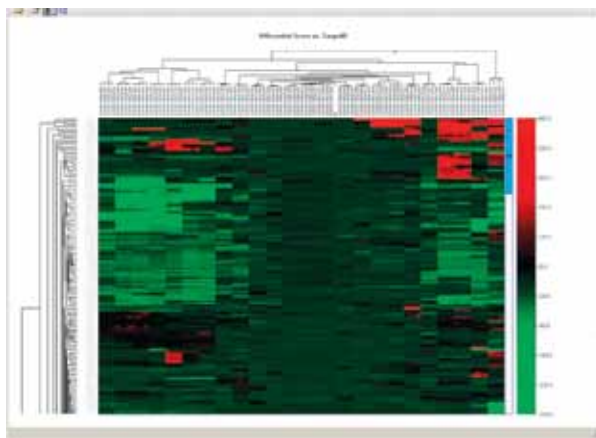


Figure 3: Gene Expression Module Heat Map



Using the heat map function in the GX Module allows easy visualization and analysis of large amounts of data. This heat map dendrogram clusters rows (Target ID) and columns (Differential Scores).

Gene Expression (GX) Module

Data from Direct Hyb, DASL, and Whole-Genome DASL gene expression profiling assays or MicroRNA profiling assays generated using the BeadArray Reader, iScan System, or BeadXpress Reader are analyzed using the Gene Expression (GX) Module. The results generated using this module provide meaningful conclusions from the continuous expression data on gene-level statistical analysis tools. Differential expression analysis can be visualized as line plots, histograms, dendrograms, box plots, heat maps, scatter plots, frequency plots, pie charts, samples tables, and gene clustering diagrams (Figure 3). Simplified data management tools include hierarchical organization of samples, groups, group sets, and all associated project analysis.

Methylation (M) Module

DNA methylation data from scanned microarray images collected from the BeadArray Reader, iScan System, or BeadXpress Reader are analyzed with the Methylation (M) Module. This module calculates methylation levels (beta values) and analyzes differences between experimental groups. CpG island methylation status is visualized across the genome with the IGV and ICB. Results from single-site resolution data are visualized as line plots, bar graphs, scatter plots, frequency plots, pie charts, histograms, dendrograms, box plots, or heat maps. Methylation data can also be combined with gene expression profiling experiments within the same GenomeStudio project to study any correlation between levels of methylated sites (beta values) and differential gene expression levels (p-values).

Protein Analysis (PT) Module

Data generated using Carboxyl VeraCode Beads on the BeadXpress Reader are analyzed using the Protein Analysis (PT) module. Users can determine analyte concentration using a standards curve or differentiate protein expression levels between samples. If applicable, protein levels can be compared to mRNA expression levels. Results can be visualized as line plots, histograms, dendrograms, frequency plots, piecharts, box plots, heat maps, scatter plots, samples tables, and gene clustering diagrams.

Sequencing Applications

DNA Sequencing (DS) Module

DNA sequencing data generated using the Genome Analyzer or HiSeq instruments and Pipeline software tools can be analyzed to discover and confirm SNPs and chromosomal breakpoint regions in the DNA Sequencing (DS) Module. Visualization tools display consensus reads in the reassembled genome and indicate SNPs with colored letters (Figure 4). Newly discovered SNPs can be exported to use in customized iSelect® genotyping array designs.

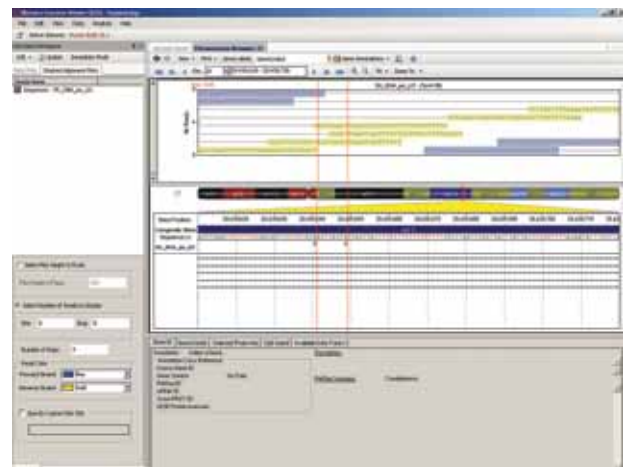
ChIP Sequencing (CS) Module

Data from whole-genome chromatin immunoprecipitation sequencing experiments performed using the Genome Analyzer or HiSeq instruments and Pipeline software can be parsed to the GenomeStudio ChIP Sequencing (CS) Module to create global binding site maps of DNA-associated proteins. Differential binding levels between experimental groups can be identified by comparing sequences, regions, and peaks in table or chromosome views.

RNA Sequencing (RS) Module

Data generated from mRNA sequencing experiments using the Genome Analyzer or HiSeq instruments and Pipeline software tools are displayed in the RNA Sequencing (RS) Module as expression levels and variants discovered. By aggregating data from the Pipeline software, the RS Module is able to count the abundance of reads falling within specific exons, genes, and splice junctions. Data are then graphically displayed as tables or plots within GenomeStudio software (Figure 3). Genome views display consensus reads in the transcriptome by aligning reads to known abundant sequences and splice junctions. Coding SNPs and splice variants are identified and confirmed visually with single-base resolution in the ICB.

Figure 4: SNPs Identified From Aligned Reads Displayed in DNA Sequencing Module



Aligned sequencing reads (yellow and purple blocks) are stacked on a reference genome in the ICB. SNPs are identified with red characters and in the called SNPs data track. Two SNPs are highlighted with a ruler indicating the position of the called SNPs in the aligned reads relative to the reference genome.

