

Supplementary Table S13. Nucleotide diversity of the three *NAT* gene paralogs in gorillas and orangutans.

	Gorillas		Orangutans	
	<i>Gorilla gorilla</i>	<i>Gorilla beringei</i>	<i>Pongo abelii</i>	<i>Pongo pygmaeus</i>
<i>NAT1</i>				
Total (2N chromosomes)	66	6	24	10
Number of used positions ¹	903	891	903	902
Number of segregating sites (<i>S</i>)	3	2	15	3
Nucleotide diversity (π) x 10 ⁻³	0.61	0.82	3.94	1.36
<i>NAT2</i>				
Total (2N chromosomes)	64	6	24	10
Number of used positions ¹	1'116	1'083	1'115	1'114
Number of segregating sites (<i>S</i>)	12 (+1 InDel) ²	1	8	7
Nucleotide diversity (π) x 10 ⁻³	1.72	0.31	1.65	1.40
<i>NATP</i>				
Total (2N chromosomes)	64	6	26	10
Number of used positions ¹	1'008	950	1'002	953
Number of segregating sites (<i>S</i>)	13	0	15 (+ 1 InDel) ²	7
Nucleotide diversity (π) x 10 ⁻³	2.77	0	3.76	2.29

¹ Number of successfully sequenced positions in common between the GAGP data and our Sanger sequencing results for *G. gorilla* and *P. pygmaeus* (only GAGP data available for *G. beringei* and *P. abelii*).

² Insertions and deletions (InDels) were not considered in the computation of nucleotide diversity.