

DNASTAR's Lasergene Genomics Suite for RNA-Seq Alignment and Analysis of Three *Bos taurus* Breeds

Matthew Keyser¹, Jacqueline Carville¹, Thomas Schwei¹, Timothy Durfee PhD¹, Amber Pollack-Berti PhD¹, Daniel Nash¹, Jennifer Stieren¹, Schuyler Baldwin¹, Richard Nelson PhD¹, Kenneth Dullea¹, John Schroeder¹, Pavel Pinkas PhD¹, Guy Plunkett III PhD^{1,2}, Frederick Blattner PhD^{1,2,3}

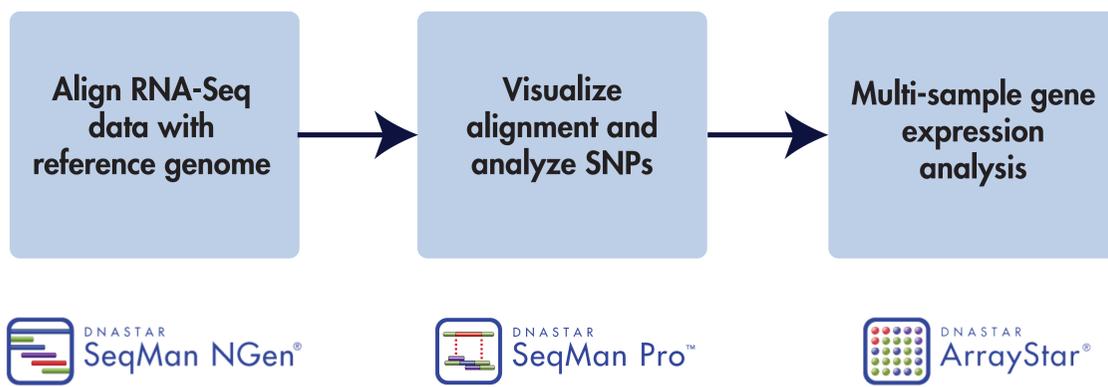
Affiliations

¹ DNASTAR, Inc., Madison, Wisconsin, USA
² University of Wisconsin, Department of Genetics, Madison, Wisconsin, USA
³ Scarab Genomics LLC, Madison, Wisconsin, USA

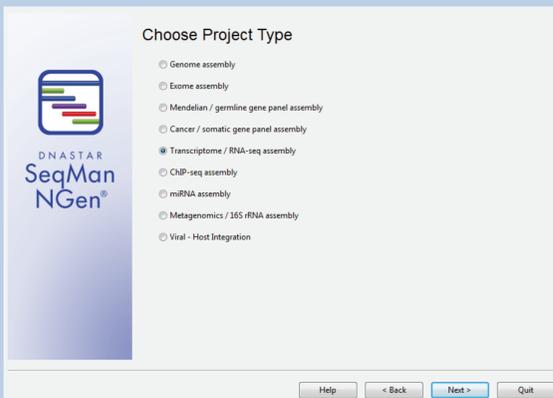
Abstract

DNASTAR offers an integrated suite of software for assembling and analyzing sequence data from all major next-generation sequencing platforms supporting key workflows on both a desktop computer as well as the DNASTAR Cloud. Our RNA-Seq alignment and analysis workflow employs the DNASTAR SeqMan NGen, SeqMan Pro, and ArrayStar applications, all components of the Lasergene Genomics Suite. Here, next-gen RNA reads from Jersey, Holstein, and Cholistani cattle are aligned against the *Bos taurus* reference sequence in SeqMan NGen. Next, visualize the three samples and perform SNP analysis in SeqMan Pro. SeqMan Pro additionally offers the ability to look at the alignment of the reads to the reference and analyze what reads map to different isoforms or exons to explore differences in splice patterns. Finally, we can import the three experiments into ArrayStar for multi-sample analysis where advanced filtering options can be utilized for large-scale gene expression analysis. Innovative algorithms and highly interactive views within these three software applications offer a powerful, integrated, and user-friendly alignment and analysis workflow for RNA-Seq data.

Workflow

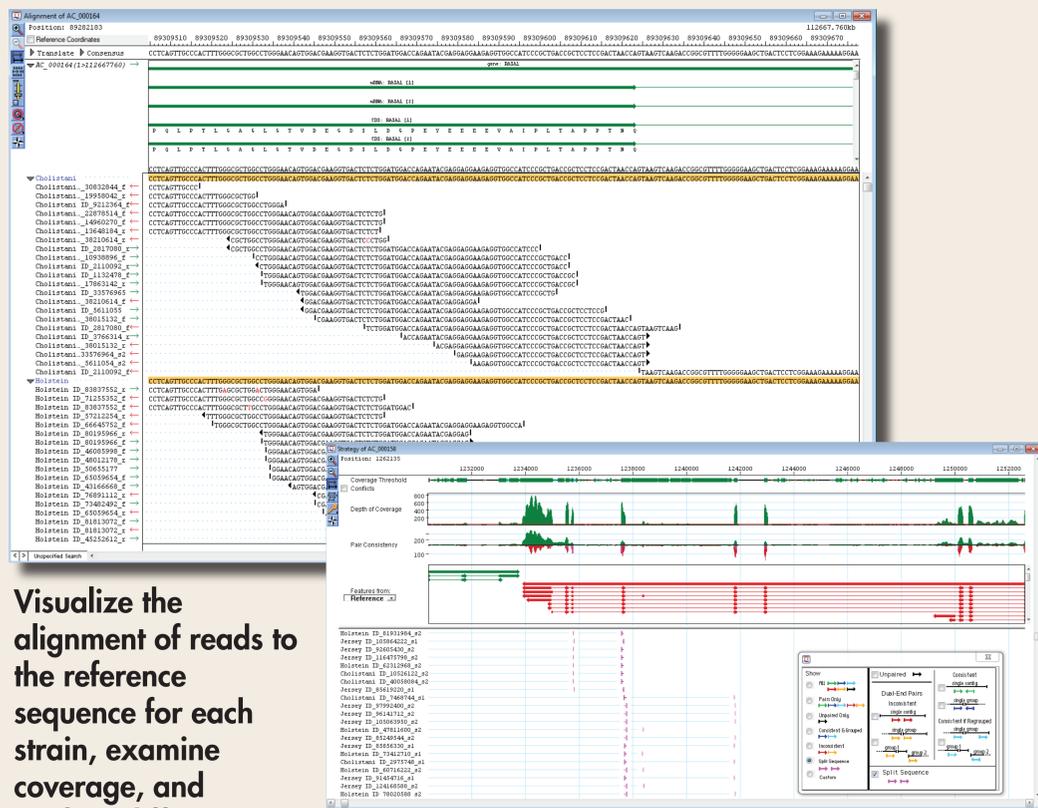


RNA-Seq Alignment



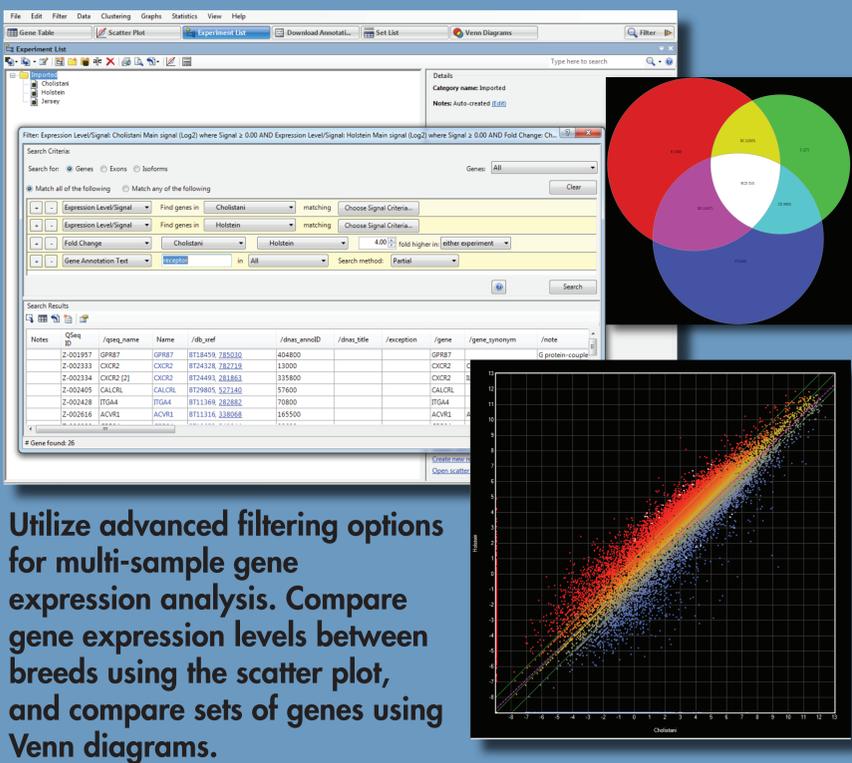
Align RNA-seq reads from Jersey, Holstein, and Cholistani cattle breeds against *Bos taurus* reference genome in SeqMan NGen.

Visualize

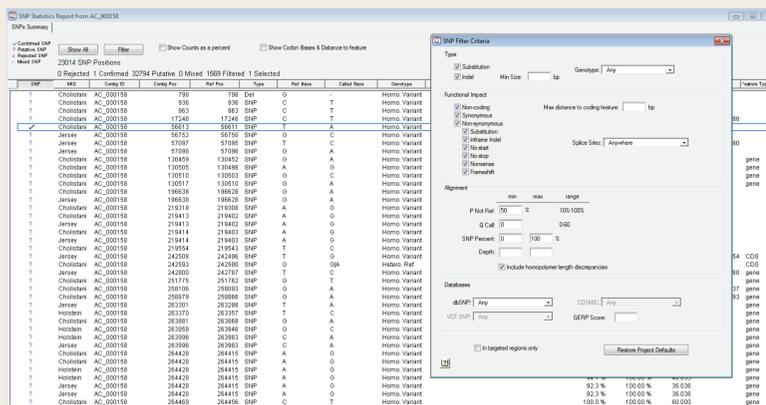


Visualize the alignment of reads to the reference sequence for each strain, examine coverage, and explore differences in splice site patterns.

Analyze



Utilize advanced filtering options for multi-sample gene expression analysis. Compare gene expression levels between breeds using the scatter plot, and compare sets of genes using Venn diagrams.



Discover SNPs using the interactive SNP report. Filter, sort, and evaluate variants.