

COMPARISON OF STR ANALYSIS RESULTS FROM .HID AND .FSA FILES USING GENEMARKER® HID

Teresa Snyder-Leiby, Xin Li, Jonathan C.S. Liu
SoftGenetics LLC, 100 Oakwood Ave., State College, PA 17803

Forensic laboratory quality assurance standards require that prior to entry into a searchable category, DNA genotypes must be verified by two concordant reviews. This may be accomplished by two individuals using the same analysis software or by two individuals using different analysis software. The recently available Applied Biosystems™ 3500 Genetic Analyzer exports STR data files in an .hid format; compatible with GeneMapper® ID-X v1.2 and the newly available GeneMarker HID v 1.95. This study demonstrates the suitability of GeneMarker HID as an analysis software option for raw data analysis from .hid files.

This analysis compared the genotyping results for 154 duplicate samples: one .hid sample set from an AB 3500 Genetic Analyzer and a replicate set of .fsa files from an AB 3130 Genetic Analyzer. Sample pairs were amplified with Identifiler® Plus, PowerPlex® 16 HS or PowerPlex® **ESI 17**. The genotyping results were concordant, obtaining the same STR profiles in both .fsa and .hid formats.

GeneMarker HID imports .hid files and provides accurate, rapid analysis of the raw data. Resultant genotypes may be exported in CODIS format, printed in a final allele report, undergo additional analysis in GeneMarker HID's mixture analysis tool, or submitted to the GeneMarker HID relationship testing database for searches and kinship analysis. GeneMarker HID is supported on Windows® 7, Vista and XP.

References:

1. Quality Assurance Standards for Forensic DNA Testing Laboratories
<http://www.cstl.nist.gov/strbase/QAS/Final-FBI-Director-Forensic-Standards.pdf>
2. Data files kindly provided by Caroline R Hill, National Institute of Standards and Technology, Biochemical Science Division, 100 Bureau Drive MS 8311, Gaithersburg, MD 20899-8311