

Table S7. Lion population pairwise  $F_{ST}$  estimates. Below the diagonal mtDNA data (12S-16S) and above the diagonal microsatellite data (22 loci).

Populations											
	GIR	UGA	KEN	NGC	SER-I	SER-II	SER-III	KRU	BOT-I	BOT-II	NAM
GIR	—	0.59490	0.42296	0.51355	0.42389	0.45582	0.42903	0.53709	0.42459	0.39594	0.47708
UGA	0.92157	—	0.13685	0.22677	0.18111	0.23260	0.18323	0.24310	0.20616	0.17590	0.30731
KEN	0.94667	1	—	0.15719	0.08134	0.11455	0.09455	0.13799	0.13843	0.09341	0.20509
NGC	0.92157	—	1	—	0.11771	0.15108	0.11405	0.26699	0.18085	0.14562	0.26318
SER-I	0.91677	0.01852	0.99644	0.01852	—	0.05463	0.04137	0.13276	0.13428	0.11136	0.22015
SER-II	0.92157	—	1	—	0.01852	—	0.06458	0.18868	0.13298	0.14046	0.25026
SER-III	0.92157	—	1	—	0.01852	—	—	0.16163	0.12167	0.09745	0.20037
KRU	0.74231	0.77174	0.84783	0.77174	0.76789	0.77174	0.77174	—	0.14698	0.14598	0.20365
BOT-I	0.92157	—	1	—	0.01852	—	—	0.77174	—	0.09483	0.17988
BOT-II	0.79987	0.84950	0.88485	0.84950	0.84608	0.84950	0.84950	0.52011	0.84950	—	0.14103
NAM	0.88021	0.93480	0.94588	0.93480	0.93141	0.93480	0.93480	0.62125	0.93480	0.06596	—

Note - the mtDNA genetic distance among African populations can be higher than between African and Asian ones.