Guidelines for IrysView® Run Metrics Report

Important: The guidelines described herein are based on internal experiences at Bionano Genomics and are provided as-is. The purpose of this technical note is to provide guidelines to customers who want to evaluate the quality of data generated from the Irys® System. For questions, please contact the Technical Support Team at support@bionanogenomics.com.

Run Metrics Report

Run metrics are useful in determining the quality and quantity of data generated by the Irys instrument. The values in the listed parameters are indicative of a good quality sample, extraction and labeling, but some metrics can vary widely between sample types (as indicated by "sample dependent"). When analyzing metrics over the course of a run, look for similar values (within 20%) from start to finish. For example, a steep drop in Quantity per Scan data can indicate that the NanoChannel is clogging on the chip.

To view metrics in IrysView, do one of the following:

- Select the Report tab, and then select the run in IrysView Molecules
- Open the *.txt file in the Detect Molecules folder for the run

For more information, see the *IrysView v2.5.1 Software Training Guide* (Document# 30035).

Raw Molecule Statistics

Raw molecule statistics are generally pre-filtered according to the following parameters: Size ≥ 20 kbp, Label SNR ≥ 3.00.

Metrics	Normal Range
Quantity per scan (Mbp)	850~4,000 (sample dependent)
Mol. N50 (kpb)	>120 (sample dependent)
Avg. Mol. SNR	8-20
Avg. Mol. Intensity	0.05~0.40
Avg. Label SNR	>10.5
Avg. Label Intensity	>0.06
Avg. Label Density	Sample Dependent (e.g. Human sample with Nt.BspQI, 8.5~11/100 kbp)

Quantity per Scan (Mbp): The amount of data collected. This value is in Mbp and corresponds to the total length of all molecules in the run divided by total scans. Too low of a value means that users may not be able to collect enough data, and too high of a value may risk clogging of the NanoChannels on the chip.

Mol. N50 (kbp): The point of half of the mass of the distribution, or the Center of Mass. The value should be as high as possible, although the value tends to be smaller for smaller genomes.

Avg. Mol. SNR: The average ratio of brightness of DNA intercalator to background noise for the dsDNA molecule (Signal to Noise).

Avg. Label SNR: The average ratio of brightness of the labels when compared to the background noise (Signal to Noise).

Avg. Label Density (per 100 kbp): The number of labeled sites per 100,000 nucleotides of DNA.

Avg. Label Intensity: The brightness of the labels.