TECH TIPS

Using GeneMapper® *ID* with Promega STR Systems

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What is GeneMapper® *ID*?

GeneMapper® *ID* combines the functionality of the GeneScan® and Genotyper® software programs into a single analysis package designed to meet the needs of human identification applications. Originally released as GeneMapper® *ID* Version 3.1 in 2003, the software was upgraded to GeneMapper® *ID* Version 3.2 in 2005 to extend operating system compatibility and analysis options and features. In addition, the newer versions of data collection software installed on ABI capillary electrophoresis instruments better integrate the transition between data collection and analysis with the GeneMapper® *ID* software and offer limited compatibility with GeneScan® and Genotyper® software. The GeneScan® and Genotyper® software applications have been discontinued by Applied Biosystems.

Can GeneMapper® *ID* be used to analyze data from the PowerPlex® Systems and other multiplex STR amplification systems?

Absolutely. The software easily extends to the analysis of nearly any STR system. The software also contains a variety of analysis features that can be used for other fragment analysis applications. Analysis of alternative STR kits with the software only requires that the user provide analysis files specific to the chemistry being used. The macros used to analyze data using the Genotyper® software have been replaced by "panel" and "bin" files. These files are text-formatted, tab-delineated tables, which can be easily customized to meet individual laboratory requirements. The panel file contains the locus size range, repeat number, stutter filter values, allelic ladder and positive control sample information, while the bin file contains bin-positioning information for making allele calls.

How can I obtain panel and bin files for analysis of PowerPlex® System data with the GeneMapper® *ID* software?

Promega offers panel and bin file sets for GeneMapper® *ID* Version 3.1 and GeneMapper® *ID* Version 3.2. These can be downloaded at: **www.promega.com/geneticidtools/panels_bins**/. After completing a brief customer information form, the panel and bin files as well as instructions are directly downloaded as a zipped file. The file sets contain the information needed for analysis of PowerPlex® 16, PowerPlex® Y, PowerPlex® ES, and PowerPlex® 1.2 Systems, as well as Penta E, Penta D, and SE33 Monoplex Systems and *GenePrint*® Fluorescent FFFL and CTTv STR Systems. For assistance in developing panel and bin sets for other Promega systems and chemistries, contact Promega Technical Services at: **genetic@promega.com**

I have been using GeneMapper® *ID* Version 3.1 with PowerPlex® 16 but have recently upgraded to GeneMapper® *ID* Version 3.2. Do I need new panel and bin files?

While your old files will work with GeneMapper® *ID* Version 3.2, we recommend obtaining panel and bin files specific for GeneMapper® *ID* Version 3.2. This version offers a number of analysis improvements over Version 3.1, including full compatibility with tri-, penta-, and hexanucleotide repeat analysis. While the pentanucleotide loci Penta E and Penta D can be successfully analyzed with GeneMapper® *ID* Version 3.1, Version 3.2 offers precise stutter filter capability for these loci. The updated panel and bin file set is required to take advantage of this improvement.

Can I use other versions of GeneMapper® software to analyze PowerPlex® reactions?

Applied Biosystems offers a separate data analysis software program named GeneMapper® Software. The most recent version is GeneMapper® software, Version 3.7. This analysis platform can be used for a variety of fragment analysis needs but is not validated for forensic use. Also, it lacks many features needed for proper analysis of forensic STR data. Promega does not recommend it as an alternative to GeneMapper® *ID* for analysis of PowerPlex® Systems.

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Our lab will be converting from GeneScan® and Genotyper® software to GeneMapper® *ID* Version 3.2. What do we need to start validating this new software?

The first step is to download the panel and bin files for GeneMapper® *ID* Version 3.2 from: **www.promega.com/geneticidtools/panels_bins**/. A "readme" file is included to help you import the panel and bin files into GeneMapper® *ID*, set up a new analysis method, and create a new size standard. For additional guidance, Applied Biosystems provides a software tutorial at: **http://docs.appliedbiosystems.com/pebiodocs/04357520.pdf**

The GeneMapper® *ID* software can be used to analyze data collected on instruments with both Macintosh® and PC operating systems. Macintosh® data must first be converted to a PC format before adding samples to a new project. Initial validation of the software might involve analysis of data sets previously processed using GeneScan® and Genotyper® software to confirm concordance of the GeneMapper® *ID* results. If you are also implementing instrument hardware or software upgrades, a more lengthy validation process may be required. Individual laboratories should consider their regulatory requirements and tailor their validations to these requirements. In the United States, the Scientific Working Group on DNA Analysis Methods (SWGDAM) and Scientific Working Group on Digital Evidence (SWGDE) have issued validation recommendations that can provide guidance.

How can I analyze samples with a 20% filter similar to the Power 20% macro that I currently use for database analysis using Genotyper®?

A 20% filter can be easily applied by setting the cut-off value (Figure 1) to 0.2000 for each repeat type present in the STR system being used. For PowerPlex® 16, the cut-off value must be set for both tetra- and pentanucleotide repeats. For the PowerPlex® Y System, the trinucleotide repeat type must also be set to accommodate the trinucleotide marker present in that system.

If I have trouble analyzing PowerPlex® data using the GeneMapper® *ID* software, whom can I contact for help?

Promega Technical Services Scientists with hands-on training with PowerPlex® Systems and Applied Biosystems instrumentation and software, including GeneMapper® *ID*, are available by phone or e-mail. These Genetic Identity Support Specialists have GeneMapper® *ID* Version 3.2 installed on their workstations, allowing you to share data files and obtain real-time support by phone. We are happy to help troubleshoot data analysis and display problems, as well as any possible chemistry issues. You can reach Promega Technical Services by phone at 800-356-9526 in the U.S. or by e-mail at: **genetic@promega.com**
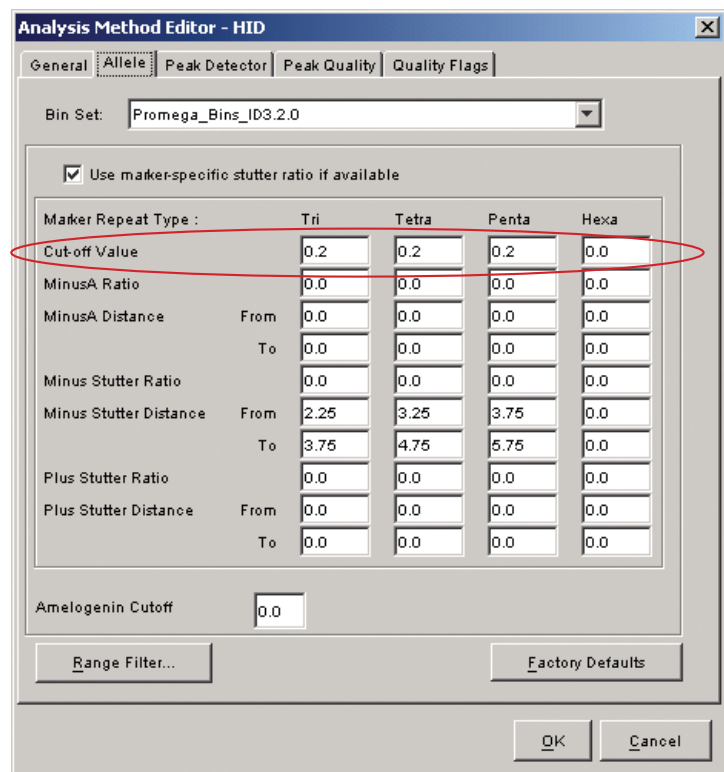

Figure 1. An example of Analysis Method Allele settings for applying a 20% filter when using the Promega PowerPlex® STR Systems and GeneMapper® *ID* Version 3.2.