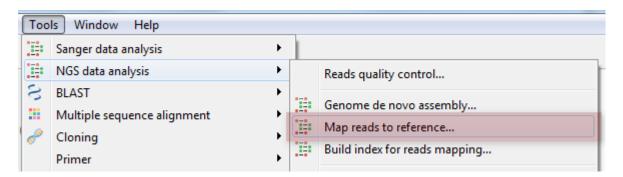
BWA-SW

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-SWBuilding Index for BWA-SW