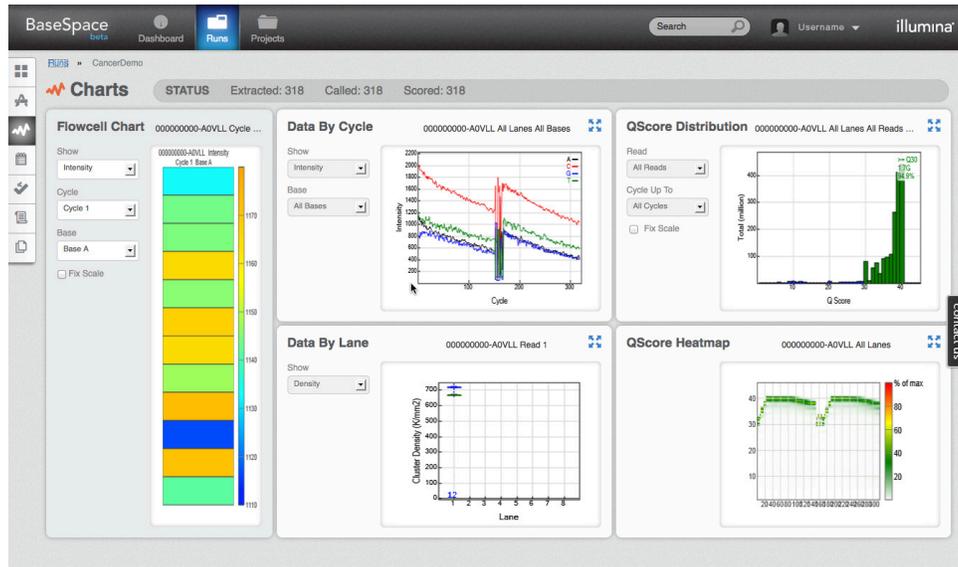


Figure 2: Monitor Run Data in Real Time



The Sequence Analysis Viewer (SAV) capabilities are now built into the BaseSpace user interface, allowing real-time, cycle-by-cycle monitoring. The Charts view shows data by lane and by cycle, with Q-Score distribution and heatmap features. Each graph can be expanded to full size.

Data Analysis Tools at Your Fingertips

Automated, Streamlined Applications Workflows

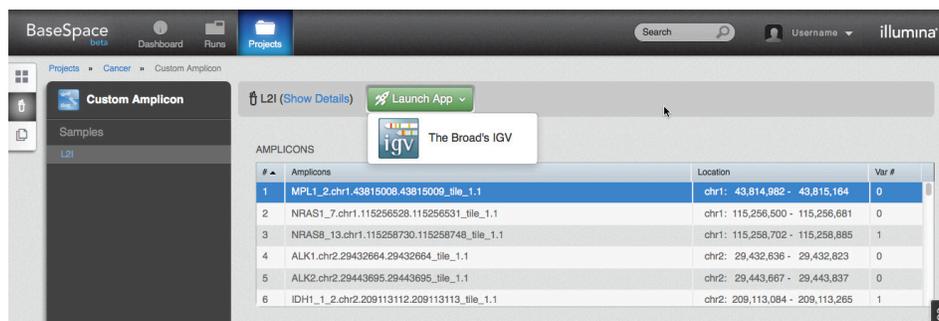
BaseSpace currently offers six integrated data analysis workflows: resequencing, amplicon resequencing, 16S metagenomics, *de novo* assembly (powered by Velvet), small RNA, and library QC. Using the Illumina Experiment Manager, the desired analysis is selected during sample sheet setup, and data is streamed directly to BaseSpace as the run commences. Upon completion of the sequencing run, BaseSpace automatically initiates the selected analysis without user intervention. The analysis is completed in a few hours, and a report is automatically generated.

BaseSpace Apps, the Right Tools for the Job

From visualization and graphical genome browsing, to annotation and filtering, to gene expression analysis, BaseSpace Apps provides an analysis ecosystem where you can pair your data with algorithms and methods developed by a growing community of bioinformatics software developers (Figure 3). With the BaseSpace Apps store, your data is just a click away from the latest analysis tools

BaseSpace also greatly simplifies third-party software development by creating a robust platform-as-a-service specific to the needs of next-generation sequencing data, and creates a channel for the access, distribution, and sharing of third-party tools. This model enables new applications to reach the widest possible user base in the shortest amount of time.

Figure 3: Launch the Latest Analysis Tools On-Demand



Browse and explore the latest apps from the bioinformatics community in the BaseSpace Apps Store, and launch them with a single click right from your dataset. Shown is Broad's Interactive Genome Viewer (IGV).

