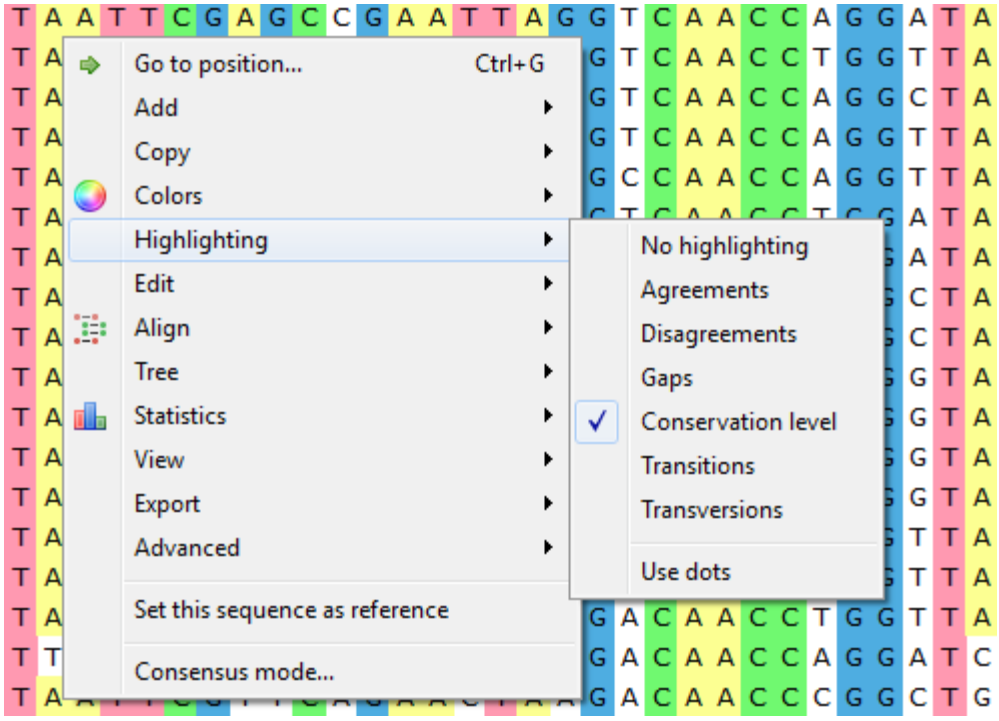
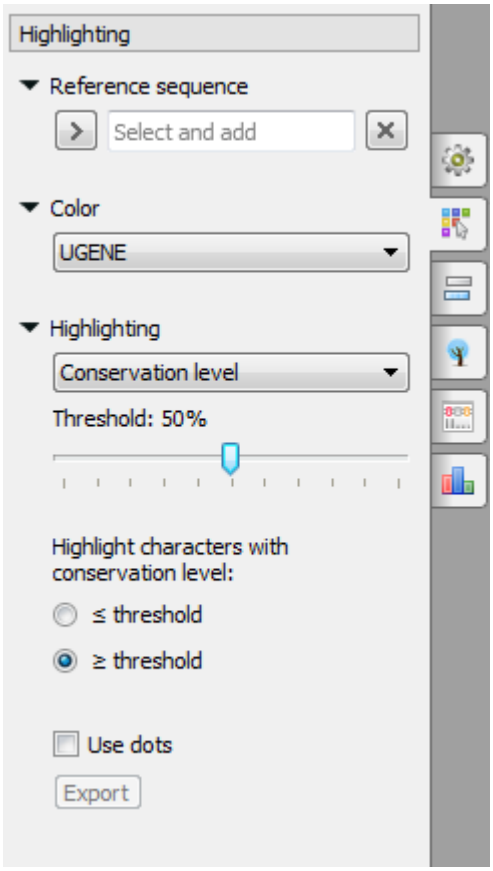
Highlighting Alignment

To apply an alignment highlighting mode, select it in the *Highlighting* context menu:



or on the *Highlighting* tab of the *Options Panel:*



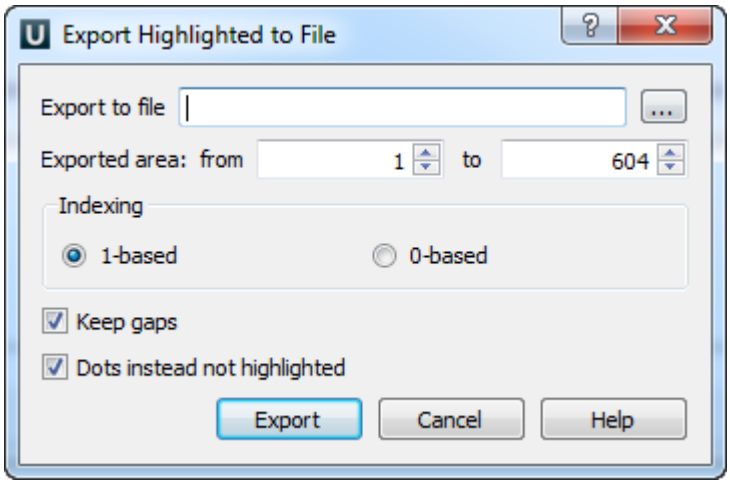
The following modes are available:

- *Agreements* — highlights symbols that coincide with the reference sequence.
- *Disagreements* — highlights nucleotides that differ from the reference sequence.
- *Gaps* - highlights gaps.
- *Conservation level* - highlights conservation level of symbols in a multiple alignment >= or <= treshhold. To select the conservation parameters use the *Highlighting* Options Panel tab.
- *Transitions* - highlights transitions.
- *Transversions* - highlights transversions.

To use dots instead of symbols which are not highlighted check the *Use dots* checkbox in the *Options Panel* or use the *Highlighting->Use dots* context menu item.

To select a reference sequence use the *Set this sequence as reference* context menu or *Reference sequence* field in the *Highlighting* tab of the *Options Panel*.

Also you can export highlighting with a help of the *Export* button in the *Options Panel* or by the *Export->Export highlighted* context menu item. The following dialog will appear:



Select file to export, exported area and click on the *Export* button. The task report will appear in the *Notifications*.