

**Supplementary Table S1.** PCR and sequencing primers used for the Sanger sequencing of the three *NAT* genes in great apes

Gene	Primer	Sequence 5'-3'	
Chimpanzees and bonobos			
<i>NAT1</i>	12540	CCTACTCAAATCCAAGTGTAAGT	FORWARD <sup>1</sup>
	12355	ACATGATAGGTCGTCAGTTGA	REVERSE <sup>1</sup>
<i>NAT2</i>	12485	GTCACACGAGGAAATCAAGTGC	FORWARD <sup>1</sup>
	12486	GTTTTCTAGCATGAATCATTCTGC	REVERSE <sup>1</sup>
<i>NATP</i>	13404	GAATCTAAGGGCAAAGTAAT	FORWARD <sup>2</sup>
	13405	TGAAAATGTGTGGTTATCATT	REVERSE <sup>3</sup>
Additional PCR and Sequencing Primers for gene <i>NAT2</i> of two BPRC chimpanzees (Oscar and Gerda)			
<i>NAT2</i>	Locus2FB	ACAGGGTCTGAGACTACTAAGAGA	FORWARD <sup>4</sup>
	Locus2RB	GGAGACGTCTGCAGGTATGT	REVERSE <sup>4</sup>
	Locus2FC	GGAAGGATCAGCCTCAGGT	FORWARD <sup>4</sup>
	Locus2RC	GATTCACAATATATTAGCCAACAATG	REVERSE <sup>4</sup>
Gorillas			
<i>NAT1</i>	12540	CCTACTCAAATCCAAGTGTAAGT	FORWARD
	12355	ACATGATAGGTCGTCAGTTGA	REVERSE
<i>NAT2</i>	12485	GTCACACGAGGAAATCAAGTGC	FORWARD
	Locus2Reverse-B	GTTTTCTAGCATGAATCACTCTGC	REVERSE <sup>5</sup>
<i>NATP</i>	Locus3Forward-B	GAATCTAAGGGCAAAGTAAT	FORWARD <sup>5</sup>
	13405	TGAAAATGTGTGGTTATCATT	REVERSE <sup>5</sup>
Orangutans			
<i>NAT1</i>	12540	CCTACTCAAATCCAAGTGTAAGT	FORWARD
	Locus1Reverse-B	ACATGATAGGTCATTAGCTGA	REVERSE <sup>6</sup>
<i>NAT2</i>	Locus2Forward-B	GCCACACAAGGATATCAAGTGC	FORWARD <sup>6</sup>
	Locus2Reverse-B	GTTTTCTAGCATGAATCACTCTGC	REVERSE <sup>6</sup>
<i>NATP</i>	Locus3Forward-C	GAATCTAAGGGCAGAAGTAAT	FORWARD <sup>6</sup>
	13405	TGAAAATGTGTGGTTATCATT	REVERSE
	Locus3Forward-D	GCCTACTCAAGGGAATCTAAGGG	FORWARD <sup>6</sup>
	Locus3Reverse-D	GCACAAATCACTATGGTTCCCAA	REVERSE <sup>6</sup>

<sup>1</sup> Newly designed on panTro2 reference sequence.

<sup>2</sup> Slightly modified from forward primer Np-L2 in Sabbagh et al. (2013).

<sup>3</sup> Slightly modified from reverse primer Np-R2 in Sabbagh et al. (2013).

<sup>4</sup> Newly designed on panTro4 (February 2011) reference sequence.

<sup>5</sup> Newly designed on gorGor3.1 (May 2011) reference sequence.

<sup>6</sup> Newly designed on ponAbe2 (July 2007) reference sequence.

## References in Supplementary Table S1

- Mortensen HM, Froment A, Lema G, Bodo JM, Ibrahim M, Nyambo TB, Omar SA, and Tishkoff SA. 2011. Characterization of genetic variation and natural selection at the arylamine N-acetyltransferase genes in global human populations. *Pharmacogenomics*. 12(11):1545-1558. doi: 10.2217/pgs.11.88
- Patin E, Barreiro LB, Sabeti PC, Austerlitz F, Luca F, Sajantila A, Behar DM, Semino O, Sakuntabhai A, Guiso N et al. . 2006a. Deciphering the ancient and complex evolutionary history of human arylamine N-acetyltransferase genes. *American journal of human genetics*. 78(3):423-436. doi: 10.1086/500614
- Patin E, Harmant C, Kidd KK, Kidd J, Froment A, Mehdi SQ, Sica L, Heyer E, and Quintana-Murci L. 2006b. Sub-Saharan African coding sequence variation and haplotype diversity at the NAT2 gene. *Hum Mutat*. 27(7):720. doi: 10.1002/humu.9438
- Podgorna E, Diallo I, Vangenot C, Sanchez-Mazas A, Sabbagh A, Cerny V, and Poloni ES. 2015. Variation in NAT2 acetylation phenotypes is associated with differences in food-producing subsistence modes and ecoregions in Africa. *BMC Evol Biol*. 15:263. doi: 10.1186/s12862-015-0543-6
- Prado-Martinez J, Sudmant PH, Kidd JM, Li H, Kelley JL, Lorente-Galdos B, Veeramah KR, Woerner AE, O'Connor TD, Santpere G et al. . 2013. Great ape genetic diversity and population history. *Nature*. 499(7459):471-475. doi: 10.1038/nature12228
- Sabbagh A, Langaney A, Darlu P, Gerard N, Krishnamoorthy R, and Poloni ES. 2008. Worldwide distribution of NAT2 diversity: implications for NAT2 evolutionary history. *BMC Genet*. 9:21. doi: 10.1186/1471-2156-9-21
- Sabbagh A, Marin J, Veyssiere C, Lecompte E, Boukouvala S, Poloni ES, Darlu P, and Crouau-Roy B. 2013. Rapid birth-and-death evolution of the xenobiotic metabolizing NAT gene family in vertebrates with evidence of adaptive selection. *BMC Evol Biol*. 13:62. doi: 10.1186/1471-2148-13-62
- The Genomes Project Consortium. 2012. An integrated map of genetic variation from 1,092 human genomes. *Nature*. 491:56. doi: 10.1038/nature11632
- Yates A, Akanni W, Amode MR, Barrell D, Billis K, Carvalho-Silva D, Cummins C, Clapham P, Fitzgerald S, Gil L et al. . 2016. Ensembl 2016. *Nucleic Acids Res*. 44(D1):D710-D716. doi: 10.1093/nar/gkv1157