

Complete Enzymatic Digestion of Double-Stranded RNA to Nucleosides Enables Accurate Quantification of dsRNA

Supplemental Information

Steven R. Strezsak, Penny J. Beuning, and Nicholas J. Skizim

Figure S1 – 200bp dsRNA

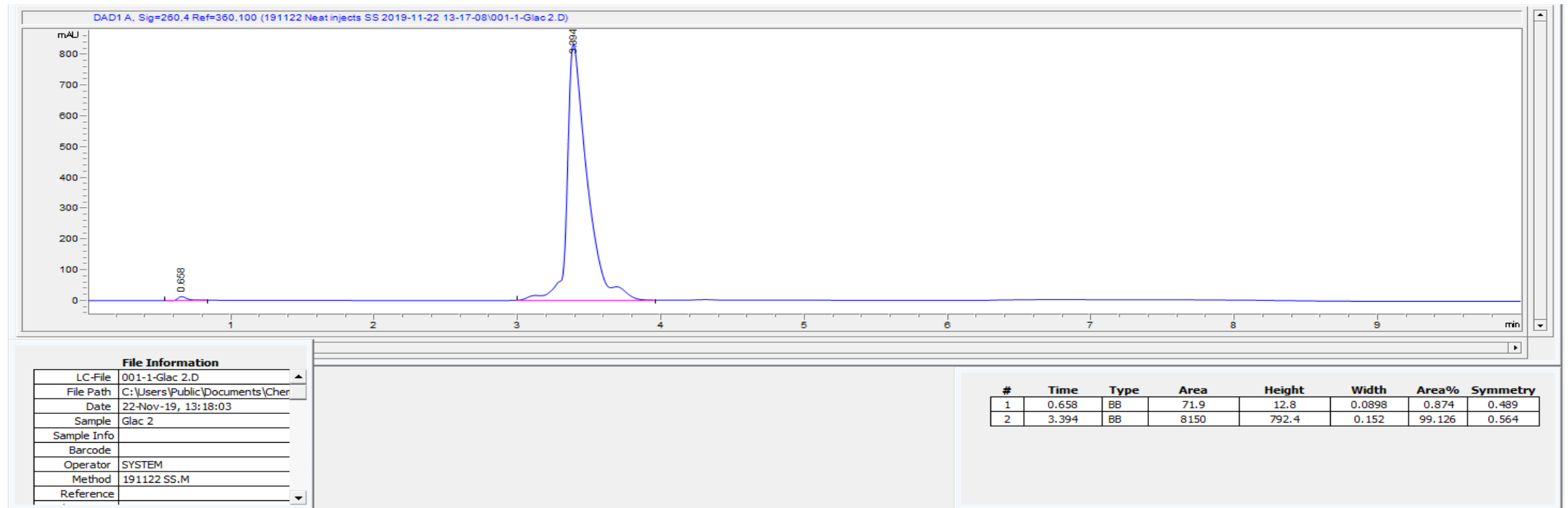


Figure S1. Chromatogram of 200 bp dsRNA post RNase I_f clean-up. dsRNA peak (3.4 mins) is 99.1% total area of chromatogram.

Figure S2 – 400bp dsRNA

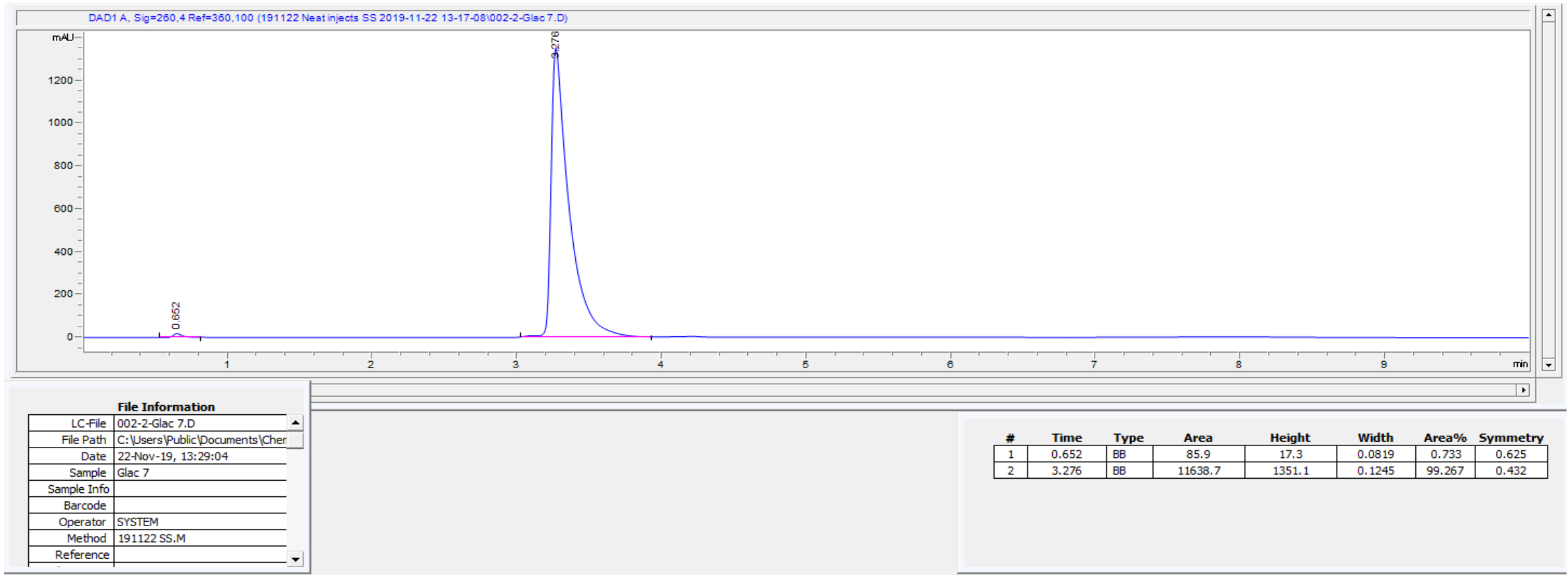


Figure S2. Chromatogram of 400 bp dsRNA post RNase I_f clean-up. dsRNA peak (3.3 mins) is 99.3% total area of chromatogram.

Figure S3 – 300bp dsRNA

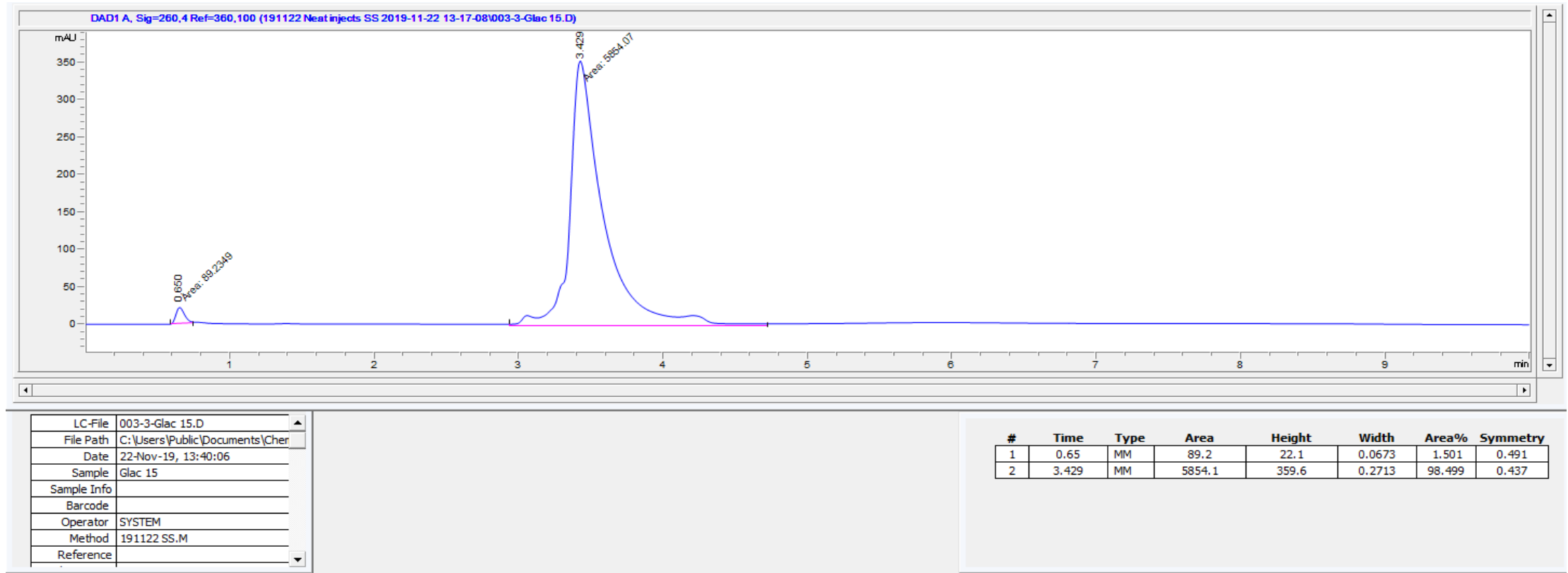


Figure S3. Chromatogram of 300 bp dsRNA post RNase I_f clean-up. dsRNA peak (3.4 mins) is 98.5% total area of chromatogram.

Figure S4 – 55bp dsRNA

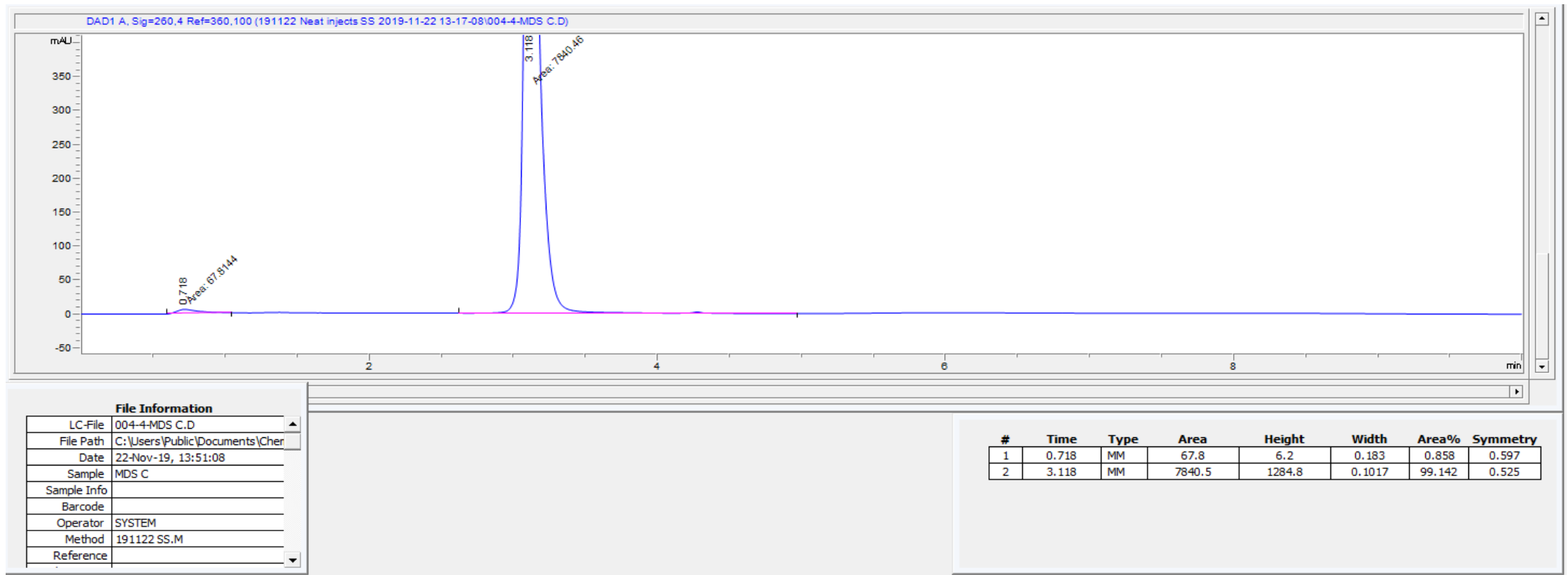


Figure S4. Chromatogram of 55 bp dsRNA post RNase I_f clean-up. dsRNA peak (3.1 mins) is 99.1% total area of chromatogram.

Figure S5 – 1000bp dsRNA

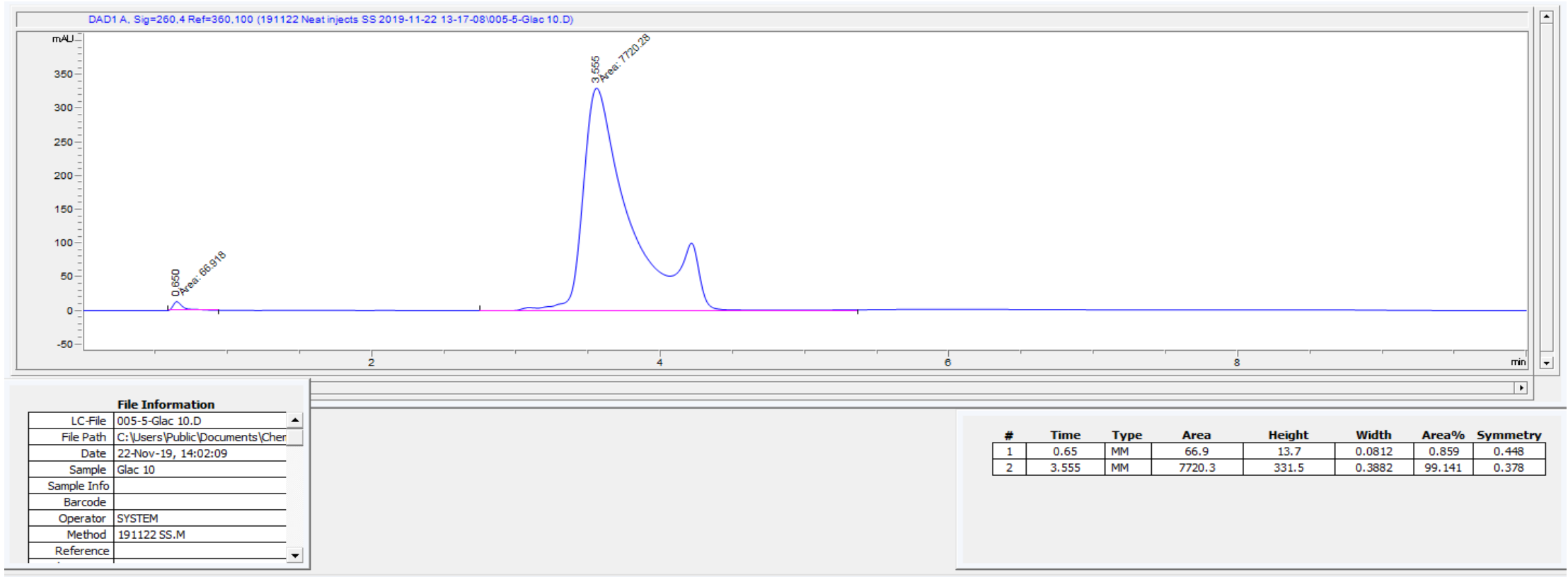


Figure S5. Chromatogram of 1000 bp dsRNA post RNase I_f clean-up. dsRNA peak (3.6 mins) is 99.1% total area of chromatogram.

Figure S6 – 55 bp dsRNA

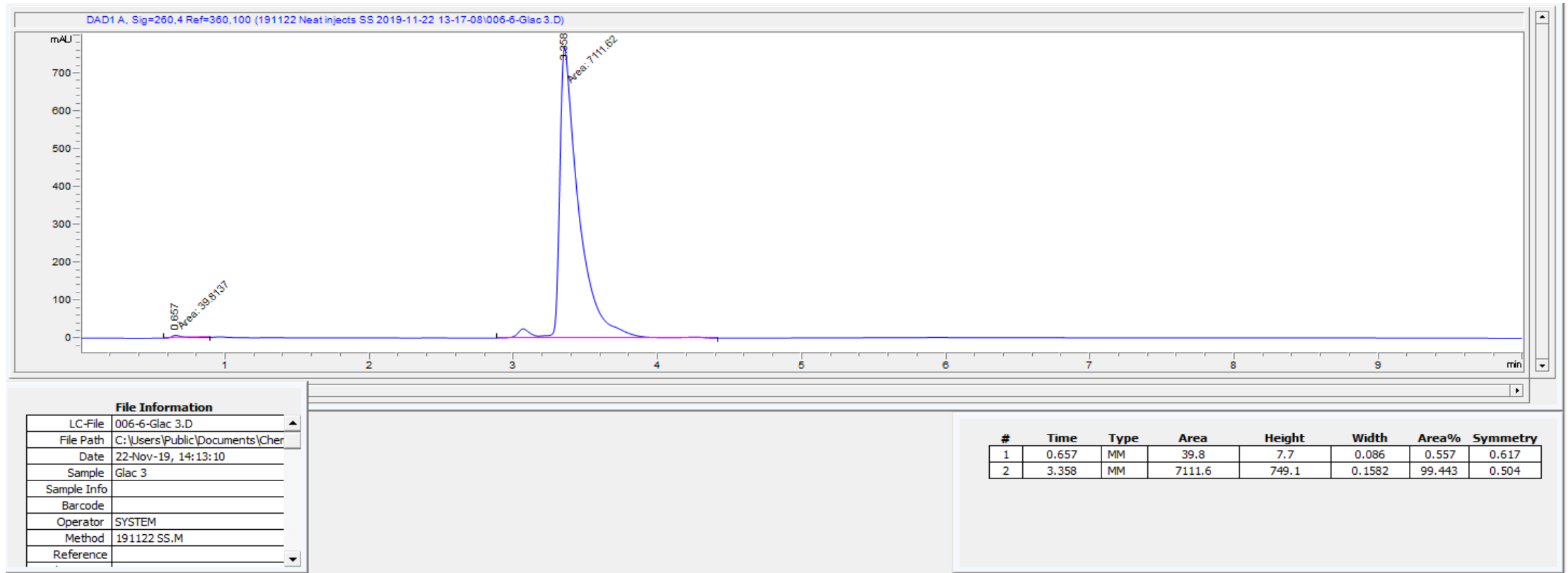


Figure S6. Chromatogram of 55 bp dsRNA post RNase I_f clean-up. dsRNA peak (3.4 mins) is 99.4% total area of chromatogram.

Figure S7 – 425bp dsRNA

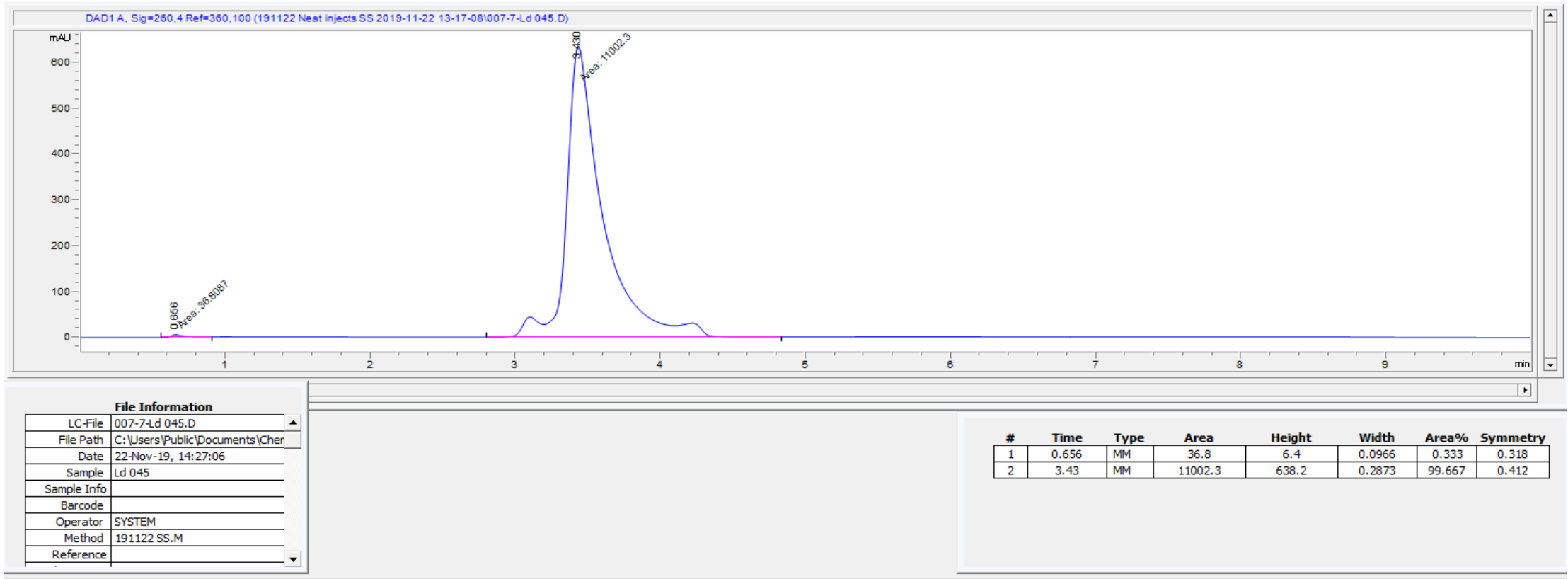


Figure S7. Chromatogram of 425 bp dsRNA post RNase I_f clean-up. dsRNA peak (3.4 mins) is 99.7% total area of chromatogram.

Figure S8 – 599bp dsRNA

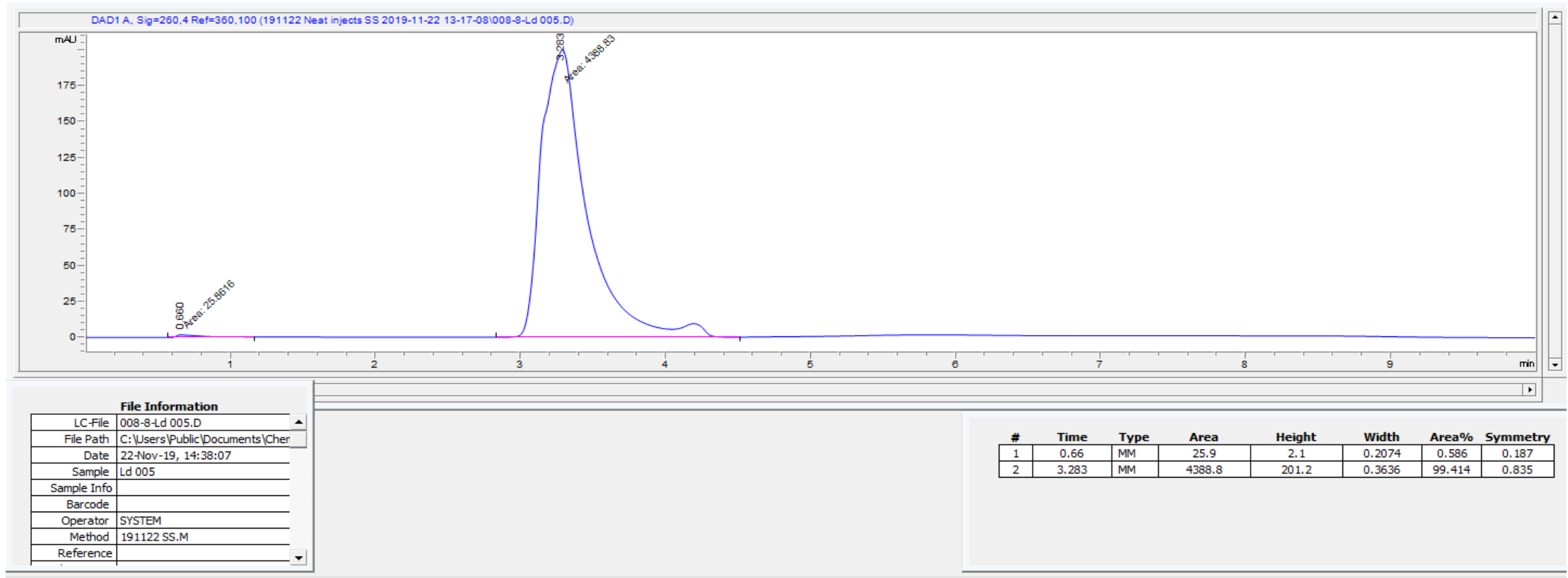


Figure s8. Chromatogram of 599 bp dsRNA post RNase I_f clean-up. dsRNA peak (3.4 mins) is 99.4% total area of chromatogram.

Figure S9 - Correlation between dsRNA length and calculated molar absorptivity coefficient

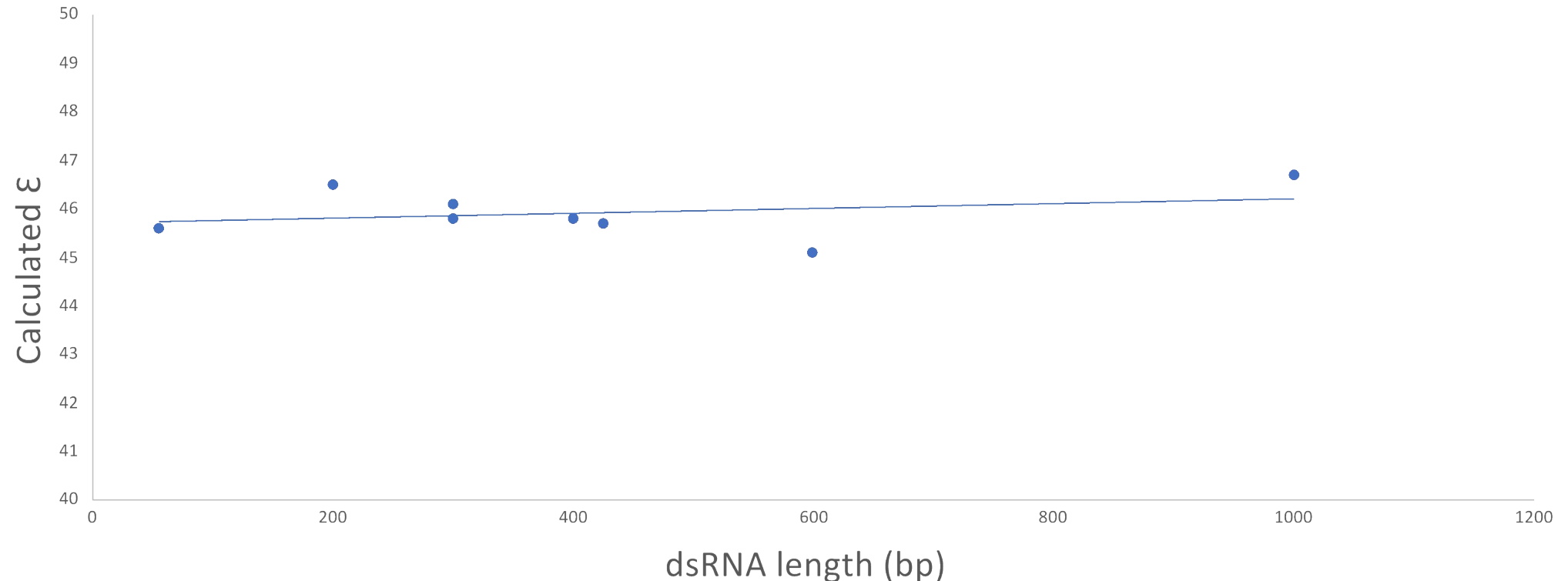


Figure S9. The goodness of fit (R^2) is low (< 0.95) when comparing the dsRNA length to the calculated absorptivity coefficient suggesting that there is no length dependency for the extinction coefficient between 55 and 1000 bp. The error bars represent the standard deviation for the calculated extinction coefficient for each sequence.

Figure S10 - Correlation between % GC content and calculated molar absorptivity coefficient

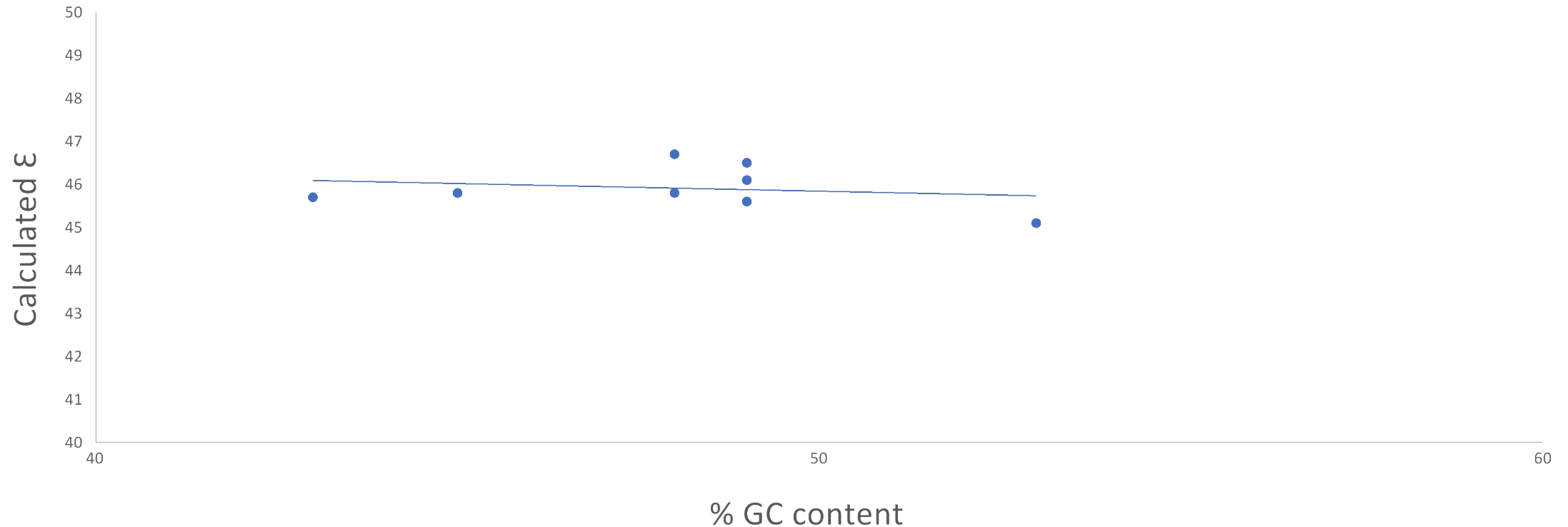


Figure S10. The goodness of fit (R^2) is low (<0.95) when comparing the % GC content to the calculated absorptivity coefficient suggesting that there is no length dependency for the extinction coefficient between 55 and 1000 bp. The error bars represent the standard deviation for the calculated extinction coefficient for each sequence.