

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

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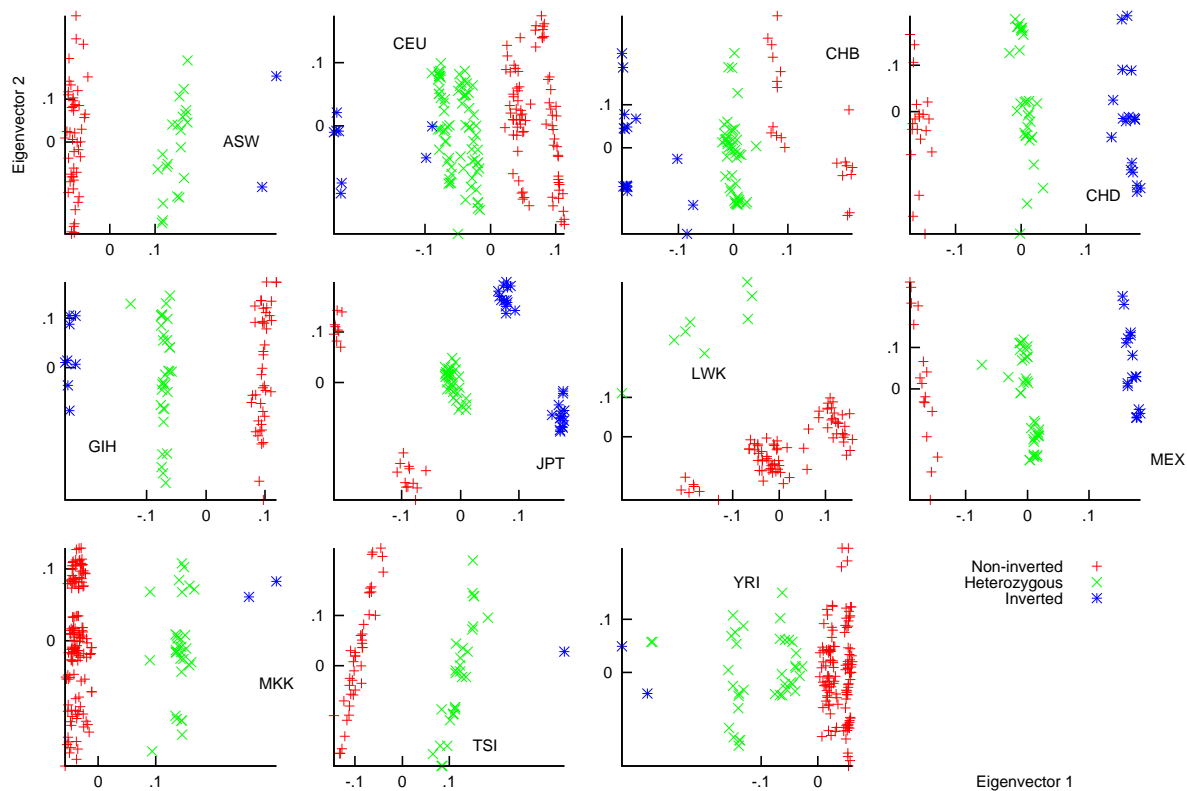


Figure S5. The first two eigenvectors obtained from PCA performed for each of the 11 HapMap populations using markers inside the predicted 3q21.3 inversion region. The inversion genotypes were obtained by inspecting Figure 9.