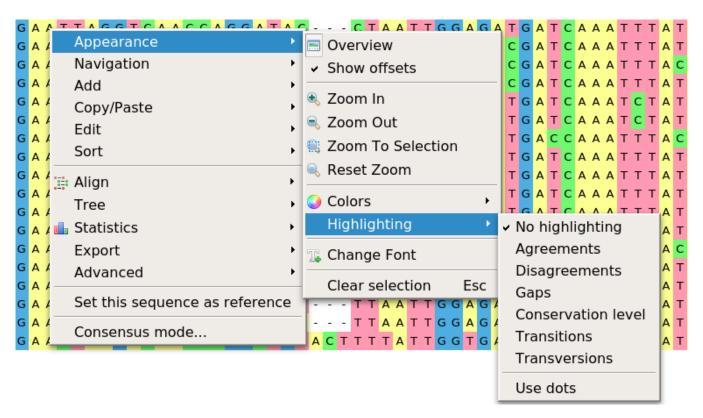
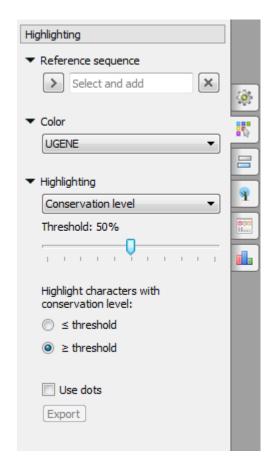
Highlighting Alignment

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



or on the Highlighting tab of the Options Panel:



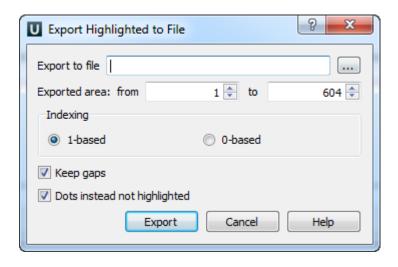
The following modes are available:

- 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*.