FIGURE S1.—This figure gives a tableau of x-y plots based on the symmetric summary statistics, $S(X)$ computed from the genetic model. The summary statistics have been rotated using the R-function `prcomp`, as described in the main text. A selection of axes are plotted against each other. All points generated under the prior predictive distribution are shown (originally in black). Superimposed, in blue, are those points that are within tolerance limits. The red point corresponds to the target data. Note that since the axes are rescaled to have the same variance in the calculation of the tolerance width, whereas the plotted axes retain the original scale, the distribution of blue points is typically elliptical. In this example, since the data are generated under the assumptions of the model, the red point is typically well placed within the blue points, which are well placed within the black points.