

Table S1. Bactrian camel mitochondrial genome sequences used for reconstructing the phylogenic tree

Species	No.of samples	Origin	Accession number
<i>Camelus bactrianus xinjiang</i>	3	BoLe, XinJiang, China	FJ171705, FJ171708, FJ171713
<i>Camelus bactrianus sunite</i>	3	ShuNite, Inner Mongolia, China	FJ171699, FJ171706, FJ171711
<i>Camelus bactrianus alashan</i>	3	ALashan, Inner Mongolia, China	FJ171702, FJ171714, FJ171716
<i>Camelus bactrianus red</i>	3	DungGovi, Mongolia	FJ171703, FJ171704, FJ171712
<i>Camelus bactrianus brown</i>	3	ÖmnöGovi, Mongolia	FJ171700, FJ171707, FJ171710
<i>Camelus bactrianus normal</i>	3	Govi-Altay, Mongolia	FJ171701, FJ171709, FJ171715
<i>Camelus bactrianus ferus</i>	3	Govi-Altay, Mongolia	EF212038, EF507800, EF507801