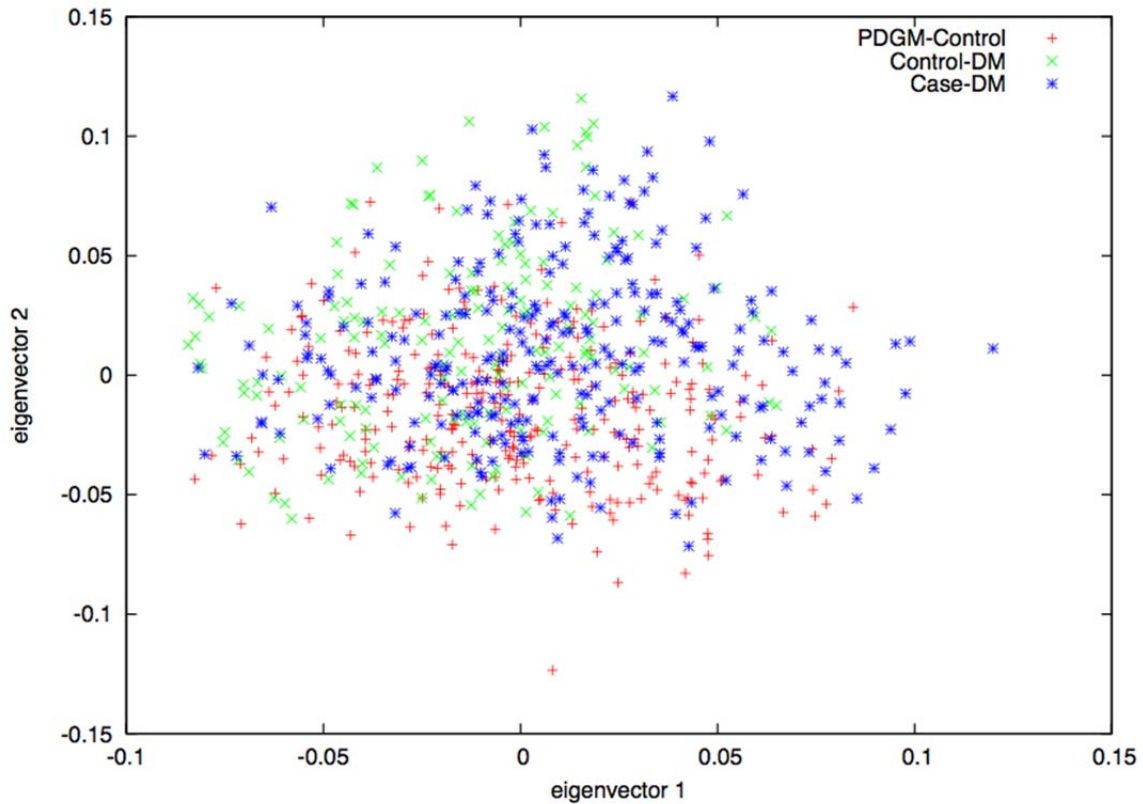


Appendix 2. Principal component analysis for the three samples groups used: Age-Macular Degeneration patients, healthy controls and population controls. The distribution of the ancestral components between case and control samples was assessed using 224 ancestry informative markers (AIMs) [24], which were SNPs with allele frequency differences (δ) ≥ 0.4 for pairwise comparisons between HapMap and Zapotecos groups.



PDGM-Control: Population controls from the Mexican Genomic Diversity Project; Control-DM: Healthy controls; Case-DM: Age-Macular Degeneration cases. Eigenvector 1 and 2 are vectors that represent the genetic diversity of the three groups analyzed.