Trimmomatic algorithm cleans raw sequencing reads from technical adapters. The Trimmomatic pre-processing step is usually performed to ensure better quality of alignment of reads on the reference genome.

For more info please see:

Bolger AM, Lohse M, Usadel B. Trimmomatic: a flexible trimmer for Illumina sequence data. *Bioinformatics*. 2014;30(15):2114-2120. doi:10.1093/bioinformatics/btu170.