

FastQC

FastQC is a stand-alone java application which will generate quality summary of your NGS data. It can take as input bam, sam and fastq files and will produce graphs and tables representing the quality of the data.

It can be downloaded at : <http://www.bioinformatics.bbsrc.ac.uk/projects/fastqc/>

Documentation about interpreting each quality module at: <http://www.bioinformatics.babraham.ac.uk/projects/fastqc/Help/3%20Analysis%20Modules/>