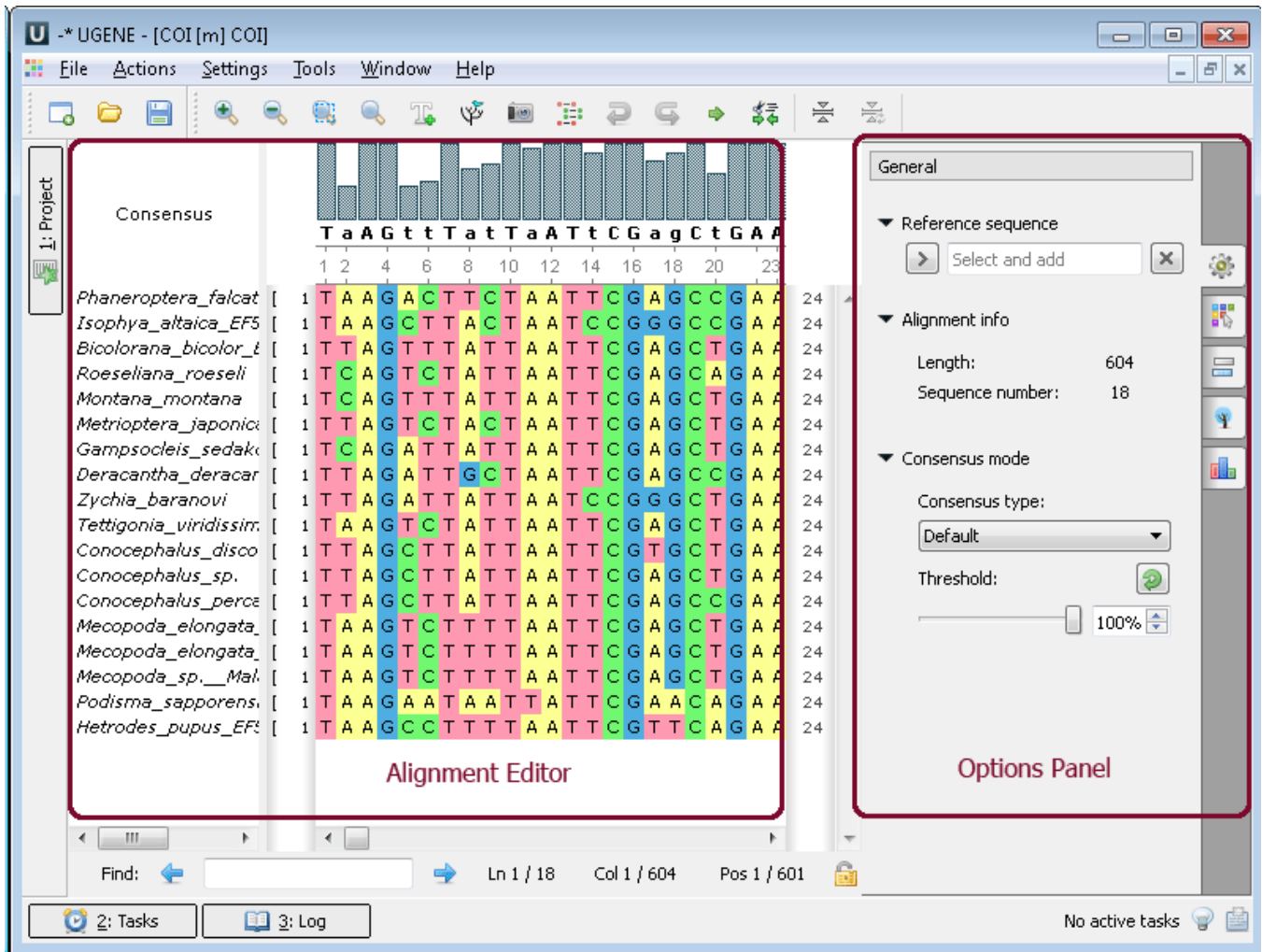


View, edit and align multiple sequence alignments

Multiple sequence alignment (MSA Editor). The *Alignment Editor* is a powerful tool for visualization and editing DNA, RNA or protein multiple sequence alignments. To activate the *Alignment Editor* open any alignment file. For example you can use the `$ugene/data/samples/CLUSTALW/COI.aln` file provided with UGENE. After opening the file in UGENE the *Alignment Editor* window appears:



The editor supports different multiple sequence alignment (MSA) formats, such as ClustalW, MSF and Stockholm. The editor provides interactive visual representation which includes:

- Navigation through an alignment;
- Optional coloring schemes (for example Clustal, Jalview like, etc.);
- Flexible zooming for large alignments;
- Export publication-ready images of alignment;
- Several consensus calculation algorithms.

Using the *Alignment Editor* you can:

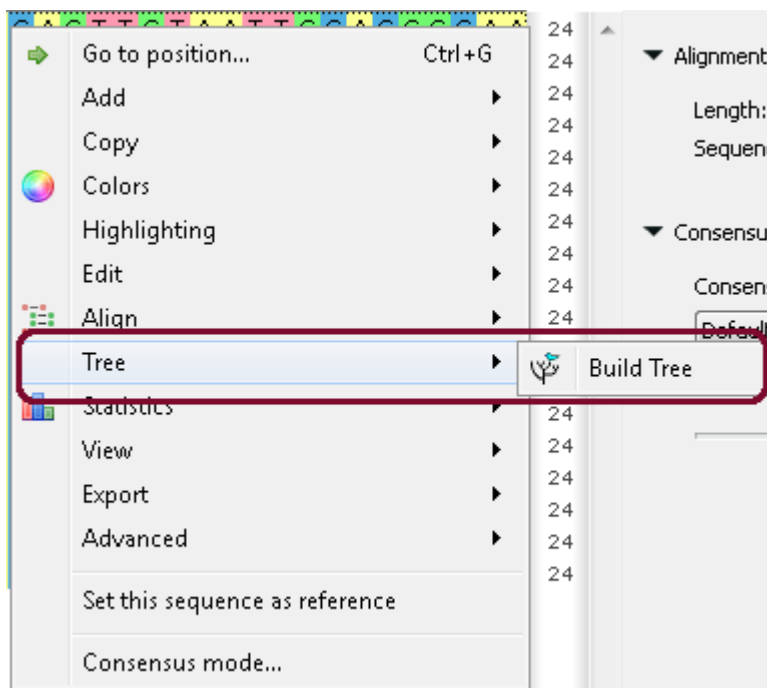
- Perform multiple sequence alignment using integrated MUSCLE and KAlign algorithms;
- Edit an alignment: delete/copy/paste symbols, sequences and subalignments;
- Build phylogenetic trees;
- Generate grid profiles;
- Build Hidden Markov Model profiles to use with HMM2/HMM3 tools.

Example 2: Build a tree from your alignment. You can do this by three different ways:

a. From the toolbar. Click to the tree icon:



b. From the context menu:



c. From the Options Panel:



After calculation the tree appears in the MSA Editor in a separate window:

U -* UGENE - [COI [m] COI]

File Actions Settings Tools Window Help

Tree view

COI2.nwk x

Find: Ln 13 / 18 Col 1 / 604 Pos 1 / 601

2: Tasks 3: Log No active tasks

	T	a	A	G	t	t	T	a
1	T	A	A	G	A	C	T	T
1	T	T	A	G	T	T	T	A
1	T	C	A	G	T	C	T	A
1	T	C	A	G	T	T	T	A
1	T	T	A	G	T	C	T	A
1	T	C	A	G	A	T	T	A
1	T	T	A	G	A	T	T	G
1	T	T	A	G	A	T	T	A
1	T	T	A	G	T	C	T	A
1	T	T	A	G	T	C	T	A
1	T	T	A	G	T	C	T	A
1	T	T	A	G	T	C	T	A
1	T	T	A	G	T	C	T	A
1	T	T	A	G	T	C	T	A
1	T	A	A	G	A	A	T	A
1	T	A	A	G	C	C	T	T
1	T	A	A	G	C	T	T	A