**Matlab® code used to obtain graphs from the similarity matrix obtained from 23andMe**

load 'matrix.dat'
thr=6;
table=tril(matrix);
table=table.\*(table >= thr);
bg=biograph(sparse(table),'','EdgeType','segmented','ShowWeights','off','ShowArrows','off','LayoutType','hierarchical');
bg.view;

**Supplementary Table 1:** Expected amount of shared genome between pairs of individuals separated by G number of generations, according to a model of independent sorting among lineages. Using data available from 23andMe we investigated the G range highlighted in gray.

|  |  |  |  |
| --- | --- | --- | --- |
| **G (number of generations apart)** | **prop of shared genome** | **Shared Mbp** | **N of potential ancestors** |
| **1** | 0.5 | 3030 | 2 |
| **2** | 0.25 | 1515 | 4 |
| **3** | 0.125 | 758 | 8 |
| **4** | 0.0625 | 379 | 16 |
| **5** | 0.03125 | 189 | 32 |
| **6** | 0.01563 | 95 | 64 |
| **7** | 0.00781 | 47 | 128 |
| **8** | 0.00391 | 24 | 256 |
| **9** | 0.00195 | 12 | 512 |
| **10** | 0.00098 | 6 | 1024 |
| **11** | 0.00049 | 3 | 2048 |
| **12** | 0.00024 | 1 | 4096 |
| **13** | 0.00012 | 1 | 8192 |



**Supplementary Figure 1** – Graphic representation of the Graph described by the adjacency matrix C(i,j). The connected subgraph at the left links 100 individuals.



**Supplementary Figure 2** – The same as in figure 3, considering only the edges corresponding to DNA-matches greater or equal to 12 Mbp. Isolated individuals and groups of two are not reported in the figure.