

## System Requirements

NimbleScan system requirements depend on the type of NimbleGen® microarrays with which you work. The key differences to note are that if you will be working with scanned images acquired from NimbleGen HD2 1-plex arrays (2.1 million probes), your system must include a 3GHz, 64-bit processor and 8GB of memory.

System Component(s)	The components below are compatible with the following array formats: <ul style="list-style-type: none"> <li>• 385K 1-plex arrays</li> <li>• 385K multiplex arrays</li> <li>• HD2 multiplex arrays</li> </ul>	The components below are compatible with the following array formats: <ul style="list-style-type: none"> <li>• 385K 1-plex arrays</li> <li>• 385K multiplex arrays</li> <li>• HD2 multiplex arrays</li> <li>• HD2 1-plex arrays</li> </ul>
Operating System	Microsoft Windows 2000®, XP®, or Vista® MacOS® 10.3 or later, with Java 1.5 or later Linux Kernel 2.4 or 2.6	Microsoft Windows Vista® x64 MacOS® 10.5, with Java 1.5 or later Linux Kernel 2.6
Processor	1GHz	3GHz, 64-bit
Memory	2GB	8GB
Hard Drive Disk Space available for installation	10MB	10MB
Monitor	XVGA 1024x768 with 16-bit colors	XVGA 1024x768 with 16-bit colors
Keyboard and Mouse	Standard	Standard

## Workaround

**HD2 1-plex users - Starting NimbleScan software to use 64-bit Java on Mac OS 10.5:** The NimbleScan installer currently does not support the 64-bit Java platform on Mac OS 10.5. Thus, if you start NimbleScan software from the desktop, the software runs 32-bit Java with a memory allowance of 1.3GB, which is not sufficient for analysis of HD2 1-plex arrays. The suggested workaround is to start NimbleScan software from a terminal that runs 64-bit Java explicitly:

1. Bring up a terminal.
2. Change directory (`cd`) to where the NimbleScan software was installed. This directory should contain the various `.jar` files included with the NimbleScan software.
3. Start NimbleScan software using the following command. Type the entire command before pressing Enter.

```
/System/Library/Frameworks/JavaVM.framework/Versions/1.5.0/Commands/java -d64 -Xmx3500m -cp `echo *.jar | tr \ :` ngs.app.ns2.NimbleScan
```

## New Functionality

**Support for NimbleGen HD2 1-plex and multiplex arrays:** Enables you to burst (multiplex formats only), visualize, align, quantify, analyze, and produce reports for these arrays. Refer to the *NimbleScan User's Guide* for more information about working with HD2 1-plex and multiplex scanned images and data.

## Enhancements

**Sample Tracking analysis** was integrated into NimbleScan 2.4 software. You no longer need to download and run a utility to make this analysis available in the software. Sample Tracking analysis reports the presence of sample tracking controls added to a sample before hybridization. This report is useful for confirming the sample identity on each array, especially on a multiplex array. Refer to Chapter 6 in the *NimbleScan User's Guide* for more information on performing a Sample Tracking analysis.

**DNA methylation analyses** were integrated into the software. You no longer need to download and run a utility to make these analyses available in the software:

- **DNA methylation Find-Peaks analysis:** Reports a p-value (positive enrichment) score for each probe from the scaled  $\log_2$ -ratio data. The report identifies statistically significant peaks, within the p-value data, which likely represent regions of DNA methylation. Refer to Chapter 6 in the *NimbleScan User's Guide* for more information on performing a DNA methylation Find-Peaks analysis.
- **DNA methylation Map-Peaks analysis:** Generates a report that maps DNA methylation peaks to the transcription start site (or other specified feature) of a gene. Refer to Chapter 6 in the *NimbleScan User's Guide* for more information on performing a DNA methylation Map-Peaks analysis.

These **CGH capabilities** were enhanced:

- **segMNT algorithm:** This algorithm has been upgraded from v1.0 to v1.1. The upgraded algorithm provides optimized performance with HD2 arrays. Refer to Appendix B in the *NimbleScan User's Guide* for details on the segMNT algorithm and how it compares to the DNACopy algorithm.
- **PDF plotting:** Additional options provide greater flexibility for analysis and display of CGH data in portable document format (PDF). Refer to Chapter 6 in the *NimbleScan User's Guide* for more information on generating PDF files for a CGH-segMNT or CGH-DNACopy analysis.