

EVALUATION OF DEGRADATION OPTION IN PROBABILISTIC GENOTYPING ANALYSIS OF STR MIXTURE DATA USING TRUEALLELE® TECHNOLOGY

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The TrueAllele® Casework system is a computerized DNA interpretation system that objectively infers genotypes from evidence data, which can then be compared to reference genotypes. Before TrueAllele® processing, an analyst reviews the quality of STR data of each sample to assess the contributor number and degradation for setting a request for processing. The Degraded option is off by default in the Request Module of the TrueAllele® Casework system. If the analyst notices a pattern of differential decay in the data where at least one contributor's peak contribution dissipates at the larger molecular weight loci at a faster rate than the others, the *Degraded* option can be turned on to account for this degradation.

To determine if the Degraded option affects the probabilistic genotyping results, the STR data from degraded samples was processed both with and without the *Degraded* option using the TrueAllele® Casework system. Furthermore, increased number of burn in and burn out cycles were used for the Degraded option to determine the effect on the probabilistic genotyping results.

This study shows that when data is degraded the use of the Degraded option with increased number of burn in and burn out cycles using the TrueAllele® Casework system can help achieve concordant probabilistic genotyping results between multiple runs. When degraded samples are processed without the use of the *Degraded* option, the probabilistic genotyping results between multiple runs are often not an accurate representation of the data and/or not concordant.