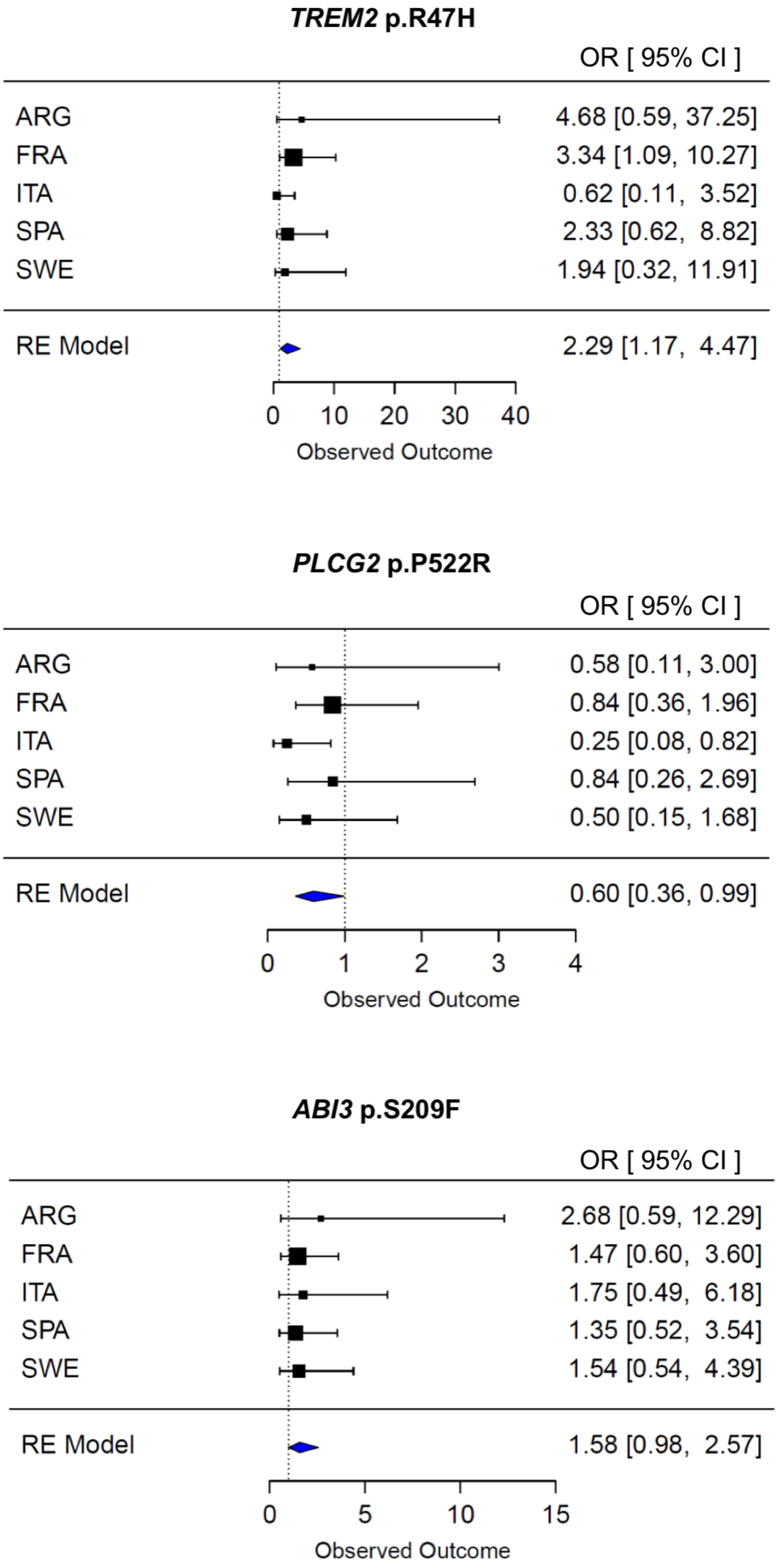

Figure S1. Meta-analysis of ARG and EADI samples. A random-effects (RE) model was used, which assumes that observed effect can vary across studies. ARG, Argentina; FRA, France; ITA, Italy; SPA, Spain; SWE, Sweden. Squared size represents population sample size.

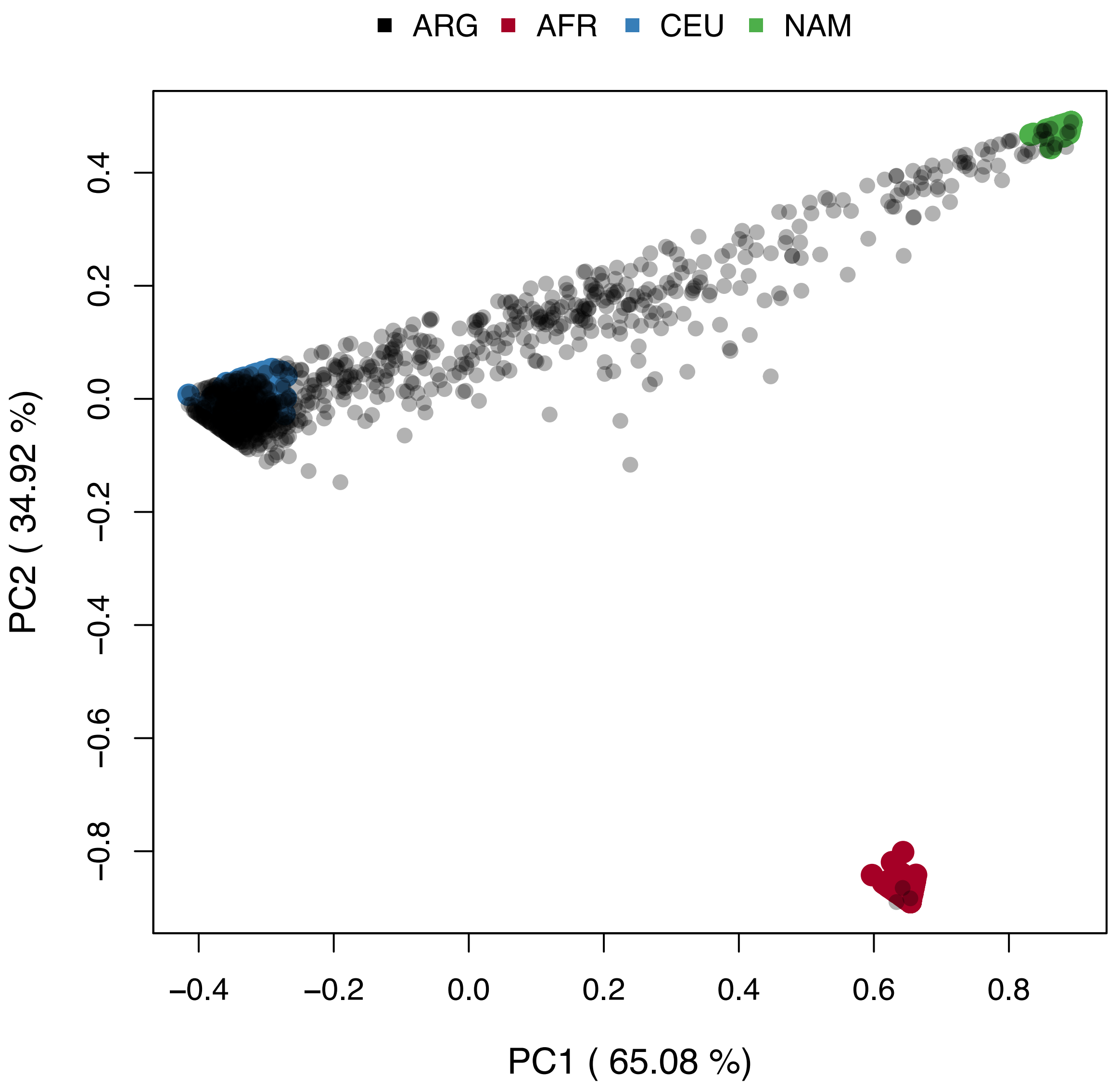

Figure S2. Ancestry of population. Principal component analysis of ancestry results. Black circles, Argentinian individuals (ARG); green circles, Native Americans (NAM); red circles, Africans (AFR); blue circles, Europeans (CEU). Percent of distribution explained by each principal component (PC) it is showed between parenthesis.

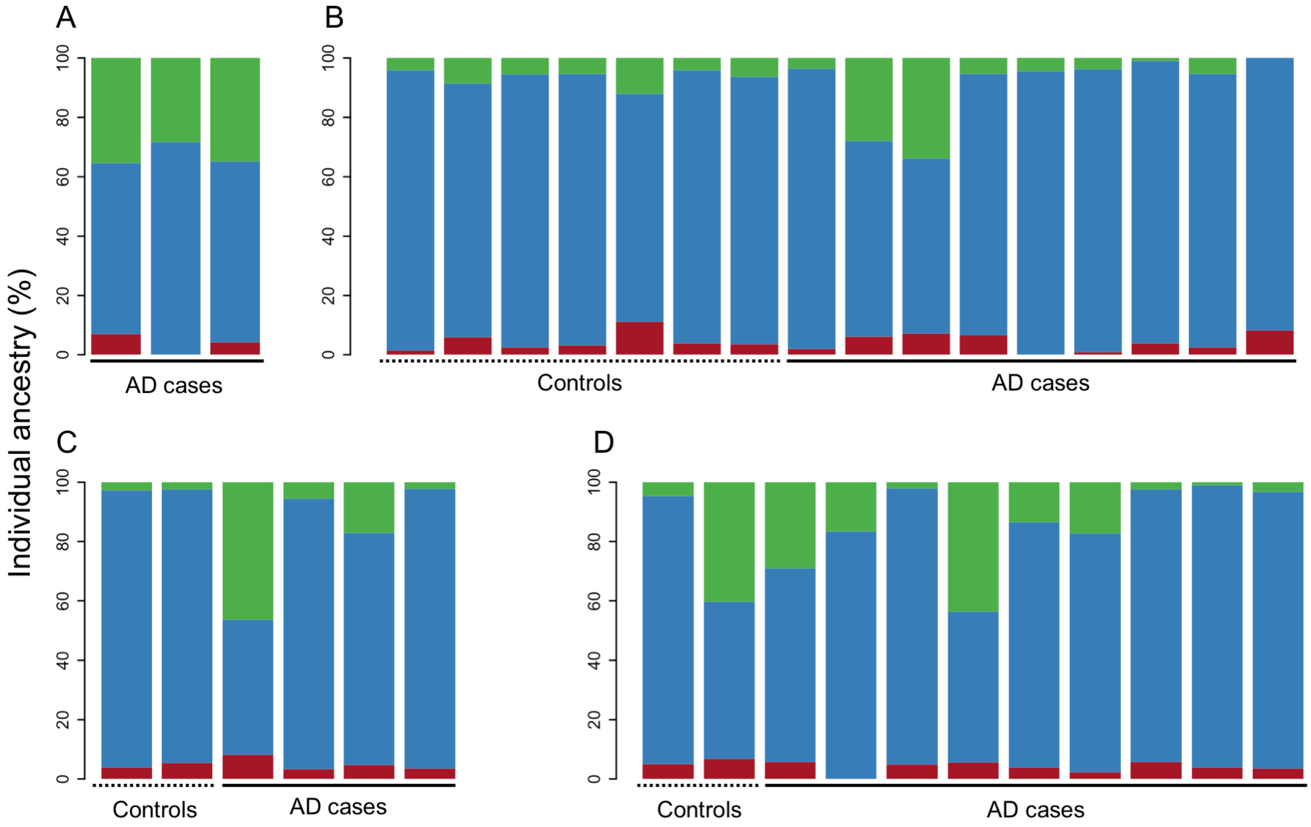

Figure S3. Individual ancestry proportion of people carrying a rare variant. Bar-plots representing each individual on the x-axis, and his percent of European (blue), African (red), and Native American (green) ancestry on the y-axis. **A.** *TREM2* p.R47H carriers. **B.** *TREM2* p.R62H carriers. **C.** *PLCG2* p.P522R carriers. **D.** *ABI3* p.S209F carriers.