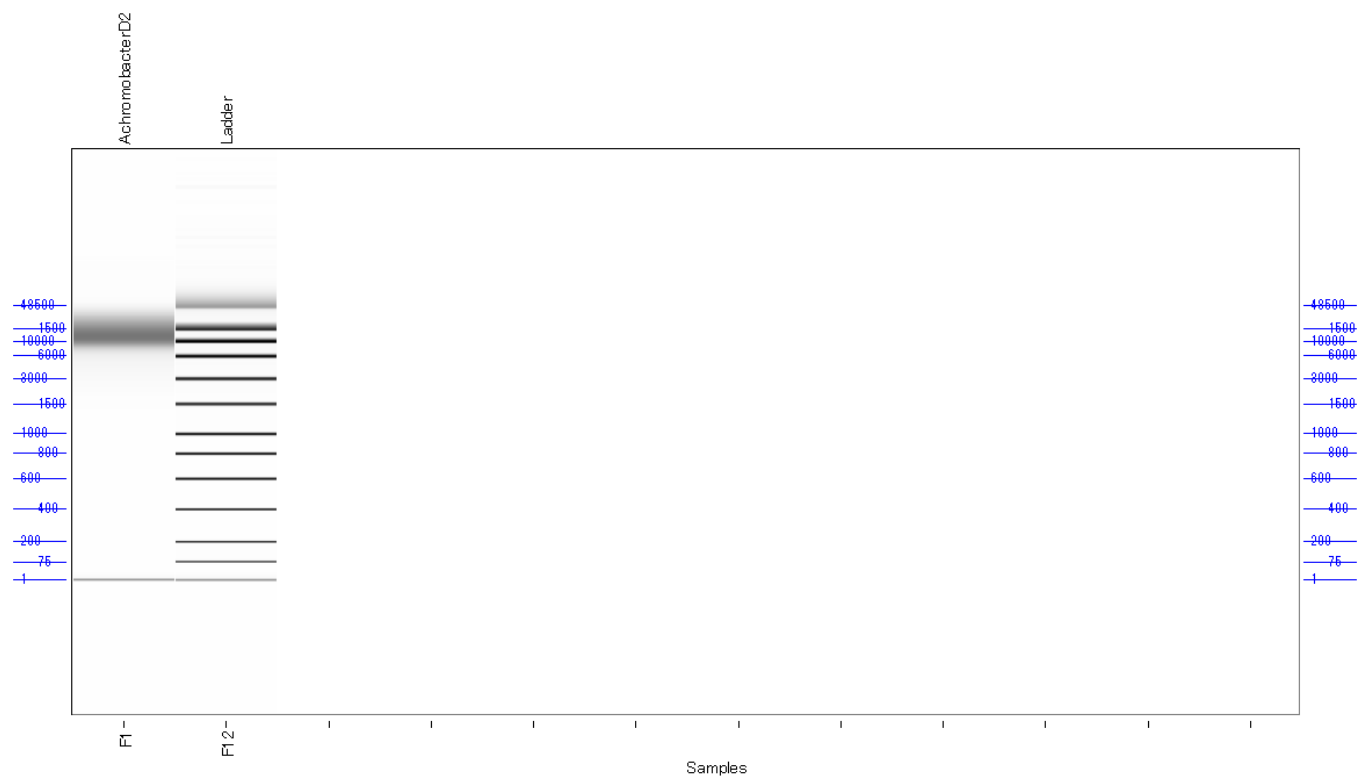


Fragment Analyzer Run Summary:**Filename and Data Path:** C:\AATI\Data\2022 10 18\15-24-45\2022 10 18 15H 24M.raw**Created:** 2022/10/18 15:40:55**# of Capillaries:** 2**Array Serial #:** 051022-16SFS**Effect Length:** 33 cm**Array Usage Count:** 228**FA Version #:** 1.2.0.11**Device Serial #:** 4193**METHOD 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



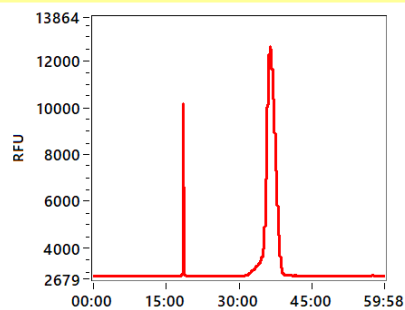
GQN Summary

Well	Sample ID	GQN	Size Threshold (bp)	Total Conc. (ng/uL)
F1	AchromobacterD2	N/A	0	7.6848
F12	Ladder			

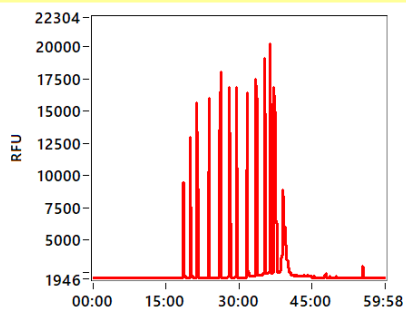
Filename and Data Path: C:\AATI\Data\2022 10 18\15-24-45\2022 10 18 15H 24M.raw

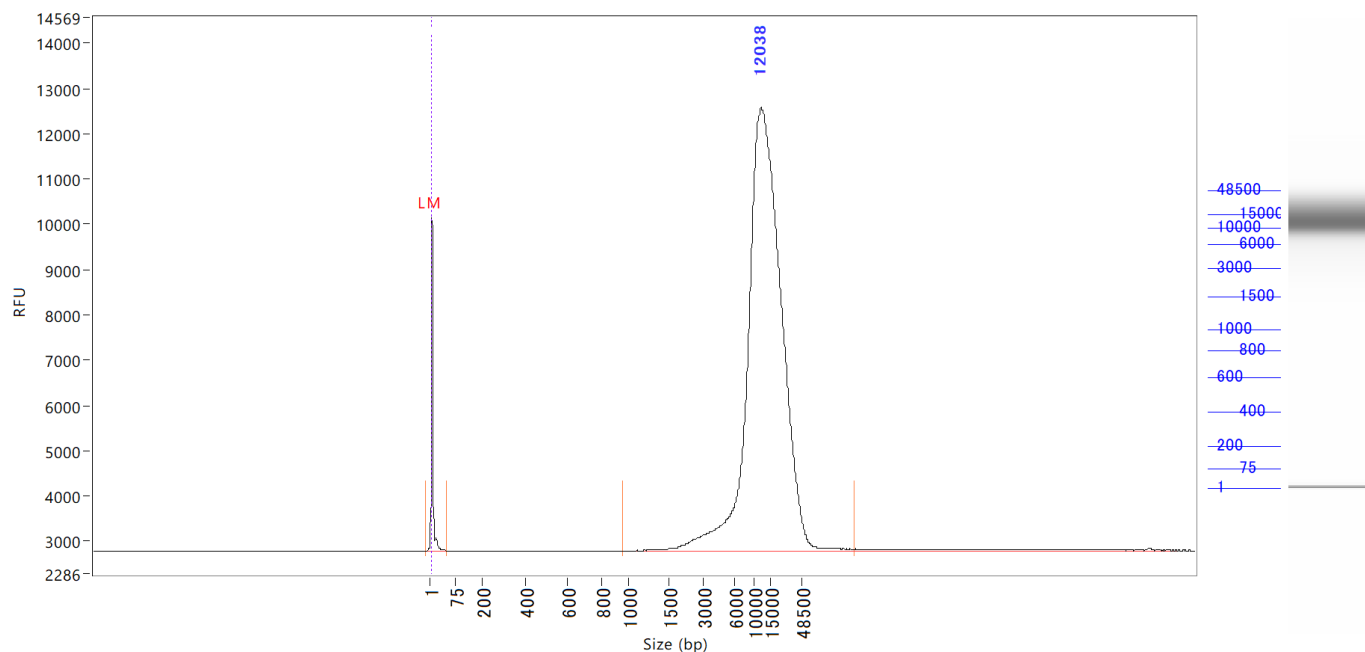
F1: AchromobacterD2

GQN: N/A (Size threshold is less than lower marker end)



F12: Ladder



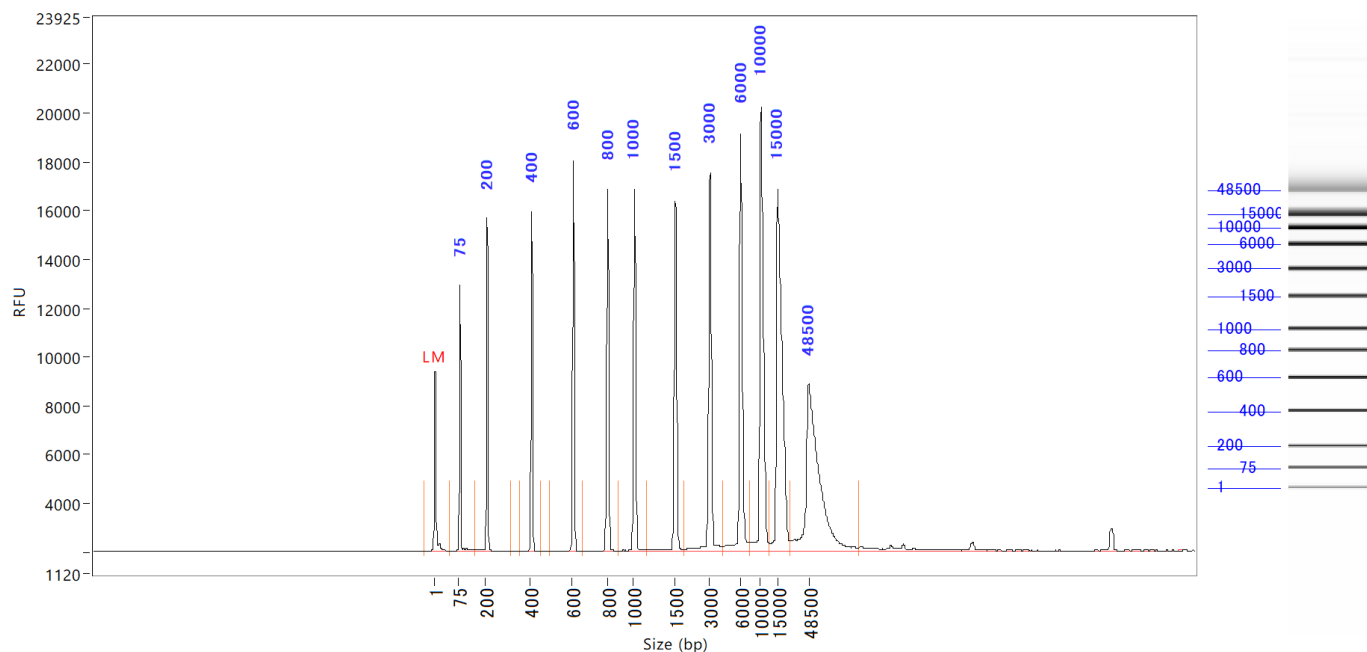
Sample: AchromobacterD2**Well Location:** F1**Created:** 2022/10/18 15:40:55

Peak	Size (bp)	Conc. (ng/uL)	From (bp)	To (bp)	Avg. Size (bp)	CV%	RFU	Corr. Peak Area
1	1 (LM)	0.0350	0	47	2	303.11	7364	42.685
2	12038	7.5720	958	>60000	16145	65.09	9813	770.188

TIC: 7.5720 ng/uL
TIM: 0.7721 nmole/L
Total Conc.: 7.6848 ng/uL

GQN: N/A (Size threshold is less than lower marker end point)
Threshold: 0

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.): 0

Sample: Ladder**Well Location:** F12**Created:** 2022/10/18 15:40:55

Peak	Size (bp)	Conc. (ng/uL)	From (bp)	To (bp)	Avg. Size (bp)	CV%	RFU	Corr. Peak Area
1	1 (LM)	0.0350	0	45	1	514.81	7376	43.505
2	75	0.4572	45	146	76	11.14	10891	47.394
3	200	0.5464	146	310	199	4.20	13637	56.646
4	400	0.5556	350	445	399	0.93	13917	57.599
5	600	0.6780	492	657	598	1.01	16022	70.294
6	800	0.6706	657	877	797	1.13	14827	69.521
7	1000	0.7009	877	1147	1000	1.43	14827	72.666
8	1500	0.7319	1147	1889	1502	3.40	14362	75.879
9	3000	0.8312	1889	4213	2997	7.38	15474	86.166
10	6000	0.9280	4213	7970	6035	6.97	17102	96.209
11	10000	1.1334	7970	12500	10188	5.53	18223	117.500
12	15000	1.3881	12500	28600	17296	16.67	14832	143.905
13	48500	1.3824	28600	>60000	55276	20.06	6831	143.318

TIC: 10.0037 ng/uL
TIM: 22.9476 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.): 0

Sample: Ladder**Well Location:** F12**Created:** 2022/10/18 15:40:55**Fit Type:** Point to Point

Calibration Curve

