Interpreting electropherograms can be an arduous task as bulk mixture pipelines produce electropherograms containing information from any number of, potentially partial, contributors, rendering Weights of Evidence (WoE) that approach zero as the mixture becomes more complex. Single cell treatments offer a way forward, by isolating, amplifying, and analyzing each cell, individually. This creates a set of electropherograms (EPGs) for each cell isolated, which are then grouped by similarity into clusters, where it is reasonable to assume a single common donor. By supposing the group of single cell EPGs (scEPGs) are replicates of one another, the logarithm of the likelihood ratio – i.e., WoE – for the cluster can be determined by comparing the probabilities of the cluster given a Person of Interest (PoI) contributed divided by the probability given a random person contributed. Though a variety of clustering approaches exist, we accomplish this by the model-based clustering application *mclust* in R. Once clustered, the group of scEPGs are evaluated and the LR for each cluster was calculated with EESCIt™, which stands for **Evidentiary Evaluation of Single Cells.** With EESIt™ being able to rapidly and reproducibly assess any number of scEPGs in any number of clusters in seconds, we perform a large-scale analysis on the implementation of two models to the EESCIt™ system: that of the normal and log-normal distributions to describe peak heights.

Specifically, 1,210 single cells were processed through a validated single cell pipeline to produce 1,210 scEPGs. The scEPGs were tested in EESCIt against the true contributor, s_{true}, and a false contributor, s_{false}, to produce logLRs with both models. As a result, there were 1,210•4 = 4,840 outcomes that were explored. When testing a sample against its true contributor, a positive logLR value is expected. Similarly, when testing a scEPG against a false contributor, a negative logLR value is expected.

Adhering to SWGDAM's guidelines for the validation of probabilistic genotyping systems, we tested the sensitivity of each model by calculating the proportion of scEPGs for which the logLR($scEPG$, s_{true})>0 and tested the specificity by calculating the proportion of scEPGs for the logLR ($scEPG$, s_{false})< 0. Preliminary results show that the normal peak model resulted in a logLR ($scEPG$, s_{true})>0 of 89.4% and a logLR ($scEPG$, s_{false})< 0 of 94.3%. The log normal model resulted in a logLR ($scEPG$, s_{true})>0 of 88.4% and a logLR (EPG, s_{false})< 0 of 92.4%. Notably, the reported sensitivities and specificities include the results when the scEPG carried minute levels of information or contained much allele drop-out. Therefore, in this study we go further and will report the robustness of these models by evaluating the logLR for each state, s_{true} or s_{false}, across total peak intensity. Additionally, Type I and Type II errors will be explored by genotype. The results for both models will be compared in the aggregate to determine which one to implement for single-cell applications.