

Supplementary file 9. Exclusive synapomorphies characterizing giraffe taxa in the mtDNA-91T dataset. Gene positions are indicated with reference to the mitochondrial genome of *G. g. giraffa* (NC_012100).

Taxon	Synapomorphy	Gene/ Region	Position	
			Gene	Alignment
<i>G. camelopardalis</i>	A=>G	cytochrome <i>b</i>	186	186
	G=>A	cytochrome <i>b</i>	288	288
	A=>G	cytochrome <i>b</i>	333	333
	C=>T	cytochrome <i>b</i>	597	597
	C=>T	cytochrome <i>b</i>	924	924
	A=>G	control region	462	1774
<i>G. c. peralta</i>	C=>T	cytochrome <i>b</i>	219	219
	C=>T	cytochrome <i>b</i>	1080	1080
	A=>G	control region	23	1315
<i>G. c. reticulata</i>	C=>T	cytochrome <i>b</i>	795	795
	C=>T	control region	94	1386
<i>G. c. rothschildi</i>	T=>C	control region	129	1422
<i>G. c. senegalensis</i>	A=>G	cytochrome <i>b</i>	732	732
	dC	control region	92	1384
	A=>G	control region	95	1387
	C=>T	control region	359	1671
	A=>G	control region	463	1775
<i>G. t. tippelskirchi</i>	C=>T	cytochrome <i>b</i>	1033	1033
<i>G. t. thornicrofti</i>	A=>G	control region	39	1331
	T=>C	control region	272	1575
	T=>A	control region	336	1640
<i>G. g. giraffa</i>	T=>C	cytochrome <i>b</i>	798	798
	iT	control region	130	1423
	A=>G	control region	170	1469
<i>G. g. wardi</i>	C=>T	cytochrome <i>b</i>	634	634
	A=>G	cytochrome <i>b</i>	705	705

i: insertion; d: deletion