Supplementary note

1. Swedish cases were ascertained from the immunodeficiency clinics at the Karolinska University Hospital Huddinge, Stockholm and the Sahlgrenska University Hospital, Gothenburg. Controls were obtained from healthy Swedish blood donors (n=360) and consecutive samples from the Swedish national neonatal screening program for phenylketonurea (PKU) (n=720).

2. German CVID cases were ascertained from the Department of Rheumatology and Clinical Immunology at the University Hospital Freiburg, Germany. Controls were obtained from anonymous healthy German blood donors (n=100) and healthy donors recruited from personnel and medical students at the University Hospital of Freiburg (n=250). All cases and controls were of European Caucasian ancestry, which was ascertained by personal interview or a self-report questionnaire.

3. American cases were ascertained from the immunodeficiency clinics at Mt. Sinai Hospital, NY and the NCI/NIH, Bethesda, MD. Controls (n=787) were selected from the NY cancer project collection, and were matched to cases based on 4 grandparent self-report, when available. All cases and controls were of European ancestry. The American cases and controls were typed for 1500 SNPs across the genome, and STRUCTURE showed no evidence for population substructure.

4. The Swedish cases and blood donor controls and the American cases and controls were typed for 260 SNPs on 27 candidate genes, and STRUCTURE showed no gross stratification between the Swedish and the American samples, nor that the ancestry of any single sample is misclassified.