

How do I interpret the Quality scores?

Quality scores range from 4 to about 60, with higher values corresponding to higher quality. The quality scores are logarithmically linked to error probabilities, as shown in the following table:

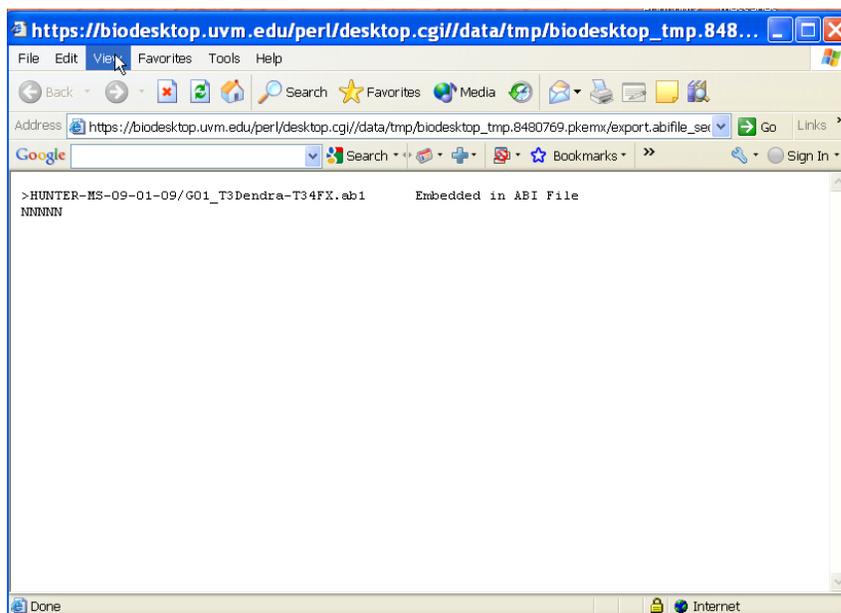
Phred quality score	Probability that the base is called wrong	Accuracy of the base call
10	1 in 10	90%
20	1 in 100	99%
30	1 in 1,000	99.9%
40	1 in 10,000	99.99%
50	1 in 100,000	99.999%

(<http://www.phrap.com/index.htm>)

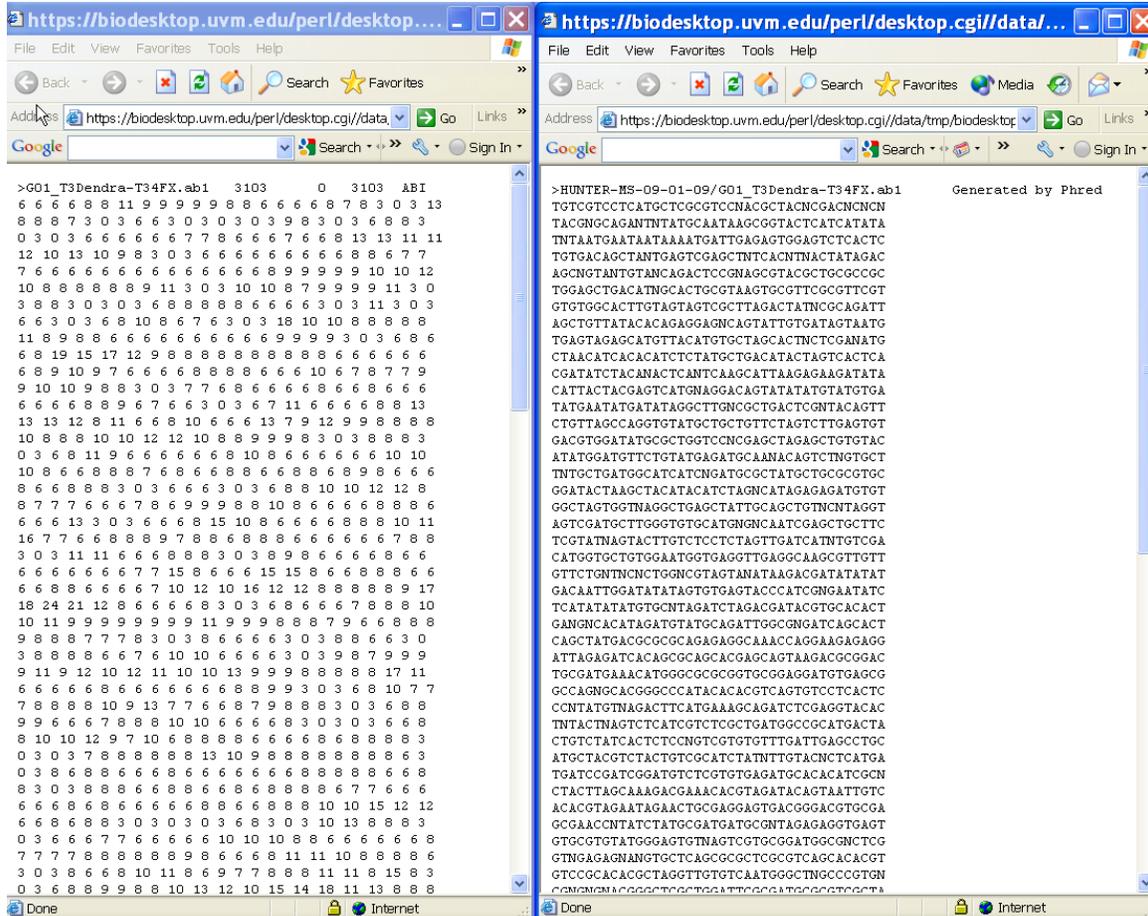
The ABI software shows I have a “No Signal”, but the phred basecaller shows that I have data.

Why is that?

When the KB base caller sees raw data that has very low to no fluorescent signal, rather than assigning low quality base calls, it assigns NNNNN's to the sequence, indicating a No Signal.



Using the same .ab1 file, Phred will generate base calls, but be sure to look at the quality scores! Single digit quality scores can have a 50-80% chance of being the wrong call.

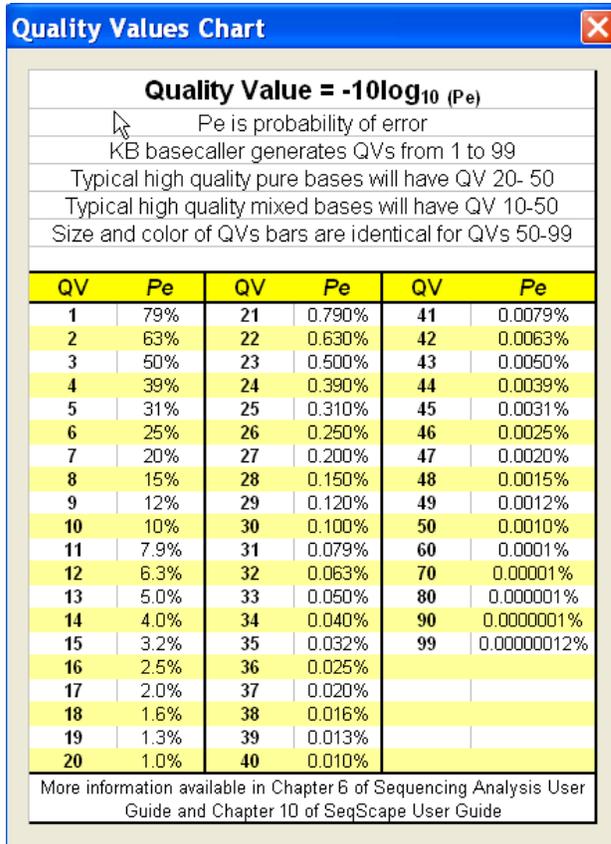


**I blasted my sequence, but there were no matches found.
Why is this?**

Check your quality score file, you most likely blasted a sequence that had very little signal and was just background noise.

Does the KB base caller generate quality scores?

Yes, the KB base caller assigns quality scores much like Phred.



In most trace viewer software packages, the quality scores are represented as bars above the sequence. A higher bar represents a higher quality score.

