

Supplementary Table S8. *NAT* genes variant calls in sequenced ancient genomes of the genus *Homo*.

Variant calls are recorded as compared to the human reference sequence (GRCh37/hg19). For *NAT1* and *NAT2*, we screened 2 kb of sequence in the region on chromosome 8 encompassing the coding exon (positions 18'079'000 to 18'081'000 for *NAT1*, and 18'257'000 to 18'259'000 for *NAT2*). For the *NATP* pseudogene, we screened 2 kb of homologous sequence (18'227'600 to 18'229'600). Non-synonymous changes are shown in bold type. Variants located beyond the stretch sequenced in individuals from this study are indicated in italics.

<i>NAT1</i> region (+18'000'000)	79124	79213	79517	80001	80015	80196	80644	80833	80901	80923	80933
hg19	<i>T</i>	<i>C</i>	<i>A</i>	G	<i>G</i>	<i>T</i>	<i>A</i>	<i>A</i>	<i>C</i>	<i>G</i>	<i>C</i>
SNP ID	<i>rs8190856</i>	<i>rs4986988</i>	<i>rs4986989</i>	rs4987076 (A445G)	<i>rs4986990 (G459A)</i>	<i>rs4986783 (G640T)</i>	<i>rs1057126</i>	<i>rs28359534</i>	<i>rs8190862</i>	<i>rs6982949</i>	<i>rs8190863</i>
Ust'-Ishim	<i>T/C</i>	<i>C/T</i>	<i>A/T</i>	G/A	<i>G/A</i>	<i>T/G</i>	<i>A</i>	<i>A</i>	<i>C/G</i>	<i>A</i>	<i>C/T</i>
Altai	<i>C</i>	<i>T</i>	<i>A</i>	A	<i>A</i>	<i>G</i>	<i>A</i>	<i>A</i>	<i>G</i>	<i>A</i>	<i>T</i>
Vindija	<i>C</i>	<i>T</i>	<i>T</i>	A	<i>A</i>	<i>G</i>	<i>T</i> ¹	<i>G</i> ¹	<i>G</i>	<i>A</i>	<i>T</i>
Denisova	<i>T</i>	<i>C</i>	<i>A</i>	G	<i>G</i>	<i>T</i>	<i>A</i>	<i>A</i>	<i>C</i>	<i>A</i>	<i>C</i>
<i>NAT2</i> region (+18'200'000)	57795	58316	58522								
hg19	<i>C</i>	G	<i>A</i>								
SNP ID	<i>rs1041983 (C282T)</i>	rs1208 (A803G)									
Ust'-Ishim	<i>C</i>	A	<i>A</i>								
Altai	<i>C/T</i>	A	<i>A</i>								
Vindija	<i>C</i>	A	<i>A</i>								
Denisova	<i>C</i>	A ²	<i>A/T</i> ³								
<i>NATP</i> region (+18'200'000)	27844	28182	28246	28291	28616	28669	29020	29104	29212	29503	29533
hg19	<i>C</i>	<i>A</i>	<i>T</i>	<i>C</i>	<i>T</i>	<i>G</i>	<i>C</i>	<i>T</i>	<i>G</i>	<i>C</i>	<i>G</i>
SNP ID	<i>rs4487818</i>		<i>rs73590295</i>	<i>rs2898473</i>	<i>rs35548819</i>	<i>rs73590297</i>	<i>rs2172426</i>	<i>rs74444655</i>	<i>rs57181121</i>	<i>rs17126565</i>	<i>rs17126568</i>
Ust'-Ishim	<i>C</i>	<i>A</i>	<i>T/C</i>	<i>A</i>	<i>T/C</i>	<i>G</i>	<i>T</i>	<i>T/C</i>	<i>G/A</i>	<i>C/G</i>	<i>G/C</i>
Altai	<i>C</i>	<i>A</i>	<i>C</i>	<i>A</i>	<i>T</i>	<i>G</i>	<i>T</i>	<i>C</i>	<i>A</i>	<i>G</i>	<i>C</i>
Vindija	<i>T</i> ¹	<i>A</i>	<i>C</i>	<i>A</i>	<i>T</i>	<i>C</i> ¹	<i>T</i>	<i>C</i>	<i>A</i>	<i>G</i>	<i>C</i>
Denisova	<i>T</i> ⁴	<i>A/G</i>	<i>T</i>	<i>A</i>	<i>T</i>	<i>G</i>	<i>C</i>	<i>T</i>	<i>G</i>	<i>C</i>	<i>G</i>

¹ Only reported in the high-coverage alignments of the Vindija Neandertal genome but not called as variant in the ancient genome browser from the Max Planck Institute for Evolutionary Anthropology.

² Apparently reported as unvariable (G) with respect to the human reference sequence in the ancient genome browser from the Max Planck Institute for Evolutionary Anthropology, but reported as A in the high-coverage sequence reads of the Denisova genome in the UCSC Genome Browser.

³ Only reported in the high-coverage sequence reads of the Denisova genome in the UCSC Genome Browser.

⁴ Apparently reported as unvariable (C) with respect to the human reference sequence in the ancient genome browser from the Max Planck Institute for Evolutionary Anthropology, but reported as T in the high-coverage sequence reads of the Denisova genome in the UCSC Genome Browser.