



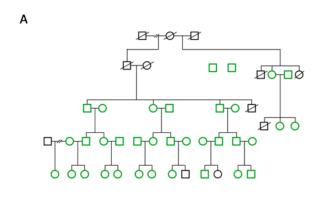
Supplementary Material

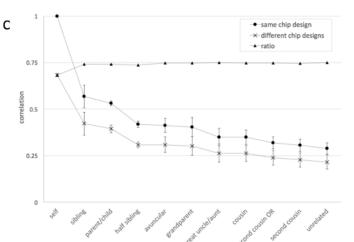
Genotype fingerprints enable fast and private comparison of genetic testing results for research and direct-to-consumer applications

Max Robinson and Gustavo Glusman*

* Correspondence: Gustavo Glusman: Gustavo@SystemsBiology.org

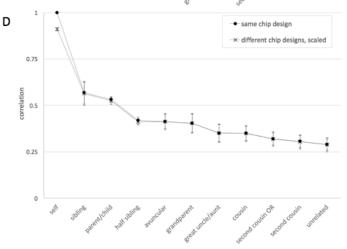
Supplementary Figure 1. Genotype fingerprints analysis of larger family pedigree. (A) Family structure. Individuals sequenced are labeled in green. (B) Number of pairs of individuals observed for different relationship distances. (C) Spearman rho vs. relationship distance when comparing fingerprints from the same chip design (circles) or different designs (crosses), and the ratio between them (triangles). (D) Spearman rho vs. relationship distance after scaling.





| Relationship | N |
|----------------------------|-----|
| self | 35 |
| sibling | 12 |
| parent/child | 39 |
| half-sibling | 2 |
| avuncular | 25 |
| grandparent | 22 |
| great uncle/aunt | 23 |
| cousin | 24 |
| second cousin once removed | 46 |
| second cousin | 40 |
| unrelated | 297 |
| | |

В



Supplementary Figure 2. Correlations between the genotype fingerprints of the 2504 individuals (rows) and the average fingerprints of the 26 populations (columns) in the 1000 Genomes Project, contrasting SNP lists V2 and V3 for the individuals and the populations. Population codes and colors as in Figures 3 and 4. Numbers in gold, white and black denote population assignments: to the same annotated population, to the same continent but different population, or to a different continent, respectively. Larger inset numbers denote totals for each of the three classification success levels.

