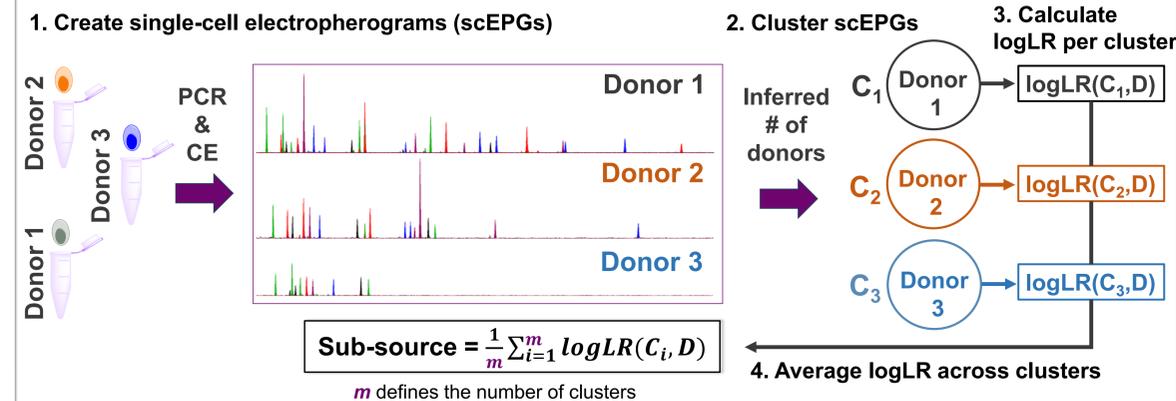


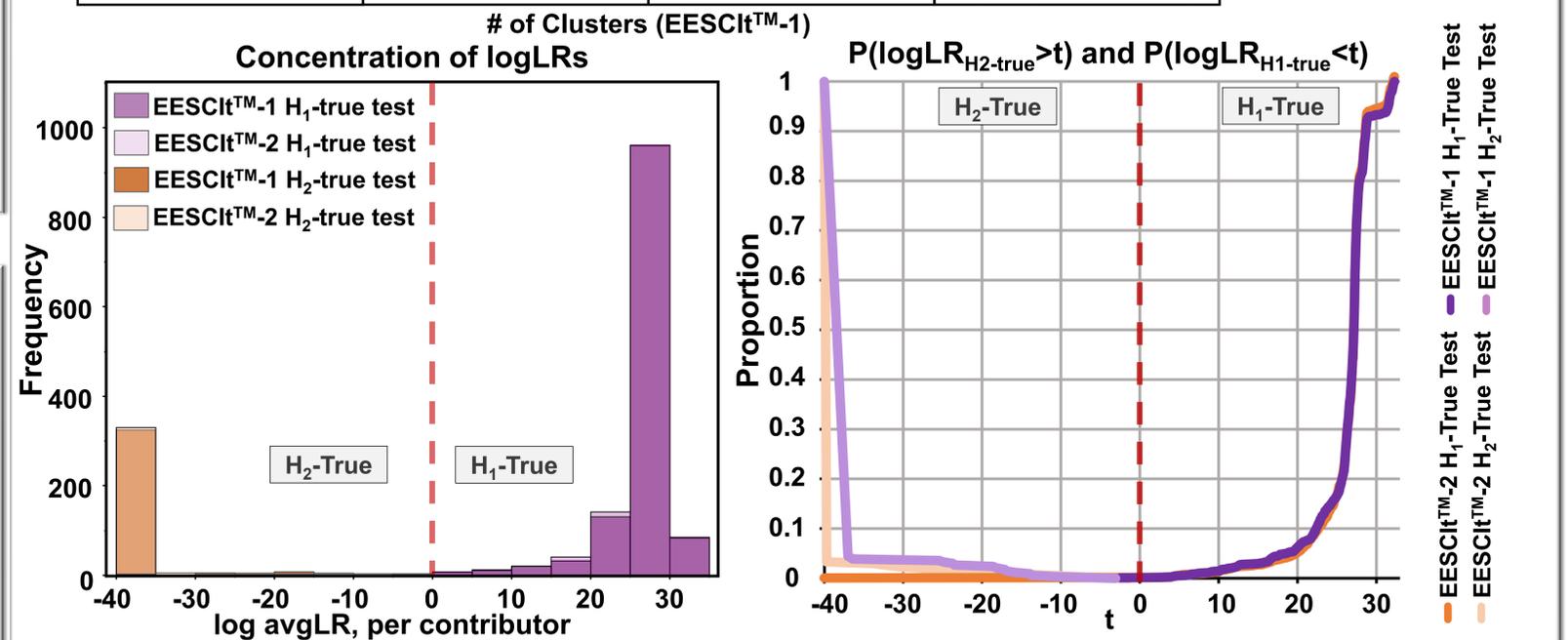
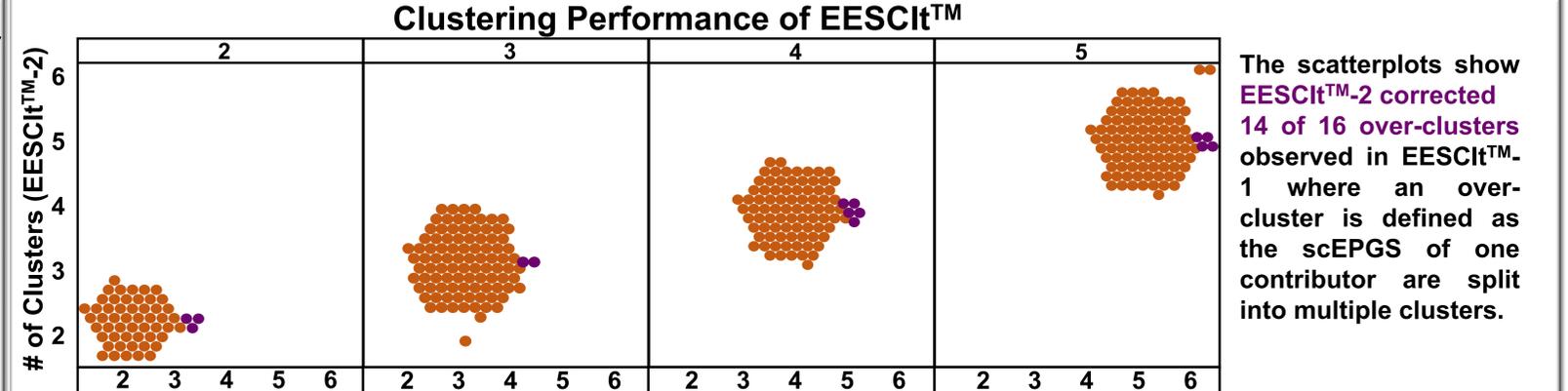
EVIDENTIARY EVALUATION OF SINGLE CELLS WITH EESCITM

Introduction

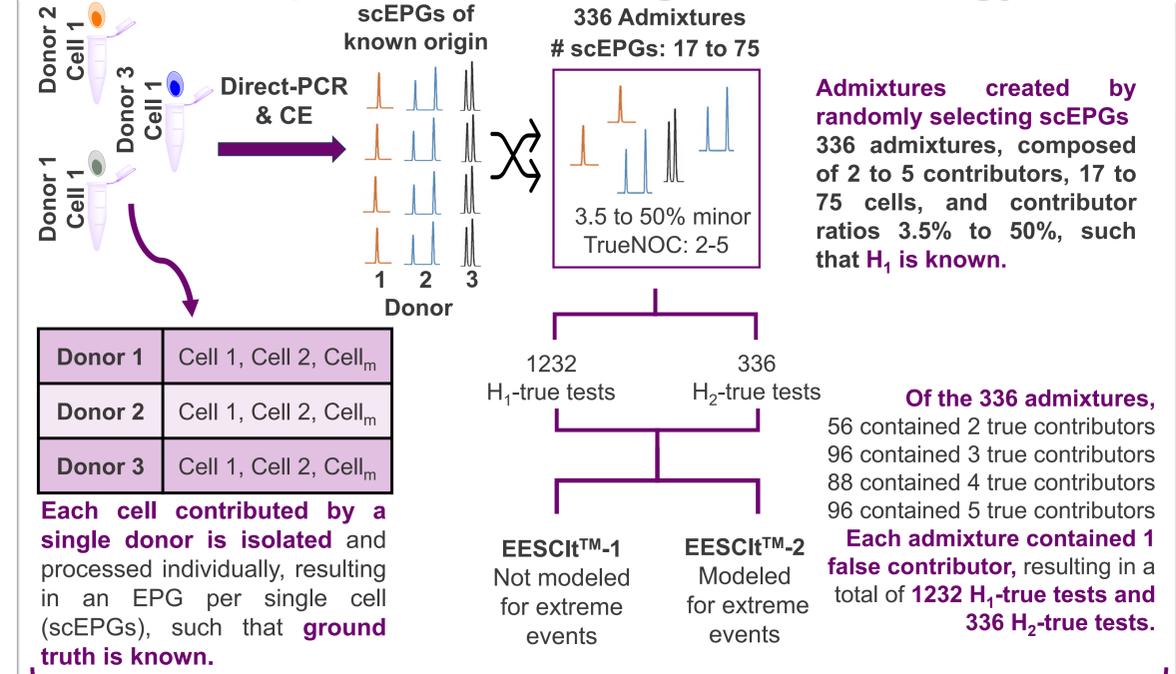


In single-cell pipelines, individual cells are isolated, amplified, and analyzed to generate single-cell electropherograms (scEPGs), which are then clustered into individual groups by EESCITM based on profile similarity where, ideally, each cluster contains scEPGs of a single donor. Each cluster is then assigned a logLR (log likelihood ratio) which is then averaged to determine the WoE, an average logLR, for a given donor. Building on previous work, where rare, extreme events were not modeled (EESCITM-1), we fine-tuned a version of EESCITM that factors extreme events (EESCITM-2) and evaluated its performance.

Results



Experimental Design/Methodology

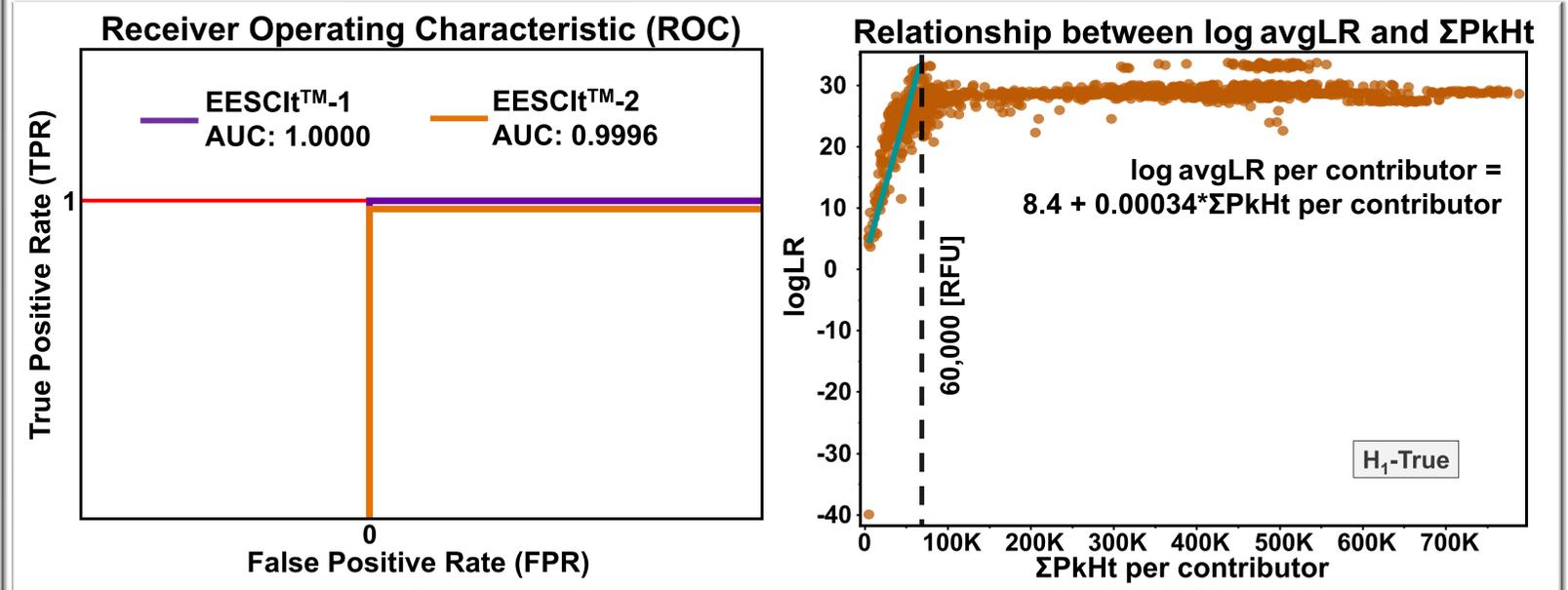
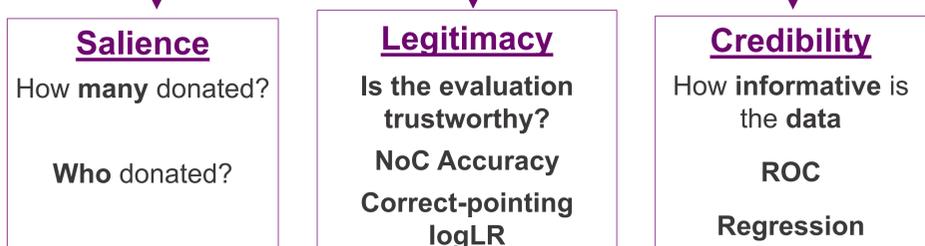


Donor 1	Cell 1, Cell 2, Cell _m
Donor 2	Cell 1, Cell 2, Cell _m
Donor 3	Cell 1, Cell 2, Cell _m

Each cell contributed by a single donor is isolated and processed individually, resulting in an EPG per single cell (scEPGs), such that ground truth is known.

Data Analytics

Saliency, Legitimacy, Credibility



The ROC curve shows EESCITM-2 is a near-perfect classifier of TPs and TNs while EESCITM-1 is a perfect classifier. In the linear regression, for each contributor, for every 2,900 RFU is a logLR increase of 1.

In conclusion, modeling for extreme events in EESCITM-2 improved clustering performance while maintaining a high discriminatory power for H₁-true tests and H₂-true tests, emphasizing the robustness of single cells in forensics.