TABLE III. A Matrix Depicting Significant Differences Between Populations

	Odzala	Lobéké	Ndoki forest	Moukalaba	Loango	ELG	CRG	Bwindi
Lobéké	------ -							
Ndoki forest	------ ↑	---↓-- -						
Moukalaba	------ -	------ -	---↑-- -					
Loango	------ -	------ -	------ -	------ -				
ELGs	------ -	------ -	↑----- ↓	-↑---- -	------ ↓			
CRGs	-↑-↑↑↑ -	---↑-↑ -	↑-↑↑↑↑ ↓	-↑↑--- -	------ -	------ -		
Bwindi	-↑-↑↑↑ -	-----↑ -	--↑--- ↓	↑↑-↑-↑ -	------ -	------ -	------ -	
Virunga	-↑-↑↑↑ -	---↑-↑ -	↑↑↑↑↑- ↓	↑↑-↑↑↑ -	↑---↑↑ -	-↑-↑↑↑ -	------ -	------ ↓

Note that each cell consists of seven entries that are always in the same order: (i) observed heterozygosity Ho, (ii) unbiased expected heterozygosity He, (iii) number of alleles NA, (iv) effective number of alleles Ne, (v) information index I, (vi) allelic richness AR, (vii) fixation index F. An upward oriented arrow indicates that the population at the top of the table has a significantly higher value at that estimate than the population on the left side. The opposite case is indicated by a downward oriented arrow. Dashes indicate that no significant differences were found. The fixation index F is the only estimate in which higher values are not associated with higher genetic diversity, but rather indicate inbreeding or undetected null alleles. In order to avoid confusion the results for that measure are separated from the six other measures by a space.