# MacVector 13.5.5

## for Mac OS X

*The online updater for this release is 44.1 MB in size*

## System Requirements

MacVector 13.5 runs on any Intel Macintosh running **Mac OS X 10.6** or higher. There are no other specific hardware requirements for MacVector – if your machine can run OS X 10.6 or above, it can run MacVector. A complete installation of MacVector 13.5 uses approximately 175 MB of disk space.

## Installation and License Activation

Install MacVector 13.5 by dragging the MacVector folder onto the Applications folder. You may be prompted for a system administrator account and password during this copy. You can then optionally drag the "Shortcut" icon for the MacVector application itself onto your desktop or onto the Dock for easy access. Don't worry if the shortcut icon appears blank, it will reset to a MacVector icon the when you first run it. Once installation is complete, you must enter a valid license owner, serial number and activation code the first time you run MacVector. This information is usually sent by e-mail but is also printed on the inside of the CD sleeve if you opted to receive MacVector on physical media. If you previously installed an earlier version of MacVector and have a serial number with a maintenance end date of September 1st 2014 or later, MacVector 13.5 will automatically use your existing license and you will not be required to enter the details again.

## Changes for MacVector 13.5.5

### Bug Fixes

A problem where features of type "????" would be created when opening a saved Align To Reference (.axml) file has been resolved.

## Changes for MacVector 13.5.4

### Bug Fixes

The Quicktest Primer fix from 13.5.3 inadvertently disabled the "mouse-over" restriction enzyme display functionality. This has been restored.

## Changes for MacVector 13.5.3

### Bug Fixes

The Contig Editor display now refreshes correctly on OS X 10.6 when loading a saved alignment.

A crash has been fixed in the Protein Analysis Toolbox.

A crash in the Quicktest Primer interface when working with large numbers of restriction enzymes has been fixed.

## Changes for MacVector 13.5.2

### Bug Fixes

A scrolling issue in the Contig Editor/Align To Reference Editor has been resolved.

A rare crash when awaking on a different network has been fixed.

## Changes for MacVector 13.5.1

### Bug Fixes

On OS X 10.6, imported sequences now retain their original file name.

An occasional crash closing modified sequences that were not saved has been fixed.

Translations in the annotated text output now correctly honor the preferences flags.

Some inconsistencies in the numbering of "untitled" sequences has been resolved.

A problem where sequence windows would disappear under OS X 10.6 has beeen resolved,

A number of display glitches in the Align To Reference editor have been fixed.

A problem where translations were sometimes missing in the Map tab when zoomed to the residue level has been fixed.

The ability to import BAM files into an Assembler Project has been restored.

Nucleic acid multiple alignment documents now have their own color group and blocking defaults.

Primers in the "Test PCR Primer Pair" mode of Primer Design can now be over 35 nt in length.

Text views now automatically resize in width to print on a single page.

## Changes for MacVector 13.5

The graphics **Symbol Editor** and floating **Graphics Palette** have been rewritten in preparation for MacVector moving to a 64-bit architecture (due with MacVector 14.0). The other main enhancements have been aimed at better handling of Next Generation Sequencing (NGS) files, particularly with the **Align To Folder** and Assembler **Velvet** *de novo* assembly functionality. There has also been some code optimization to better handle the analysis of large genomic sequences, particularly noticeable with the Pustell Matrix "dot-plot" functionality.

### Align To Reference Enhancements

The **Align To Reference** alignment algorithm and the **Editor** now handle alignments around a circular sequence. Note that this is only the case for the "Sequence Confirmation" algorithm. The cDNA Alignment algorithm still assumes the target sequence is linear.

You can now select one or more sequence "Reads" in the **Align To Reference Editor** and save those reads to a fasta or fastq formatted file by choosing **File | Export…** and selecting the required format in the resulting dialog. In particular, this lets you run alignments of up to 500,000 NGS reads against a reference sequence and then specifically export all of the aligned (or non-aligned) reads for further analysis.

## Align To Folder Enhancements

Align To Folder can now perform alignments against fasta and fastq files with many millions of reads.

You can now retrieve the "hits" from an Align To Folder run to one of three destinations – the MacVector Desktop (i.e. opening each hit in a window on the screen), to a folder (where each hit is written out as a separate file) or to a single file (where the hits are concatenated into a single fasta or fastq file). The key to this functionality is that you can select lines in the Folder Description List window as follows;
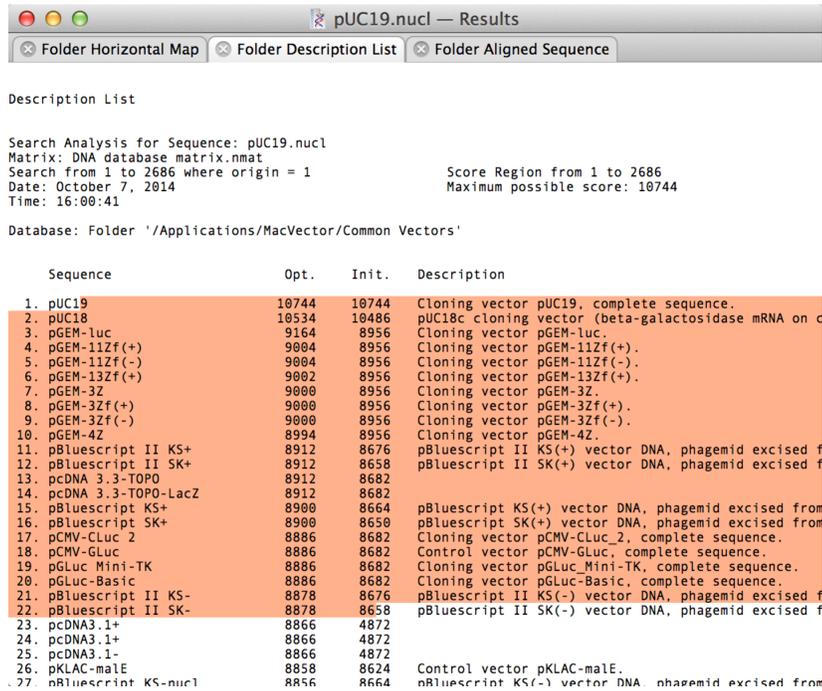


When any part of a line is highlighted, that "hit" is considered "selected". You can then choose on the options from the Database menu;

**Database | Retrieve To Desktop** – this opens windows on the desktop containing the selected sequences. If the matching sequence was a single file (e.g. in MacVector or GenBank format) the original file is opened. If the hit is a Read within a large fasta or fastq file, a new sequence window is created and populated with the Read sequence.

**Database | Retrieve To Disk** – this saves the hits to individual files in the selected destination folder. If the matching sequence was a single file (e.g. in MacVector or GenBank format), the file is simply copied to the destination so that all features and feature appearance information is maintained.

**Database | Retrieve To File** – this saves the sequence information (plus any quality information in the case of fastq data) of all selected hits into a single file in either fasta or fastq format.

Taken together, these enhancements let you use **Align To Folder** to pull out rare matching reads from large NGS datasets for use in further analysis or DNA Assembly. In beta testing, this has been used to "clone" genes from MiSeq RNA-Seq runs using Protein source sequences aligned to Fastq data.

## Pustell Matrix ("Dot Plot") Enhancements

The performance of large (i.e. genome-sized) Pustell Matrix dot plot alignments has been dramatically improved. You can now scan and display pairs of bacterial genomes in just a few seconds to easily identify inversions, duplications and rearrangements in their gene organization. You can zoom in and out of the dot plot display in real time to explore the relationships right down to the residue level.

## Nucleic Acid Subsequence Enhancements

A small but significant change has been made to the graphical output of this. If you select a pair of hits in the Map results tab, then choose **Edit | Copy**, the sequences of the actual subsequences are substituted into the copied sequence. This allows you to maintain primers in a nucleic acid subsequence file and use the **Nucleic Acid Subsequence** analysis option to quickly identify and "clone" predicted PCR fragments even if the primers have mismatches or tails added to them.

## Assembler Enhancements

Reference alignments (from **Bowtie**) now have a separate coverage report tab that lists the read coverage for every gene and CDS feature in the reference sequence. You can use this to (e.g.) accurately measure relative expression levels of mRNA in RNA-Seq experiments or plasmid copy number in whole cell DNA sequencing experiments.

**Velvet** now does a much better job at trimming poor quality residues from input sequences.

**Velvet** now handles paired sequences that have identical names.

You can now export unassembled reads from **Bowtie** and **Velvet** alignments as fasta or fastq files. This lets you filter out reads that match specific sequences so you can focus subsequent alignments using a subset of reads.

## Miscellaneous Enhancements

You can now reset the circular origin of circular sequences to any arbitrary position. Simply click between the residues where you want the new origin to be, then right-click (or <control>-click) and choose **Set Circular Origin** from the popup menu.

Informative tooltips have been restored in all views. There is a setting to turn this on/off in **MacVector | Preferences | General**.

The cDNA **Align To Reference** algorithm now does a much better job of displaying segmented reads in the **Map** view.

A number of issues with saving trace files have been resolved. In particular, you can now use the bsml format to save annotations with chromatogram information.

# Support information

For assistance with MacVector, please contact your local MacVector, Inc office. You will need a current MacVector maintenance contract to be eligible for technical support other than for basic installation problems. New sales of MacVector include 12 months of support that also entitles you to any upgrades to MacVector released during the maintenance period.

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When contacting Customer Support with a technical problem, please be prepared to give your product serial number as well as a detailed description of your problem and any error messages you encounter. Visit the MacVector Web site for details of any available updates, and any relevant information that could not be added to these release notes in time for publication:

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http://www.macvector.com
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