Supplementary information to the paper “Paleo-oscillomics: inferring aspects of Neanderthal language abilities from gene regulation of neural oscillations”

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S1. Evidence of selective sweeps in genes of interest in AMHs (based on Green et al. 2010)

\textit{AUTC2} (chr7:6862946-69274862, hg18) (S value = -8.7)
DYRK1A (chr21:37580123-37789088, hg18) (S value = -4.5)
ELP4 (chr11:31018381-31627465, hg18) (S value = -6.89)
FOXP1 (chr3:71482762-71697708, hg 18) (S value = -5.16)
ROBO1 (chr3:79287548-79620463, hg18) (S value = -5.57)
S2. DMRs affecting to genes in interest in AMHs (based on Gokhman et al. 2017)

COLAA2
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FOXP1
S3. DMRs affecting to gene of interest in Neanderthals (based on Gokhman et al. 2017)

DMRs that discriminate between the human groups are ranked according to their significance level (column 1). The coordinates of the DMR (columns 2 to 4) are referred to the GRCh37/hg19 assembly of the human genome. Methylation maps are from one Denisovan individual, two Neanderthals (Altai Neanderthal and Vindija Neanderthal), four ancient AMHs (Ust’-Ishim, Loschbour, Stuttgart and La Braña 1) and two present-day individuals (Bone1 and Bone2) (columns 6 to 13). The data considered in the analysis are highlighted in red (Neanderthal) and green (modern humans). We further provide with an average methylation value for Neanderthal samples (column 14) and AMH samples (column 15). Column 16 displays whether methylation signals are found within a CpG island (1) or outside a CpG island (0). Columns 17 to 24 show the position of the DMRs related to the closest genes and their transcription starting sites (TSS).
S4. DECIPHER patients bearing CNVs affecting to the full sequence of genes of interest (Table 2)

AUTS2

DECIPHER patient 279043
CACNA1C

DECIPHER Patient 290015
COL4A2

DECIPHER patient 278109

DECIPHER patient 273803
EGRI

DECIPHER patient 304609
FMRI

DECIPHER patient 284912
**FOX1**

**DECIPHER Patient 264639**