

Assay Class: High Sensitivity DNA Assay  
Data Path: C:\...s and Settings\Bioanalyzer\2015-05-21\2015-05-21\_004\_RJ.xad

Created: 5/21/2015 3:24:31 PM  
Modified: 5/21/2015 3:58:04 PM

**Electrophoresis File Run Summary**

Instrument Information:

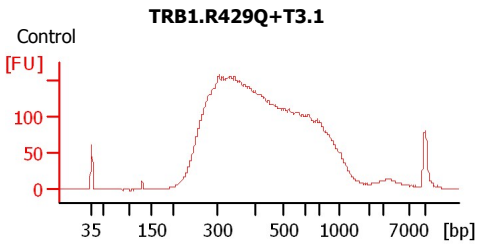
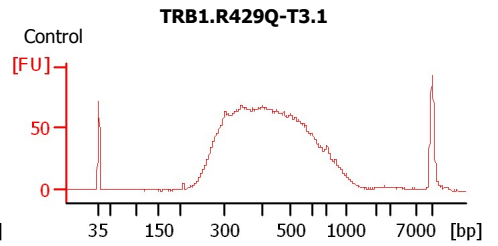
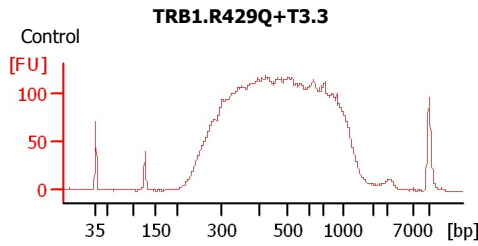
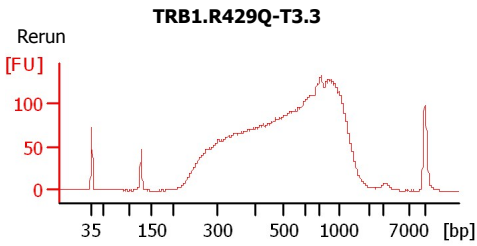
Instrument Name: DE13701086                      Firmware: C.01.069  
Serial#: DE13701086                              Type: G2938B

Assay Information:

Assay Origin Path: C:\Program Files\Agilent\2100 bioanalyzer\2100 expert\assays\dsDNA\High Sensitivity DNA.xsy  
Assay Class: High Sensitivity DNA Assay  
Version: 1.03  
Assay Comments: Copyright © 2003-2010 Agilent Technologies

Chip Information:

Chip Lot #:  
Reagent Kit Lot #:  
Chip Comments:



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**Electrophoresis File Run Summary (Chip Summary)**

Sample Name	Sample Comment	Rest. Digest	Status	Observation	Result Label	Result Color
TRB1.R429Q-T3.3	Rerun	<input type="checkbox"/>	✓			
TRB1.R429Q+T3.3	Control	<input type="checkbox"/>	✓			
TRB1.R429Q-T3.1	Control	<input type="checkbox"/>	✓			
TRB1.R429Q+T3.1	Control	<input type="checkbox"/>	✓			
Ladder		<input type="checkbox"/>	✓			

**Chip Lot #**

**Reagent Kit Lot #**

**Chip Comments :**

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**Electrophoresis Assay Details**

**General Analysis Settings**

Number of Available Sample and Ladder Wells (Max.) : 12  
Minimum Visible Range [s] : 32  
Maximum Visible Range [s] : 138  
Start Analysis Time Range [s] : 33  
End Analysis Time Range [s] : 137.5  
Ladder Concentration [pg/μl] : 1950  
Uses Standard Area for Ladder Fragments  
Lower Marker Concentration [pg/μl] : 125  
Upper Marker Concentration [pg/μl] : 75  
Used Upper Marker for Quantitation  
Standard Curve Fit is Point to Point  
Show Data Aligned to Lower and Upper Marker

**Integrator Settings**

Integration Start Time [s] : 33.05  
Integration End Time [s] : 137  
Slope Threshold : 0.8  
Height Threshold [FU] : 5  
Area Threshold : 0.1  
Width Threshold [s] : 0.6  
Baseline Plateau [s] : 0.5

**Filter Settings**

Filter Width [s] : 0.5  
Polynomial Order : 4

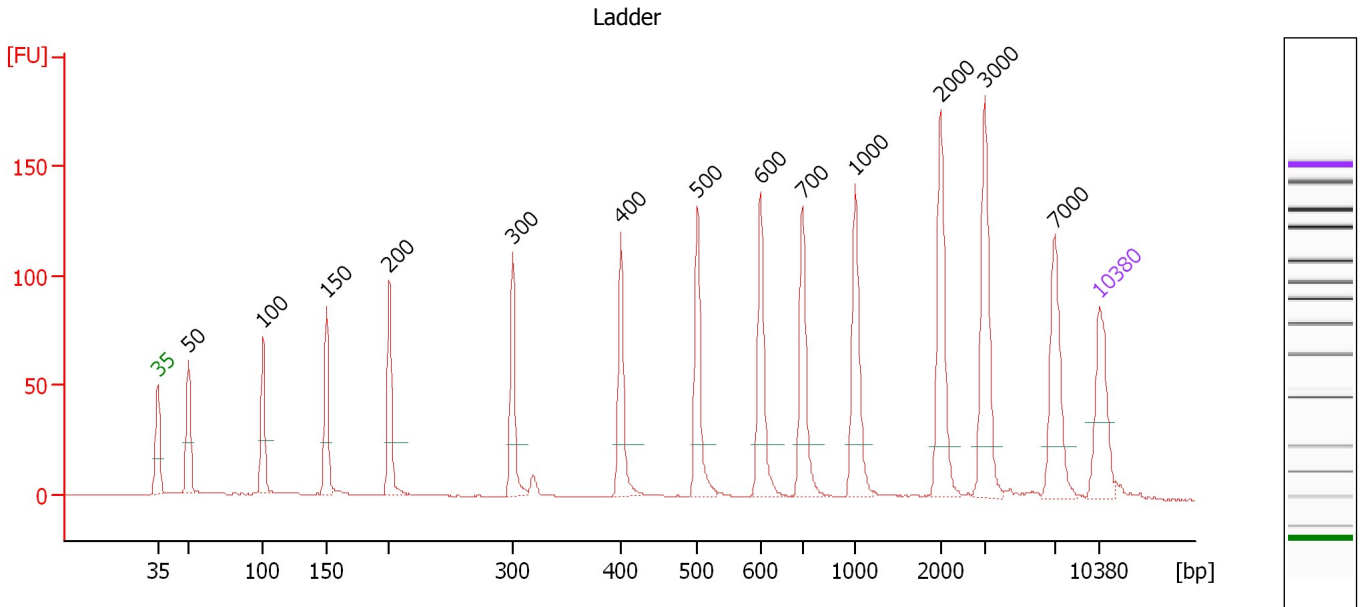
**Ladder**

Ladder Peak	Size	Area
1	35	160
2	50	210
3	100	208
4	150	221
5	200	242
6	300	270
7	400	305
8	500	306
9	600	336
10	700	321
11	1000	366
12	2000	413
13	3000	411
14	7000	400
15	10380	214

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**Electropherogram Summary**



**Overall Results for Ladder**

Noise: 0.2

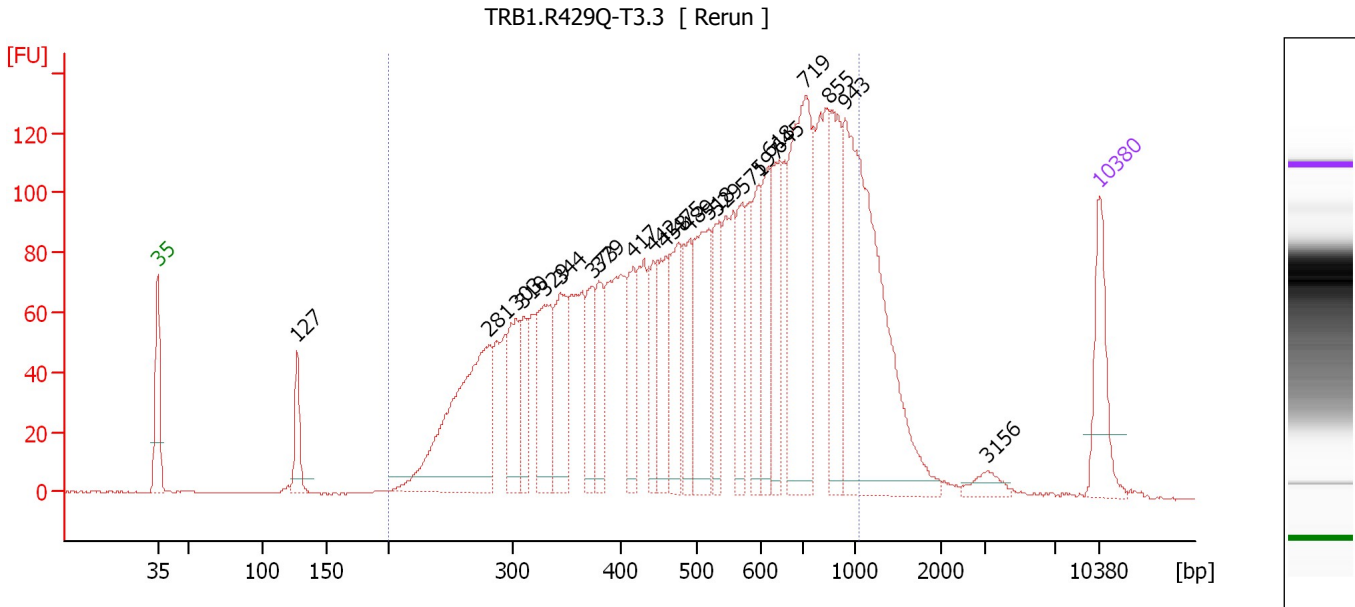
**Peak table for Ladder**

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	35	125.00	5,411.3	Lower Marker	43.00
2	50	150.00	4,545.5	Ladder Peak	45.29
3	100	150.00	2,272.7	Ladder Peak	50.83
4	150	150.00	1,515.2	Ladder Peak	55.54
5	200	150.00	1,136.4	Ladder Peak	60.21
6	300	150.00	757.6	Ladder Peak	69.37
7	400	150.00	568.2	Ladder Peak	77.43
8	500	150.00	454.5	Ladder Peak	83.10
9	600	150.00	378.8	Ladder Peak	87.77
10	700	150.00	324.7	Ladder Peak	90.89
11	1,000	150.00	227.3	Ladder Peak	94.82
12	2,000	150.00	113.6	Ladder Peak	101.14
13	3,000	150.00	75.8	Ladder Peak	104.44
14	7,000	150.00	32.5	Ladder Peak	109.61
15	10,380	75.00	10.9	Upper Marker	113.00

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**Electropherogram Summary Continued ...**



**Overall Results for sample 1 : TRB1.R429Q-T3.3**

Number of peaks found: 23                      Corr. Area 1: 3,282.7  
 Noise: 0.2

**Peak table for sample 1 : TRB1.R429Q-T3.3**

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	35	125.00	5,411.3	Lower Marker	43.00
2	127	64.97	774.7		53.38
3	281	354.77	1,910.3		67.67
4	303	104.41	521.5		69.64
5	310	65.75	321.2		70.19
6	329	133.47	614.7		71.71
7	344	124.88	549.4		72.95
8	373	76.42	310.0		75.29
9	379	72.08	288.0		75.75
10	417	87.39	317.9		78.37
11	442	72.95	249.8		79.84
12	458	94.57	313.0		80.71
13	475	113.73	362.9		81.67
14	489	77.14	238.8		82.50
15	518	170.47	499.0		83.93
16	529	84.02	240.5		84.48
17	571	89.70	238.2		86.41
18	597	85.45	216.8		87.65
19	618	102.29	250.8		88.33
20	645	93.38	219.5		89.16
21	719	305.38	643.5		91.14
22	855	136.90	242.5		92.93
23	943	453.18	728.2		94.08
24	3,156	17.66	8.5		104.64
25	10,380	75.00	10.9	Upper Marker	113.00

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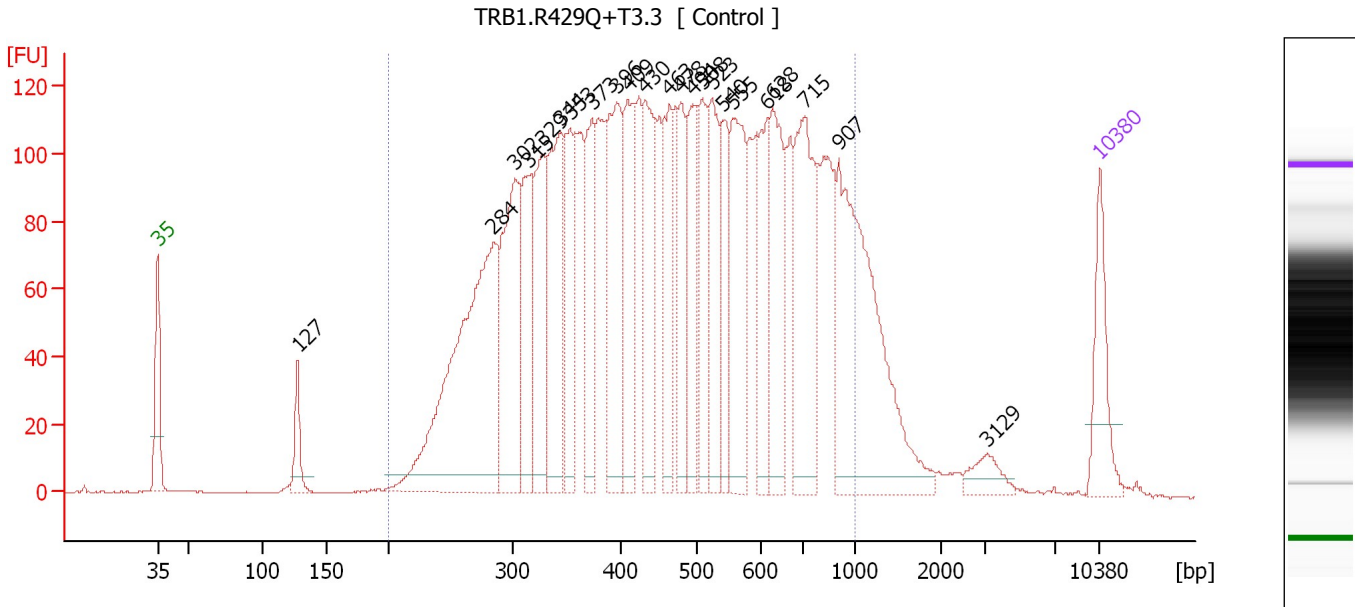
**Electropherogram Summary Continued ...****... Region table for sample 1 : TRB1.R429Q-T3.3**

<b>From [bp]</b>	<b>Average Size [bp]</b>	<b>To [bp]</b>	<b>Corr. Area</b>	<b>Molarity [pmol/l]</b>	<b>% of Total</b>	<b>Size distribution in CV [%]</b>	<b>Conc. [pg/μl]</b>	<b>Co lor</b>
200	540	1,032	3,282.7	12,779.1	89	37.3	3,694.41	■

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**Electropherogram Summary Continued ...**



**Overall Results for sample 2 : TRB1.R429Q+T3.3**

Number of peaks found: 23                      Corr. Area 1: 4,062.0  
 Noise: 0.3

**Peak table for sample 2 : TRB1.R429Q+T3.3**

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	35	125.00	5,411.3	Lower Marker	43.00
2	127	61.07	727.0		53.40
3	284	597.26	3,180.9		67.95
4	302	287.02	1,439.8		69.54
5	315	167.46	806.0		70.56
6	329	187.99	866.6		71.68
7	344	227.70	1,002.0		72.94
8	353	128.91	553.3		73.64
9	373	151.64	615.6		75.27
10	396	238.88	914.4		77.09
11	409	159.59	591.4		77.93
12	430	172.13	606.2		79.14
13	463	116.58	381.4		81.01
14	478	124.36	394.3		81.85
15	494	131.41	402.8		82.78
16	508	130.93	390.5		83.48
17	523	149.15	432.1		84.18
18	540	103.64	290.8		84.97
19	555	193.86	529.3		85.67
20	618	113.83	279.1		88.33
21	628	175.87	424.1		88.66
22	715	245.79	521.0		91.08
23	907	402.48	672.6		93.60
24	3,129	28.36	13.7		104.61
25	10,380	75.00	10.9	Upper Marker	113.00

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**Electropherogram Summary Continued ...****... Region table for sample 2 : TRB1.R429Q+T3.3**

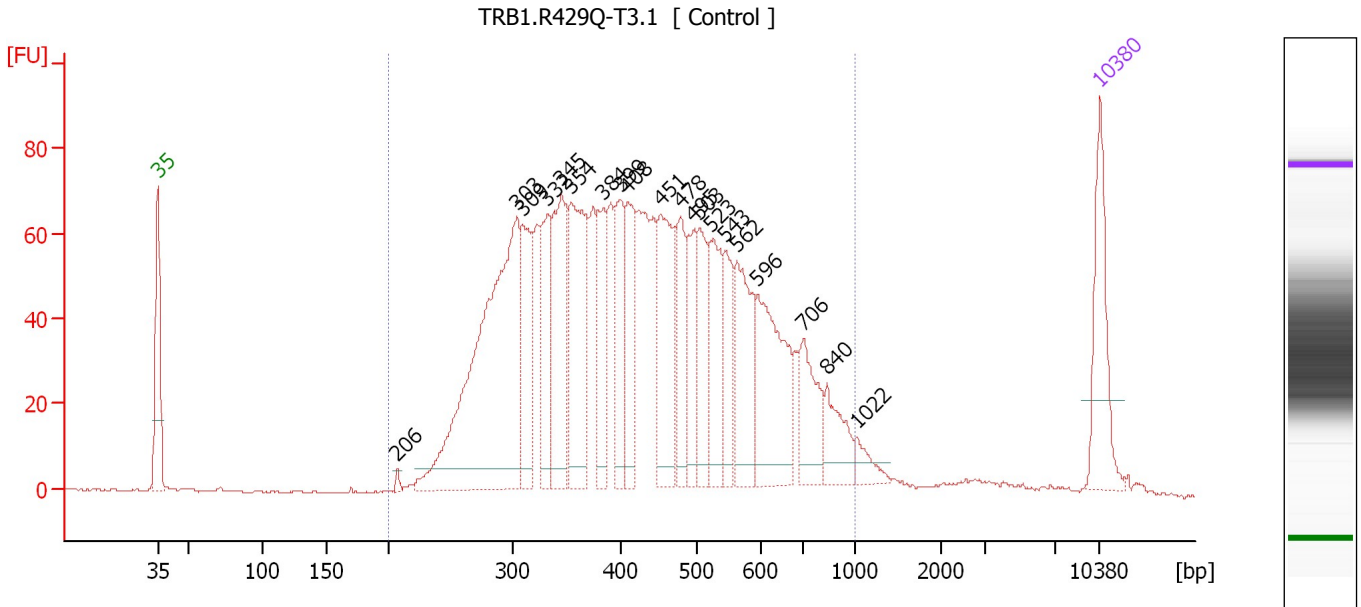
<b>From [bp]</b>	<b>Average Size [bp]</b>	<b>To [bp]</b>	<b>Corr. Area</b>	<b>Molarity [pmol/l]</b>	<b>% of Total</b>	<b>Size distribution in CV [%]</b>	<b>Conc. [pg/μl]</b>	<b>Co lor</b>
200	489	1,000	4,062.0	18,785.0	92	36.3	5,080.64	■



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**Electropherogram Summary Continued ...**



**Overall Results for sample 3 : TRB1.R429Q-T3.1**

Number of peaks found: 20                      Corr. Area 1: 2,080.2  
 Noise: 0.3

**Peak table for sample 3 : TRB1.R429Q-T3.1**

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	35	125.00	5,411.3	Lower Marker	43.00
2	206	4.68	34.5		60.75
3	303	496.52	2,479.1		69.65
4	309	98.48	483.2		70.08
5	332	90.68	414.1		71.93
6	345	158.79	697.8		72.98
7	354	171.60	735.2		73.69
8	384	82.46	325.5		76.12
9	399	81.72	310.2		77.36
10	408	91.03	338.1		77.88
11	451	141.54	475.8		80.31
12	478	75.07	237.7		81.88
13	495	67.37	206.2		82.83
14	503	75.16	226.3		83.26
15	523	94.23	273.2		84.16
16	543	60.59	169.1		85.11
17	562	109.43	294.8		86.02
18	596	145.54	370.0		87.59
19	706	71.60	153.7		90.97
20	840	46.56	84.0		92.73
21	1,022	17.44	25.8		94.96
22	10,380	75.00	10.9	Upper Marker	113.00

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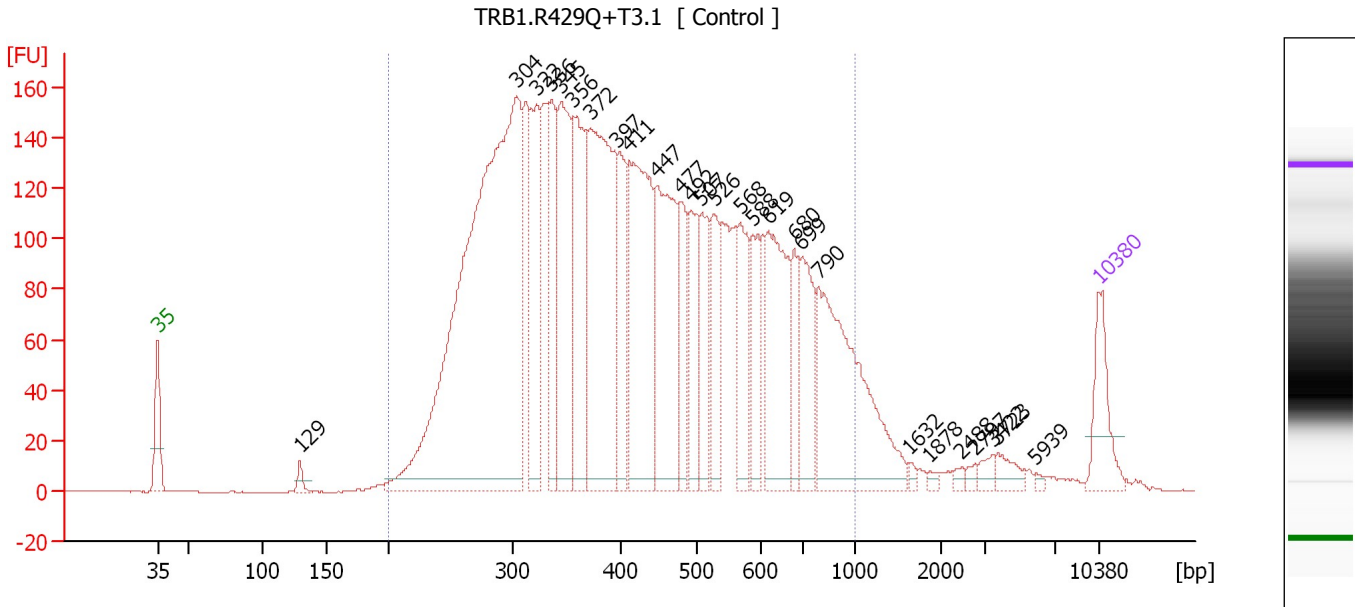
**Electropherogram Summary Continued ...****... Region table for sample 3 : TRB1.R429Q-T3.1**

<b>From [bp]</b>	<b>Average Size [bp]</b>	<b>To [bp]</b>	<b>Corr. Area</b>	<b>Molarity [pmol/l]</b>	<b>% of Total</b>	<b>Size distribution in CV [%]</b>	<b>Conc. [pg/<math>\mu</math>l]</b>	<b>Co lor</b>
200	447	1,000	2,080.2	10,512.7	96	32.5	2,716.00	■

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**Electropherogram Summary Continued ...**



**Overall Results for sample 4 : TRB1.R429Q+T3.1**

Number of peaks found: 27                      Corr. Area 1: 4,823.2  
 Noise: 0.3

**Peak table for sample 4 : TRB1.R429Q+T3.1**

Peak	Size [bp]	Conc. [pg/μl]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
1	35	125.00	5,411.3	Lower Marker	43.00
2	129	20.85	244.4		53.59
3	304	1,559.29	7,763.6		69.72
4	322	248.39	1,167.4		71.17
5	336	200.00	902.8		72.24
6	345	330.83	1,454.2		72.97
7	356	258.48	1,099.6		73.90
8	372	550.26	2,242.2		75.16
9	397	161.06	615.4		77.15
10	411	404.05	1,491.3		78.02
11	447	336.08	1,138.4		80.11
12	477	119.85	380.5		81.81
13	492	148.30	456.9		82.64
14	507	120.13	359.2		83.42
15	526	115.93	333.7		84.34
16	568	138.83	370.3		86.28
17	588	104.89	270.4		87.21
18	619	243.53	595.9		88.37
19	680	78.54	175.0		90.27
20	699	141.90	307.7		90.85
21	790	393.00	754.1		92.06
22	1,632	6.86	6.4		98.82
23	1,878	6.06	4.9		100.37
24	2,488	7.64	4.7		102.75
25	2,797	6.86	3.7		103.77

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**Electropherogram Summary Continued ...**

**... Peak table for sample 4 : TRB1.R429Q+T3.1**

Peak	Size [bp]	Conc. [pg/ $\mu$ l]	Molarity [pmol/l]	Observations	Aligned Migration Time [s]
26	3,422	14.25	6.3		104.98
27	3,723	23.19	9.4		105.37
28	5,939	4.03	1.0		108.24
29	10,380	75.00	10.9	Upper Marker	113.00

**Region table for sample 4 : TRB1.R429Q+T3.1**

From [bp]	Average Size [bp]	To [bp]	Corr. Area	Molarity [pmol/l]	% of Total	Size distribution in CV [%]	Conc. [pg/ $\mu$ l]	Color
200	446	1,000	4,823.2	24,920.8	94	36.9	6,211.13	

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**Gel Image**