Compare identified SNPs across individuals and to known SNPs

An advanced application that integrates many of the most powerful functionalities in the software includes assembling and analyzing multiple samples using one reference template, probabilistic identification of SNPs, small indels and genotype calls with known variants correlated to their dbSNP and COSMIC IDs and GERP scores, review of SNPs from analysis samples within a single project identification of structural variations, and for large-scale projects with hundreds of individual data sets, tools for SNP quantitation, filtering, set comparison, clustering and indication of the gene disruption impact from called SNPs, as well as gene ontology.

DNASTAR Software Pipeline

DNASTAR offers an integrated suite of software for assembling and analyzing sequence data from all major next-generation sequencing platforms supporting key workflows on a desktop computer. Supported workflows include reference-guided and de novo genome and transcriptome assembly and analysis, metagenomics sample assembly, targeted resequencing, exome assembly, and RNA-Seq, ChIP-Seq and miRNA alignment and analysis.

Interactive views within the software facilitate fast, comprehensive analysis, helping scientists move quickly from raw next-gen sequencing data to genetic and genomic quantitation, filtering, set comparison, clustering and indication of the gene disruption impact from called SNPs, as well as gene ontology.

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Compare identified SNPs across individuals and to known SNPs

Examine data from different individuals

Analyze individual assemblies

Analyze gene disruption and gene ontology

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