

**General information:** **Line 1 and 2** should contain the **title** of the study and an **author** name with Email address for contact as well as the detailed **geographic background** of the haplotypes. Also use regional characterization if appropriate.

**First block of sequences:** the first line of a block denotes the sequence range (here denoted in **line 3**); below the haplotypes are denoted line by line

optional:  
**Second block of sequences:** as haplotypes 4 and 5 have a different sequence range than haplotypes 1, 2, and 3, a **new range** is given in **line 7**; ht 5 shall not be considered for further analysis and is therefore commented out

	A	B	C	D	E	F	G	H	I	J
1	# Population data of 250 individuals from Austria; Walther Parson (walther.parson@i-med.ac.at)									
2	# 100 samples from Innsbruck, 100 samples from Salzburg, 50 samples from Vienna									
3	#! 16024-576									
4	haplotype1	H1c	1	16519C	263G	523DEL	524DEL	477C		
5	haplotype2	R0	1							
6	haplotype3	R0	1							
7	#! 16024-16365 73-340									
8	haplotype4	T2b	1	16126C	16294T	16296T	16304C	73G	263G	315.1C
9	#haplotype5	?	1	16223T	73G	263G	315.1C			
10										

**Column A:**  
haplotype names;  
don't use blanks,  
special characters  
and umlauts (ä, ö, ü)

**Column B:**  
haplogroups;  
unknown  
haplogroups are  
denoted as ,?'

**Column C:**  
frequencies; in this  
context they are all 1  
because of individual  
haplotype notation

**Column D and further columns:**  
differences to the rCRS;  
use forensic notation as outlined in  
the ISFG recommendations for  
mtDNA typing