

IntRa-Q Software Manual

You can get the results in a practical way with the help of our special IntRa-Q Software.

Step 1: After the run, firstly please adjust the baseline threshold values to 1000 for each dye (Figure 1 -2).

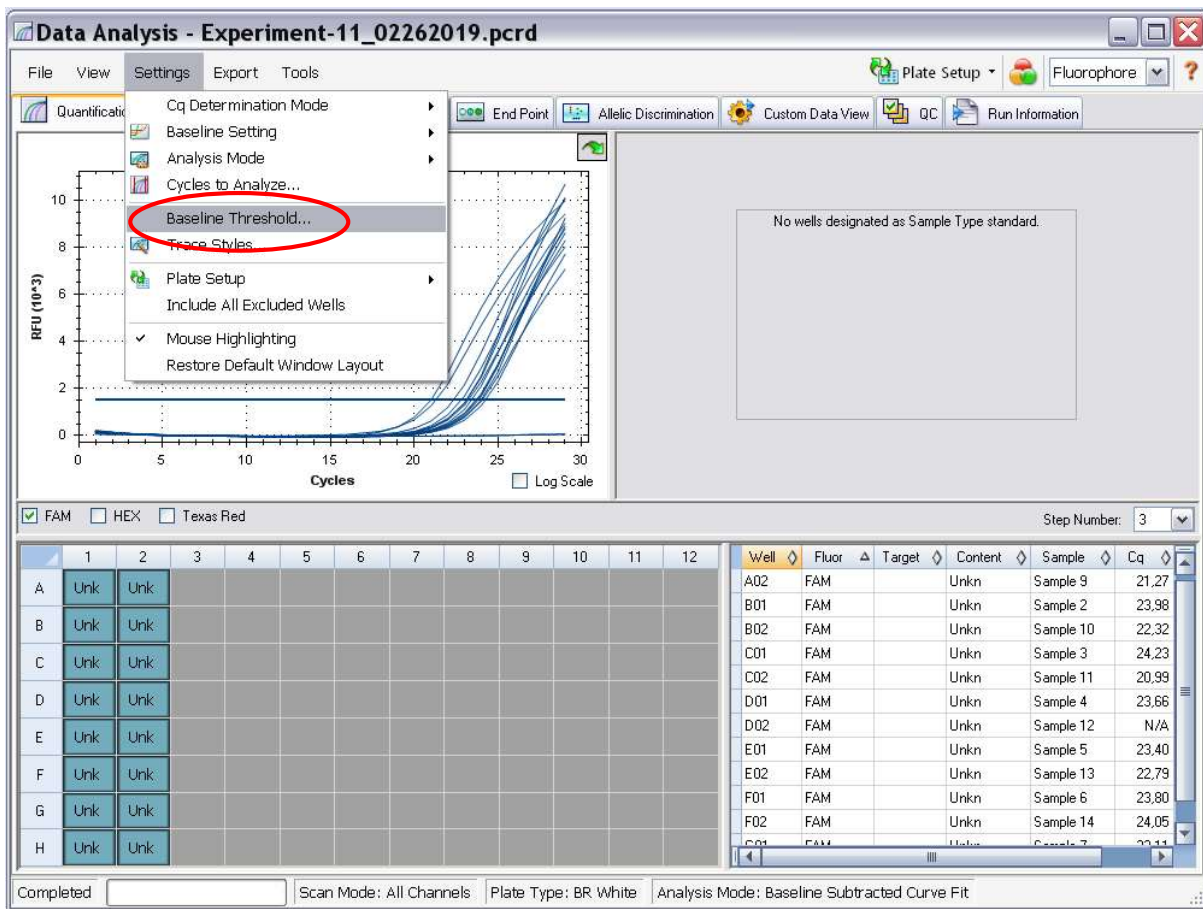


Figure - 1

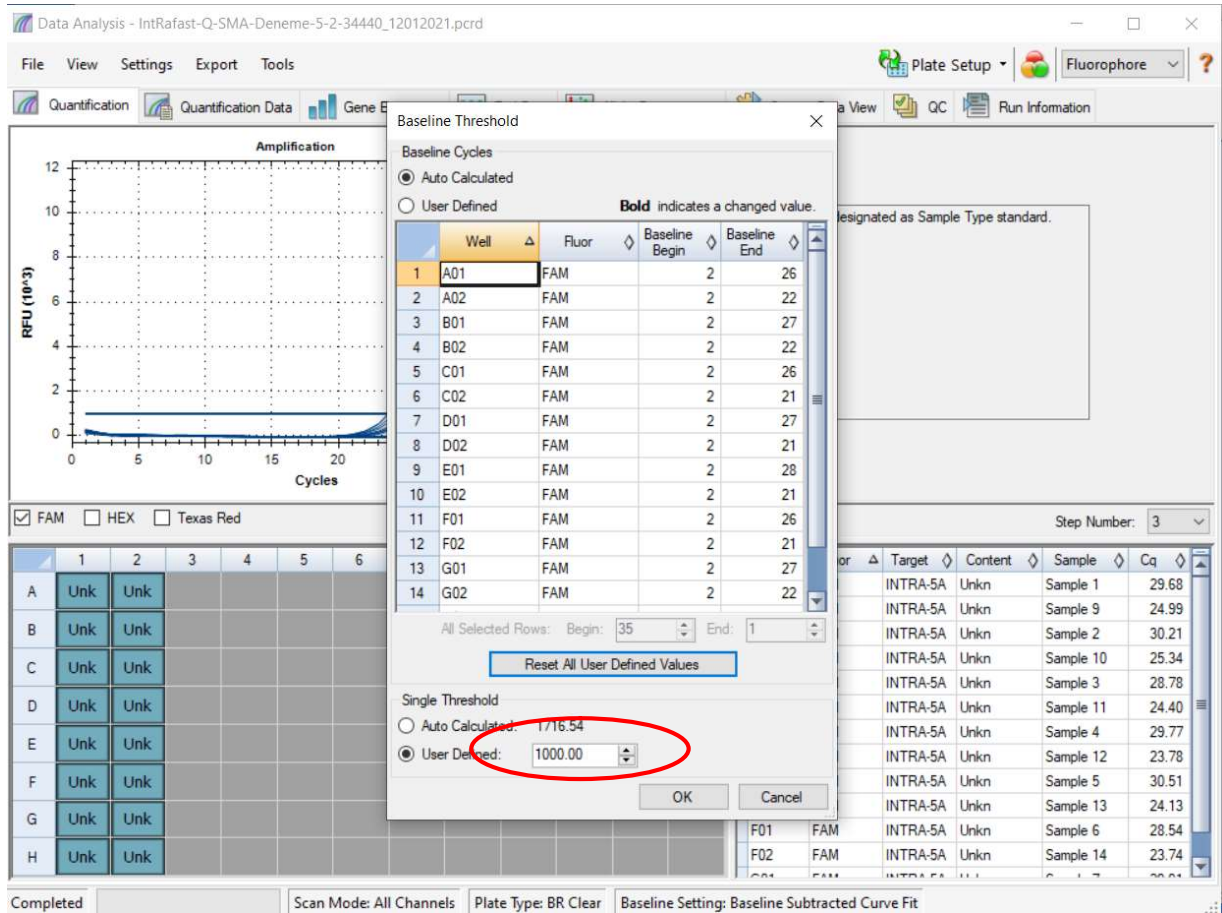


Figure - 2

Step 2: Export the data files from run file to a folder as Excel 2013 format. Export > Export All Data Sheets > Excel 2003 (*.xls) (Figure – 3).

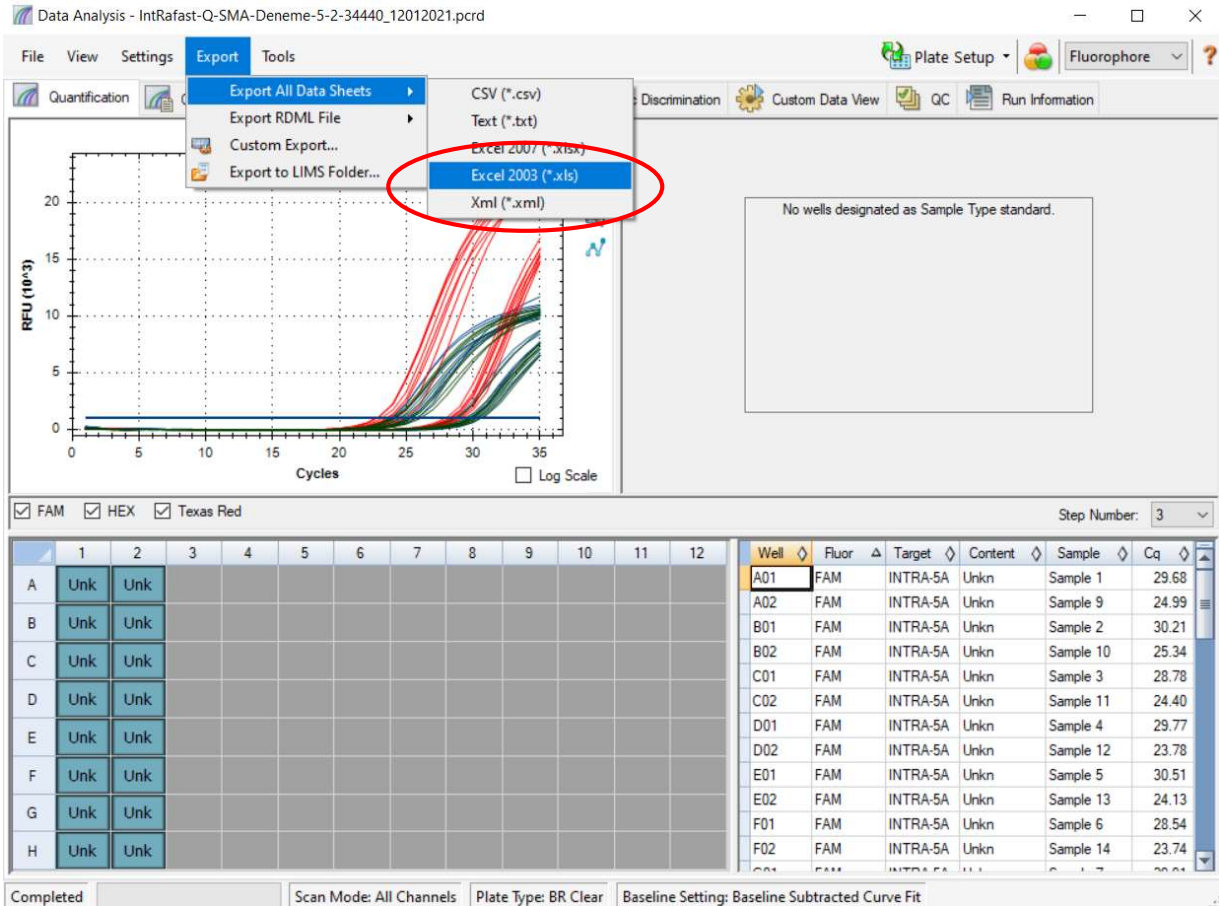


Figure - 3

Step 3: Click to IntRa-Q Software icon to open the software. Choose the parameter you want to analyze. For this example, SMN1 Exon 7 (Figure - 4).

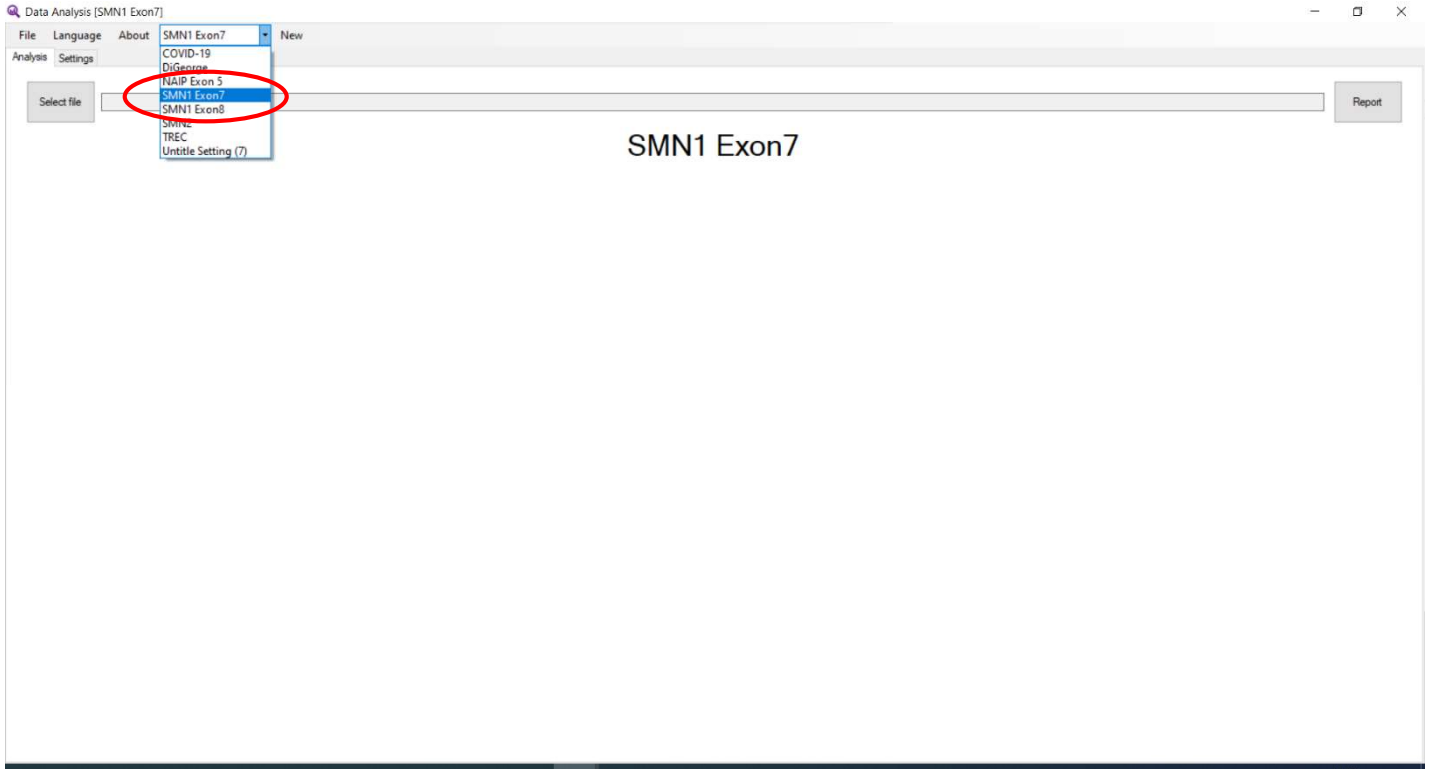


Figure – 4

Step 4: Select the daha file from the folder you saved and click the open (Cq Results files) (Figure 5 - 6).

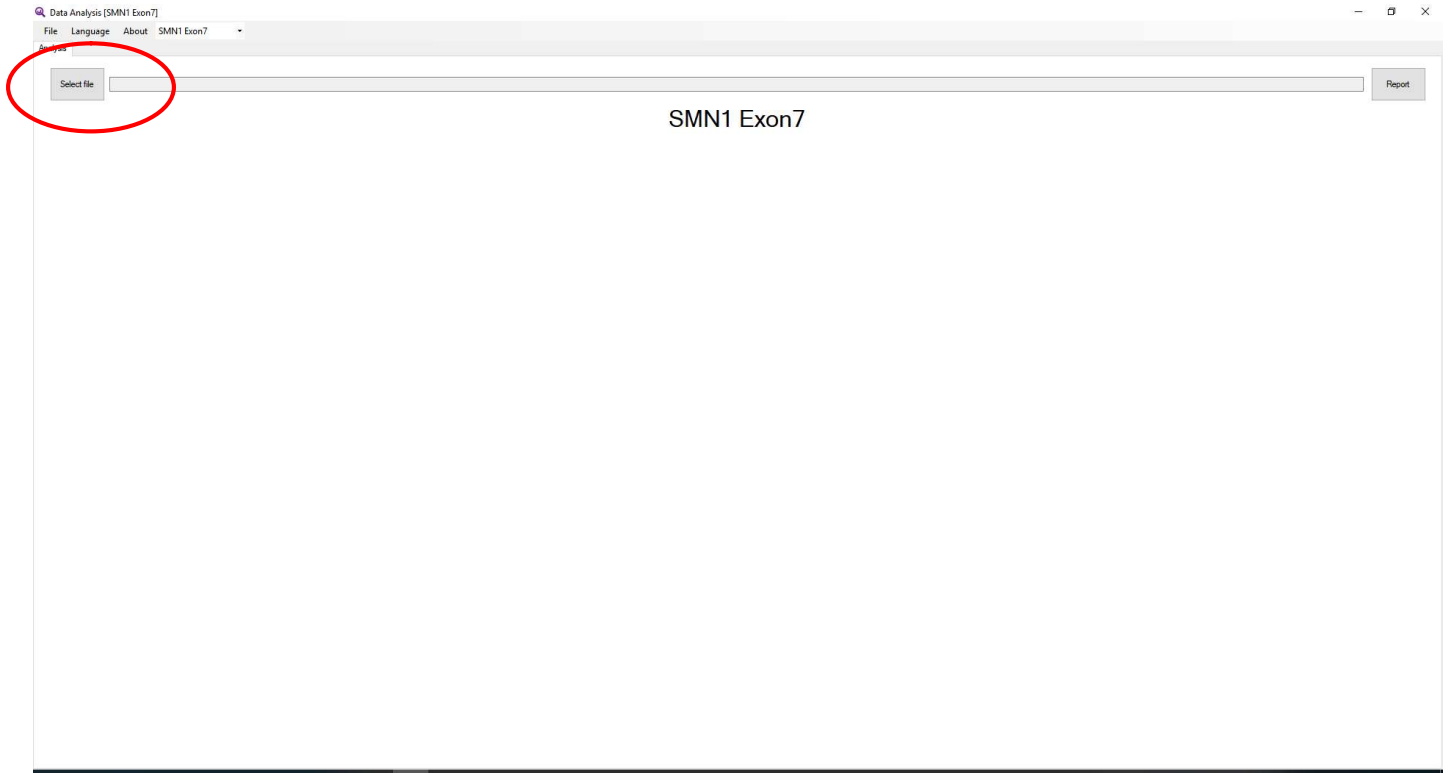


Figure - 5

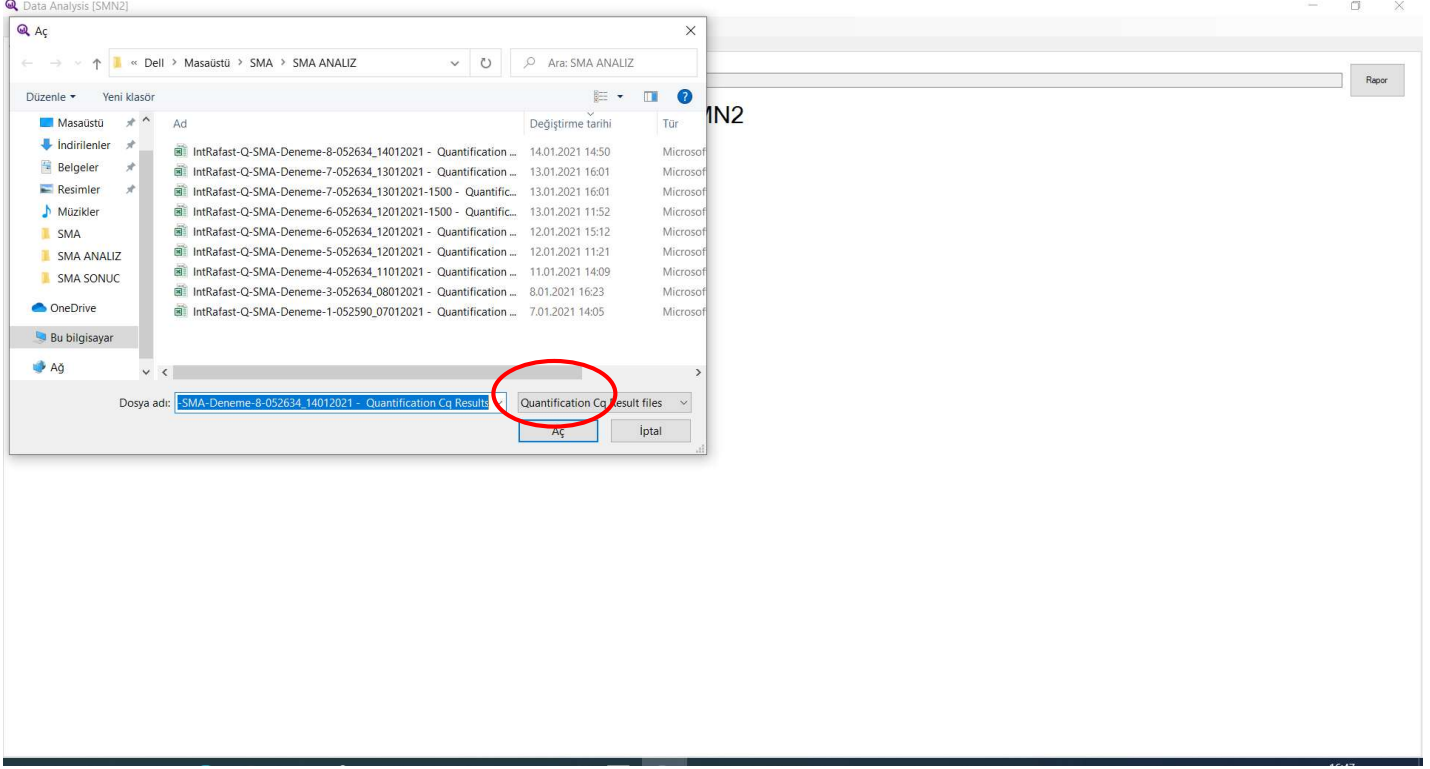


Figure - 6

Step 5: The results will be automatically appeared on the screen. **Gray:** Wild-Type, **Red :** Carrier State, **Black:** Homozygous Deletion, **Yellow:** No DNA, **Blue:** Repeat. You can save all the results as pdf file by clicking **"Report"** (Figure - 7).

Data Analysis [SMN1 Exon7]

File Language About SMN1 Exon7 New

Analysis Settings

Select file C:\Users\Del1\Desktop\SMA\ANALIZ\IntRafast-Q-SMA-Deneme-5-2-34440_12012021 - Quantification Cq Results.xls

Report

SMN1 Exon7

| | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 |
|---|-------------------------------|--------------------------------|---|---|---|---|---|---|---|----|----|----|
| A | Sample 1 Carrier 5.94 | Sample 9 Carrier 6.34 | | | | | | | | | | |
| B | Sample 2 Carrier 7.29 | Sample 10 Carrier 5.79 | | | | | | | | | | |
| C | Sample 3 Wild-Type 1.54 | Sample 11 Wild-Type 2.61 | | | | | | | | | | |
| D | Sample 4 Wild-Type 2.94 | Sample 12 Wild-Type 2.85 | | | | | | | | | | |
| E | Sample 5 Wild-Type 3.98 | Sample 13 Wild-Type 3.97 | | | | | | | | | | |
| F | Sample 6 Wild-Type 1.46 | Sample 14 Wild-Type 2.80 | | | | | | | | | | |
| G | Sample 7 Wild-Type 2.51 | Sample 15 Wild-Type 2.73 | | | | | | | | | | |
| H | Sample 8 Wild-Type 2.33 | Sample 16 Wild-Type 2.33 | | | | | | | | | | |

Figure - 7

Step 6: Choose the other parameter you want to analyze. For this example Exon 8. Repeat the steps from step 4 (Figures 8 - 9 - 10).

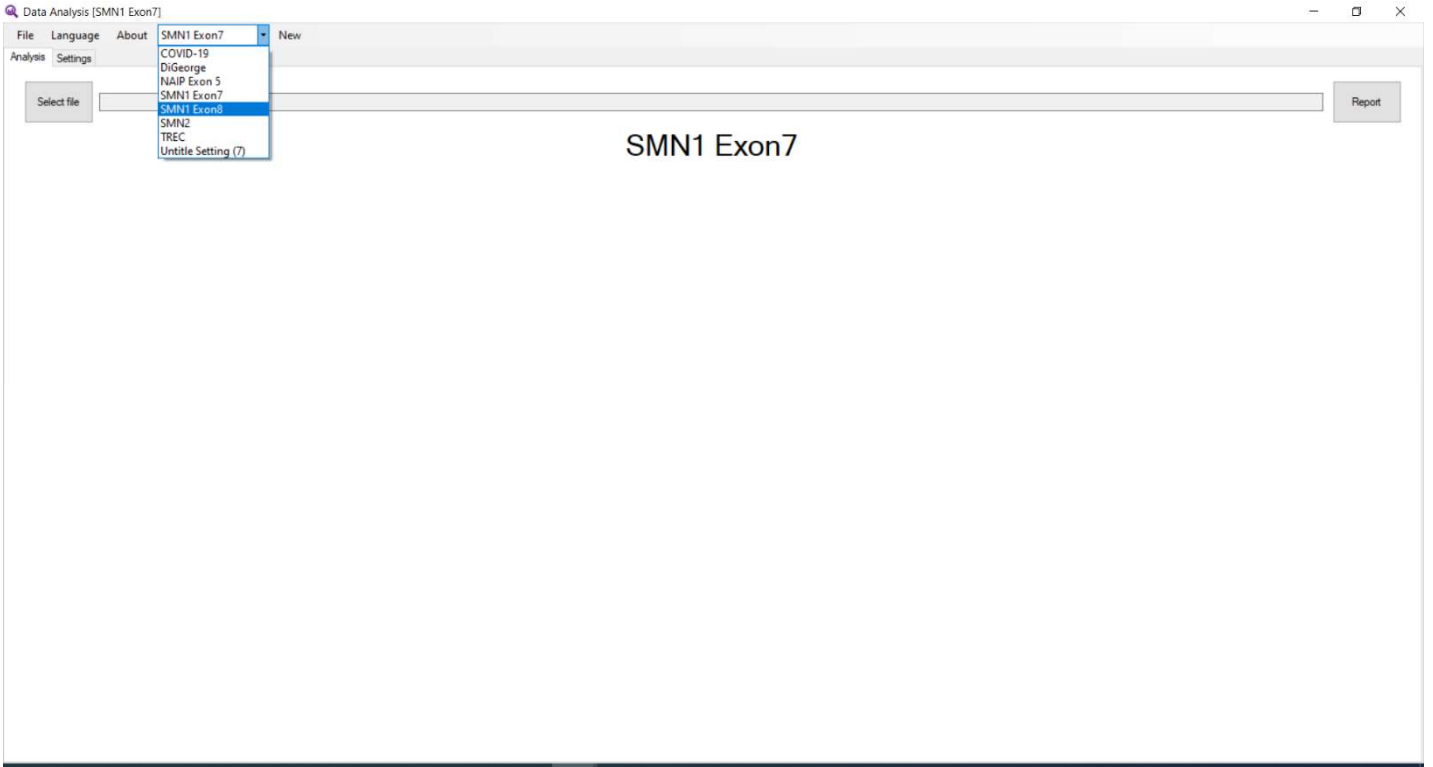


Figure - 8

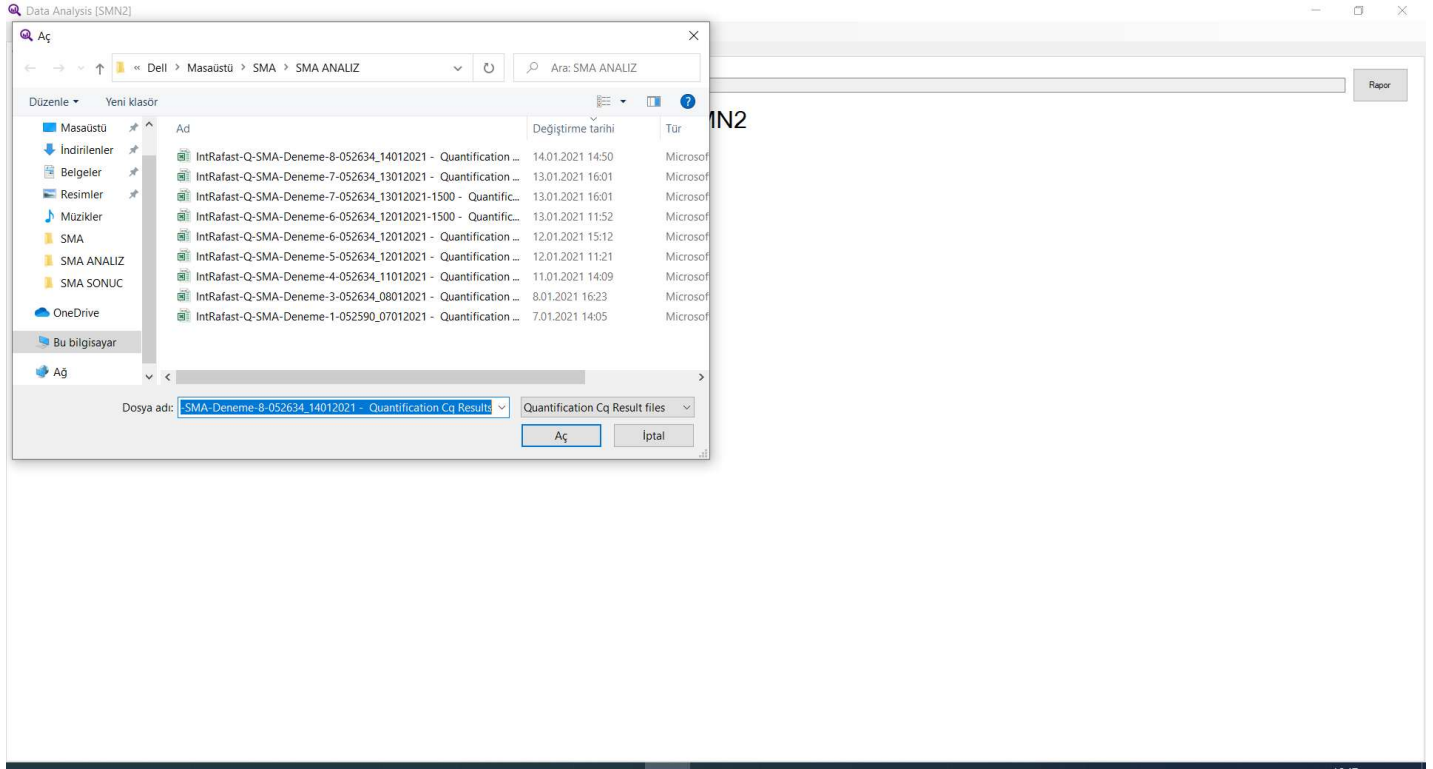


Figure - 9

Data Analysis [SMN1 Exon8]

File Language About SMN1 Exon8 New

Analysis Settings

Select file C:\Users\Del1\Desktop\SMA\SMA ANALIZ\Int Rafast-Q-SMA-Deneme-5-2-34440_12012021 - Quantification Cq Results.xls Report

SMN1 Exon8

| | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 |
|---|-------------------------------|--------------------------------|---|---|---|---|---|---|---|----|----|----|
| A | Sample 1 Carrier 6.84 | Sample 9 Carrier 7.03 | | | | | | | | | | |
| B | Sample 2 Carrier 7.64 | Sample 10 Carrier 8.08 | | | | | | | | | | |
| C | Sample 3 Wild-Type 2.73 | Sample 11 Wild-Type 3.06 | | | | | | | | | | |
| D | Sample 4 Wild-Type 2.92 | Sample 12 Wild-Type 3.60 | | | | | | | | | | |
| E | Sample 5 Wild-Type 4.05 | Sample 13 Wild-Type 3.82 | | | | | | | | | | |
| F | Sample 6 Wild-Type 1.49 | Sample 14 Wild-Type 3.20 | | | | | | | | | | |
| G | Sample 7 Wild-Type 2.86 | Sample 15 Wild-Type 2.97 | | | | | | | | | | |
| H | Sample 8 Wild-Type 2.79 | Sample 16 Wild-Type 3.36 | | | | | | | | | | |

Figure - 10