HYBRID DETERMINATION METHODS

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    To determine wether an individual is substantially admixed I first ran a STRUCTURE (version 2.3.4) analysis using all group size (k) values from 2 to 8 using all 1,344 *Zea mays* individuals from Mexico. I then used the resulting q-values in the web Application, "Structure Harvester" (version 0.6.93)(http://taylor0.biology.ucla.edu/structureHarvester/), to determine the best fitting k value based on delta k: The second order rate of change of the likelihood. The best fitting k was determined to be 3. I then made a histogram of "other teosinte attribution" in R, which means I determined what subspecies the individual was by it's largest q-value attribution then, if it is a teosinte, added the q-value attribution of the remaining teosinte to the dataset used to make the histogram. I decided based on the histogram that 25% other attribution was the best threshold to use. I then determined the most obvious admixed groups visually and set the criterion for inclusion into each group by falling into coordinate-based region surrounding the admixed populations. There were 3 such groups assigned and the coordinate cutoffs are X, X and X respectively.