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# Bionano VIA™ MultiScale BAM Reference Builder 4.0 Release Notes

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A

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# Revision History

| REVISION | NOTES |
| --- | --- |
| A | Initial release. |

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# New Features in Version 4.0

1. Support for samples containing ChrM.

2. Command line utility to convert the binary msr file to a tab delimited text file (`.tsv or .tsv.gz`). Command to run: `java -jar msbam-reference-export.jar.`

3. Calculation of read depth now includes clipped reads and improper pair reads.

4. A new option to either use or not use BAM QC measures to select files for reference creation.

    a. A checkbox selection **Exclude Input Files based on QC** has been added to the UI

    b. If used, samples that fail (above threshold of 20%) will not be used. QC metric used to exclude files:

        i. BaseQ<30

        ii. MapQ<30

        iii. Invalid Reads

        iv. Nonusable Reads

    c. The reference file header stores the value of the parameter along with the metrics and cut-off thresholds

# Bug Fixes in Version 4.0

These are the bugs fixed in 4.0 that existed in previous version(s) and were not included in an incremental build release.

1. When re-building a reference file using some BAM files and some raw depth files, all intermediate depth files get deleted incorrectly and result in a "file not found error." Now, only the raw depth file associated with the selected BAM file is deleted before re-building the reference.

# Technical Assistance

For technical assistance, contact Bionano Genomics Technical Support.

You can retrieve documentation on Bionano products, SDS's, certificates of analysis, frequently asked questions, and other related documents from the Support website or by request through e-mail and telephone.

| TYPE | CONTACT |
|------|---------|
| **Email** | support@bionano.com |
| **Phone** | Hours of Operation: <br> Monday through Friday, 9:00 a.m. to 5:00 p.m., PST <br> US: +1 (858) 888-7663 |
| **Website** | www.bionano.com/support |
| **Address** | Bionano Genomics, Inc. <br> 9540 Towne Centre Drive, Suite 100 <br> San Diego, CA 92121 |