

5.4 Smear DNA Analysis (gDNA QC for NGS)

The **Smear** function can help user to understand the major size and the distribution of the fragmented genomic DNA.

To conduct the analysis, do the following steps:

- Step 1. Click the Smear tab (Figure 5-19 A) (Alternatively, you can select Smear from the Toolbar).
- Step 2. Enter the percentage of the target distribution (e.g. 50%) or the bp range of the target region (Figure 5-19 B-C). Then, click Apply. Figure 5-19 D shows the detail information of the assigned region, including the Average bp and concentration of the region (nmol/L).
- Step 3. Modify the Interval of the size range if necessary, and then click Apply to apply the setting. Doing so will help you get the more detail of the distribution (Figure 5-19 E).
- Step 4. In addition, you can edit the other zone by selecting Zone2 and the editing rules are the same as mentioned above. This function helps user get the ratios between Zone1 and Zone2 which provided more information about these two Zones (Figure 5-19 F).
- Step 5. All information about the distribution will show up in the below table.
- Step 6. Click the right button on the right panel to export the report (Figure 5-20). User can export a report with two zones information, select “both zone” at Smear zone

***Note:** To use the Smear function, the result data must be calculated.

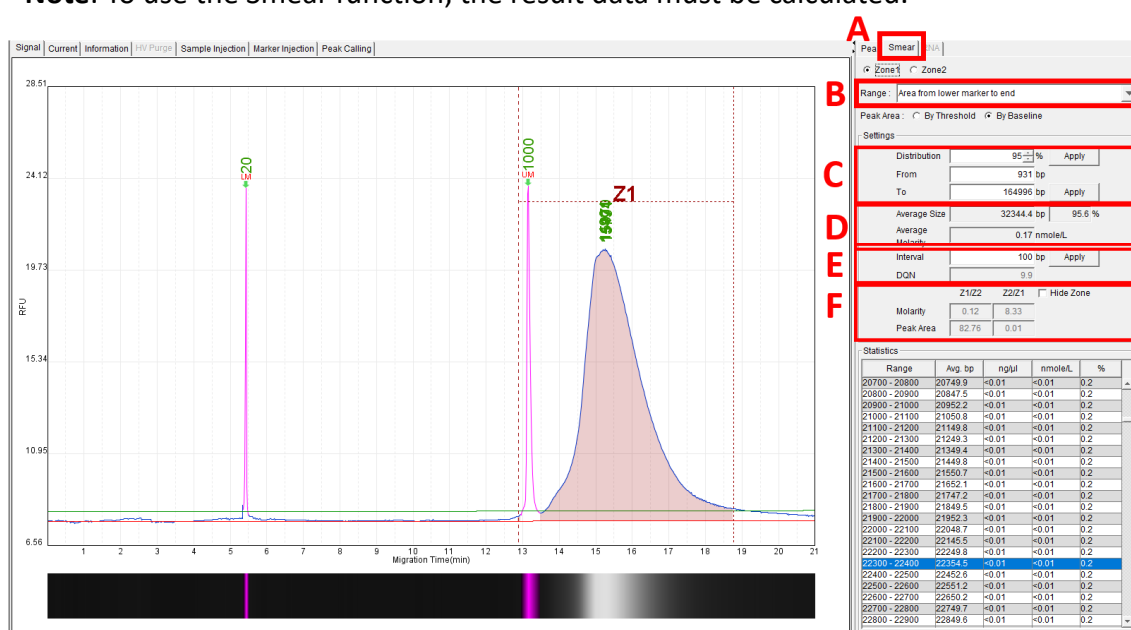
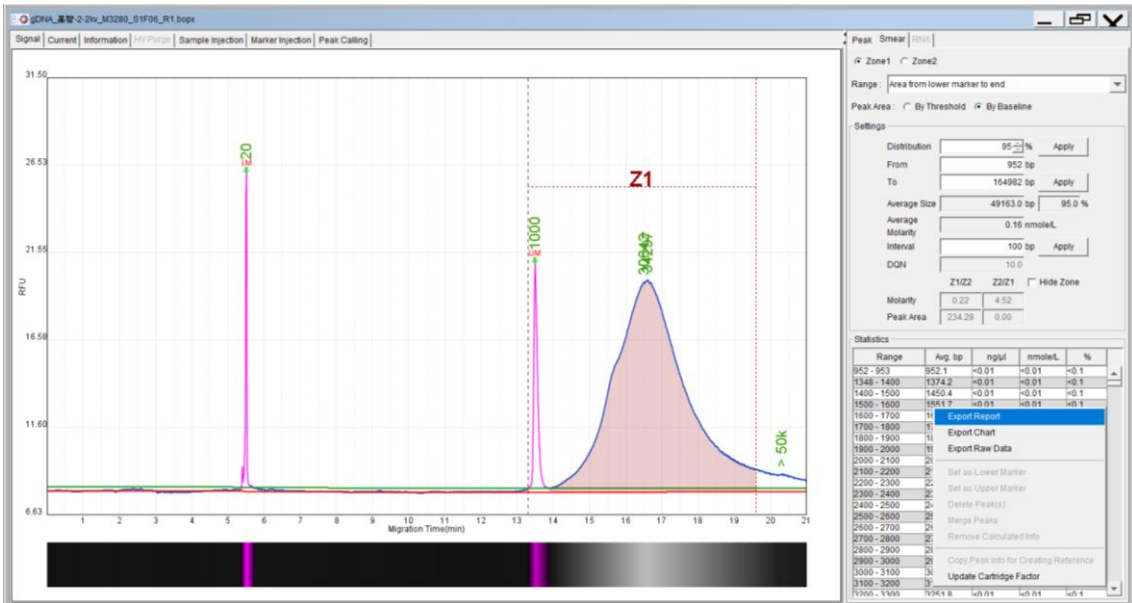


Figure 5-19 Fragmented Genomic DNA Sample Result



Report Format

Export Type :

Individual Folder

Application Type :

Standard(DNA) Smear RNA Peak Calling

Signal View :

Window Best Fit(LM-UM) Best Fit(LM-End) Original

X Axis :

Time Size

Gel View :

Best Fit(LM-UM) Best Fit(LM-End) Original

Result List :

Result Name Sample Description

Smear Zone :

Only Zone1 Both Zone

Small Chart Description :

Sample Position Sample ID

File Format :

Preview PDF WORD EXCEL

OK

Figure 5-20 Export the Smear Report