

Figure S2

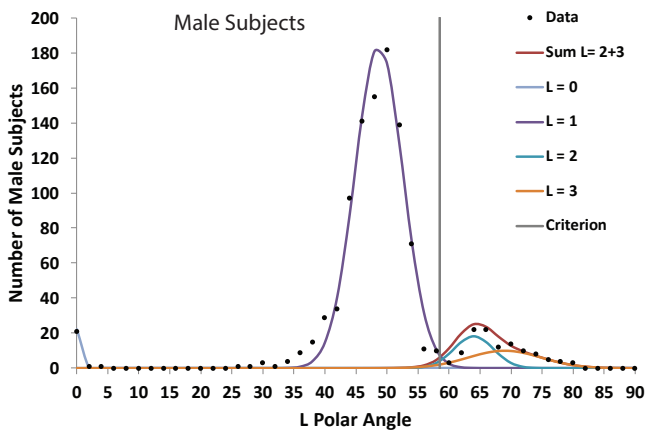


Figure S2. Illustration of the method used for clustering subjects with 1L gene compared to individuals with more than 1L gene. The black dots plot out the histogram values for polar angles from Figure 2 of the main text for the distribution for all males that had their color vision tested. Polar angle is related to the total number of L genes a male has. The histogram was fit to 1 Gaussian function representing all subjects with 1 L gene. Individuals estimated to have more than 1 L gene were fit with the sum of two Gaussian functions, one representing individuals with 2L genes and one representing individuals with 3L gene. The standard deviations are larger as the total number of genes increases. The place where the Gaussians cross is taken as the criterion separating 1 L gene subjects from those with >1 L genes. The area under the curves where they overlap provides an estimate of the rate of misclassification errors.