

EVALUATION OF CUSTOM 2311 SNP MIXTURE PANEL FOR THE DECONVOLUTION OF COMPLEX MIXTURES

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One of the main challenges in forensic DNA analysis is the ability to separate (*i.e.*, deconvolute) the individual donors from a complex DNA mixture (*i.e.*, three or more individuals). Probabilistic genotyping (*e.g.*, using STRMix software) in conjunction with standard STR typing has enabled the resolution of more than three mixtures when assumptions, such as the number of contributors and reference profiles, are provided towards estimating evidentiary weight for mixture interpretation. Recently, a custom 2311 single nucleotide polymorphisms (SNP) panel was developed by the Massachusetts Institute of Technology Lincoln Laboratory (MIT-LL) which can resolve highly complex mixtures containing up to ten individuals without conditioned assumptions (*e.g.*, the number of contributors). Advantages of that panel, compared to STR typing and probabilistic genotyping, include increased discriminatory power due to the simultaneous analysis of significantly more loci, relatively low drop-in rate, and lack of stutter artifacts. This current study assessed the custom SNP panel and corresponding custom ID Prism Mixture Software, which included testing of 1) serially diluted single source samples (*i.e.*, 10 ng-10 pg) to evaluate method sensitivity and reproducibility, 2) blind mixture samples to determine robustness and accuracy of the method, and 3) several mixtures prepared to simulate complex forensic mixtures (*i.e.*, 2-10 person mixtures) in various proportions (*e.g.*, 30 pg-10 ng) and total template amounts (*e.g.*, 10 pg-10 ng) to identify potential limitations of the method. Results from this study, demonstrated that sufficient library yields for sequencing were achieved with as little as 10 pg of input DNA. Moreover, this method was able to resolve complex mixtures (*e.g.*, up to ten individuals) and identified both major and minor contributors with DNA input ratios as low as 1:100 for 1st degree relatives. Mixture proportions obtained from the ID Prism software output were concordant with the expected proportions and the software provided a user-friendly interface for interpretation.