MANUAL OF SMA *PLUS* SOFTWARE

You can get the results in a practical way with the help of our special SMA *Plus* Software.

Step 1: After the run, before the anaylsis, please adjust the baseline threshold value stated below for each dye (Figure 1 -2).

TS value should be 1500 for each dye in blood kits.

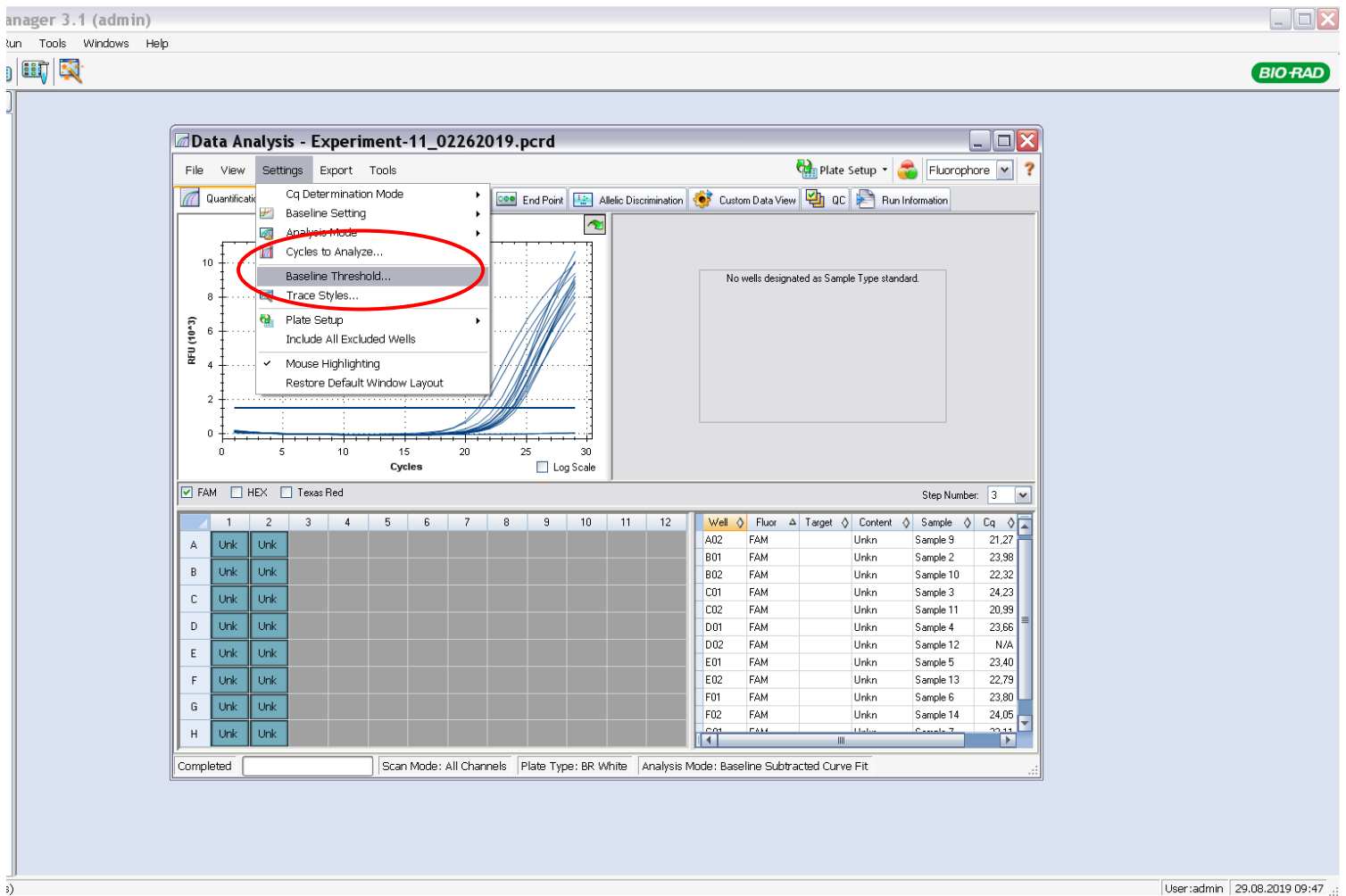**TS value should be 1000 for each dye in NBS kits.**
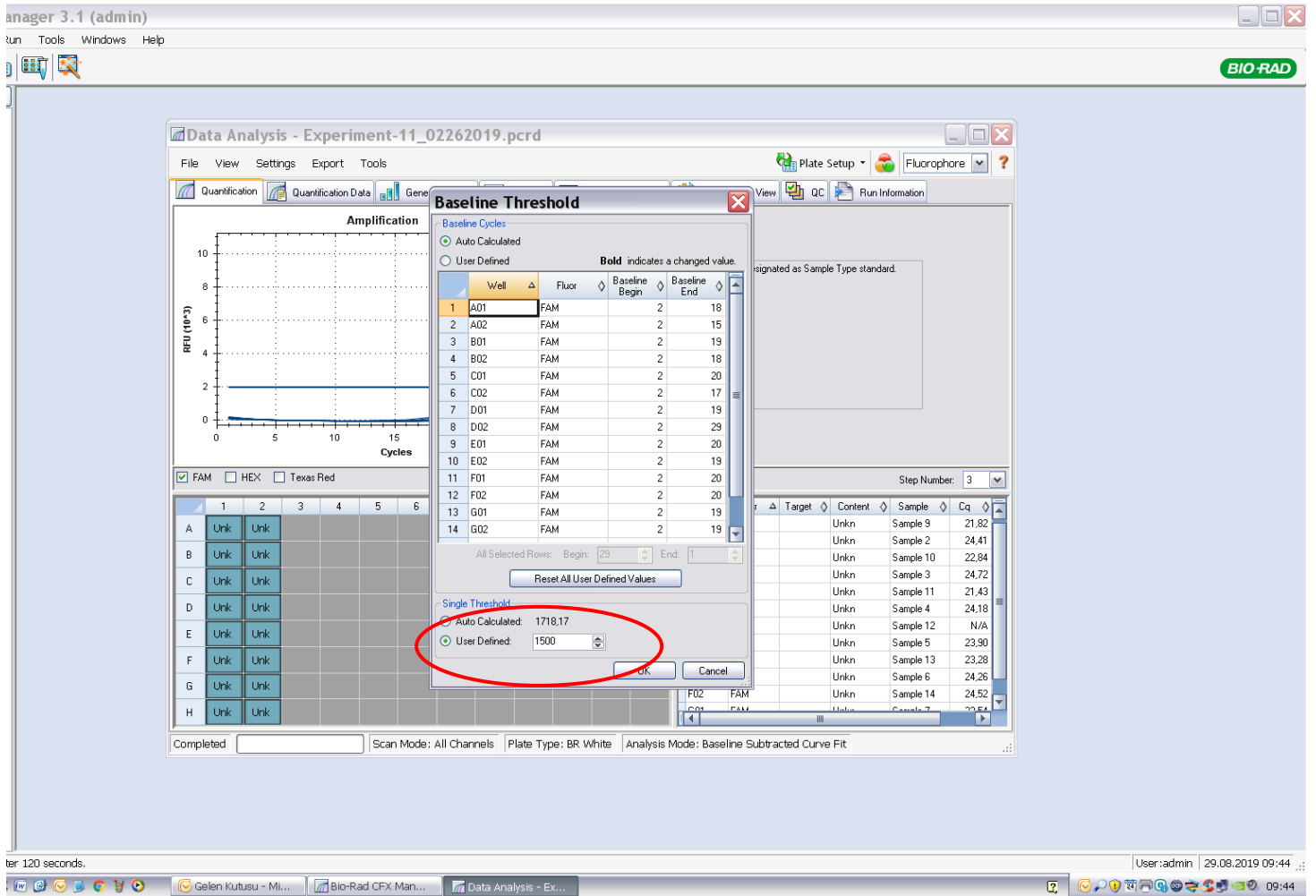

Figure - 1

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).
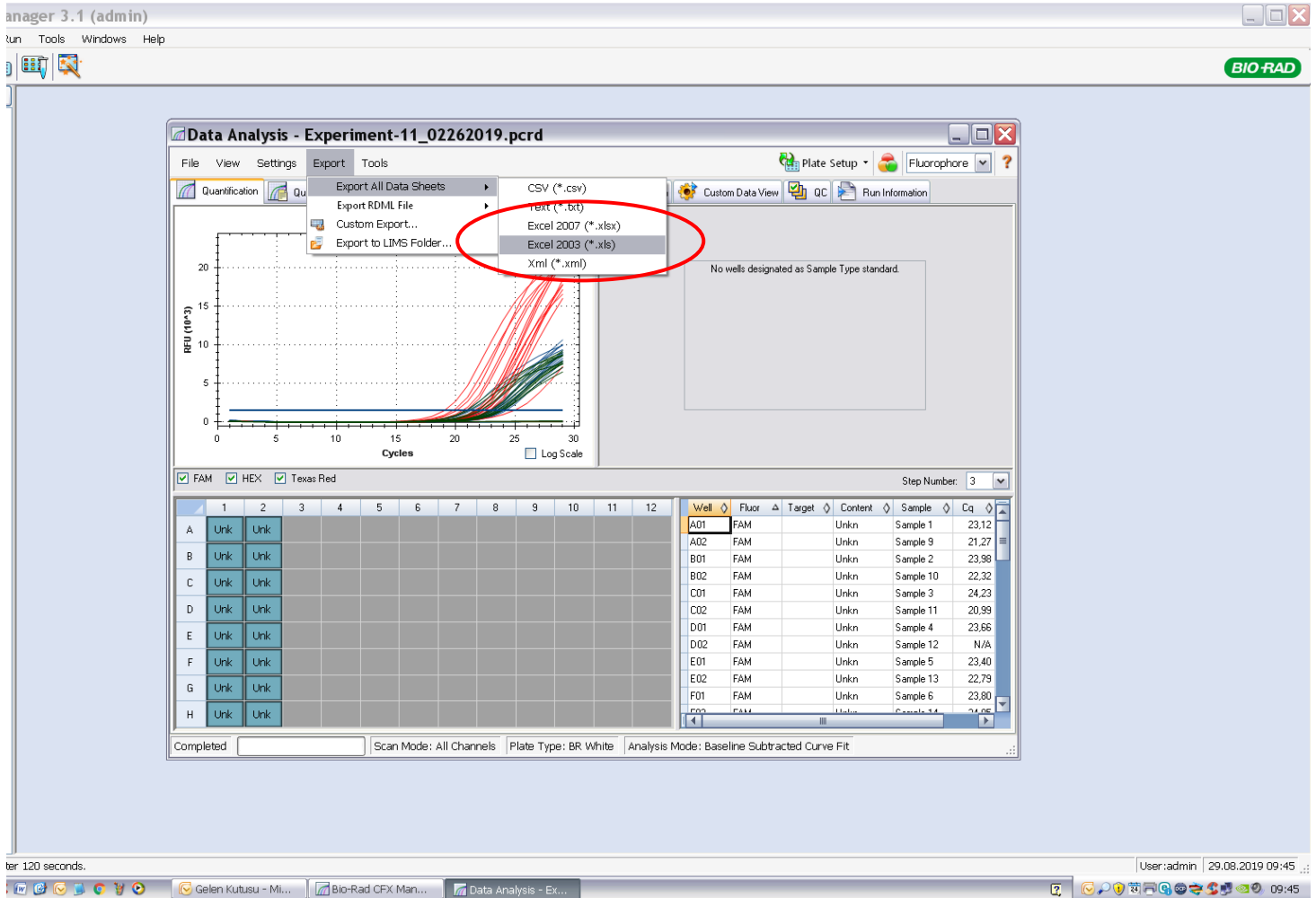

Figure - 3

Step 3: Click to SMA *Plus* Software ikon, open the SMA plus software. Choose the parameter you want to analyze. For this example, SMN1 Exon 7 (Figure - 4).
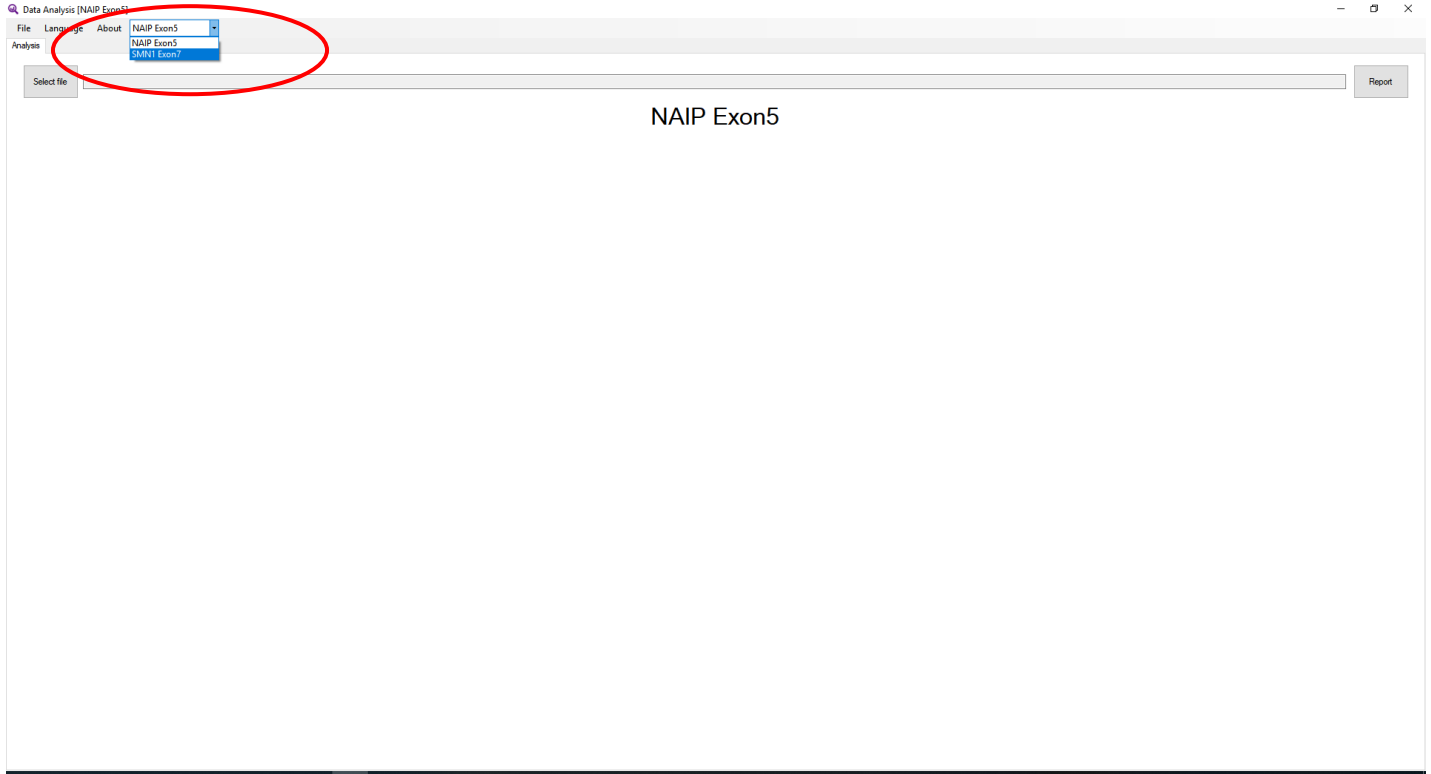

Figure – 4

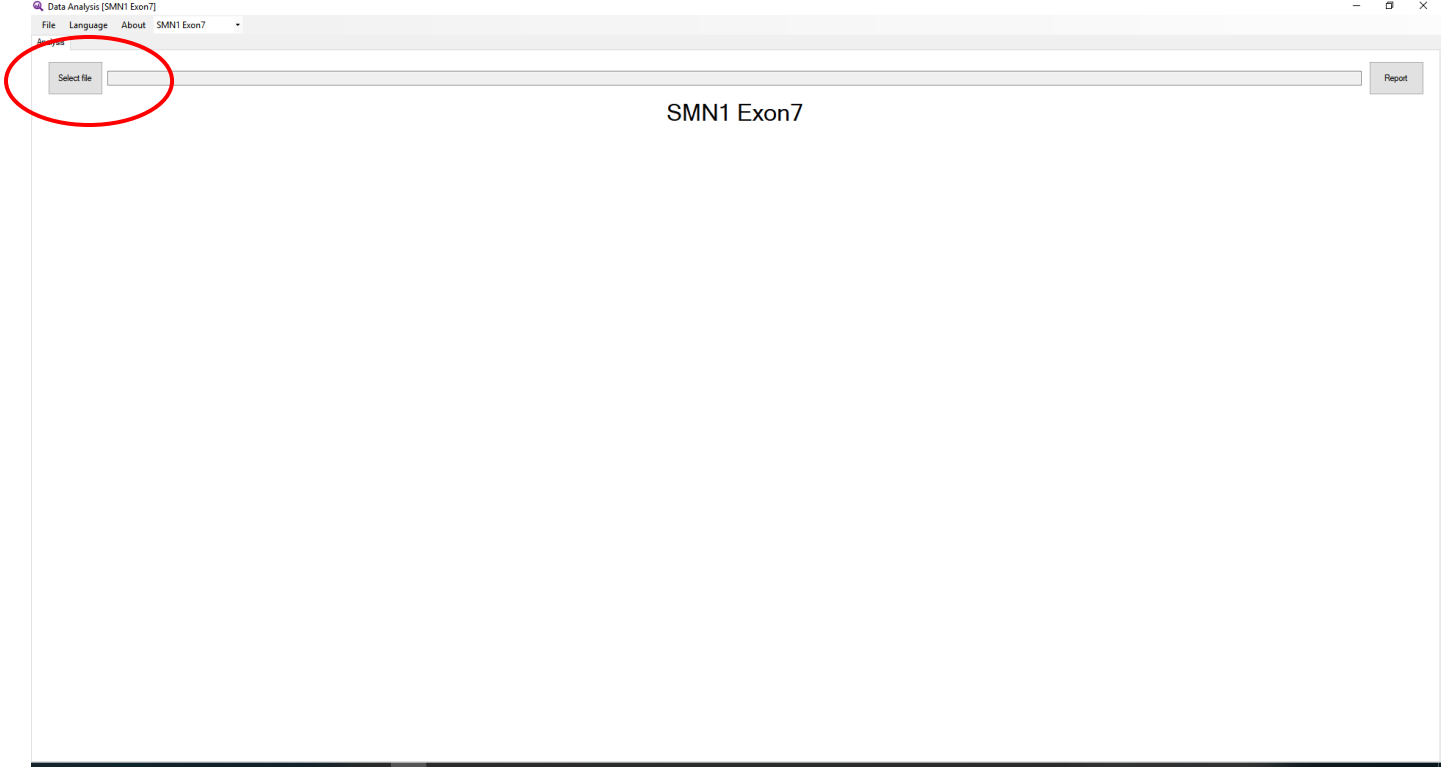**Step 4:** Select the daha file from the folder you saved and click the open (Cq Results files) (Figure 5 - 6).
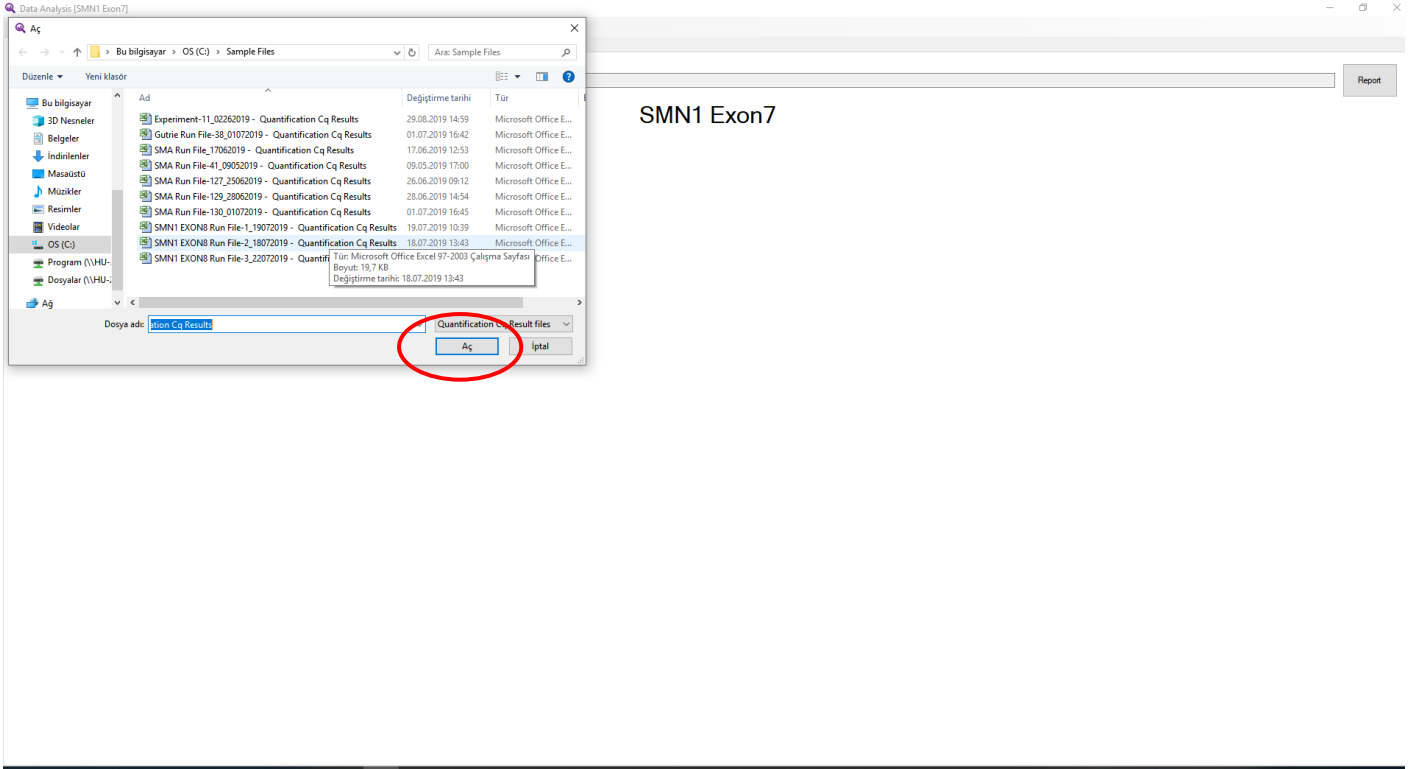

Figure - 5

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).
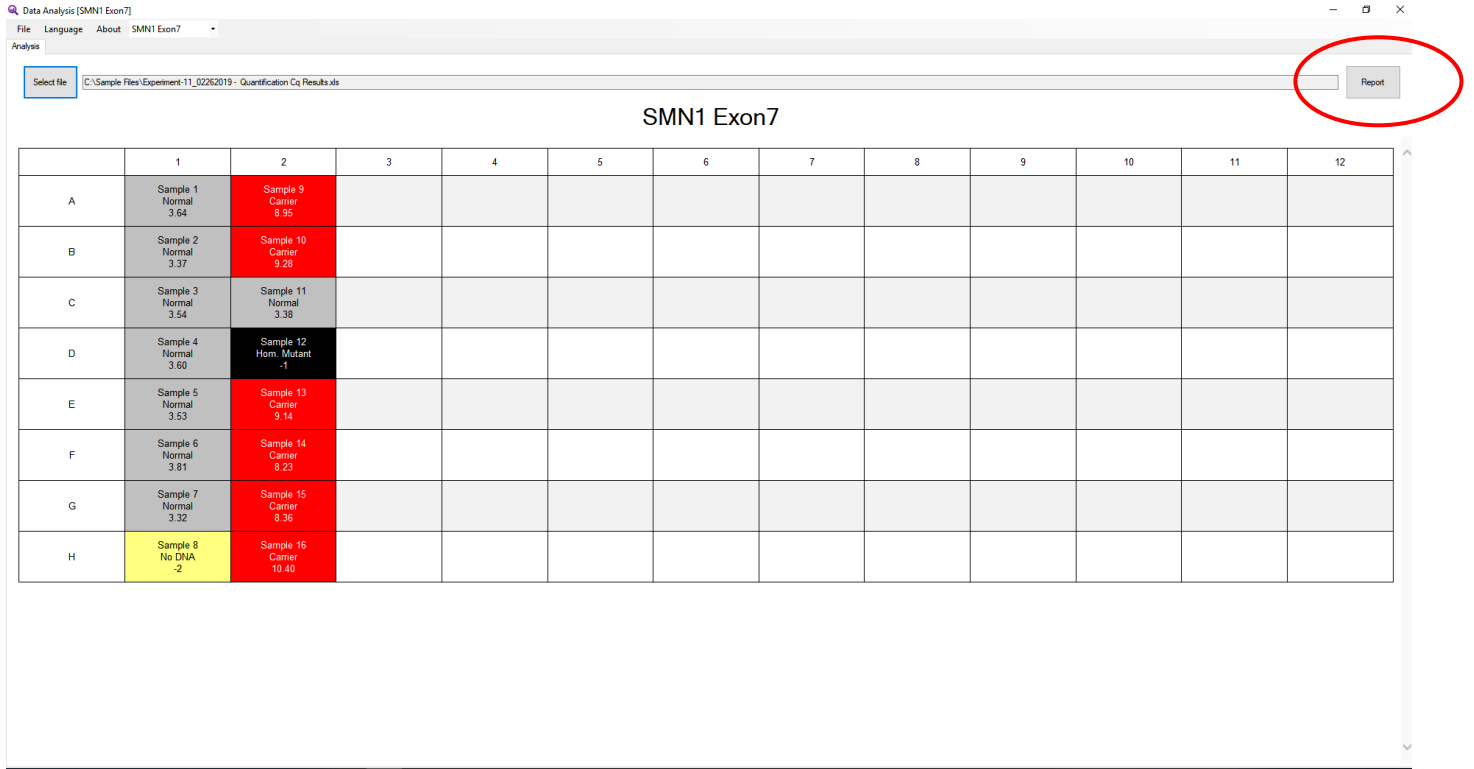

Figure - 7

Step 6: Choose the other parameter you want to analyze. For this example NAIP Exon 5. Repeat the steps (step 1-5) in the previous parameter analysis and than continue step 6 and the following figures (Figures 8 - 9 - 10).
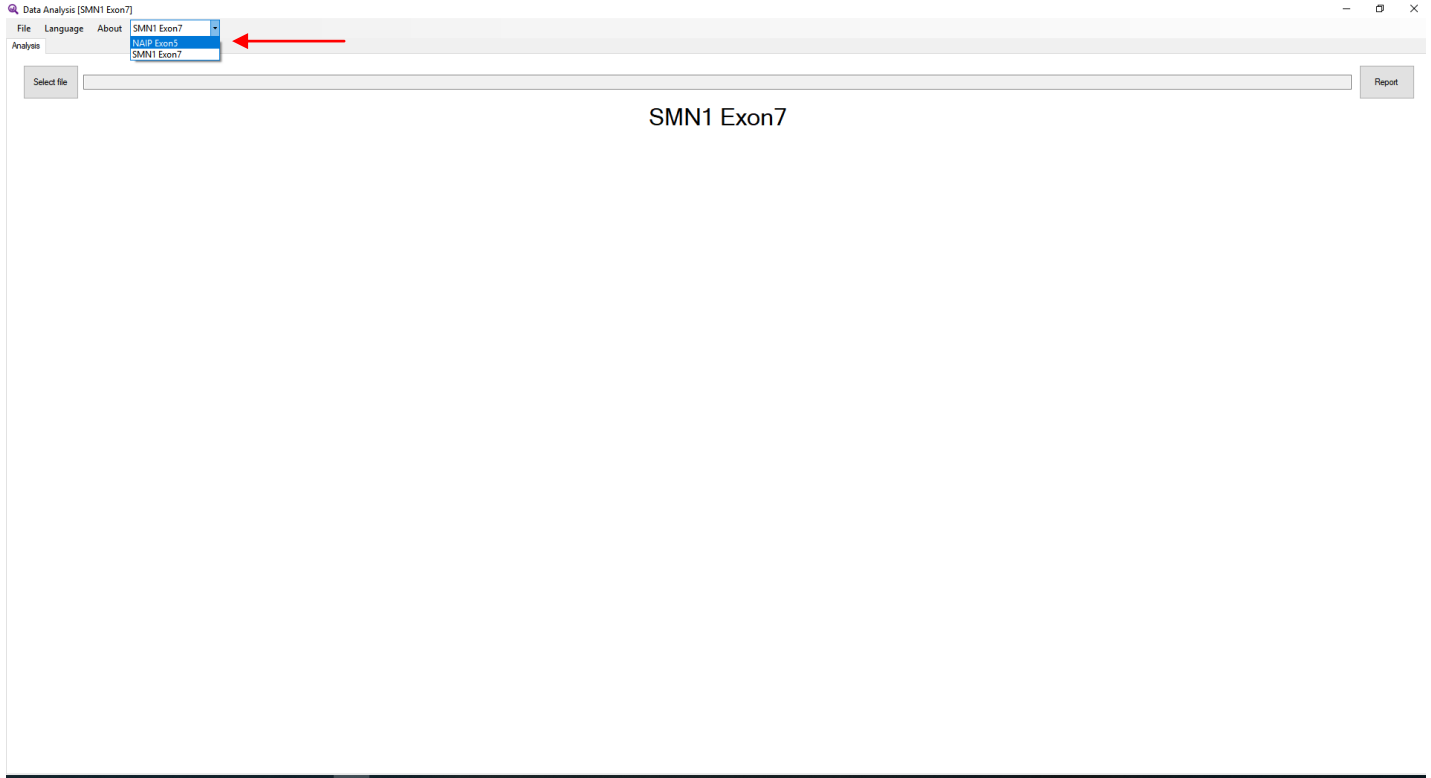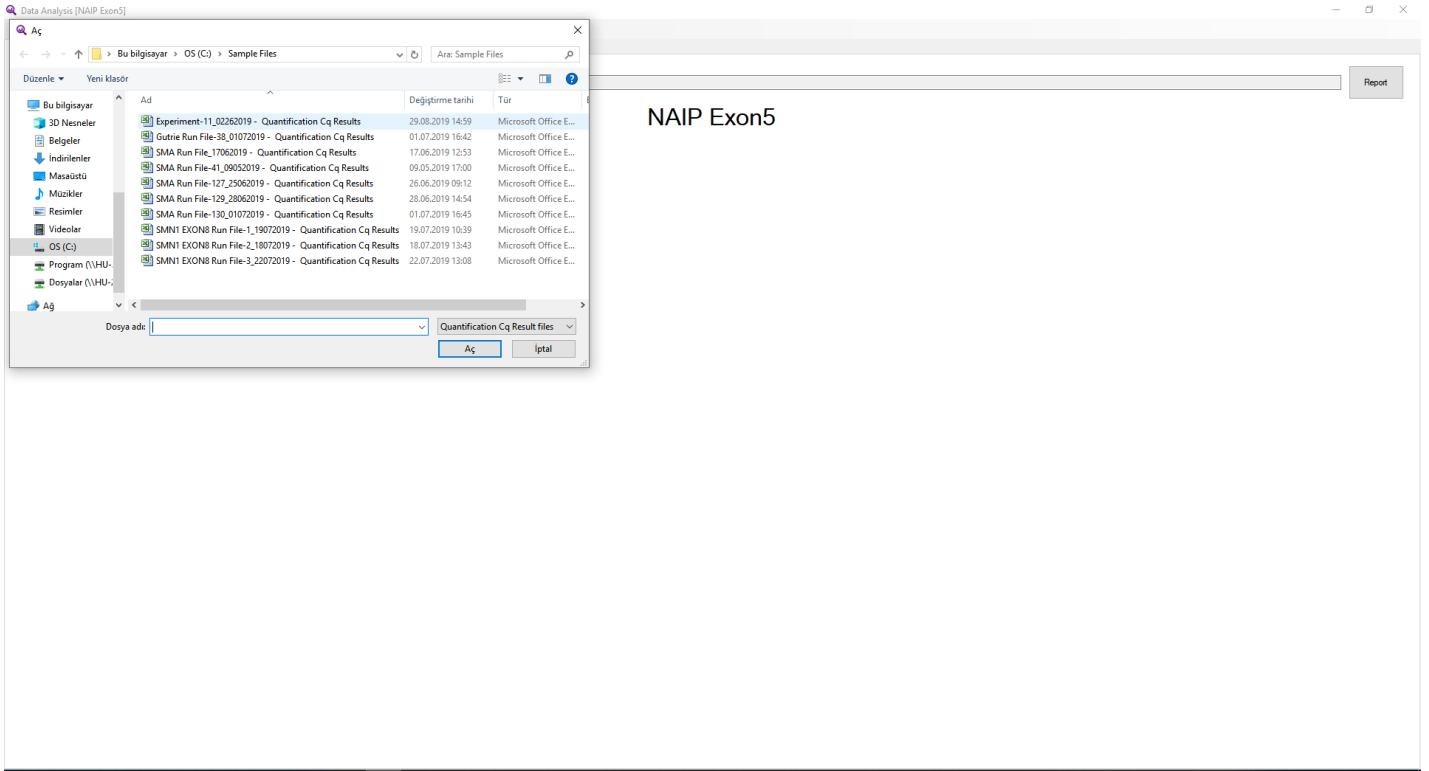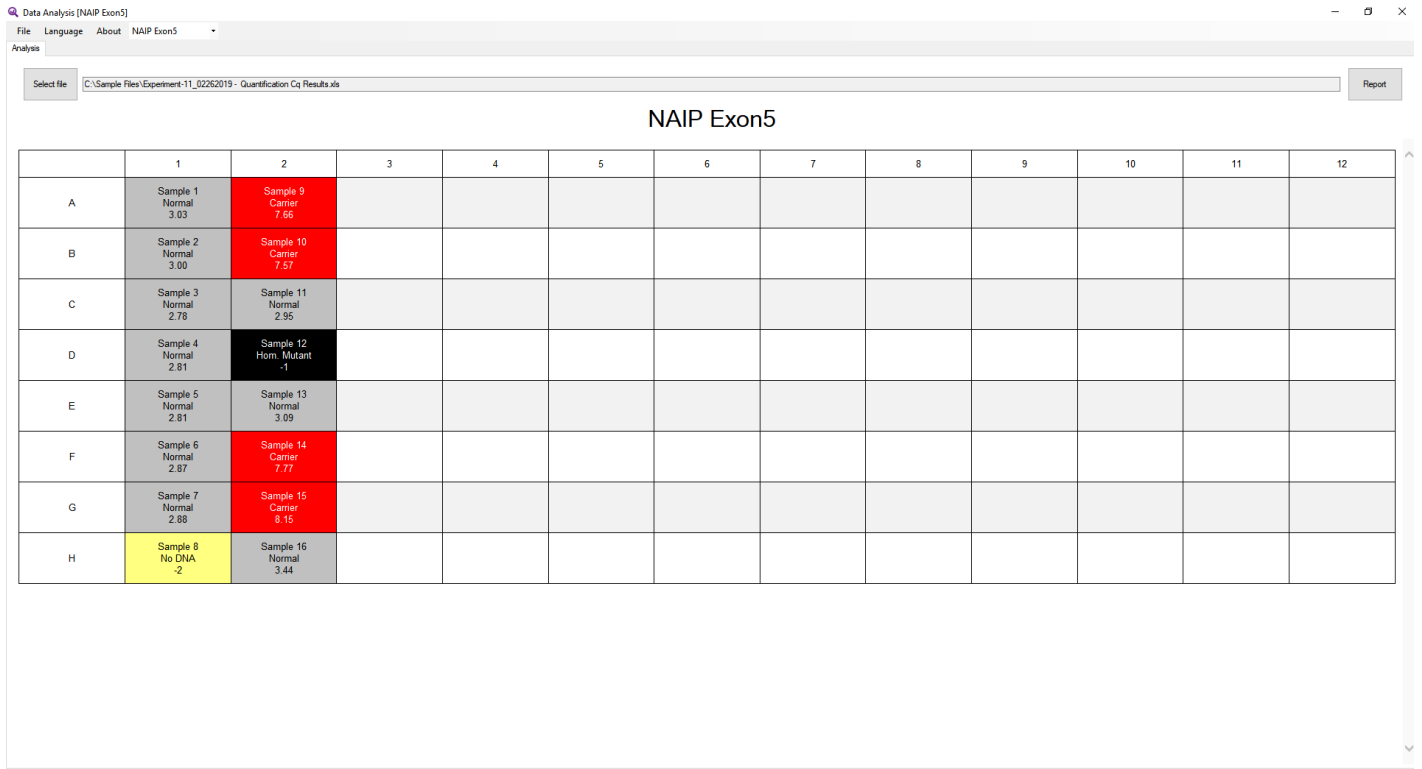

Figure - 8

Figure - 9

Figure - 10