## **BWA**

BWA is a fast light-weighted tool that aligns relatively short reads to a reference sequence. Click this link to open BWA homepage. BWA is embedded as an external tool into UGENE.

Open Tools DNA assembly submenu of the main menu.



Select the *Align short reads* item to align short reads to a DNA sequence using *BWA*. Or select the *Build index* item to build an index for a DNA sequence which can be used to optimize aligning of short reads.

- Aligning Short Reads with BWABuilding Index for BWA