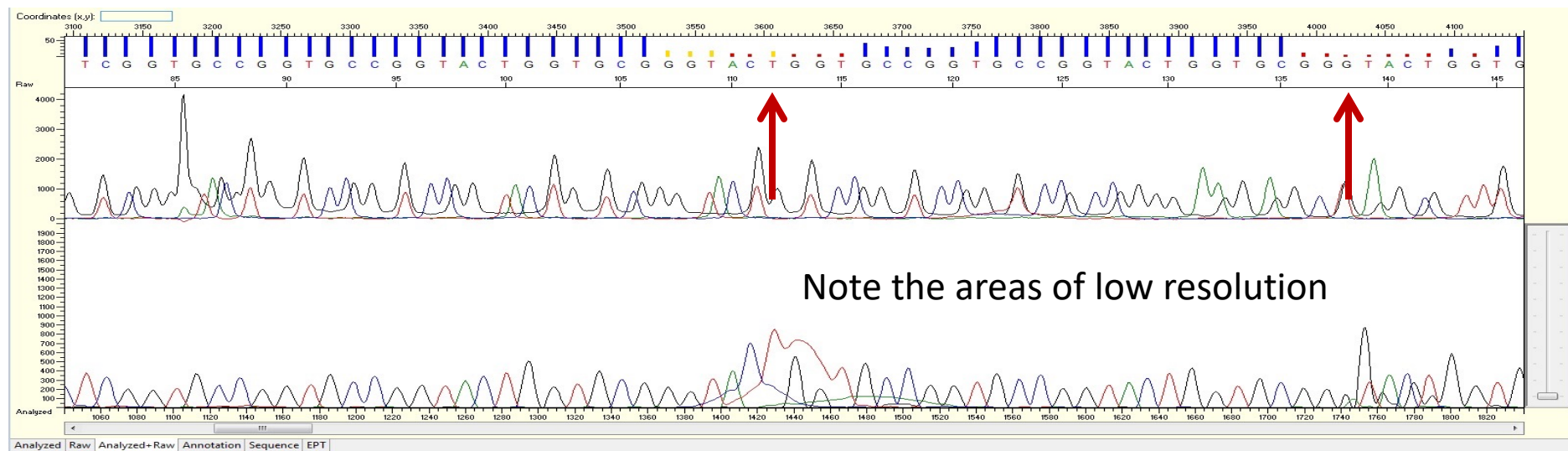
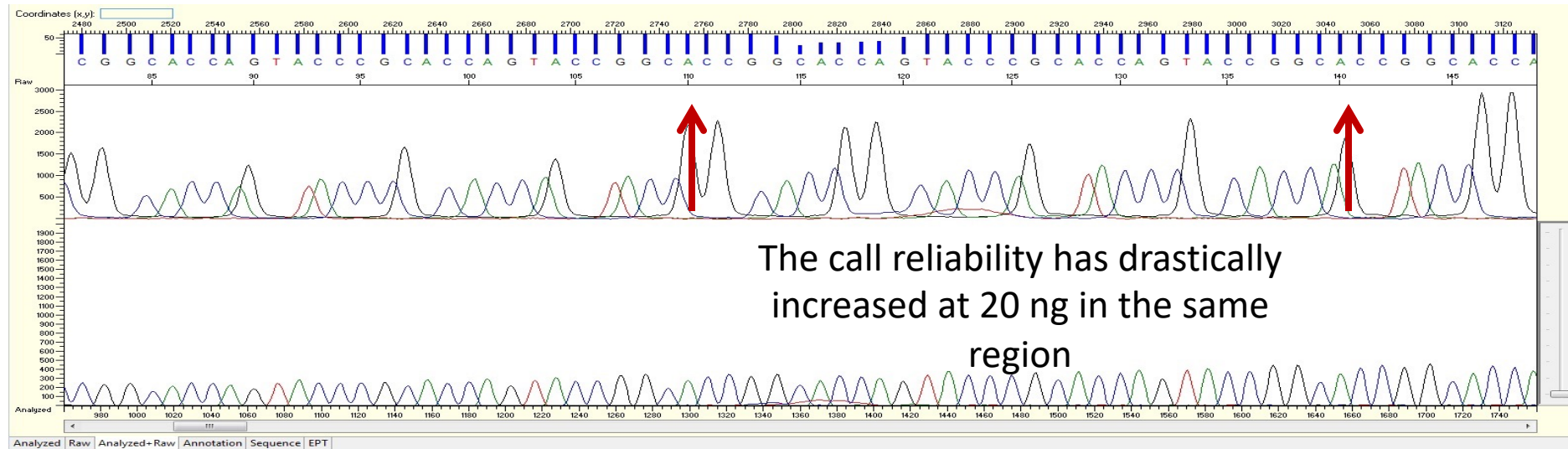


Concentration Matters

10 ng of sample (note: we request 50 ng of DNA in 10ul and run 5ul on the 3130xl)



20 ng of sample (note: we request 50 ng of DNA in 10ul and run 5ul on the 3130xl)



Legend

Trace Score



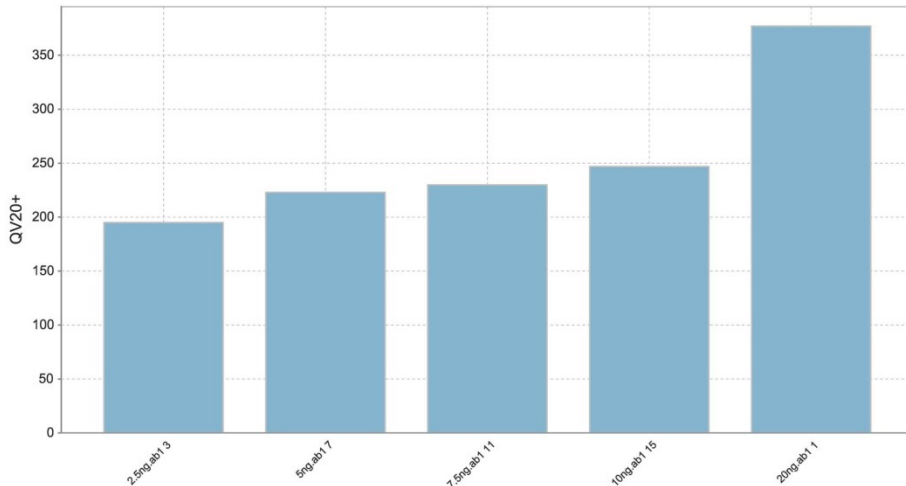
CRL



Trace File Name	Well#	Cap#	Trace Score	CRL	QV20+	Signal Intensity				Comments
						A	C	G	T	
10ng.ab1	H3	15	49	255	247	301	411	623	420	
2.5ng.ab1	B3	3	48	224	195	254	411	809	353	
20ng.ab1	A1	1	57	298	377	545	571	1006	266	← Note the increased signal intensity and trace scores for 20 ng
5ng.ab1	D3	7	51	230	223	230	382	834	338	
7.5ng.ab1	F3	11	51	255	230	358	673	838	640	

QV20+ Report

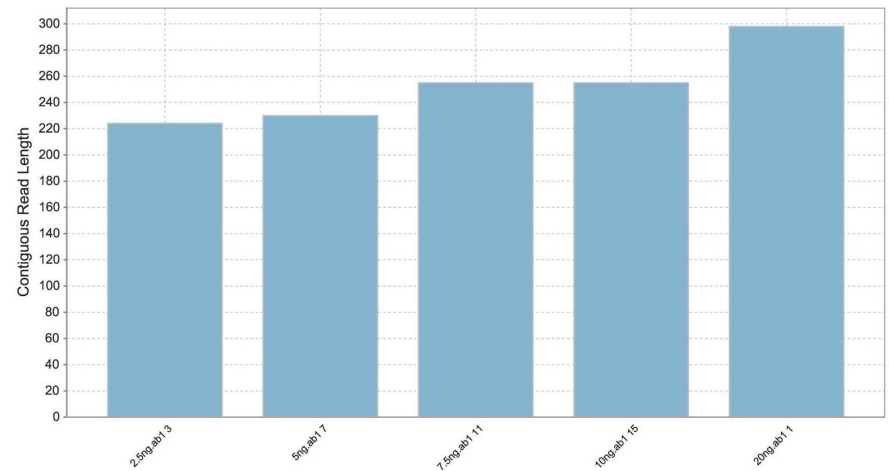
QV20+ value is the total number of bases in the entire trace that have basecaller quality value greater than or equal to 20.
 QV20+ : N = 5, Range = 195 - 377, Median = 247, Mean = 254, StandardDev = 71



QV20+ value is the total number of bases in the entire trace that have basecaller quality value greater than or equal to 20 (99% probability the call is correct).

Contiguous Read Length Report

The Contiguous Read Length (CRL) is the longest uninterrupted stretch of bases with quality higher than a specified limit. In the evaluation of the quality of each base, not only the quality value of that base is used, but also those of adjacent bases within a specified window size.
 Contiguous Read Length : N = 5, Range = 224 - 298, Median = 255, Mean = 252, StandardDev = 29



The Contiguous Read Length is the longest uninterrupted stretch of bases with quality higher than a specific limit.