

Investigation of Inversion Polymorphisms in the Human Genome using Principal Components Analysis

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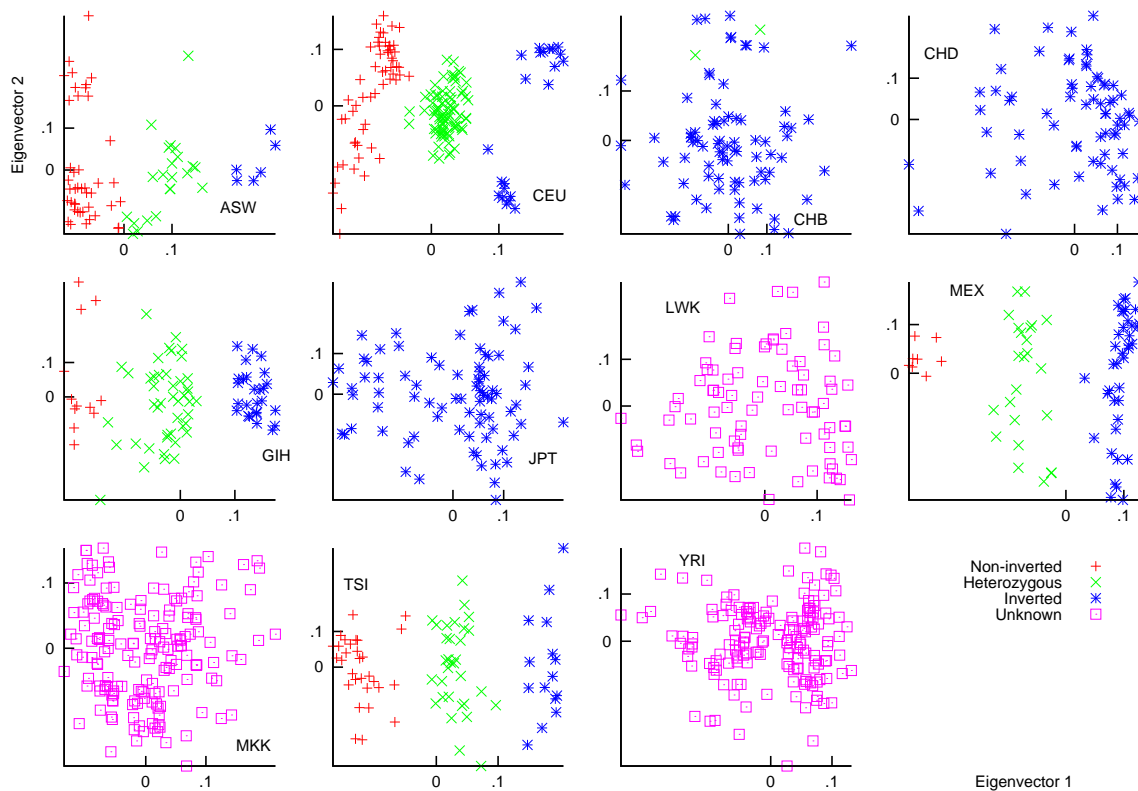


Figure S1. The first two eigenvectors obtained from PCA performed for each of the 11 HapMap populations using markers inside the 8p23.1 inversion region. The inversion genotypes were obtained by inspecting these single-population PCA results together with those from the PCA for pooled data shown in Figure 1 and Figures S2 and S3.