

## **File format of Y-STR/Y-SNP submissions to the YHRD**

Each row represents an unique male individual with Y-STR and optionally Y-SNP information together with the geographical position of sampling and the ethnic origin of that individual.

### **ID** - Reference (*mandatory*)

Give an anonymized identifier (e.g. ID01, ID02, ...) for reference. This information will not be public available.

### **Population** - Population name (*mandatory*)

Give a string which best describes you sample. It should be composed of a geographical position (e.g. „City, Country“, „Region, Country“ or „Country“) and the ethnicity in square brackets.

### **DYS19, DYS389I, DYS389II, DYS390, DYS391, DYS392, DYS393, DYS385** (*mandatory*)

Alleles of each locus of the minimal Y-STR Haplotype. Intermediate alleles are separated by dots („.“) and duplicated alleles by colon („:“). Type a single zero („0“) to indicate a deletion (even on duplicated loci, e.g. DYS385).

### **DYS438, DYS439, DYS437, DYS448, DYS456, DYS458, DYS635, YGATAH4** (*optional*)

Alleles of each locus of the extended Y-STR Haplotype (Powerplex-Y or Y-Filer). Type zero („0“) to indicate a deletion. If you didn't analyze a certain locus or got no results indicate that (entire row or single cell) with „-“.

### **Y-SNP Marker 1, Y-SNP Marker 2, ..., Y-SNP Marker N** (*optional*)

For each marker (from 1 to N) name the column and give the state of each individual at each marker with „-“ (ancestral), „+“ (derived) or „-1“ (not analyzed).

### **Final Marker** (*optional, mandatory if Y-SNP markers are given*)

Give the final marker name (last marker with derived state).

### **Haplogroup** (*optional, mandatory if Y-SNP markers are given*)

Give the phylogenetic haplogroup name. This information is used for validation purposes.