



## 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:

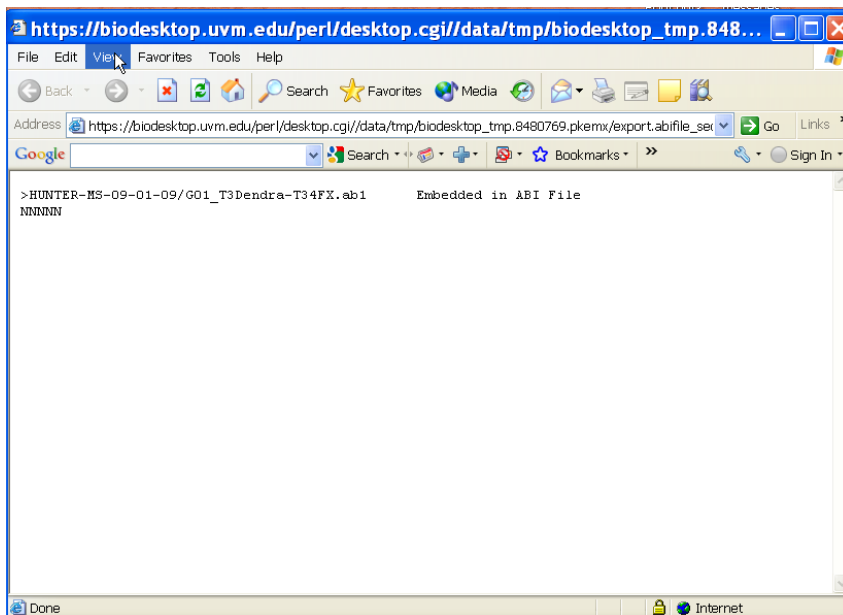
Phred quality score	Probability that the base is called wrong	Accuracy of the base call
10	1 in 10	90%
20	1 in 100	99%
30	1 in 1,000	99.9%
40	1 in 10,000	99.99%
50	1 in 100,000	99.999%

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

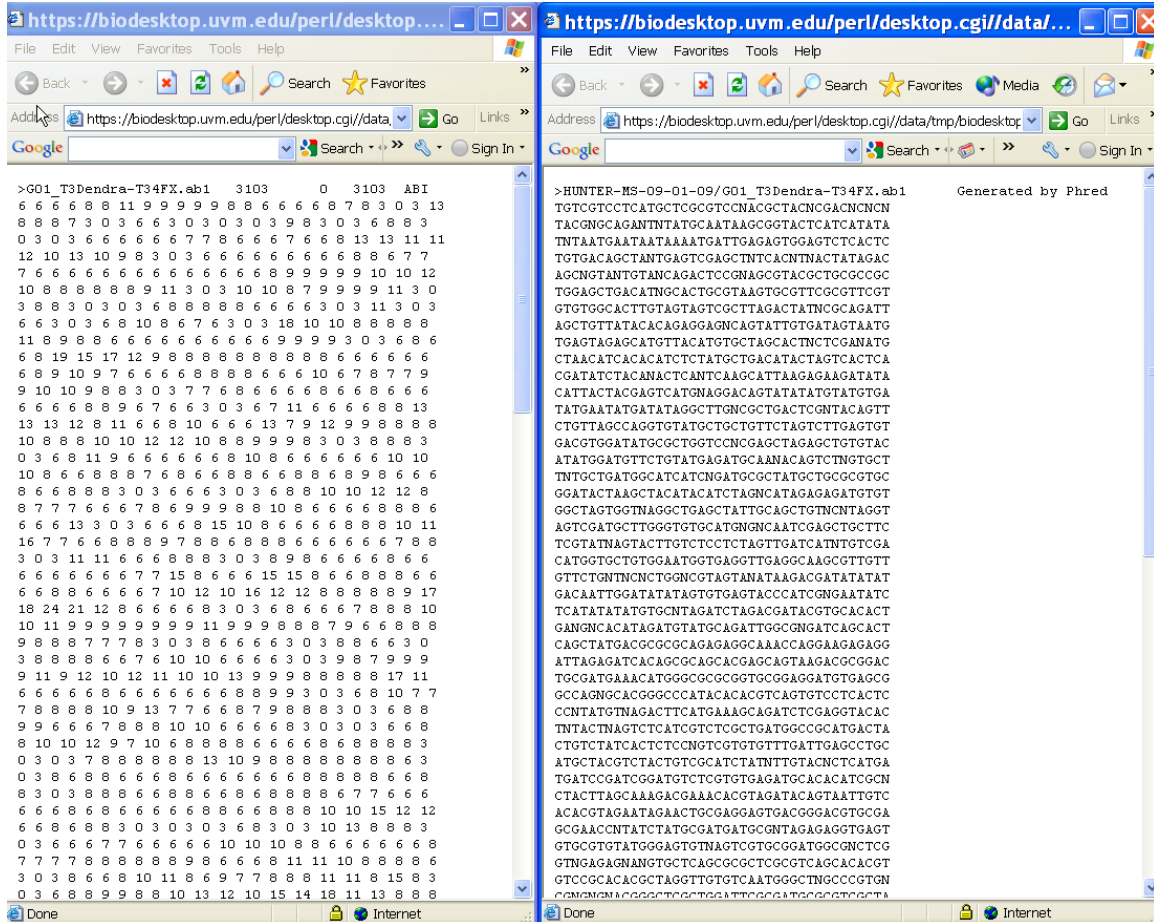
**The ABI software shows I have a “No Signal”, but the phred basecaller shows that I have data.**

**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.



