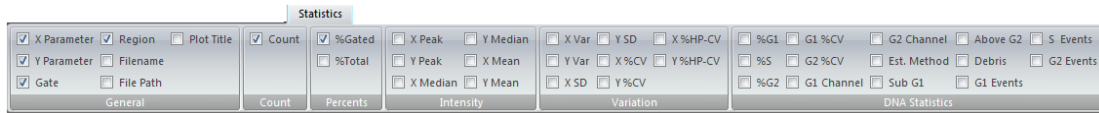


Statistics Tab

In VenturiOne you can select a statistic to be displayed on the plots in the **Plots** area. You can select this statistic on the **Statistics** tab of the **Ribbon**. You can also select which statistic(s) are displayed in the **Results** table.



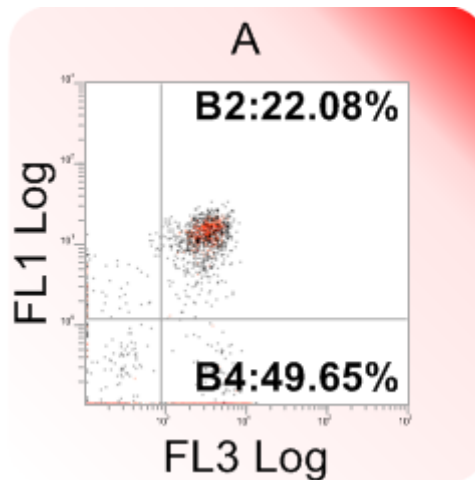
Statistics Tab Behavior

The **Statistics** tab behaves differently depending on which tab in the **Workspace** is selected.

When in the **Plots** tab of the **Workspace** only one statistic can be checked at any time. The currently checked statistic is displayed adjacent to the region for all regions on all plots in the **Plots** area. If you check a new statistic the previously checked one is automatically unchecked.

By default the **%Gated** statistic is displayed on plots.

When **% Gated** is checked on the **Statistics** tab the **% Gated** value is displayed in the plots, as illustrated below:



Results will not be truncated, so any statistic that is too large to appear on a plot will be hidden.

You can display just the region name by ensuring all check boxes are deselected.

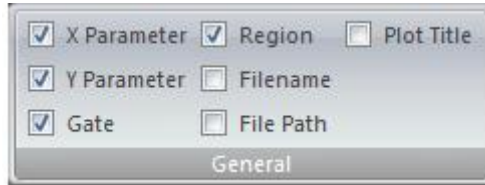
The statistics in the **General** and the **DNA** groups cannot be displayed on plots and the controls in these groups are disabled when in the **Plots** tab of the **Workspace**.

When in the **Results** tab of the **Workspace** any number of statistics can be checked and the statistical values for the checked statistics are displayed in the **Results** table.

When in the **Reports** tab of the **Workspace** the **Statistics** tab is only enabled when a **Stats Box** is selected. Statistical values for the checked statistics are displayed in the **Stats Box**.

General Group

The statistics in this group, when checked, are displayed in the **Results** table and in selected **Stats Boxes** on the reports.



X Parameter displays the X parameter of the plot containing the region.

Y Parameter displays the Y parameter of the plot containing the region.

Gate displays the name of the gate on which the region is gated.

Region displays the name of the region or the DNA plot name.

Filename displays the LMD file name.

File Path displays the LMD full path and file name.

Plot Title displays the title of the plot.

Count Group

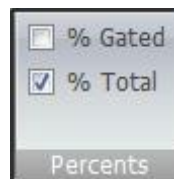
The statistic in this group, when checked, is displayed on **Plots**, in the **Results** table and in selected **Stats Boxes** on the reports.



Count displays the number of events in the region.

Percents Group

The statistics in this group, when checked, are displayed on **Plots**, in the **Results** table and in selected **Stats Boxes** on the reports.

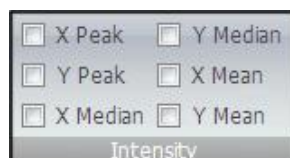


% Gated displays the percentage of events in the region compared to all the events in the parent gate.

% Total displays the percentage of events in the region compared to all the events in the file.

Intensity Group

The statistics in this group, when checked, are displayed on **Plots**, in the **Results** table and in selected **Stats Boxes** on the reports.



The **Intensity** group displays statistical options that express the intensity of the generated populations. The options are defined below:

X Peak displays the peak channel (mode) for the x-axis histogram of a region.

Y Peak displays the peak channel (mode) for the y-axis histogram of a region. Where the region is only a single parameter region the entry on the results table is left blank.

X Median displays the median average for the x-axis histogram of a region.

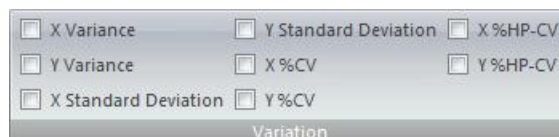
Y Median displays the median average for the y-axis histogram of a region. Where the region is only a single parameter region the entry on the results table is left blank.

X Mean displays the mean average for the x-axis histogram of a region.

Y Mean displays the mean average for the y-axis histogram of a region. Where the region is only a single parameter region the entry on the results table is left blank.

Variation Group

The statistics in this group, when checked, are displayed on **Plots**, in the **Results** table and in selected **Stats Boxes** on the reports.



The **Variation** group displays options that express the variation of populations. The options are defined below:

X Variance displays the variance for the x-axis histogram of a region.

Y Variance displays the variance for the y-axis histogram of a region. Where the region is only a single parameter region the entry on the results table is left blank.

X Standard Deviation displays the standard deviation for the x-axis histogram of a region.

Y Standard Deviation displays the standard deviation for the y-axis histogram of a region. Where the region is only a single parameter region the entry on the results table is left blank.

X %CV displays the Coefficient of Variation for the X scale range of events. This allows comparison of the variation of populations that have significantly different mean values; it is displayed as a percentage. The X %CV is calculated by dividing the Standard Deviation by the Arithmetic Mean and is displayed as a percentage.

Y %CV displays the Coefficient of Variation for the Y scale range of events. This allows comparison of the variation of populations that have significantly different mean values; it is displayed as a percentage. The Y %CV is calculated by dividing the Standard Deviation by the Arithmetic Mean and is displayed as a percentage.

X %HP-CV displays the Half-Peak Coefficient of Variation for the X scale range of events. The X %HP-CV uses a Standard Deviation calculated from the scale width between the half peak points either side of the Peak. Once the Standard Deviation is calculated it is divided by the Arithmetic Mean and displayed as a percentage.

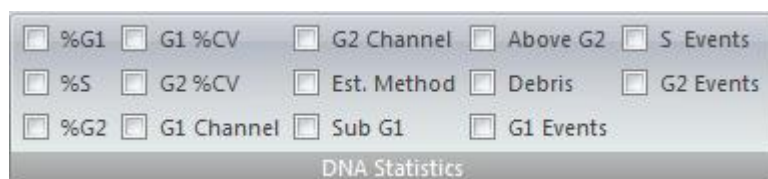
Y %HP-CV displays the Half-Peak Coefficient of Variation for the Y scale range of events. The Y %HP-CV uses a Standard Deviation calculated from the scale width between the half peak points either side of the Peak. Once the standard deviation is calculated it is divided by the Arithmetic Mean and displayed as a percentage.

DNA Statistics Group

The **DNA Statistics** group displays the statistical options associated with the DNA Cell Cycle plots.

The statistics in this group, when checked, are displayed in the **Results** table and in selected **Stats Boxes** on the reports.

When a cell cycle plot is present in the **Plots** area, the statistics in the **DNA Statistics** group are checked by default.



%G1 displays events in the G1 phase, represented as a percentage of the total of events in G1, G2 and S phase.

%S displays events in the S phase, represented as a percentage of the total of events in G1, G2 and S phase.

%G2 displays events in the G2 phase, represented as a percentage of the total of events in G1, G2 and S phase.

G1 %CV displays the Coefficient of Variation for the G1 phase. This is calculated by dividing the G1 phase Standard Deviation by the Arithmetic Mean and is displayed as a percentage.

G2 %CV displays the Coefficient of Variation for the G2 phase. This is calculated by dividing the G2 phase Standard Deviation by the Arithmetic Mean and is displayed as a percentage.

G1 Channel displays the position of the G1 calculated peak channel.

G2 Channel displays the position of the G2 calculated peak channel.

Est. Method displays the estimate method used. This can be Automatic or User.

Sub G1 displays the number of events above the lower threshold divider and below the G1 phase.

Above G2 displays the number of events below the upper threshold divider and above the G2 phase.

Debris displays the number of DNA debris events. These are the events outside the threshold limits.

G1 Events displays the number of events in the G1 phase.

S Events displays the number of events in the S phase.

G2 Events displays the number of events in the G2 phase.