



# 1.7.0 Software Release Notes

For Navigator Software™ version 1.7.0

## Hardware Requirements

The software operates current 4500, WAVE (3500) and WAVE-MD instruments and runs on any computer that was running a previous version of the software.

## Software Requirements

The 1.7.0 client and server software can be installed on a new system or can upgrade version 1.6.3 or later.

The upgrades will not work automatically with versions earlier than 1.6.3 or with unpublished versions. Contact Transgenomic Customer Service for instructions on how to perform these upgrades.

## Upgrade Instructions

Two upgrade guides are now provided in PDF format. A Navigator server upgrade guide should be included on the server upgrade CD. In addition, a new client upgrade guide should be included on the client CD.

Please read all upgrade instructions carefully for 1.7.0

## New Features in Version 1.7.0

**Table 1: New Features**

Fragment Collector	<ol style="list-style-type: none"> <li>1. The fragment collector wash time has always been fixed at eight seconds. The user can now specify the wash time.</li> <li>2. A second vial naming convention has been added to Navigator™. The user can now report and view vials in A1, A2, B1, etc.</li> <li>3. First vial offset has been enabled</li> </ol>
Speed Plate	Added ability to exclude injection name index.
Import-Export	<ol style="list-style-type: none"> <li>1. Added protocol functionality</li> <li>2. Improved virtual method import</li> </ol>
Instrument Configuration	Equilibration can now be configured to include one or more blank injections. This eliminates the need to manually insert blank injections every time a different method is run.
Interface	Eliminated USB key on the 4500.
Protocols	<p>Added protocol template and protocol functionality.</p> <p>A protocol template is essentially a blue print for an assay. It contains all of the amplicons and methods that will be utilized on the WAVE system. Additionally, it contains the physical tray configuration, as well as the analysis parameters that will be used for mutation calling. Protocol templates are ideal for users that perform multi-exon assays. A set of subjects are run against multiple amplicons with one or more methods per amplicon.</p> <p>A protocol is an instantiation of a protocol template. In other words it is an actual run of a protocol template. At this point, a set of actual subjects are ready to run on the WAVE system. There is no limit to the number of protocols that can be created from just one protocol template.</p> <p>Utilizing protocols as part of a workflow provides many benefits:</p> <ol style="list-style-type: none"> <li>1. A protocol template can be used repeatedly to guarantee a consistent workflow.</li> <li>2. Sample tray setup time is significantly decreased. All of the injections will be automatically created based upon the protocol template.</li> <li>3. Automated mutation calling can be performed once a method has completed.</li> <li>4. Protocol injection data is grouped by amplicon and method, instead of by tray. This makes it much easier to access and analyze data.</li> <li>5. Every injection can be assigned a mutation call, which will be persisted in the WAVE system database.</li> <li>6. Reviewers will be utilized when making mutation calls. This provides traceability for the analysis done on each injection.</li> <li>7. A history of the mutation calls, comments, call date, control injections and reviewers is maintained in Navigator™.</li> </ol>

**Table 1: New Features**

	<ol style="list-style-type: none"> <li>8. Extensive protocol reporting and export functionality can be utilized to generate impressive and useful results.</li> </ol>
Reports	<ol style="list-style-type: none"> <li>1. Injection run report has been added. This report allows the user to see all of the injections that were run in a given time range.</li> <li>2. Added ability to save reports by object name. Analysis report can be saved by injection name. Subject report can be saved by subject name. Protocol Amplicon report can be saved by amplicon name.</li> <li>3. Analysis report performance increase.</li> </ol>
Sample Trays	The sample tray position can now be modified even after the tray has been created.

## Major Fixes in Version 1.7.0

**Table 2: Major Fixes**

Backup Utility	<ol style="list-style-type: none"> <li>1. Recovery no longer fails when the c:\temp directory does not exist.</li> <li>2. Support request no longer fails if log files are missing. Previously if one of the logs was missing, it would corrupt the support request file.</li> </ol>
Import/Export	Corrected handling of virtual method import with the same timestamp.
Interface	Turbo oven leaks were not always detected immediately. This has been corrected.
Oven Calibration	Wave-MD and 4500 oven calibrations would fail if the Oven Calibration maintenance event was modified. The maintenance event can no longer be modified.
Peak Picker	<ol style="list-style-type: none"> <li>1. The peak picker algorithm now clears the previous peaks and baseline, even when no new peaks are calculated. Previously, the old peaks would remain on the analysis page.</li> <li>2. When new baselines are calculated, they are immediately updated on the analysis page. Previously, the data had to be reloaded before the new baseline would appear.</li> </ol>

## Known Issues in Version 1.7.0

**Table 3: Known Issues**

DNA tab	<p>The size limit in the editor for sequence context is 30,000 characters. When importing large sequences from mutationDiscovery.com, the file is parsed into multiple "blocks" not exceeding the 30,000 character limit.</p> <p>In some cases, imported web data (from mutationDiscovery.com) does not show features when the format button is pressed. As a workaround, please close the client and log back in.</p> <p>Deleting sequence across line breaks may inappropriately prevent the user from editing the end of the sequence. The user may select another sequence, then reselect the initial sequence to continue editing.</p>
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## Questions About 1.7.0

Please contact Transgenomic Technical Support by visiting: <http://www.transgenomic.com> and following the Support link.

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