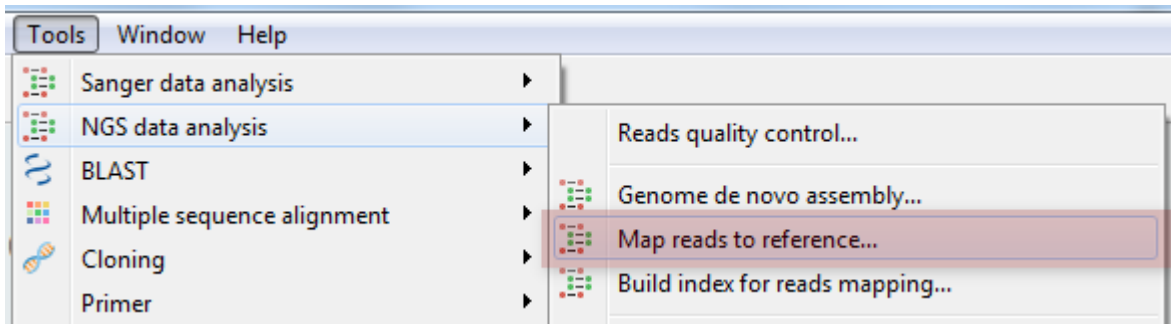


# BWA

*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 BWA](#)
- [Building Index for BWA](#)