Start with a standard processing method such as: MAS 5.0, RMA, or dChip

Convert to log base 2 scale.

Create a data matrix with rows representing transcripts and columns representing samples.

Create a rank matrix of the same dimension as the data matrix and populate each column with the ranks of the transcripts in that column (sample) based on expression value.

Calculate the variance of each row (transcript) in the rank matrix.

Discard rows with the highest rank variance and also remove the corresponding rows from the data matrix.

Repeat 4 times, removing 1/4 of the difference between the starting transcript count and the selected number of approximate rank invariant transcripts to use each time.

The transcripts represented by the remaining rows are the Global Rank-invariant Set (GRiS).

For each sample, create a calibration curve by comparing the GRiS reference values to the GRiS values for that sample.

Reference values for each GRiS transcript are calculated by taking the trimmed mean across all samples.

Use lowess to smooth the calibration curve for each sample.

Repeat for each sample.

Done