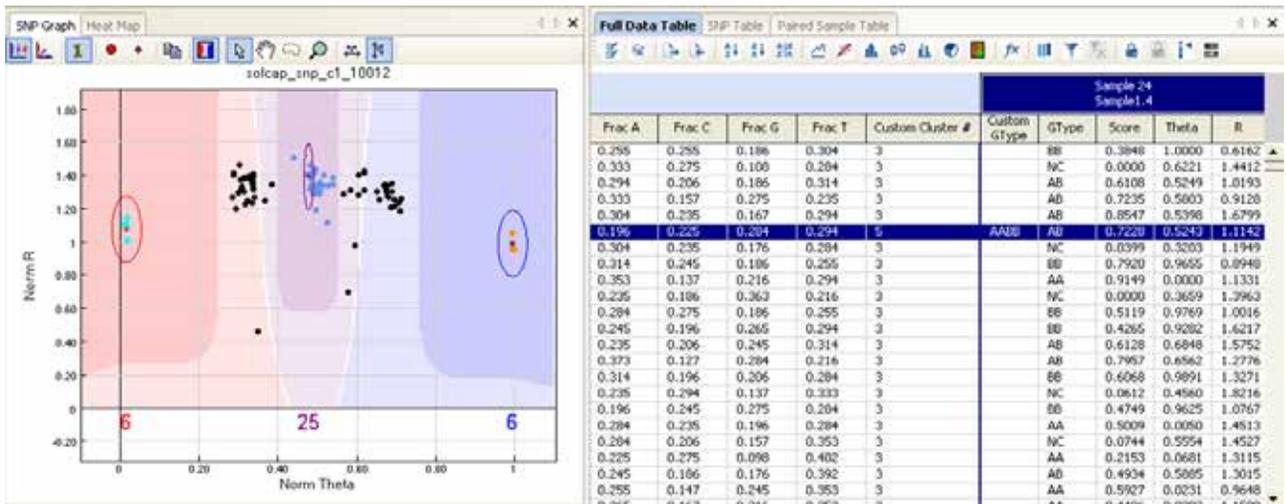


Figure 3: SNP Graph and Full Data Table After Custom GType Value is Changed to 5



Changing the Custom Cluster # value to 5 results in three changes to the data handling:

- The colors of the genotype positions in the first, third, and fifth cluster of the SNP Graph will change from the default colors.
- The Custom GType column for any genotypes falling inside the call region for the first, third, and fifth clusters will be populated. For example, any samples at this SNP with a genotype in the first cluster will have the Custom GType populated with an AAAA.
- A new context menu, unique to loci with a Custom Cluster # of 5, will be available by right-clicking in the SNP Graph (not shown).

Custom GType Column

At this stage, the second and fourth clusters are in the no-call region of the SNP Graph, and the Custom GType column for these samples remains blank. The genotype dots are black to indicate the current status as a no-call. The next step is to call the genotypes for the second and fourth clusters manually. These calls will not be perpetuated in the cluster file nor will these cluster positions be applicable to future samples added to the same project; however, they can be saved within the current project for generating subsequent final reports (described later in this document).

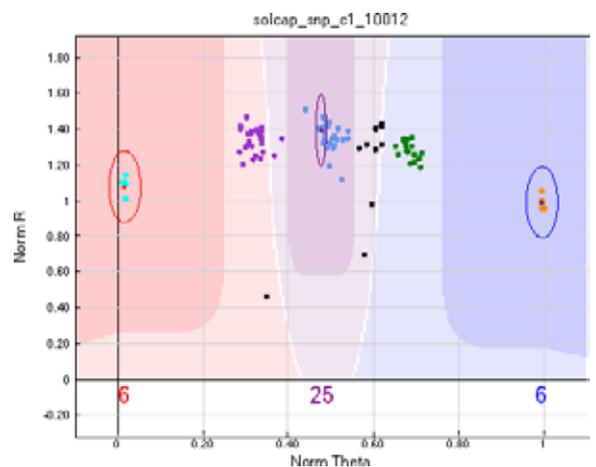
To call the genotypes on the second and fourth clusters, select the samples in the SNP graph for one of the two clusters. Using the default cursor, click the left mouse button and drag a selection square around the genotypes. When you release the mouse button, the selected genotypes will be highlighted yellow.

With the genotype positions highlighted in the SNP Graph, right-click to view the new context menu, which allows the user to define the Custom GTypes as AAAA, AAAB, AABB, BBBA or BBBB.

- For the second cluster, select **Define AAAB Genotype Using Selected Samples** from the context menu.
- For the fourth cluster, select **Define BBBA Genotype Using Selected Samples** from the context menu.

The Custom GType column for the selected samples will be populated using the assigned genotype. The color of the highlighted samples will change from black to a color that is specific to the assigned genotype, AAAB or BBBA, as shown in Figure 4. (Typically the user must click off the locus, then click back to the locus to view the color change.)

Figure 4: SNP Graph with Custom Genotype Calls



This example shows the cluster positions of the potato SNP from Figure 2 with all five clusters called. Note that the samples with genotypes that fall between the third and fourth cluster are left in the no-call region.

Without additional information about the biology of the organism, GenomeStudio v1.8 leaves these dots black by default. Individual researchers may decide to call genotypes for dots that show unusual spread or appear in between clusters, depending on the available background information and the experimental design. In the absence of any additional information, however, best practices favor a no-call rather than a potentially incorrect call.

