Choosing 20 as the cutoff for FASTQ “Phred score”

* [Clinical Applications for Next-Generation Sequencing](http://www.sciencedirect.com/science/book/9780128017395)**,** 2016, Pages 19–37
* Chapter 2 – Basic Bioinformatic Analyses of NGS Data
* “The reads are usually trimmed, to remove low-quality reads, either using a fixed trimming from both ends or using a phred score-based trimming, using a score of 20 as the cutoff.”
* <http://www.sciencedirect.com/science/article/pii/B9780128017395000027>
* “For many purposes, a Phred Score of 20 or above is acceptable, because this means that whatever it qualifies is 99% accurate, with a 1% chance of error.”
* <https://gatkforums.broadinstitute.org/gatk/discussion/4260/phred-scaled-quality-scores>