

Fragment Analyzer Run Summary:

Filename and Data Path: C:\AATI\Data\2022 10 17\09-33-46\2022 10 17 09H 33M.raw

Created: 2022/10/17 9:50:01

of Capillaries: 2

Array Serial #: 051022-16SFS

Effect Length: 33 cm

Array Usage Count: 221

FA Version #: 1.2.0.11

Device Serial #: 4193

METHOD INFORMATION

Method Name: DNF-468-33 - HS Genomic DNA 50Kb.mthds

Gel Prime: No

Full Conditioning: Yes

Gel Prime to Buffer: No

Gel Selection: Gel 2

Perform Prerun: 5.0 kV, 30 sec.

Rinse: No

Marker 1: No

Rinse: Tray: 3, Row: H, # Dips: 1

Sample Injection: 5.0 kV, 15 sec.

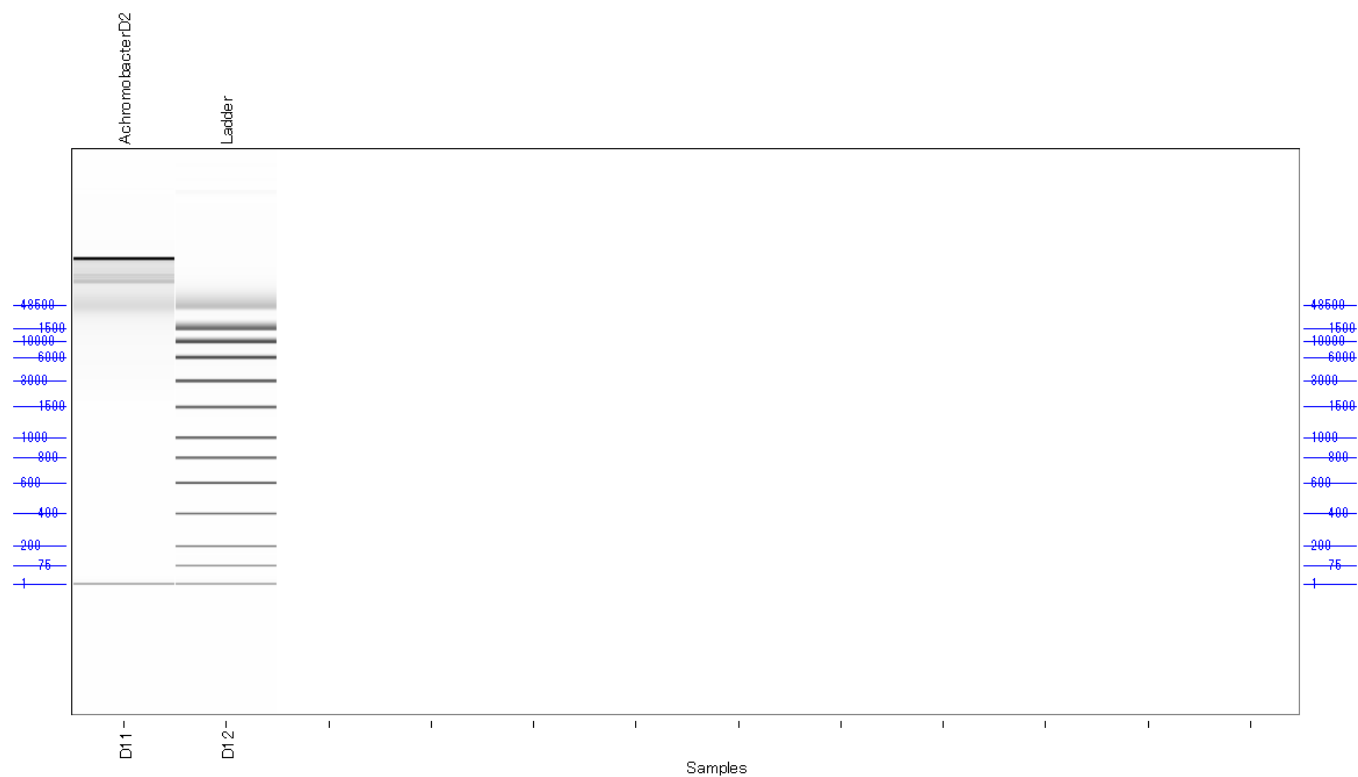
Separation: 5.0 kV, 60.0 min.

Tray Name: Tray-2

Analysis Mode: gDNA

NOTES

Gel Image

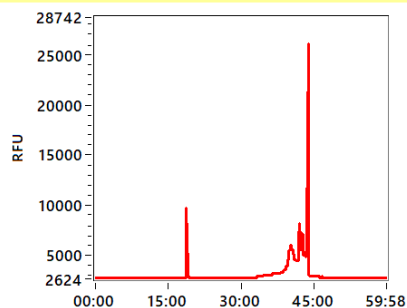


GQN Summary

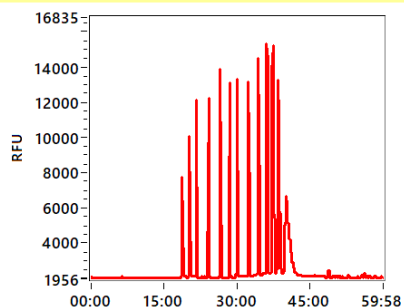
Well	Sample ID	GQN	Size Threshold (bp)	Total Conc. (ng/uL)
D11	AchromobacterD2	8.9	15000	8.2472
D12	Ladder			

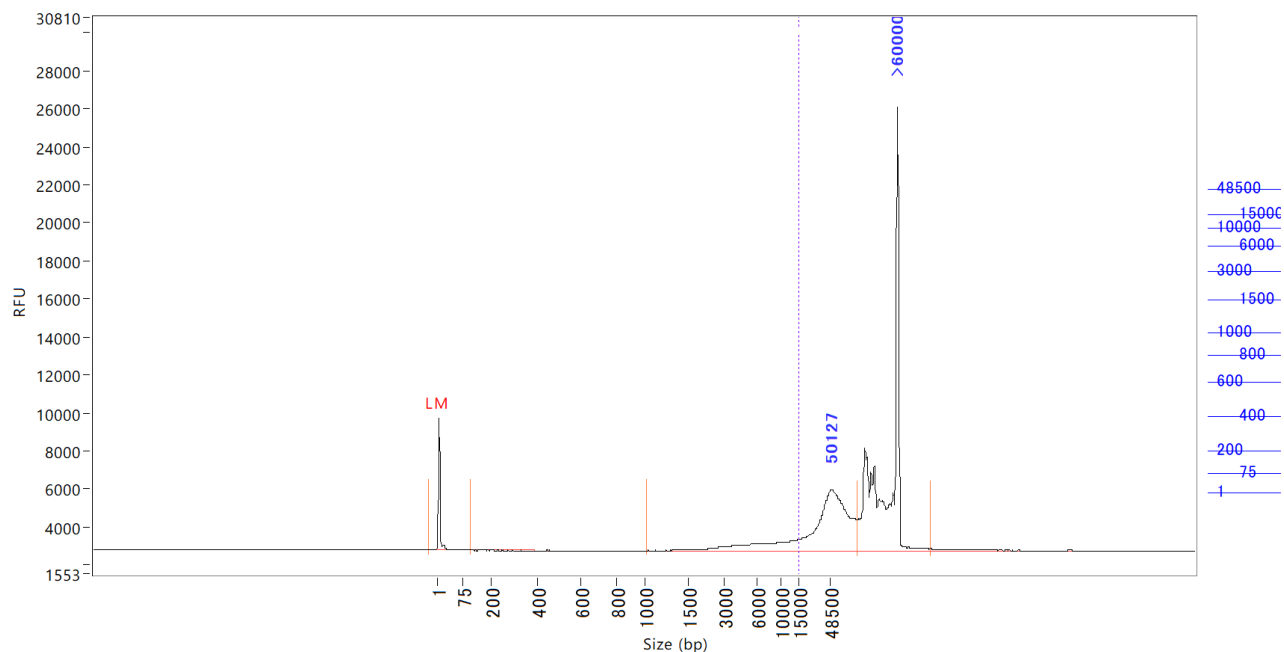
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D11: AchromobacterD2
GQN: 8.9



D12: Ladder



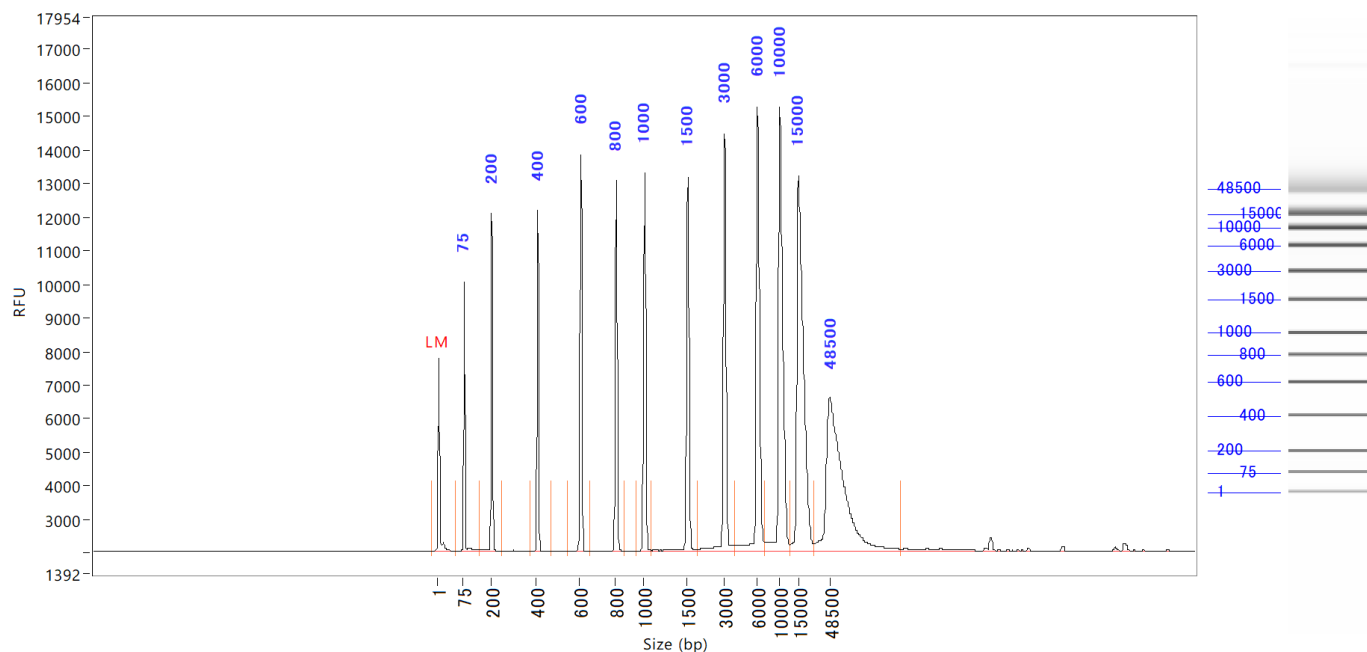
Sample: AchromobacterD2**Well Location:** D11**Created:** 2022/10/10 9:50:01

Peak	Size (bp)	Conc. (ng/uL)	From (bp)	To (bp)	Avg. Size (bp)	CV%	RFU	Corr. Peak Area
1	1 (LM)	0.0345	0	104	1	361.89	6936	40.343
2	50127	3.4460	1022	>60000	39923	56.32	3196	335.977
3	>60000	4.6557	>60000	>60000	>60000	14.38	23378	453.928

TIC: 8.1017 ng/uL
 TIM: 0.2151 nmole/L
 Total Conc.: 8.2472 ng/uL

GQN: 8.9
 Threshold: 15000

Sample Peak Width (sec): 50 Sample Min Peak Height: 100 Sample Baseline V to V?: Y Sample Baseline V to V pts: 3
 Sample Filter: Binomial # of Pts for Filter: 3 Sample Start Region (min): 0 Sample End Region (min): 60
 Manual Baseline Start (min): 15 Manual Baseline End (min): 59
 Marker Peak Width (sec): 5 Marker Min Peak Height: 500 Marker Baseline V to V?: N Marker Baseline V to V pts: 3
 Lower Marker Selection: First Peak > 500 RFU Upper Marker Selection: Last Peak > 500 RFU
 Ladder Size (bp): 1, 75, 200, 400, 600, 800, 1000, 1500, 3000, 6000, 10000, 15000, 48500
 Quantification Using: Ladder Final Concentration (ng/uL): 0.8333 Dilution Factor: 12.0
 Min. RFU for Data Processing: 3 Size Threshold (b.p.): 15000

Sample: Ladder**Well Location:** D12**Created:** 2022/10/17 9:50:01

Peak	Size (bp)	Conc. (ng/uL)	From (bp)	To (bp)	Avg. Size (bp)	CV%	RFU	Corr. Peak Area
1	1 (LM)	0.0345	0	50	2	369.59	5738	33.898
2	75	0.4428	50	146	76	11.56	8022	36.273
3	200	0.5139	146	245	198	3.01	10051	42.104
4	400	0.5211	368	462	399	0.98	10140	42.689
5	600	0.6276	543	656	599	0.77	11811	51.419
6	800	0.6172	656	855	798	1.01	11046	50.559
7	1000	0.6494	939	1076	997	0.89	11266	53.204
8	1500	0.7037	1076	1891	1497	3.64	11143	57.651
9	3000	0.8230	1891	3935	2986	6.50	12438	67.425
10	6000	0.9526	3935	7390	6001	6.96	13243	78.042
11	10000	1.2037	7390	12667	10200	6.49	13202	98.607
12	15000	1.4679	12667	31094	17605	18.94	11175	120.256
13	48500	1.4696	31094	>60000	57791	24.17	4592	120.396

TIC: 9.9926 ng/uL
TIM: 21.9070 nmole/L
Total Conc.: 9.9996 ng/uL

Sample Peak Width (sec): 20 Sample Min Peak Height: 100 Sample Baseline V to V?: Y Sample Baseline V to V pts: 3
Sample Filter: Binomial # of Pts for Filter: 3 Sample Start Region (min): 0 Sample End Region (min): 60
Manual Baseline Start (min): 15 Manual Baseline End (min): 59
Marker Peak Width (sec): 5 Marker Min Peak Height: 500 Marker Baseline V to V?: N Marker Baseline V to V pts: 3
Lower Marker Selection: First Peak > 500 RFU Upper Marker Selection: Last Peak > 500 RFU
Ladder Size (bp): 1, 75, 200, 400, 600, 800, 1000, 1500, 3000, 6000, 10000, 15000, 48500
Quantification Using: Ladder Final Concentration (ng/uL): 0.8333 Dilution Factor: 12.0
Min. RFU for Data Processing: 3 Size Threshold (b.p.): 15000

Sample: Ladder**Well Location:** D12**Created:** 2022/10/17 09:50:01**Fit Type:** Point to Point

Calibration Curve

