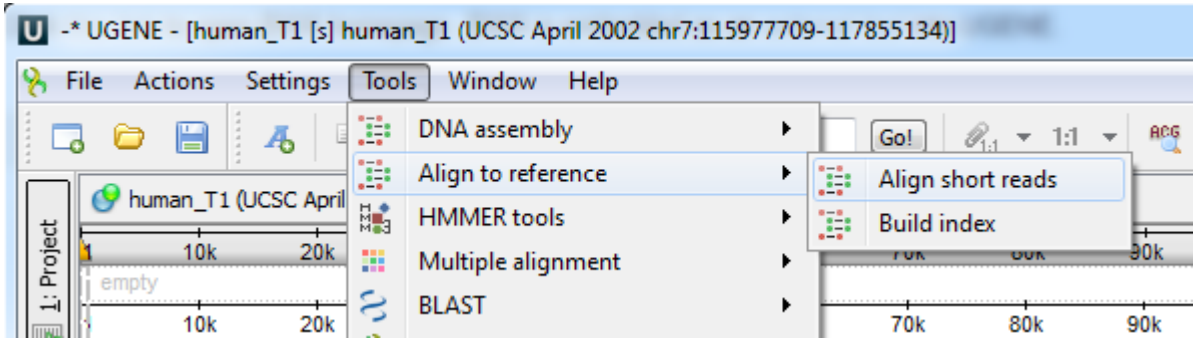


# BWA-SW

*BWA* is a fast light-weighted tool that aligns relatively short reads to a reference sequence. Click [this link](#) to open *BWA* homepage. *BWA-SW* share similar features such as long-read support and split alignment. *BWA-SW* is embedded as an *external tool* into UGENE.

Open *Tools* *Align to reference* submenu of the main menu.



Select the *Align short reads* item to align short reads to a DNA sequence using *BWA-SW*. 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-SW](#)
- [Building Index for BWA-SW](#)