**Assessing the variance in the “corrected” one-per-family datasets**

 To remove family structure from the datasets, we recommend resampling the dataset to include only one member from each family in the dataset. We also recommend resampling the dataset a large number of times because the range of values one could obtain is quite large if only a single one-per-family dataset is used (Fig. S3).

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**Figure S3**. Illustration of the range of values that were obtained by creating only a single one-per-family dataset (see main text for details). The plot shows pairwise FST values between schistosome infrapopulations of 12 human patients. Blue circles show the pairwise FST values of the raw, uncorrected datasets and green circles show the mean FST values of 1000 resampled datasets that include only one member of each family. Dotted lines show the range of pairwise FST values that were obtained from the one-per-family datasets. Note the large range of values, although most are smaller than the values from the raw datasets (red circles indicate the exceptions). The 95% confidence intervals that surround the mean of the 1000 samples are too small to plot (i.e., 1000 samples resulted in high accuracy and precision).