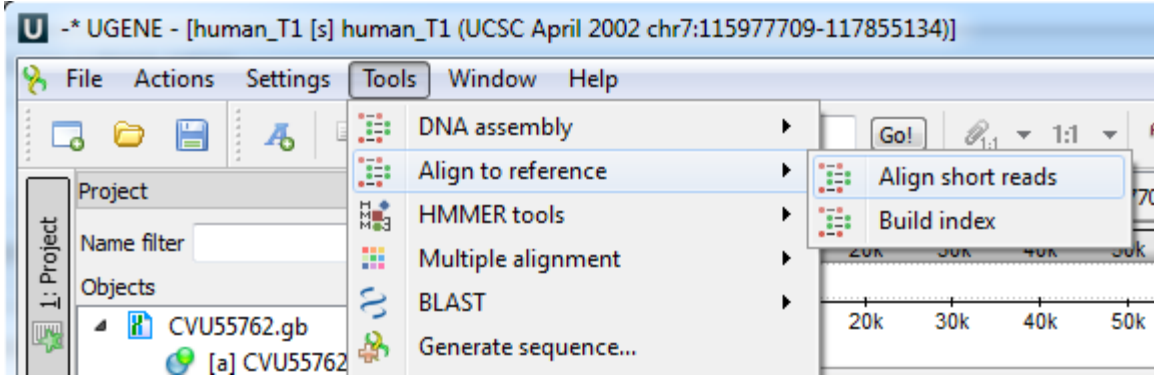


# BWA-MEM

*BWA* is a fast light-weighted tool that aligns relatively short reads to a reference sequence. Click [this link](#) to open *BWA* homepage. *BWA-MEM* is generally recommended for high-quality queries as it is faster and more accurate. *BWA-MEM* also has better performance than *BWA-backtrack* for 70-100bp Illumina reads.

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-MEM*. 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-MEM
- Building Index for BWA-MEM