



cnvPartition v2.3.4 CNV Analysis Plug-in for GenomeStudio™ and KaryoStudio Software

1. General Information

The cnvPartition CNV Analysis Plug-in is a software library that works with Illumina's GenomeStudio data analysis software and KaryoStudio cytogenetics software. This document provides information about downloading, installing, and using the cnvPartition CNV Analysis Plug-in.

2. Version History

Build	Date
v2.3.4 for GenomeStudio and KaryoStudio Software	03/09/09
<ul style="list-style-type: none">Increased accuracy for calling smaller-sized CNVs.Improved logic for detecting CNVs on the sex chromosomes. Based on gender information from the sample sheet, single copies of X chromosomes are ignored for males.	
Build	Date
v2.2.1 for GenomeStudio and KaryoStudio Software	01/22/09
<ul style="list-style-type: none">cnvPartition v2.2.1 is compatible with Illumina's GenomeStudio and KaryoStudio software. NOTE: There are two different versions of cnvPartition v2.2 for KaryoStudio—one for 32-bit systems and one for 64-bit systems. Be sure to install the version of cnvPartition that is compatible with your computer.The cnvPartition algorithm now ignores Y-chromosome probes for females.The cnvPartition algorithm now ignores probes with NaN or a missing value for the Log R Ratio.Changed the minimum value for MinHomozygousRegionSize from 10Mb to 5Mb	
Build	Date
v1.2.0 for BeadStudio	10/10/08
<ul style="list-style-type: none">Added configuration fileAll chromosomes starting with letter "M" are now recognized as mitochondrial.B Allele Frequency is now ignored for Intensity Only probes.Added configuration option to detect extended regions of homozygosity such as copy-neutral LOH (default = True)Added configuration option for the minimum size of a detected region of homozygosityAdded configuration option to ignore CNV regions with less than a minimum number of probes defined by the user (default=3)	



Build	Date
v1.0.2 for BeadStudio	3/11/08
<ul style="list-style-type: none">Added Confidence Threshold parameter—any CNV region with a confidence lower than this value will be removed from the CNV output. The recommended default is 35.Added Probe Gap Size Threshold parameter—a CNV region overlapping with a probe gap larger than this value will not be created. Helps prevent CNV regions from being found across centromeres and other large probe gaps. The recommended default is 1,000,000 base pairs.The internal expected Log R Ratio mean and standard deviation values for each copy number value have been changed to better reflect actual Log R Ratio values seen in normal HapMap samples. This results in higher overall accuracy and precision.	
Build	Date
v1.0.1 for BeadStudio	1/29/08
<ul style="list-style-type: none">Improved detection of smaller CNVsBoth Log R Ratio and B Allele Frequency are used as inputs.Mitochondrial SNPs can be included in an analysis (optionally).The CNV Confidence score is now calculated.	
Build	Date
v0.9.3 for BeadStudio	09/04/07
<ul style="list-style-type: none">Improved classification of CN = 0 regions (homozygous deletions)Lowered the Min SNPs Per Bin parameter default to ten (from 30) to improve detection of CN = 0 regions (homozygous deletions)	
Build	Date
v0.9.2 for BeadStudio	07/23/07
<ul style="list-style-type: none">First release	

3. Downloading and Installing the cnvPartition CNV Analysis Plug-in

1. Download the cnvPartition CNV Analysis Plug-in from one of three places:

- The GenomeStudio Portal
- The software downloads section of [iCom](#)
- The [illumina•connect](#) web page

If you are installing the cnvPartition plug-in to use with GenomeStudio software, the setup program places the *.dll and configuration file into this GenomeStudio directory on your computer:

[C:\Program Files\Illumina\GenomeStudio\CNVAlgorithm\cnvPartition](#)





If you are installing the cnvPartition plug-in to use with KaryoStudio software, the setup program places the *.dll and configuration file into this KaryoStudio directory on your computer:

<C:\Program Files\Illumina\Illumina KaryoStudio\CNVAlgorithm\cnvPartition>

2. Run the setup program for the plug-in.
3. Follow the instructions in the installation prompts.

4. Using the cnvPartition CNV Analysis Plug-in

1. Do one of the following:
 - a. Open a genotyping project using GenomeStudio software.
 - b. Open a cytogenetics project using KaryoStudio.
2. [\[KaryoStudio\]](#) Note the version number of cnvPartition displayed in the software application title bar. This version of KaryoStudio will automatically be used to process your data.
[\[Optional\]](#) Adjust the cnvPartition parameters as needed (see Section 5 of this document).
3. [\[GenomeStudio\]](#) Select **Analysis | CNV Analysis**.
The CNV Analysis dialog appears.
4. Select **Create New CNV Analysis | cnvPartition v2.2.1**.
5. In the CNV Analysis Name area, enter a name for this CNV analysis.
[\[Optional\]](#) Adjust the cnvPartition parameters as needed (see Section 5 of this document).
6. Click **Calculate New CNV Analysis**.
7. When the analysis is complete, click **OK**.
8. After running the analysis using GenomeStudio software, you can view the results in many ways:
 - c. In the **Full Data Table**, in the CNV Value and CNV Confidence columns
 Use the column chooser  to display the CNV Value and CNV Confidence columns.
 - d. In the **CNV Region Display** tool, by selecting **Analysis | Show CNV Region Display**
 - e. In the **IGV (Illumina Genome Viewer)**, by selecting **View | CNV Analysis as Bookmarks**
 - f. In the **Bookmark Viewer**, by going to the IGV and selecting **View | Bookmark Viewer**.

5. Configuring the cnvPartition Plug-in

Starting with v1.2.0 of the cnvPartition Plug-in, the parameters can be changed via an editable configuration file. When you install the cnvPartition Plug-in, a configuration file is installed on your computer in this location:

<C:\Program Files\Illumina\GenomeStudio\CNVAlgorithm\cnvPartition> for GenomeStudio software, or

<C:\Program Files\Illumina\Illumina KaryoStudio\CNVAlgorithm\cnvPartition> for KaryoStudio

When you modify and save the default configuration file, your changes are preserved for future sessions.

NOTE: You can also adjust cnvPartition parameters from within GenomeStudio software, but not from within KaryoStudio software.



Perform the following steps to adjust cnvPartition Plug-in parameters from within GenomeStudio software:

1. In a GenomeStudio genotyping project, go to **Analysis | CNV Analysis**.
The CNV Analysis dialog appears.
2. Select cnvPartition v2.2.1 from the dropdown menu.
3. In the Options area of the CNV Analysis dialog, modify the parameters as needed.

The following table lists cnvPartition parameters, descriptions, and related information for GenomeStudio software.

Parameter Name	Description	Default Value	Mandatory	Visible in GUI?
ChiSquareThreshold	Minimum Chi Square value needed to detect a region of extended homozygosity See the DNA Copy Number Analysis Technical Note for more details.	23.5	True	False
ConfidenceThreshold	CNV regions with a confidence threshold below this value are excluded from analysis results.	35	True	True
DetectExtendedHomozygosity	Detect regions of extended homozygosity (regions exhibiting LOH but no change in copy number)	True	True	True

Note: The algorithm for detecting regions of homozygosity is similar to that used in the LOH Detector Autobookmarking Plug-in, and is described in detail in the DNA Copy Number Analysis Technical Note available at illumina.com. This algorithm is run only on regions with a copy number of 2 as detected by cnvPartition.

Additionally, the calculated ChiSquare for the homozygous region is used to populate the CNV Confidence value reported in the Full Data table, and is not subject to filtering by the ConfidenceThreshold parameter. Homozygous regions can be filtered independently of CNV regions using the MinHomozygousRegionSize, ChiSquareThreshold and/or MinHomozygoteCount parameters. CNV regions can be filtered independently of homozygous regions using the ConfidenceThreshold and/or MinProbeCount parameters.

To run only CNV detection, toggle DetectExtendedHomozygosity to False.

To detect only extended homozygous regions, set ConfidenceThreshold to a very high value, such as 10,000,000. Because even phenotypically normal samples contain many regions of homozygosity, you may want to set this threshold higher, to minimize the number of found regions.

GapSizeThreshold	Regions within probe gaps larger than this value are not considered to be within CNV regions. This helps prevent CNVs from being called across large probe gaps, such as centromeres.	1,000,000	True	False
------------------	---	-----------	------	-------



Parameter Name	Description	Default Value	Mandatory	Visible in GUI?
IncludeMitochondria	Set this flag to True if you want to include mitochondrial chromosomes in this analysis. NOTE: KaryoStudio excludes mitochondrial chromosomes from analysis.	False	True	False
IncludeSexChromosomes	Set this flag to True if you want to include X, Y, and XY (pseudoautosomal) chromosomes in this analysis. NOTE: KaryoStudio excludes pseudoautosomal regions from analysis.	False	True	True
LogDiagnosticInfo	Log diagnostic info to a file in the application's temp file directory. The log directory location on Windows XP machines is: C:\Documents and Settings\<username>\Local Settings\Application Data\Illumina\cnvPartition	False	True	False
MinHomozygoteCount	Minimum number of homozygotes needed to detect a region of extended homozygosity See the DNA Copy Number Analysis Technical Note for more details.	50	True	True
MinHomozygousRegionSize	Homozygous regions smaller than this are not detected	5 Mb	True	True
MinProbeCount	Regions with probe counts smaller than this are removed from analysis results.	3	True	False

6. Technical Support

Direct questions about installing and using the cnvPartition CNV Analysis Plug-in to Illumina Technical Support at techsupport@illumina.com, 1.800.809.4566 (toll-free), or +1.858.202.4566 (outside North America).



© 2008-9 Illumina, Inc. All rights reserved.

Illumina, Solexa, Making Sense Out of Life, Oligator, Sentrix, GoldenGate, DASL, BeadArray, Array of Arrays, Infinium, BeadXpress, VeraCode, IntelliHyb, iSelect, CSPPro, and GenomeStudio are registered trademarks or trademarks of Illumina, Inc. All other brands and names contained herein are the property of their respective owners.

The cnvPartition CNV Analysis Plug-in incorporates portions of code from the Cephes Math Library.

Cephes Math Library Release 2.8: June, 2000 Copyright 1984, 1987, 1995, 2000 by Stephen L. Moshier

Contributors: * Sergey Bochkhanov (ALGLIB project). Translation from C to pseudocode.

See subroutines comments for additional copyrights.

Redistribution and use in source and binary forms, with or without modification, are permitted provided that the following conditions are met:

-Redistributions of source code must retain the above copyright notice, this list of conditions and the following disclaimer.

-Redistributions in binary form must reproduce the above copyright notice, this list of conditions and the following disclaimer listed in this license in the documentation and/or other materials provided with the distribution.

-Neither the name of the copyright holders nor the names of its contributors may be used to endorse or promote products derived from this software without specific prior written permission.

THIS SOFTWARE IS PROVIDED BY THE COPYRIGHT HOLDERS AND CONTRIBUTORS "AS IS" AND ANY EXPRESS OR IMPLIED WARRANTIES, INCLUDING, BUT NOT LIMITED TO, THE IMPLIED WARRANTIES OF MERCHANTABILITY AND FITNESS FOR A PARTICULAR PURPOSE ARE DISCLAIMED. IN NO EVENT SHALL THE COPYRIGHT OWNER OR CONTRIBUTORS BE LIABLE FOR ANY DIRECT, INDIRECT, INCIDENTAL, SPECIAL, EXEMPLARY, OR CONSEQUENTIAL DAMAGES (INCLUDING, BUT NOT LIMITED TO, PROCUREMENT OF SUBSTITUTE GOODS OR SERVICES; LOSS OF USE, DATA, OR PROFITS; OR BUSINESS INTERRUPTION) HOWEVER CAUSED AND ON ANY THEORY OF LIABILITY, WHETHER IN CONTRACT, STRICT LIABILITY, OR TORT (INCLUDING NEGLIGENCE OR OTHERWISE) ARISING IN ANY WAY OUT OF THE USE OF THIS SOFTWARE, EVEN IF ADVISED OF THE POSSIBILITY OF SUCH DAMAGE.