

Supplementary Table S6. AMOVA Φ_{ST} estimates for the three *NAT* genes between pairs of *Pan* species and sub-species.

Except for the analyses involving the San Diego sample, all results are shown as Φ_{ST} values, with associated *P*-values in brackets (adjusted *P*-values after slash). For analyses involving the San Diego sample, the proportion of significant *P*-values associated with the 122 sub-samples is reported. Significant values are shown in bold.

	<i>P. t. verus</i> (San Diego sample)	<i>P. t. ellioti</i>	<i>P. t. troglodytes</i>	<i>P. t. schweinfurthii</i>	<i>P. paniscus</i>	
NAT1	<i>P. t. verus</i> (BPRC sample)	0 %	0.068 (0.04 / 0.24)	0.026 (0.26 / 0.78)	0.059 (0.06 / 0.30)	0.332 (<0.00001 / 0)
	<i>P. t. verus</i> (San Diego sample)		0 %	0 %	0 %	100 %
	<i>P. t. ellioti</i>			0 (0.35 / 0.78)	0.032 (0.19 / 0.76)	0.315 (<0.00001 / 0)
	<i>P. t. troglodytes</i>				0 (0.76 / 0.78)	0.271 (0.001 / 0)
	<i>P. t. schweinfurthii</i>					0.270 (0.0004 / 0)
NAT2	<i>P. t. verus</i> (BPRC sample)	0 %	0.739 (< 0.00001 / 0)	0.730 (< 0.00001 / 0)	0.781 (< 0.00001 / 0)	0.915 (< 0.00001 / 0)
	<i>P. t. verus</i> (San Diego sample)		100 %	100 %	100 %	100 %
	<i>P. t. ellioti</i>			0.675 (< 0.00001 / 0)	0.722 (< 0.00001 / 0)	0.890 (< 0.00001 / 0)
	<i>P. t. troglodytes</i>				0 (0.71 / 0.71)	0.778 (< 0.00001 / 0)
	<i>P. t. schweinfurthii</i>					0.775 (< 0.00001 / 0)
NATP	<i>P. t. verus</i> (BPRC sample)	75.41 %	0.418 (< 0.00001 / 0)	0.483 (< 0.00001 / 0)	0.315 (< 0.00001 / 0)	0.951 (< 0.00001 / 0)
	<i>P. t. verus</i> (San Diego sample)		100 %	100 %	100 %	100 %
	<i>P. t. ellioti</i>			0.035 (0.20 / 0.40)	0.024 (0.24 / 0.40)	0.879 (< 0.00001 / 0)
	<i>P. t. troglodytes</i>				0.093 (0.07 / 0.21)	0.919 (< 0.00001 / 0)
	<i>P. t. schweinfurthii</i>					0.940 (< 0.00001 / 0)