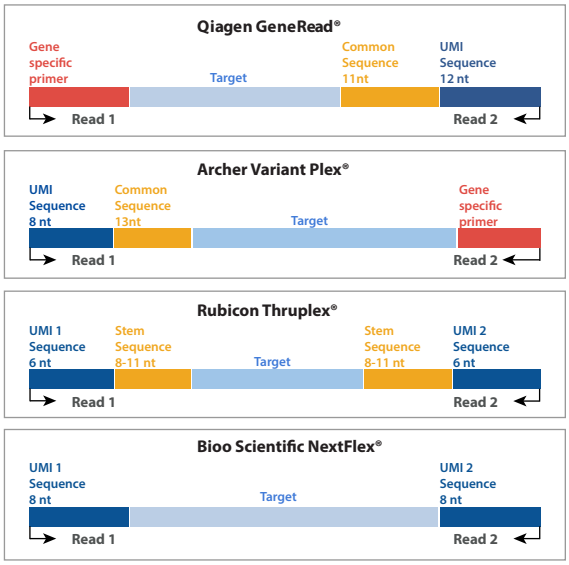
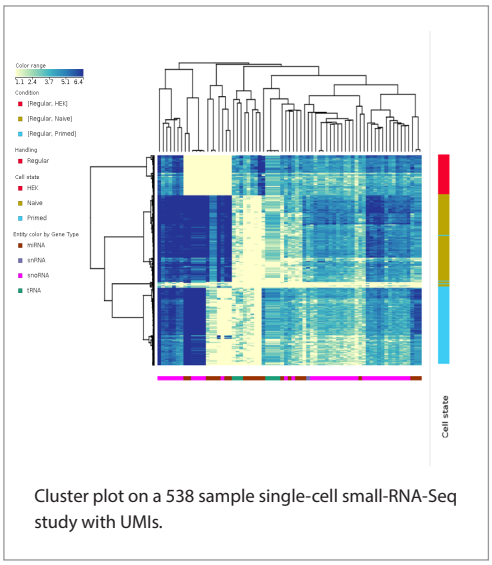
strandngs

Large Scale Transcriptomics and Unique Molecular Identifiers Support from Strand NGS v3.1

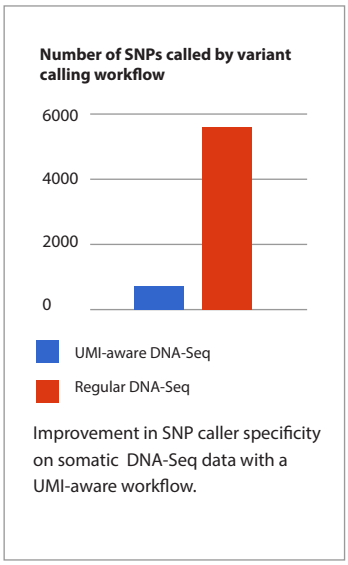
UMI-ready DNA-, RNA-, and small RNA-Seq



UMI Protocols with native support in Strand NGS. Strand NGS v3.1 also supports custom, user-specified UMI protocols.



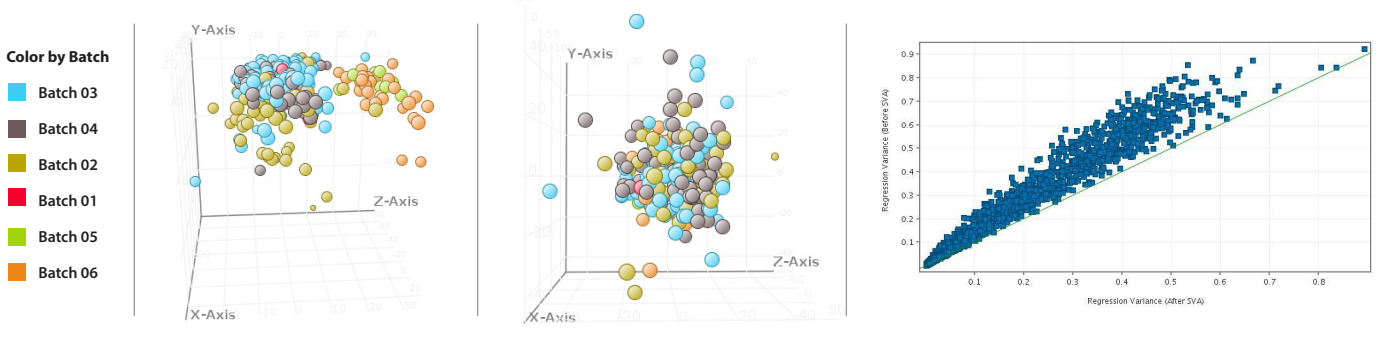
Cluster plot on a 538 sample single-cell small-RNA-Seq study with UMIs.



Improvement in SNP caller specificity on somatic DNA-Seq data with a UMI-aware workflow.

Unique Molecular Identifiers, or UMIs, are short sequences (6-12bp) added to sequencing libraries prior to PCR amplification. UMIs can improve the accuracy of RNA-Seq quantification and lead to improved specificity in low-frequency variant calling for DNA-Seq. Strand NGS v3.1 implements a complete, end-to-end UMI workflow for DNA-, RNA-, and small-RNA-Seq.

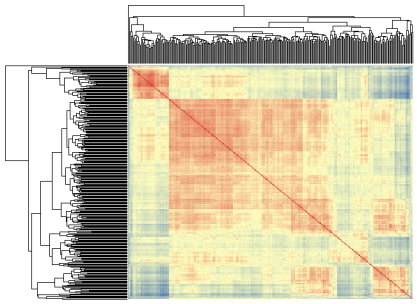
Confounding variable analysis for RNA- and small-RNA-Seq



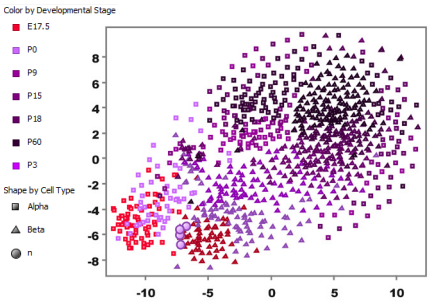
Legend, before-after PCA plots (left and center) and gene regression variance scatter (right), showing the effect of confounding variable analysis (CVA) on a 283 sample Pan cancer RNA-Seq study. The PCA plots show how CVA removes the effect of batch; the regression variance plot shows how CVA reduces the original variance, resulting from batch effect, on all genes.

Confounding variable analysis (CVA) is a statistical approach to remove unwanted variance from datasets. Strand NGS v3.1 implements an intuitive interface based on Surrogate Variable Analysis (SVA), for CVA.

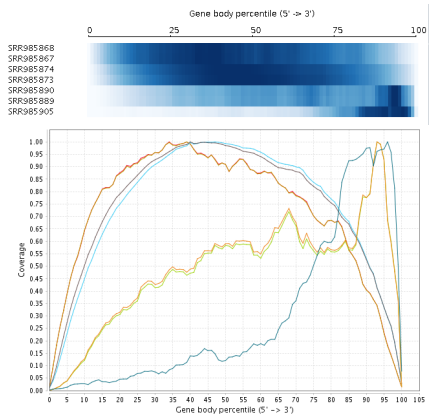
Analysis of large-scale RNA-Seq and small-RNA-Seq data



Correlation of gene expressions on a 283-sample RNA-Seq Pan Cancer study.



t-SNE plot on a 931-sample single-cell study showing the separation between alpha and beta-cells between birth and maturation.



Gene body coverage on a RNA-Seq study, showing coverage bias towards the 3' end in certain samples.

Large-scale RNA and small-RNA-Seq. Strand NGS v3.1 contains enhancements for the analysis and visualization of hundreds of samples in RNA- and small-RNA-Seq. Highlights include a pleasingly-graded color scheme for publication quality plots; a gene body coverage diagram; the t-SNE plot as an alternative to PCA for clustering and classification of large-scale data; and several other features.

Strand Life Sciences Pvt. Ltd
5th Floor, Kirloskar Business Park, Bellary Road, Hebbal, Bangalore 560024
Phone:+91-80-40 (787263) Fax: +91-80-4078-7299