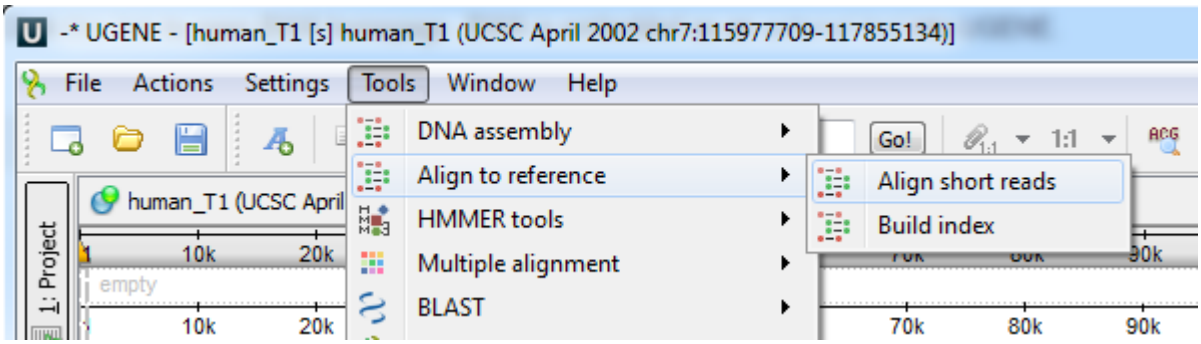
# BWA-SW

*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