User Guide
Standard (S2) Cartridge Kit (C105201/C105801)

A. Specifications

Specifications	Description
DNA Sizing Range	20-5000 bp
L.O.D	0.1 ng/µl
Resolution	4-10 bp
Sample number (per cartridge)	200 runs
Shelf life	6 months

* Best resolution is determined by the 15-622 DNA Size Marker (C109200).

For new cartridge, please follow unpacking guide to unpack and use 20bp-1000bp Alignment Marker to do calibration.

B. Sample Preparation

Sample volume requirement

0.2 ml tube: 20 µl

0.1 ml tube (C104252): 10 µl

Micro Vial: 2 µl

Recommended sample concentration

Fragment sample: 0.1-10 ng/µl

***NOTE: When fragment sample concentration is over 10 ng/µl, please 10X dilute sample by 1X dilution buffer.**

Smear sample: 2-50 ng/µl

***NOTE: When smear sample concentration is over 50 ng/µl, please 10X dilute sample by 0.1X dilution buffer.**

***NOTE: If sample is eluted in water, adding dilution buffer to make the sample in 0.2X or 0.1X dilution buffer condition.**

- **Section B-1: sample size in 20-1000 bp**
- **Section B-2: sample size in 20-5000 bp**

B-1. Sample size within range from 20 bp to 1000 bp

Marker required:

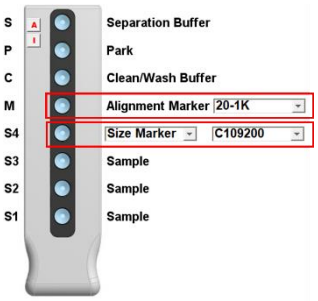
20bp-1000bp Alignment Marker (C109100): 20 µl

15-622bp Size Marker (C109200): 20 µl

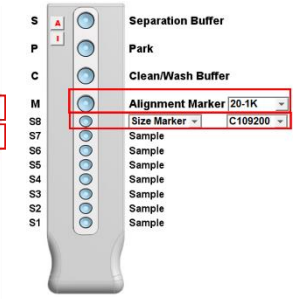
***NOTE: All the markers should be loaded at regular 0.2 ml PCR tube, Except for the size marker for *Qsep*$_1$ 12-well tray (size marker put at "S8" position needs to use 0.1ml tube (C104252)).**

Click "Change Buffer", place alignment marker and size marker at corresponding position:

Qsep$_1$ 8-well tray



Qsep$_1$ 12-well tray



B-2. Sample size within range from 10 bp to 5000 bp

Marker required:

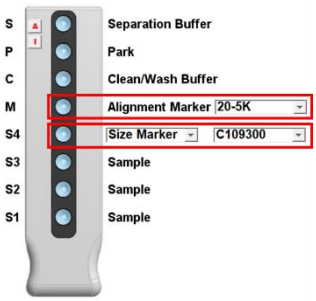
20bp-5000bp Alignment Marker (C109102): 20 µl

50-3000bp Size Marker (C109300): 20 µl

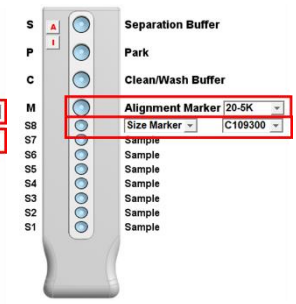
***NOTE: All the markers should be loaded at regular 0.2 ml PCR tube, except the size marker for *Qsep*$_1$ 12-well tray (size marker put at "S8" position needs to use 0.1 ml tube (C104252).**

Click "Change Buffer", place alignment marker and size marker at corresponding position:

Qsep$_1$ 8-well tray



Qsep$_1$ 12-well tray



***NOTE: If sample is eluted in nuclease-free water, please use dilution buffer to dilute it**

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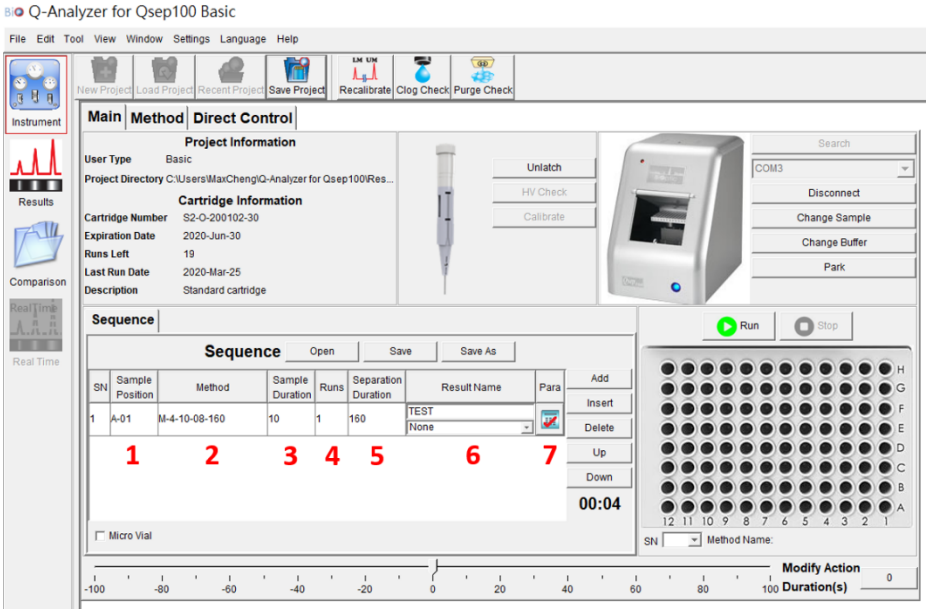
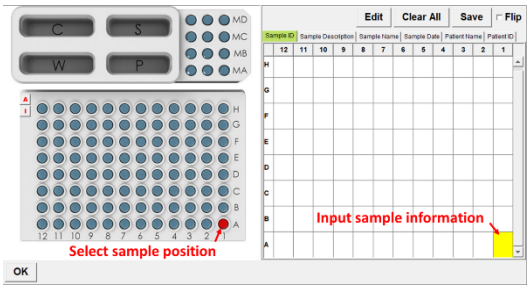
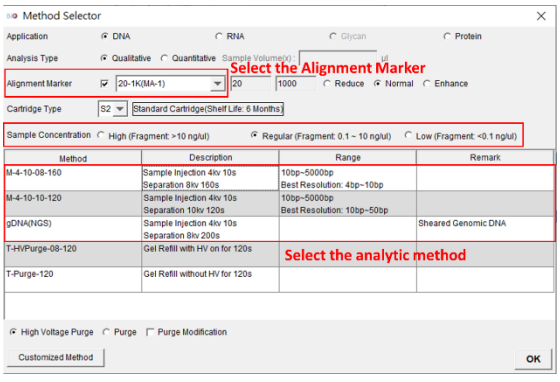
C. Software Operation



1. Place sample and select corresponding position, then input Sample information (optional).



2. Select alignment marker and analytic method in Method Selector.



*NOTE: Based on sample concentration to adjust injection condition

Sample concentration	High (2kV, 10s)	Regular (4kV, 10s)	Low (8kV, 10s)
Fragment DNA	> 10 ng/μl	0.1-10 ng/μl	0.01-0.1 ng/μl
Smear DNA	> 50 ng/μl	2-50 ng/μl	0.5-2 ng/μl

3. Sample Duration: adjust the sample injection time to increase/decrease injection amount.

*NOTE: Do not set the injection time over 20 sec.

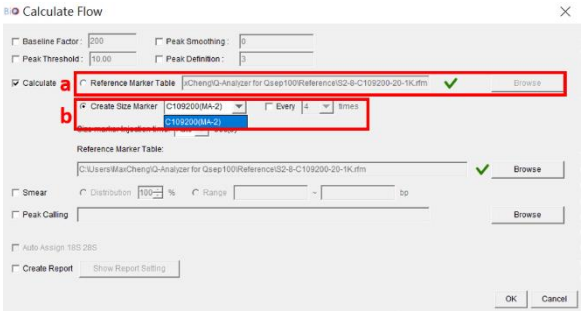
4. Runs: reputation time.

5. Separation Duration: adjust the duration to extend/reduce the separation time.

*NOTE: Step 3-5 are optional.

6. Input the result name for result file.

7. Click “Para”  . Choose to use reference (a) or create size marker (b) to do the calculation.



*NOTE: When using create size marker function, select the size marker you use. e.g. 20-1k is paired with C109200, 20-5k is paired with C109300.

8. Click “Run” to start analysis. 

*NOTE: Please renew the alignment marker every 20 runs.

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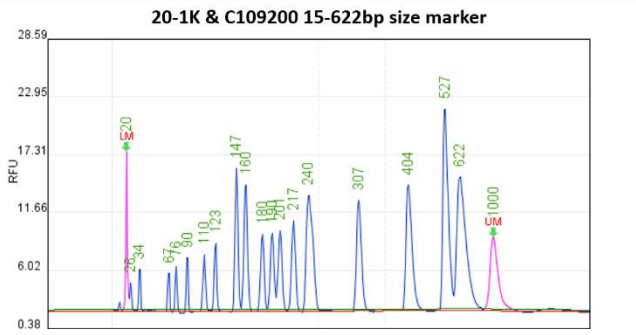
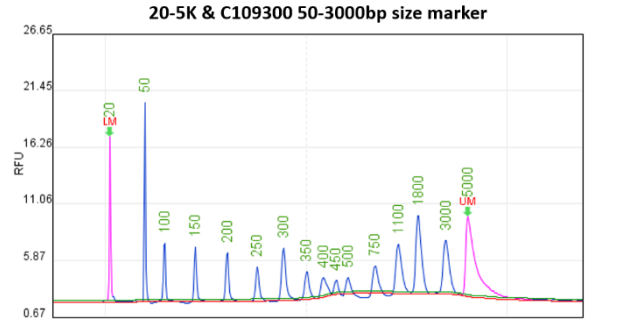
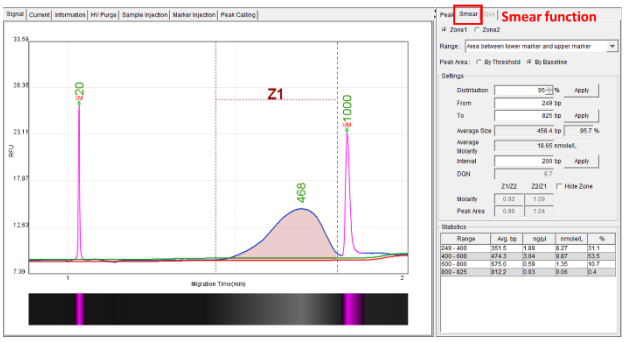
D. Result and Application

- **Alignment Marker & Size Marker**





- **Fragmented & Library Sample Validation**



Distribution:	96.1 %	**Average Size:**	462.7 bp
From:	271 bp	**Average Molarity:**	18.62 nmole/L
To:	903 bp	**DQN:**	9.6

Range	Avg. bp	ng/µl	nMole / L	Percent
271 - 400	352.7	1.86	8.12	30.6
400 - 600	474.3	3.04	9.87	53.5
600 - 800	675.0	0.59	1.35	10.7
800 - 903	844.9	0.11	0.19	1.3

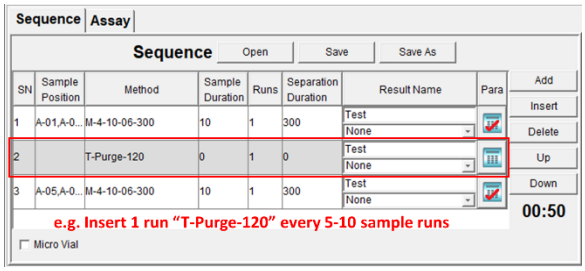
Using smear function to get average size, molarity, and size distribution of fragmented DNA or library DNA sample

E. Troubleshooting

Please ensure that the system is working well, and the operation follows the instructions first.

Sometimes there will be some residues left in DNA sample after extraction.
These residues might cause unstable current at sample injection or separation steps. Here is a list of solutions to help fix the occurrence.

1. Use dilution buffer to dilute the sample.
2. Centrifuge the sample for a while to make the residues accumulate at the bottom of the tube.
3. Insert a “T-purge-120” method between several sample runs.
   e.g. insert 1 run “T-Purge-120” every 5-10 sample runs.



F. Cartridge Discard

Please wear the gloves before discarding cartridge.

1. Bend the cartridge tip.
2. Open the cap on gel reservoir and remove the inner cap.
3. Pour the gel into the chemical waste container.
4. Cartridge can throw it into the bin.

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