

Accessing and using sequencing data

Alt-text Figure 1 - Example FASTQ read. Four text lines are used to represent each read

Illustrative examples of FASTQ read. Detailed description in figure legend: Four text lines are used to represent each read. The first line is the unique name of the read, the second line is the nucleotide sequence, the third line is the 'break' line, and the fourth line is the quality scores (one for each base sequenced).