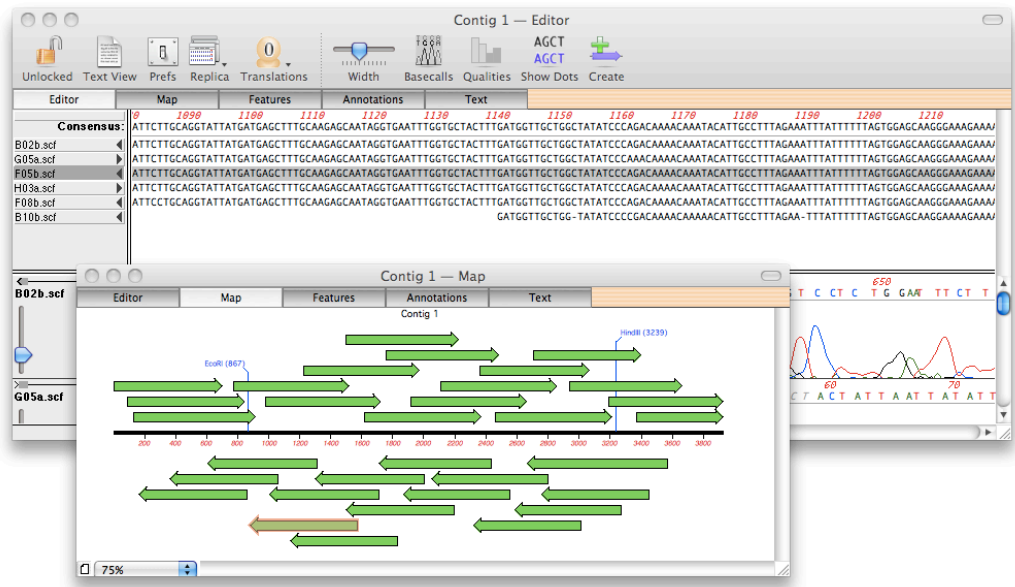


are observed, you can quickly identify alternative protein sequences by performing an open reading frame analysis. Alternatively see a realtime 3/6 frame translation of your contigs in the integrated contig editor.



Next Generation Sequencing.

Short read data may be imported in Fastq format and assembled using the latest version of phrap. Illumina, 454 and Solid data are all supported in fastq format. Each read in a project contains metadata of which type of sequencer it was generated from.

Supports Numerous File Formats. Effortlessly import ABI, SCF, and ALF formatted chromatogram files, MacVector, Fastq or FASTA formatted sequence files.

Easy to use interface. Navigating around your assemblies has never been easier. Display an entire contig in the graphical Map view, and select a read to instantly zoom straight to that region in the Editor

view at sequence level. Click on a base in the alignment and see the trace data associated with that base below.

Integrated within MacVector Analyze contigs directly in MacVector. Run restriction enzyme analysis, design primers and align contigs directly from the contig editor view.

Job Manager Assembler uses the MacVector job manager to control basecalling and assembly. Allows you to continue working whilst running longer assemblies

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