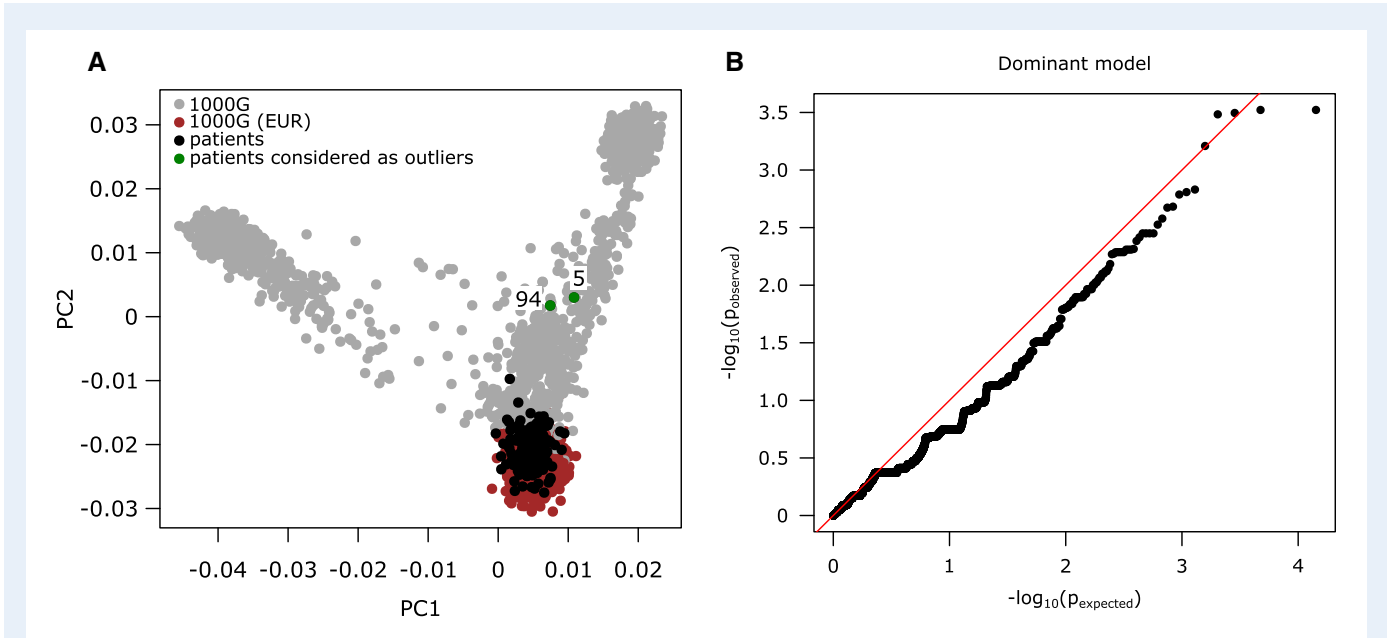


human reproduction SUPPLEMENTARY DATA



**Supplementary Figure S1** Assessment of the population structure of the patients and the quality of the variant set.

(A) Principal component (PC) analysis of the 1000 Genomes individuals (gray and red) overlapped with the initial 166 individuals from this project (black and green). The 1000 Genomes European individuals are labeled in red. Two individuals for this project, marked in green, were considered outliers and were removed from the analysis. (B) Observed versus expected gene mutation burden in the dataset. The analysis considered only synonymous variants with gnomAD\_NFE allele frequency <5%.