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TapeStation Software

4200 TAPESTATION INSTRUMENTS

Modified from: https://www.agilent.com/cs/library/usermanuals/public/G2964-90000_TapeStation_USR_ENU.pdf

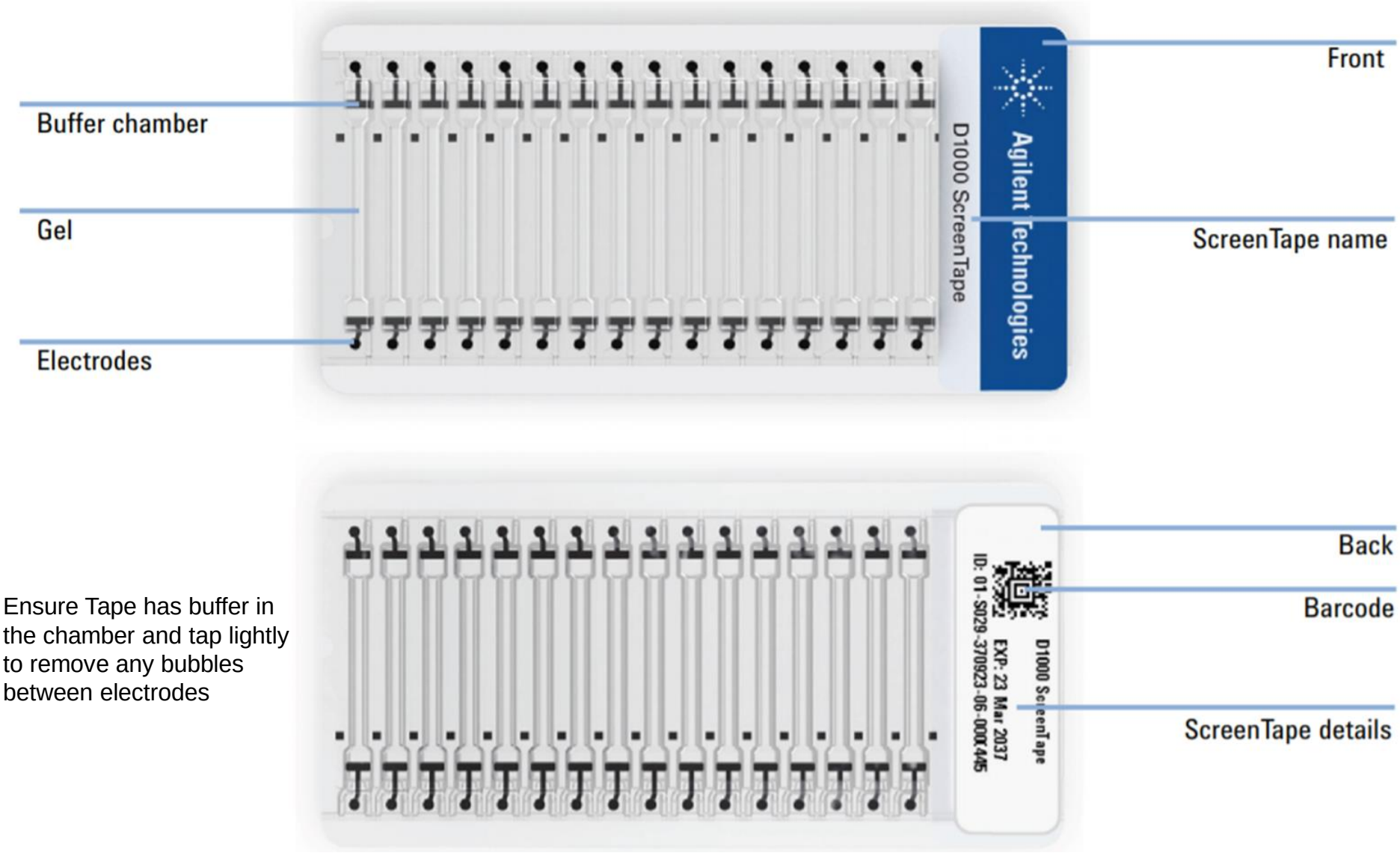
	DNA			RNA	
	D1000	HS D1000	Genomic DNA	RNA	HS RNA
Sizing range	35 to 1000bp	35 to 1000bp	200 to >60kbp	100 to 6000nt	100 to 6000nt
Required sample volume	1µl of sample	2µl of sample	1µl of sample	1µl of sample	2µl of sample
					
Quantification range	0.1 – 50ng/µl	10 – 1000pg/µl	10 – 100ng/µl	25 – 500ng/µl	500 – 10,000pg/µl
Limit of detection	LOD 0.1 ng/uL	LOD 5 pg/uL	LOD 0.5 ng/uL	LOD 5 ng/µL	LOD 100 pg/µL
			DNA Integrity Number (DIN)	RNA Integrity Number equivalent (RIN^e)	

Not Shown
D5000 & HSD5000
Sizing Range: 100-5000 bp

Same Volume and Concentration Requirements as D1000 and HSD1000 Respectively

Note: Only tapes sold by Bauer Core are shown, other assays available through Agilent Technologies

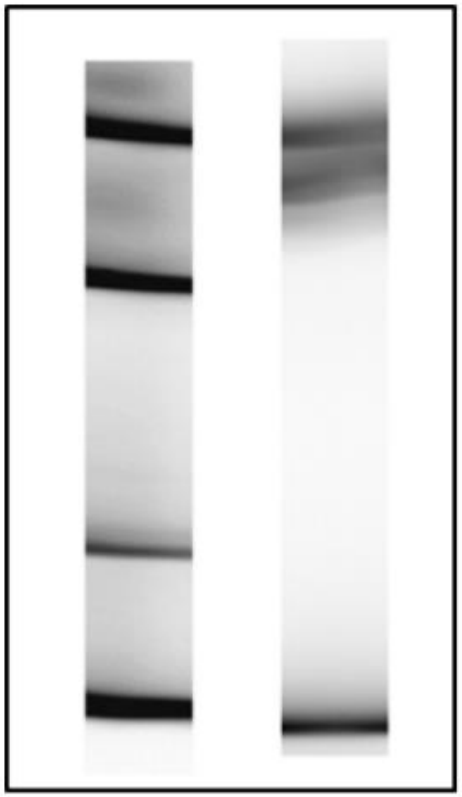
Modified from: http://www.integratedsci.com.au/news/article/tapestation2200-promotion.html



Ensure Tape has buffer in the chamber and tap lightly to remove any bubbles between electrodes

Modified from: https://www.agilent.com/cs/library/usermanuals/public/4200-TapeStation_SystemManual.pdf

Effect of Bubbles



Bubbles within the gel lane significantly affect results.

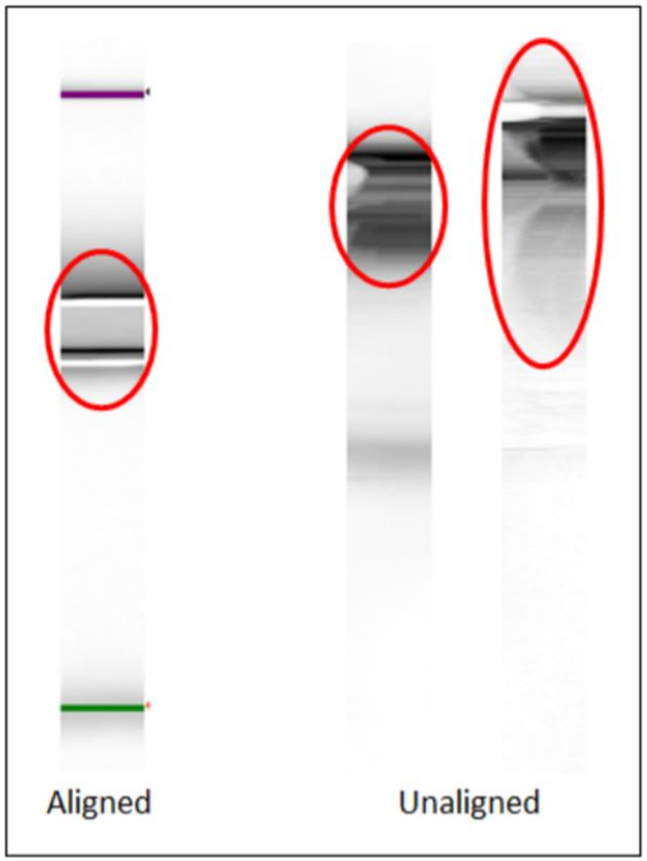


Figure 14 Effect of bubbles at the gel interface on TapeStation Analysis software results - Gel view/unaligned

Air bubbles present at the top of the buffer chamber are normal and acceptable.

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Common TapeStation Software Results and Questions

ALL IMAGES FROM AGILENT TECHNOLOGIES TAPESTATION GUIDES FOR THE 4200 & 2200

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DNA Assays

Concentration too Low

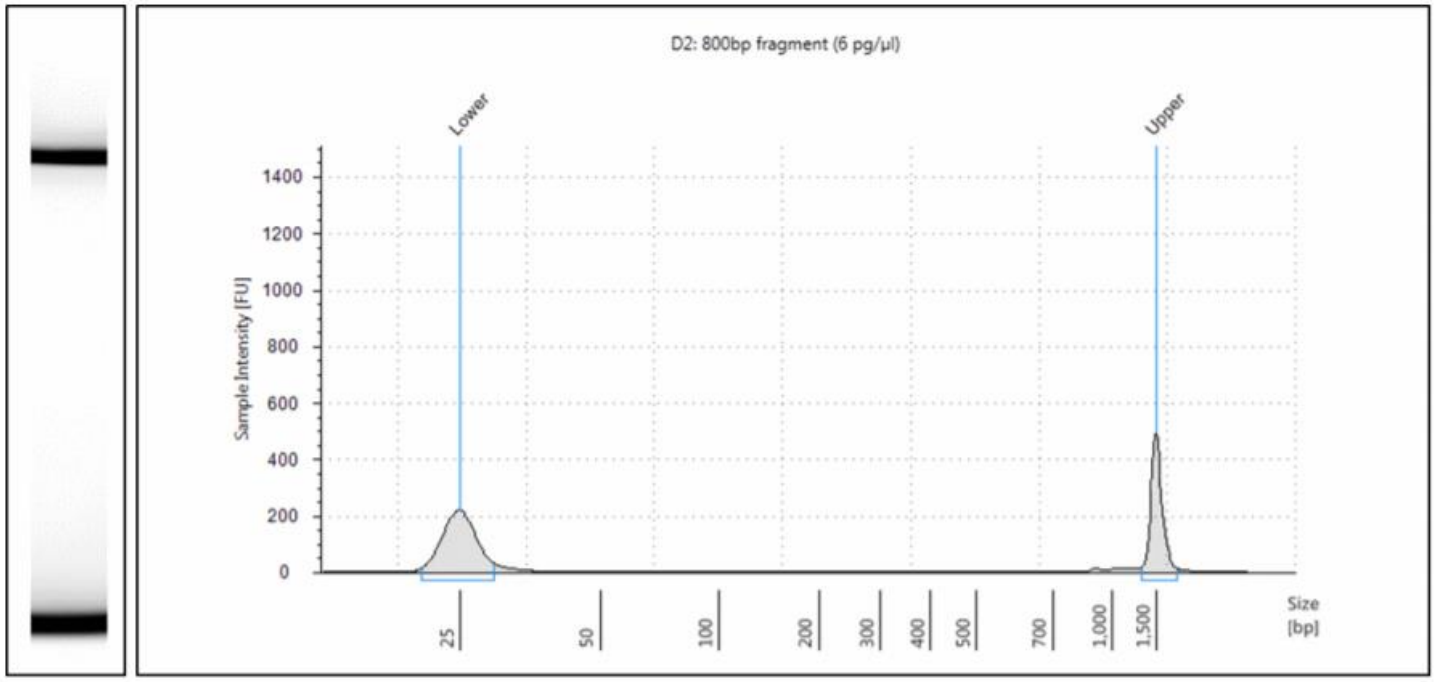

Figure 31 Example of missing sample peak due to too low concentrated sample in the High Sensitivity D1000 assay in the **Gel** view (Left) and **Electropherogram** view (Right) of the TapeStation Analysis software.

Concentration too High

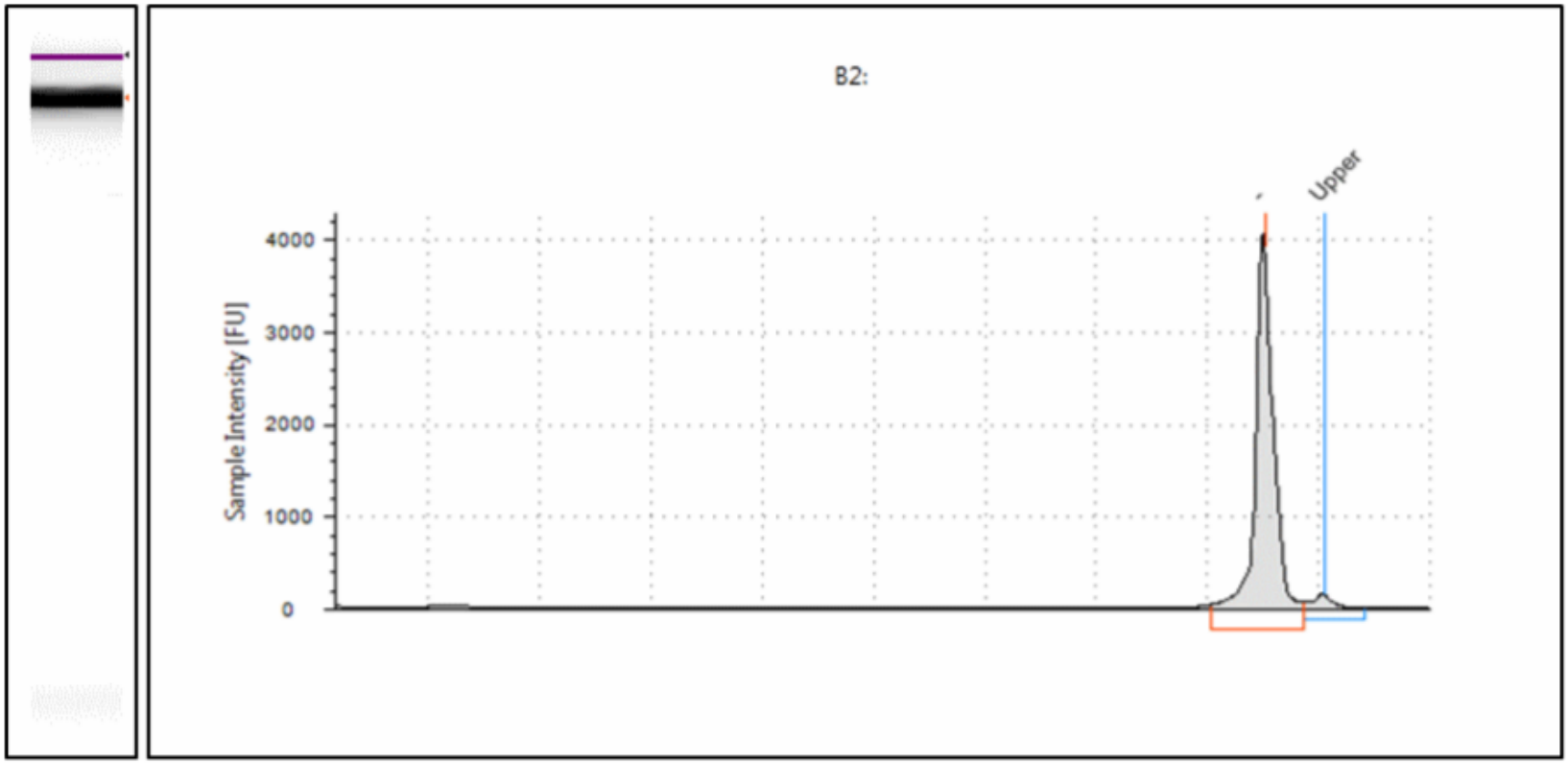

Figure 30 Example of missing marker peak due to too concentrated sample in the High Sensitivity D1000 assay in the **Gel** view (Left) and **Electropherogram** view (Right) of the TapeStation Analysis software.

- It is important to choose the correct assay based on the concentration of the sample. Using sample concentrations outside the specified quantitative ranges will lead to inaccurate quantification.
- For correct volumes and quantitative range, please refer to the appropriate Quick Guide ("Sample Preparation" on page 60).

Figure 16 Effect of correct (A1) and incorrect consumables/protocol (B1 – D1) on the D1000 Ladder peak intensity and Marker assignment in the D1000 ScreenTape assay.

Importance of Size Range

If applicable use an assay with a broader sizing range.

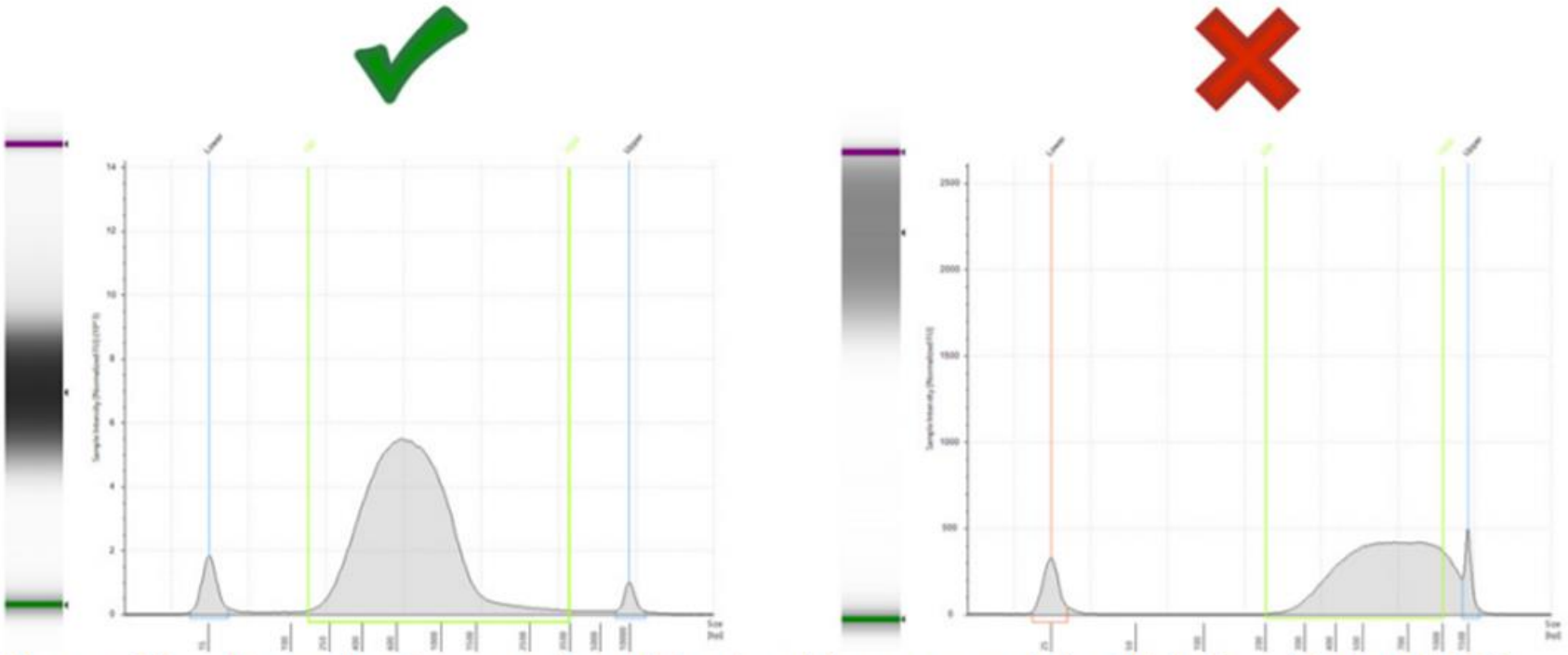

Figure 29 Example of a sample within the sizing range of the High Sensitivity D5000 assay (left) and the same sample merging with the upper marker (right) in the High Sensitivity D1000 assay.

Sizing Range

In order to achieve accurate results the samples used must be within the sizing range as stated in the respective assay Quick Guide. Signal of sample merging with either Upper and/or Lower Marker will not be taken into consideration in concentration calculation. Additional sample overlaying with the marker will alter the known concentration of the marker that is used for concentration calculation. This will influence the overall quantification performance of this lane (Table 3 on page 60).

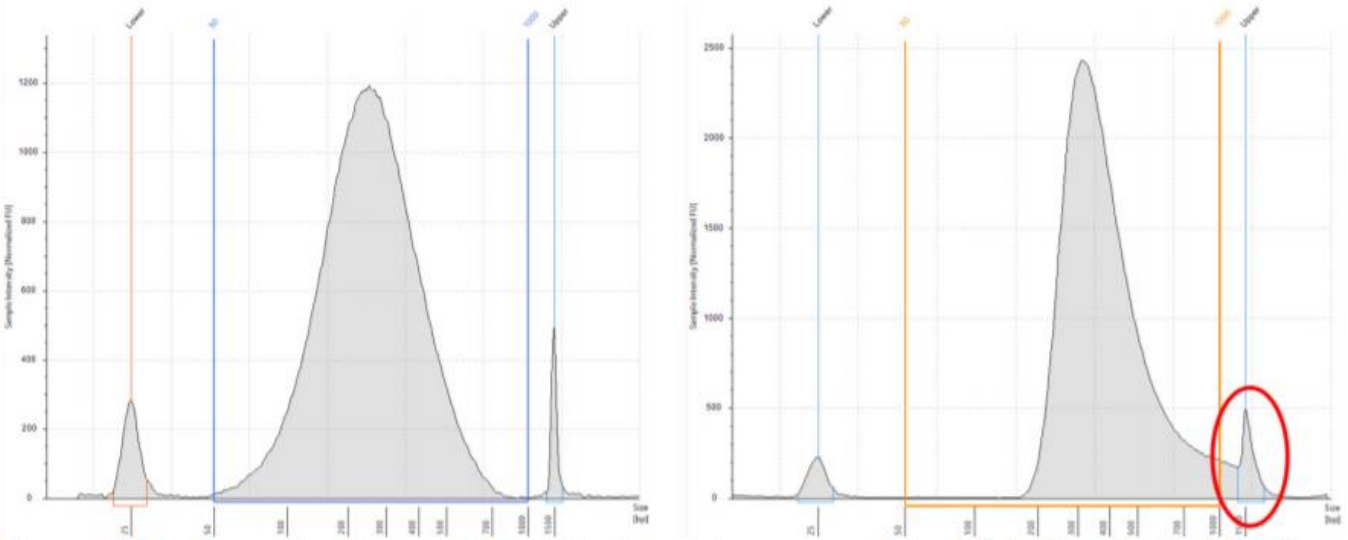

Figure 28 Example of a sample within the sizing range of the High Sensitivity D1000 assay (Left) and a sample merging with the Upper Marker (Right) in the **Region** view of the TapeStation Analysis software.

If applicable use an assay with a broader sizing range.

Peak Integration

In DNA assays, concentration values are calculated using the area of the sample peak compared to the known concentration of the upper marker.

The user must ensure that both marker and sample peaks are properly integrated, by manually adjusting the peak when necessary. An example of correct upper marker peak integration is shown below.

NOTE

In assays with no upper marker (RNA, High Sensitivity RNA, Genomic DNA, and Cell-free DNA assay) quantification is calculated using the lower marker.

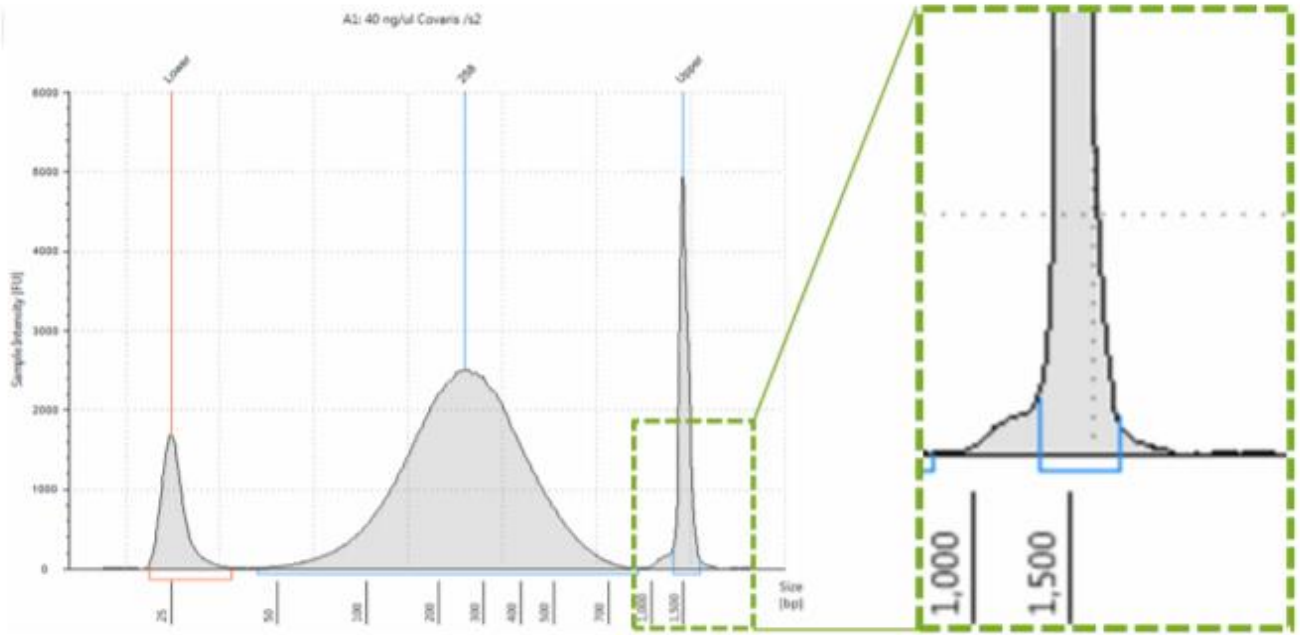

Figure 23 Correct upper marker integration for DNA ScreenTape assays. Figure shows D1000 ScreenTape assay.

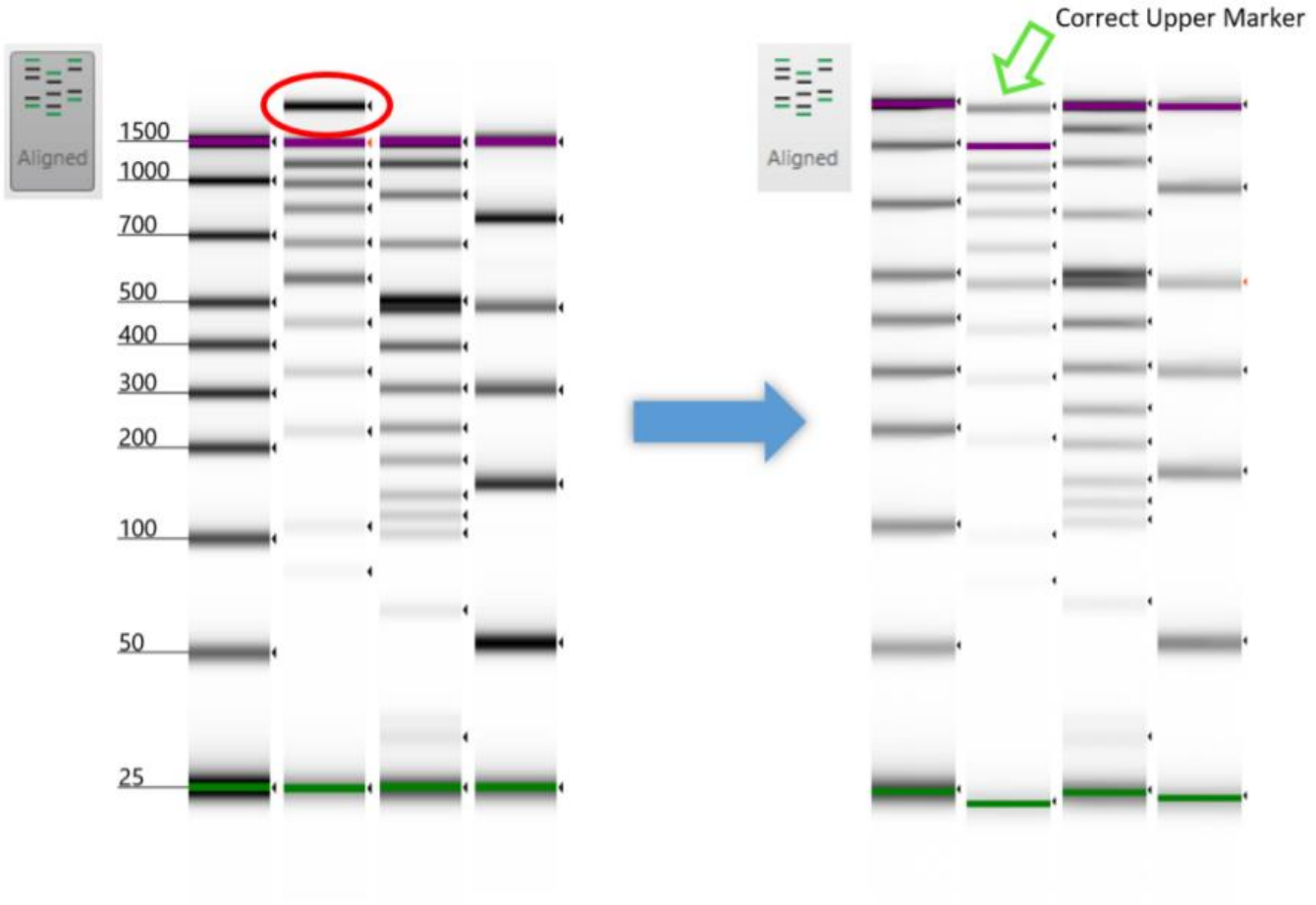

Figure 25 Example of an incorrect (Left) assigned Upper Marker and how to identify the correct Upper Marker (Right) in the D1000 ScreenTape assay in the TapeStation Analysis software.

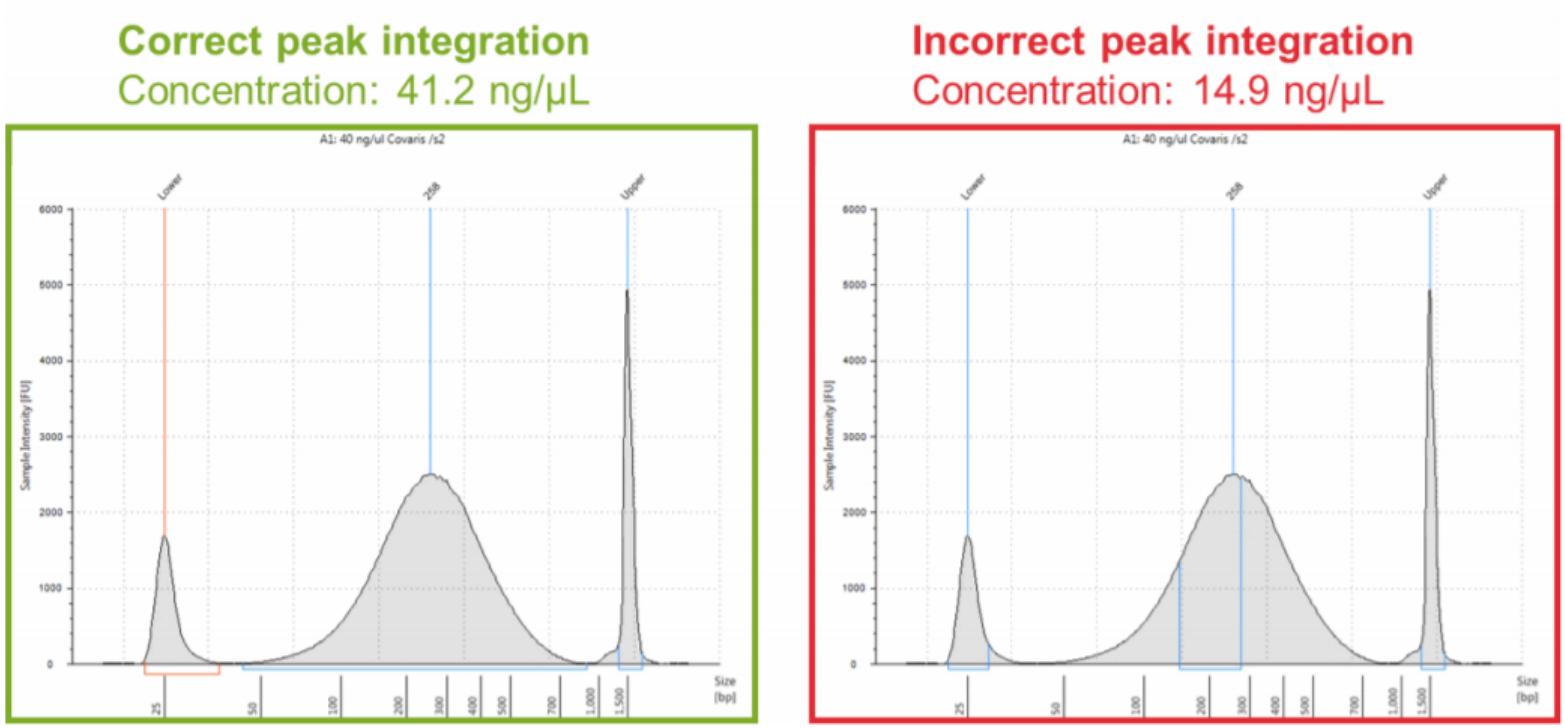

Figure 24 Example of correct (A) and incorrect (B) sample peak integration, and their effect on reported sample concentration.

Electropherogram vs. Region- Conc.

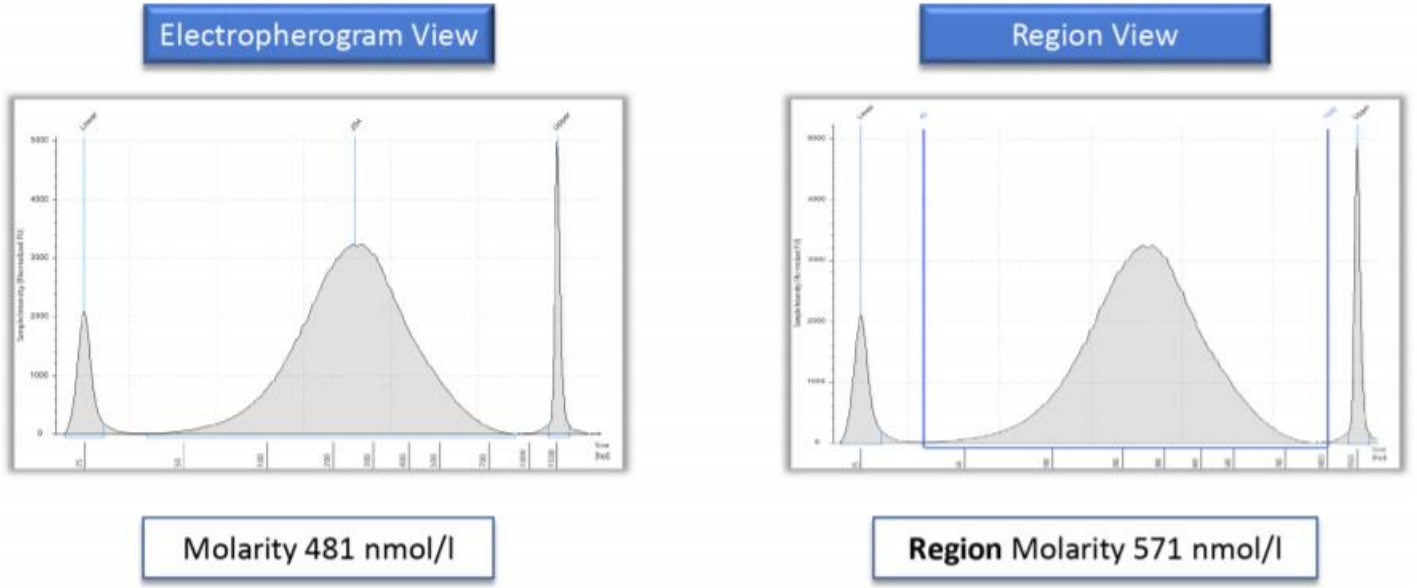

Figure 27 The concentration data obtained in Electropherogram and Region views of the TapeStation Analysis software.

Electropherogram vs. Region- Sizing

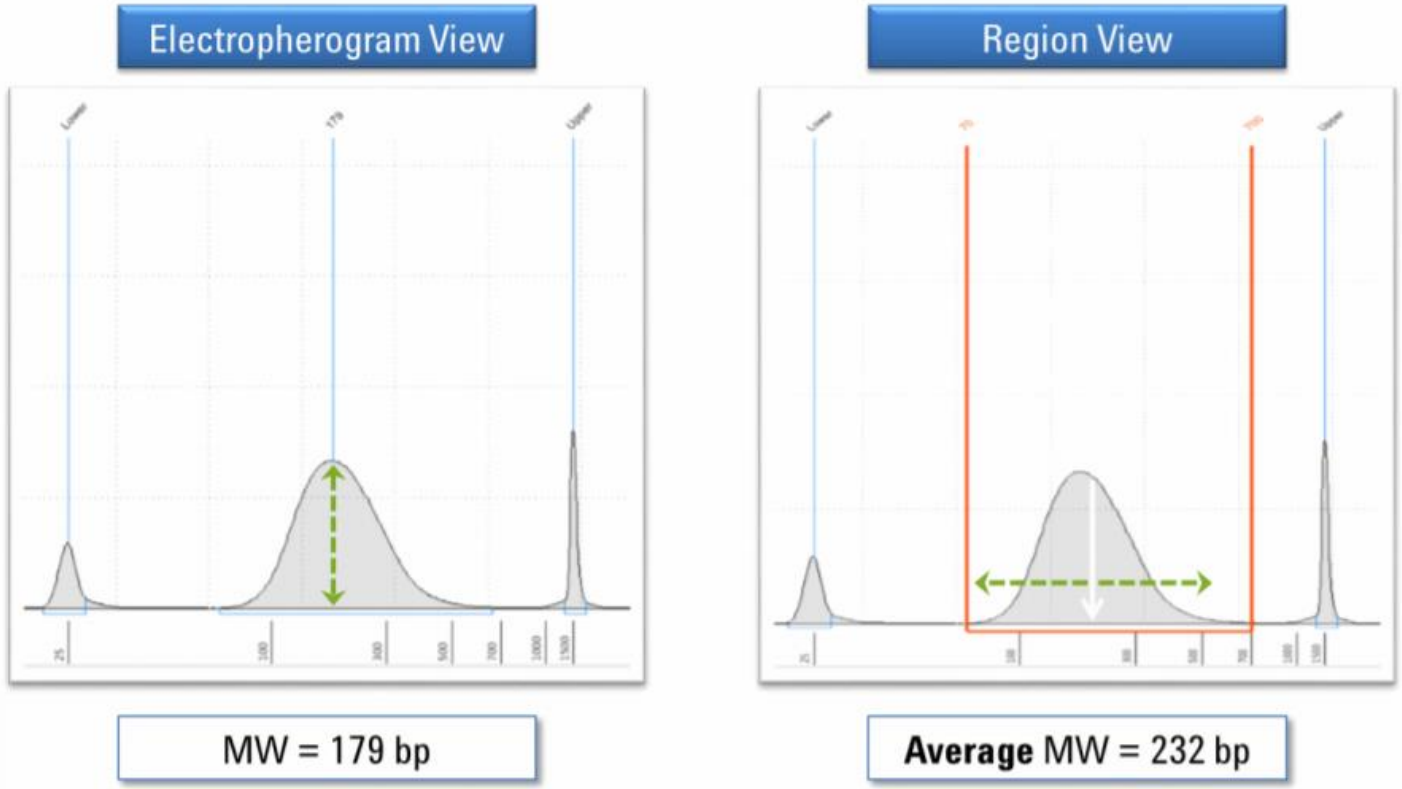

Figure 26 The sizing data obtained in Electropherogram and Region views of the TapeStation Analysis software.

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RNA Assays

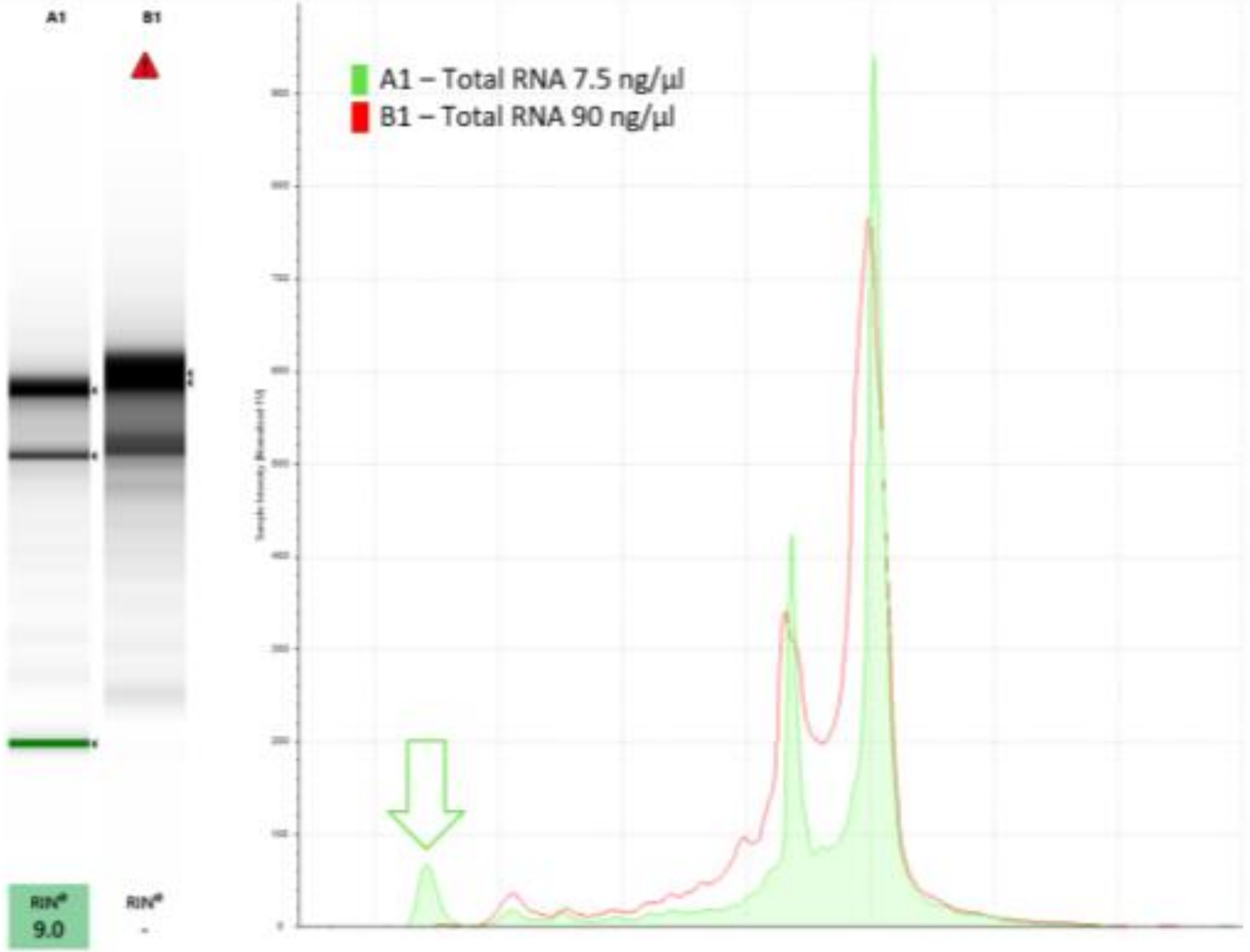

Figure 32 Example of a sample within (A1) and outside (B1) the quantitative range of the High Sensitivity RNA assay in the **Gel** view (Left) and **Comparison** view (Right) of the TapeStation Analysis software. The **Lower Marker** peak (green arrow) is missing in the overconcentrated sample.

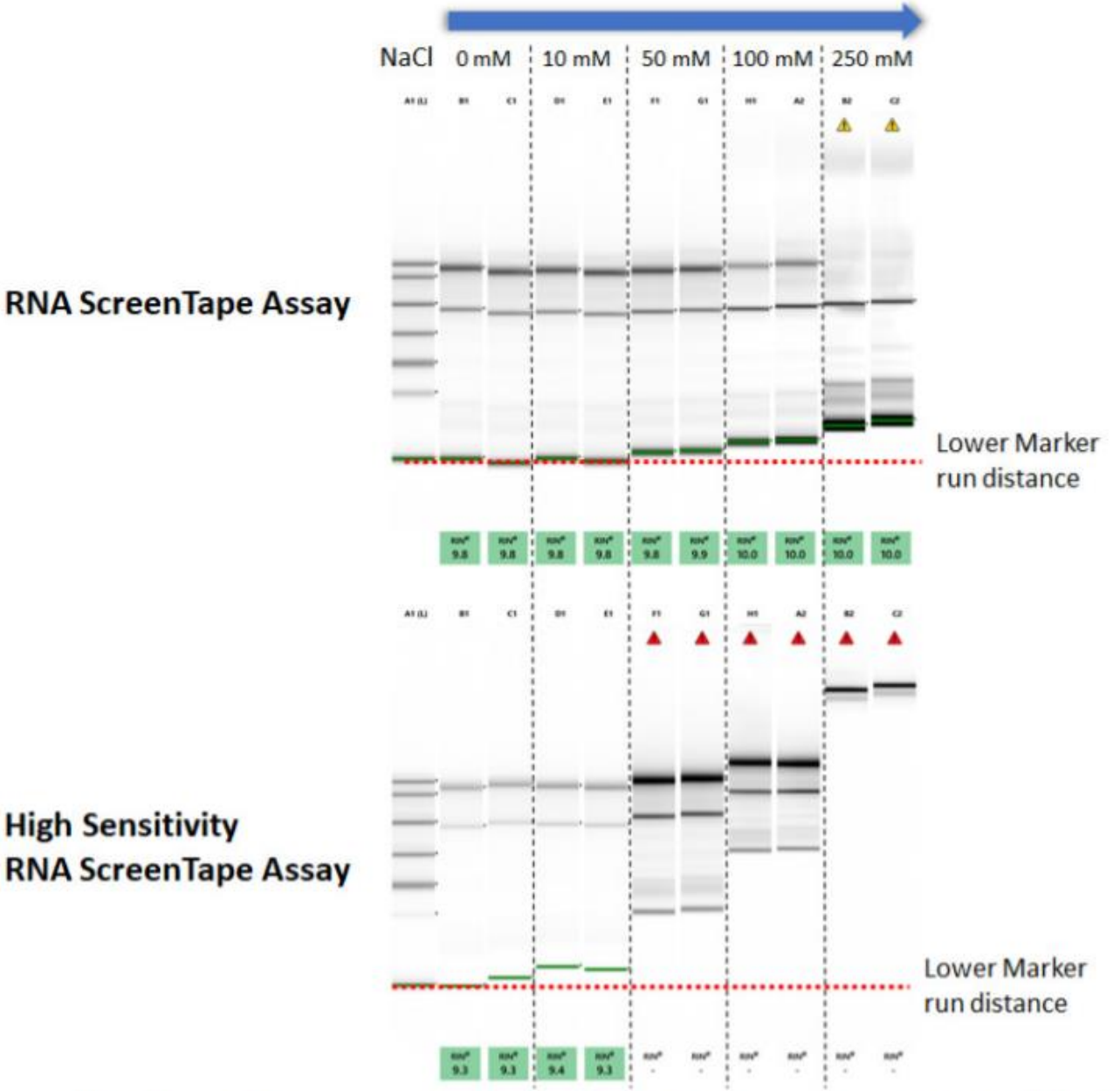

Figure 33 Effects of increasing salt concentrations in the sample matrix on the RNA and High Sensitivity RNA Screentape Assay in the unaligned **Gel** view of the TapeStation Analysis software.

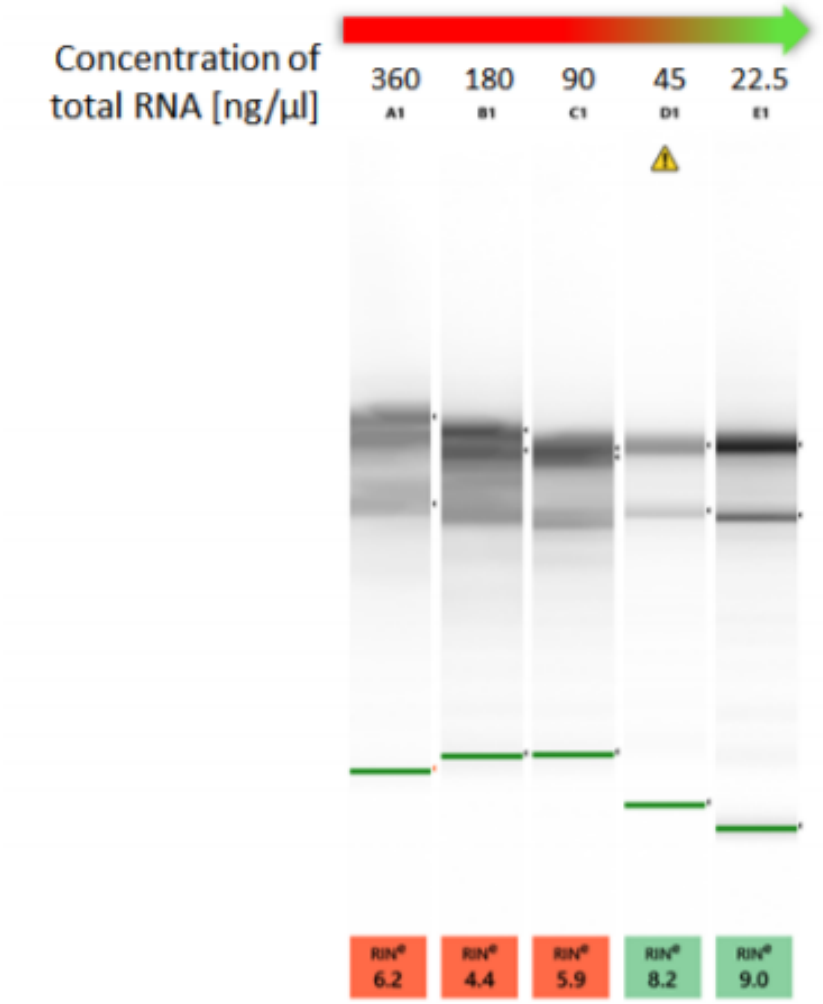

Figure 34 Effects of overconcentrated samples on run distance of the Lower Marker and RIN^e values in the High Sensitivity RNA ScreenTape assay in the Gel view of the TapeStation Analysis software.

References

https://www.agilent.com/cs/library/usermanuals/public/G2964-90000_TapeStation_USR_ENU.pdf

https://www.agilent.com/cs/library/usermanuals/public/4200-TapeStation_SystemManual.pdf