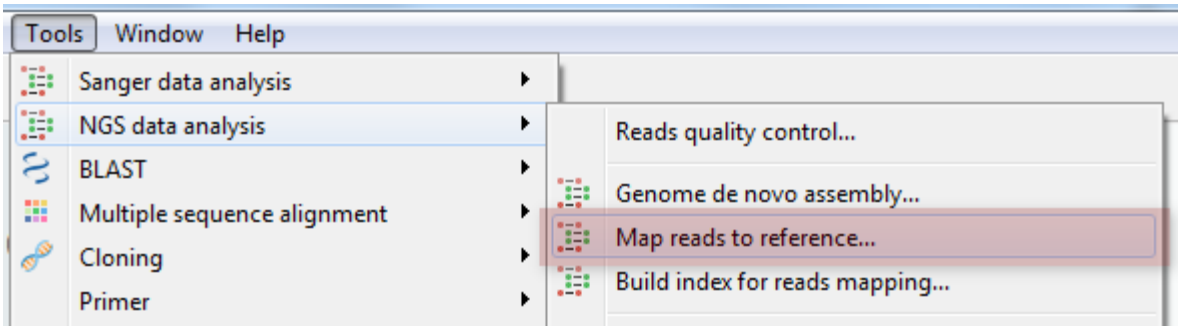
BWA-MEM

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