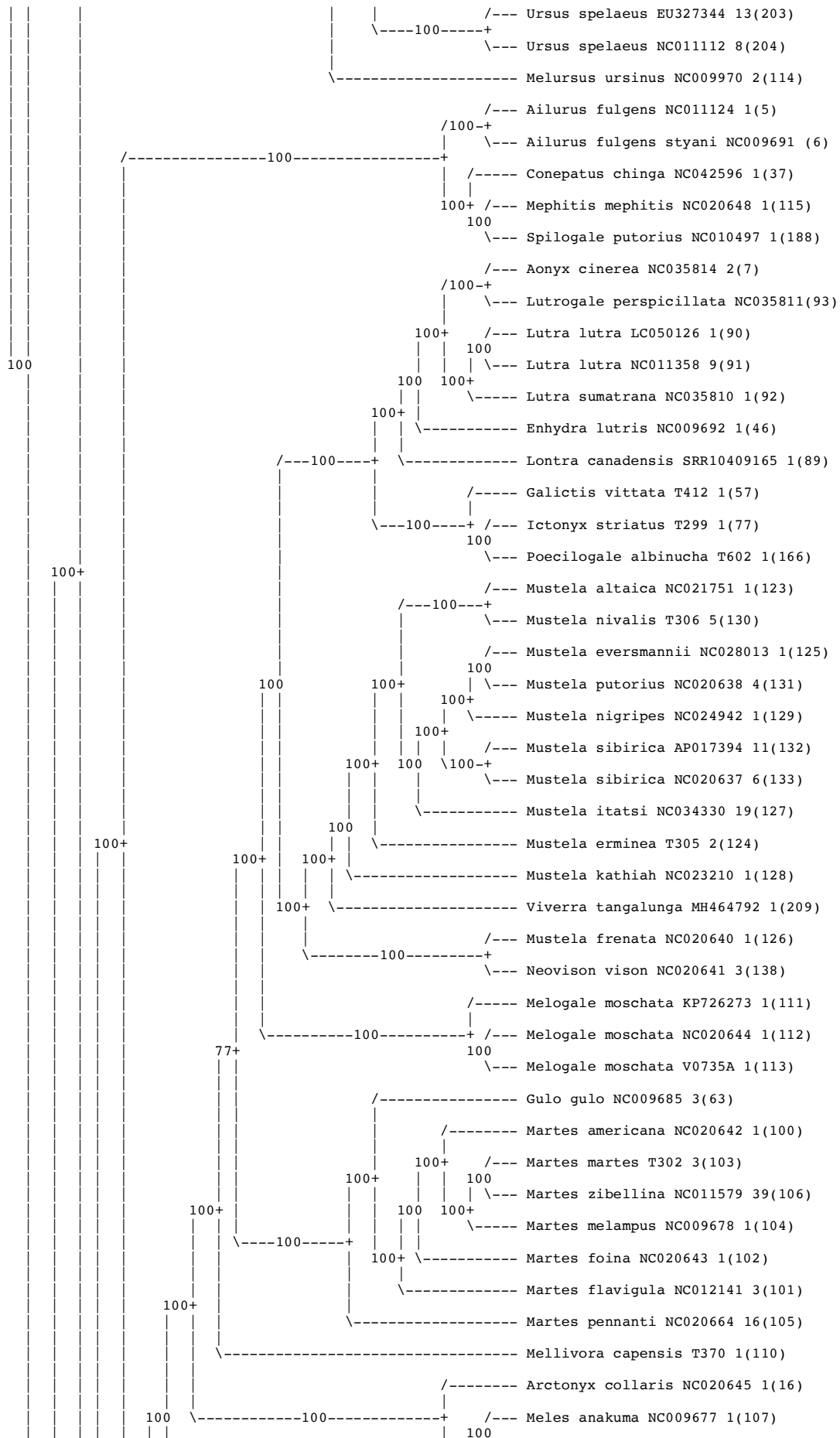
<sup>7</sup> Forest Parks & Wildlife Department Gilgit-Baltistan, Pakistan.

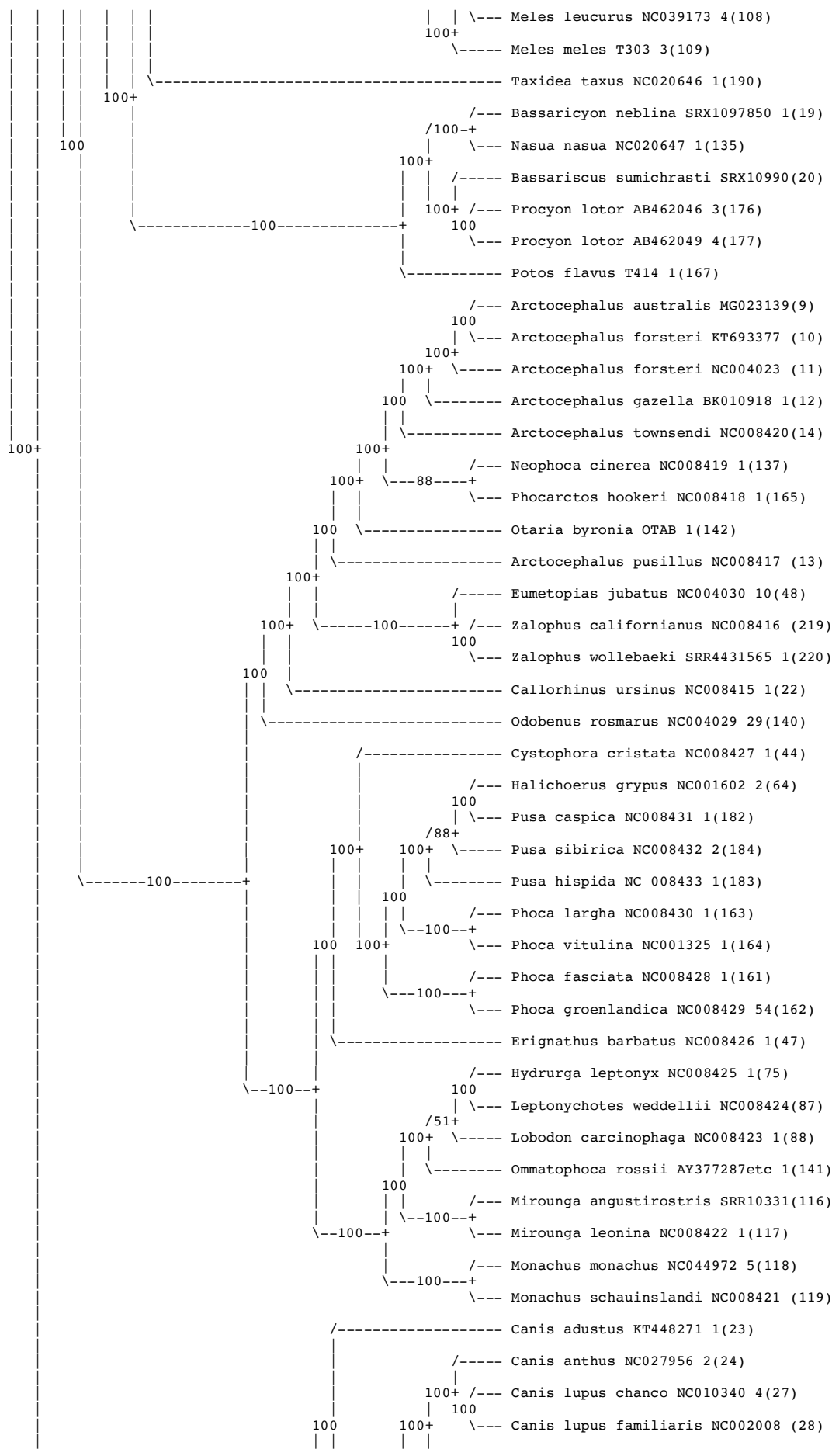
\* Correspondence: [alexandre.hassanin@mnhn.fr](mailto:alexandre.hassanin@mnhn.fr)





























.....	415.00	41.50%
.....*	233.50	23.35%
.....	197.50	19.75%
.....	123.00	12.30%
.....	123.00	12.30%
.....	99.00	9.90%
.....	97.50	9.75%
.....**	39.50	3.95%

2 groups at (relative) frequency less than 1% not shown