August 31, 2005

Dear Valued GeneMapper® *ID* Customer,

The purpose of this communication is to address customer's questions regarding the presentation of sample information in GeneMapper® *ID* software v3.2.

When a sample file using GeneMapper® *ID* software v3.2 is created during data collection, all of the specific information, e.g. injection time and voltage for that particular sample is imbedded in the file.

A project can be created within GeneMapper® *ID* software v3.2 for analysis of a given set of sample data files in a run folder. The information listed within the "Sample Info" tab of GeneMapper® *ID* software v3.2 adopts a single set of values for all samples within a folder of data imported into the software. The values adopted are randomly chosen from one sample file within the folder. This is for reporting only, the original file information is not lost or overwritten.

What does this mean? If files that are run using two different injection conditions are combined into the same project folder then, for some of those files, the injection conditions presented in the "Sample Info" tab will be different from the run conditions that were actually used for those particular sample files. For example, if you were to combine files from a 5 sec 3 KV injection with files from a 10 sec 3 KV injection into the same run folder, GeneMapper® *ID* software v3.2 will report only the information for the selected file. However, information in the files is not overwritten. If the files are split into separate folders where all files in a folder have the same run conditions then the correct values will be reported.

GeneMapper® *ID* software v3.2 assumes that all of the files in a project are run under the same conditions and selects a single file to report run conditions. To align the reported injection parameters with the parameters imbedded in the sample file, users should arrange sample files injected using different parameters into separate folders. In choosing to do this, users must make sure there is at least one allelic ladder present in each new folder created in order for genotyping to occur. The user can then import all of the run folders into one project and analyze the data simultaneously.

If you have any further questions about this issue or would like to know more about the new features contained in GeneMapper® *ID* software v3.2 please contact your local field applications specialist or technical support professionals at 1-800-831-6844, press 5, press*, press 1, press 3.

Sincerely yours,

Applied Biosystems Human Identification Team