

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