README file: Constructing and plotting a principle component analysis for the *Medicago polymorpha* deep GBS populations

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In this experiment, we run a simple PCA on the *M. polymorpha* deep GBS populations. This is done to look at the clustering patterns of each population and is a way to verify the results that we see in the STRUCTURE analysis. This will be done using a single input file, called ‘Mpol\_deep\_pops\_whole\_labels.csv’. The first two columns of the input data are the Unique IDs of the individuals, and the populations to which they belong. Subsequent columns indicate the polymorphic loci.

The analysis is run using the r package adegenet (Jombart, T.) The file is named ‘PCA analysis and plot.R’. The code will calculate the percent variance at each axis, and requires an input of how many axes to run.

Reference: Jombart, T. 2015. An introduction to adegenet 2.0.0. http://adegenet.r-forge.r-project.org/files/tutorial-basics.pdf