

Geneious R10: A Bioinformatics Platform for Biologists

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One of the challenges of bioinformatics is the abundance of applications, websites and algorithms available to the research community. Sharing data between these programs can be difficult and many require the user to navigate difficult command-line interfaces.

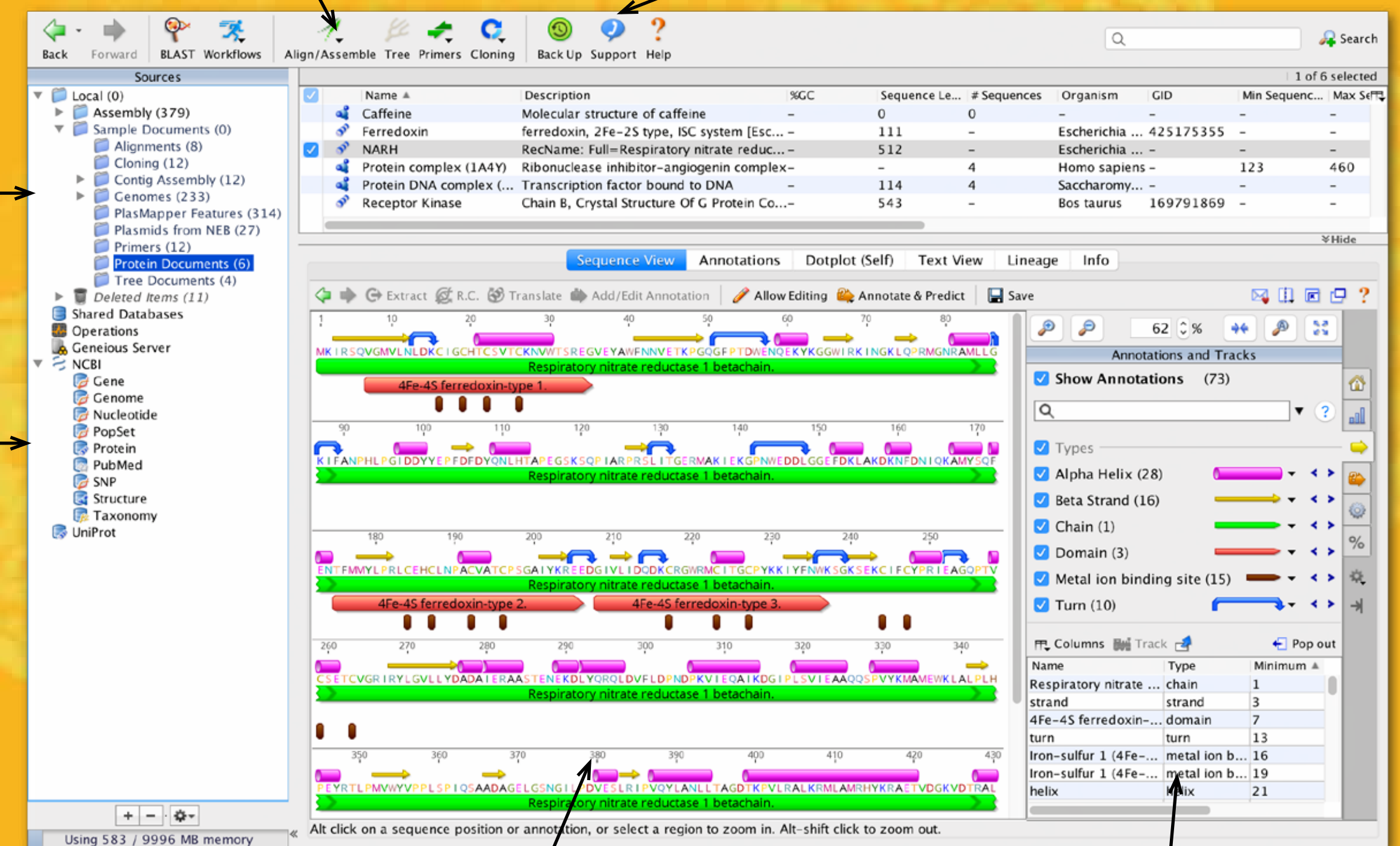
Geneious R10 provides a solution to these problems by incorporating industry-leading algorithms and applications for genomic & protein sequence analyses via a single robust desktop program. Researchers can easily query, manage, share, and analyze all of their sequence data intuitively within a user-friendly interface. The R10 platform provides tools for next-generation sequence analysis, chromatogram assembly, sequence alignment, phylogenetics, primer design, cloning and microsatellite analyses, and includes the ability to make custom workflows to automate your analysis pipelines. Geneious also offers intuitive data management features, such as drag-and-drop file interface, local file directory organization, and the ability to connect to shared relational databases. Geneious development is driven by feedback from the scientific community, and its stable java framework and public API allow users to extend the software by creation of their own plugins.

Quickly access your favourite functions

Dedicated support from experienced bioinformaticians

Intuitive file management system

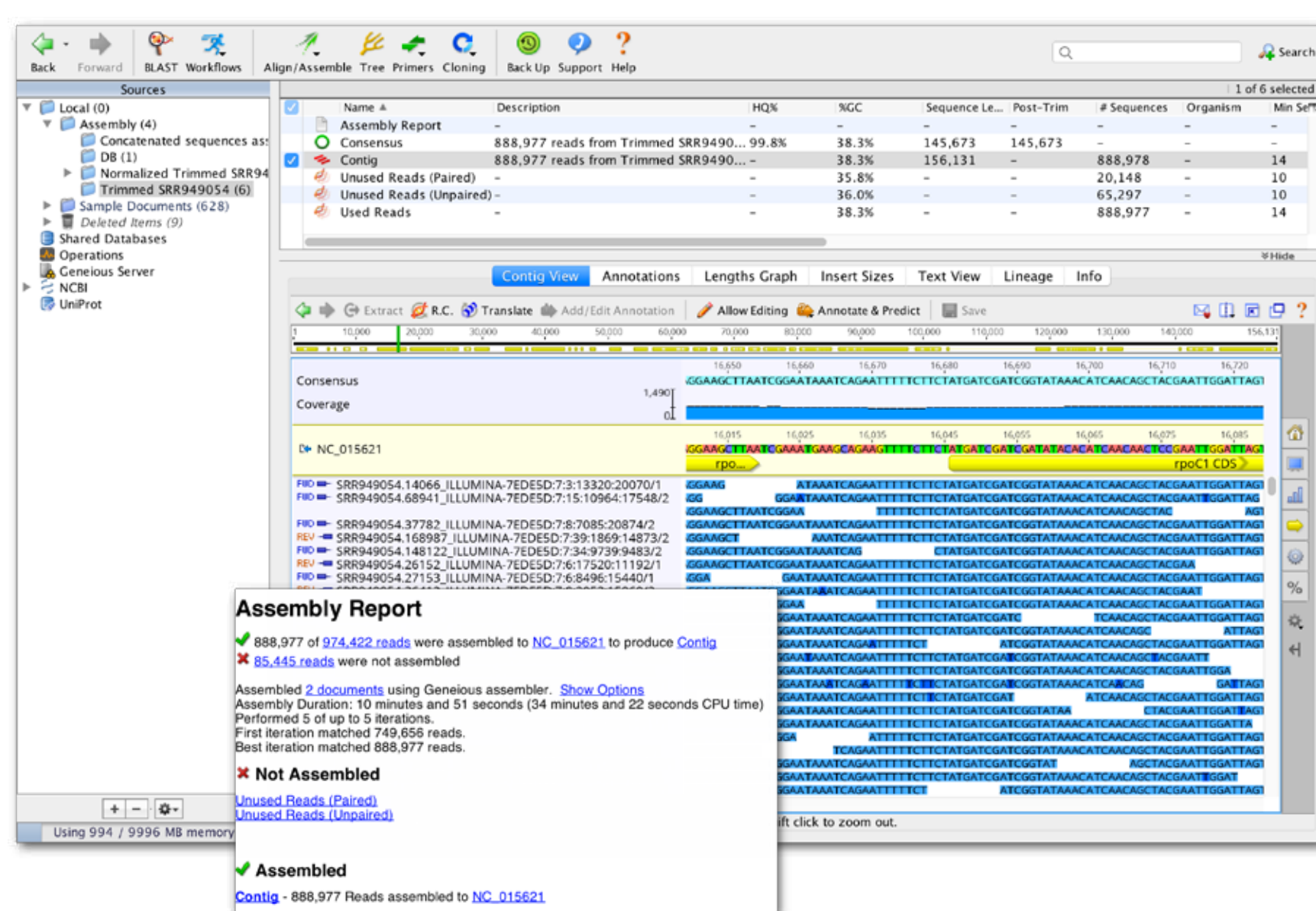
Directly access NCBI databases



Rich annotations in a fully customisable sequence viewer

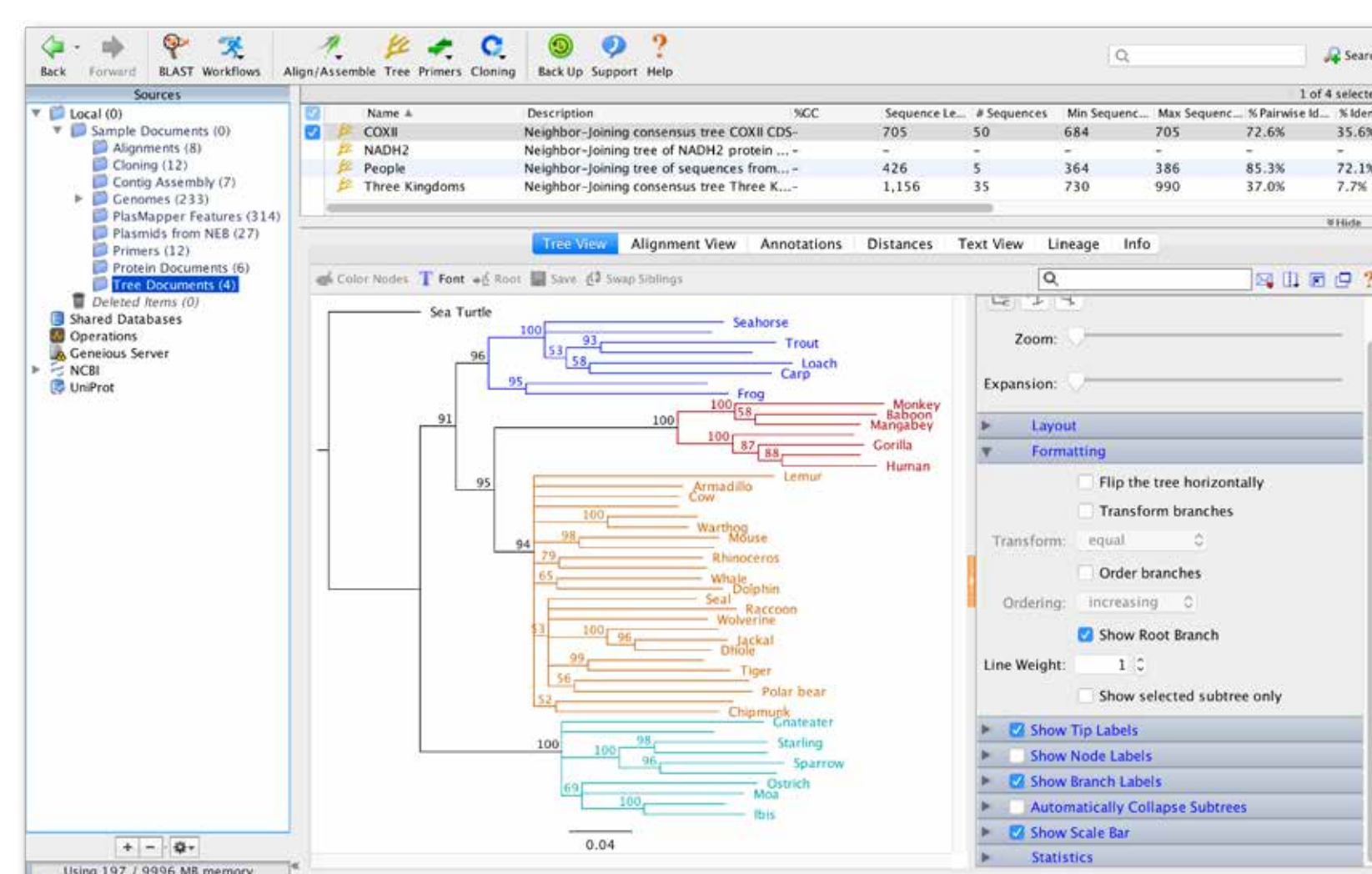
Sequence statistics, annotations and graphs at your fingertips

Sequence Assembly



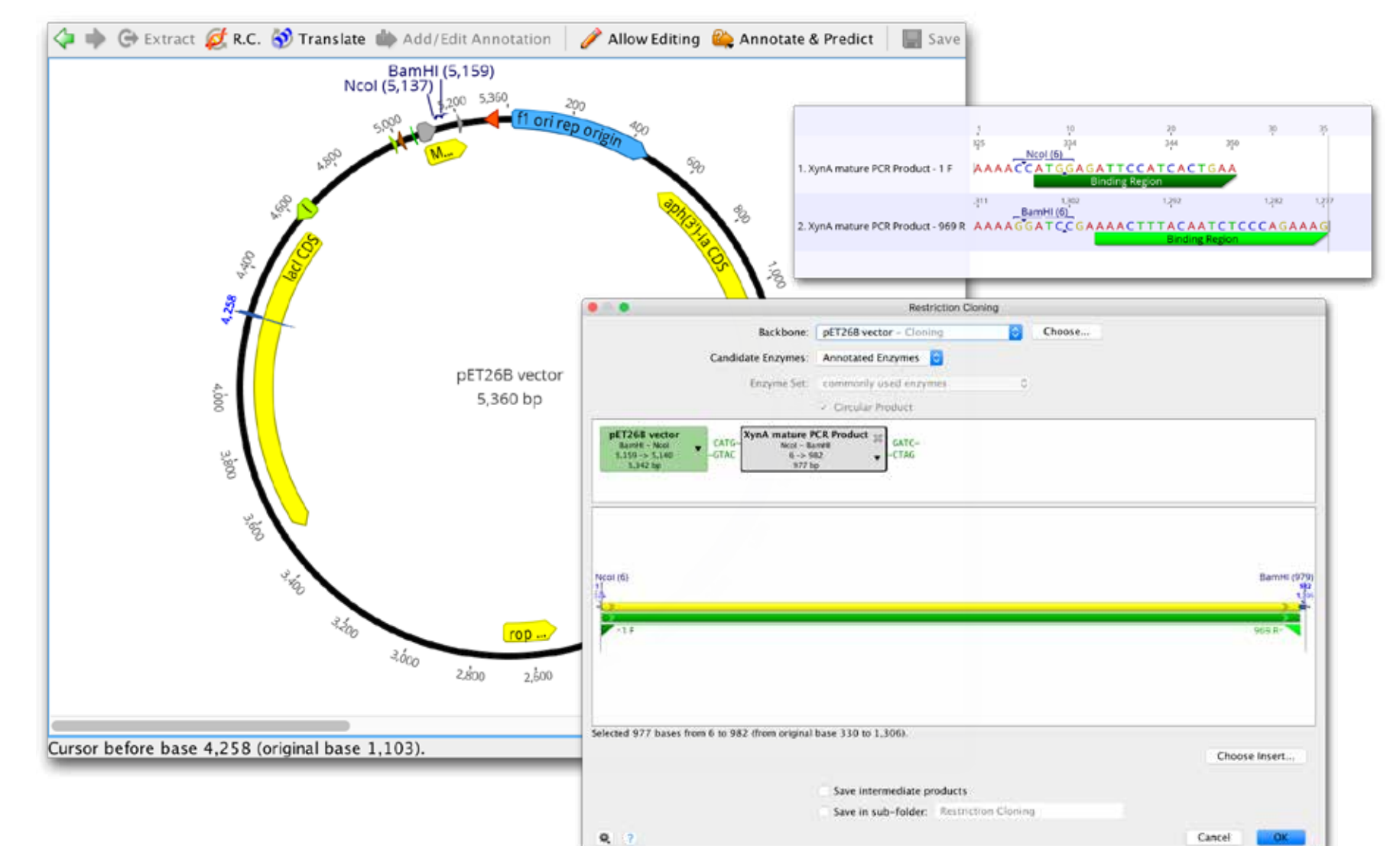
- Assemble data from Sanger, Illumina, Ion Torrent, 454, PacBio platforms using the Geneious assembler, or plugins for Velvet, MIRA, Bowtie2, Tophat, BMap and Tadpole
- Assemble RNA-Seq data with the Geneious reference assembler, Tophat or BMap
- Improved long read handling and structural variant mapping ^{New in R10}
- Pre-processing tools for NGS data including trimming, filtering, pairing and barcode sorting.
- Beautiful assembly visualization including coverage graphs and annotation tables

Alignment and Phylogenetics



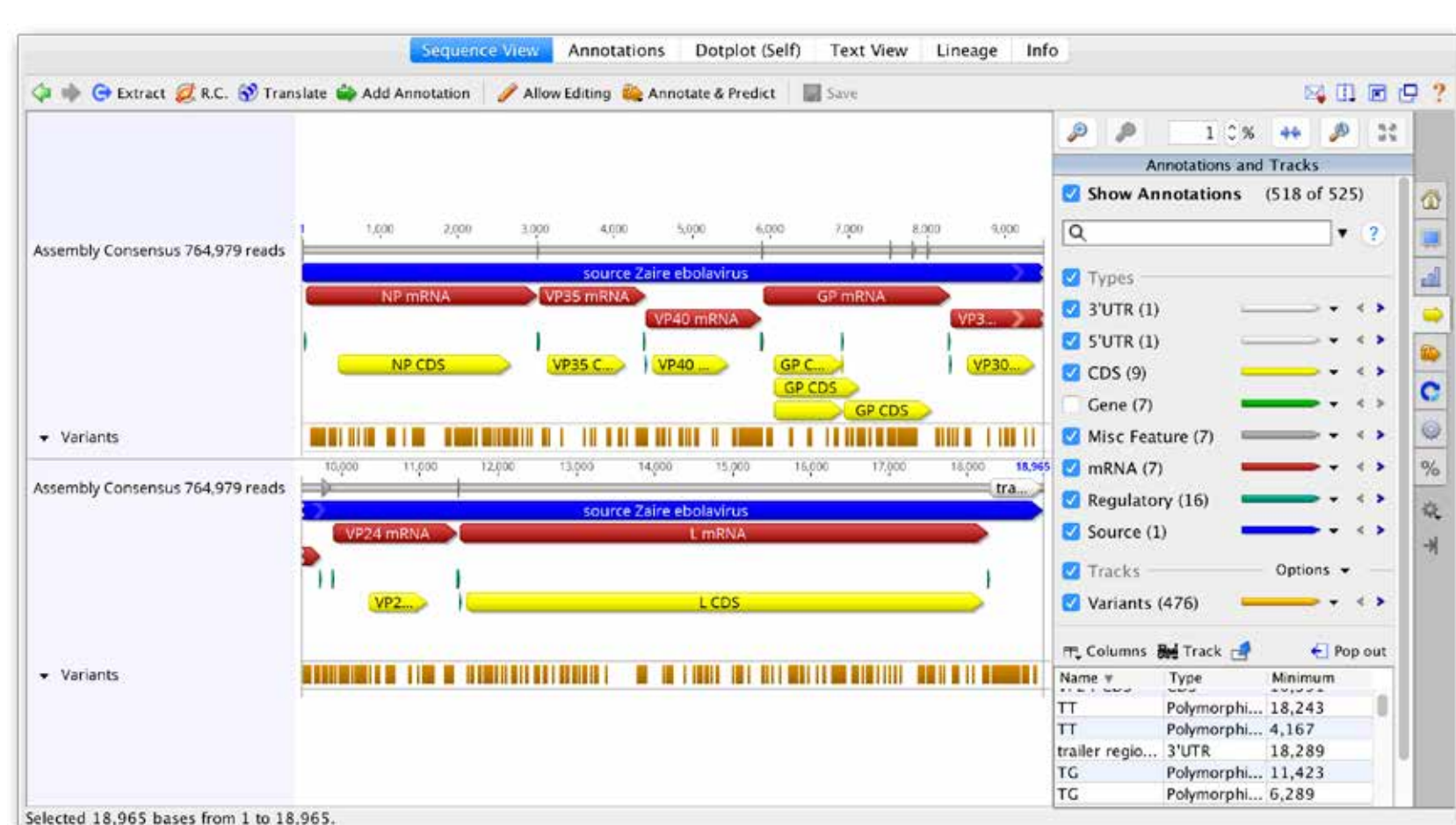
- Alignment with ClustalW, MUSCLE, MAFFT, MAUVE and LASTZ
- Mask alignment sites for tree building ^{New in R10}
- Build neighbour-joining and UPGMA trees with the Geneious tree-builder
- Build trees using PHYML, Garli, RaxML, FastTree and MrBayes
- Fully customizable tree visualisation and editing, with support for large trees
- Export publication quality trees to high quality vector format like svg, pdf or eps.

Primer Design and Cloning



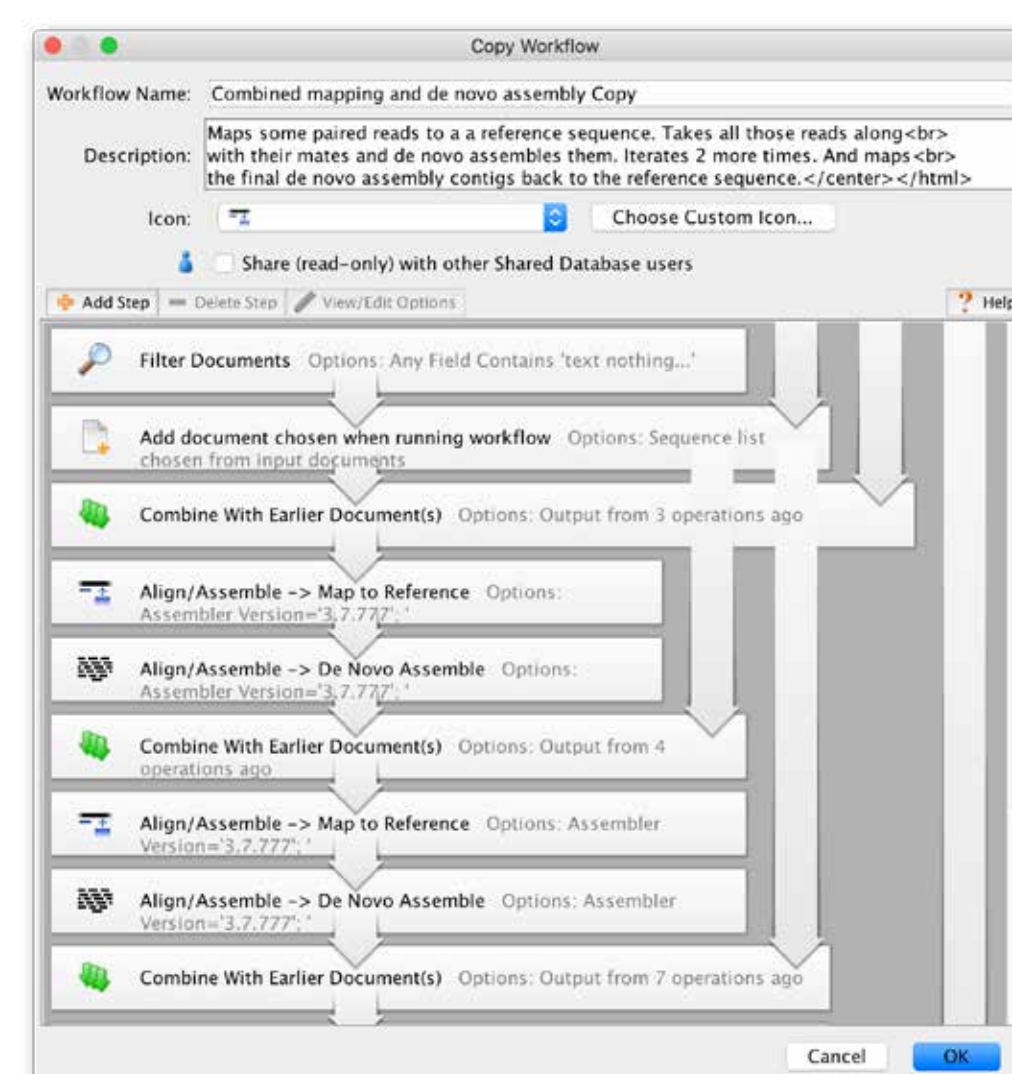
- Design and test primers with Primer3
- Simulate PCR reactions and restriction digests
- Design cloning strategies for Restriction cloning ^{New redesigned tool in R10}
TOPO cloning
Gibson assembly (TALEN)
Gateway Cloning
CRISPR
GoldenGate
- Improved lineage tracking ^{New in R10}

Analyse and Annotate



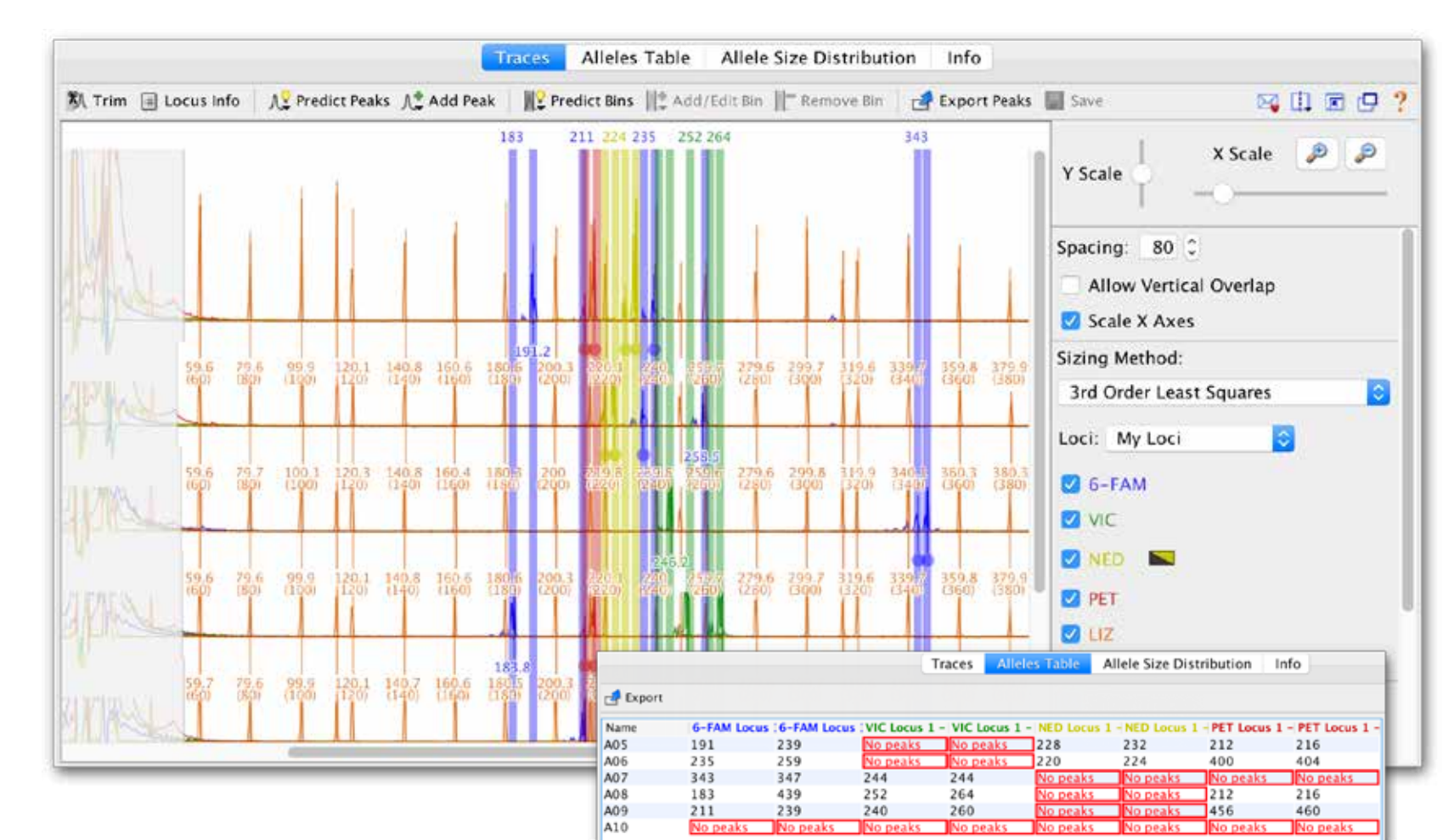
- Find and annotate genes by comparison with existing sequences and annotations in public or local databases
- Powerful SNP detection annotates variants while screening out sequencing errors
- Export single sample variant calls to a VCF file

Customise Your Geneious



- Streamline your analysis and automate common tasks with a custom workflow
- Open-source plugin development kit allows you to extend Geneious functionality: Add your favourite algorithm, database or visualization

And More...



- Import microsatellite AB1 fragment files and visualize traces
- GenBank Submission tool
- Chimera filtering of NGS amplicon datasets ^{New in R10}

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