Fig. 1

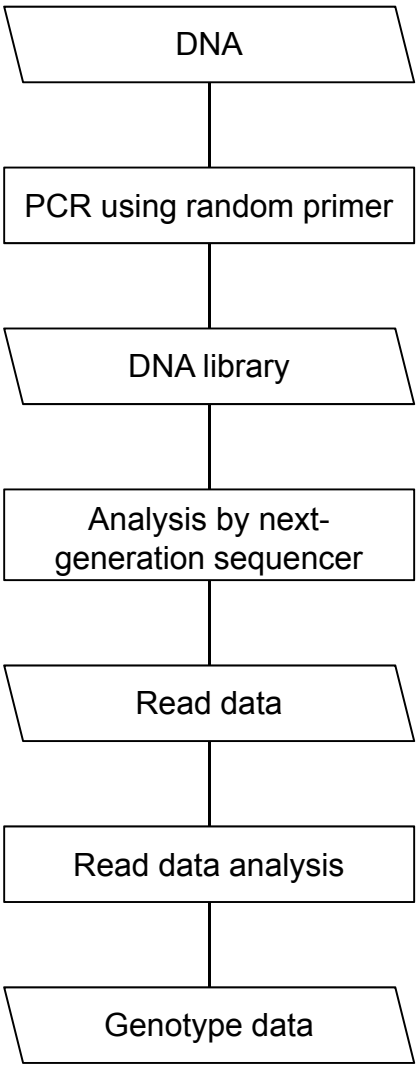

DNA
PCR using random primer
DNA library
Analysis by next-generation sequencer
Read data
Read data analysis
Genotype data

Fig. 2

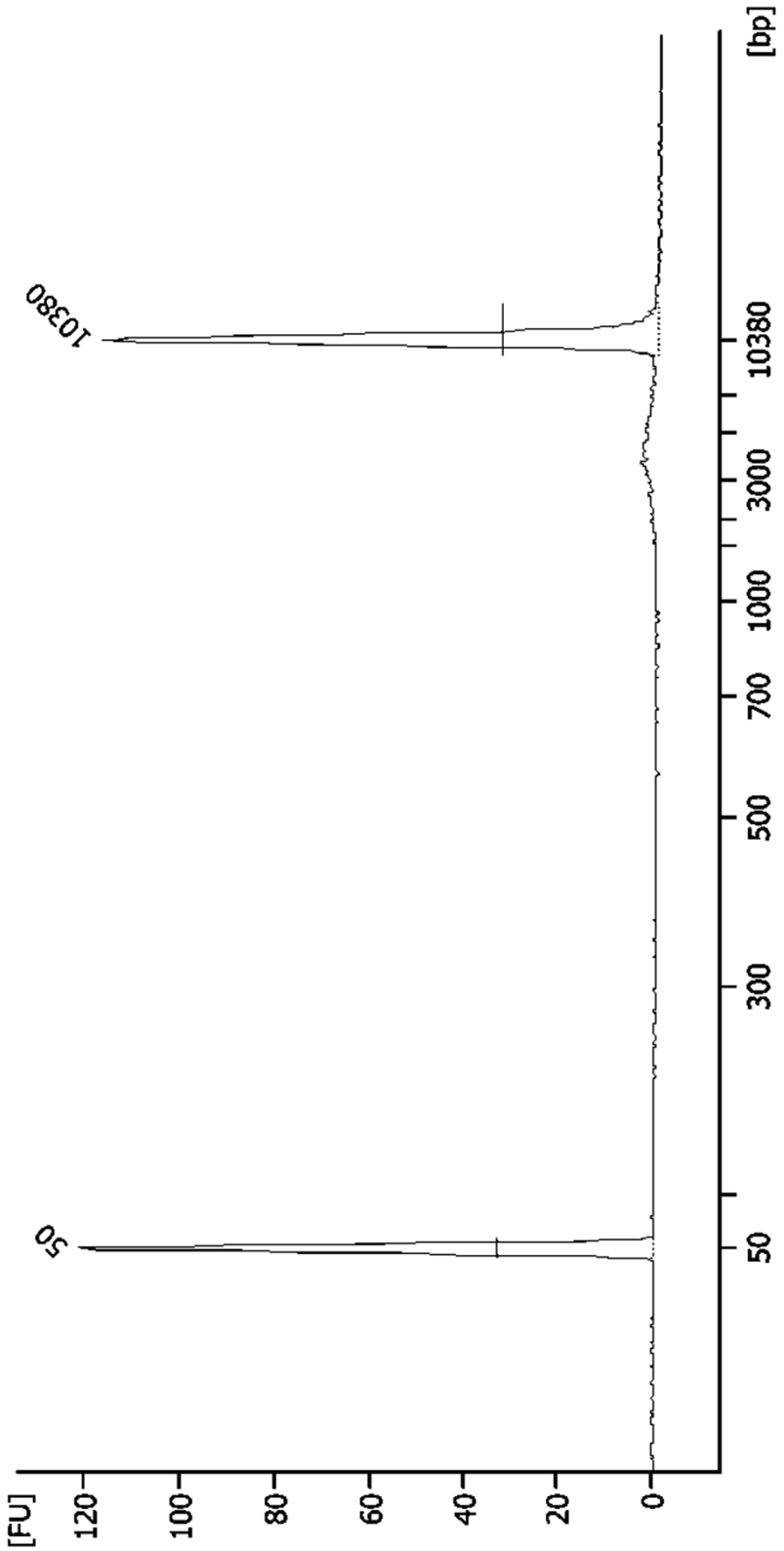

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Fig. 3

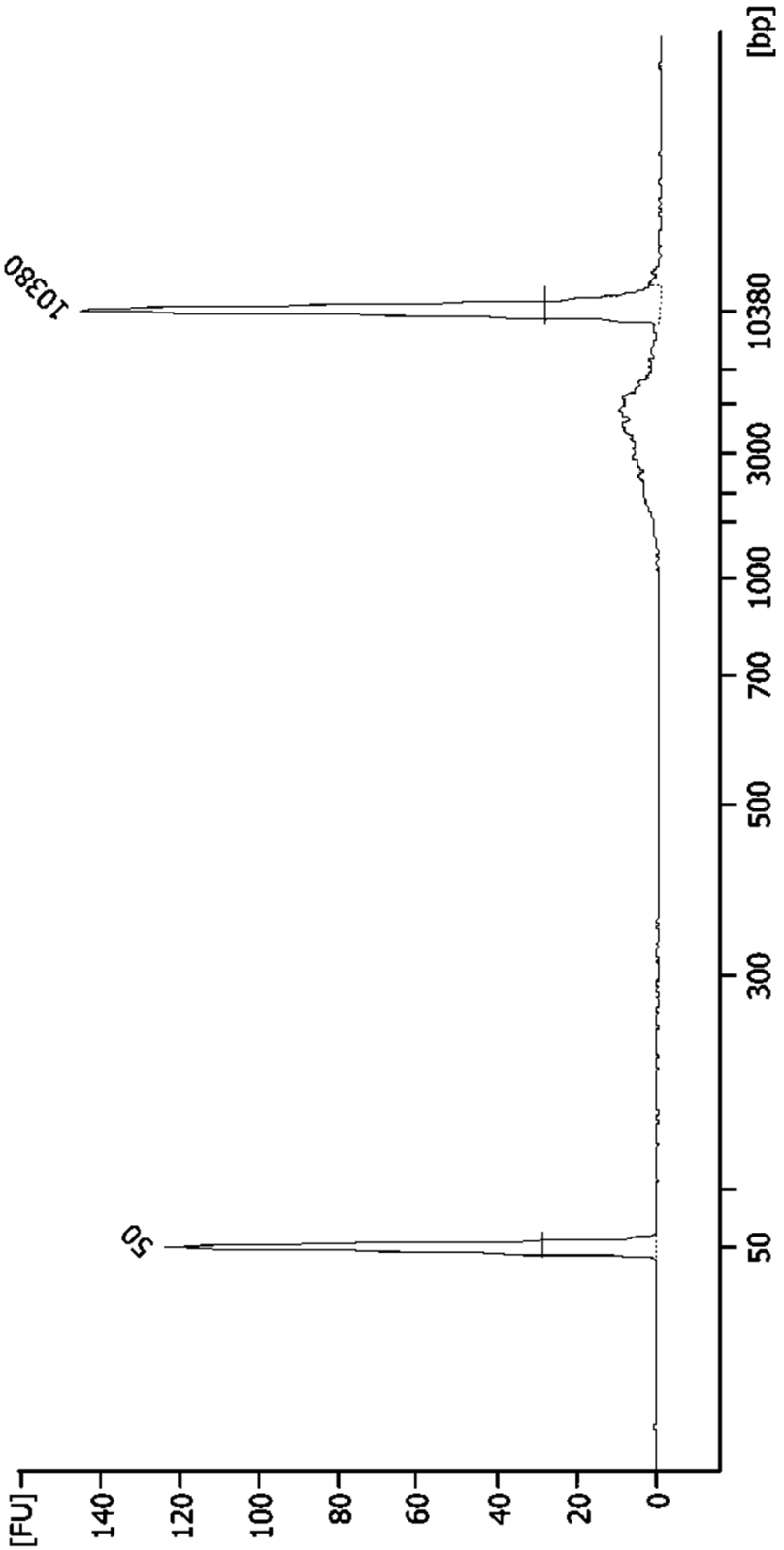

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Fig. 4

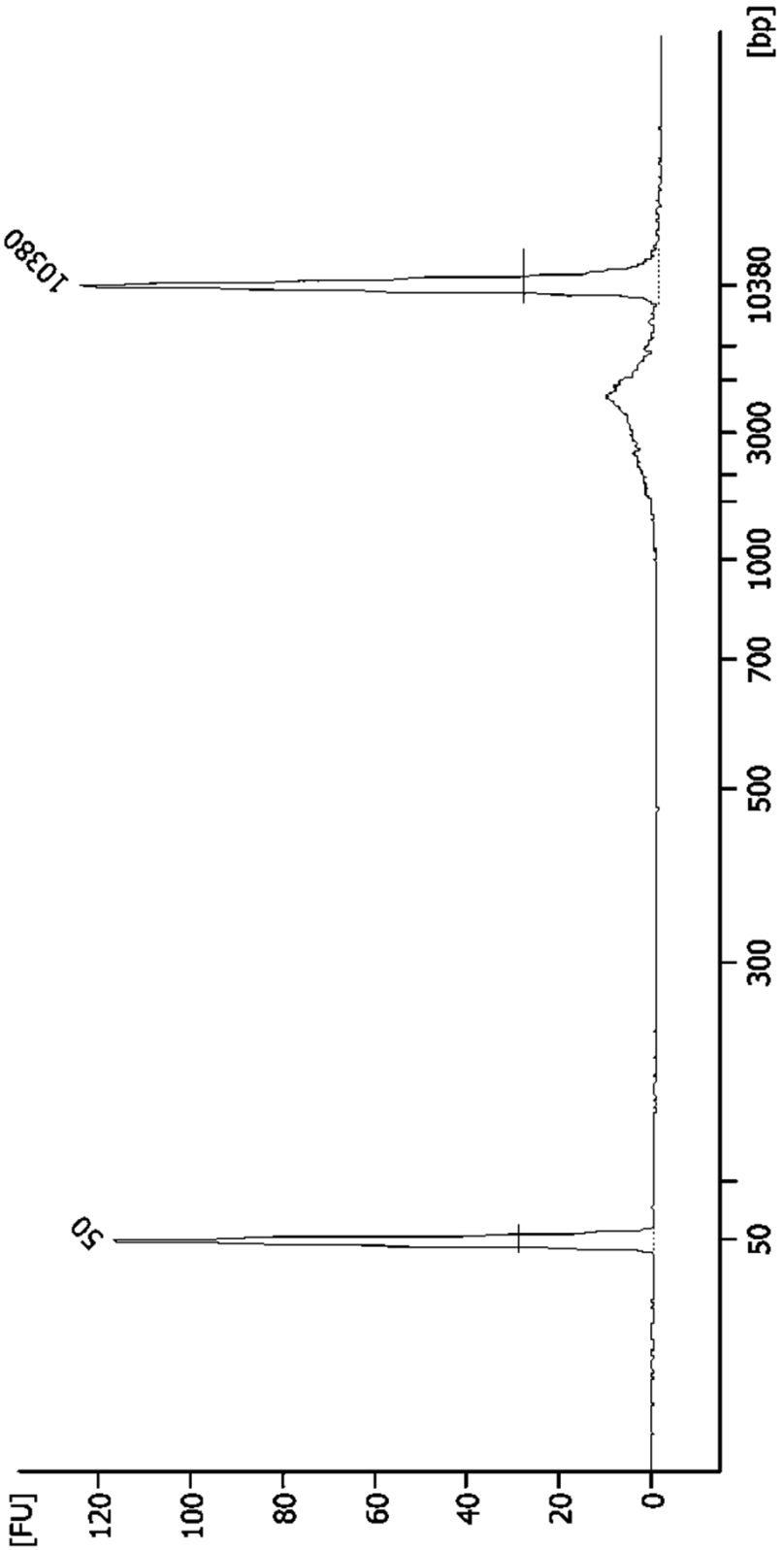

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Fig. 5

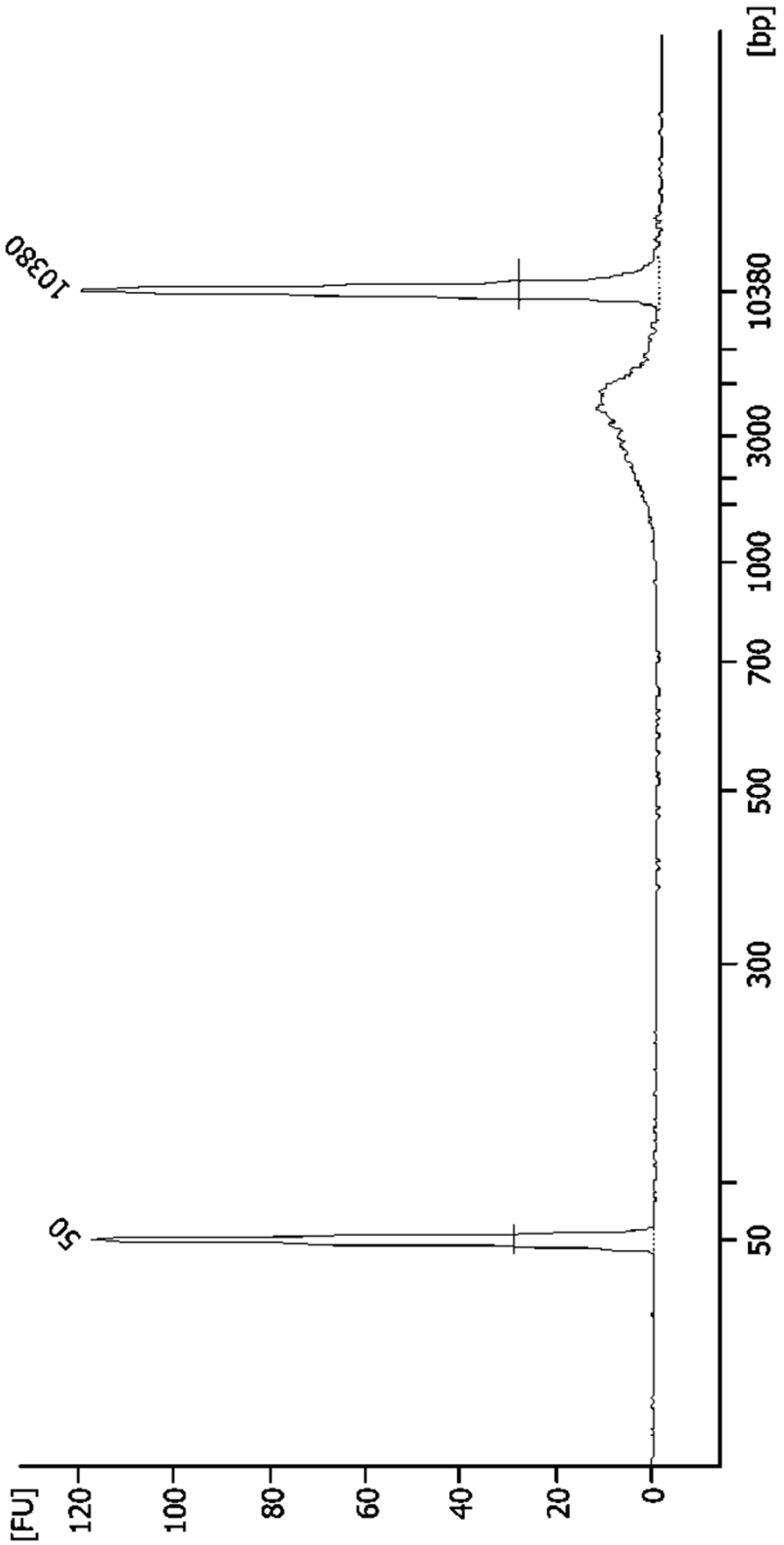

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Fig. 6

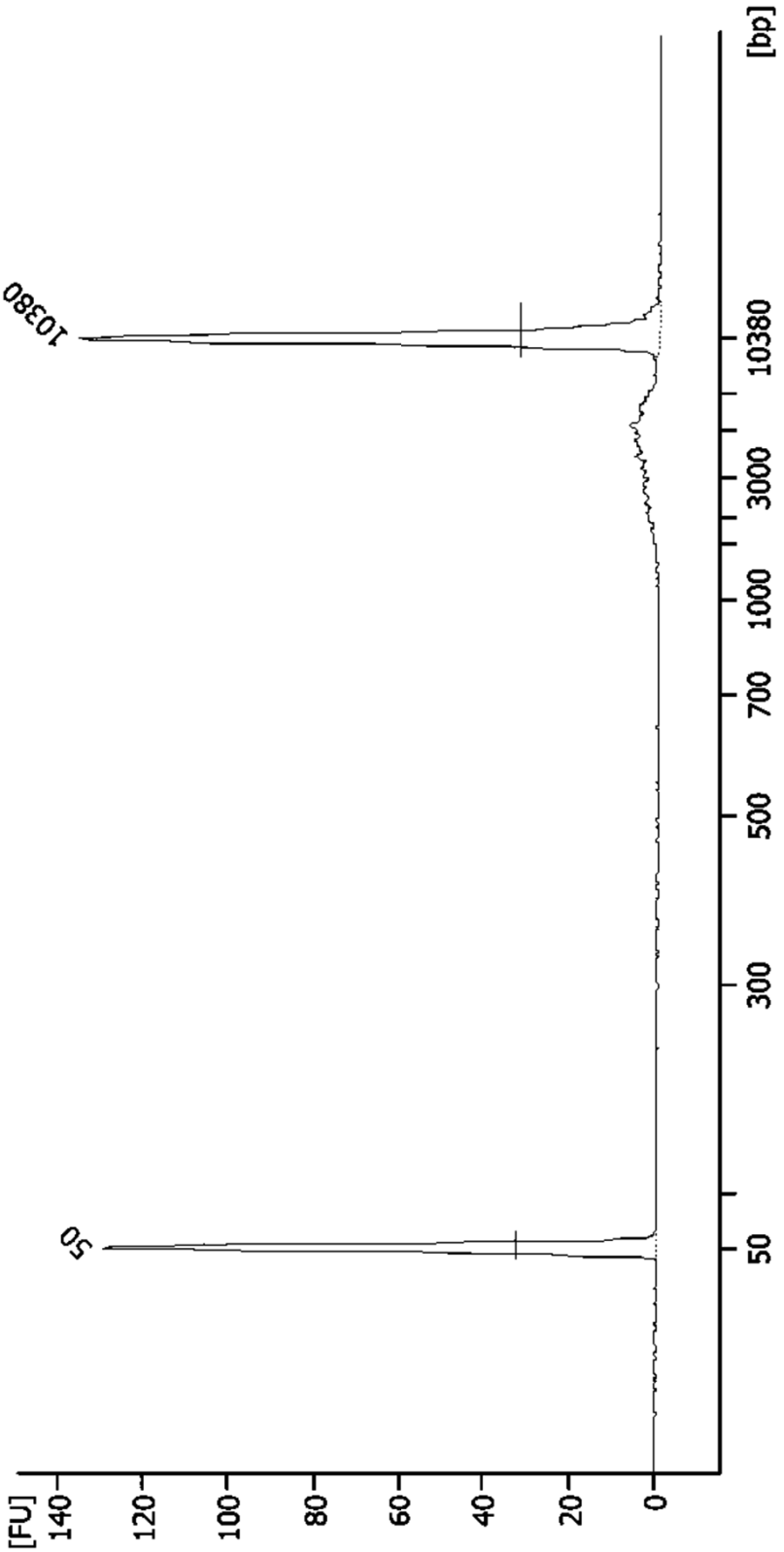

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Fig. 7

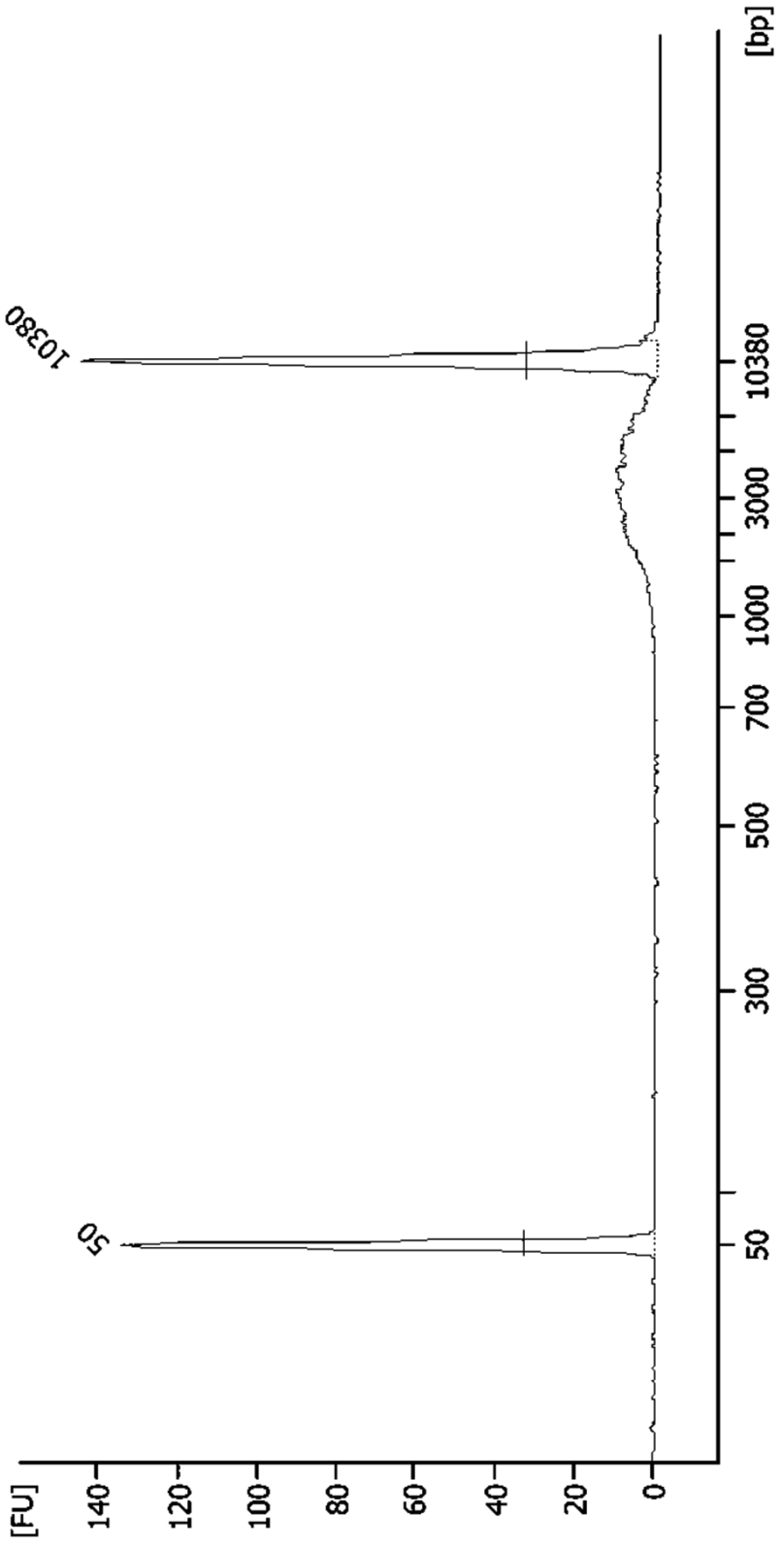

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Fig. 8

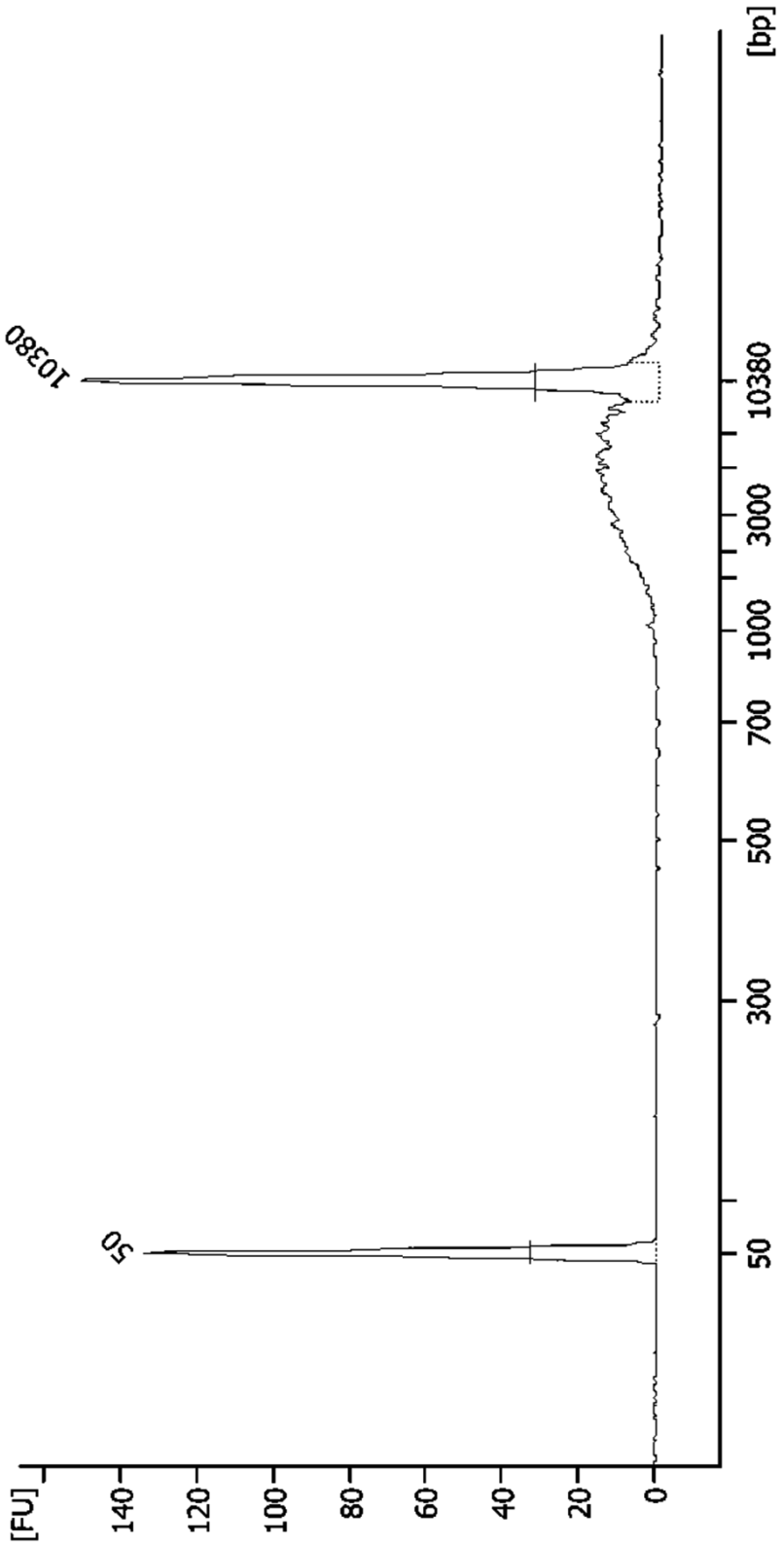

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Fig. 9

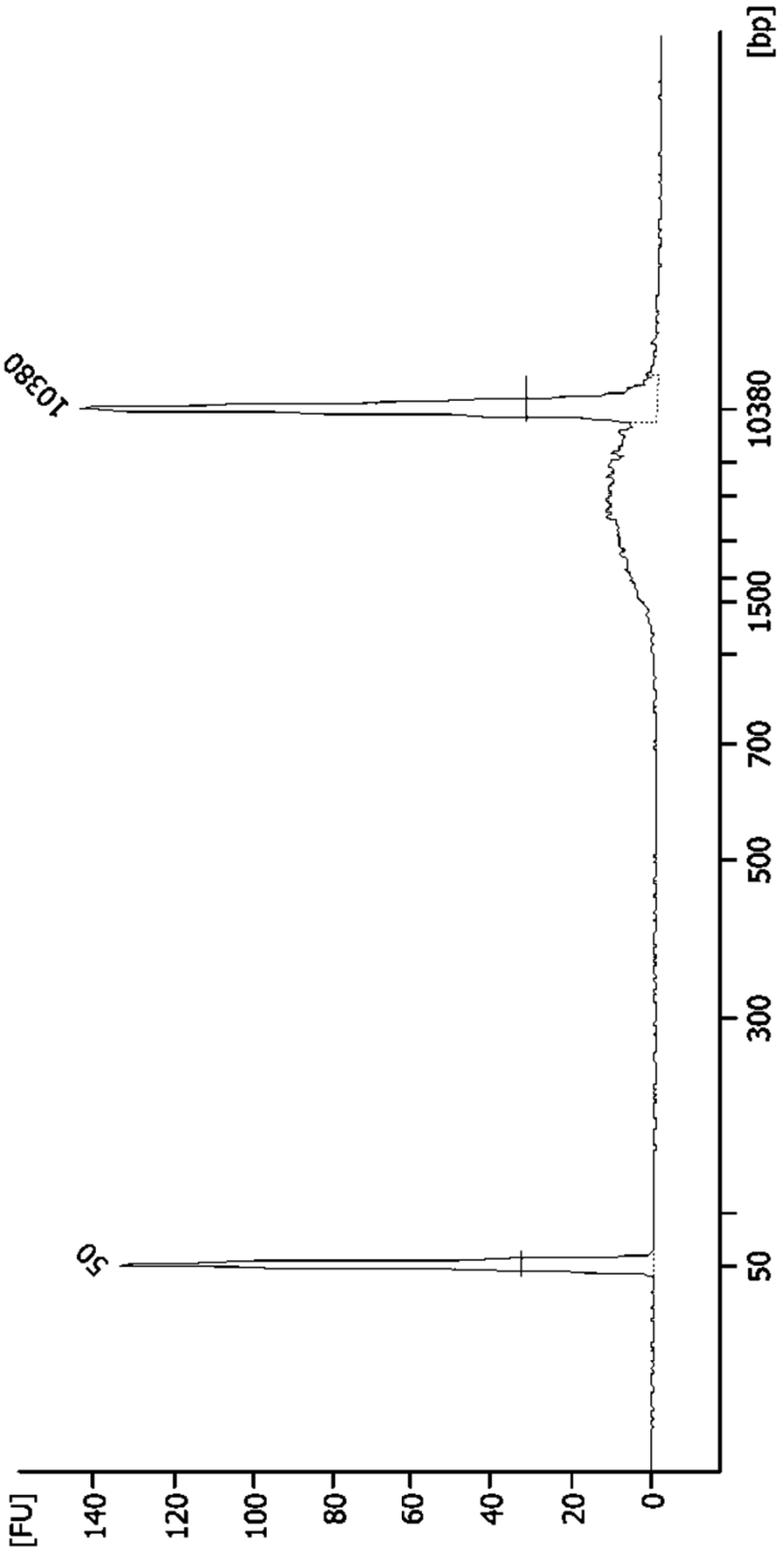


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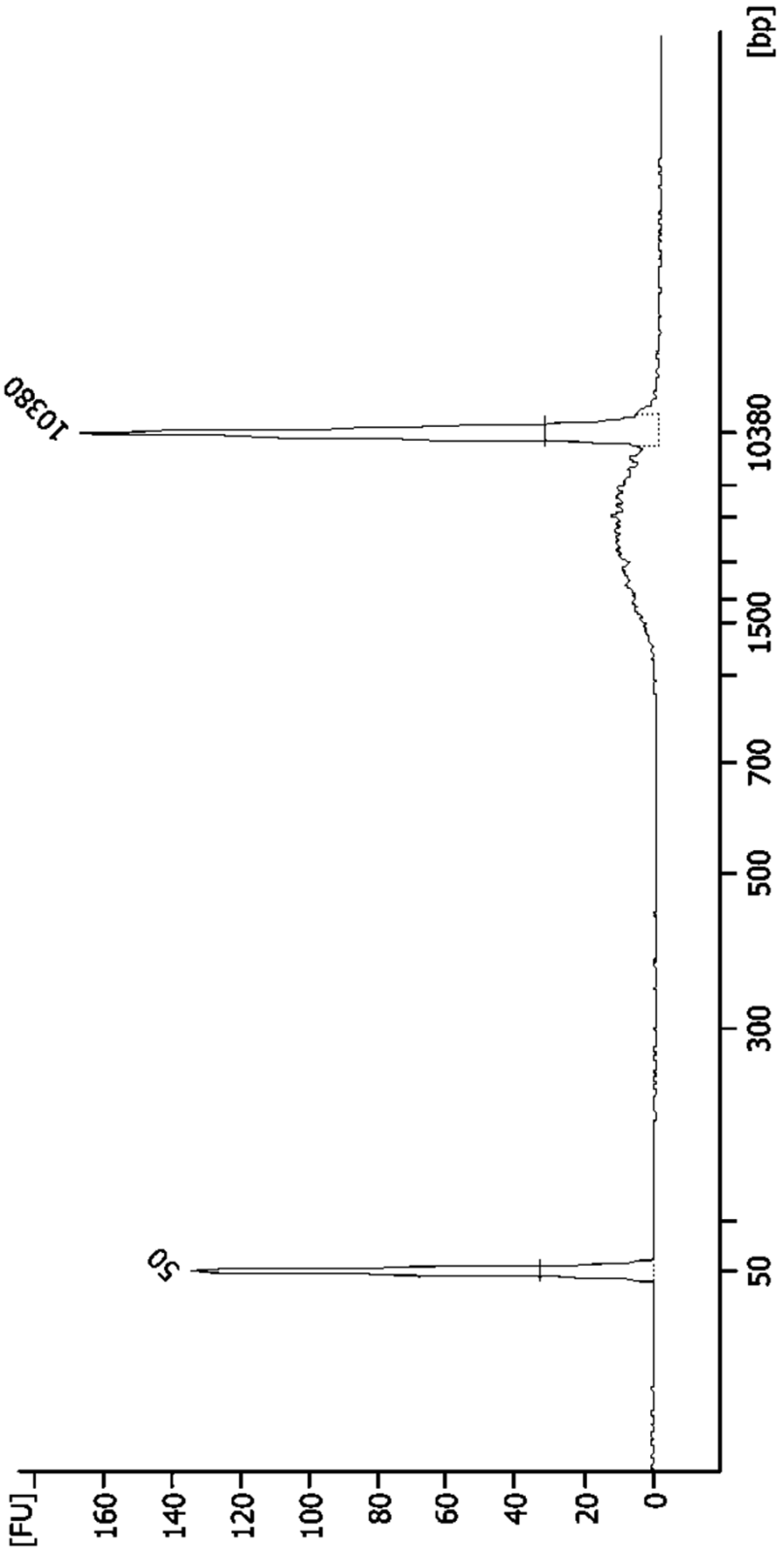

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Fig. 11

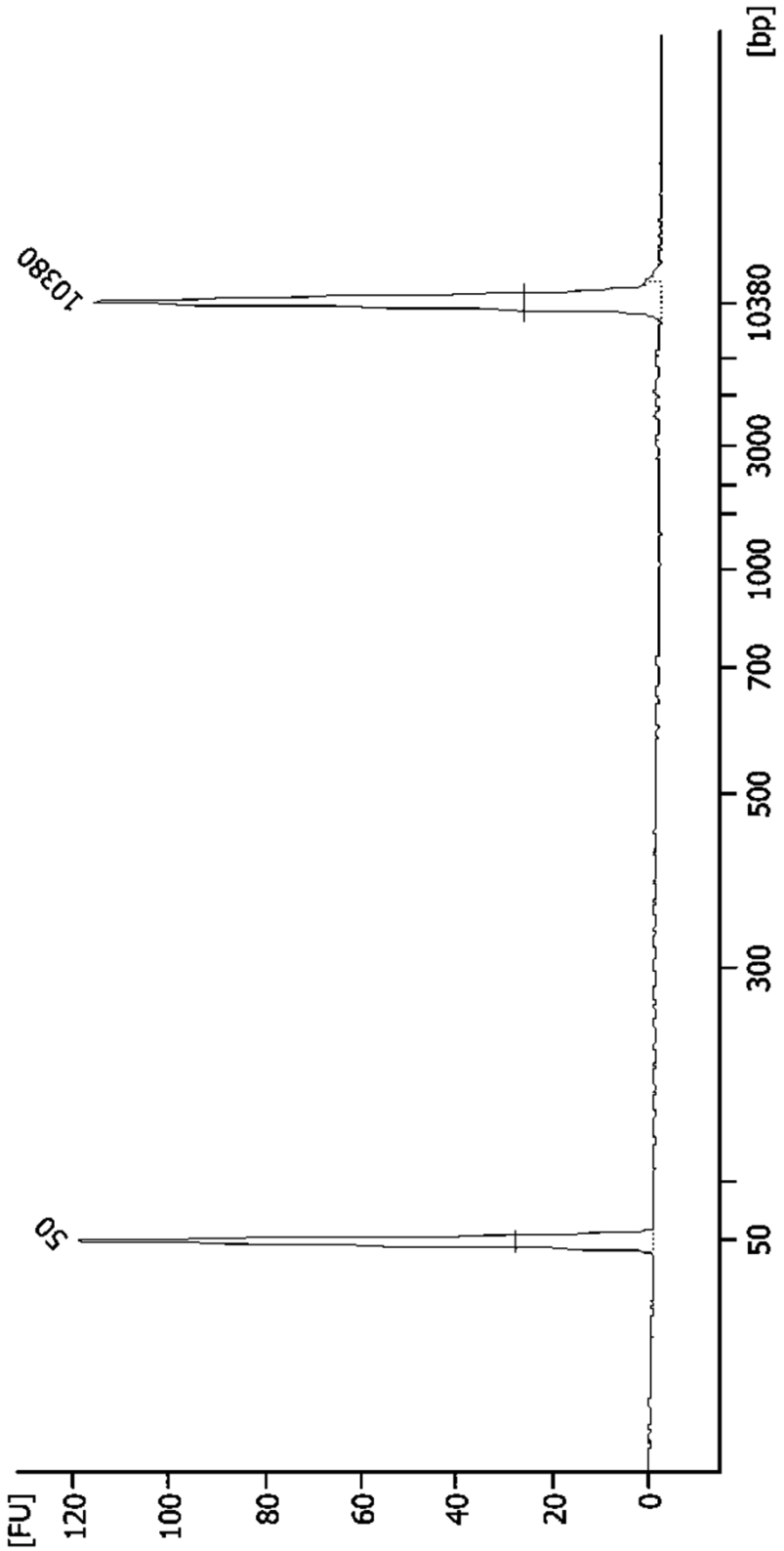

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Fig. 12

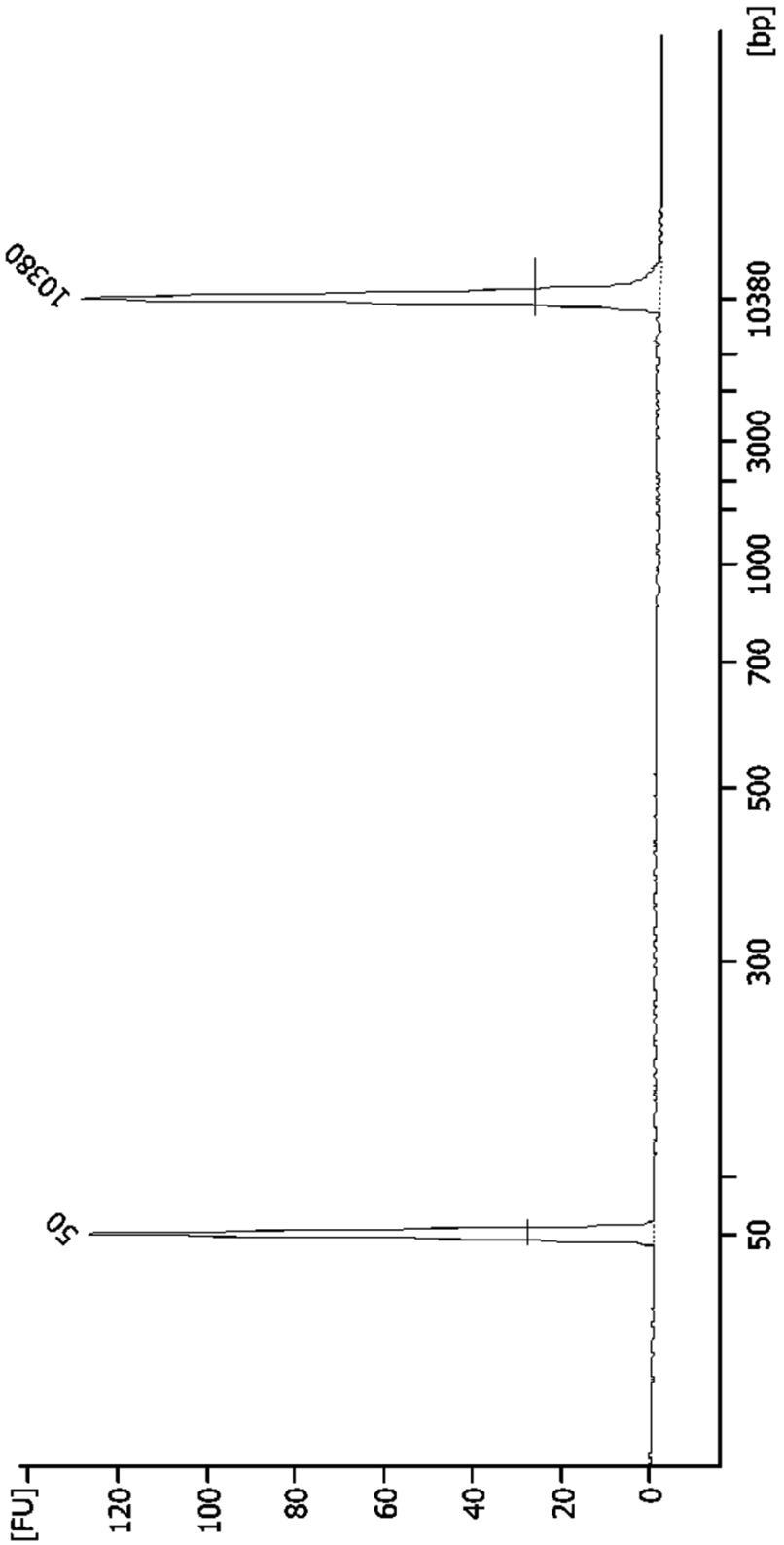

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Fig. 13

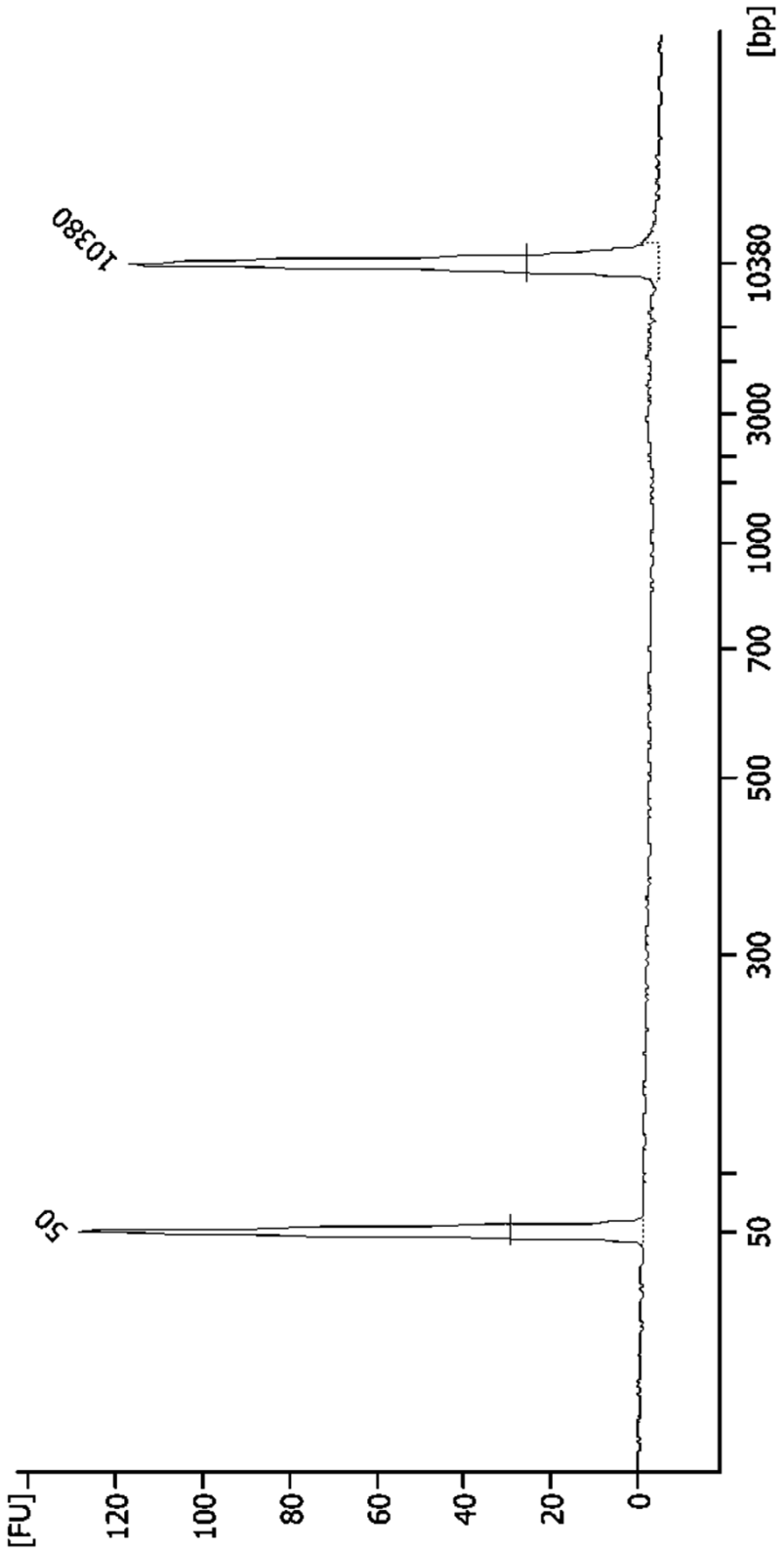

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Fig. 14

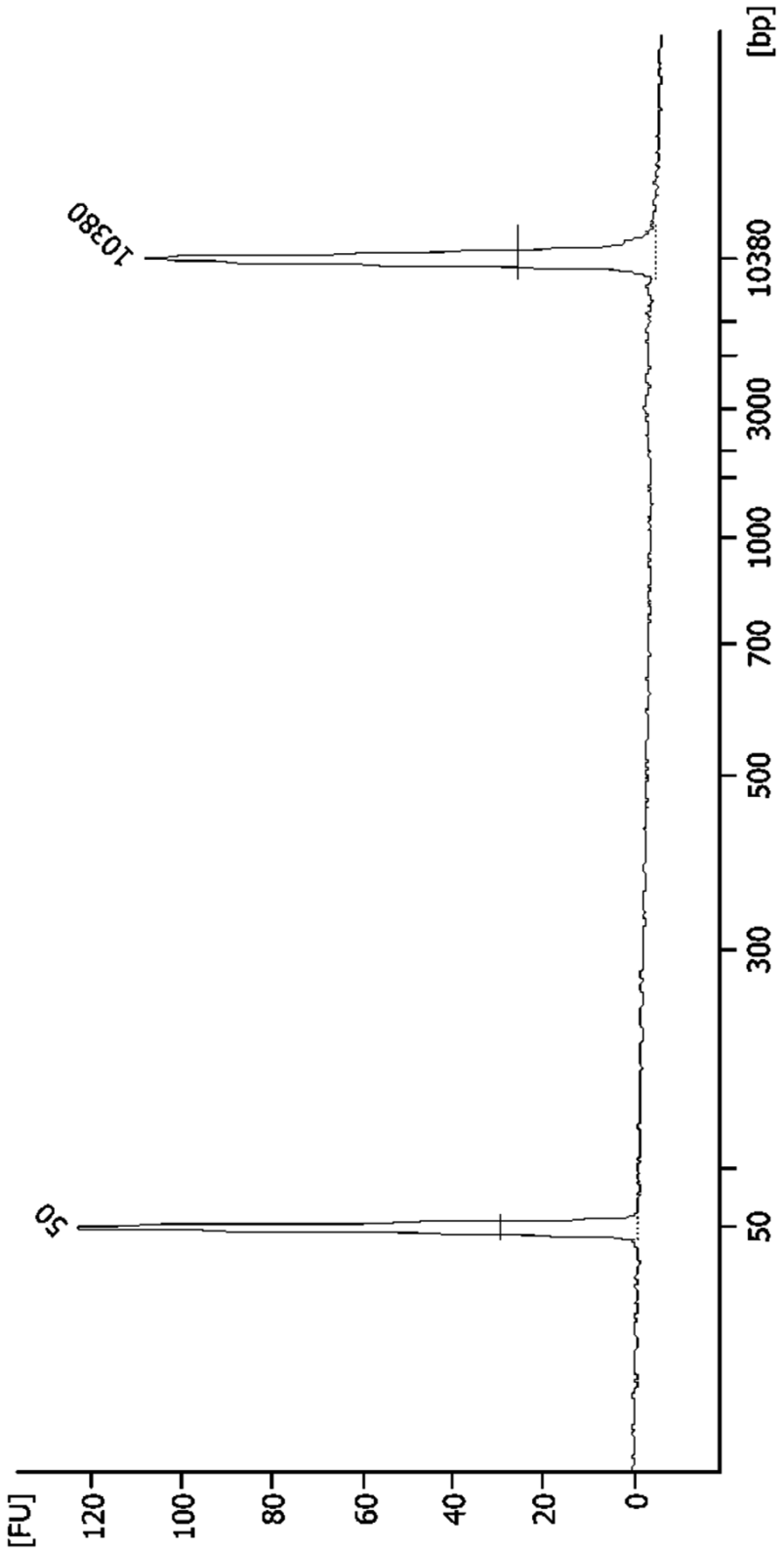

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Fig. 15

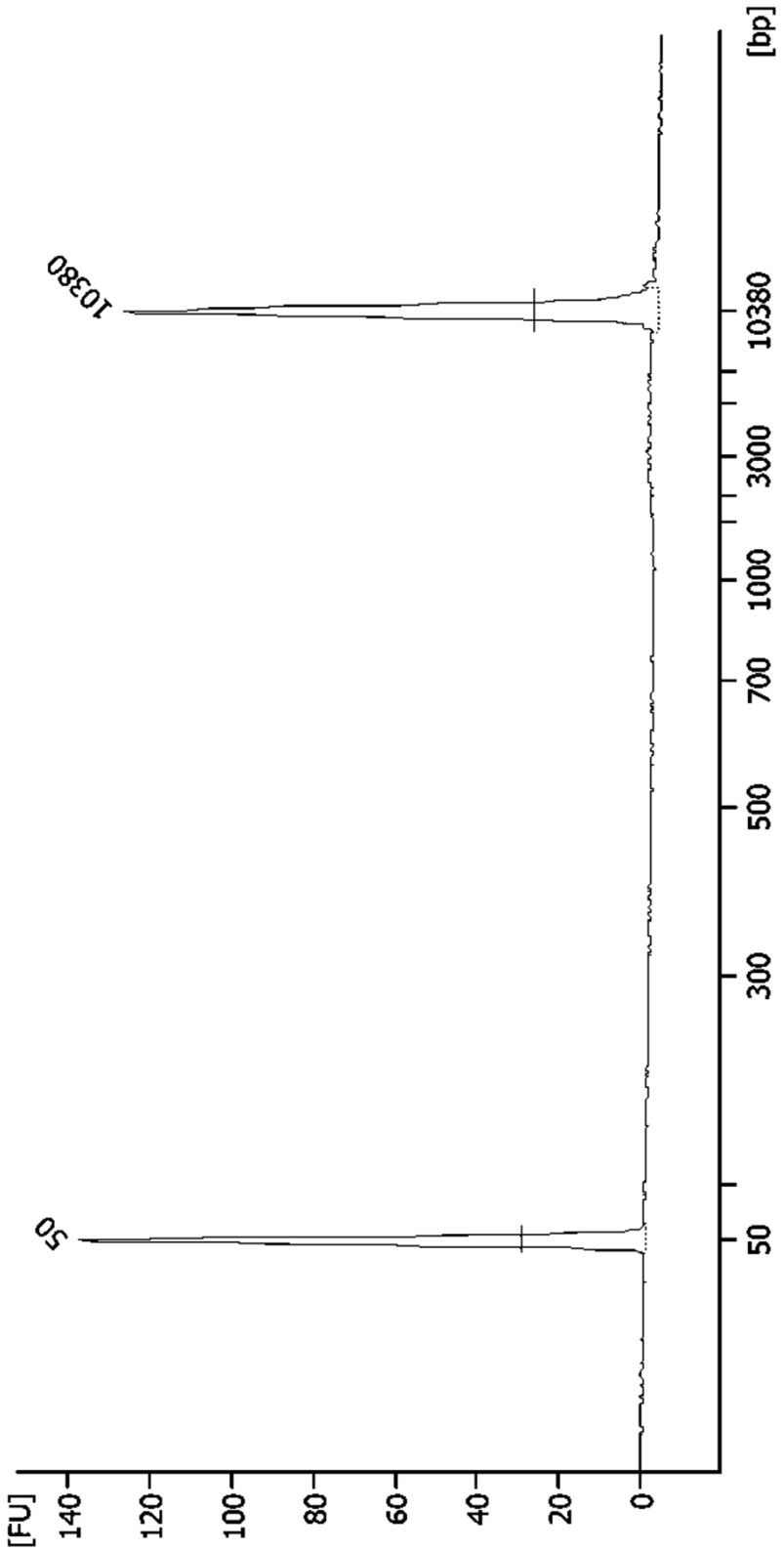

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Fig. 16

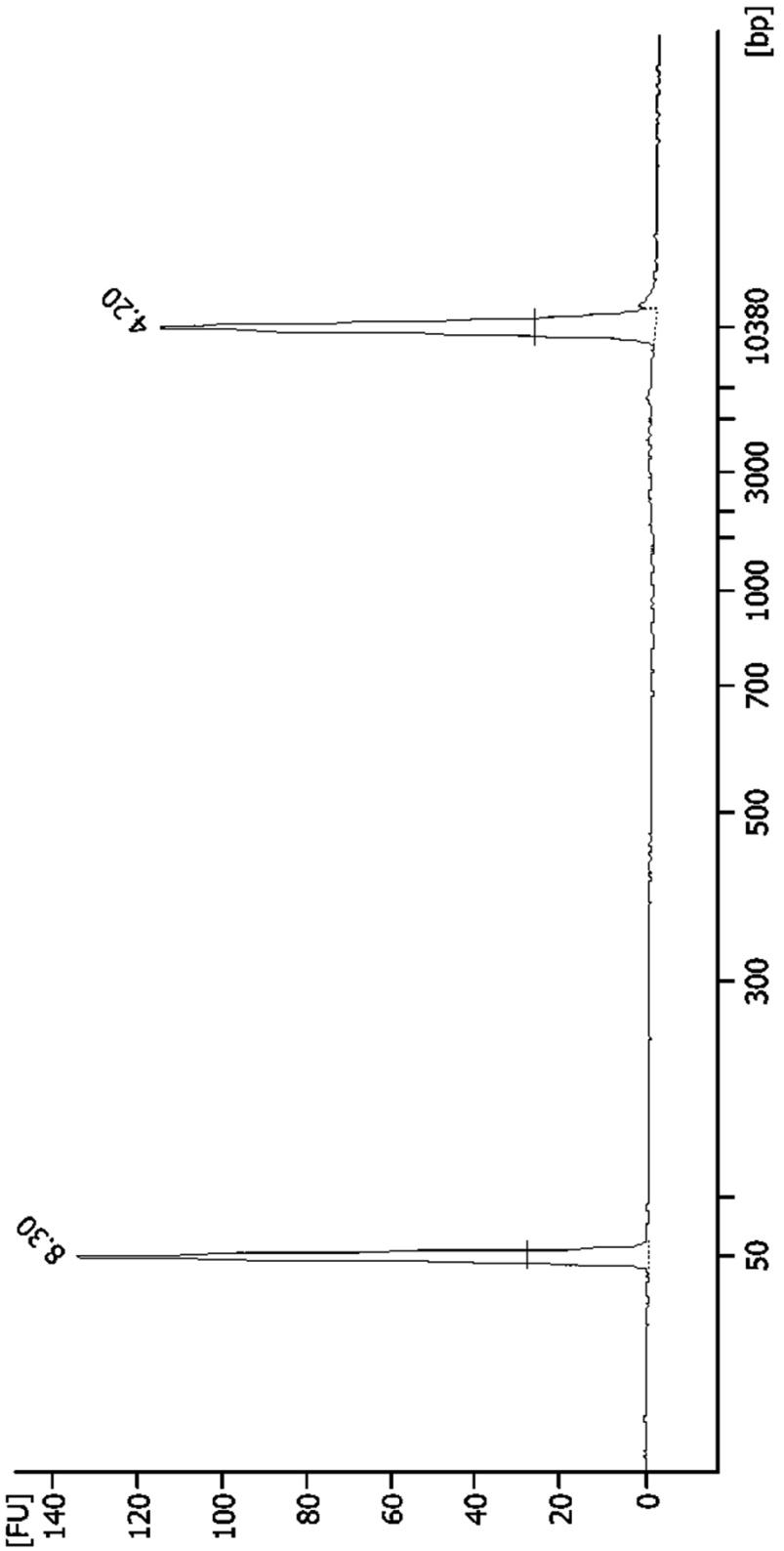

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Fig. 17

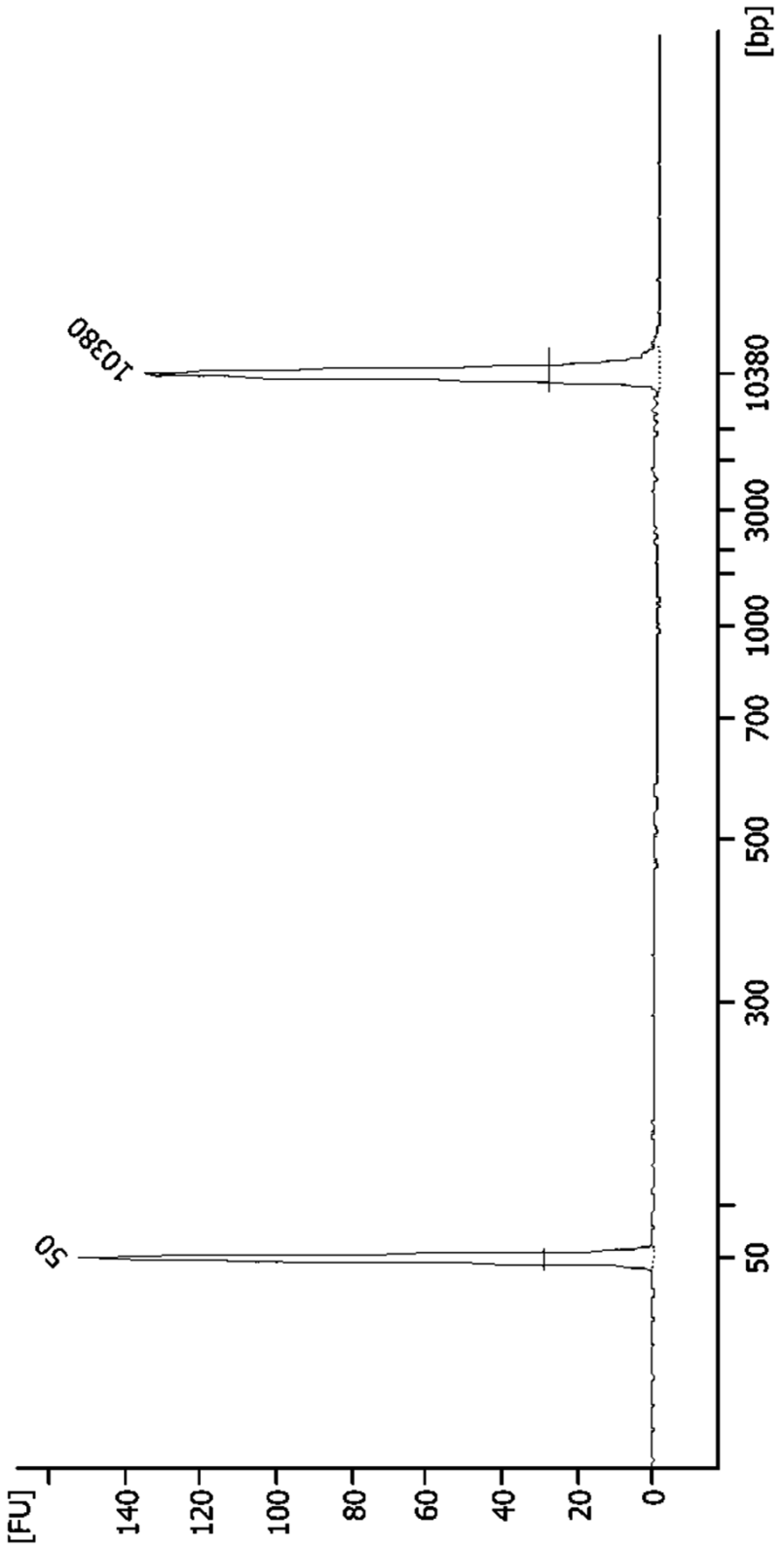

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Fig. 18

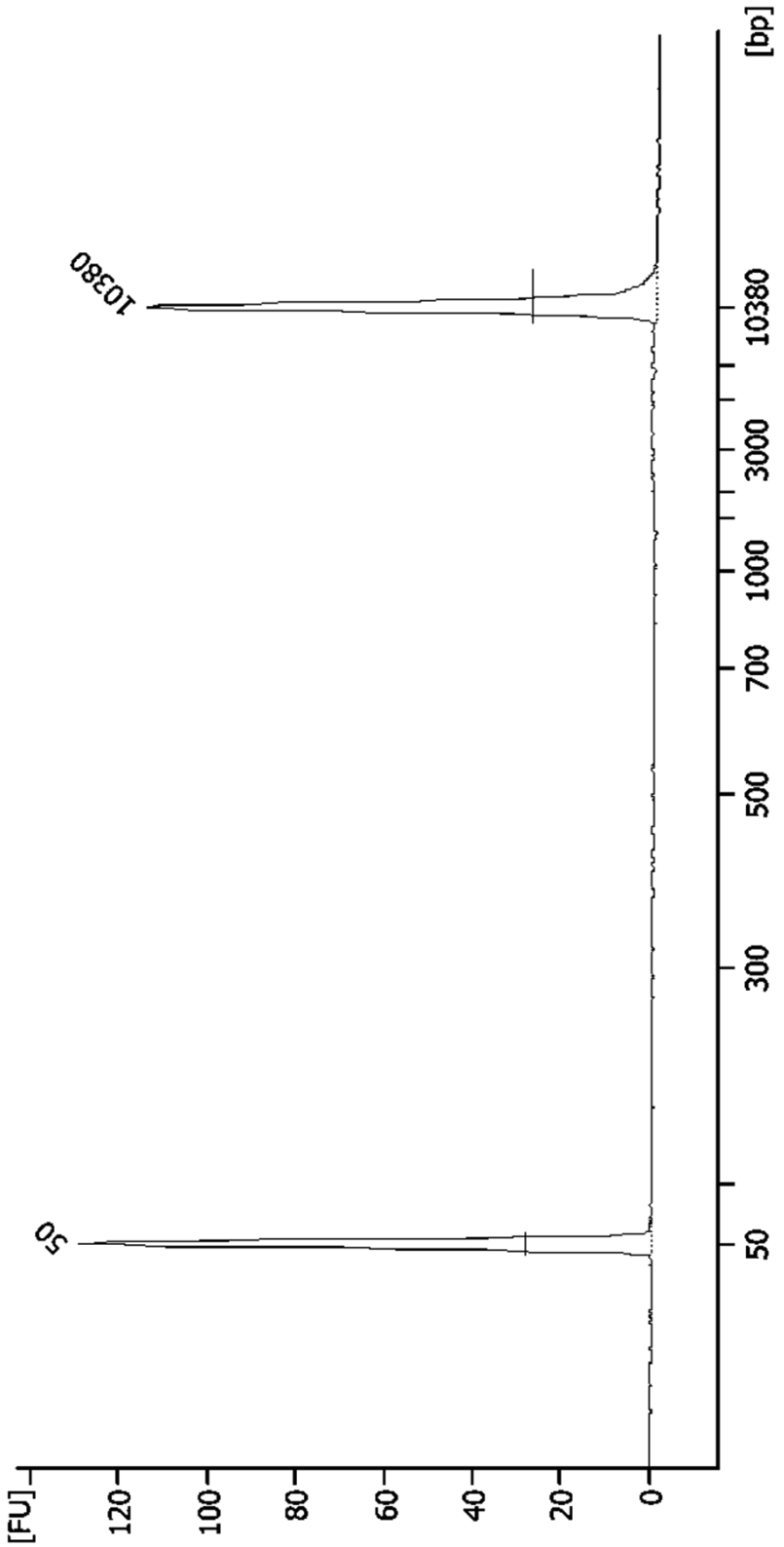

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Fig. 19

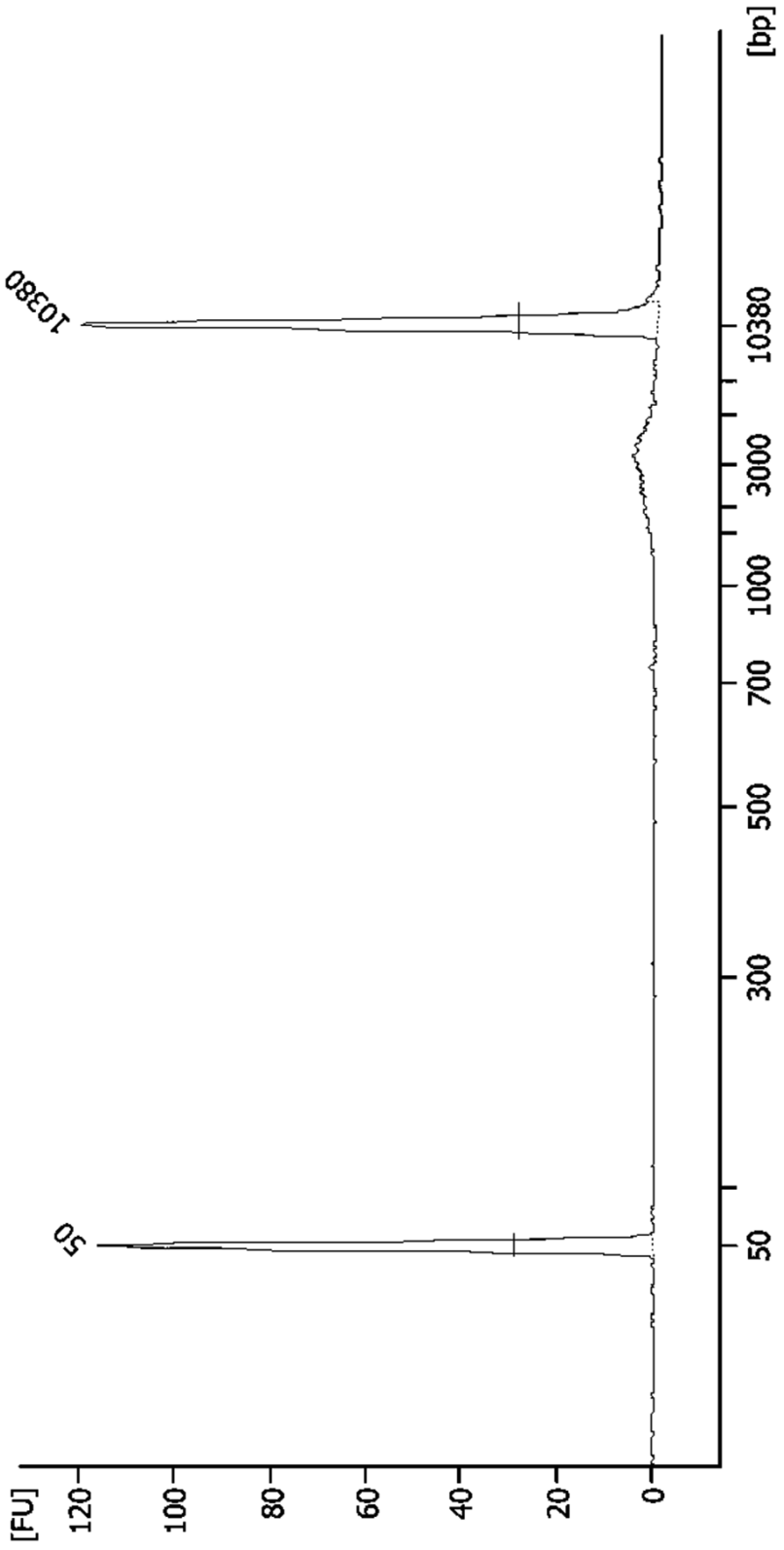

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Fig. 20

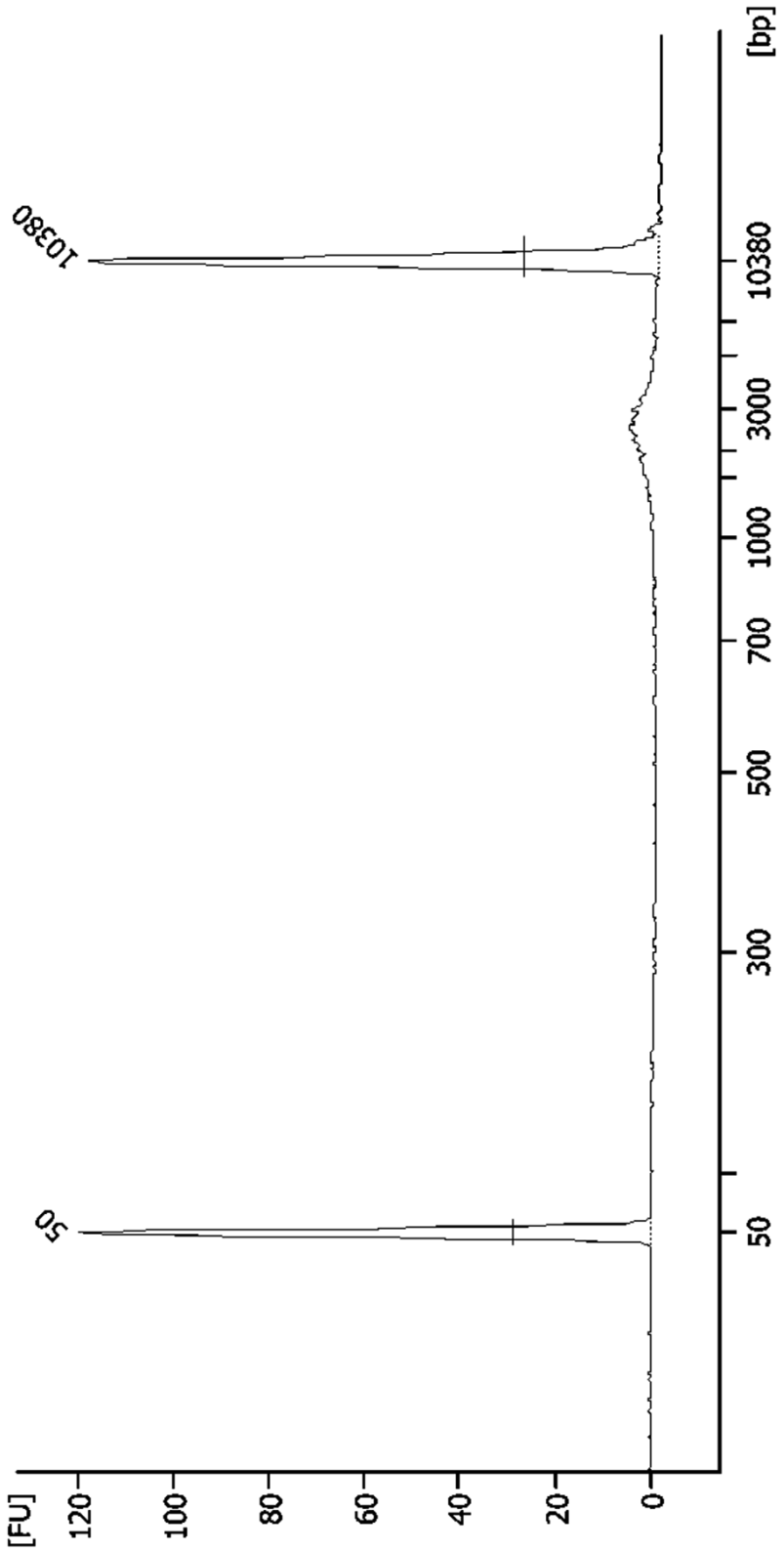

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Fig. 21

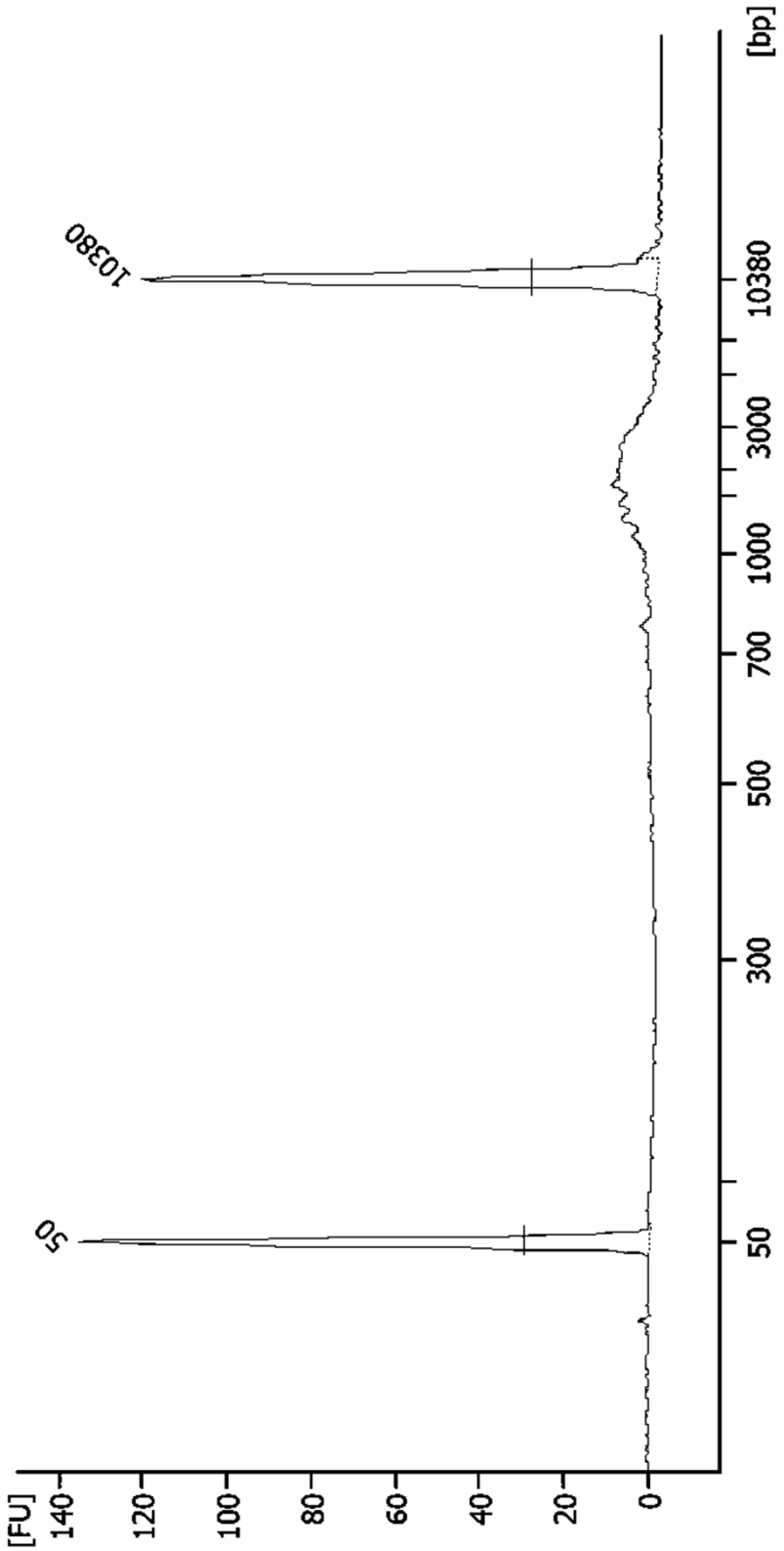

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Fig. 22

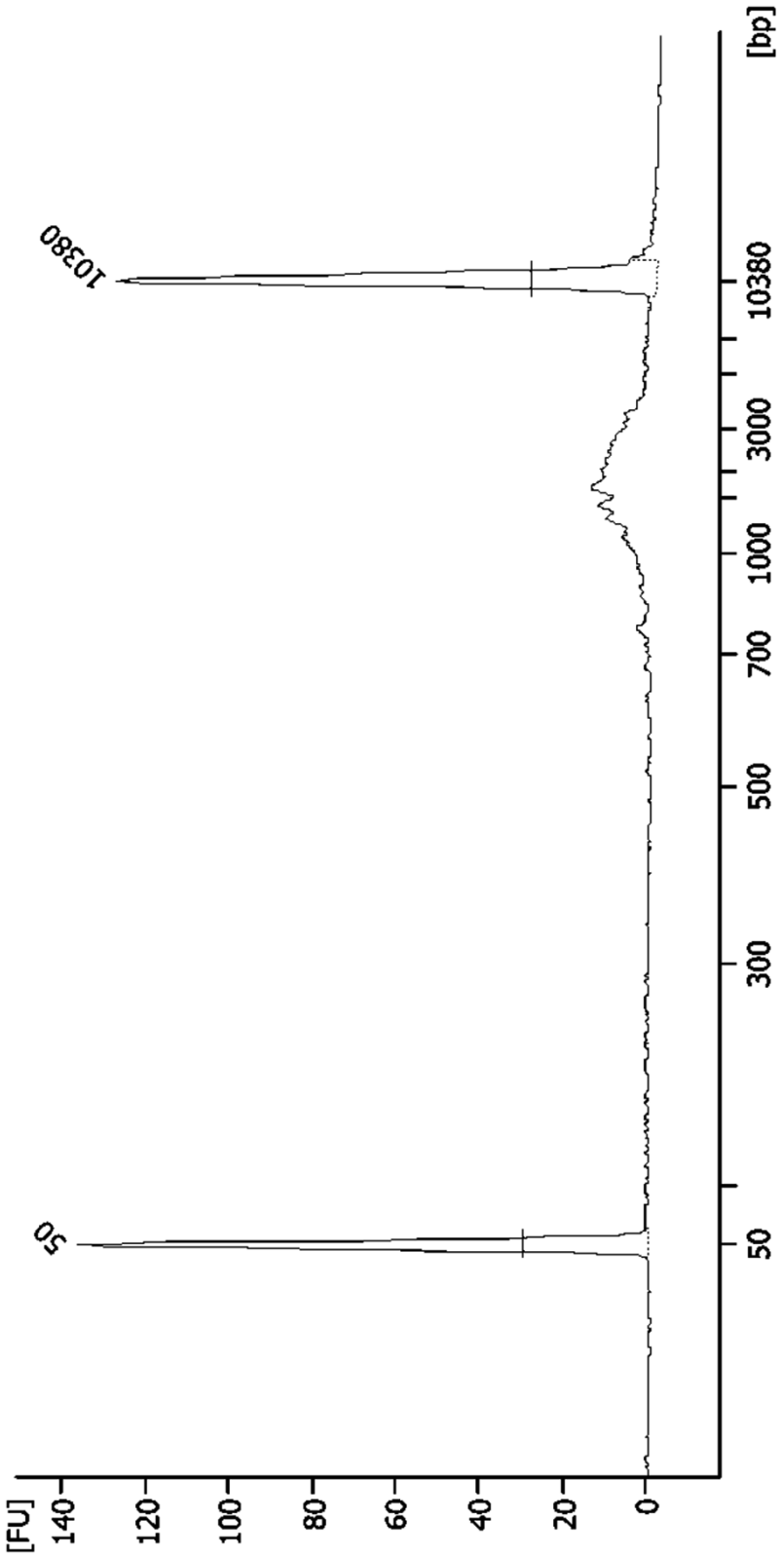

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Fig. 23

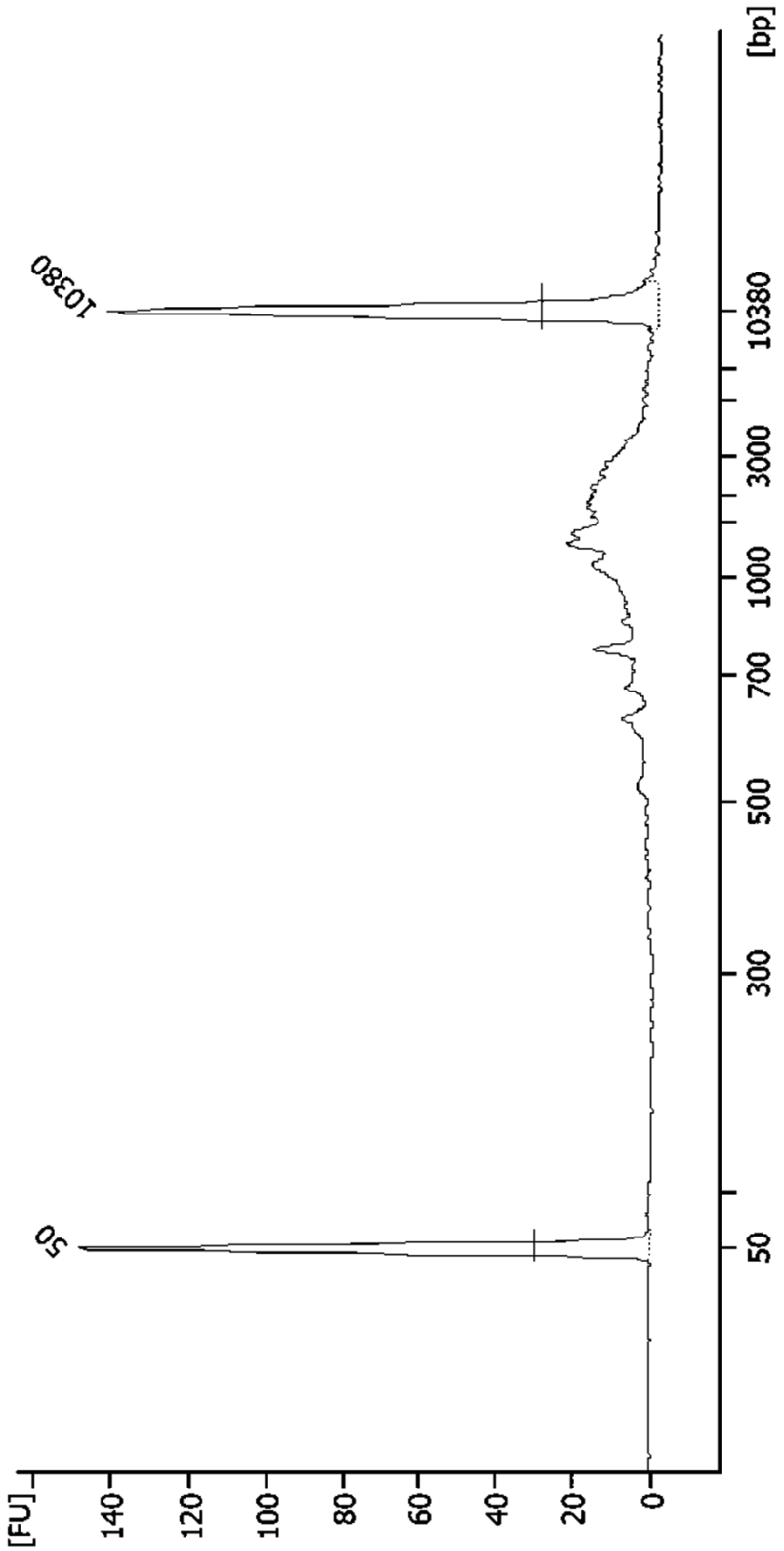

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Fig. 24

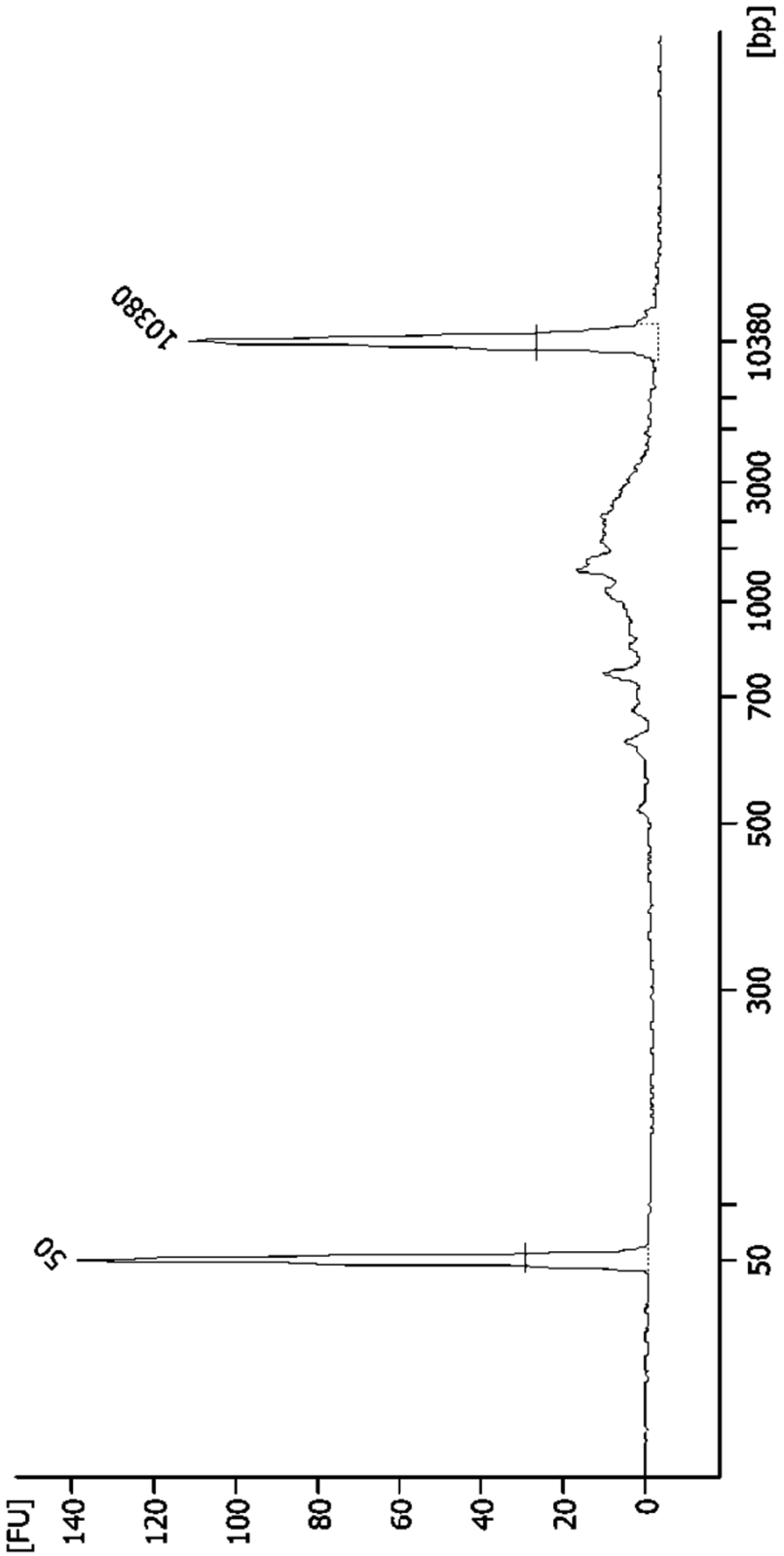

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Fig. 25

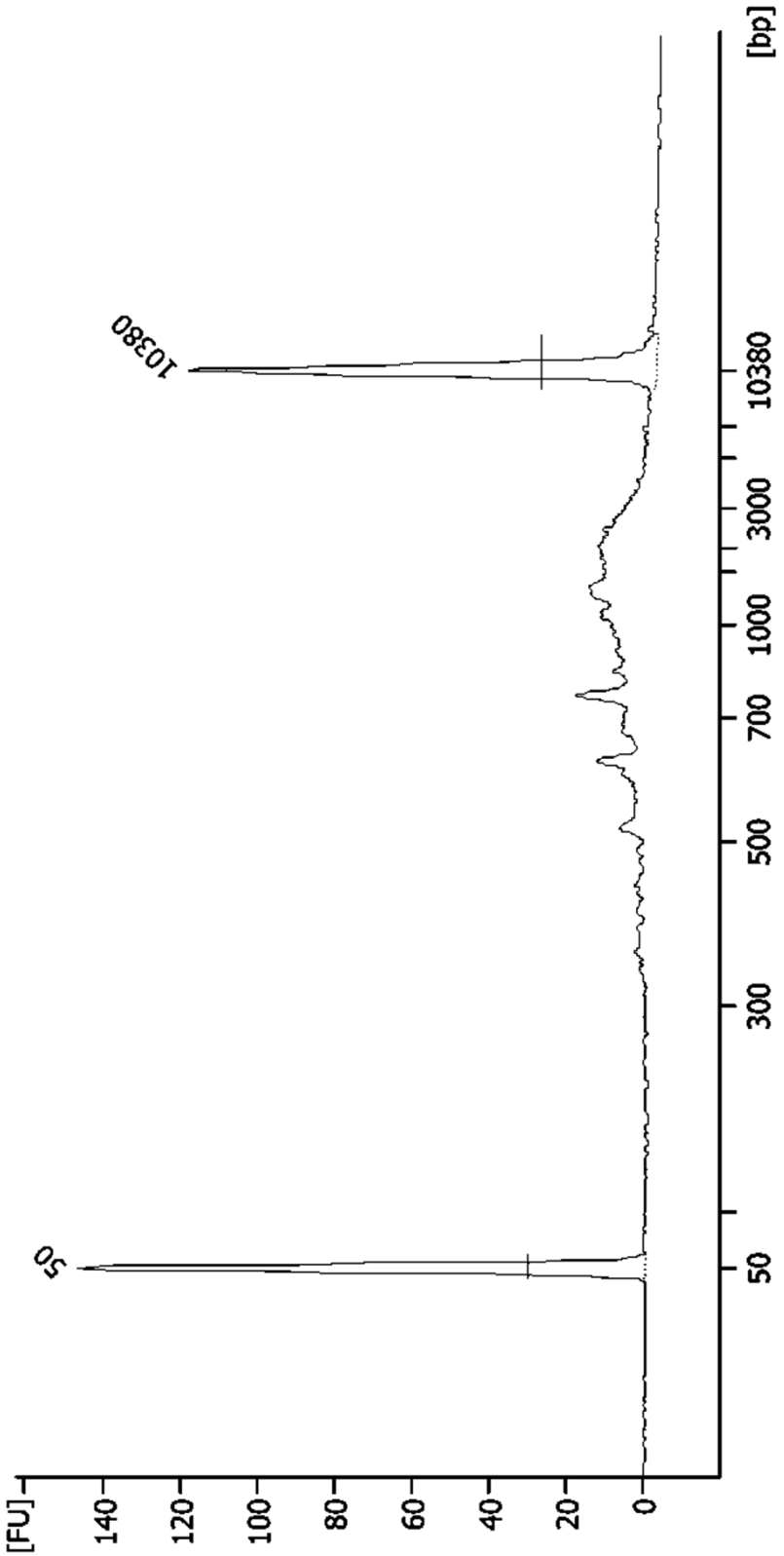

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Fig. 26

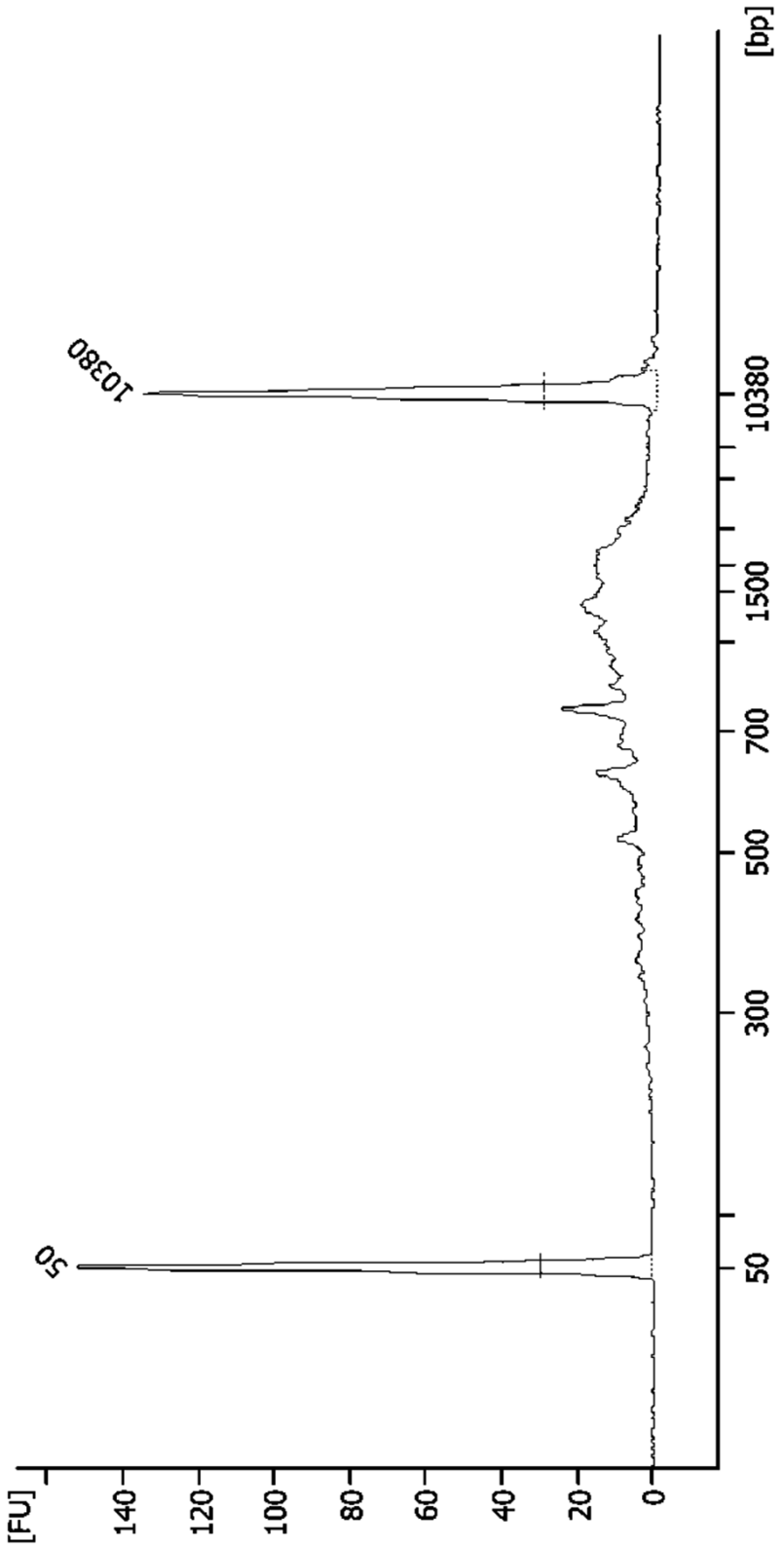


Fig. 27

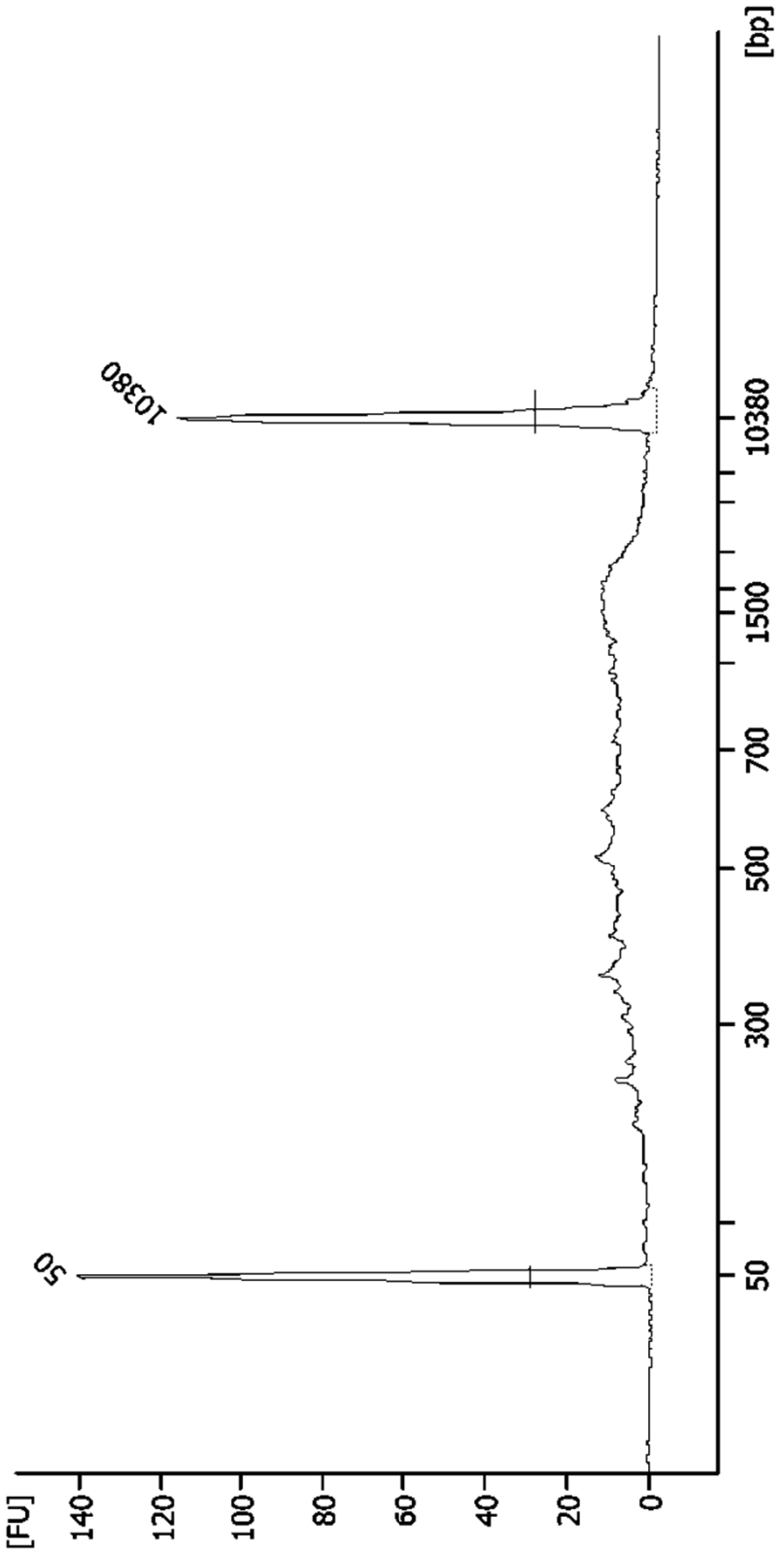


Fig. 28

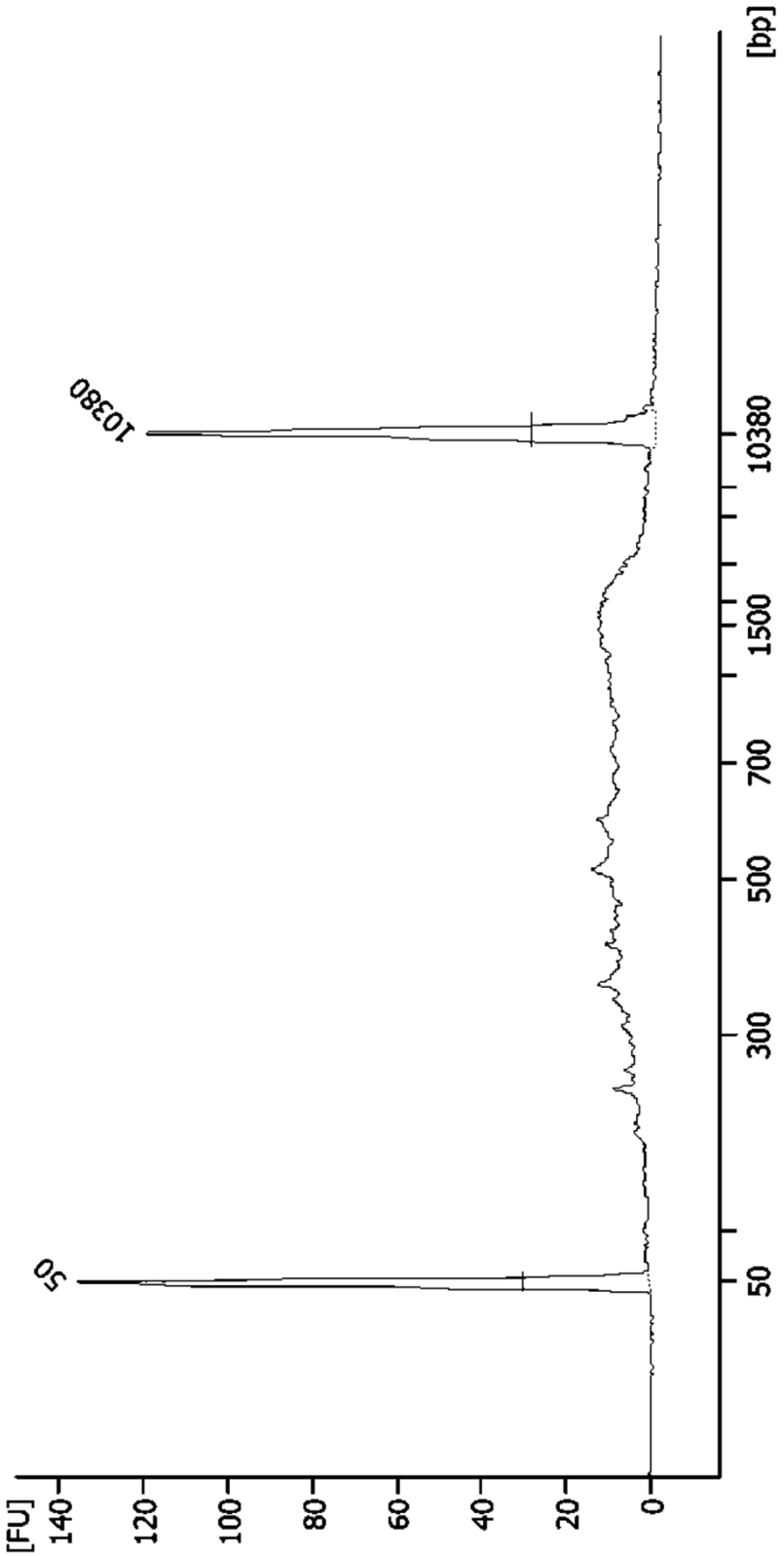


Fig. 29

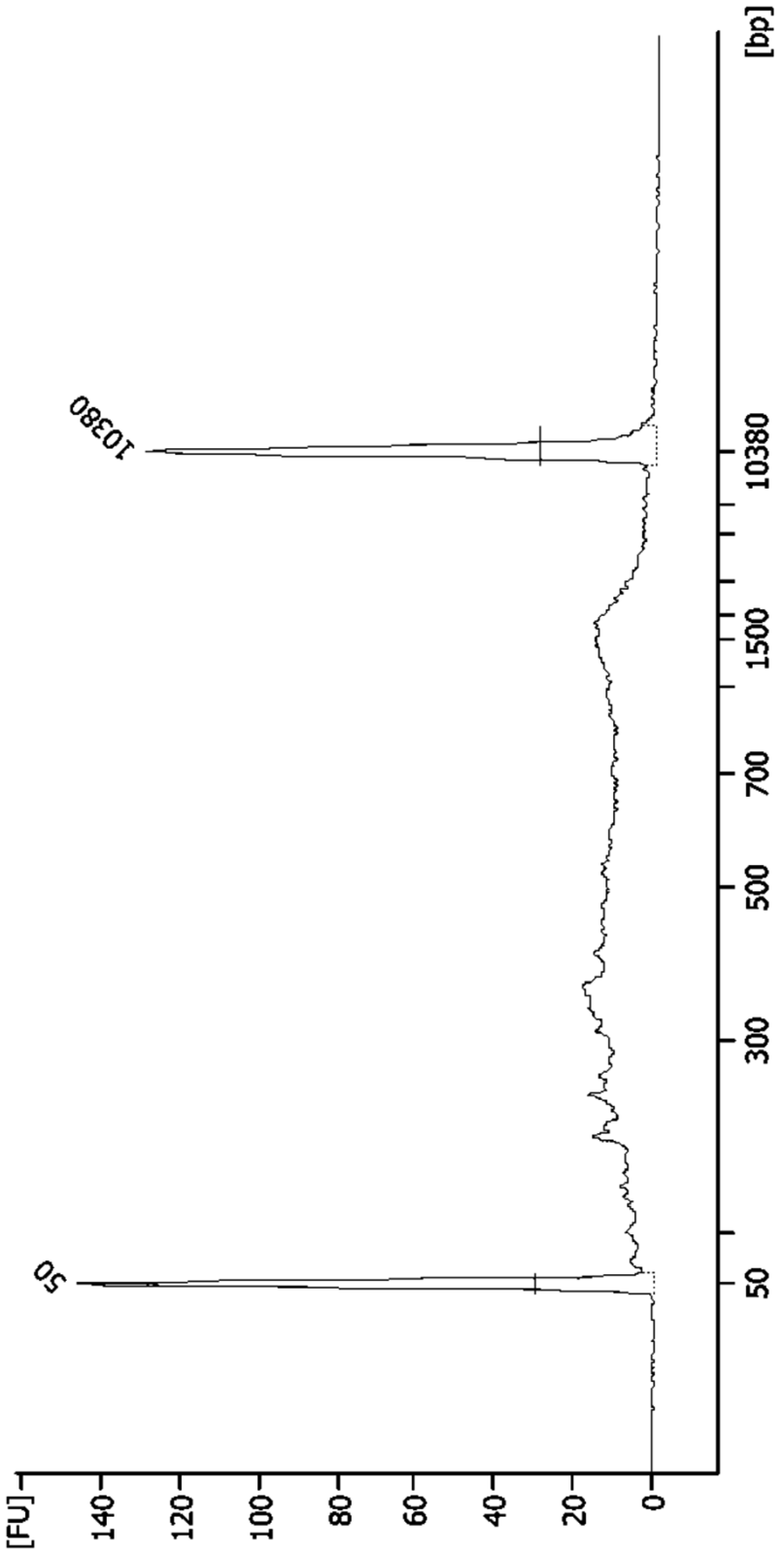


Fig. 30

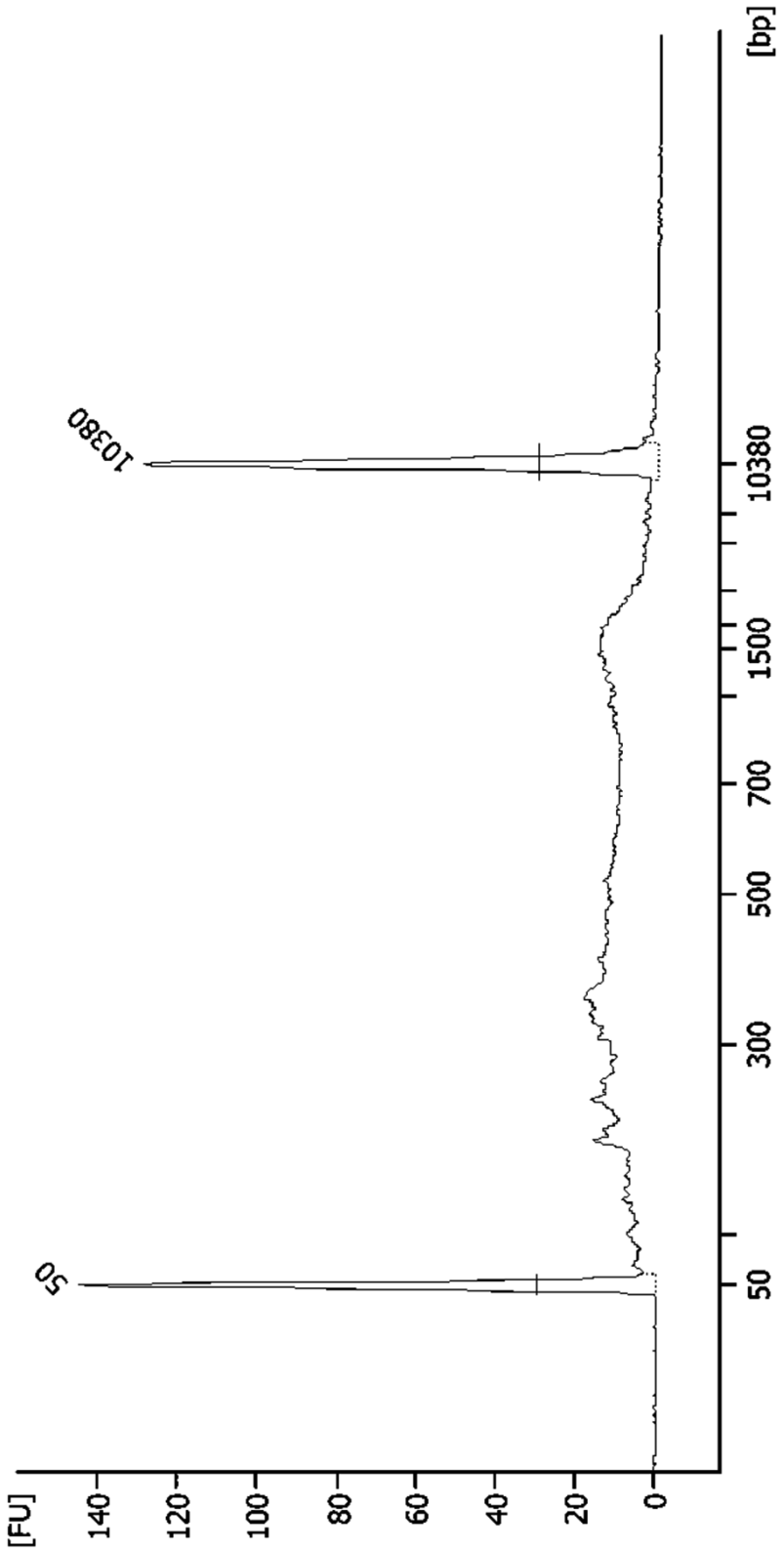


Fig. 31

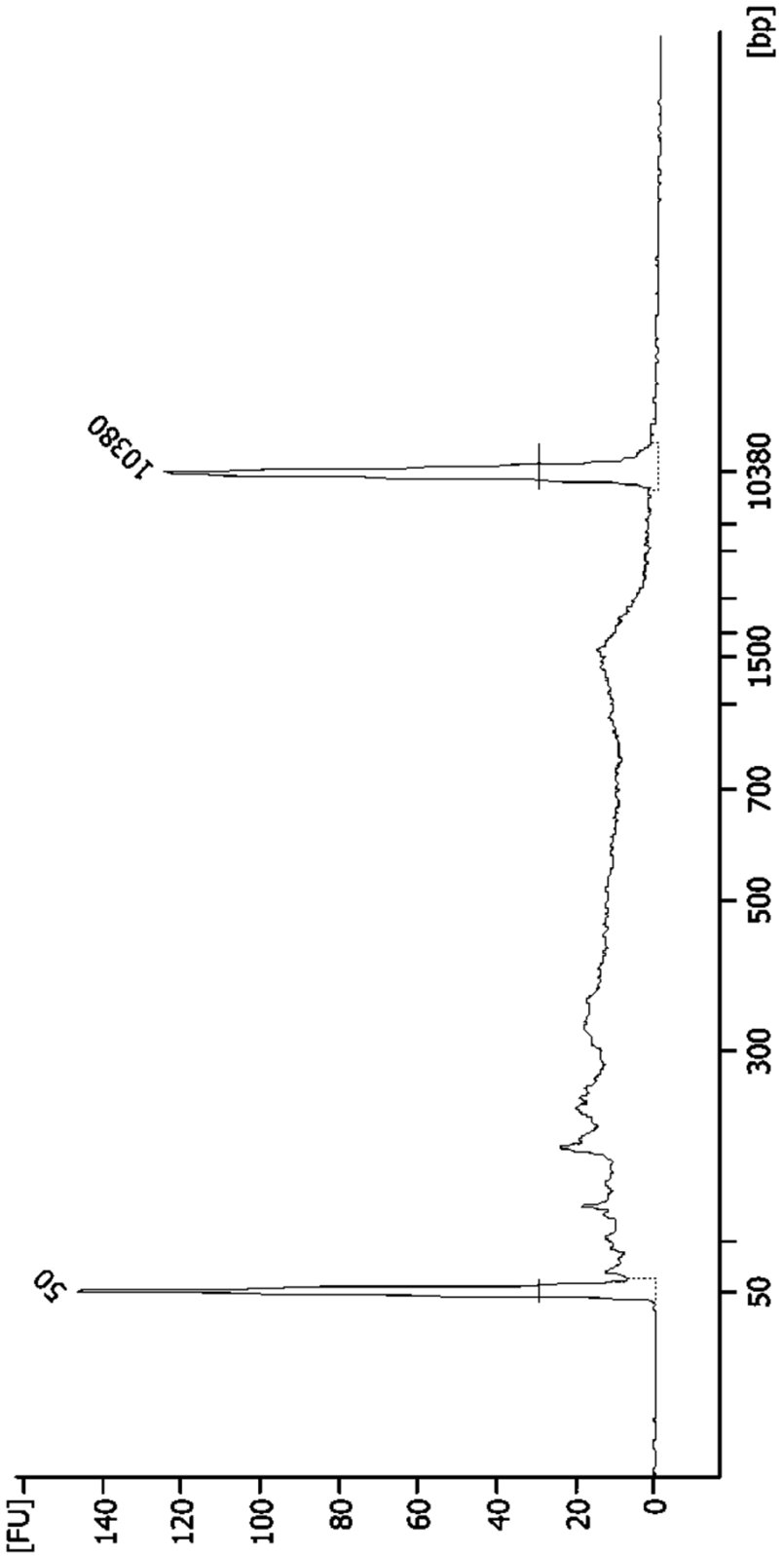


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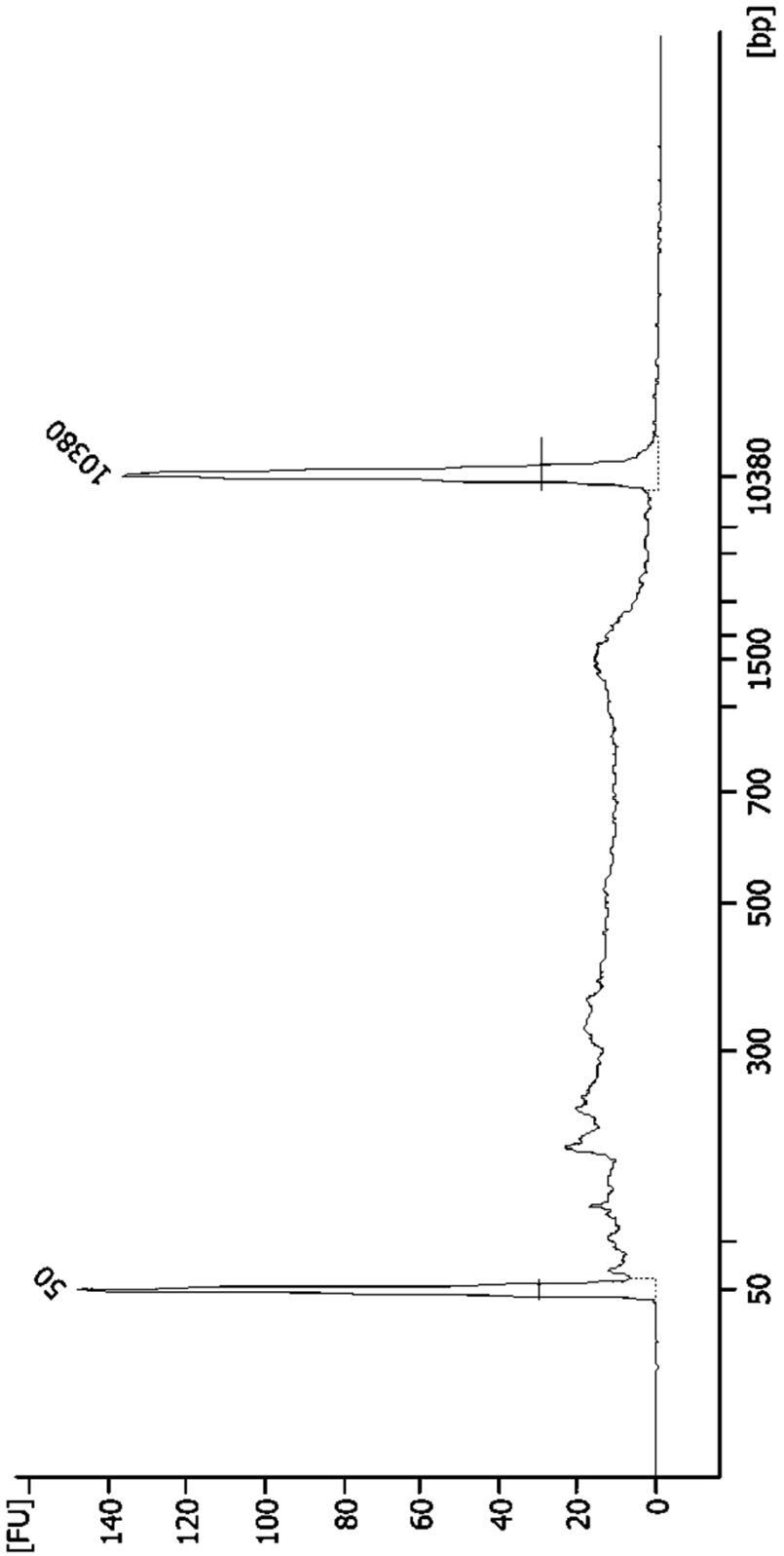


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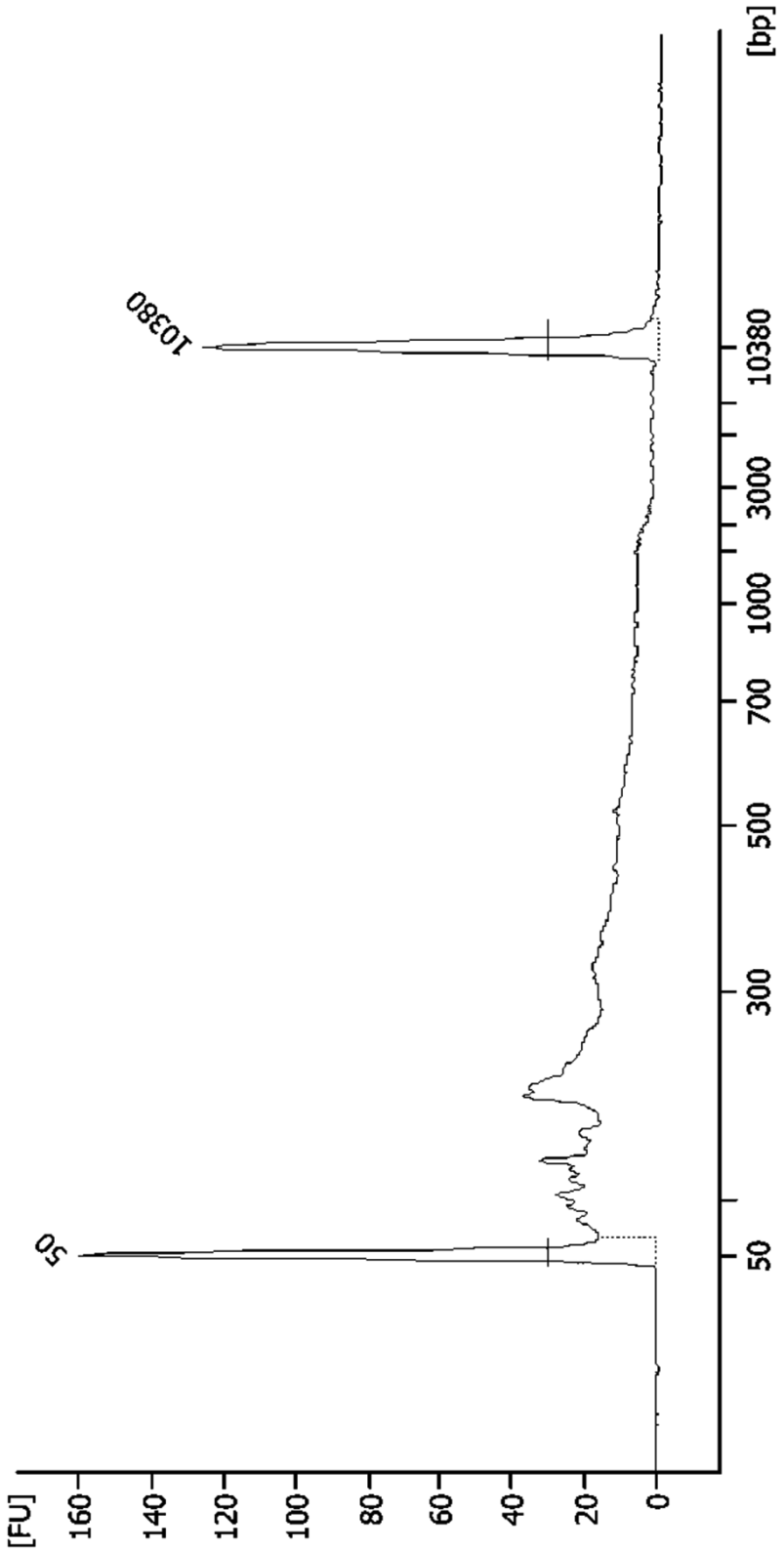

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Fig. 34

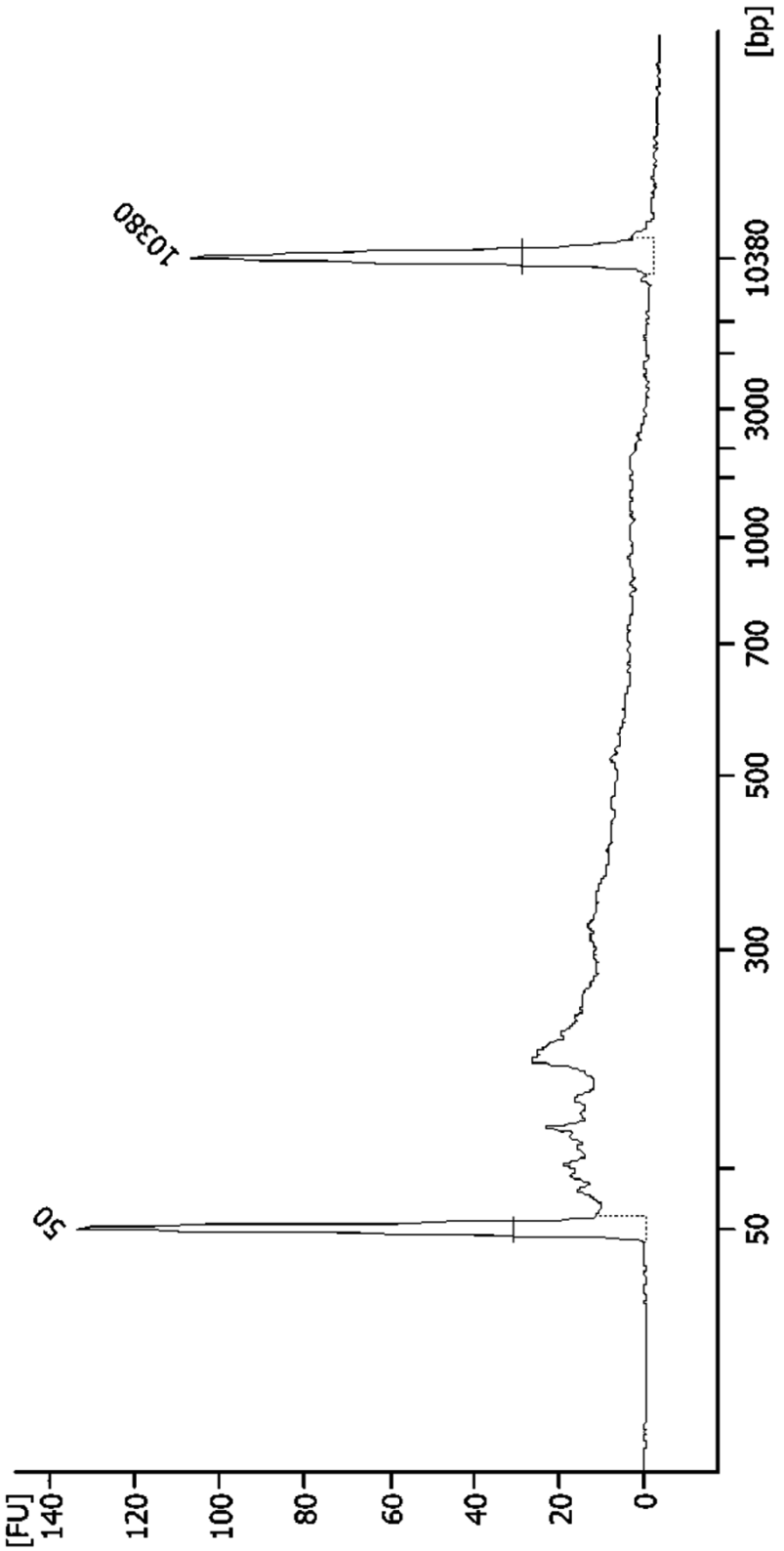

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Fig. 35

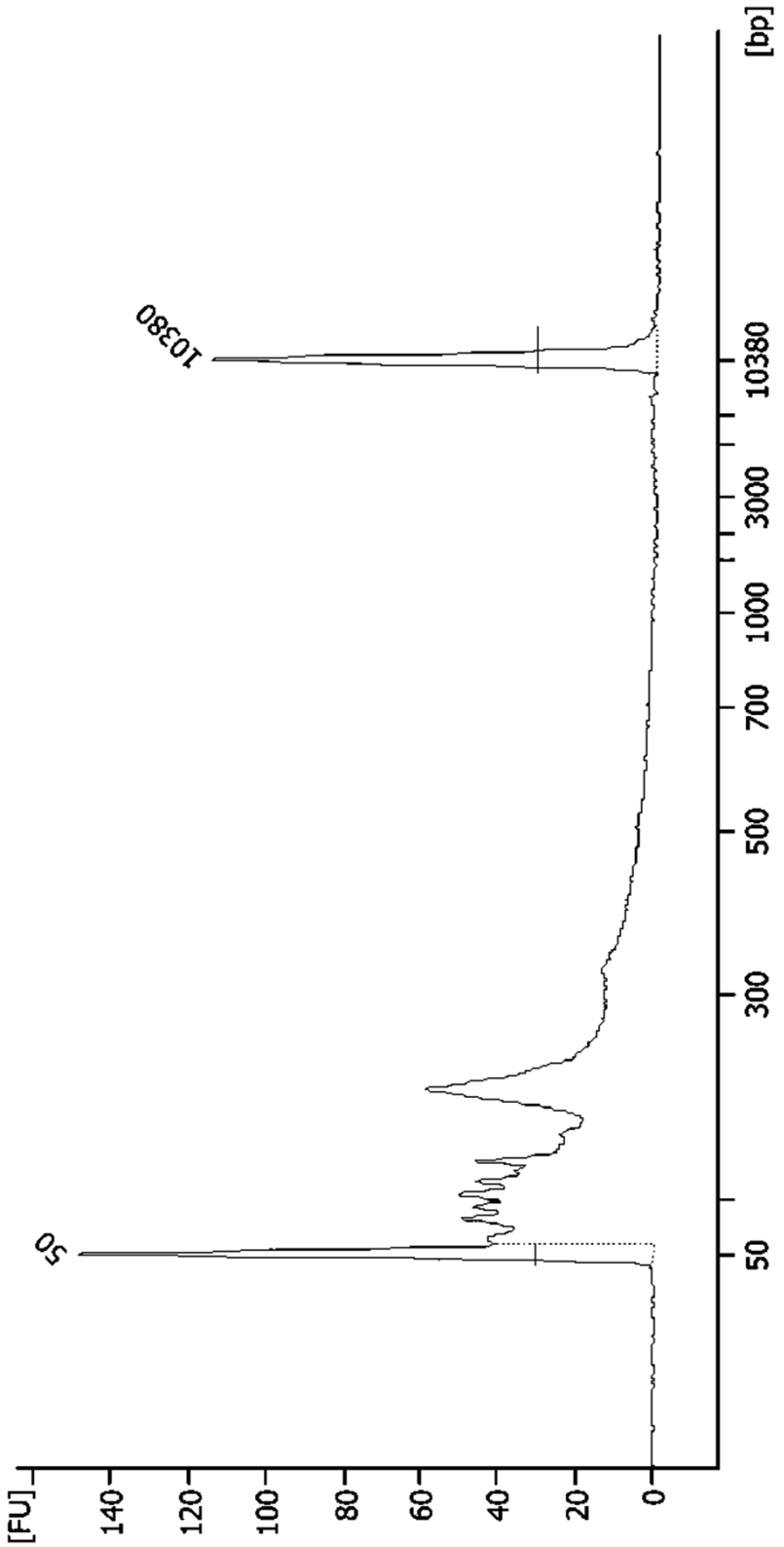

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Fig. 36

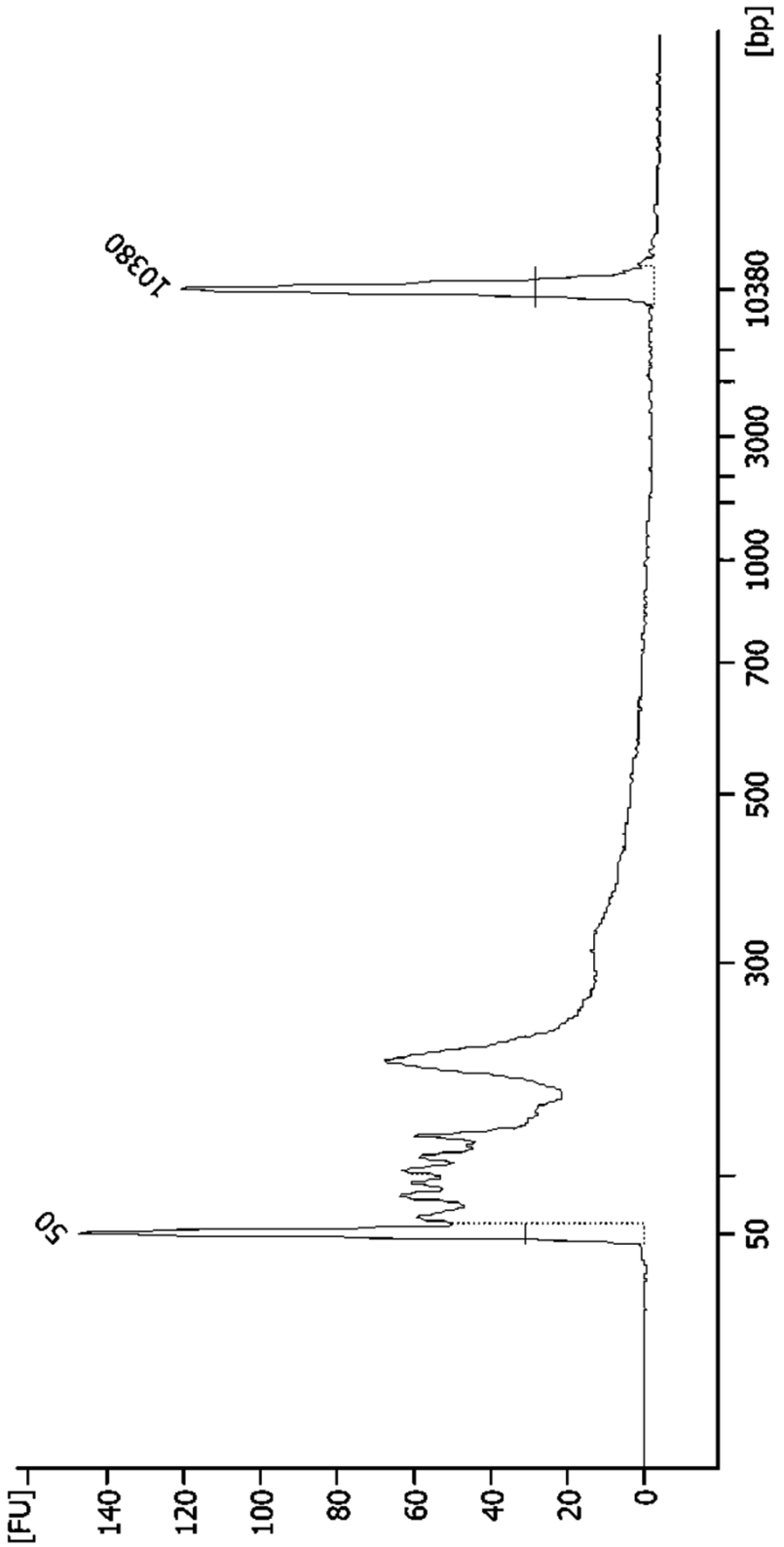

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Fig. 37

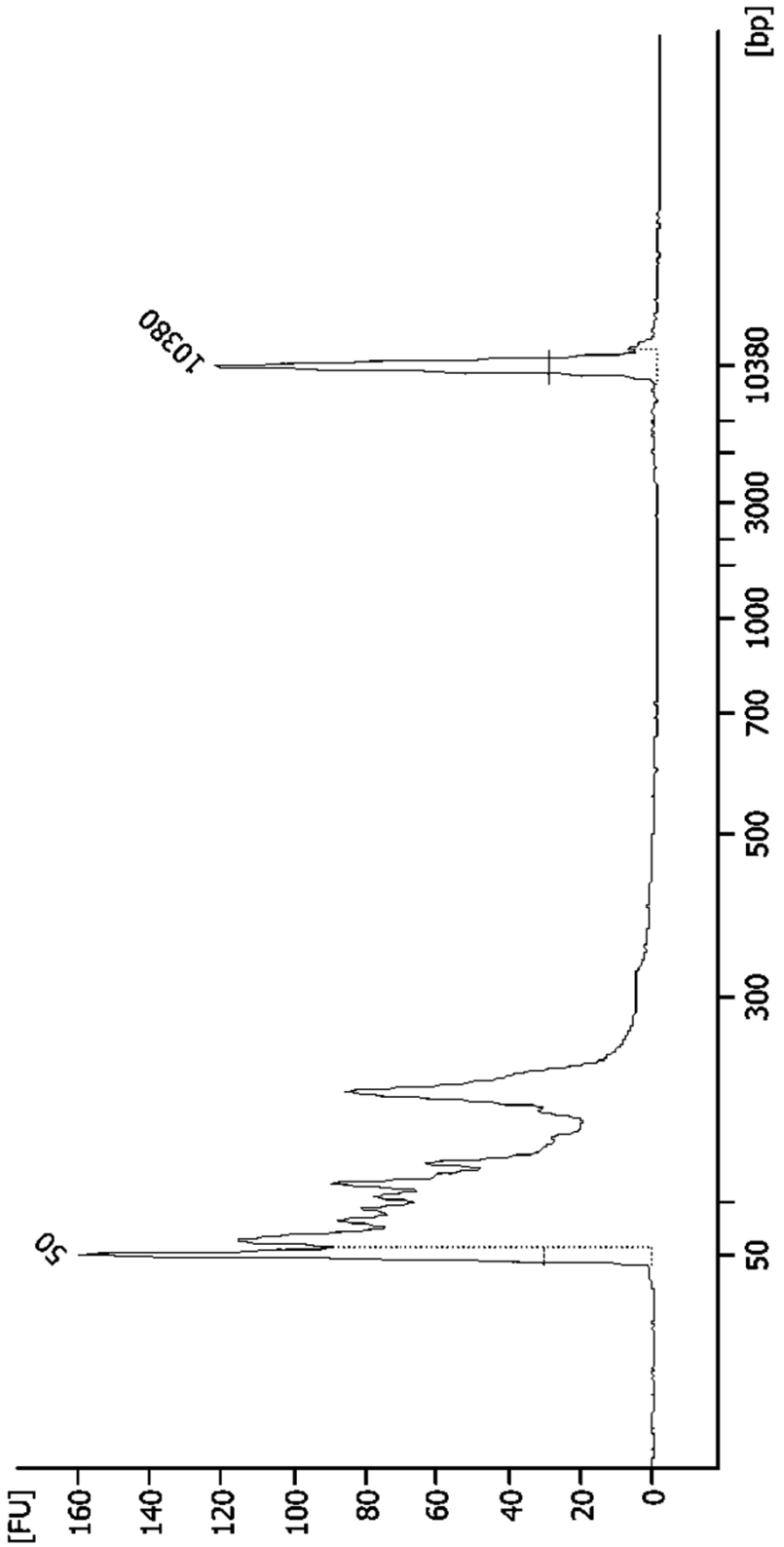

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Fig. 38

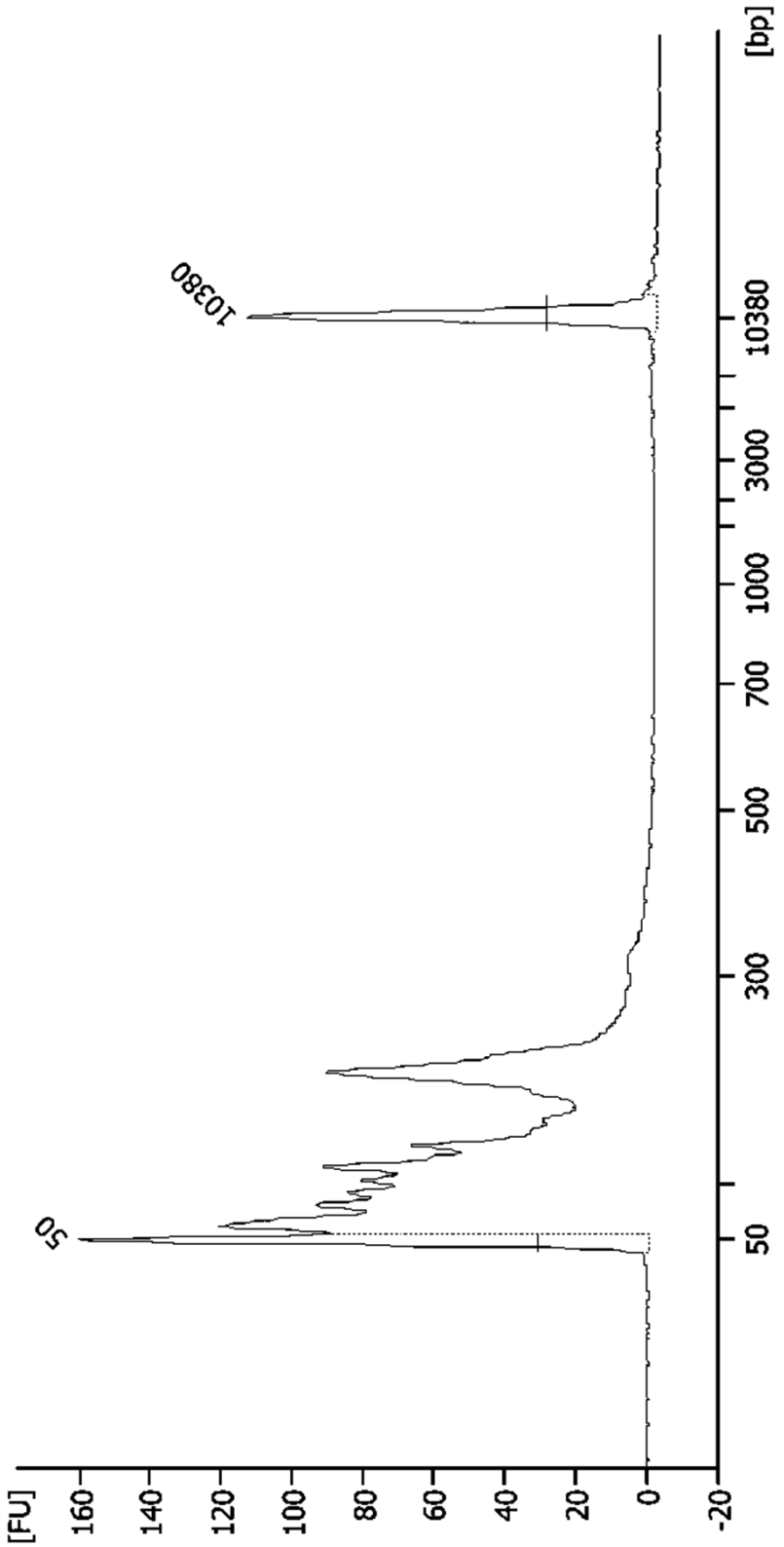

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Fig. 39

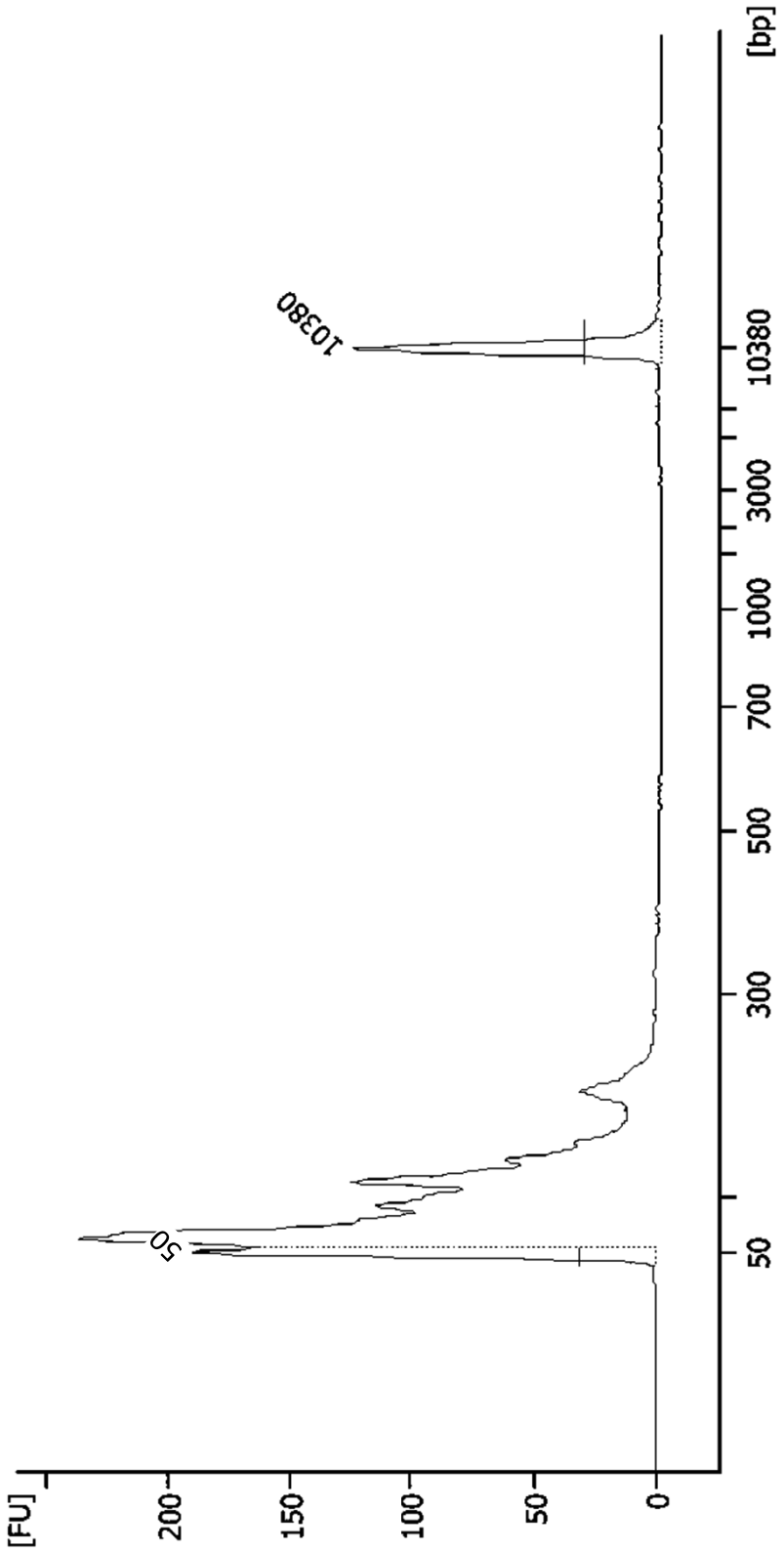


Fig. 40

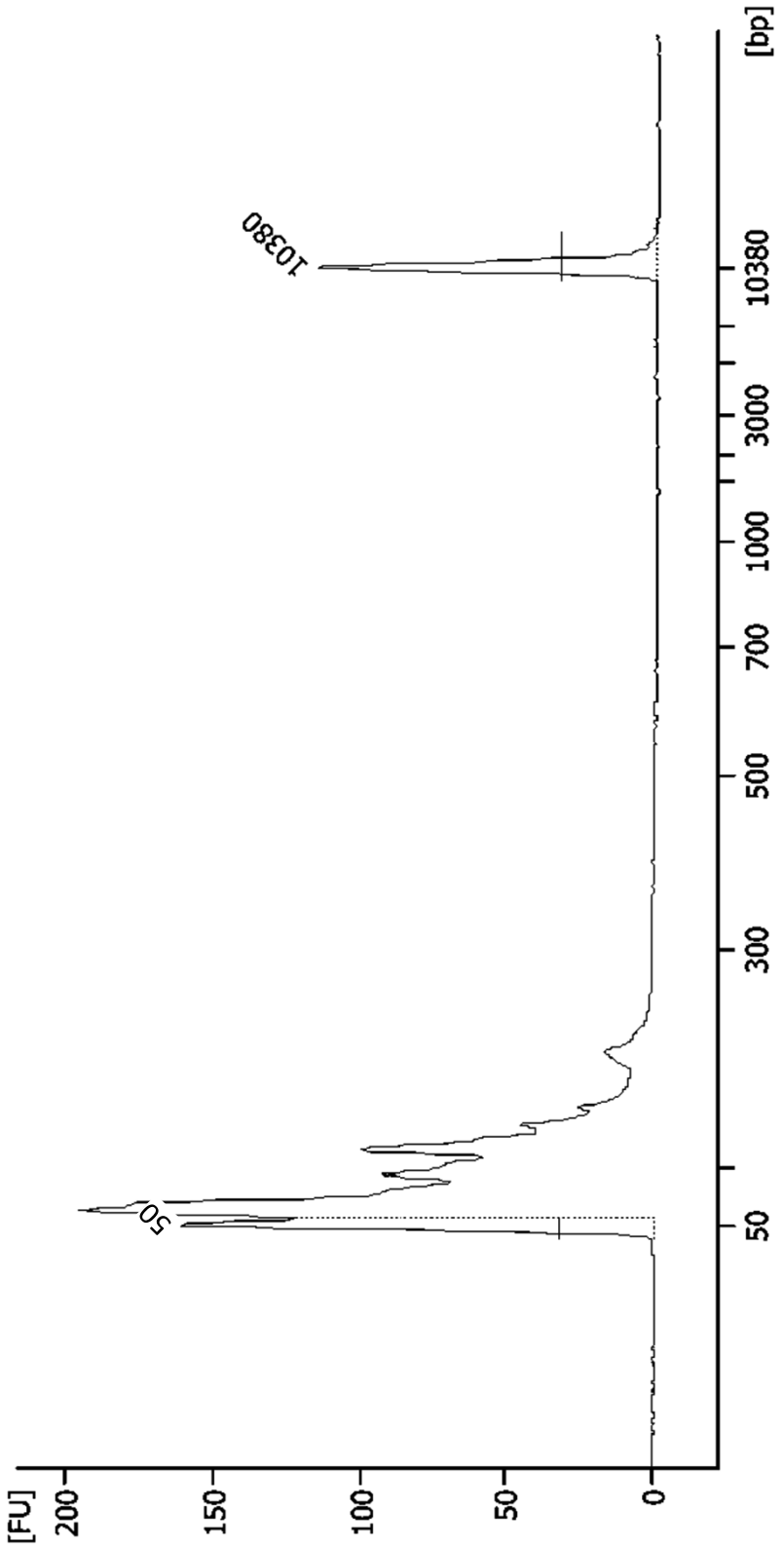


Fig. 41

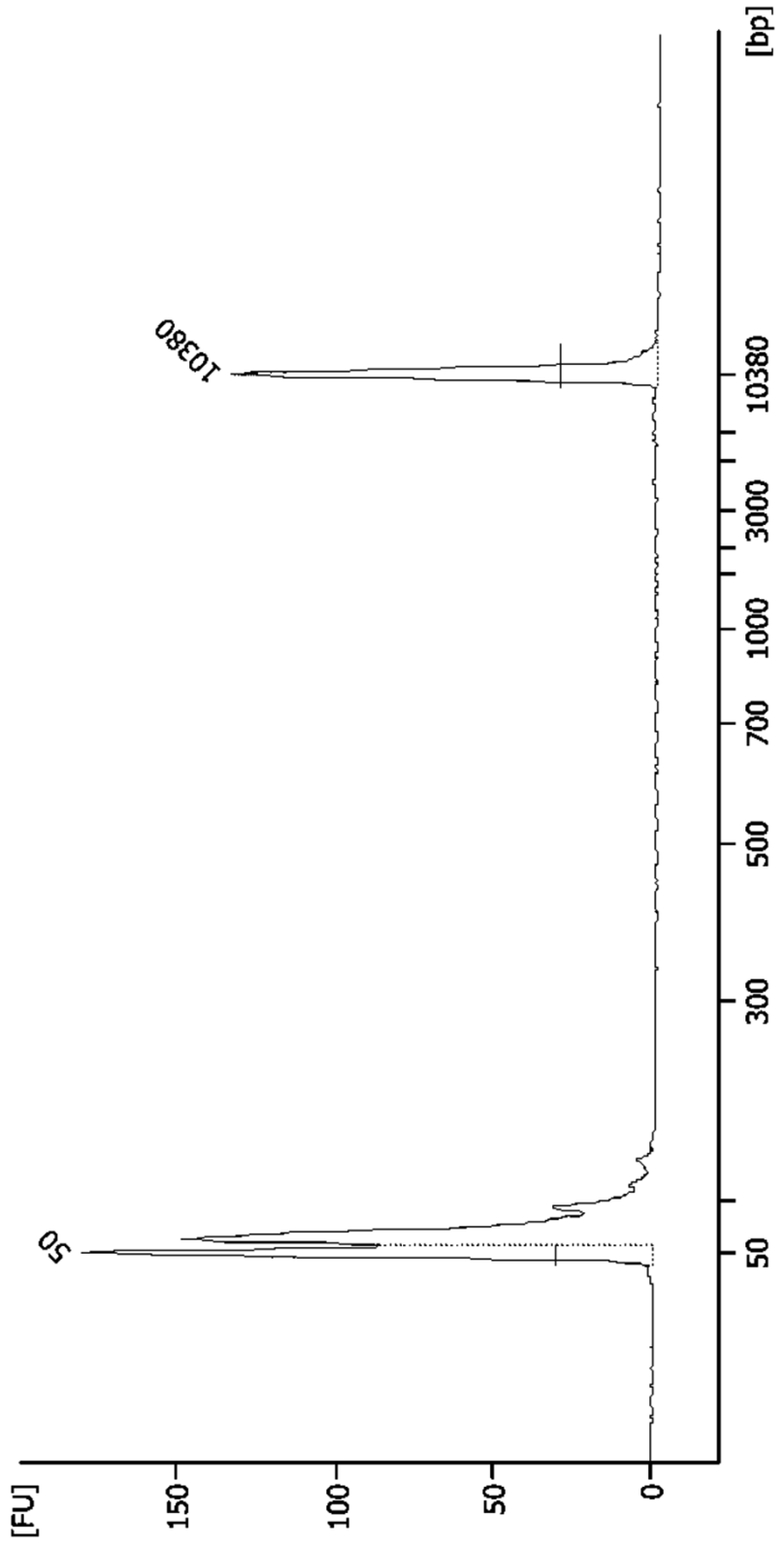


Fig. 42

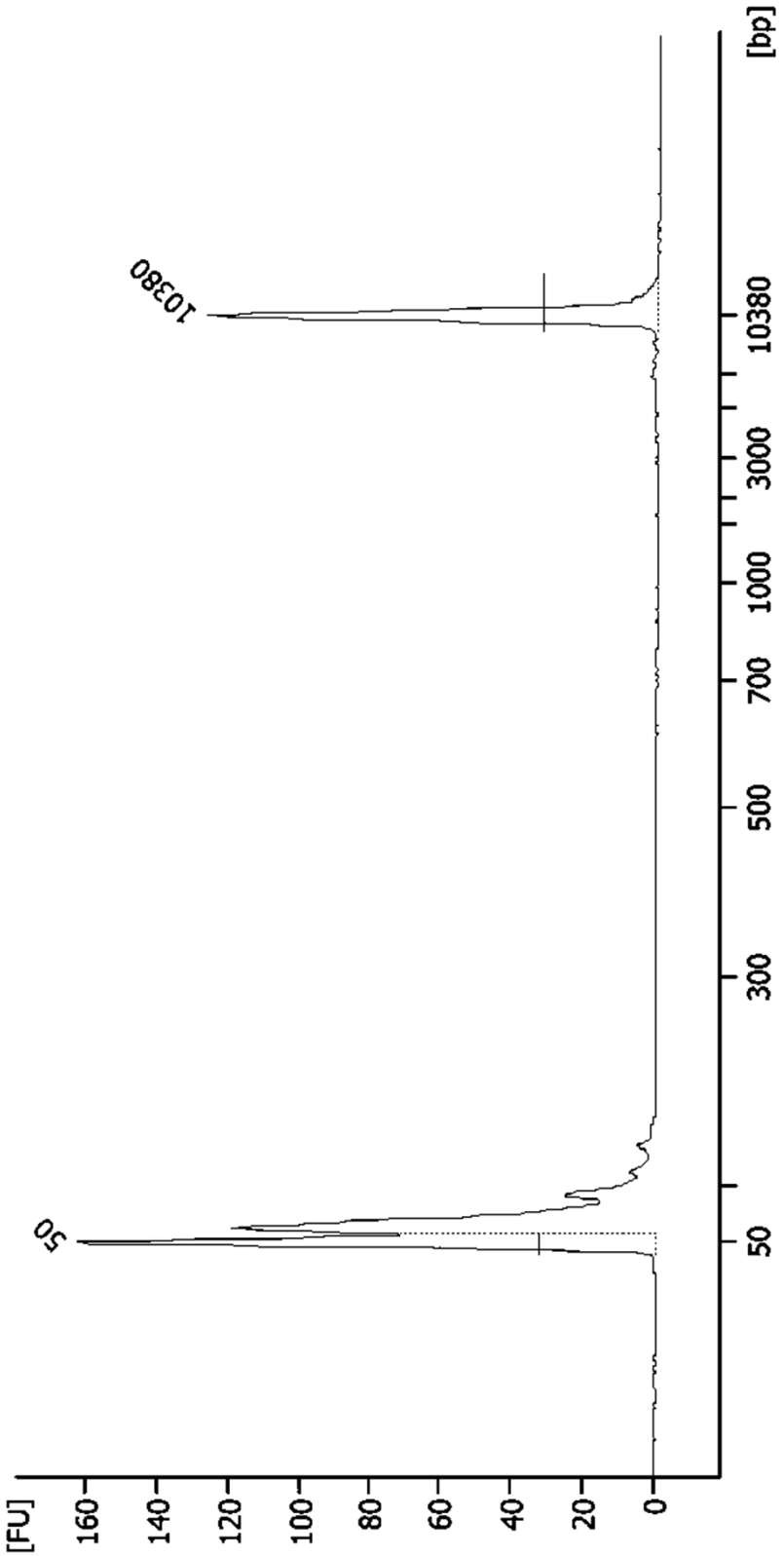

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Fig. 43

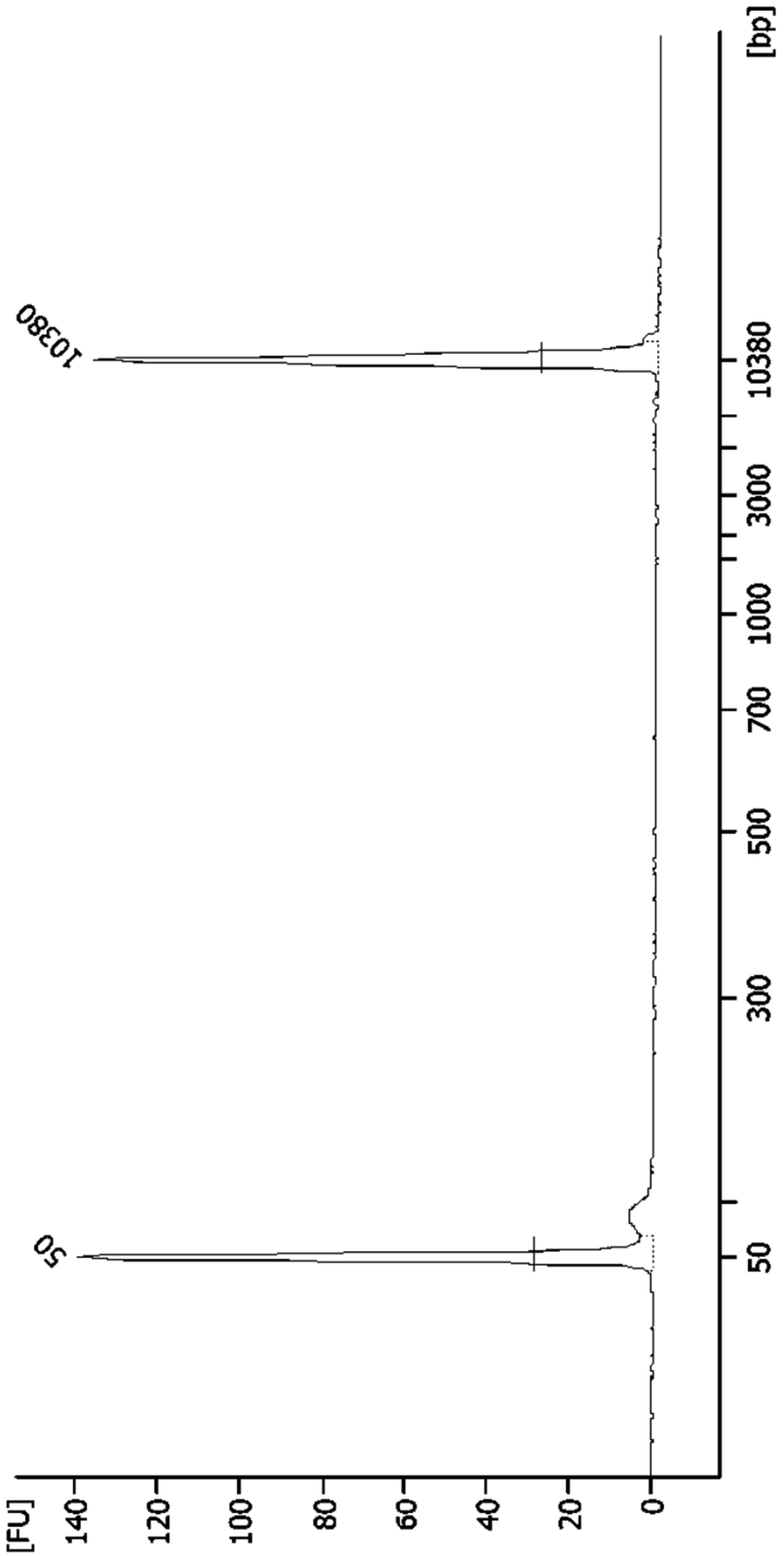

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Fig. 44

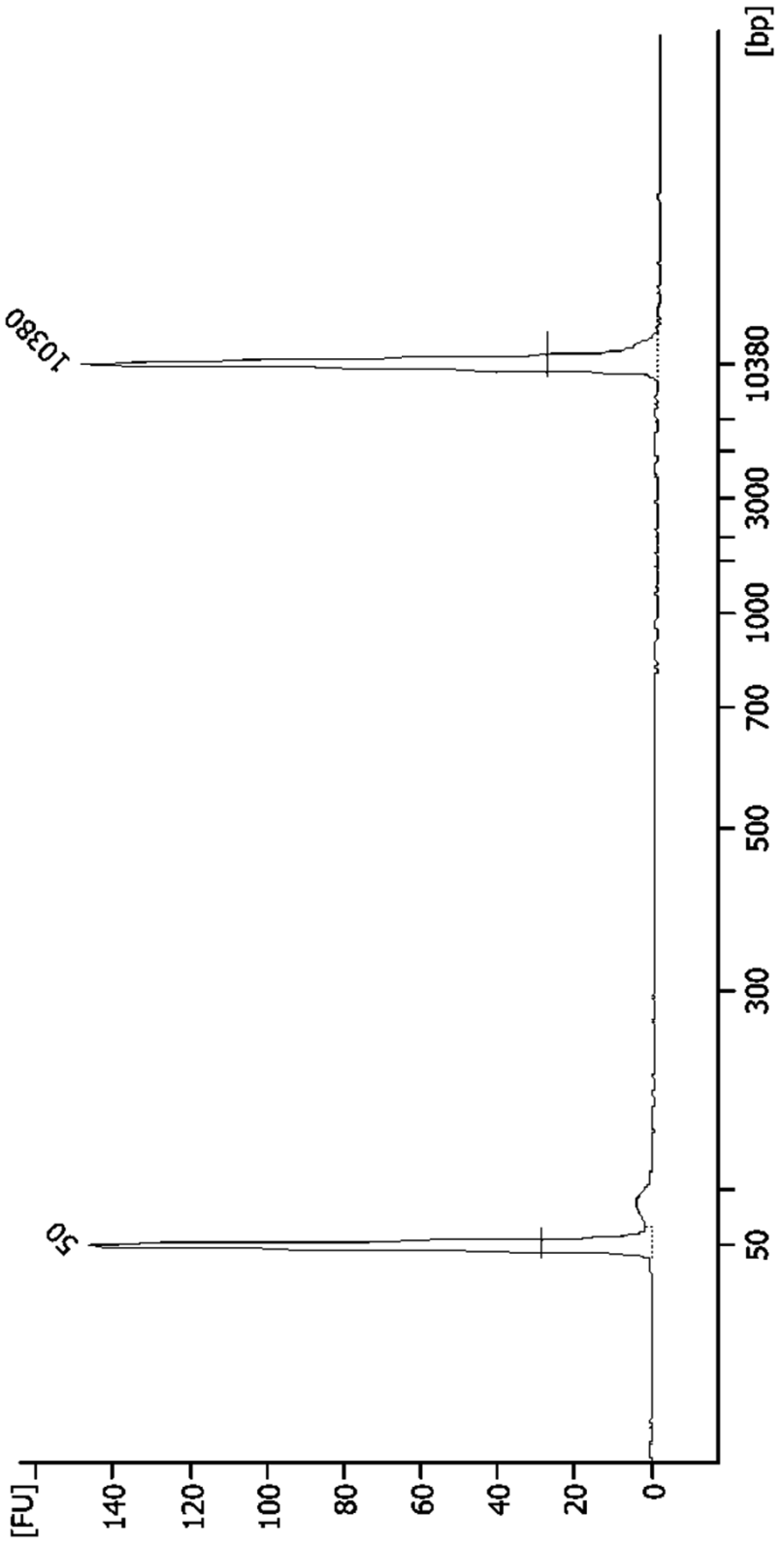

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Fig. 45

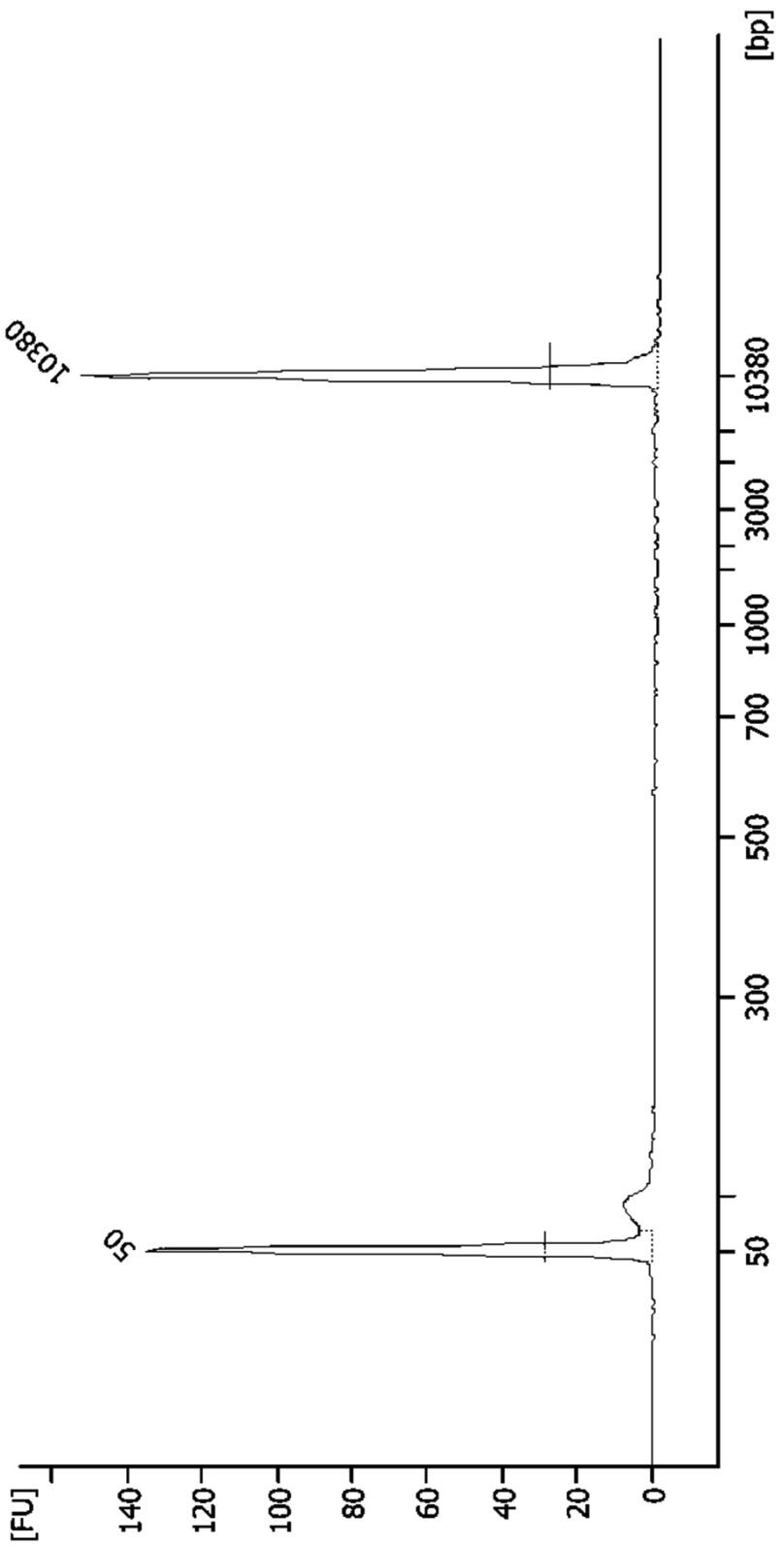

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[bp]

Fig. 46

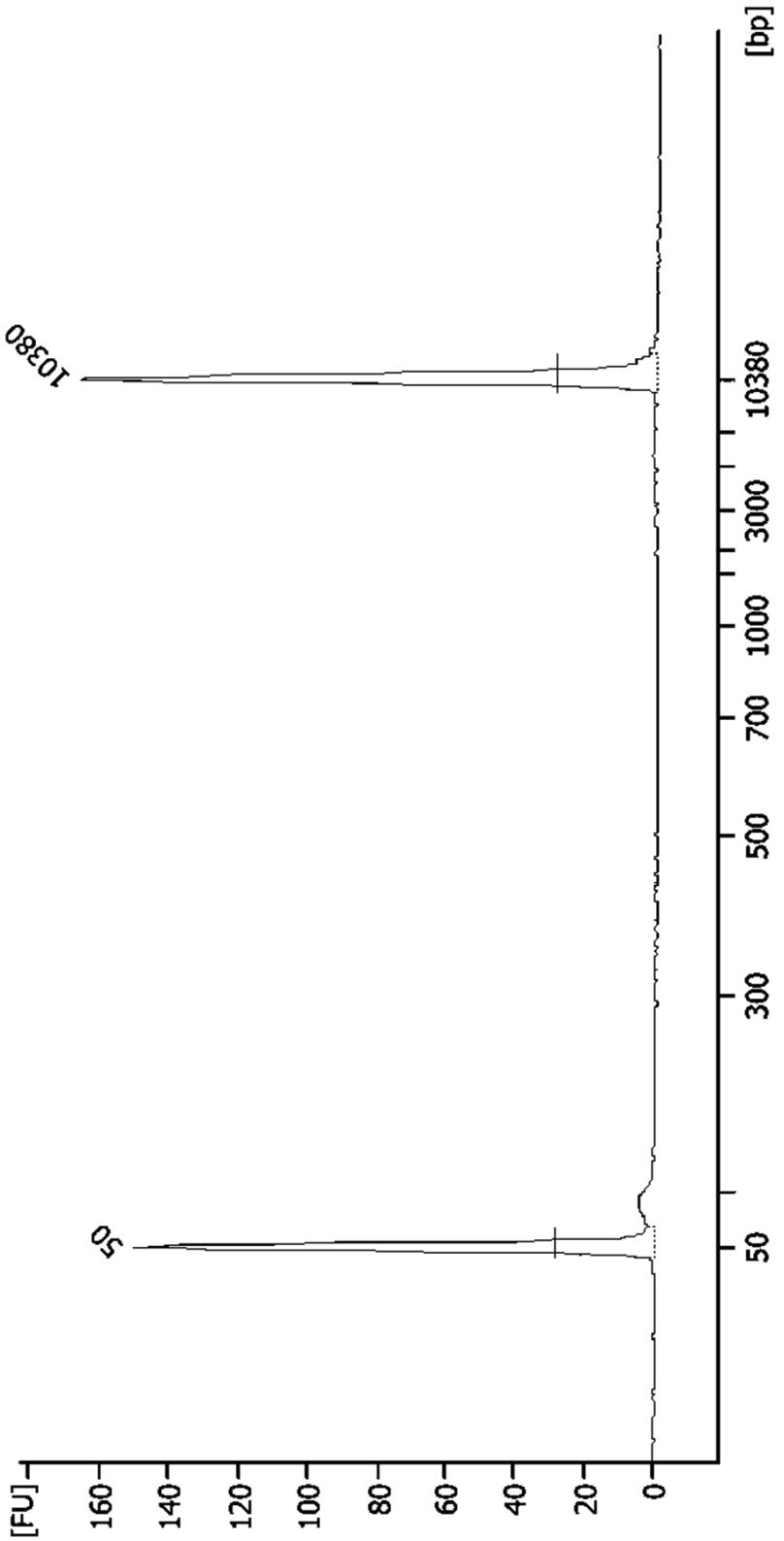

[FU]
160
140
120
100
80
60
40
20
0
50
10380
50
300
500
700
1000
3000
10380
[bp]

Fig. 47

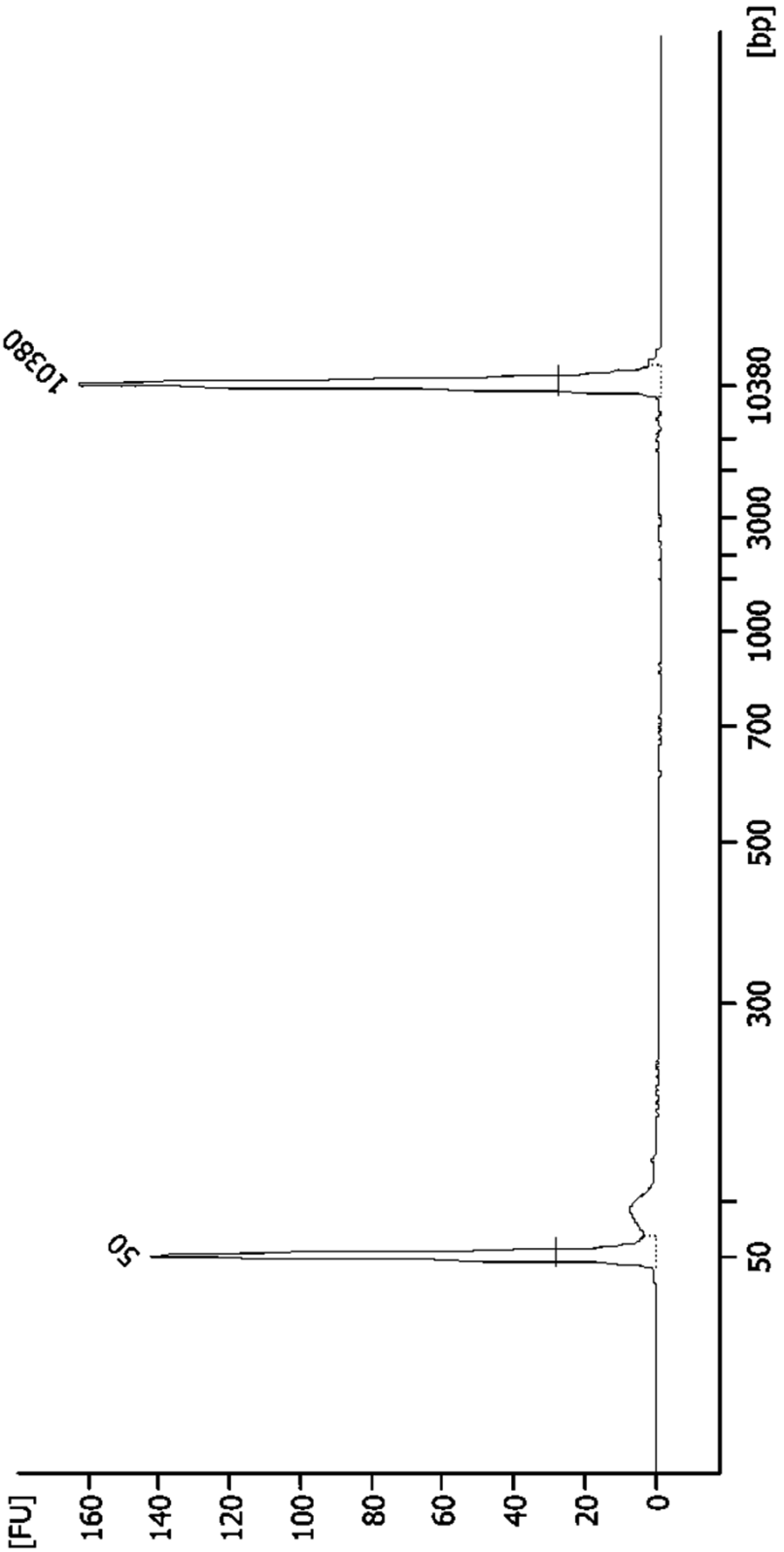

[FU]
160
140
120
100
80
60
40
20
0
50
10380
50
300
500
700
1000
3000
10380
[bp]

Fig. 48

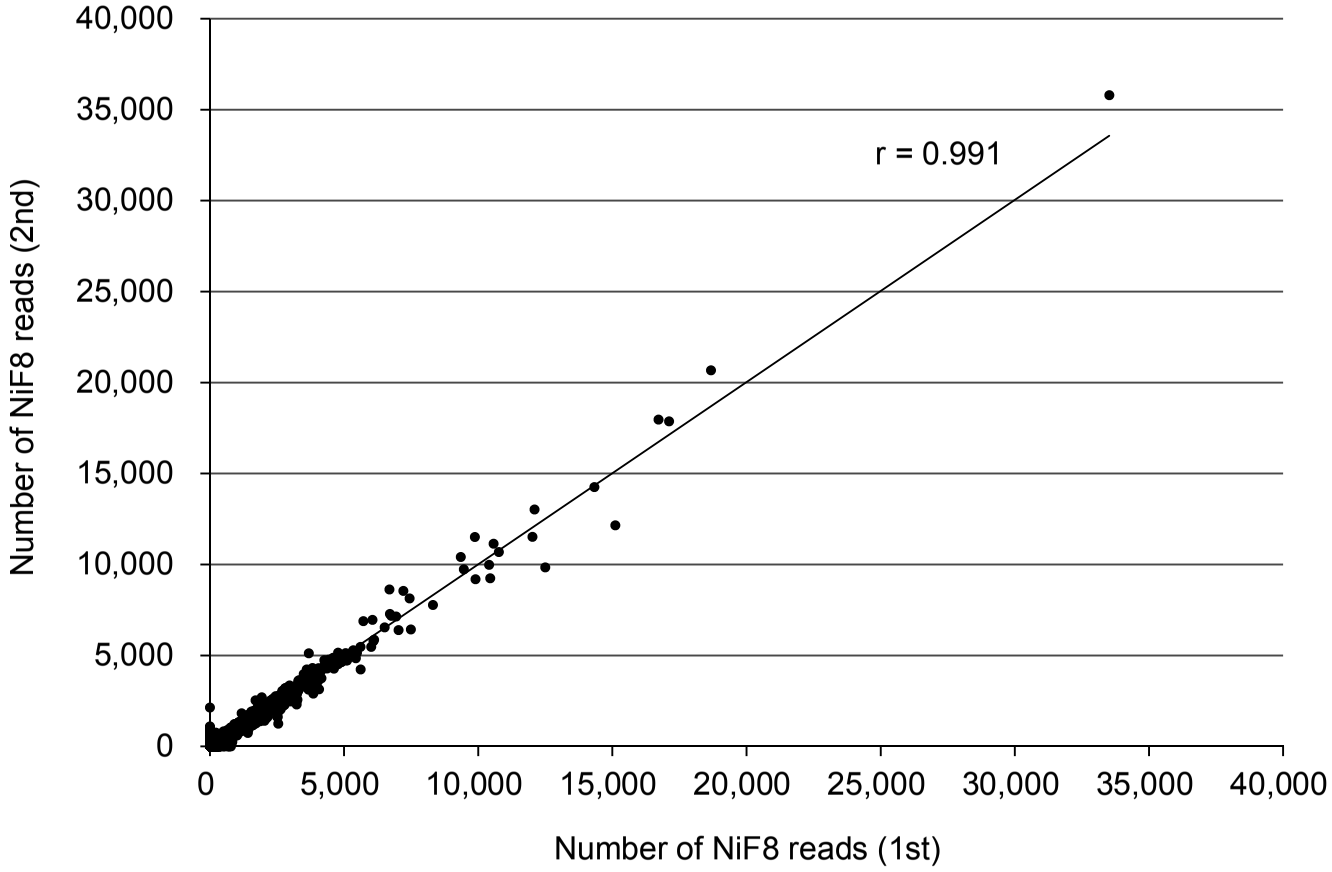

40,000
35,000
30,000
25,000
20,000
15,000
10,000
5,000
0
Number of NiF8 reads (2nd)
r = 0.991
0
5,000
10,000
15,000
20,000
25,000
30,000
35,000
40,000
Number of NiF8 reads (1st)

Fig. 49

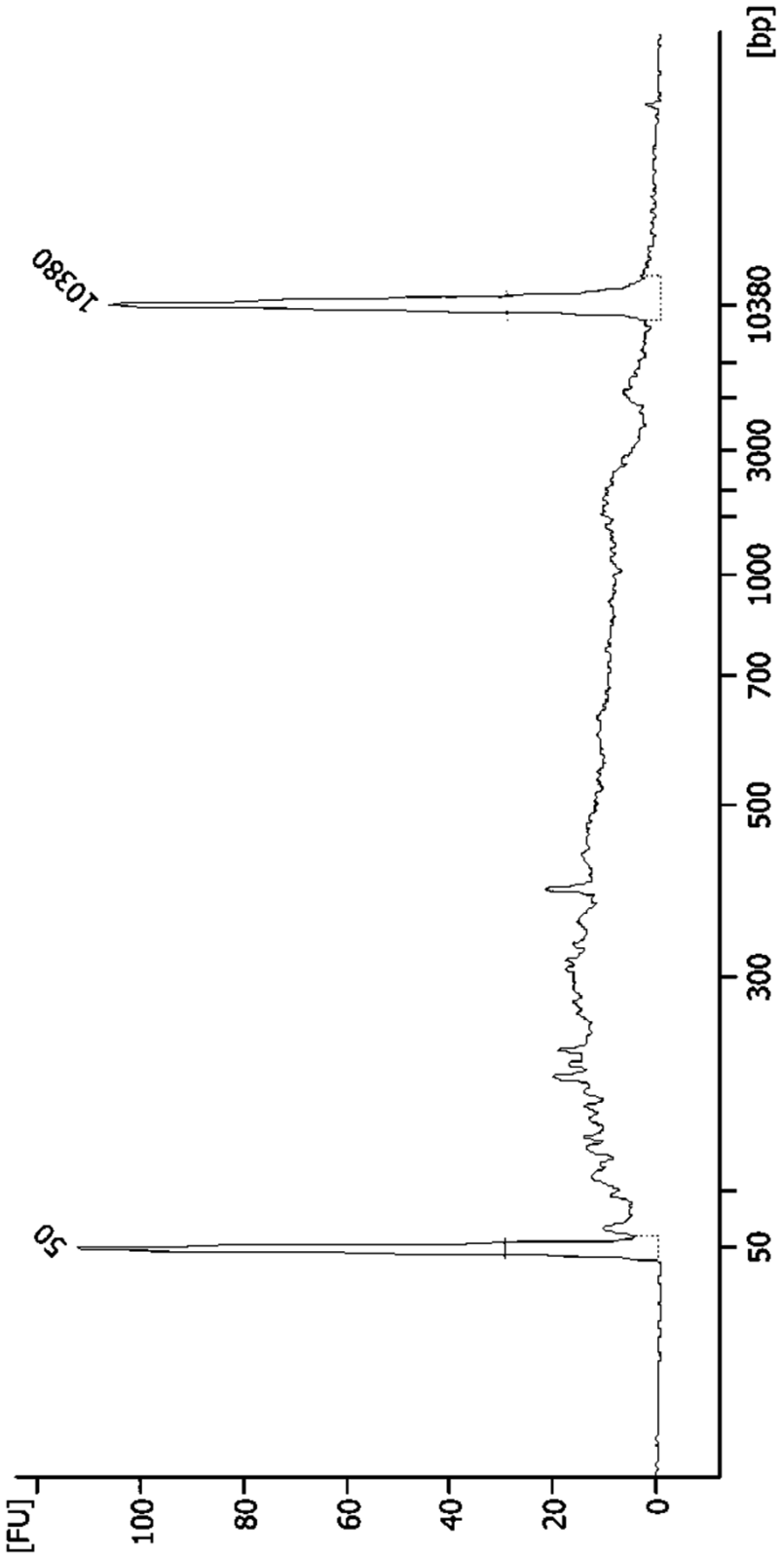


Fig. 50

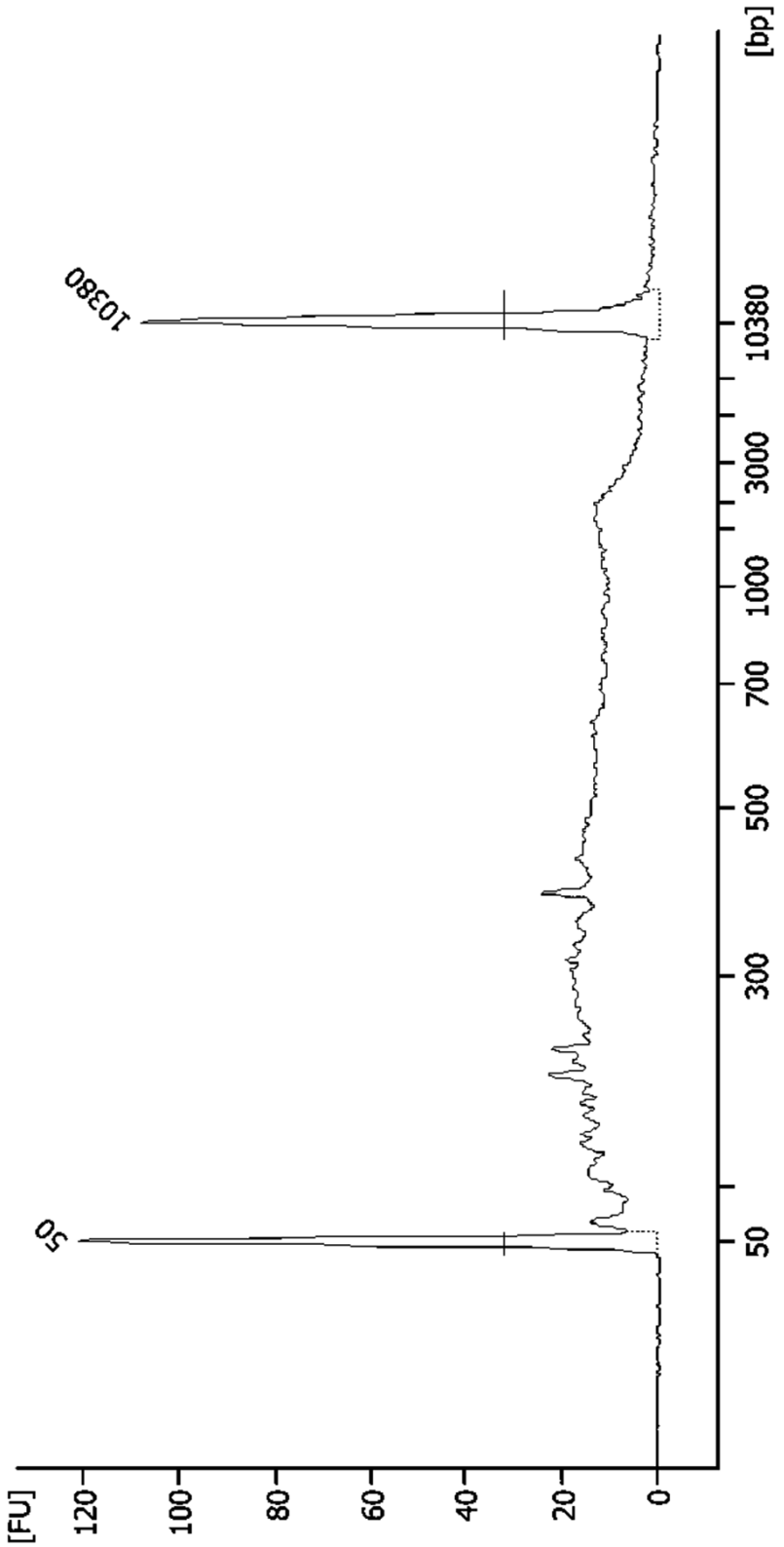

[FU]
120
100
80
60
40
20
0
50
300
500
700
1000
3000
10380
[bp]
50
10380

Fig. 51

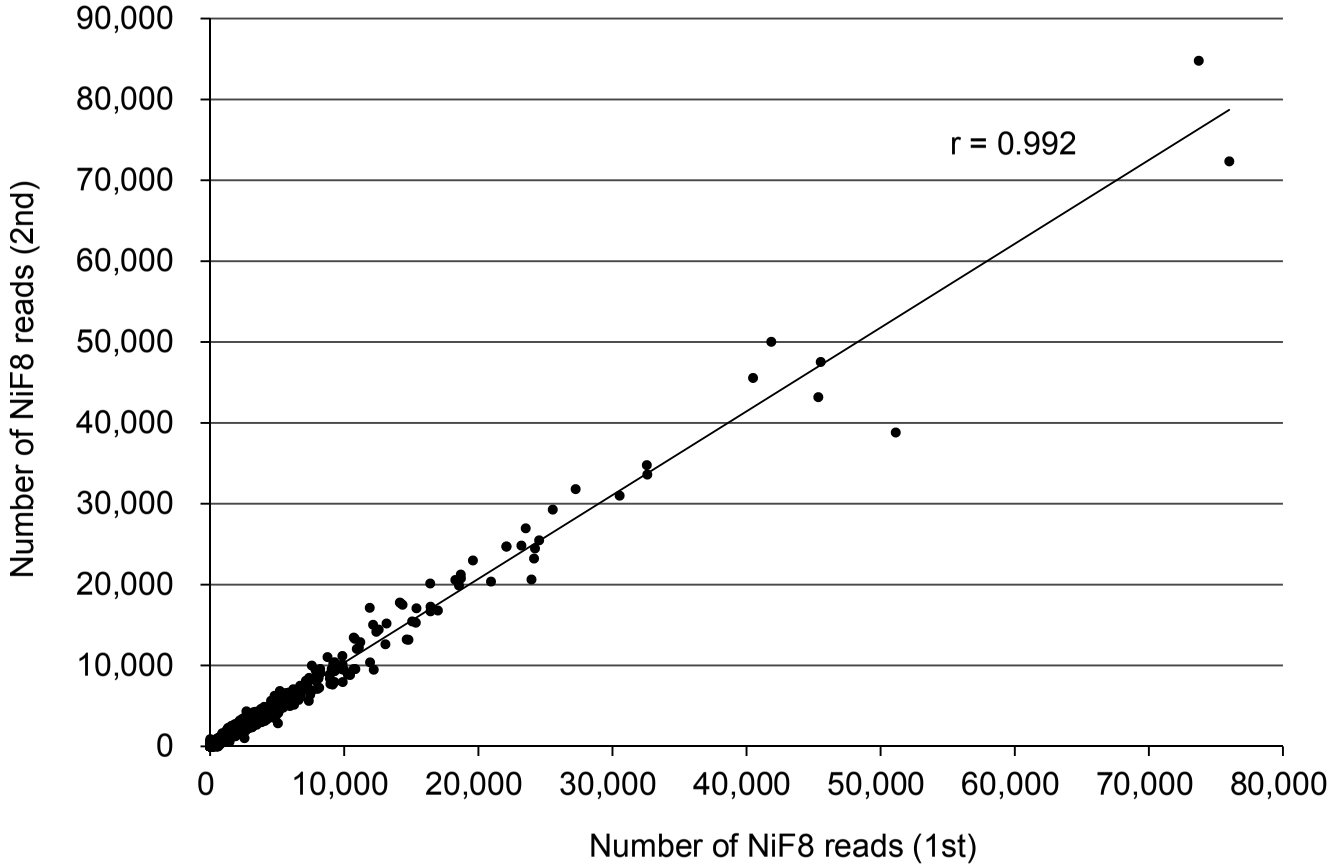

90,000
80,000
70,000
60,000
50,000
40,000
30,000
20,000
10,000
0
Number of NiF8 reads (2nd)
r = 0.992
0
10,000
20,000
30,000
40,000
50,000
60,000
70,000
80,000
Number of NiF8 reads (1st)

Fig. 52

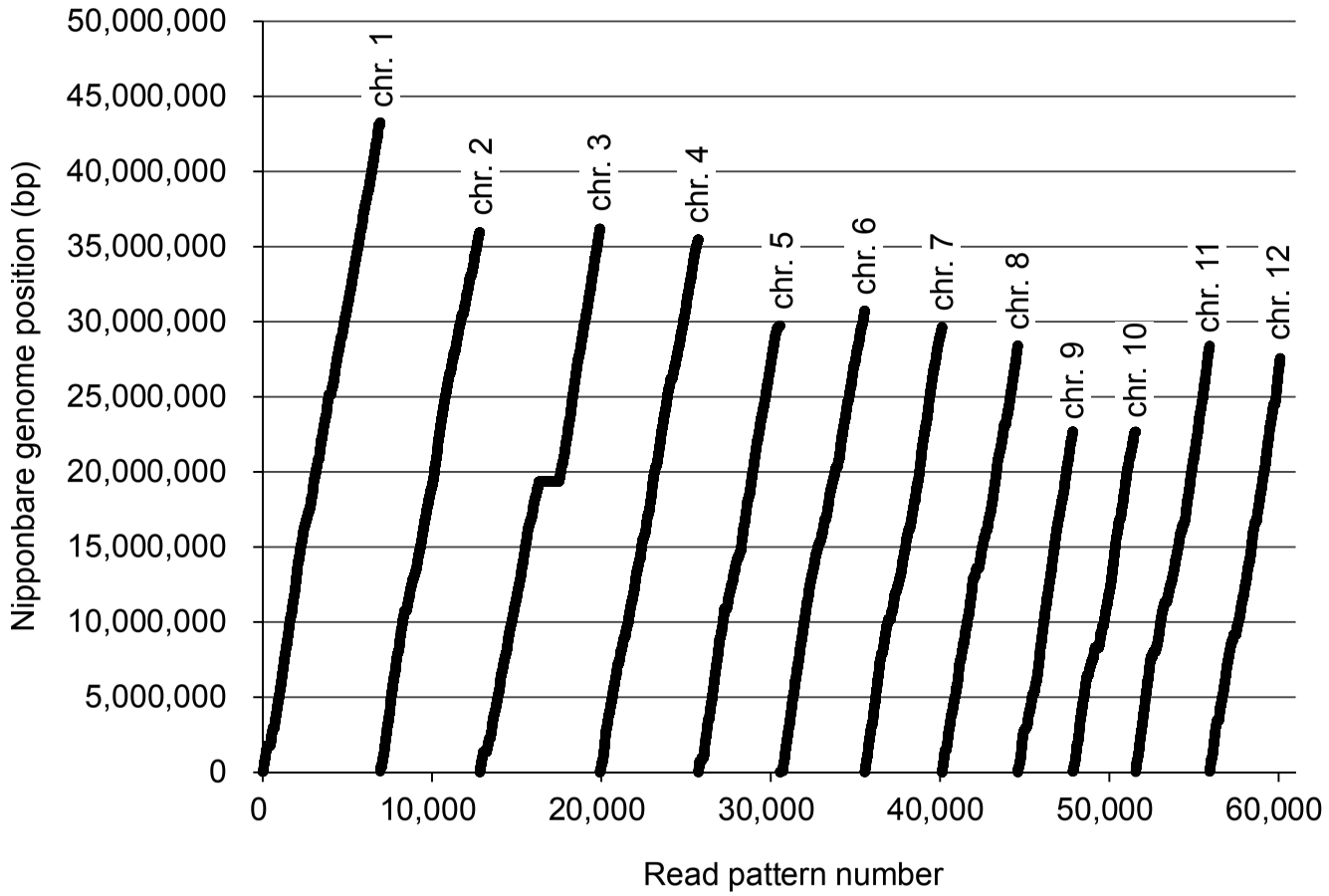

Nipponbare genome position (bp)
50,000,000
45,000,000
40,000,000
35,000,000
30,000,000
25,000,000
20,000,000
15,000,000
10,000,000
5,000,000
0
chr. 1
chr. 2
chr. 3
chr. 4
chr. 5
chr. 6
chr. 7
chr. 8
chr. 9
chr. 10
chr. 11
chr. 12
0
10,000
20,000
30,000
40,000
50,000
60,000
Read pattern number

Fig. 53

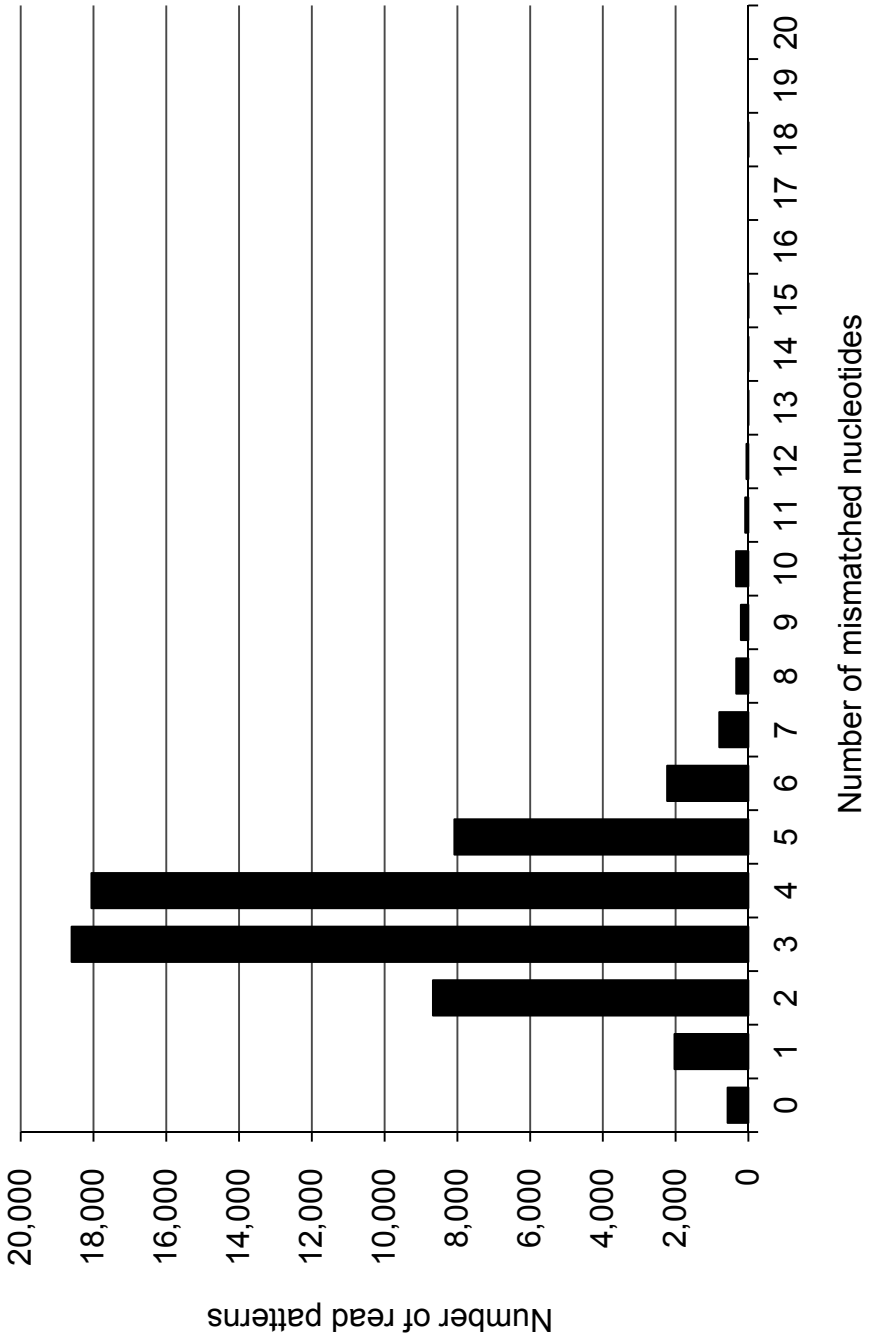

Number of read patterns
20,000
18,000
16,000
14,000
12,000
10,000
8,000
6,000
4,000
2,000
0
0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20
Number of mismatched nucleotides

Fig. 54

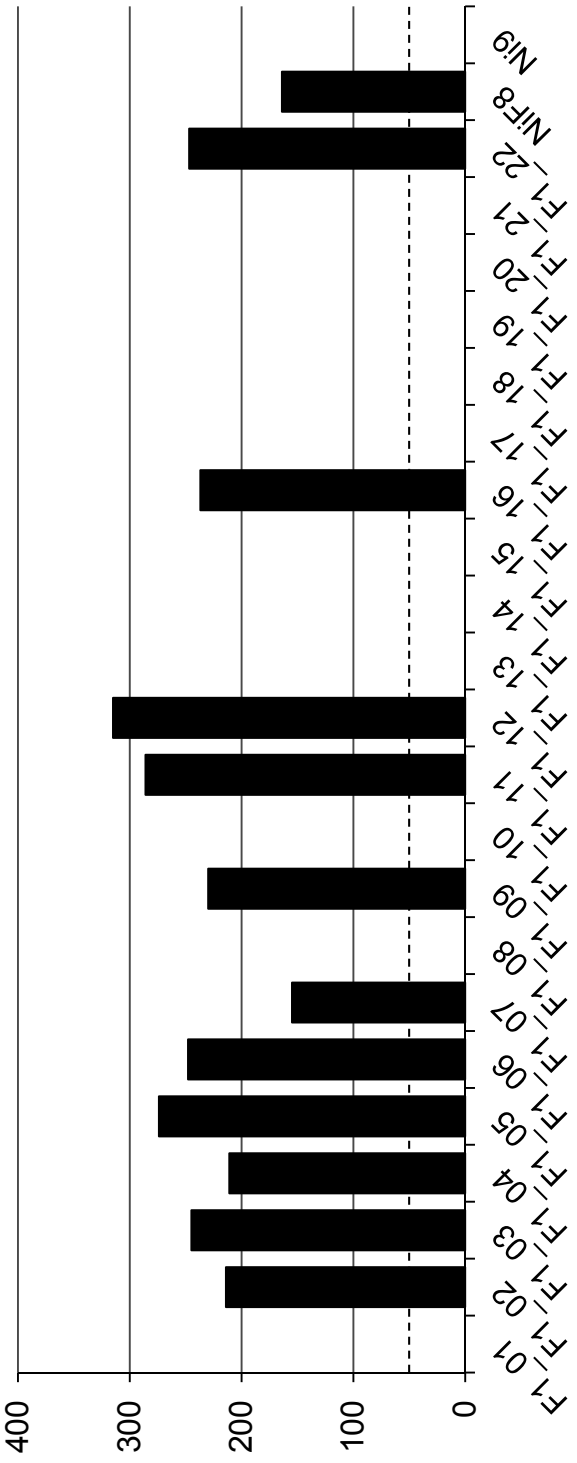

400
300
200
100
0
F7/01
F7/02
F7/03
F7/04
F7/05
F7/06
F7/07
F7/08
F7/09
F7/10
F7/11
F7/12
F7/13
F7/14
F7/15
F7/16
F7/17
F7/18
F7/19
F7/20
F7/21
F7/22
NiF8
Ni9

Fig. 55

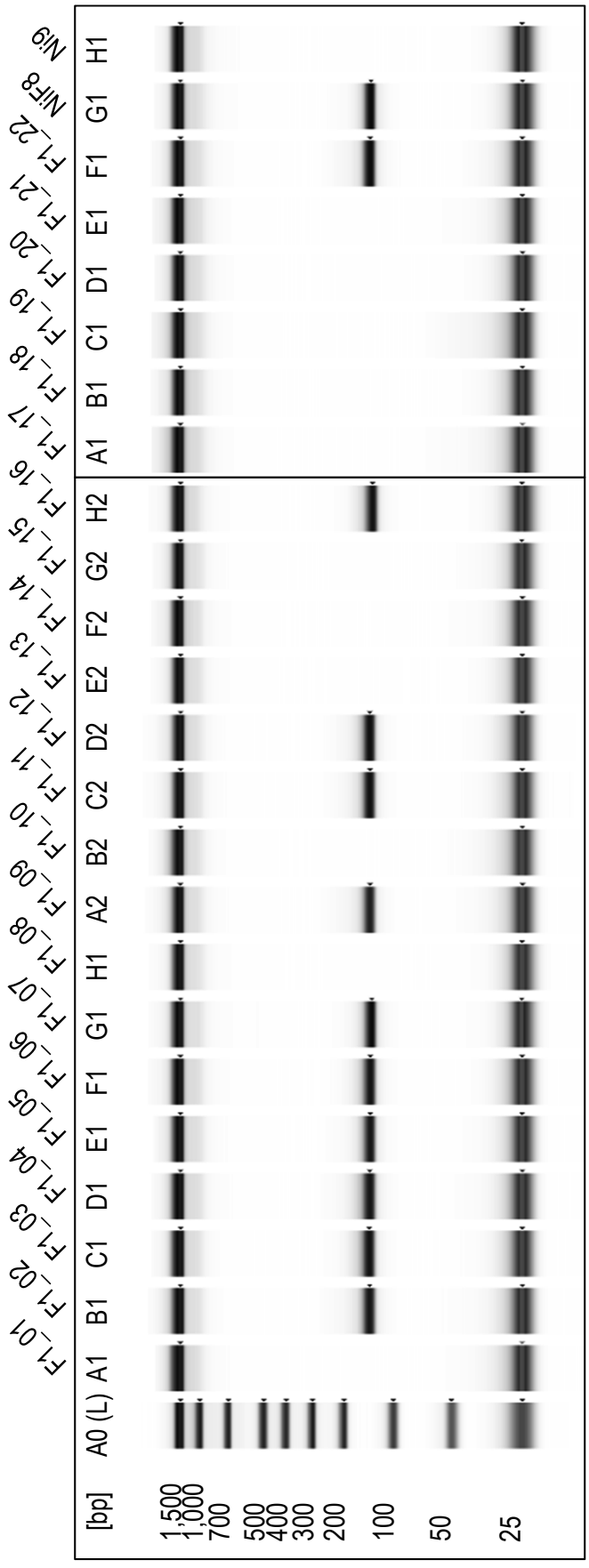

[bp]
1,500
1,000
700
500
400
300
200
100
50
25
A0 (L)
A1
B1
C1
D1
E1
F1
G1
H1
A2
B2
C2
D2
E2
F2
G2
H2
F1_01
F1_02
F1_03
F1_04
F1_05
F1_06
F1_07
F1_08
F1_09
F1_10
F1_11
F1_12
F1_13
F1_14
F1_15
F1_16
F1_17
F1_18
F1_19
F1_20
F1_21
F1_22
NIF8
N19

Fig. 56

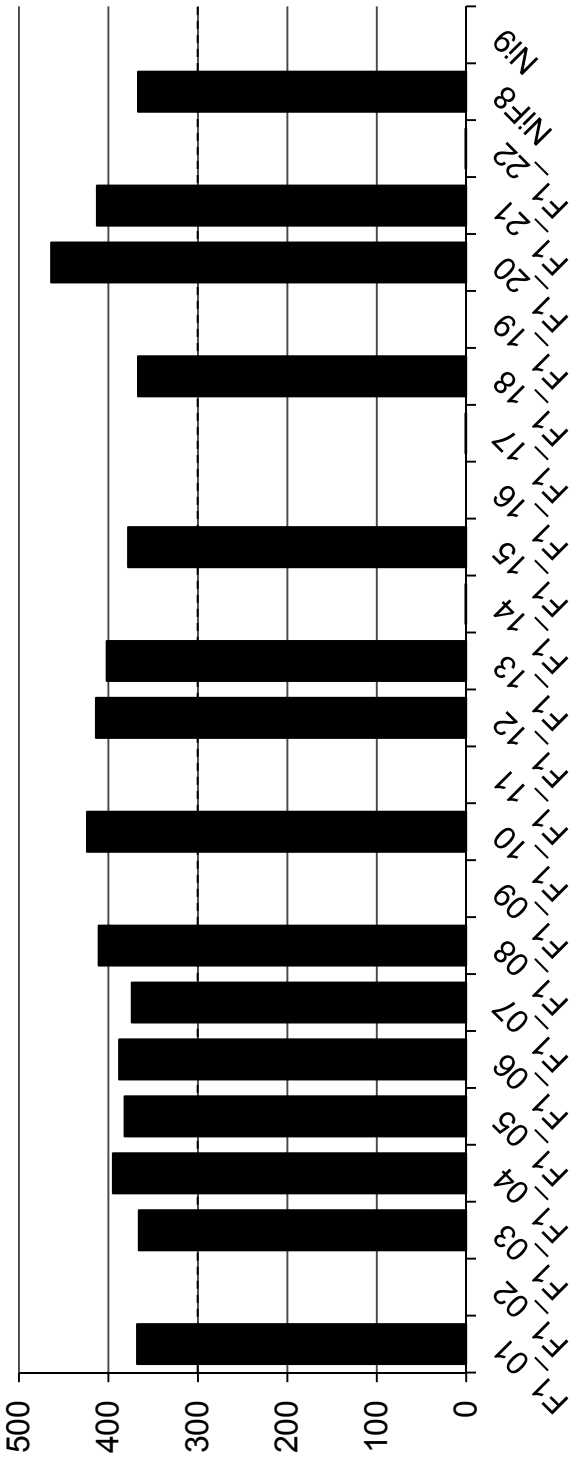

500
400
300
200
100
0
F7
F7_01
F7_02
F7_03
F7_04
F7_05
F7_06
F7_07
F7_08
F7_09
F7_10
F7_11
F7_12
F7_13
F7_14
F7_15
F7_16
F7_17
F7_18
F7_19
F7_20
F7_21
F7_22
Ni-F8
Ni-9

Fig. 57

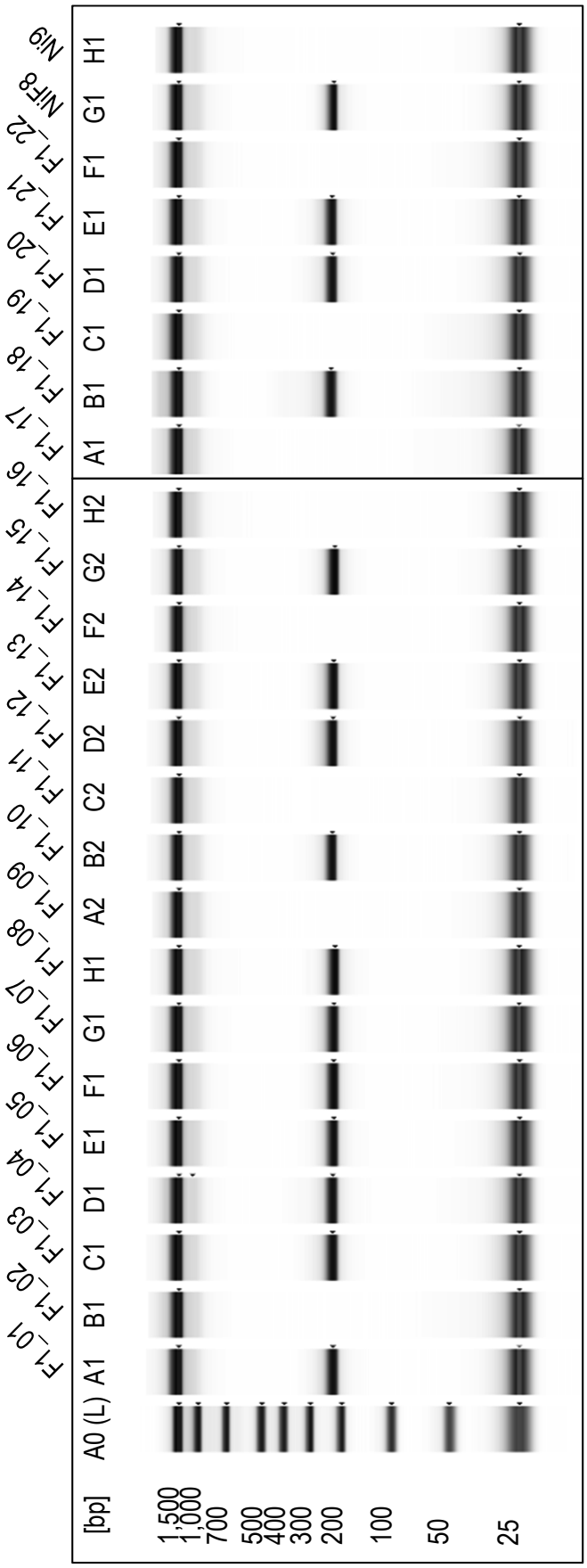

[bp]
1,500
1,000
700
500
400
300
200
100
50
25
A0 (L)
A1
B1
C1
D1
E1
F1
G1
H1
A2
B2
C2
D2
E2
F2
G2
H2
01
02
03
04
05
06
07
08
09
10
11
12
13
14
15
16
17
18
19
20
21
22
NIF8
N19

Fig. 58

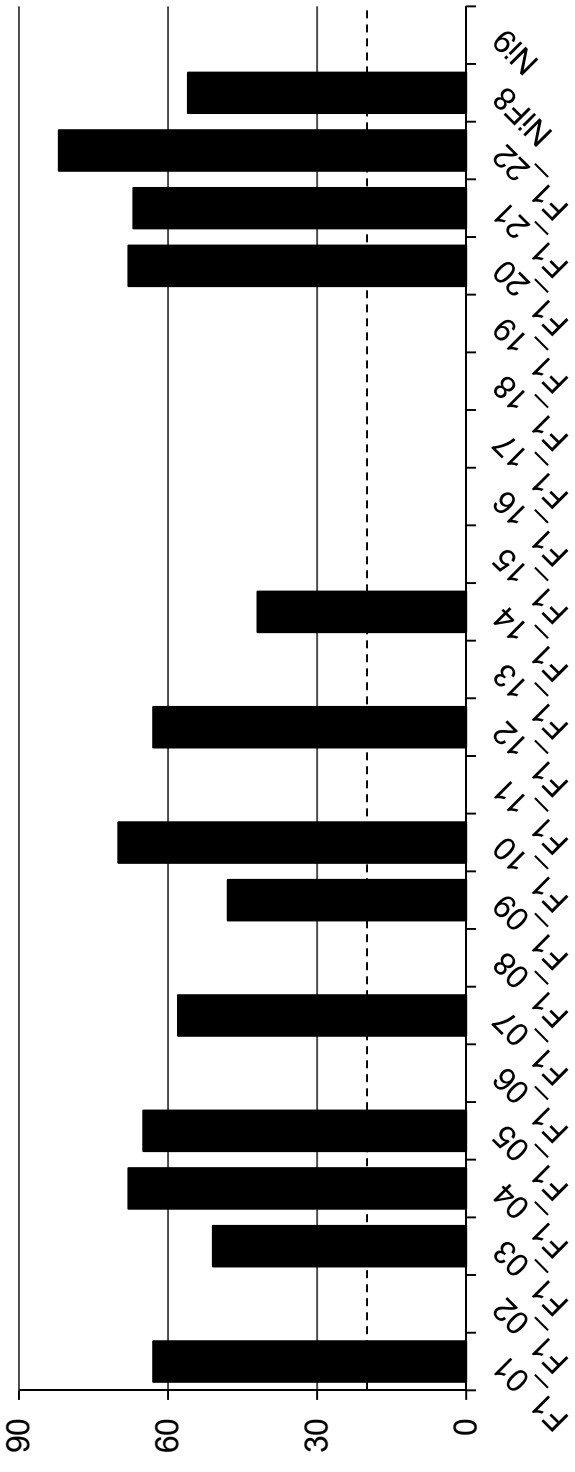

90
60
30
0
F7/01
F7/02
F7/03
F7/04
F7/05
F7/06
F7/07
F7/08
F7/09
F7/10
F7/11
F7/12
F7/13
F7/14
F7/15
F7/16
F7/17
F7/18
F7/19
F7/20
F7/21
F7/22
NiF8
Ni9

Fig. 59

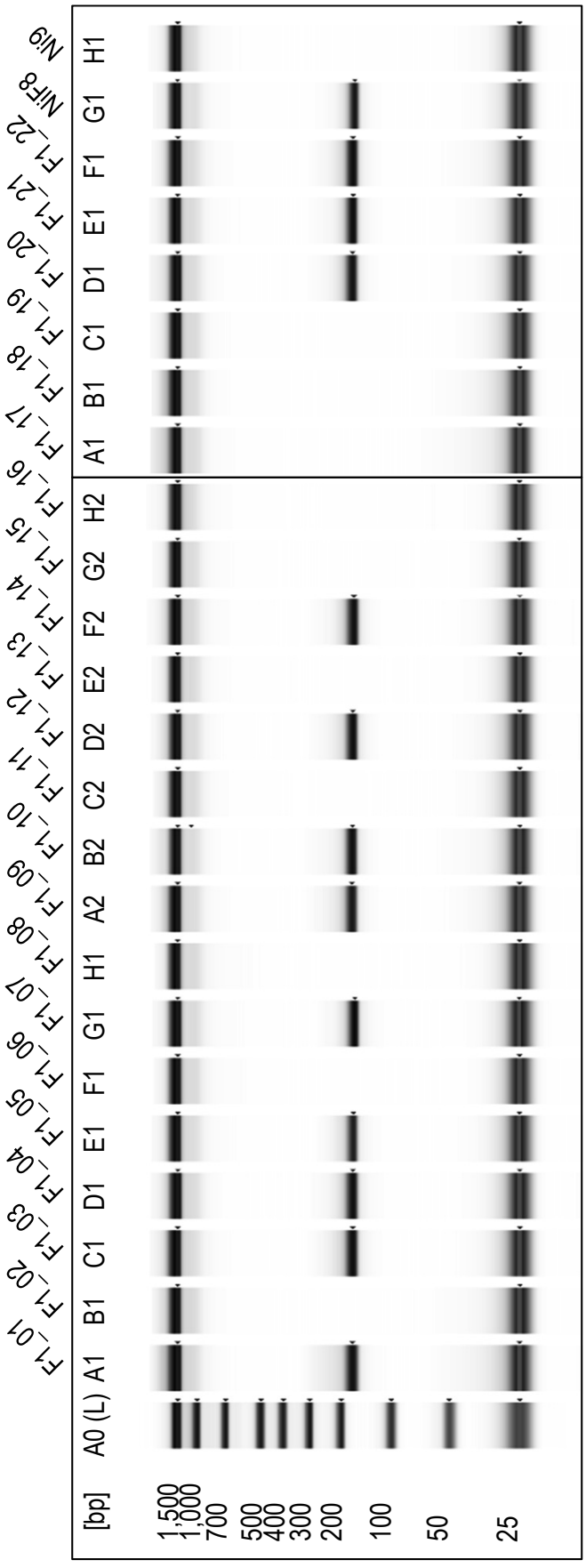

[bp]
1,500
1,000
700
500
400
300
200
100
50
25
A0 (L)
A1
B1
C1
D1
E1
F1
G1
H1
A2
B2
C2
D2
E2
F2
G2
H2
A1
B1
C1
D1
E1
F1
G1
H1
01
02
03
04
05
06
07
08
09
10
11
12
13
14
15
16
17
18
19
20
21
22
NIF8
N19

Fig. 60

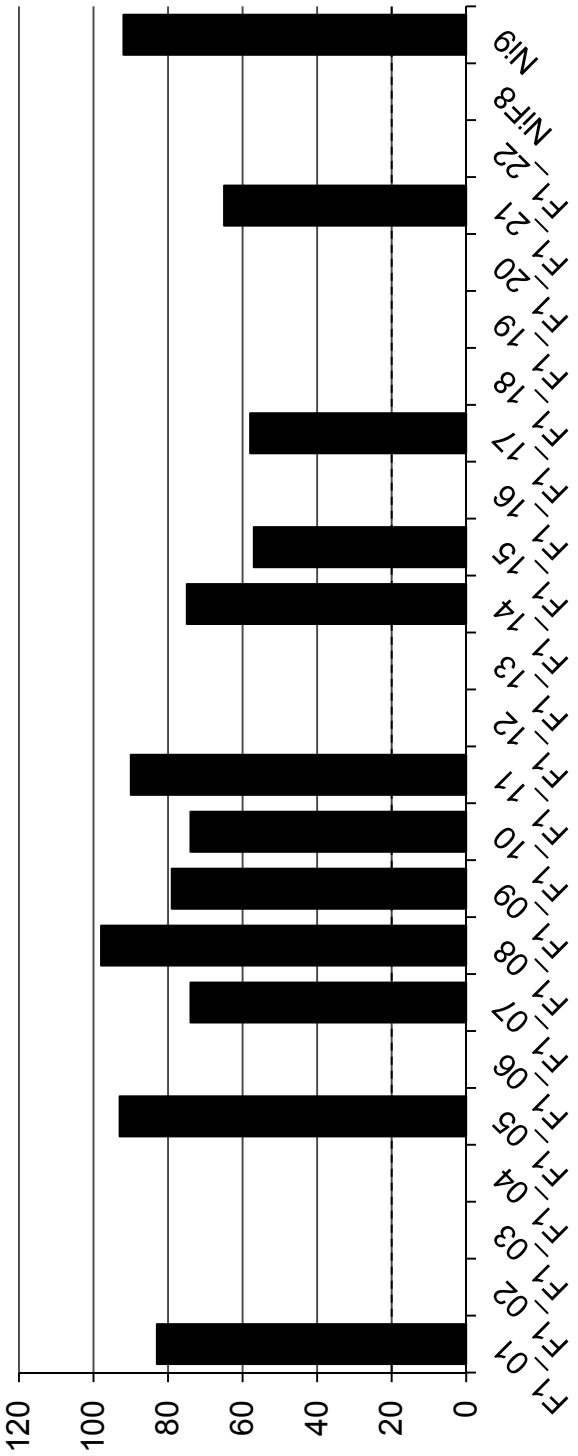

120
100
80
60
40
20
0
F7/01
F7/02
F7/03
F7/04
F7/05
F7/06
F7/07
F7/08
F7/09
F7/10
F7/11
F7/12
F7/13
F7/14
F7/15
F7/16
F7/17
F7/18
F7/19
F7/20
F7/21
F7/22
NiF8
Ni9

Fig. 61

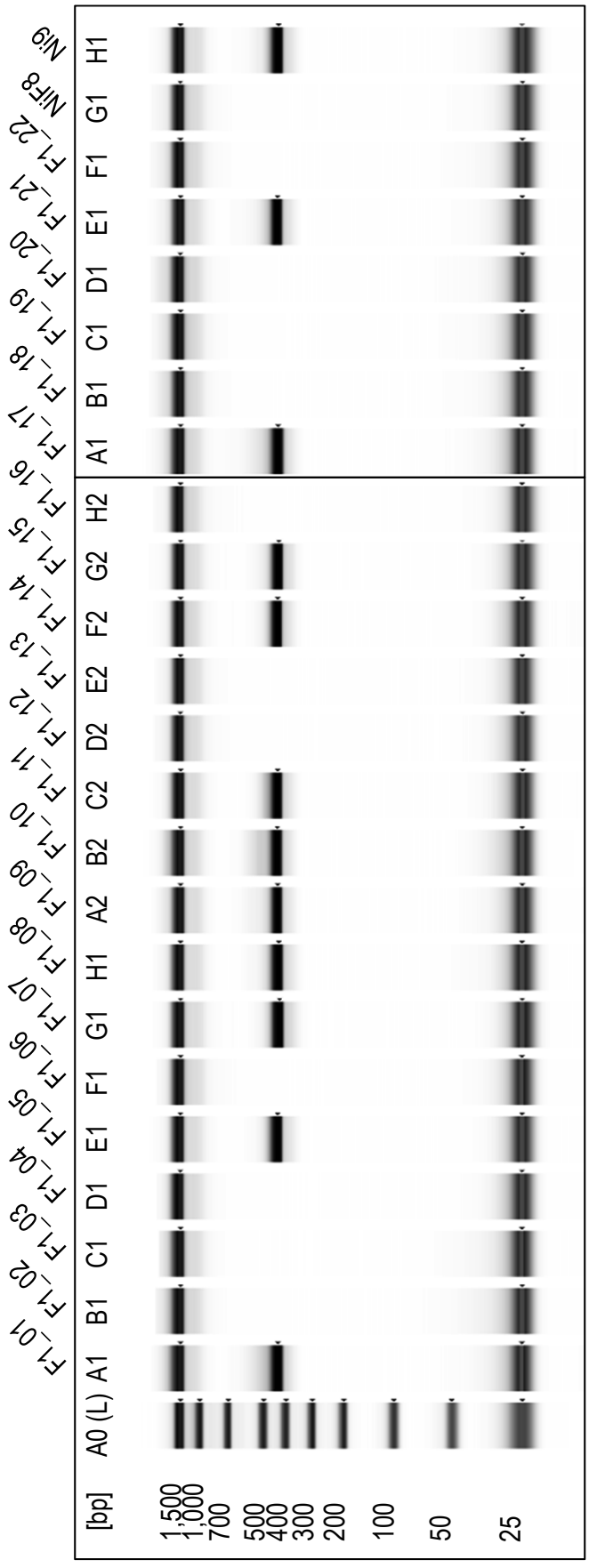

[bp]
1,500
1,000
700
500
400
300
200
100
50
25
A0 (L)
A1
B1
C1
D1
E1
F1
G1
H1
A2
B2
C2
D2
E2
F2
G2
H2
F1_01
F1_02
F1_03
F1_04
F1_05
F1_06
F1_07
F1_08
F1_09
F1_10
F1_11
F1_12
F1_13
F1_14
F1_15
F1_16
F1_17
F1_18
F1_19
F1_20
F1_21
F1_22
NIF8
NI9

Fig. 62

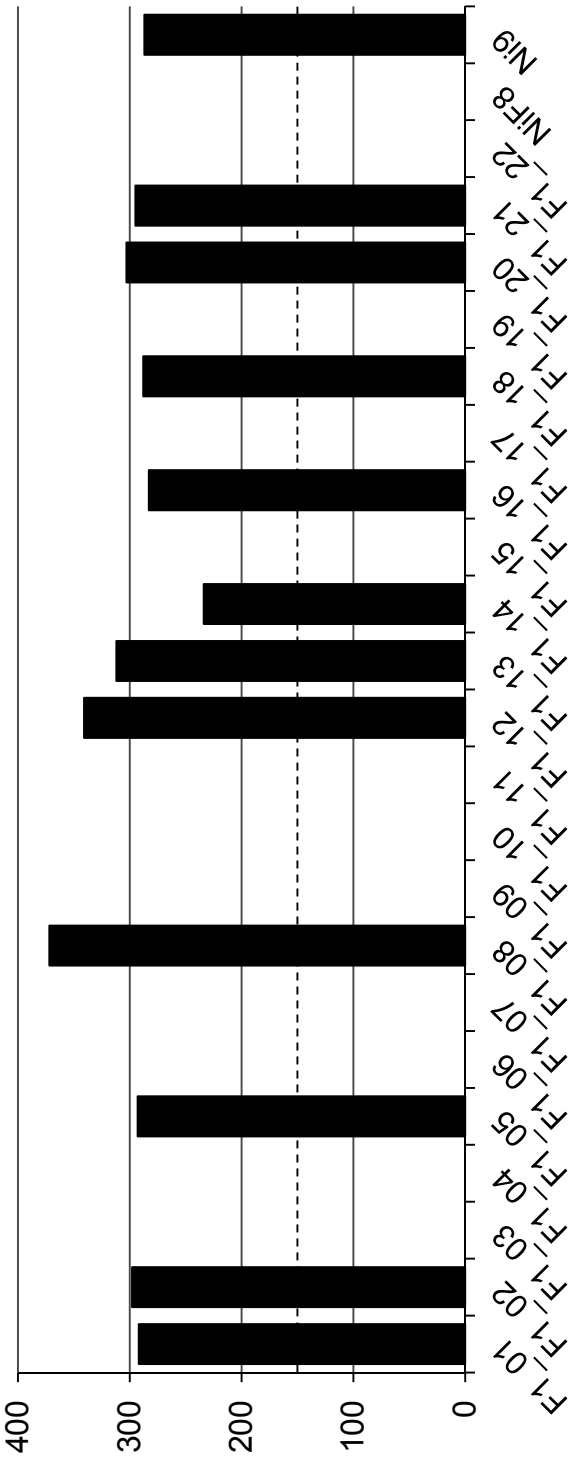

400
300
200
100
0
F7/01
F7/02
F7/03
F7/04
F7/05
F7/06
F7/07
F7/08
F7/09
F7/10
F7/11
F7/12
F7/13
F7/14
F7/15
F7/16
F7/17
F7/18
F7/19
F7/20
F7/21
F7/22
NiF8
Ni9

Fig. 63

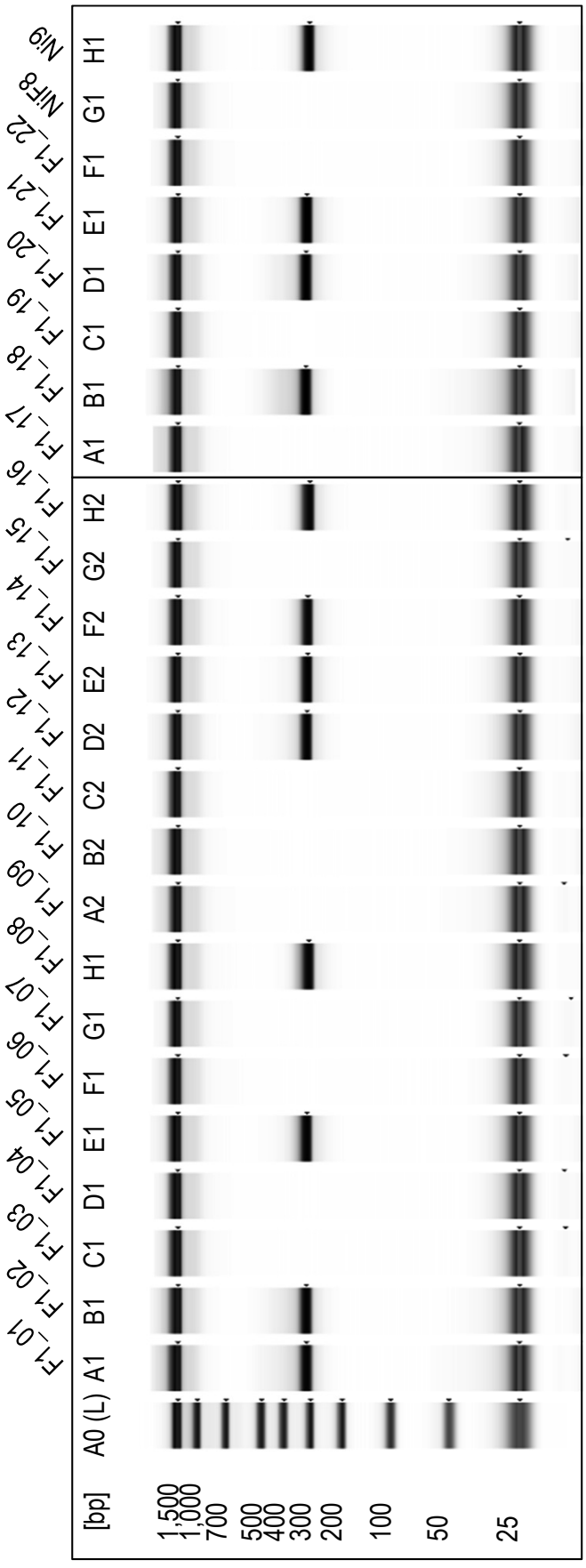

[bp]
1,500
1,000
700
500
400
300
200
100
50
25
A0 (L)
A1
B1
C1
D1
E1
F1
G1
H1
A2
B2
C2
D2
E2
F2
G2
H2
F1_01
F1_02
F1_03
F1_04
F1_05
F1_06
F1_07
F1_08
F1_09
F1_10
F1_11
F1_12
F1_13
F1_14
F1_15
F1_16
F1_17
F1_18
F1_19
F1_20
F1_21
F1_22
NIF8
N19

Fig. 64

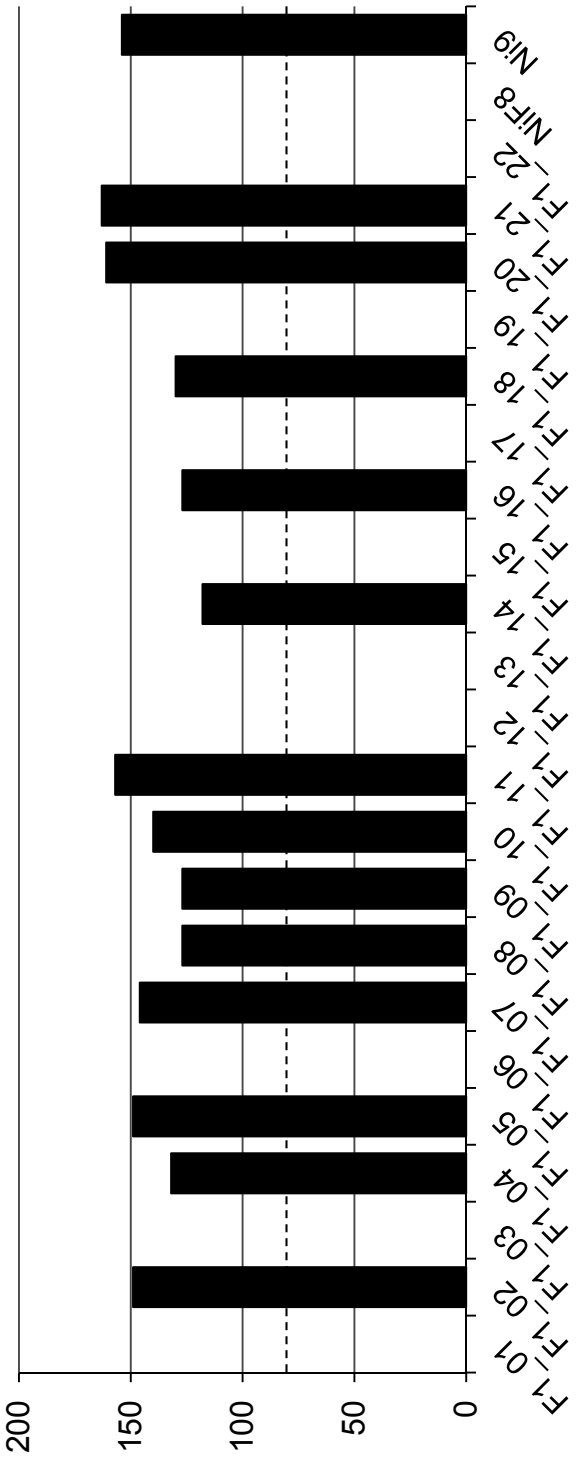

200
150
100
50
0
F7/01
F7/02
F7/03
F7/04
F7/05
F7/06
F7/07
F7/08
F7/09
F7/10
F7/11
F7/12
F7/13
F7/14
F7/15
F7/16
F7/17
F7/18
F7/19
F7/20
F7/21
F7/22
NiF8
Ni9

Fig. 65

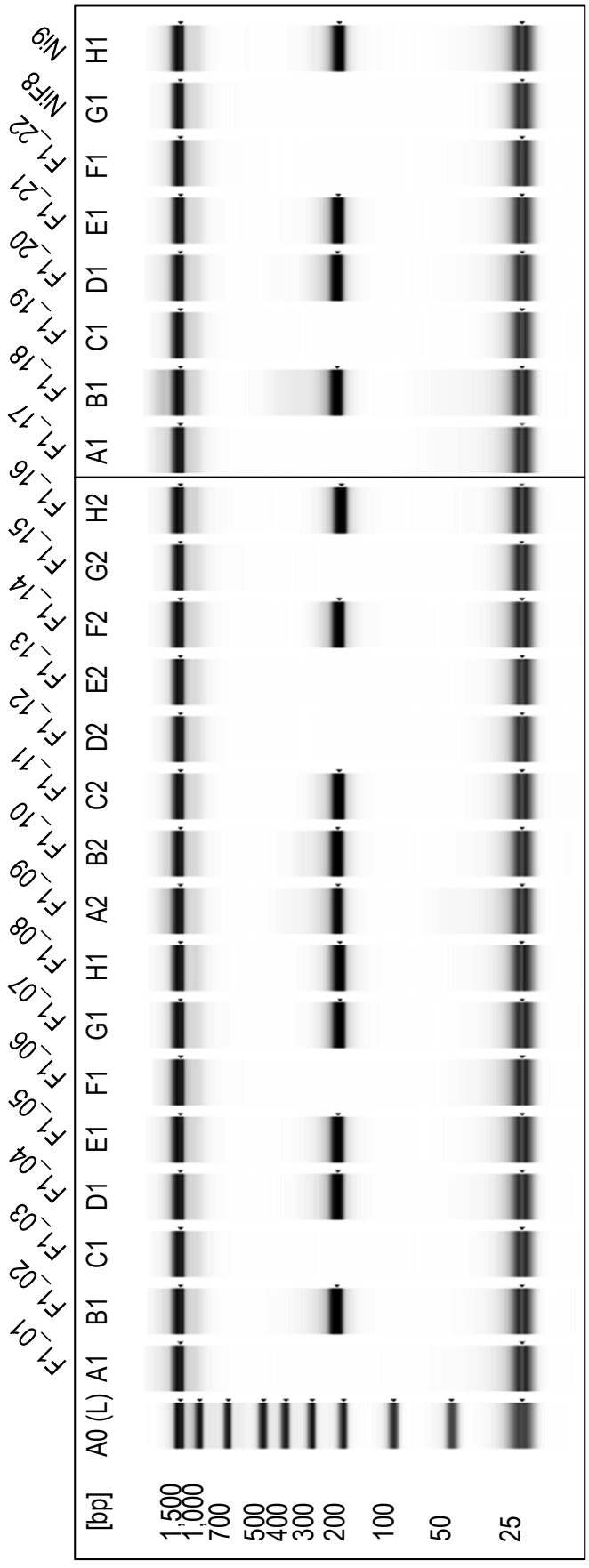

[bp]
1,500
1,000
700
500
400
300
200
100
50
25
A0 (L)
A1
B1
C1
D1
E1
F1
G1
H1
A2
B2
C2
D2
E2
F2
G2
H2
01
02
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04
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07
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09
10
11
12
13
14
15
16
17
18
19
20
21
22
NIF8
N19

Fig. 66

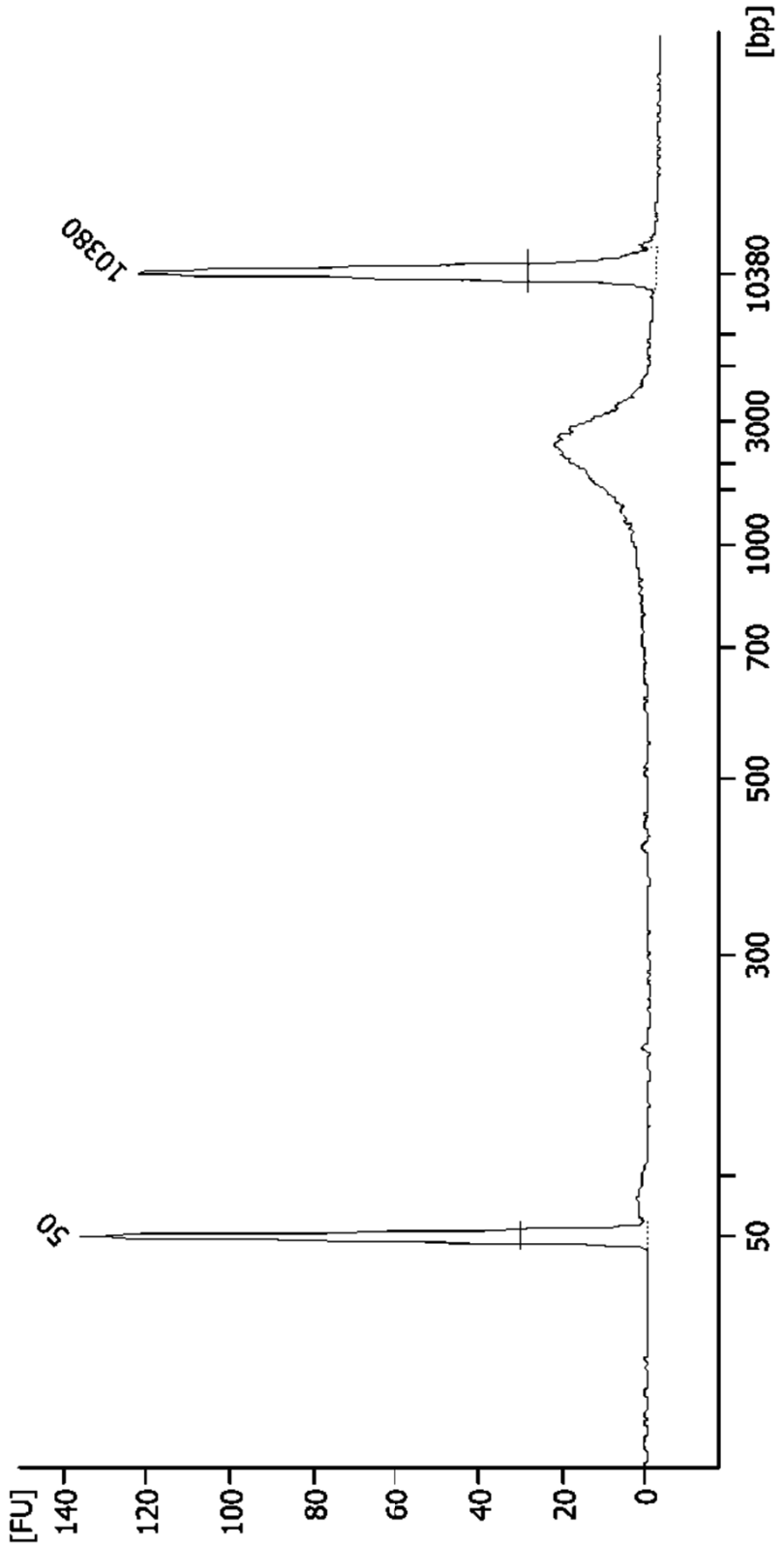

[FU]
140
120
100
80
60
40
20
0
50
300
500
700
1000
3000
10380
[bp]
50
10380

Fig. 67

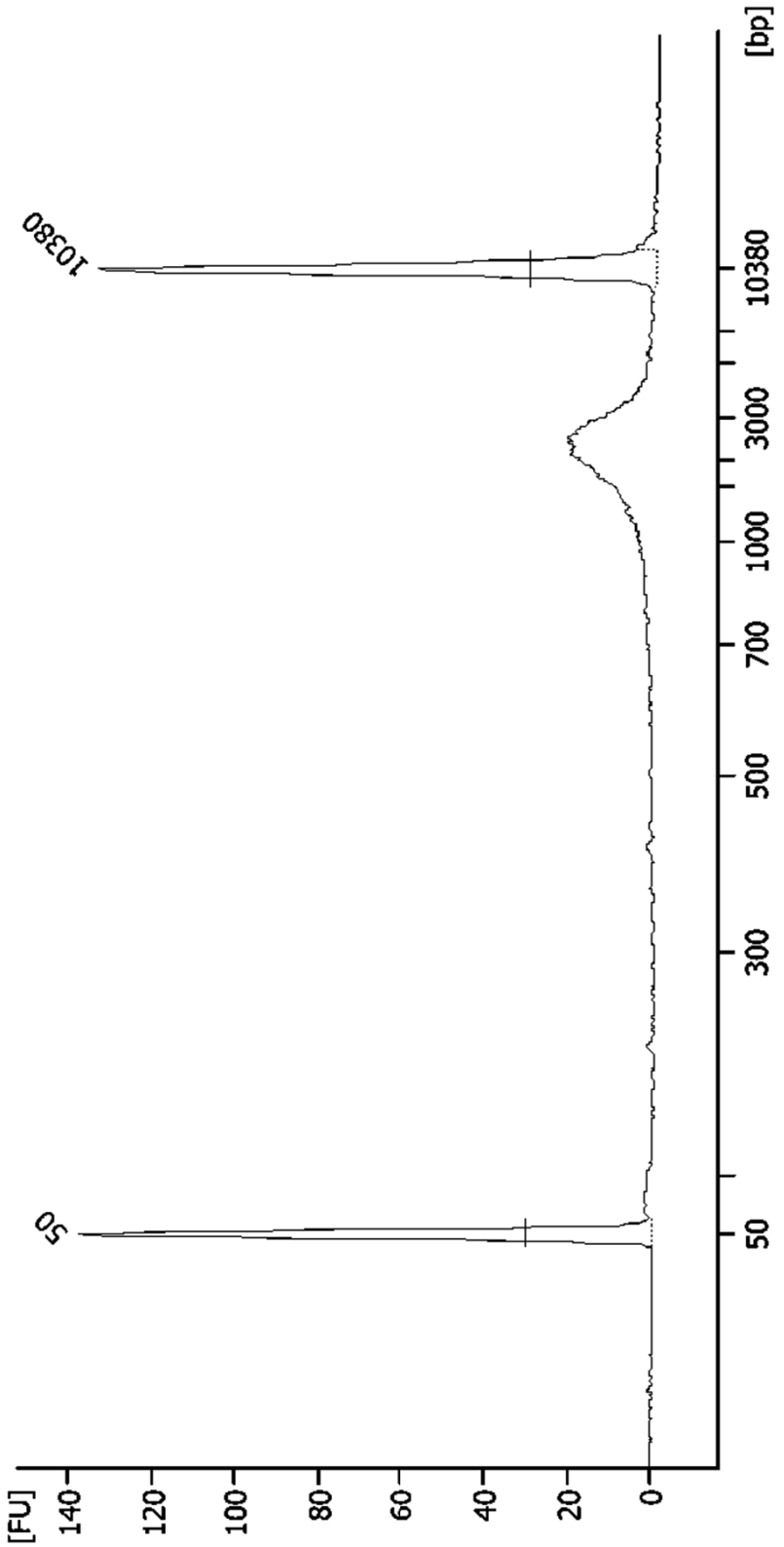

[FU]
140
120
100
80
60
40
20
0
50
10380
50
300
500
700
1000
3000
10380
[bp]

Fig. 68

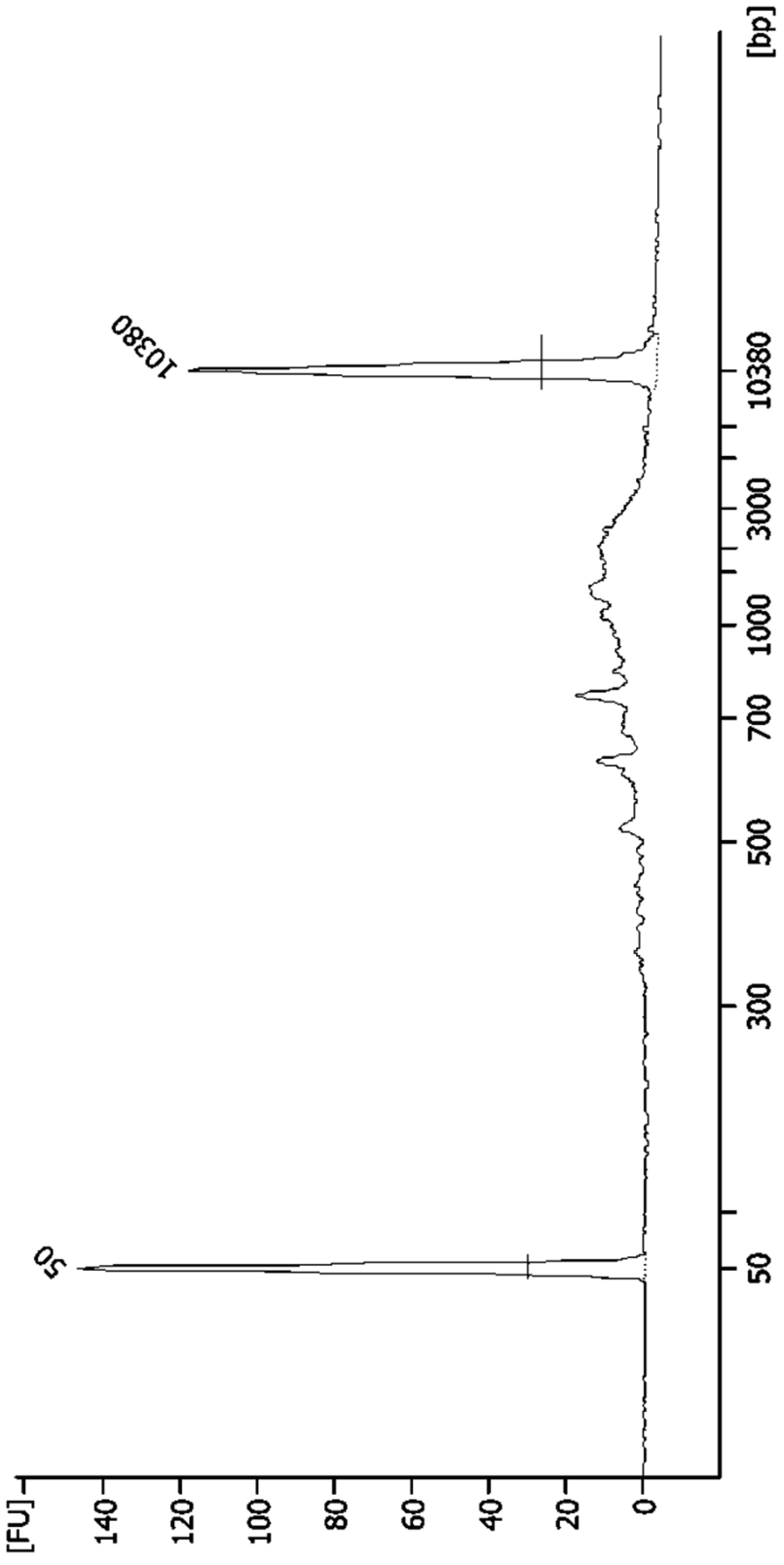

[FU]
140
120
100
80
60
40
20
0
50
300
500
700
1000
3000
10380
[bp]
50
10380

Fig. 69

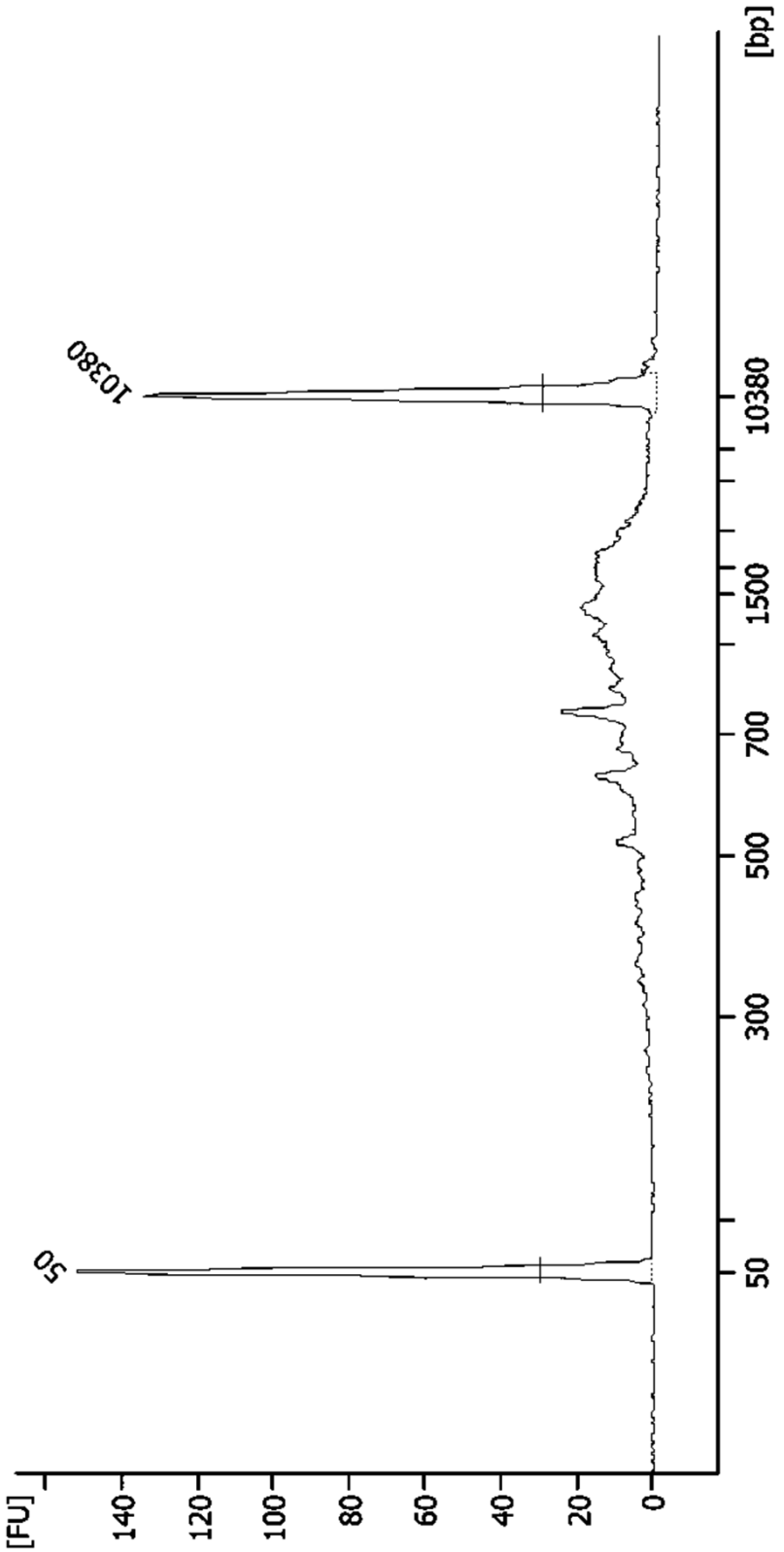


Fig. 70

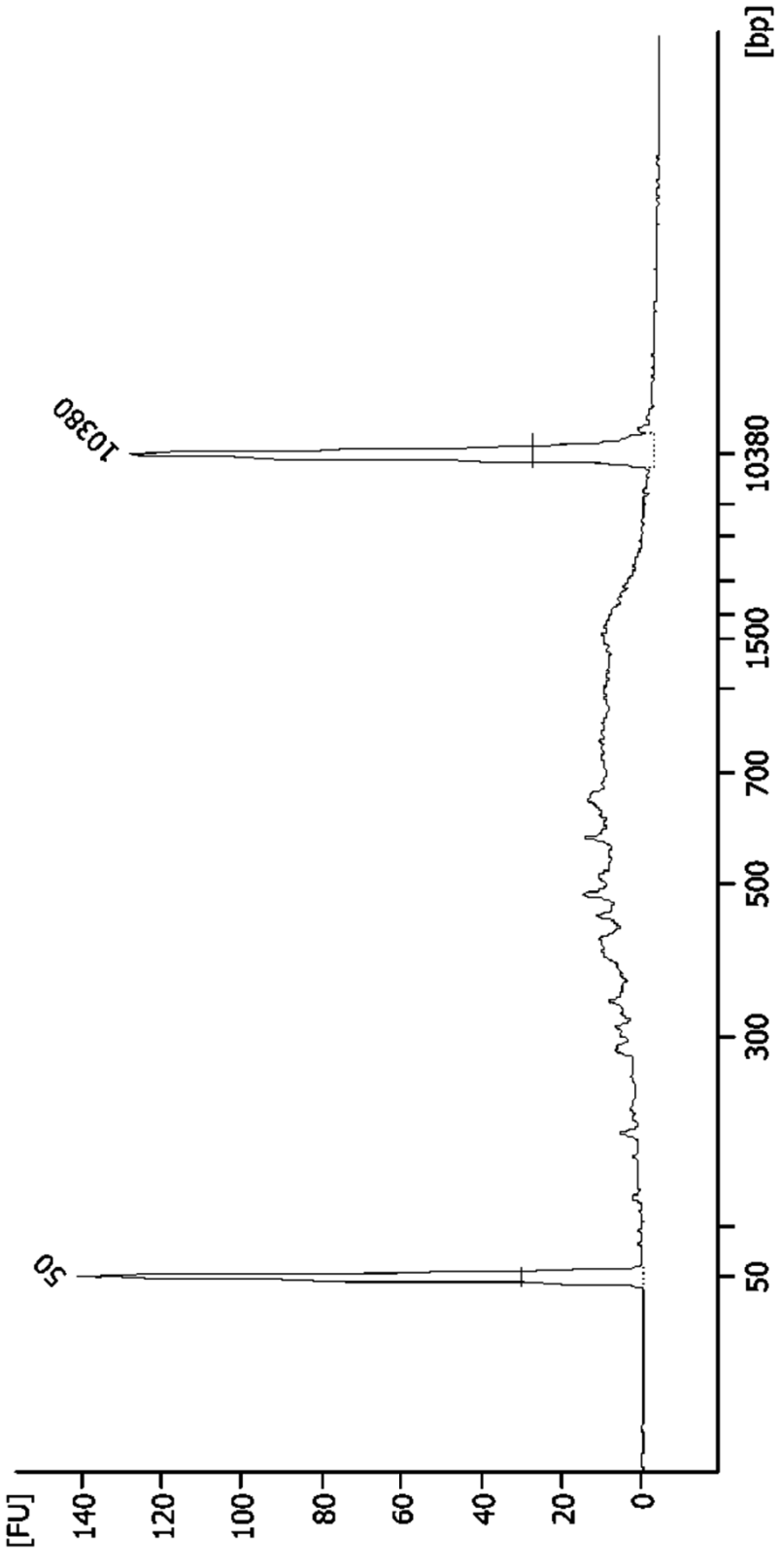


Fig. 71

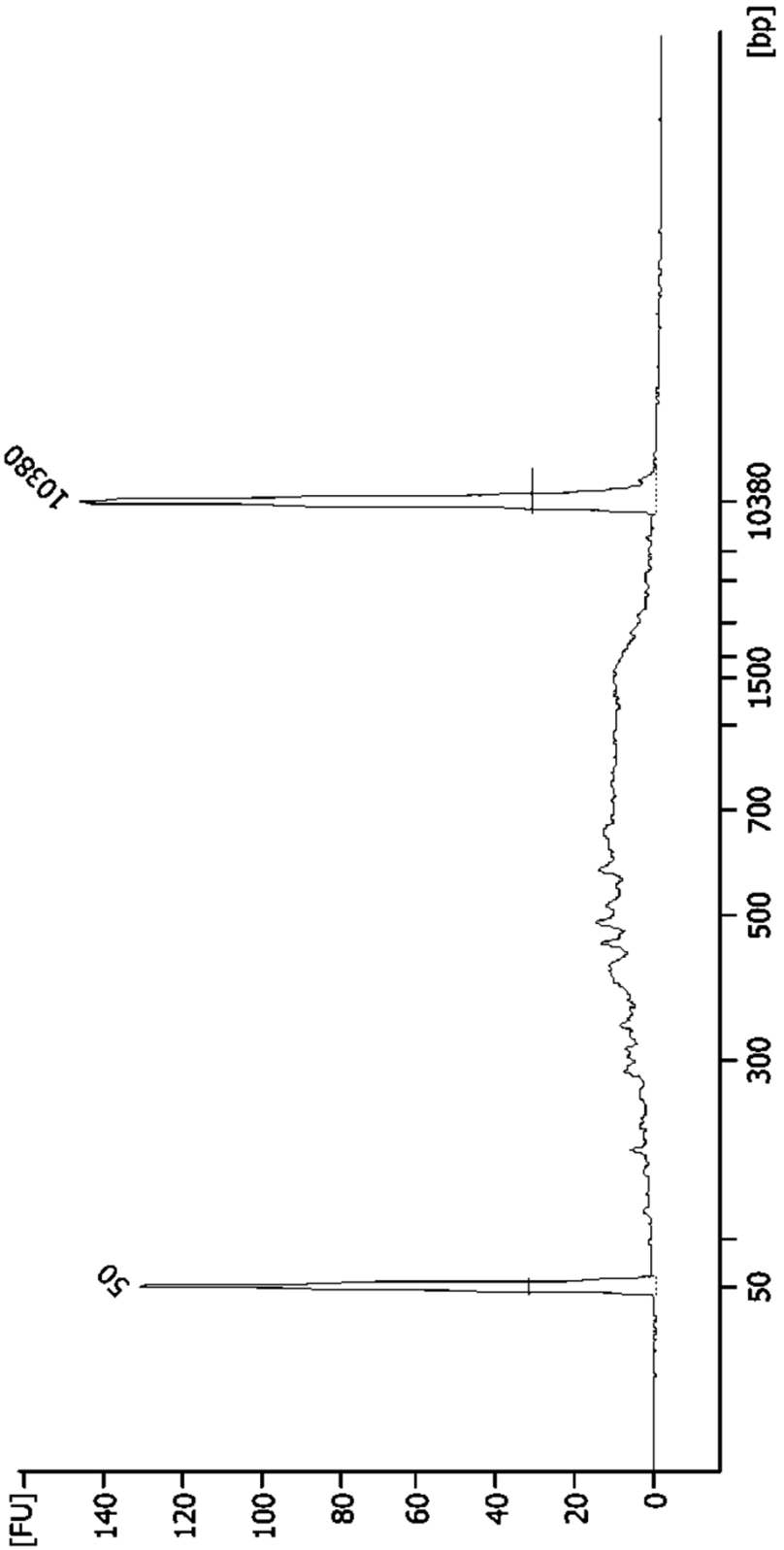


Fig. 72

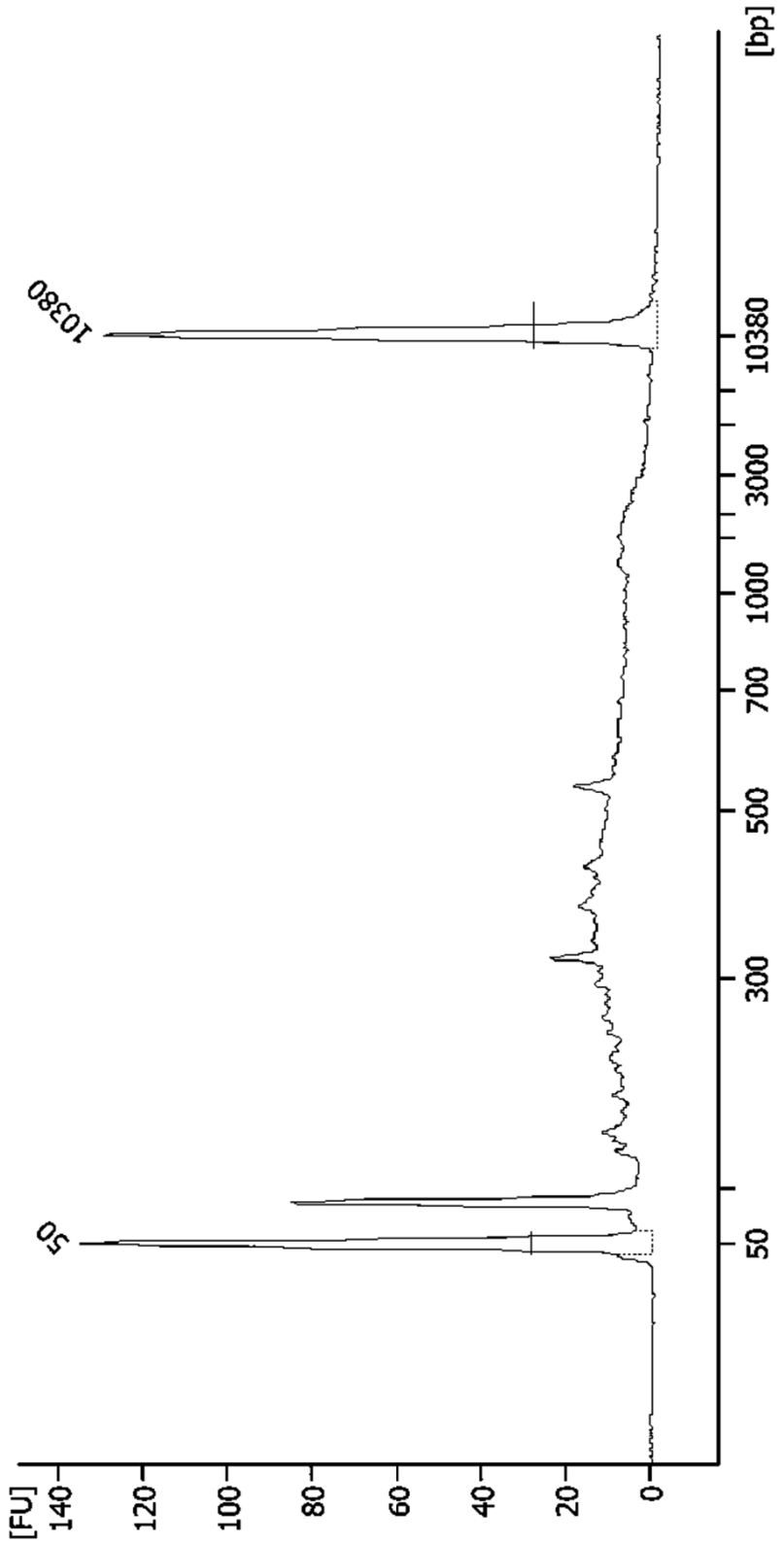

[FU]
140
120
100
80
60
40
20
0
50
10380
50
300
500
700
1000
3000
10380
[bp]

Fig. 73

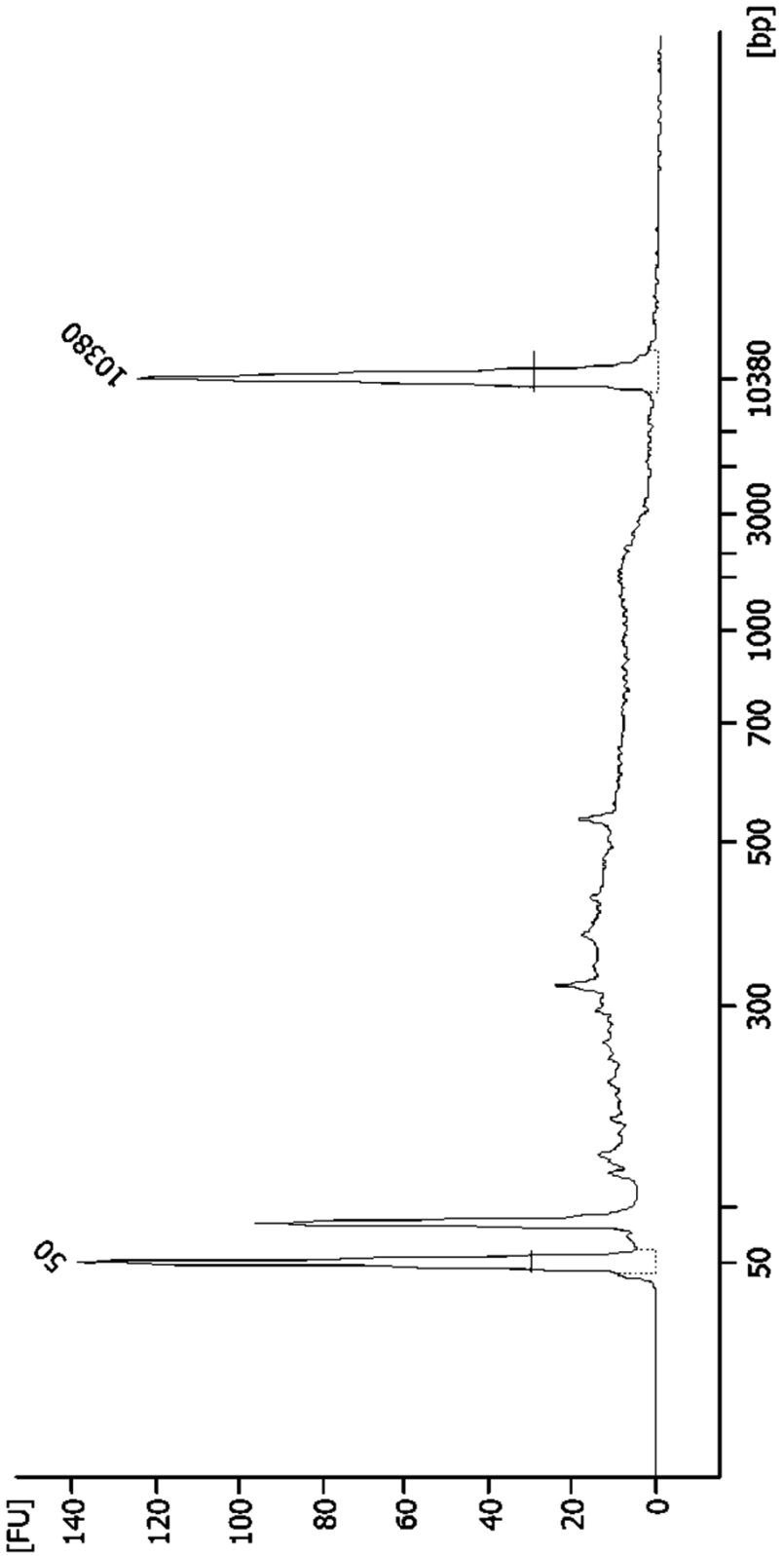

[FU]
140
120
100
80
60
40
20
0
50
10380
50
300
500
700
1000
3000
10380
[bp]

Fig. 74

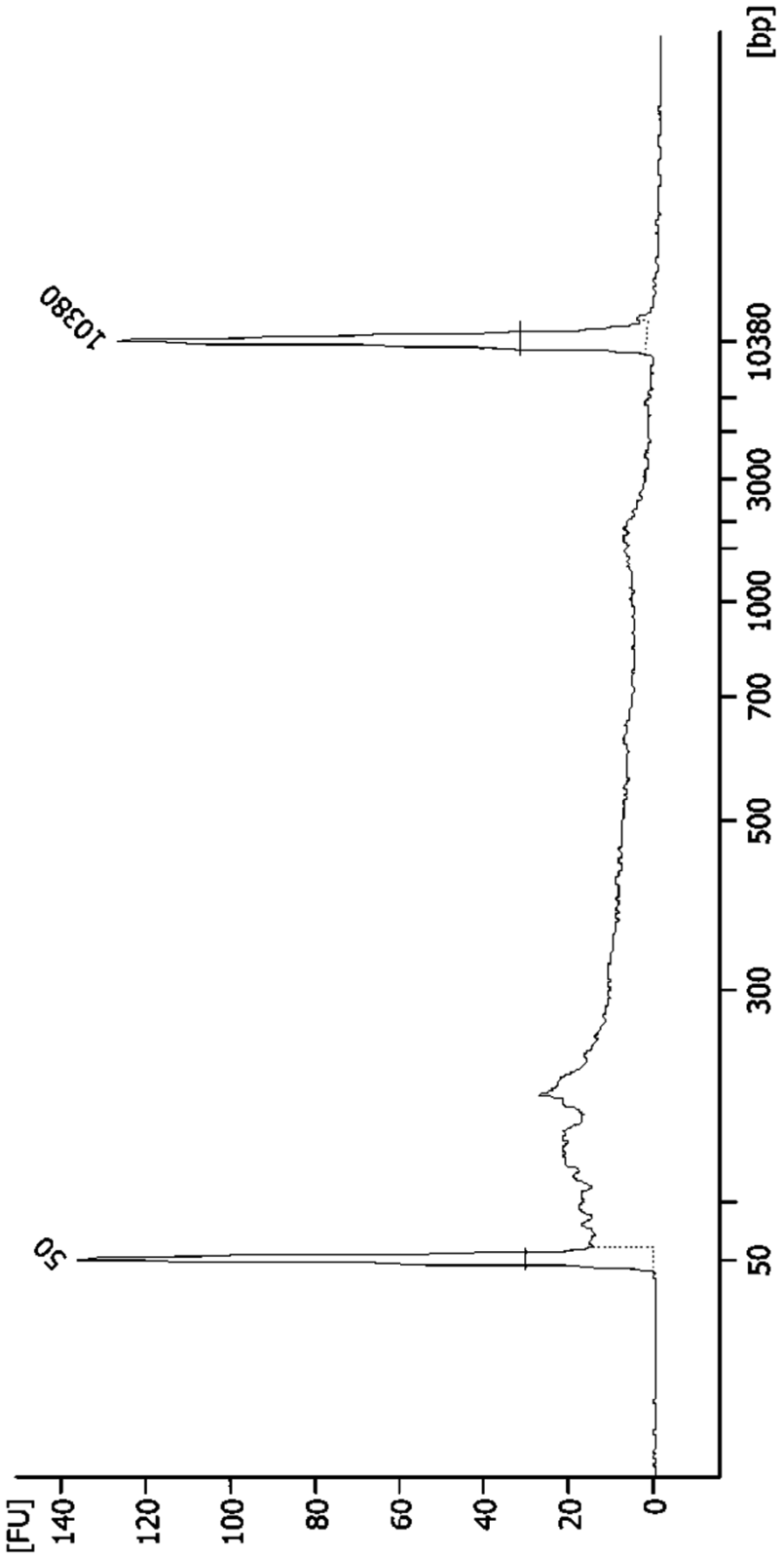

[FU]
140
120
100
80
60
40
20
0
50
10380
50
300
500
700
1000
3000
10380
[bp]

Fig. 75

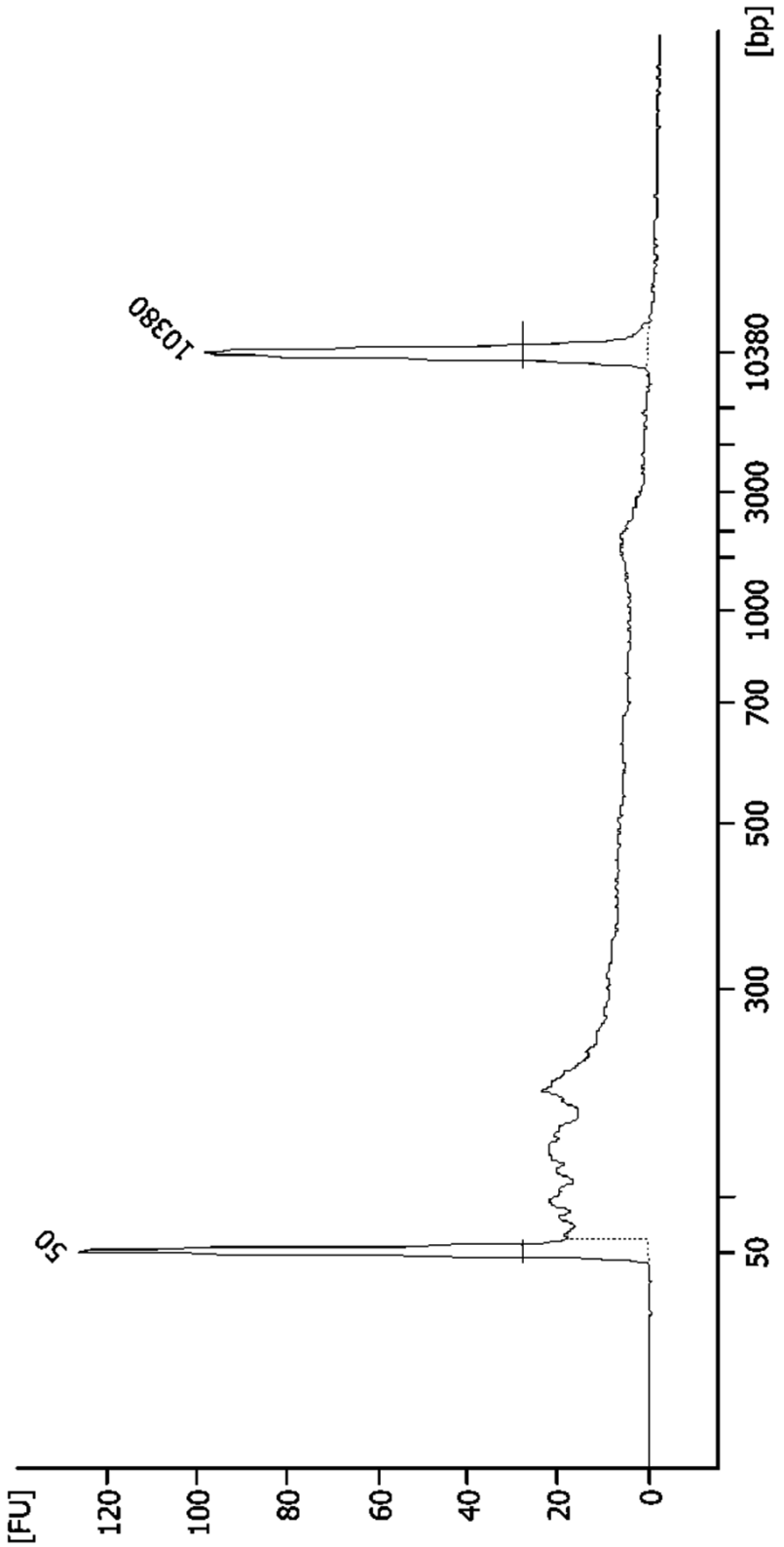

[FU]
120
100
80
60
40
20
0
50
10380
50
300
500
700
1000
3000
10380
[bp]

Fig. 76

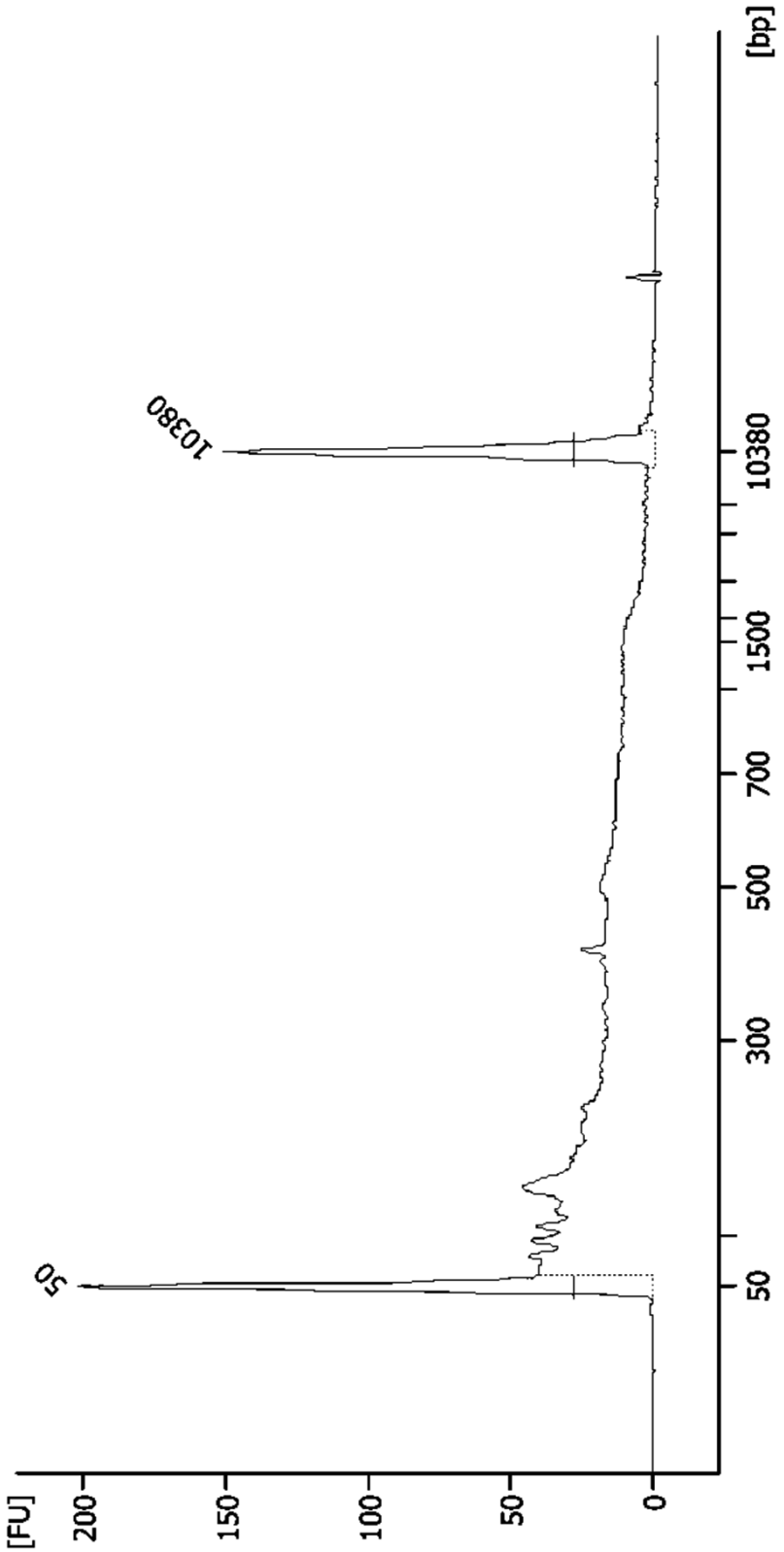


Fig. 77

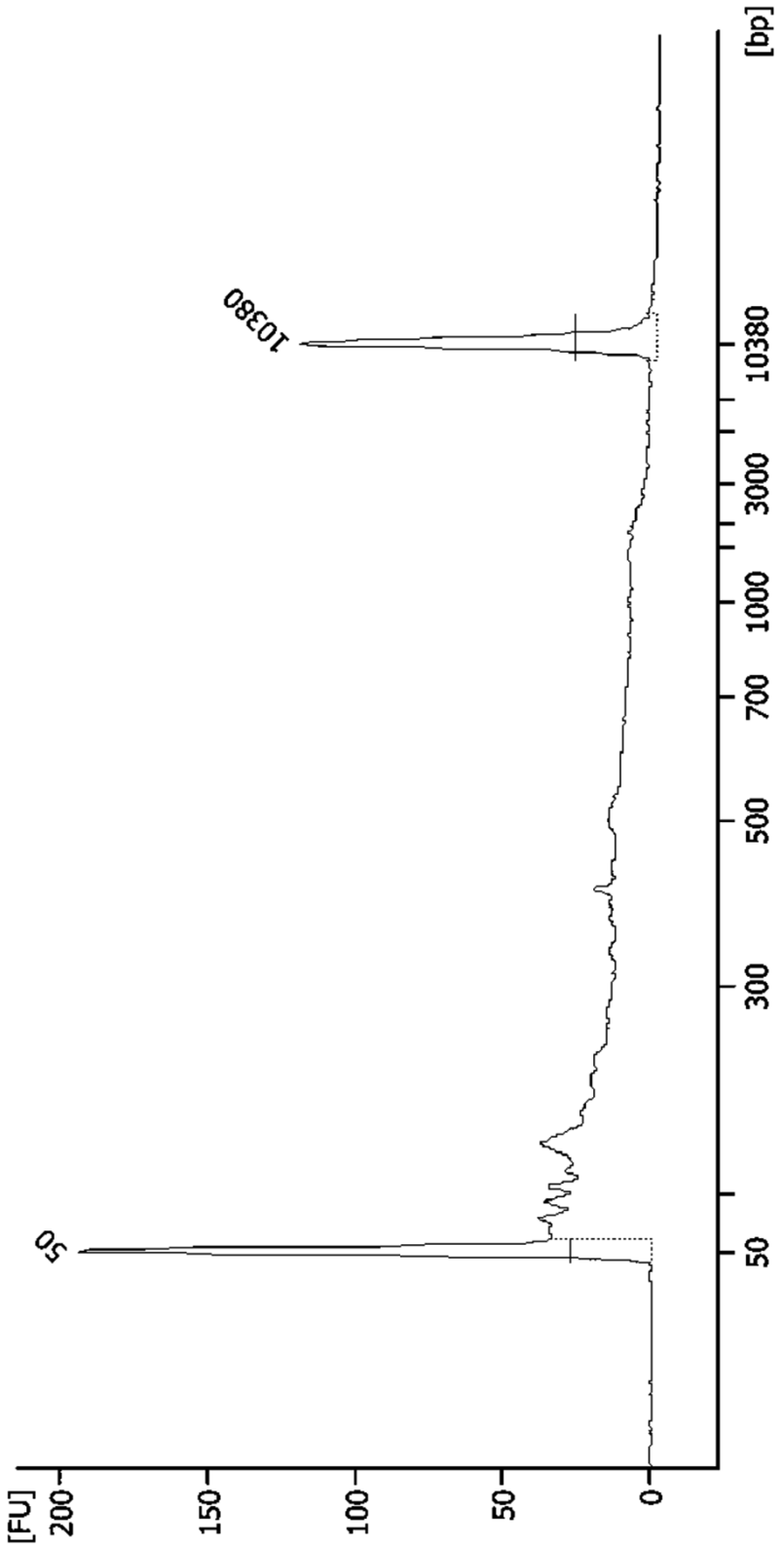


Fig. 78

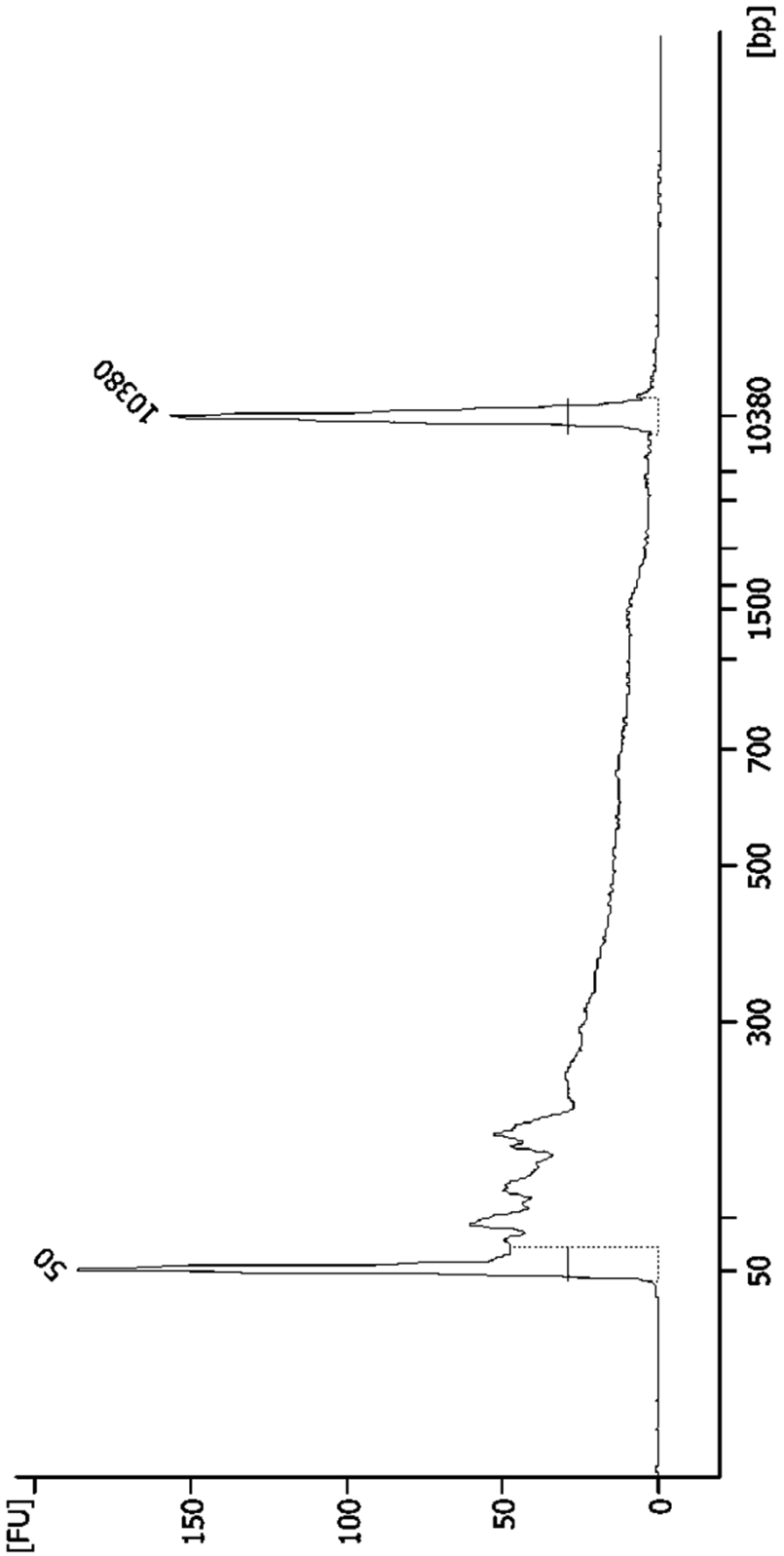


Fig. 79

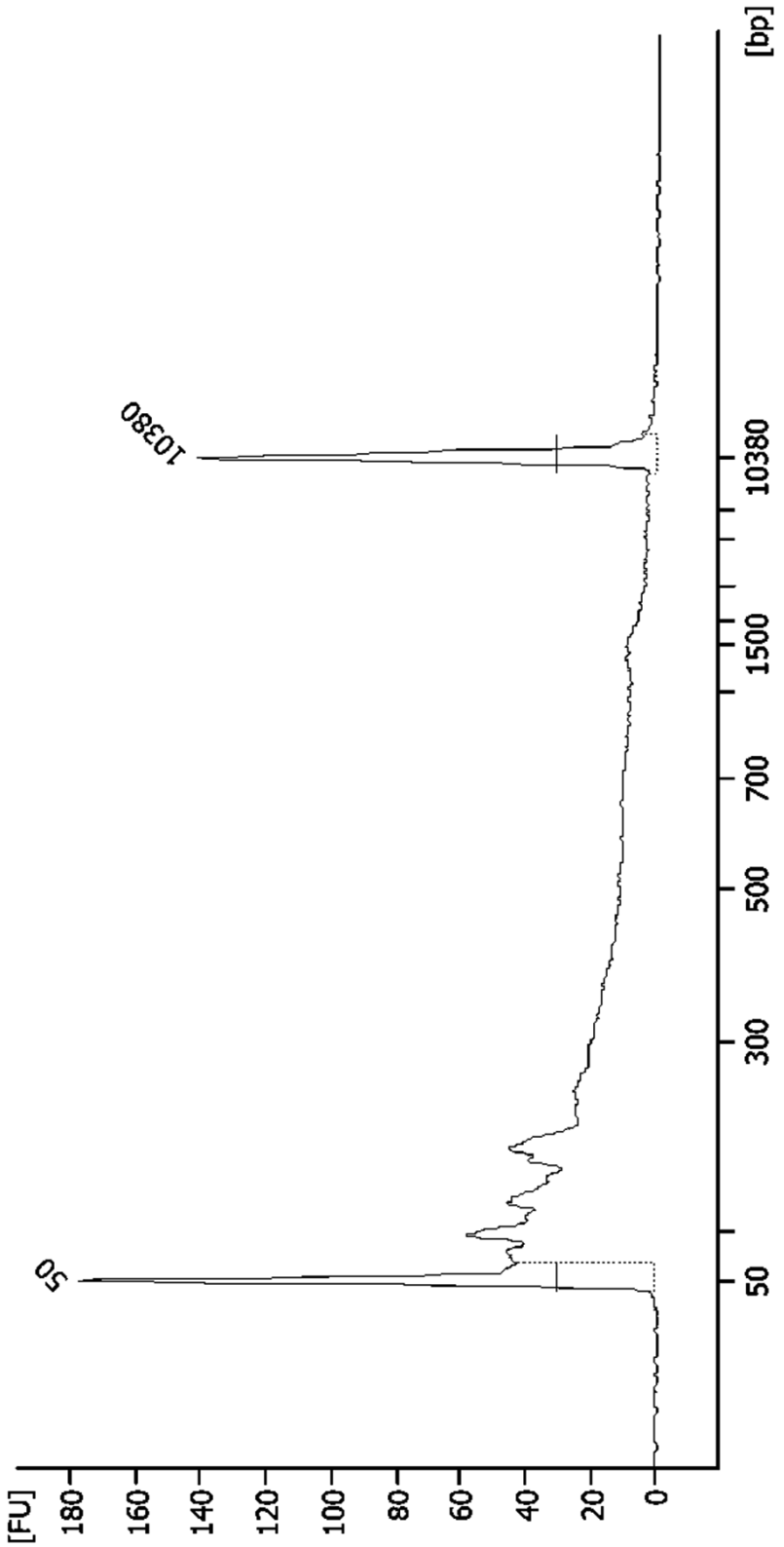

[FU]
180
160
140
120
100
80
60
40
20
0
50
10380
50
300
500
700
1500
10380
[bp]

Fig. 80

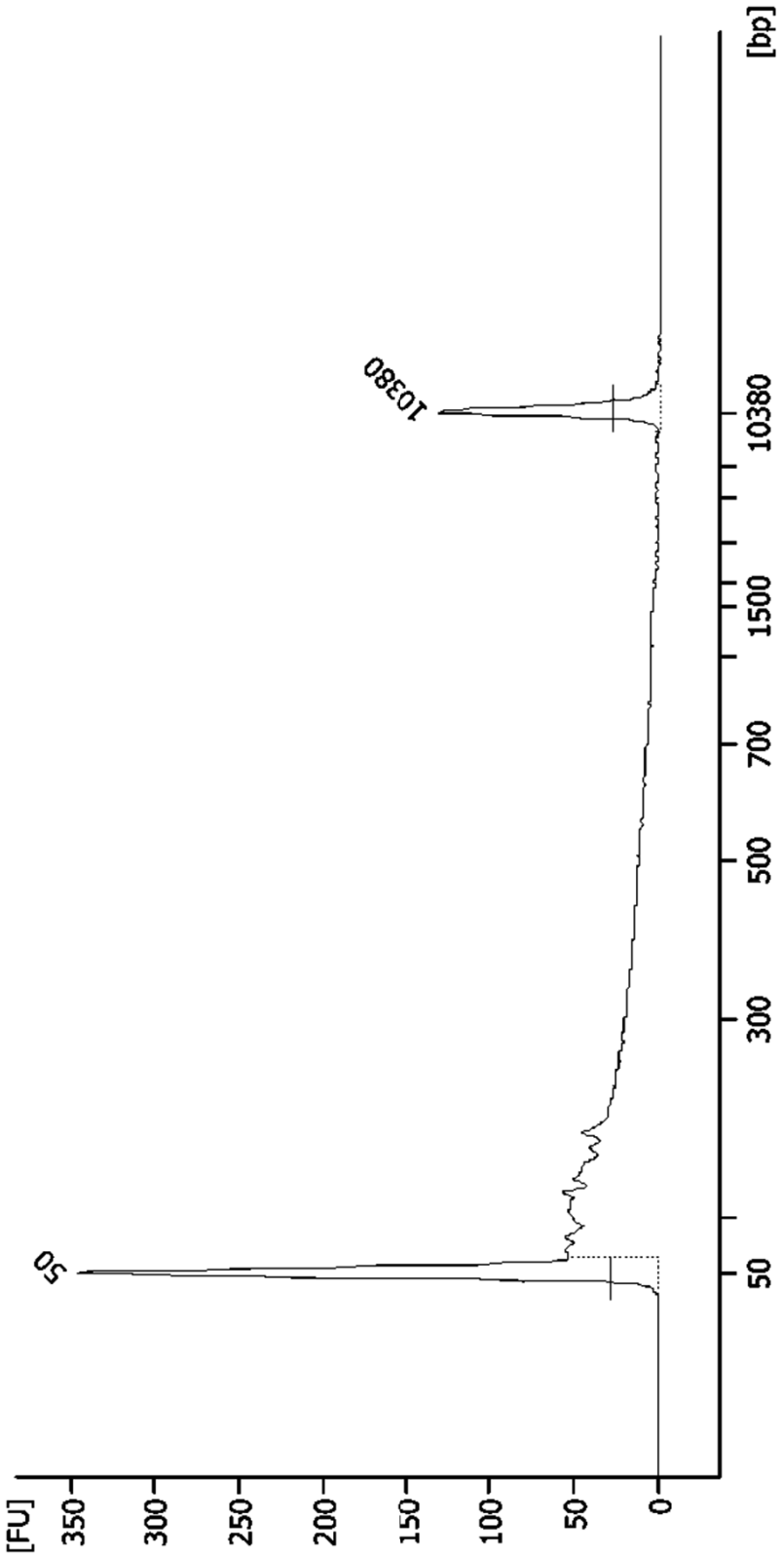

[FU]
350
300
250
200
150
100
50
0
50
10380
[bp]
50
300
500
700
1500
10380

Fig. 81

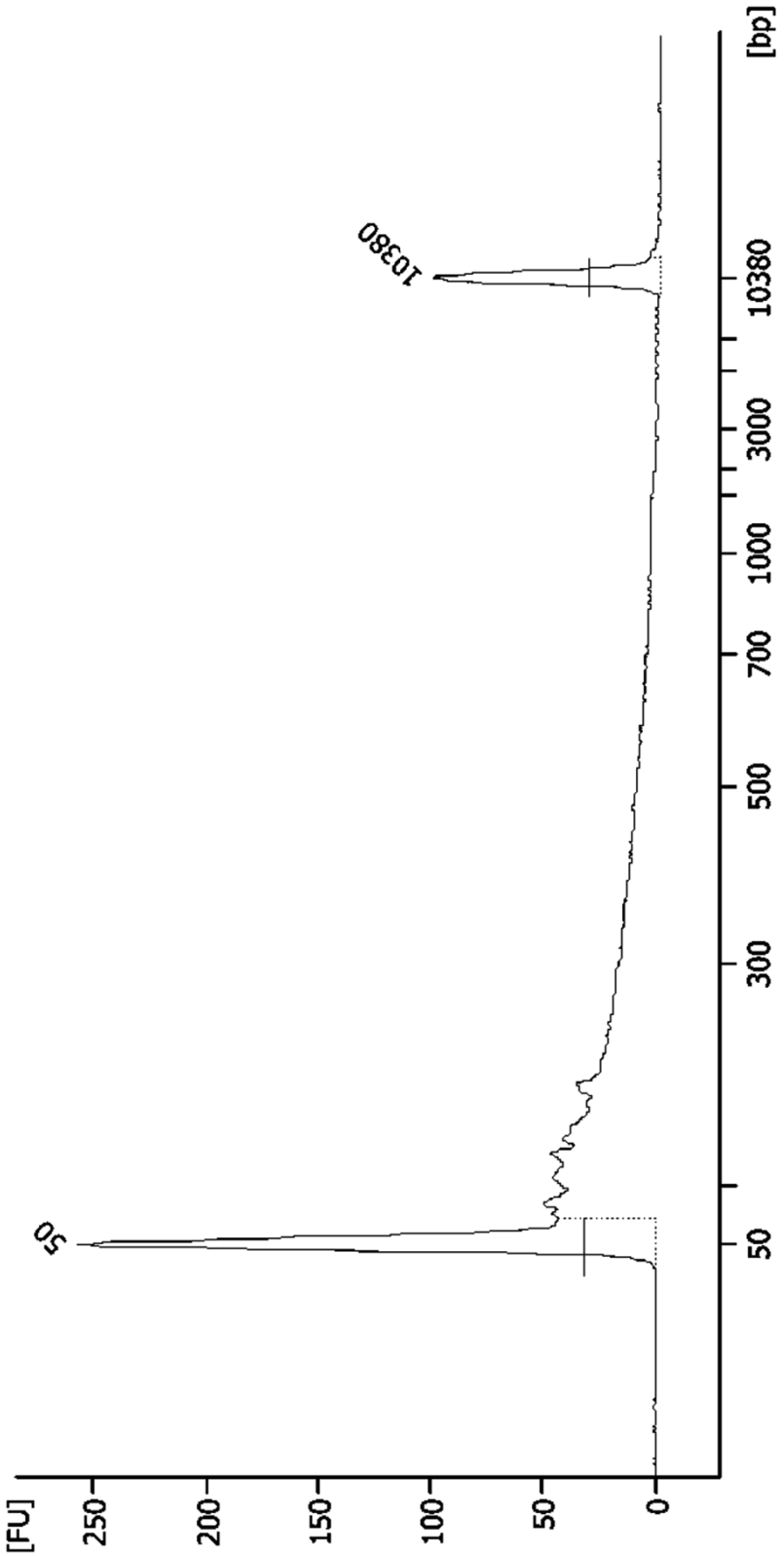

[FU]
250
200
150
100
50
0
50
10380
50
300
500
700
1000
3000
10380
[bp]

Fig. 82

$y = 3E+08x^{-6.974}$ ($r = 0.985$)

Primer concentration		Primer length															
μM	Factor relative to reference	8	9	10	11	12	14	16	18	20	22	24	26	28	29	30	35
0.6	Reference	×	×	×	×	×	×	×	×	×	×	×	×	×	×	×	×
2	3.3-fold	×	×	×	×	×	×	×	×	×	×	×	×	×	×	×	×
4	6.7-fold	×	×	×	×	×	○	○	○	○	○	○	○	○	×	×	×
6	10.0-fold	×	×	×	×	×	○	○	○	○	○	○	○	○	○	○	×
8	13.3-fold	×	×	×	×	○	○	○	○	○	○	○	○	○	○	×	×
10	16.7-fold	×	×	×	×	○	○	○	○	○	○	○	○	○	○	×	×
20	33.3-fold	×	×	×	○	○	○	○	○	○	○	○	×	×	×	×	×
40	66.7-fold	×	○	○	○	○	○	○	○	○	×	×	×	×	×	×	×
60	100.0-fold	×	○	○	○	○	○	○	○	○	×	×	×	×	×	×	×
100	166.7-fold	-	×	○	○	○	○	○	○	×	-	-	-	-	-	-	-
200	333.3-fold	-	×	○	○	×	×	×	×	×	-	-	-	-	-	-	-
300	500.0-fold	-	×	×	×	×	×	×	×	×	-	-	-	-	-	-	-

$y = 8E+08x^{-5.533}$ ($r = 0.967$)

Fig. 83

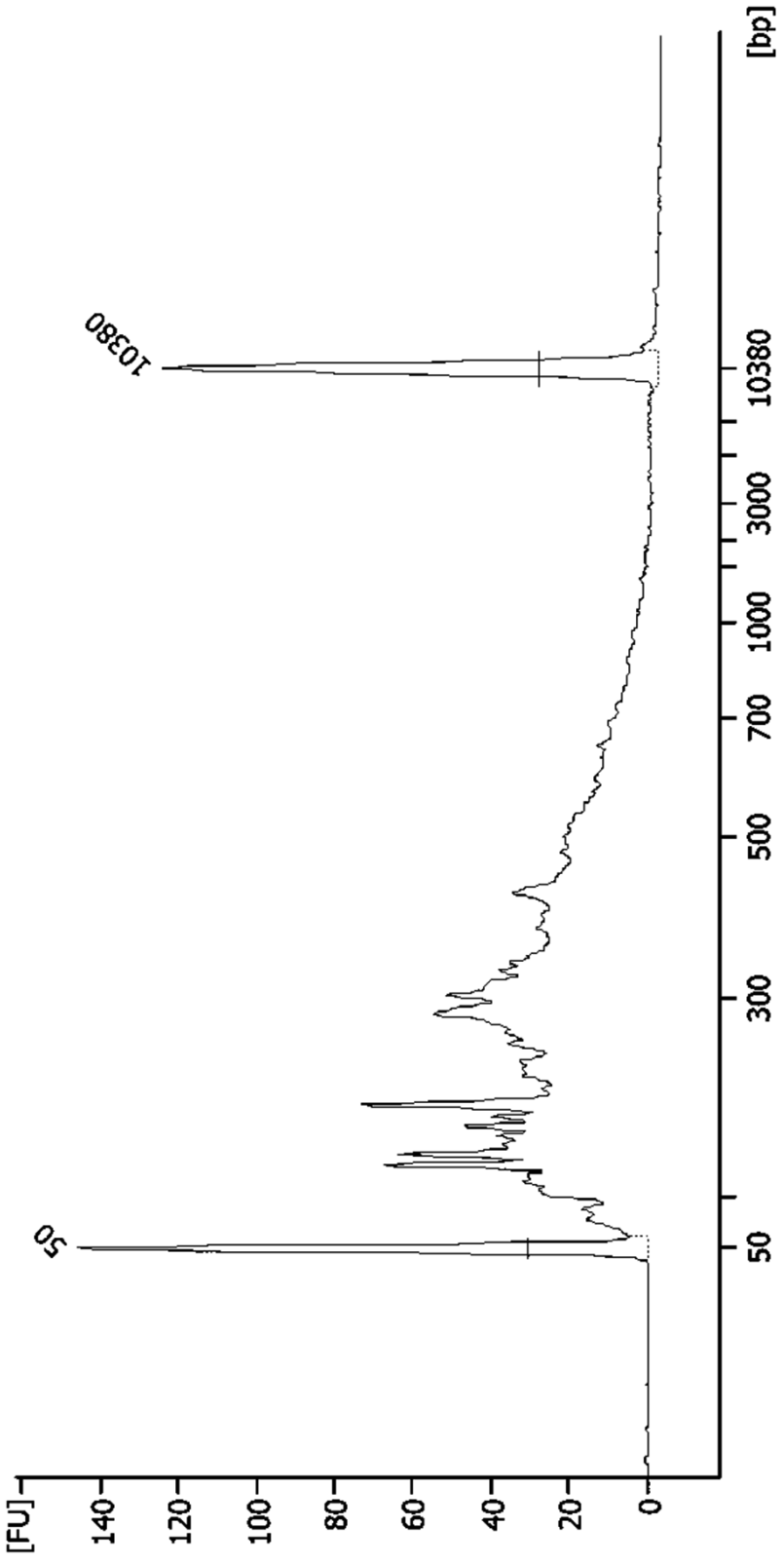

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120
100
80
60
40
20
0
50
10380
50
300
500
700
1000
3000
10380
[bp]

Fig. 84

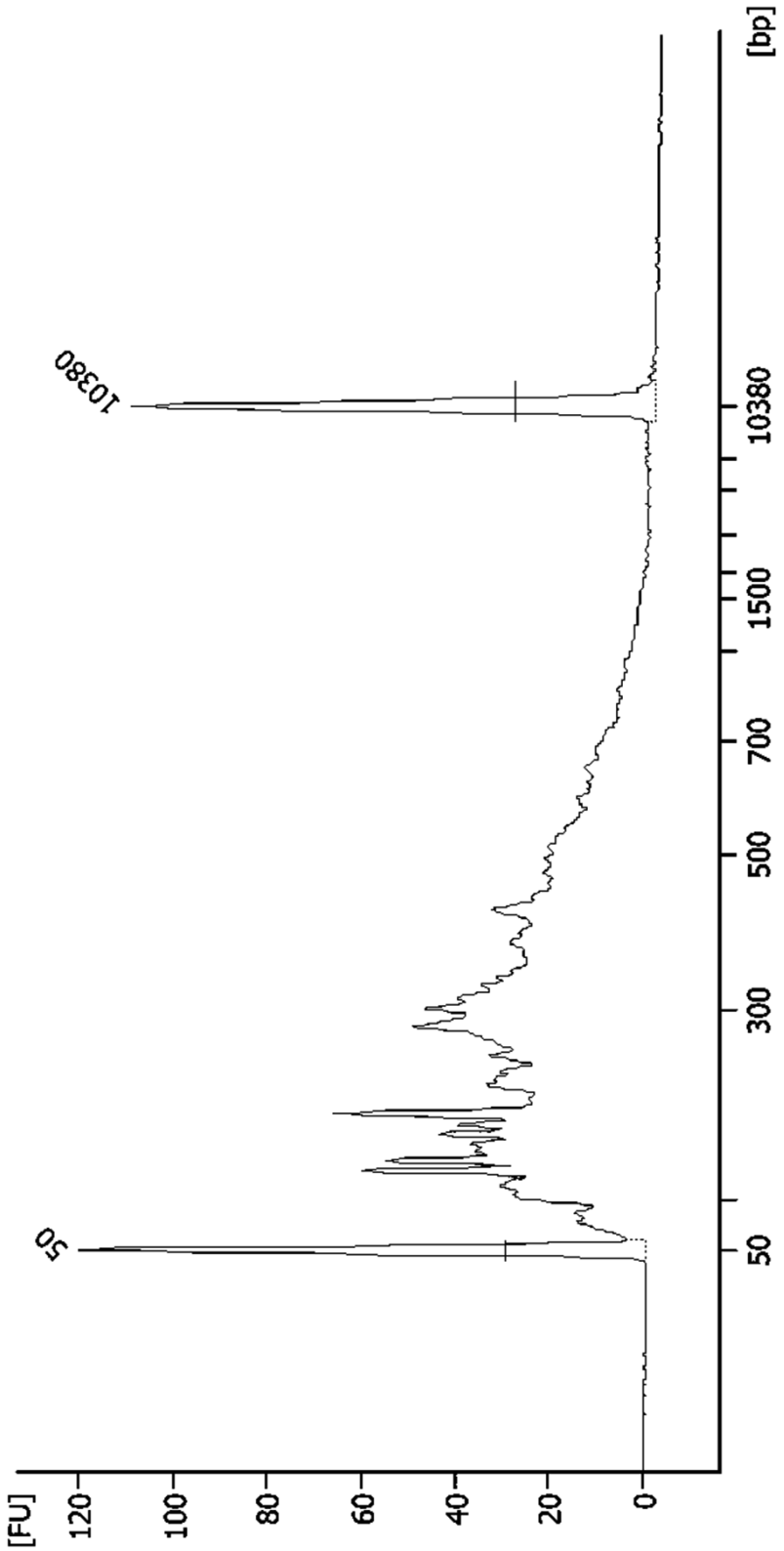


Fig. 85

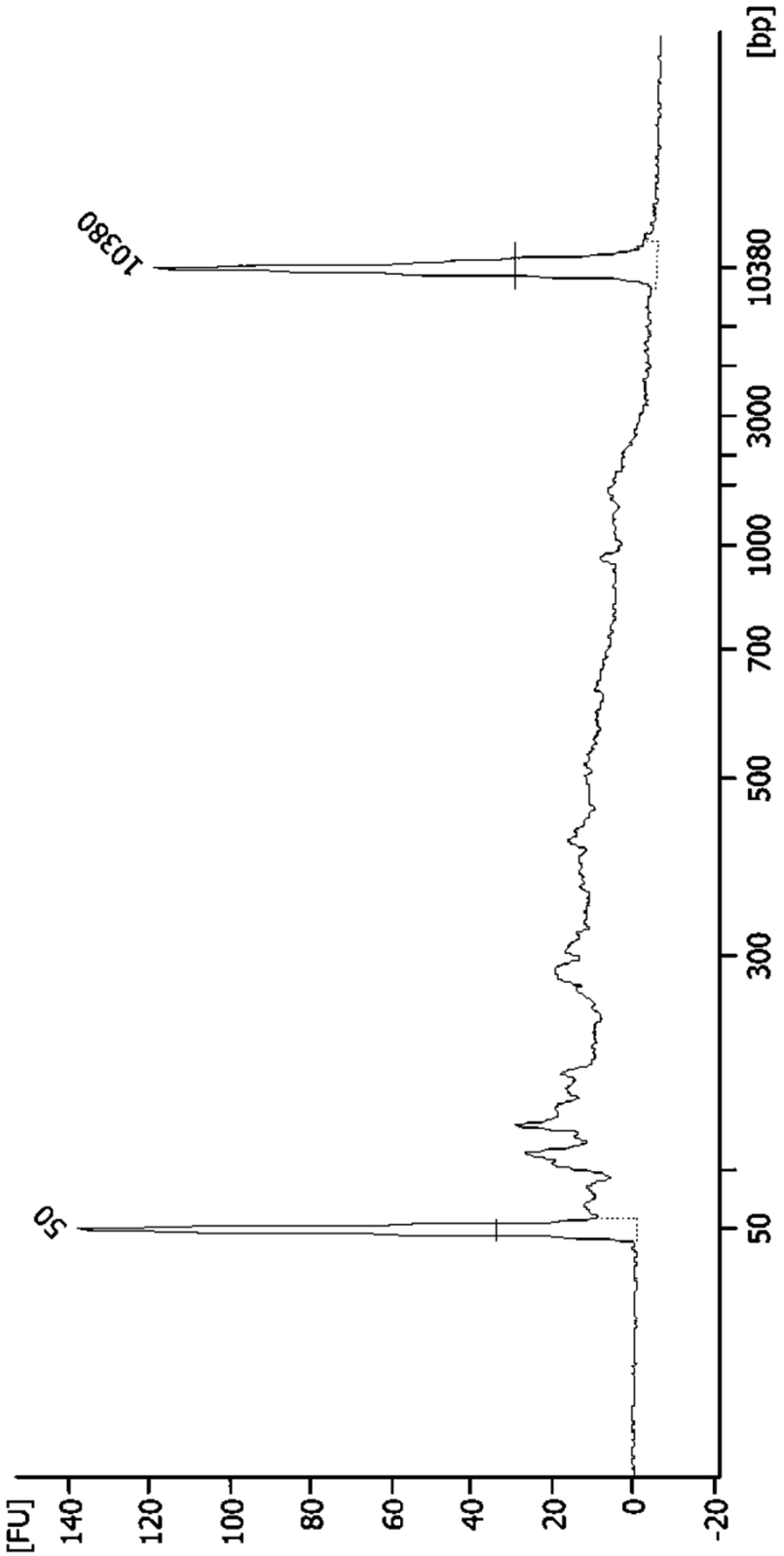

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120
100
80
60
40
20
0
-20
50
300
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700
1000
3000
10380
[bp]
50
10380

Fig. 86

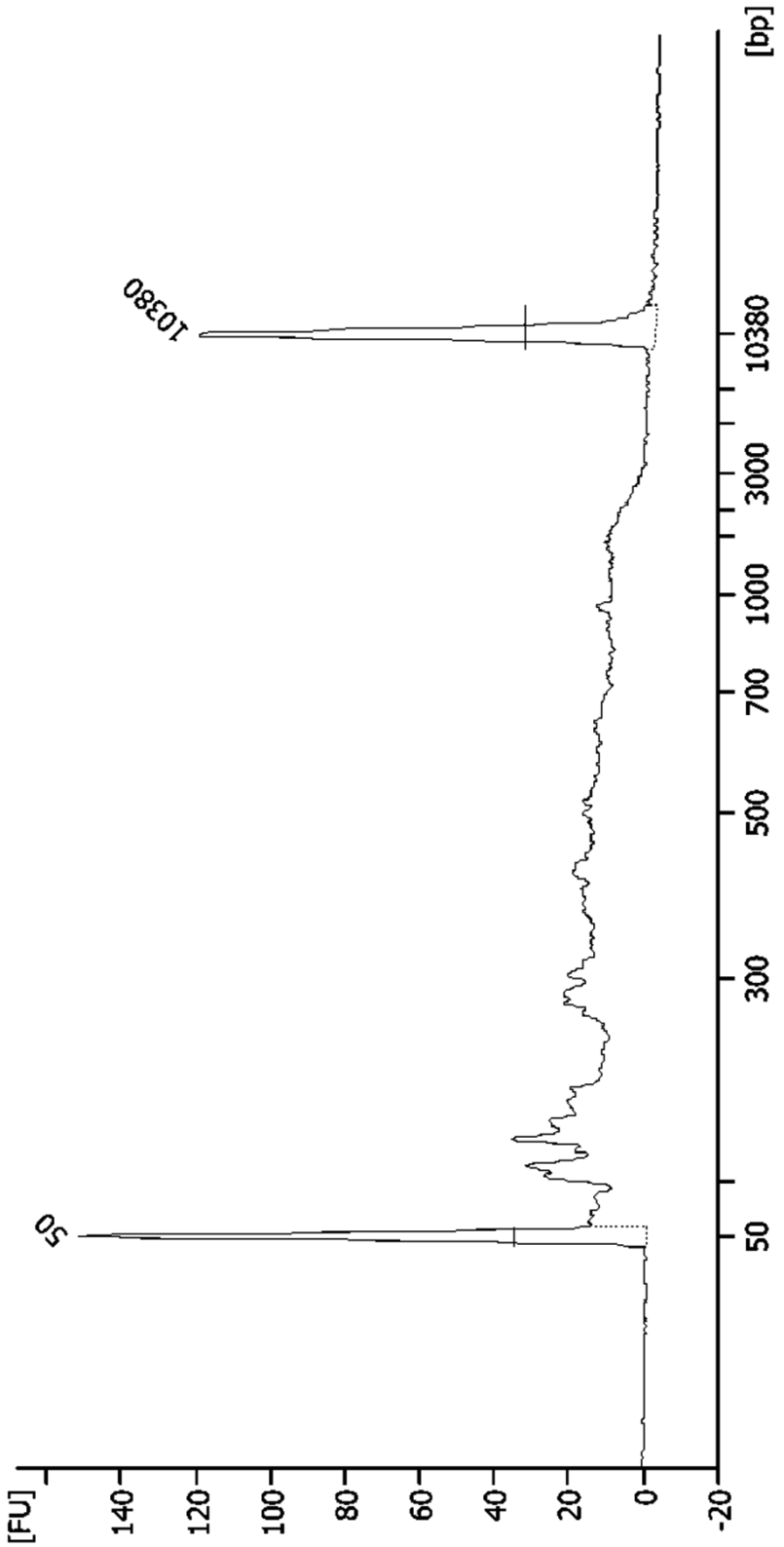

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140
120
100
80
60
40
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-20
50
10380
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10380
[bp]

Fig. 87

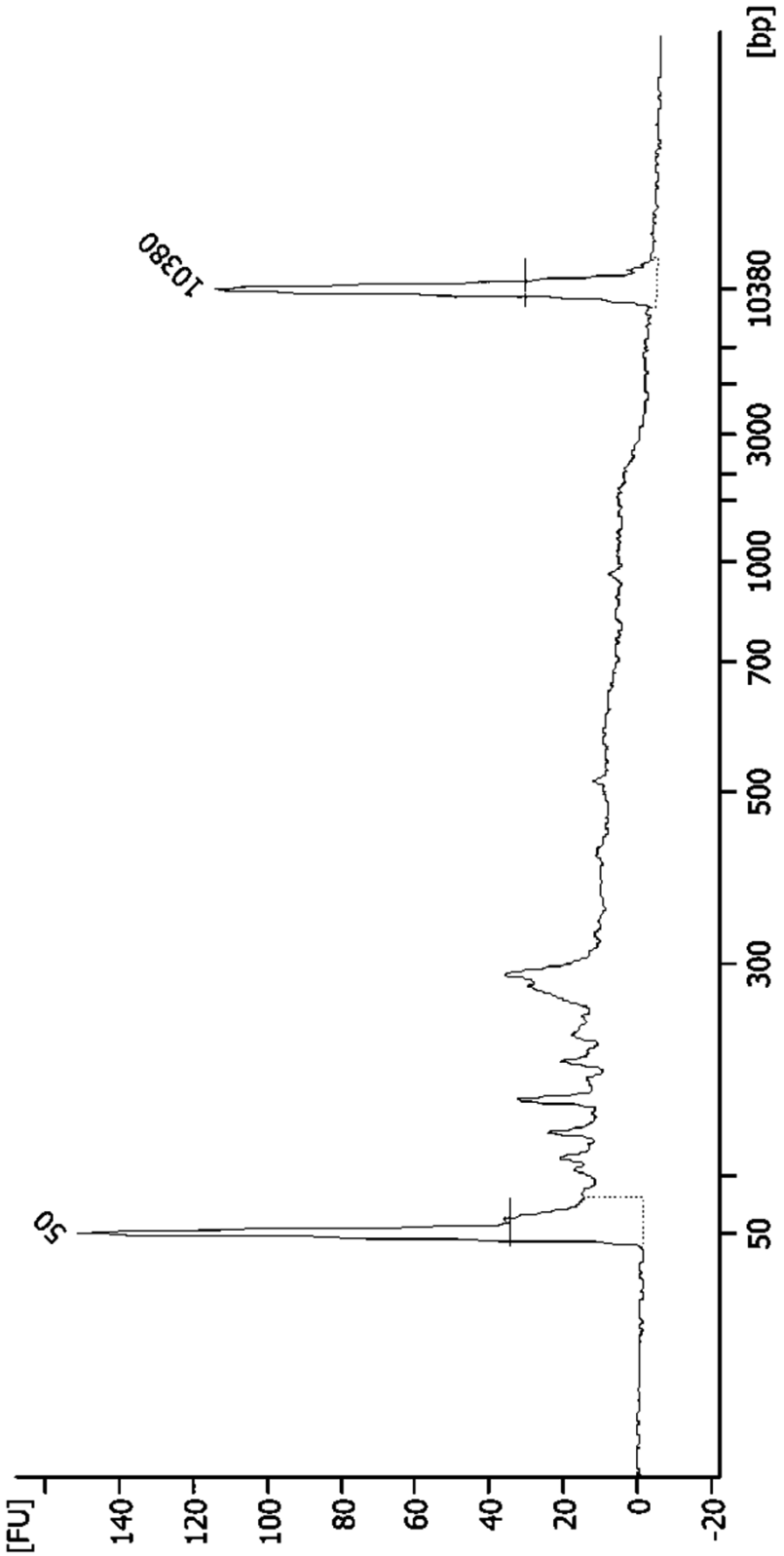

[FU]
140
120
100
80
60
40
20
0
-20
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10380
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10380
[bp]

Fig. 88

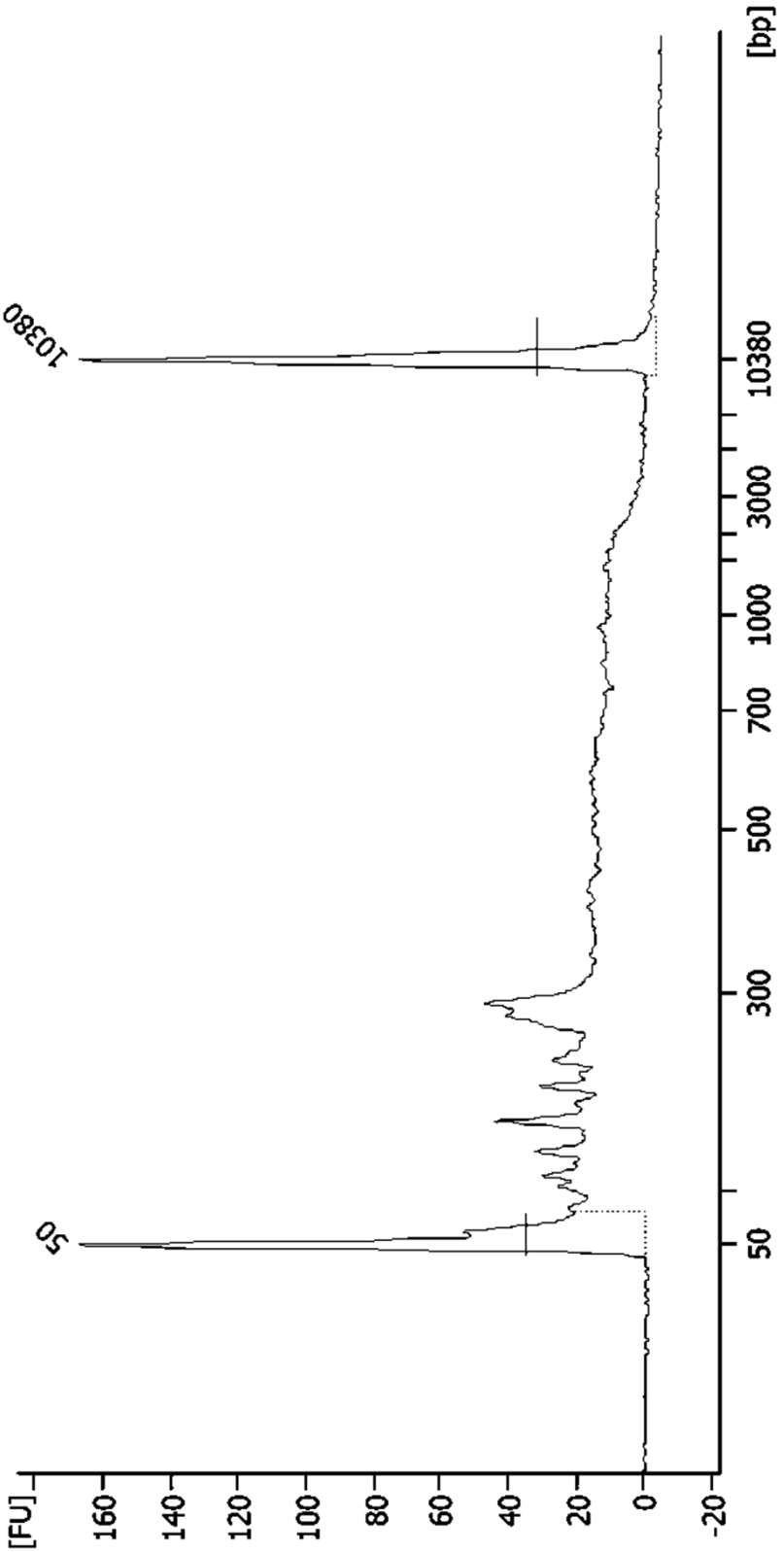

[FU]
160
140
120
100
80
60
40
20
0
-20
50
300
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3000
10380
[bp]
50
10380

Fig. 89

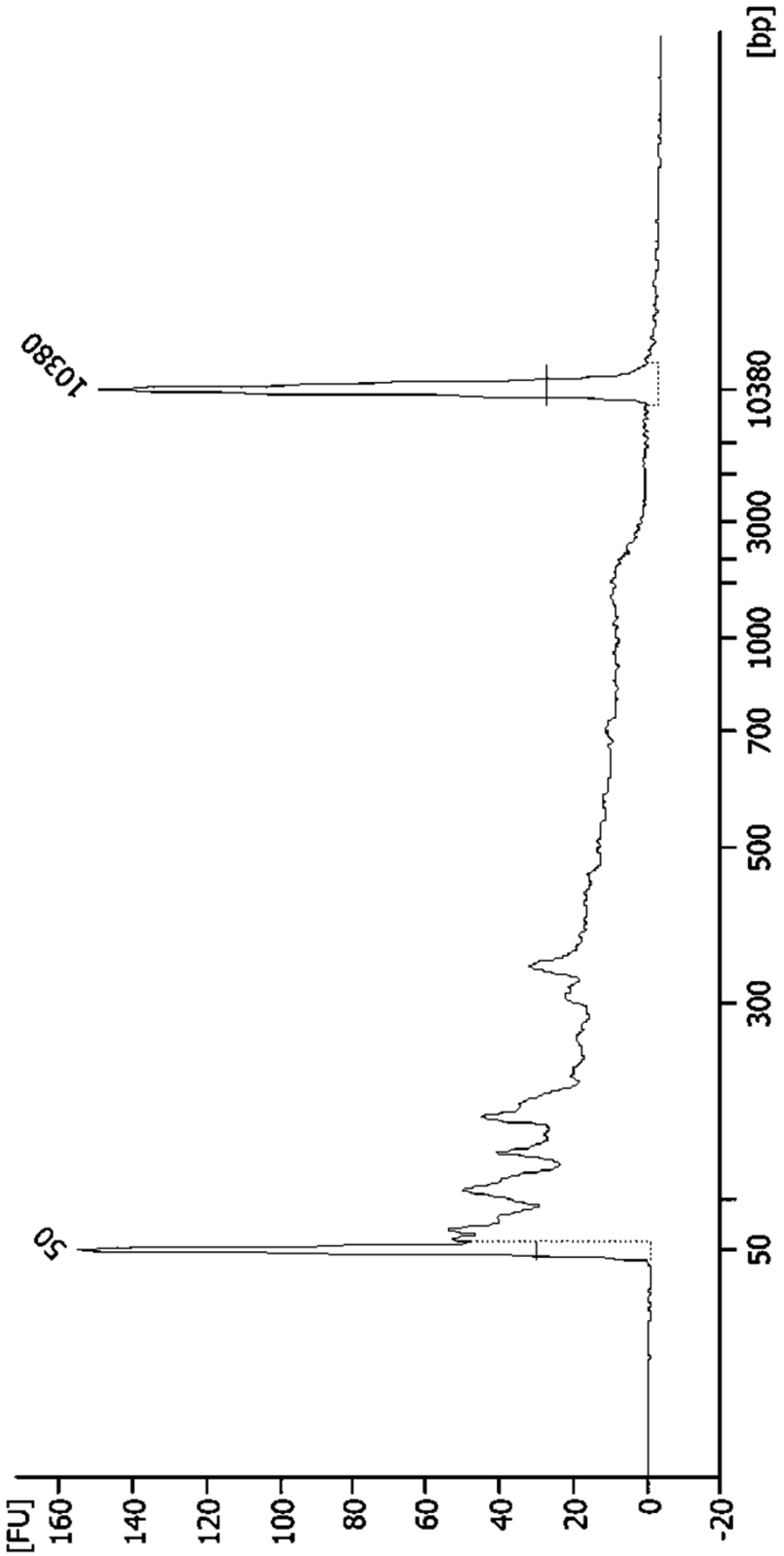

[FU]
160
140
120
100
80
60
40
20
0
-20
50
10380
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10380
[bp]

Fig. 90

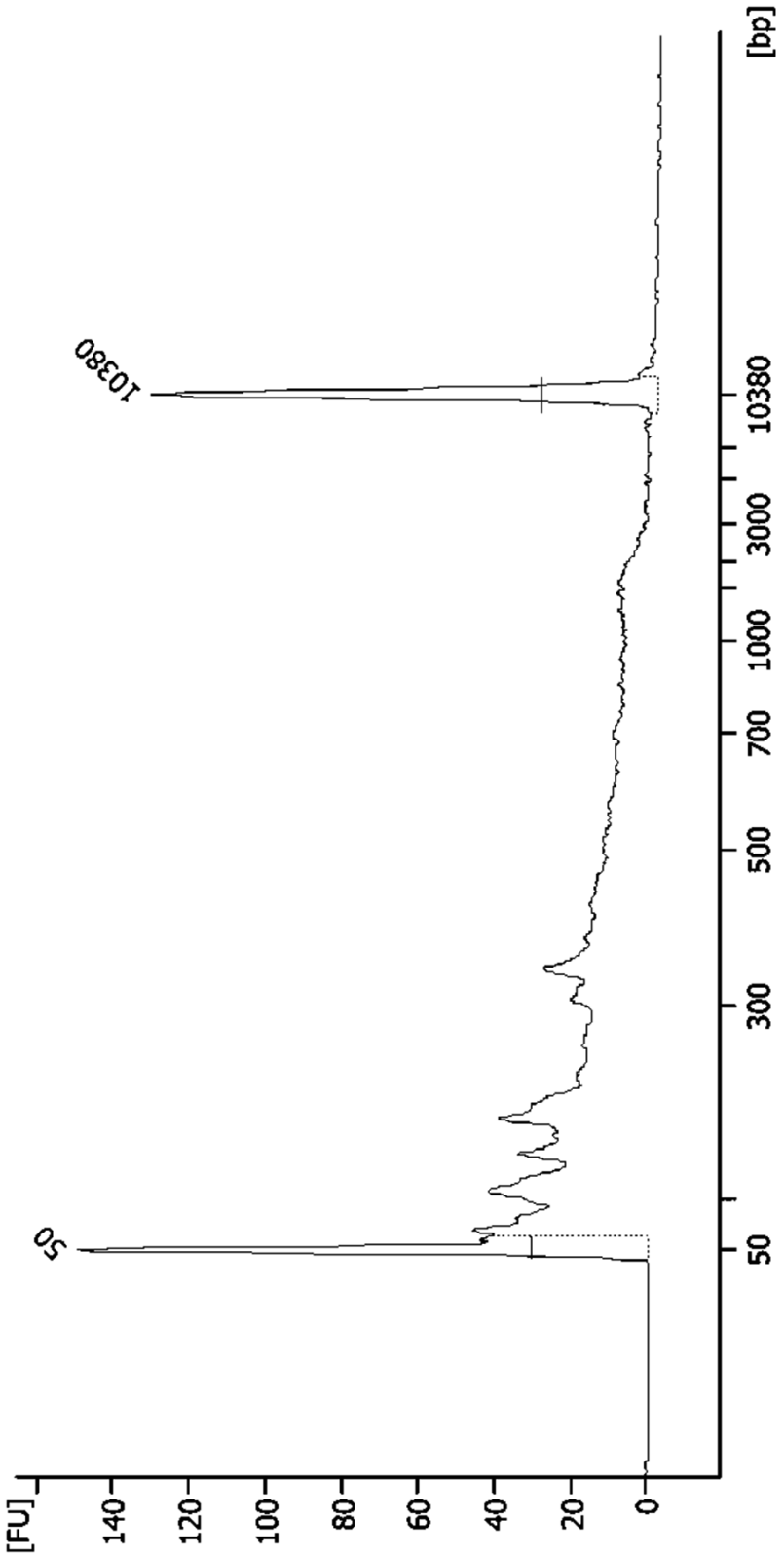

[FU]
140
120
100
80
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10380
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3000
10380
[bp]

Fig. 91

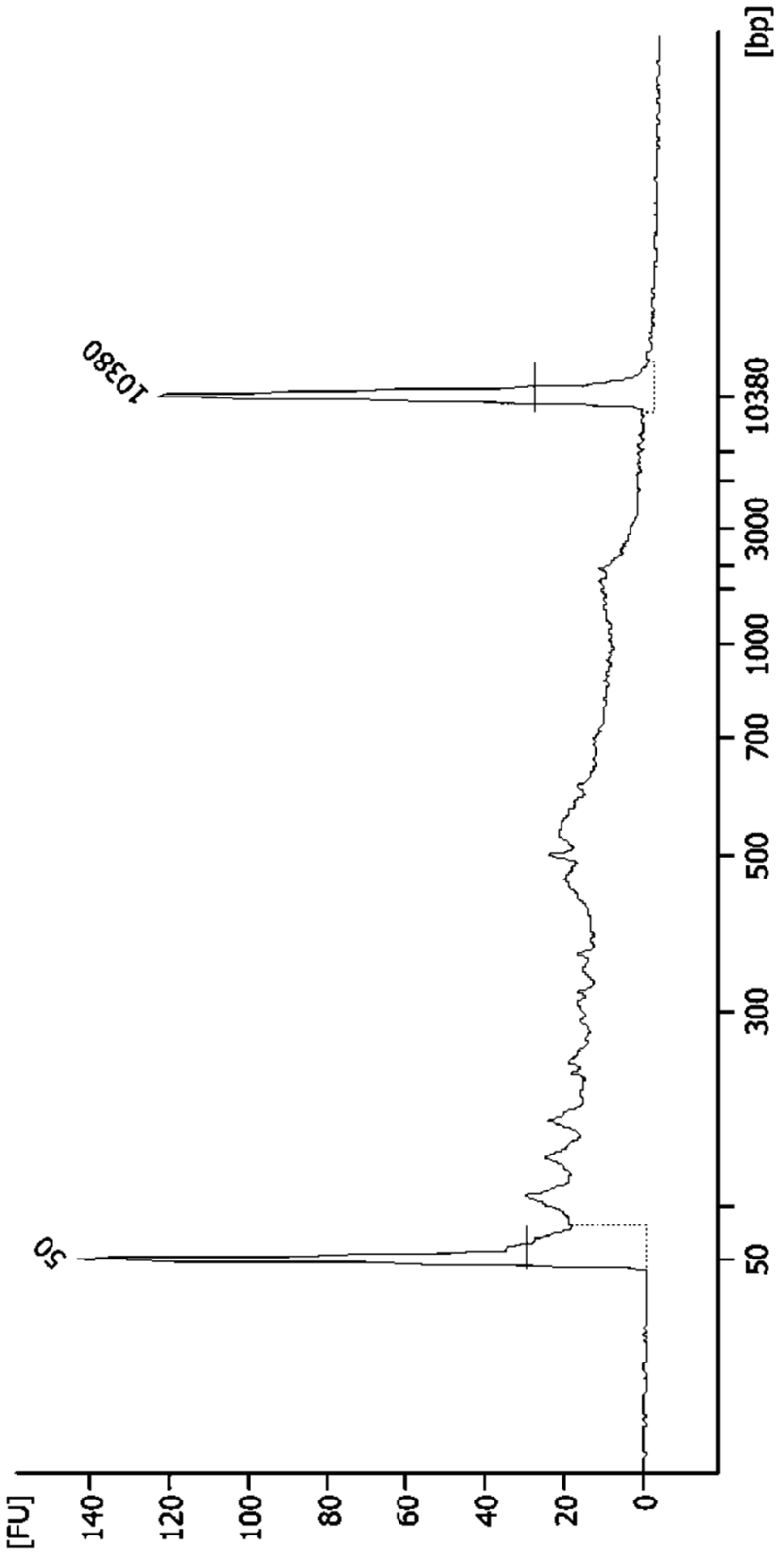

[FU]
140
120
100
80
60
40
20
0
50
10380
50
300
500
700
1000
3000
10380
[bp]

Fig. 92

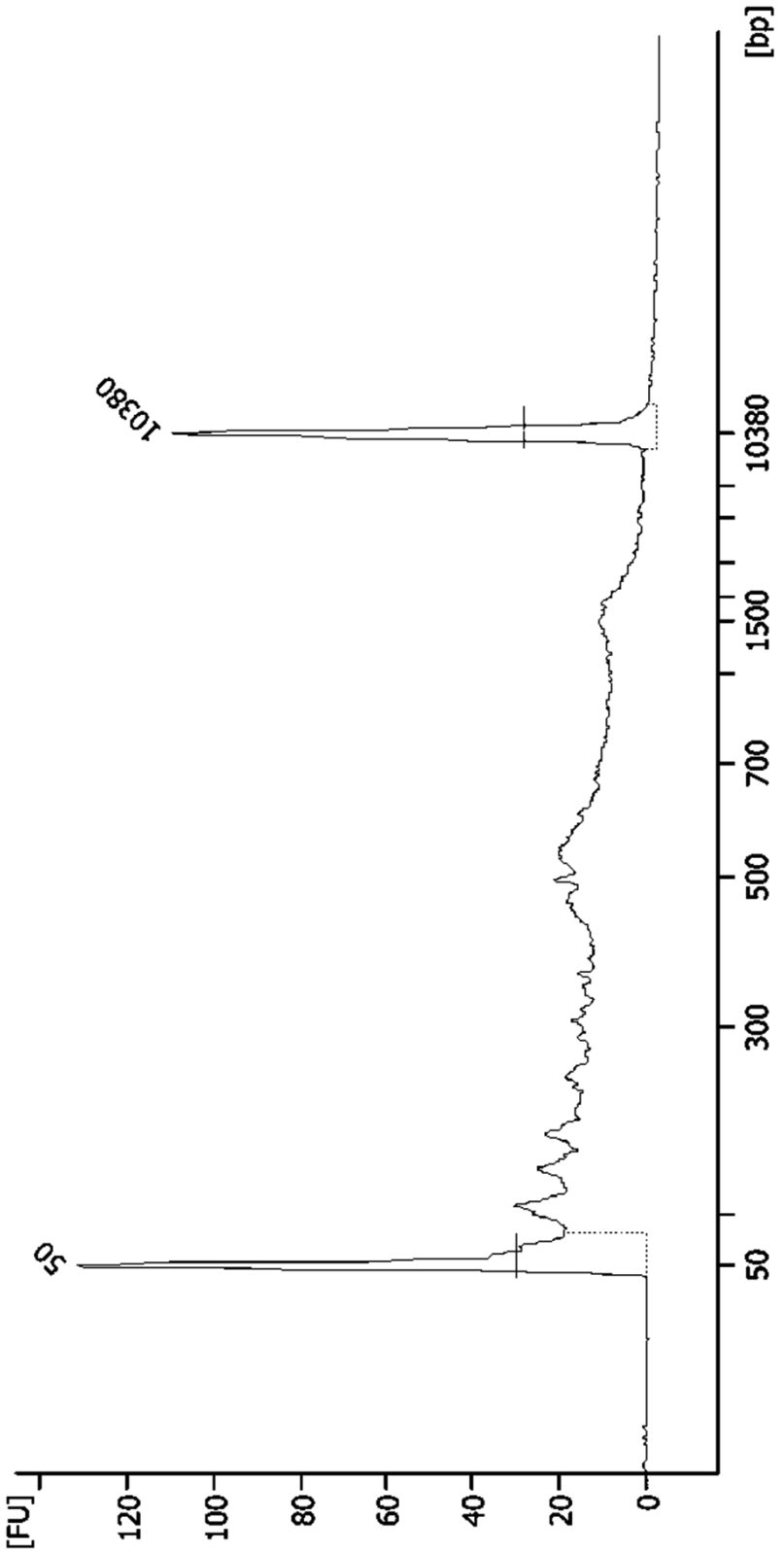


Fig. 93

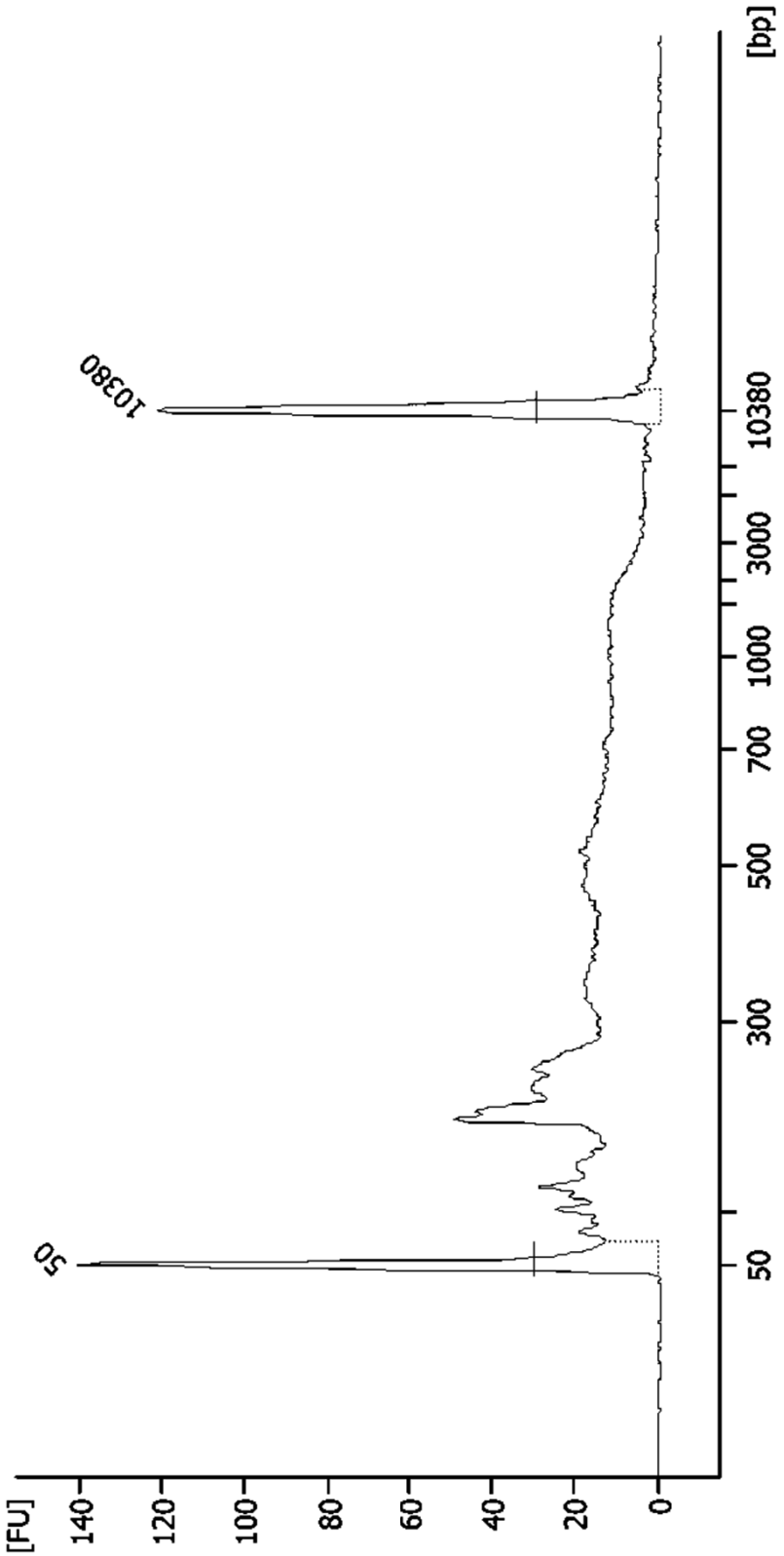

[FU]
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120
100
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0
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10380
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300
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1000
3000
10380
[bp]

Fig. 94

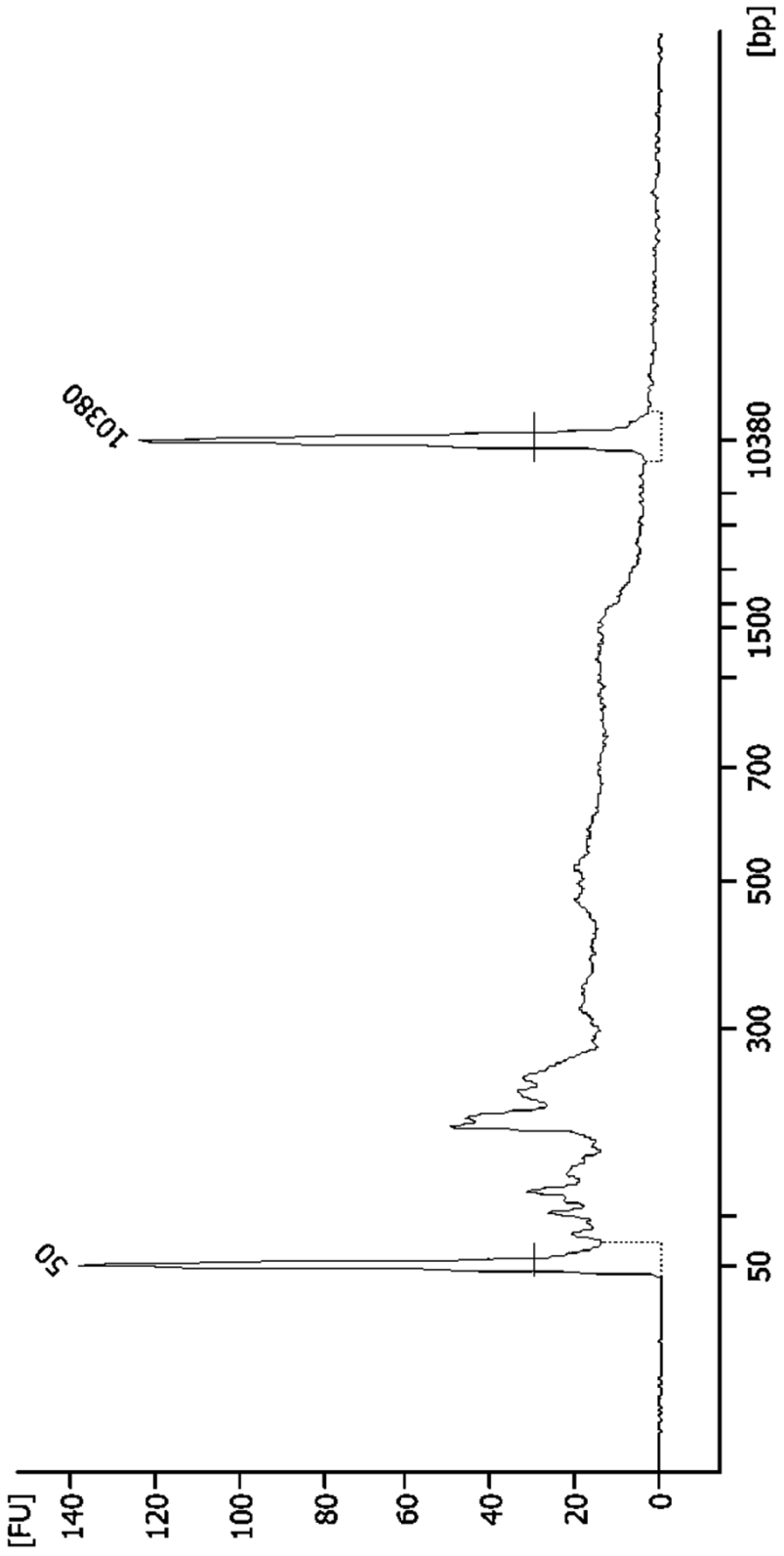


Fig. 95

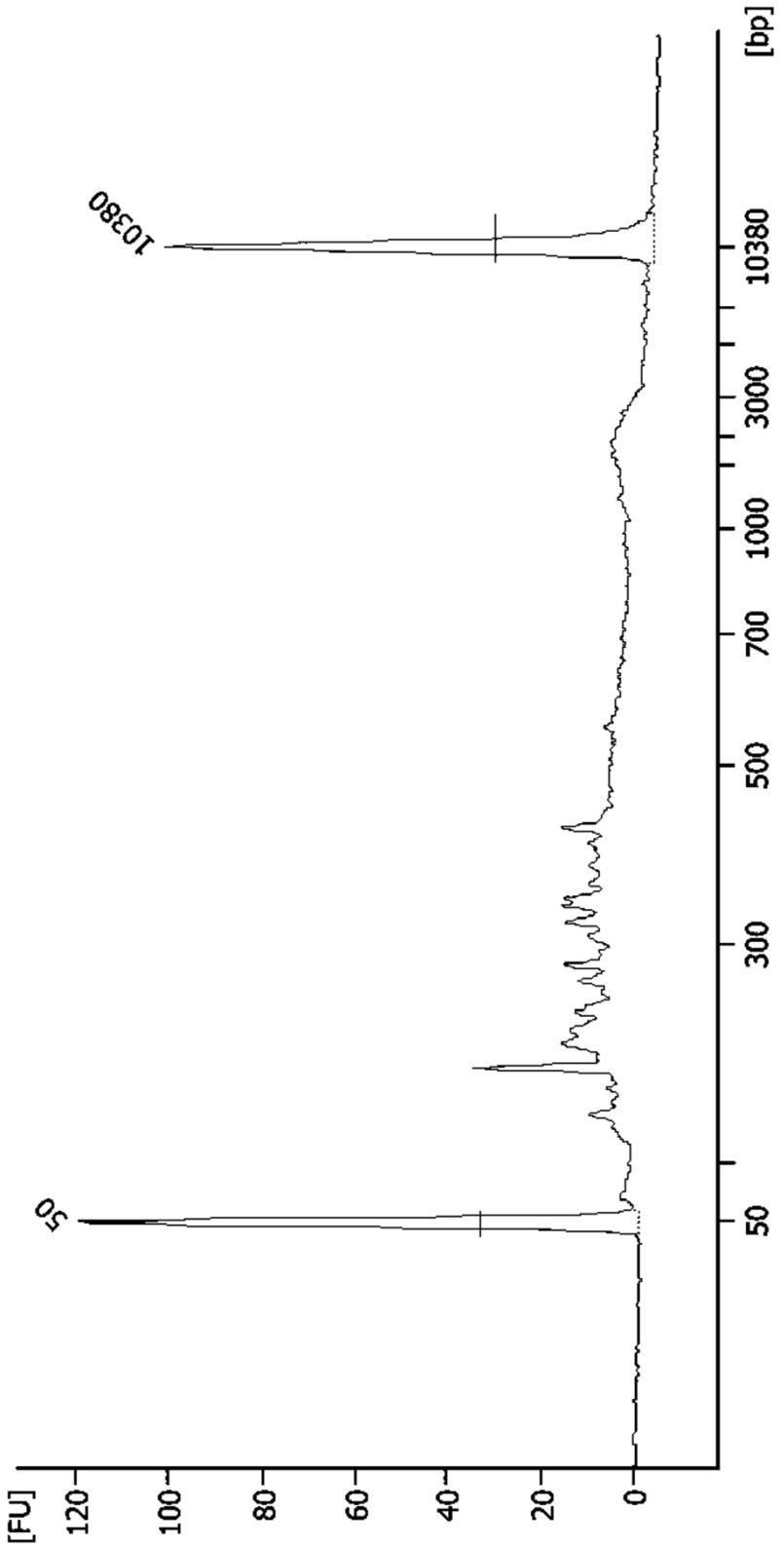

[FU]
120
100
80
60
40
20
0
50
300
500
700
1000
3000
10380
[bp]
50
10380

Fig. 96

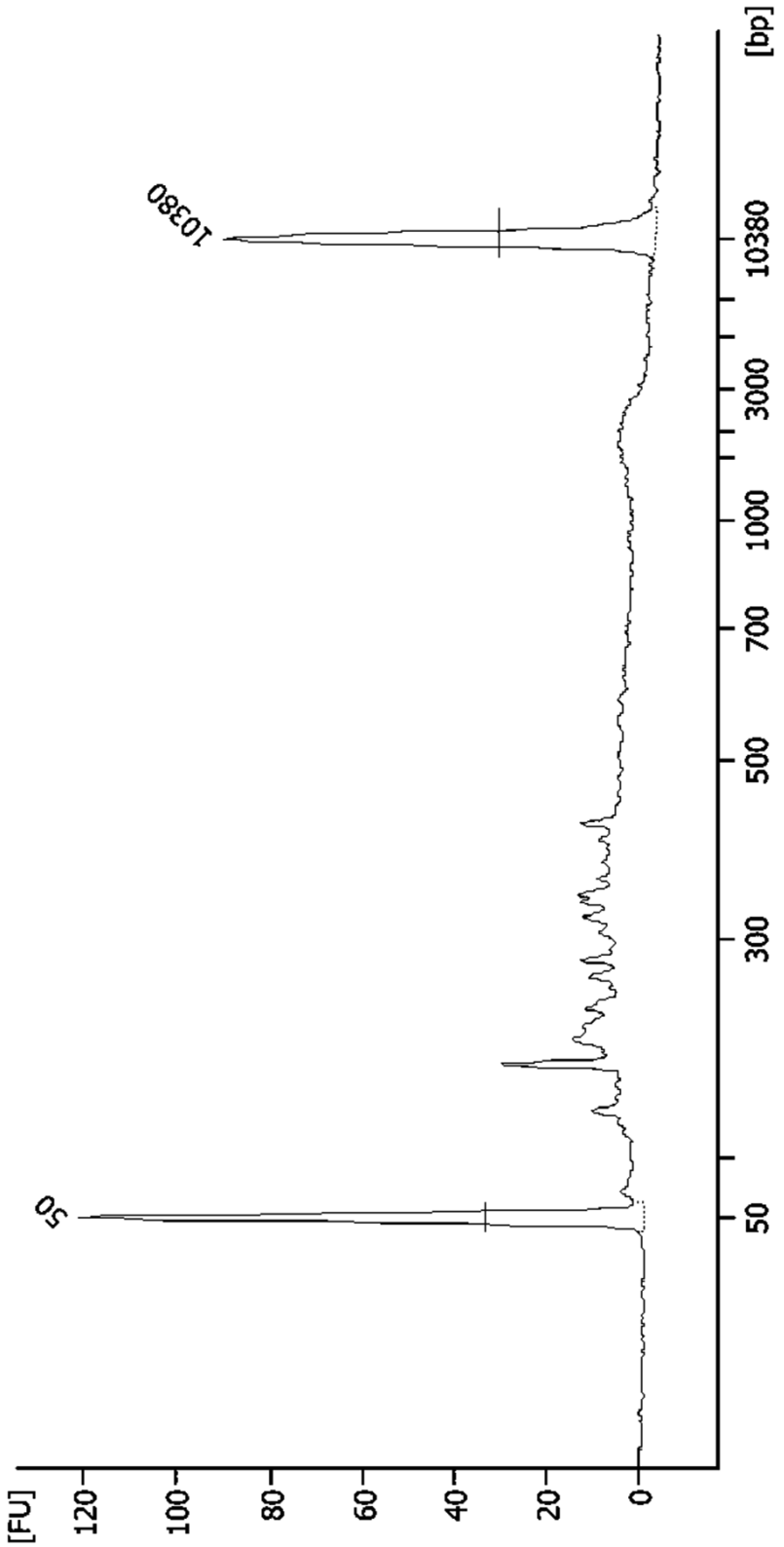

[FU]
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100
80
60
40
20
0
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10380
50
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500
700
1000
3000
10380
[bp]

Fig. 97

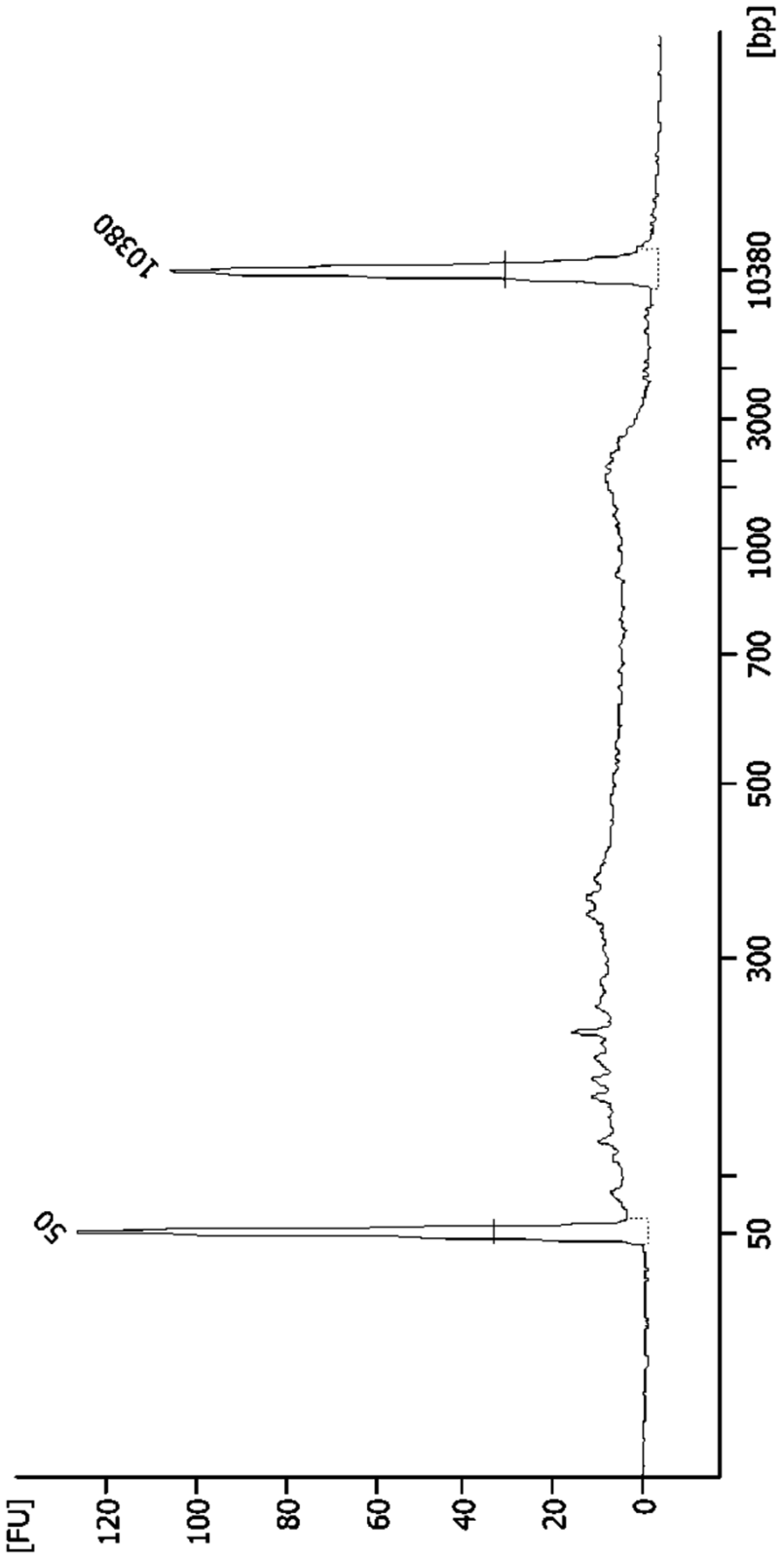

[FU]
120
100
80
60
40
20
0
50
300
500
700
1000
3000
10380
[bp]
50
10380

Fig. 98

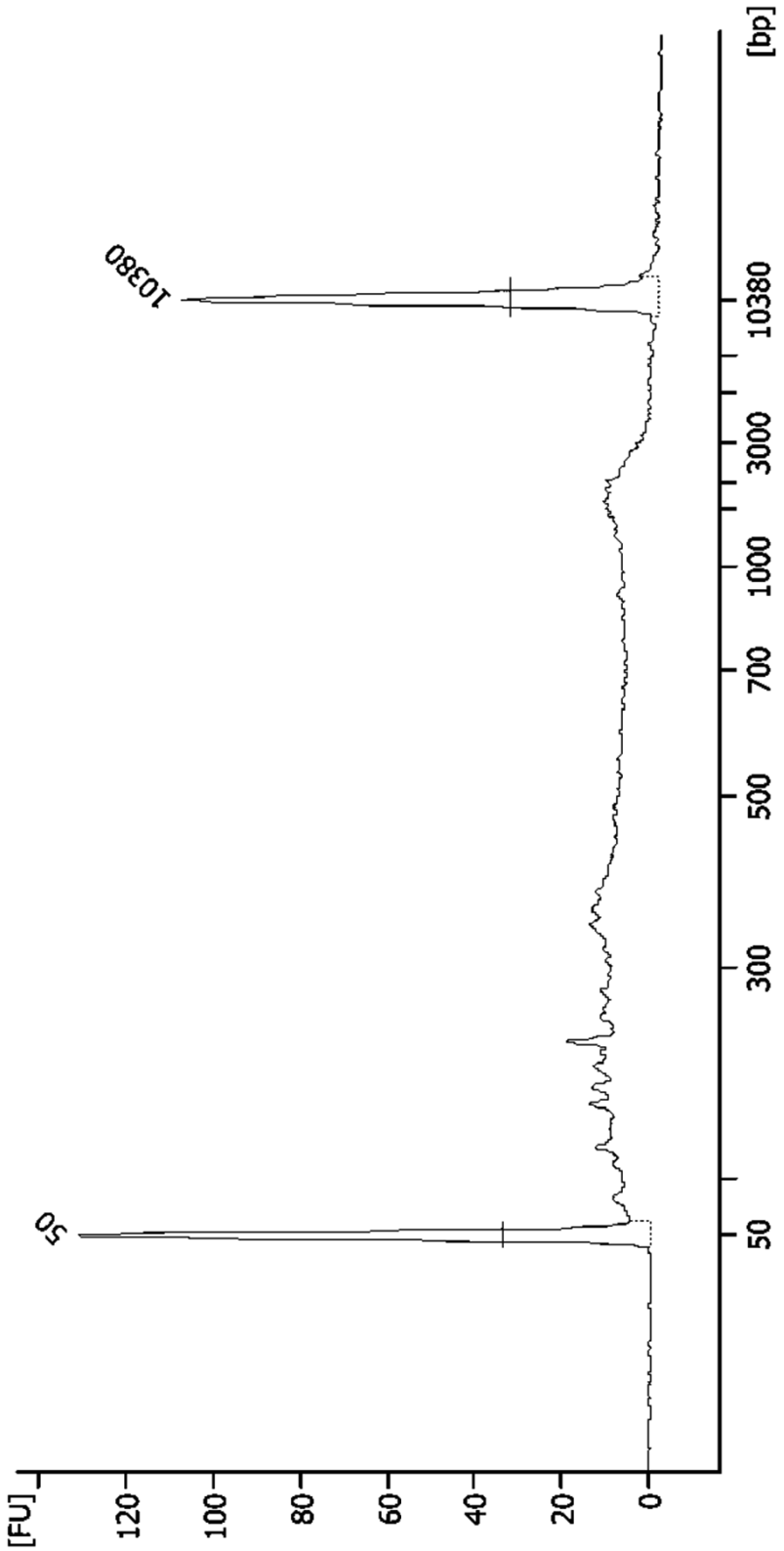

[FU]
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100
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60
40
20
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50
10380
50
300
500
700
1000
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10380
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Fig. 99

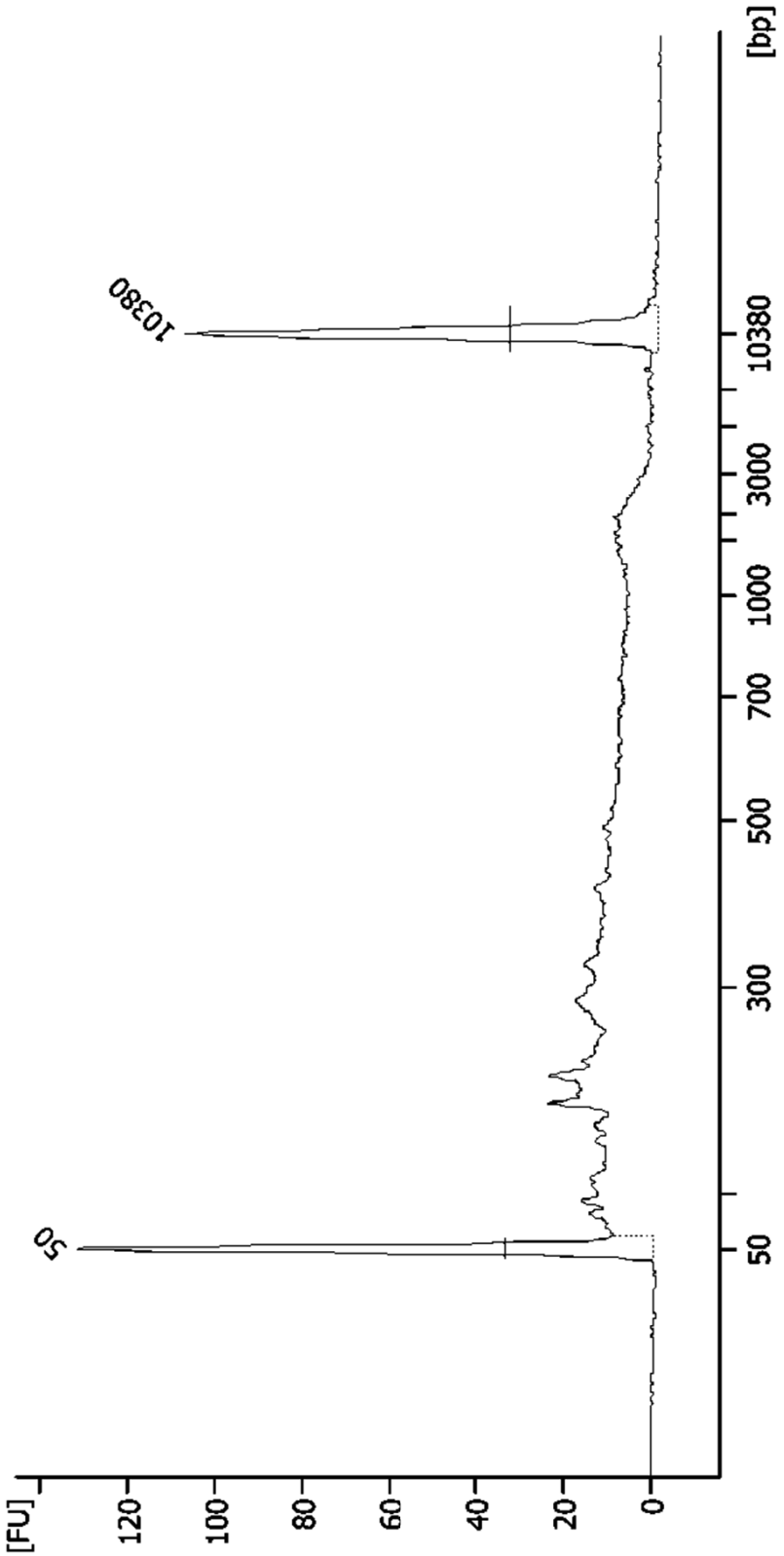

[FU]
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60
40
20
0
50
10380
50
300
500
700
1000
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Fig. 100

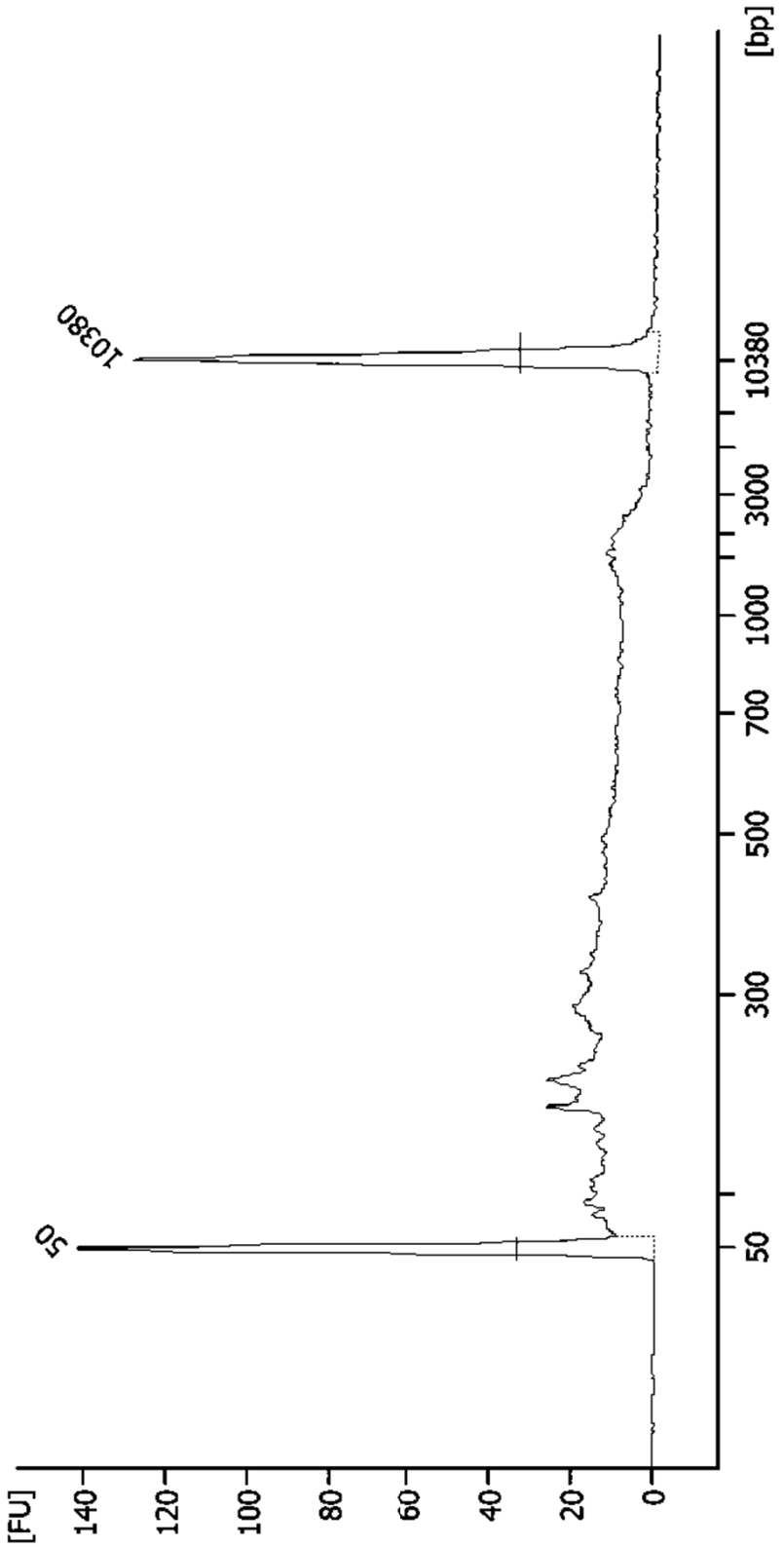

[FU]
140
120
100
80
60
40
20
0
50
10380
50
300
500
700
1000
3000
10380
[bp]

Fig. 101

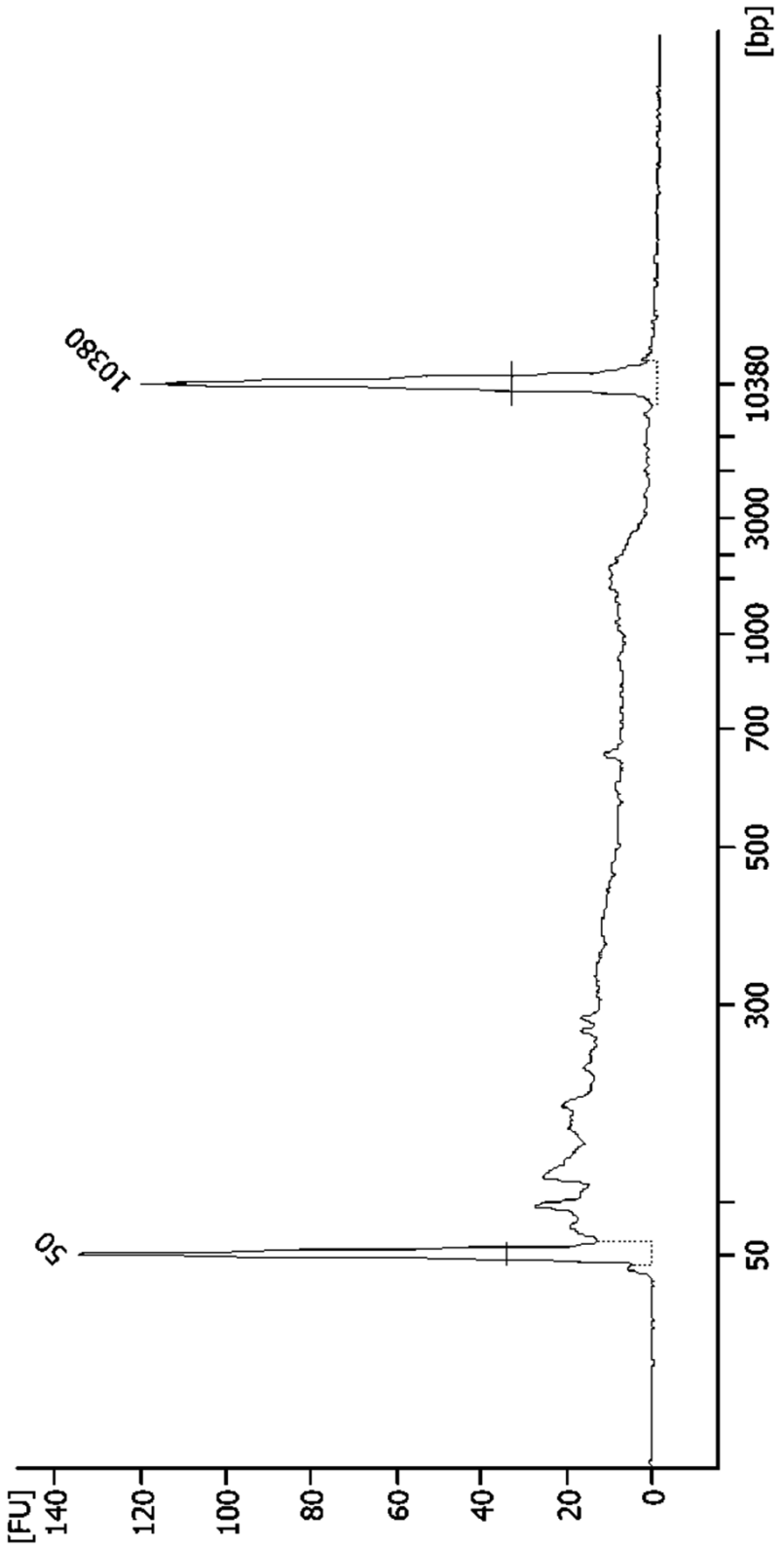

[FU]
140
120
100
80
60
40
20
0
50
300
500
700
1000
3000
10380
[bp]
50
10380

Fig. 102

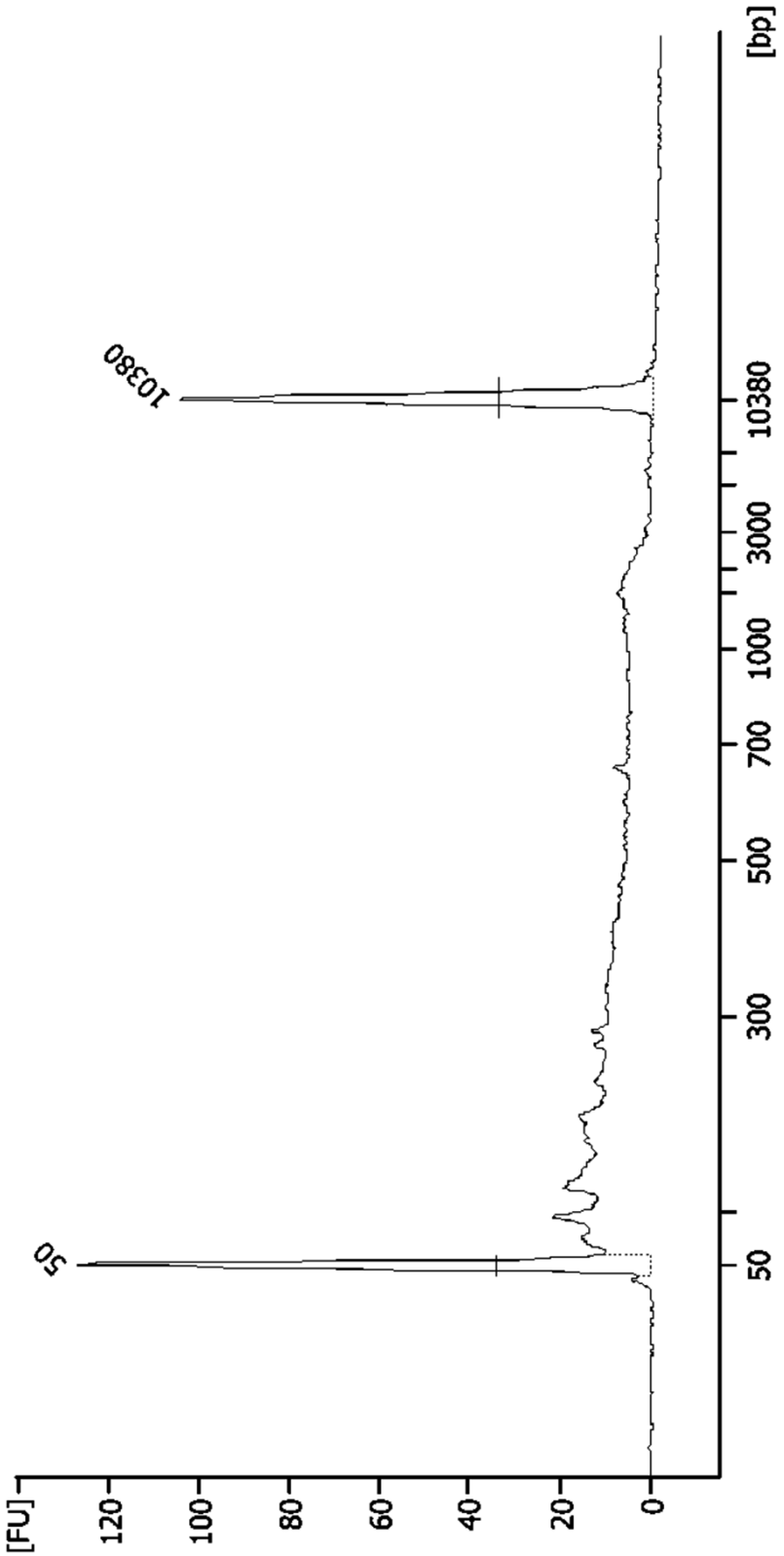

[FU]
120
100
80
60
40
20
0
50
10380
50
300
500
700
1000
3000
10380
[bp]

Fig. 103

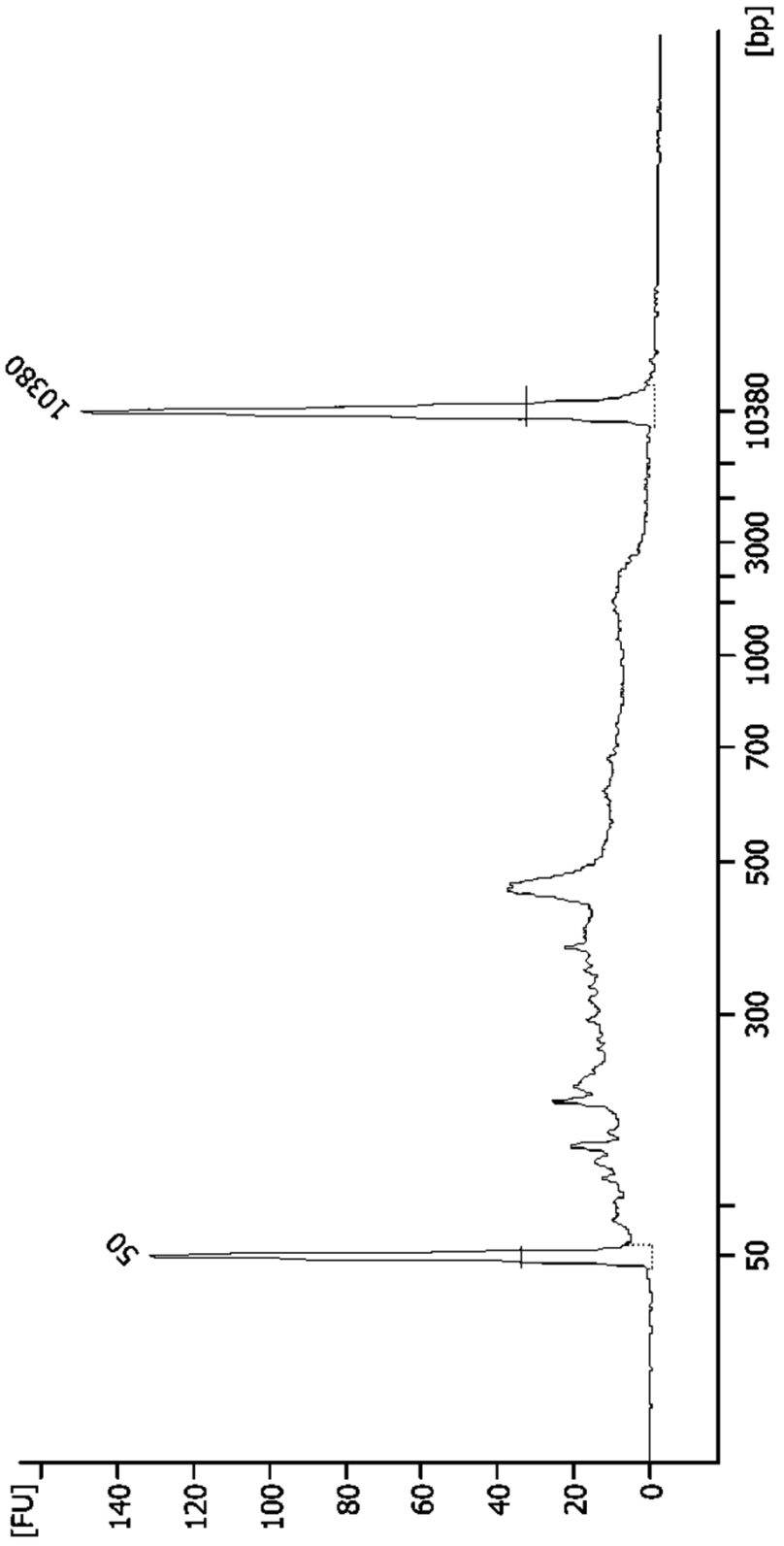

[FU]
140
120
100
80
60
40
20
0
50
10380
50
300
500
700
1000
3000
10380
[bp]

Fig. 104

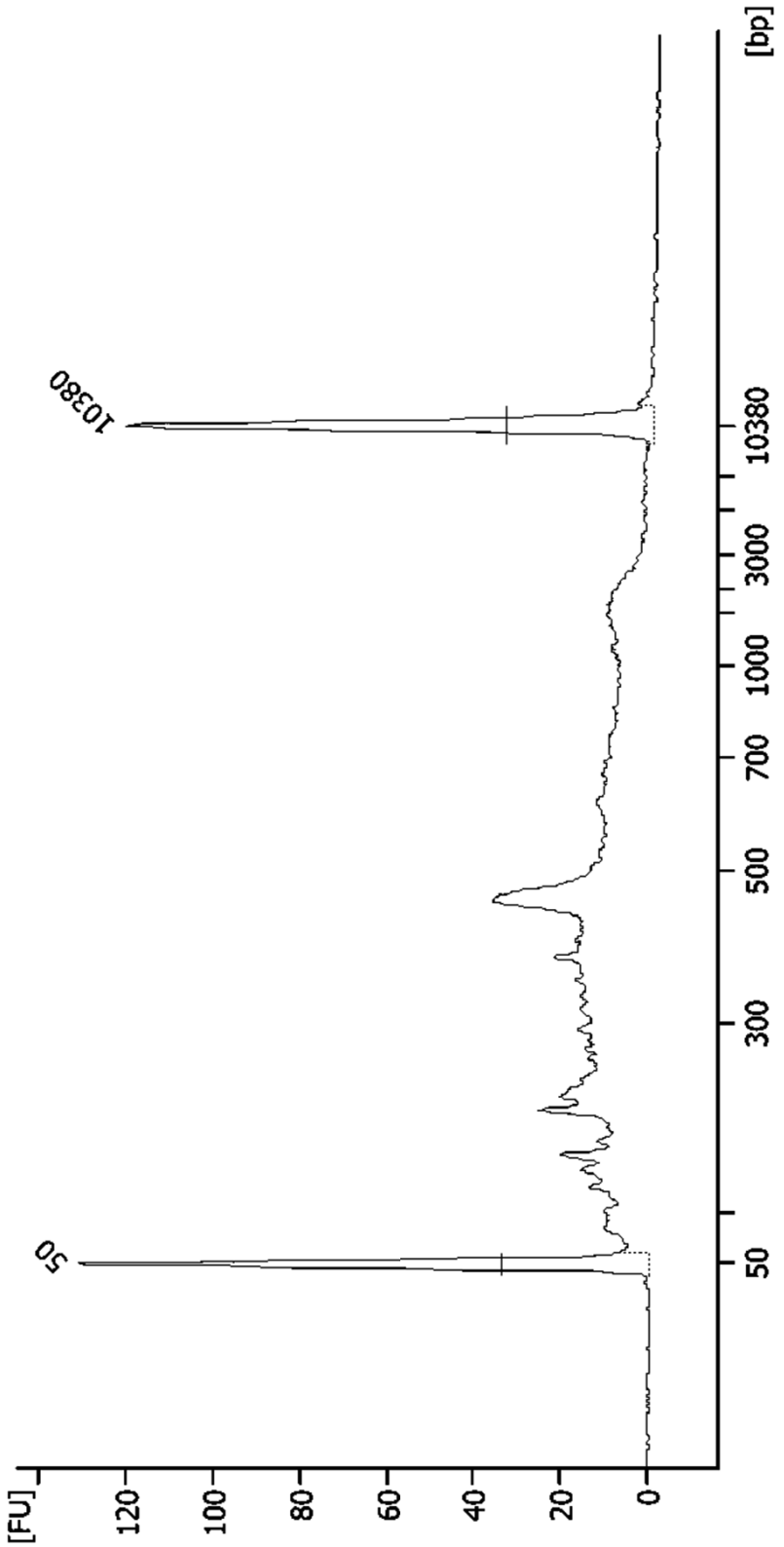

[FU]
120
100
80
60
40
20
0
50
10380
50
300
500
700
1000
3000
10380
[bp]

Fig. 105

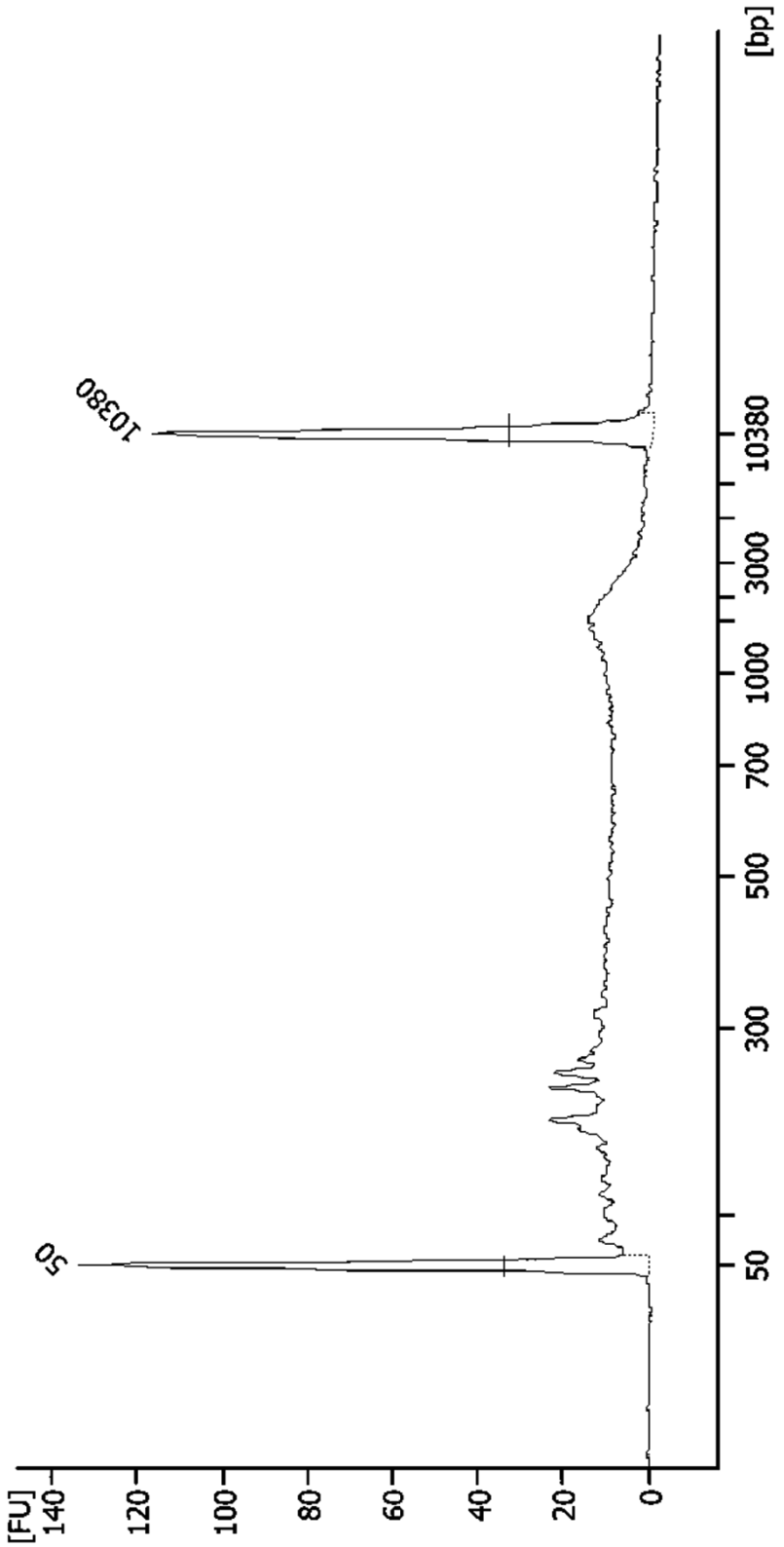

[FU]
140
120
100
80
60
40
20
0
50
10380
50
300
500
700
1000
3000
10380
[bp]

Fig. 106

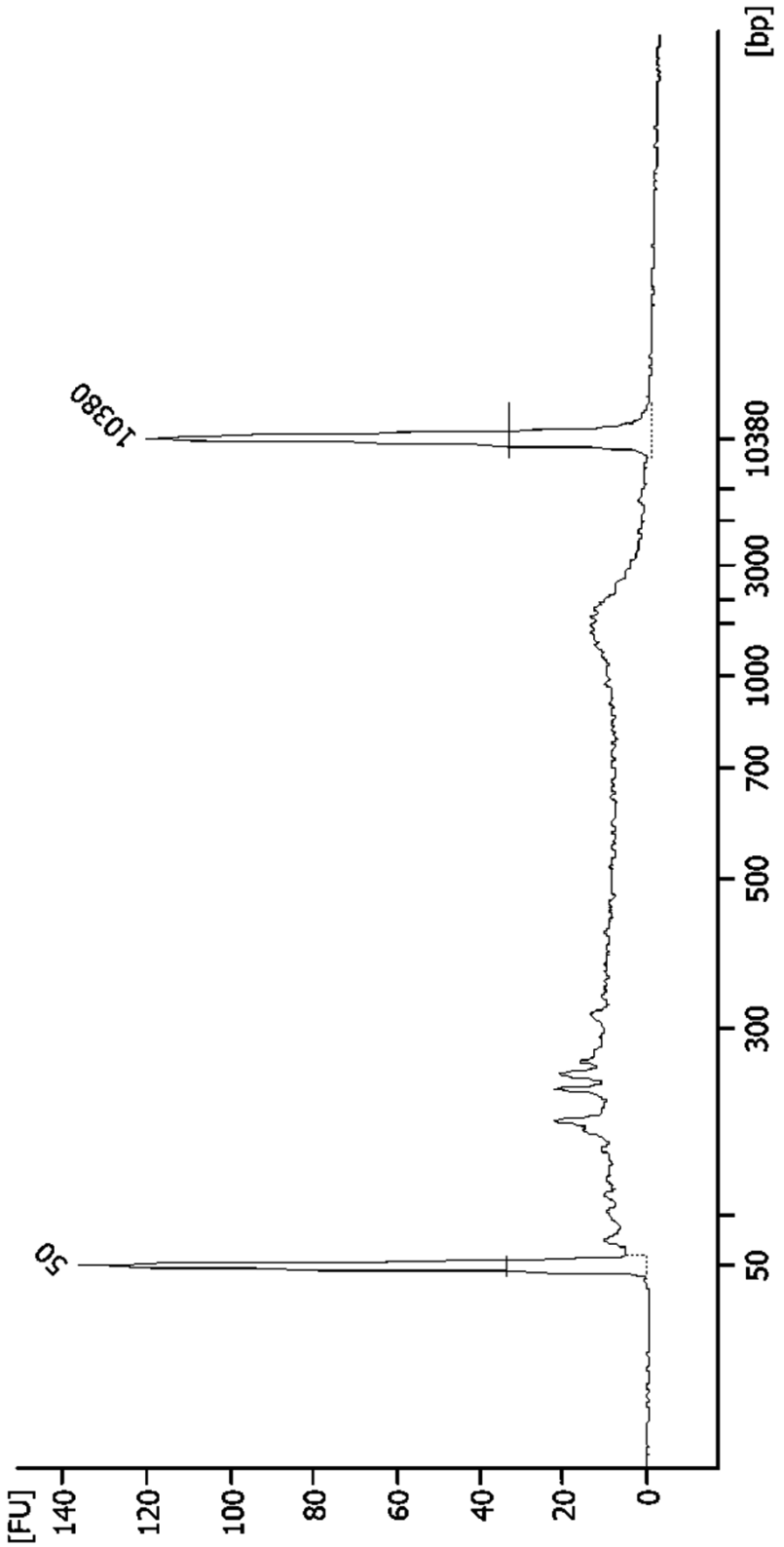

[FU]
140
120
100
80
60
40
20
0
50
10380
50
300
500
700
1000
3000
10380
[bp]

Fig. 107

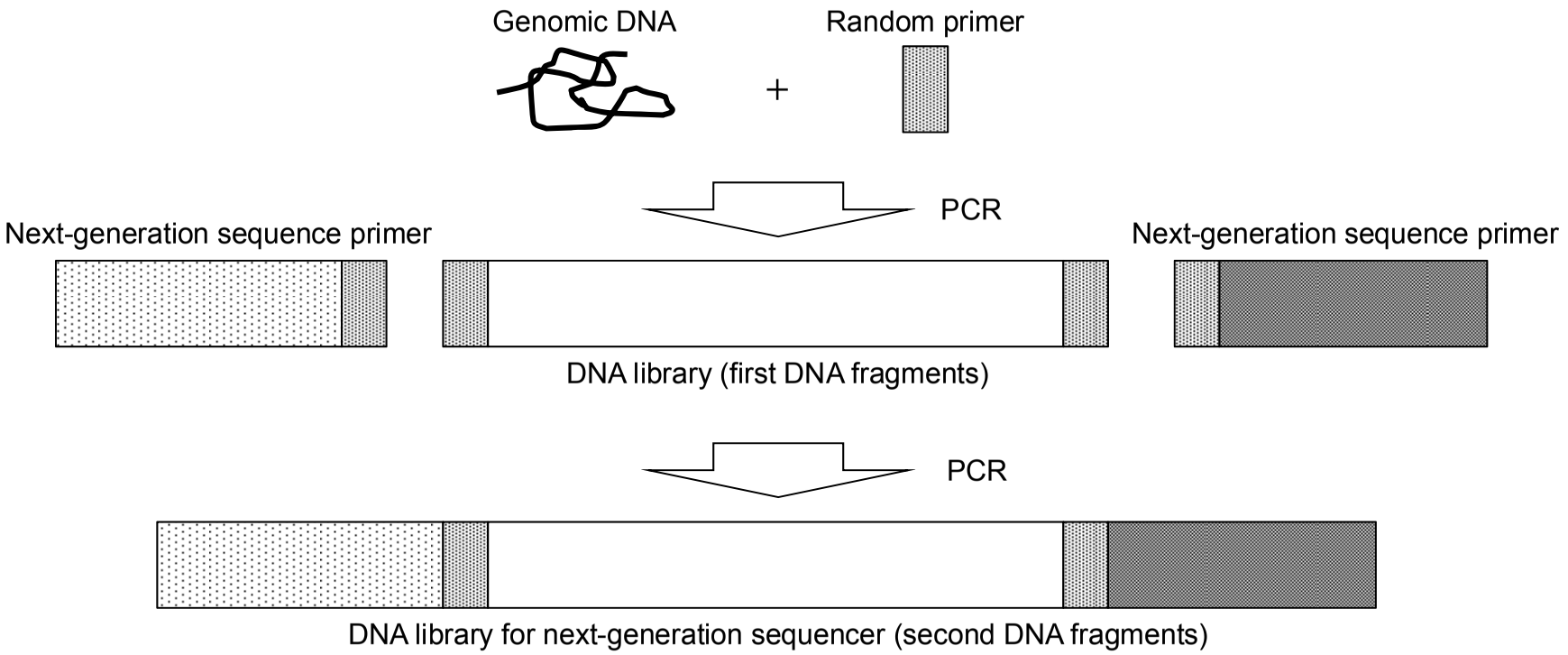

Genomic DNA
Random primer
+
PCR
Next-generation sequence primer
Next-generation sequence primer
DNA library (first DNA fragments)
PCR
DNA library for next-generation sequencer (second DNA fragments)

Fig. 108

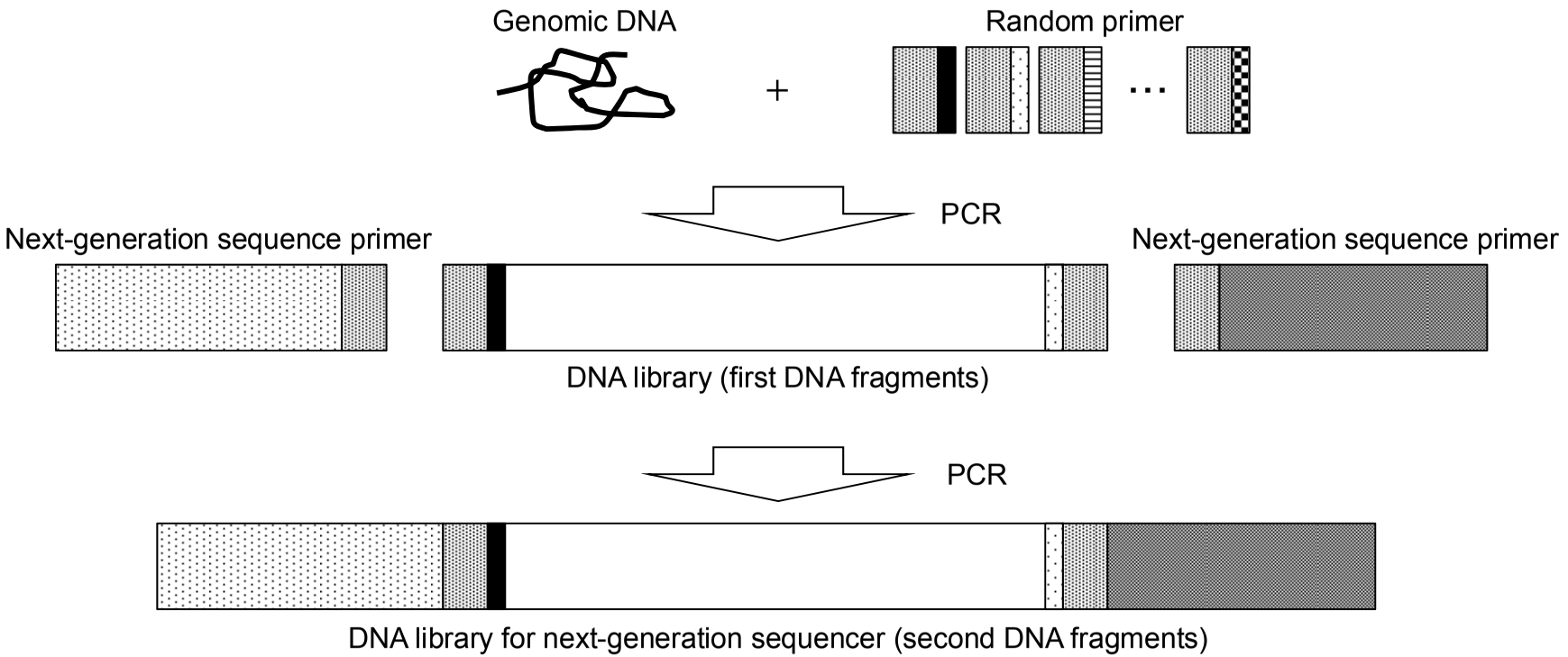

Genomic DNA
Random primer
+
...
PCR
Next-generation sequence primer
Next-generation sequence primer
DNA library (first DNA fragments)
PCR
DNA library for next-generation sequencer (second DNA fragments)

Fig. 109

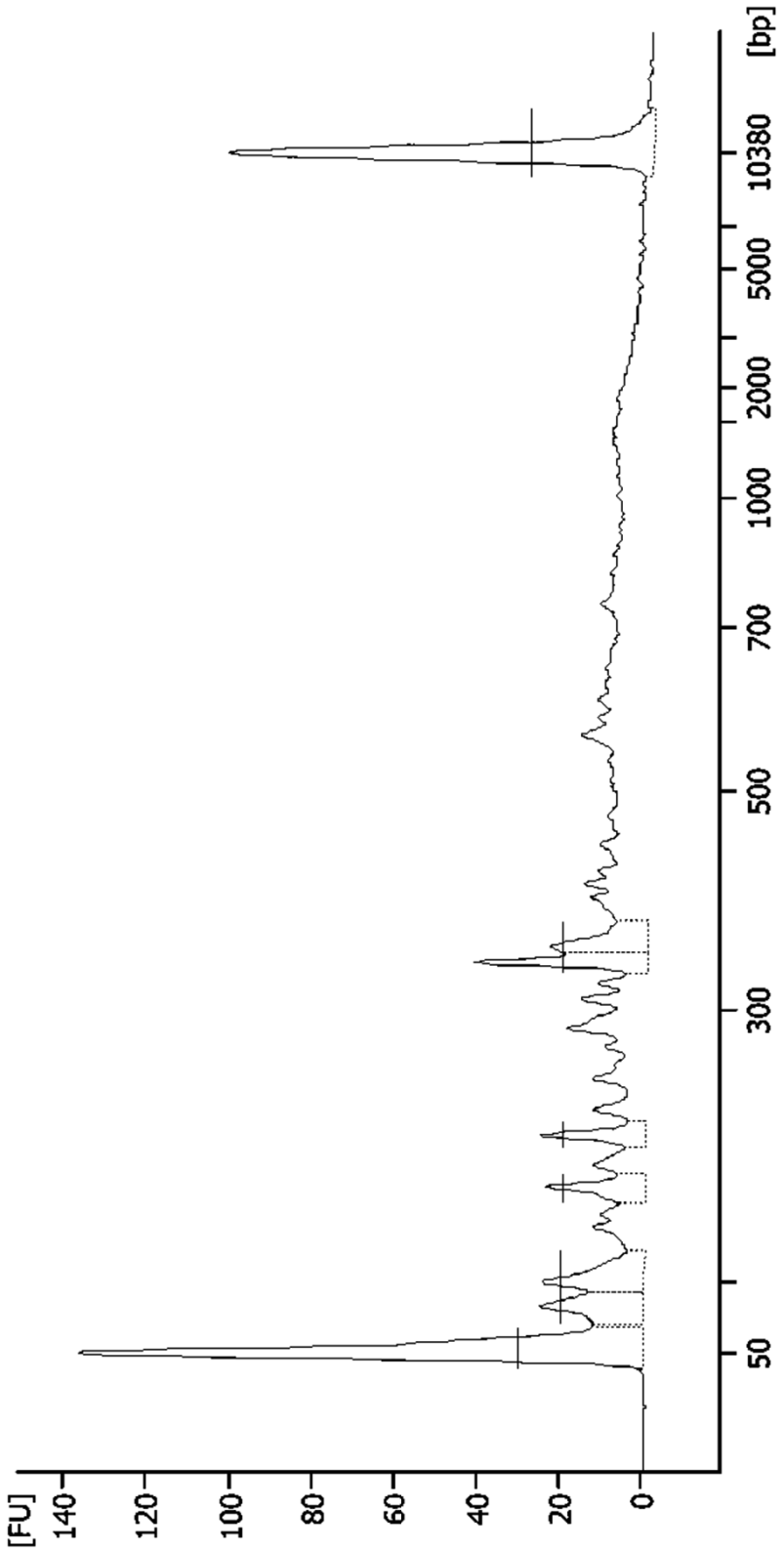

[FU]
140
120
100
80
60
40
20
0
50
300
500
700
1000
2000
5000
10380
[bp]

Fig. 110

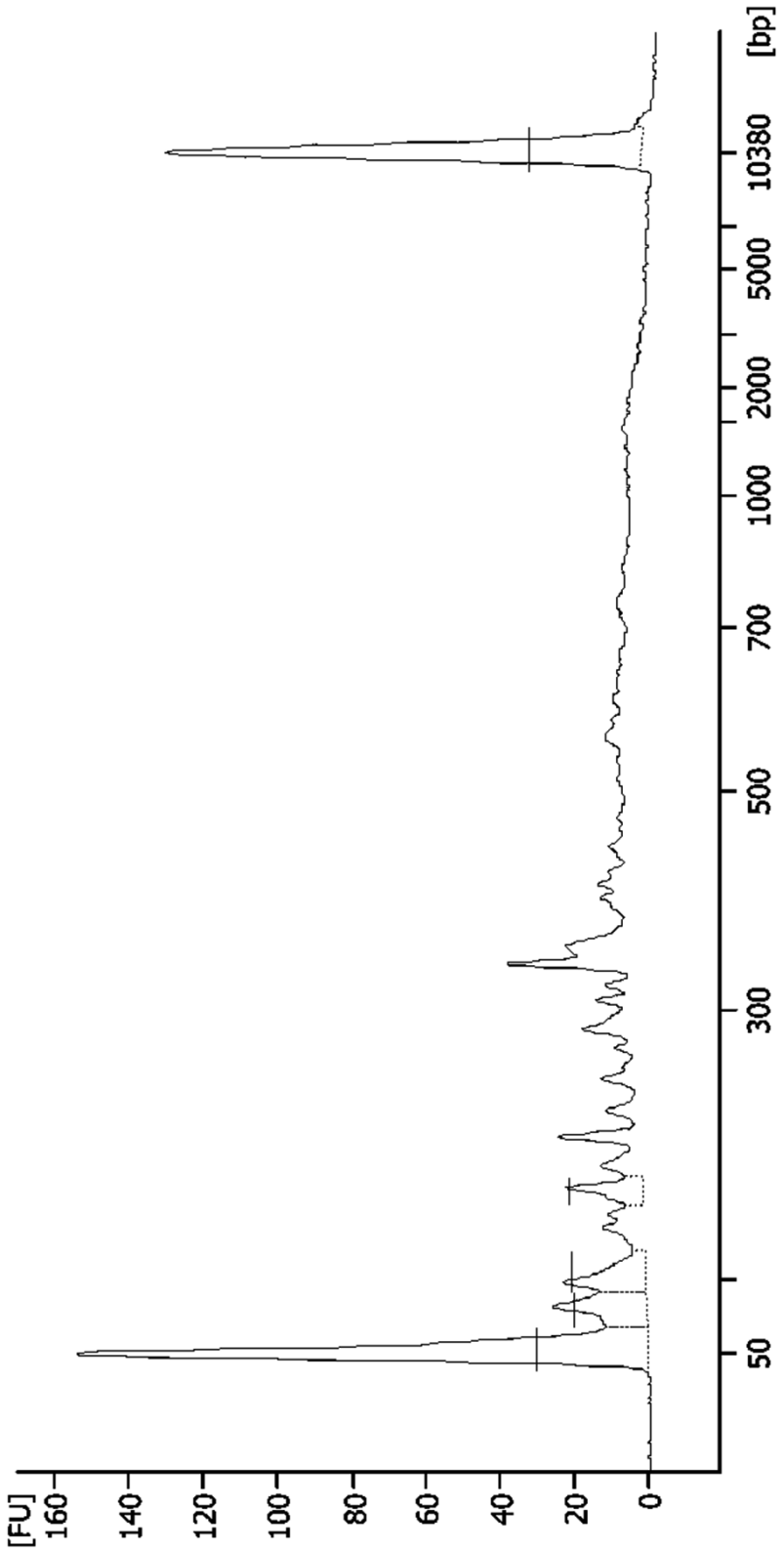

[FU]
160
140
120
100
80
60
40
20
0
50
300
500
700
1000
2000
5000
10380
[bp]

Fig. 111

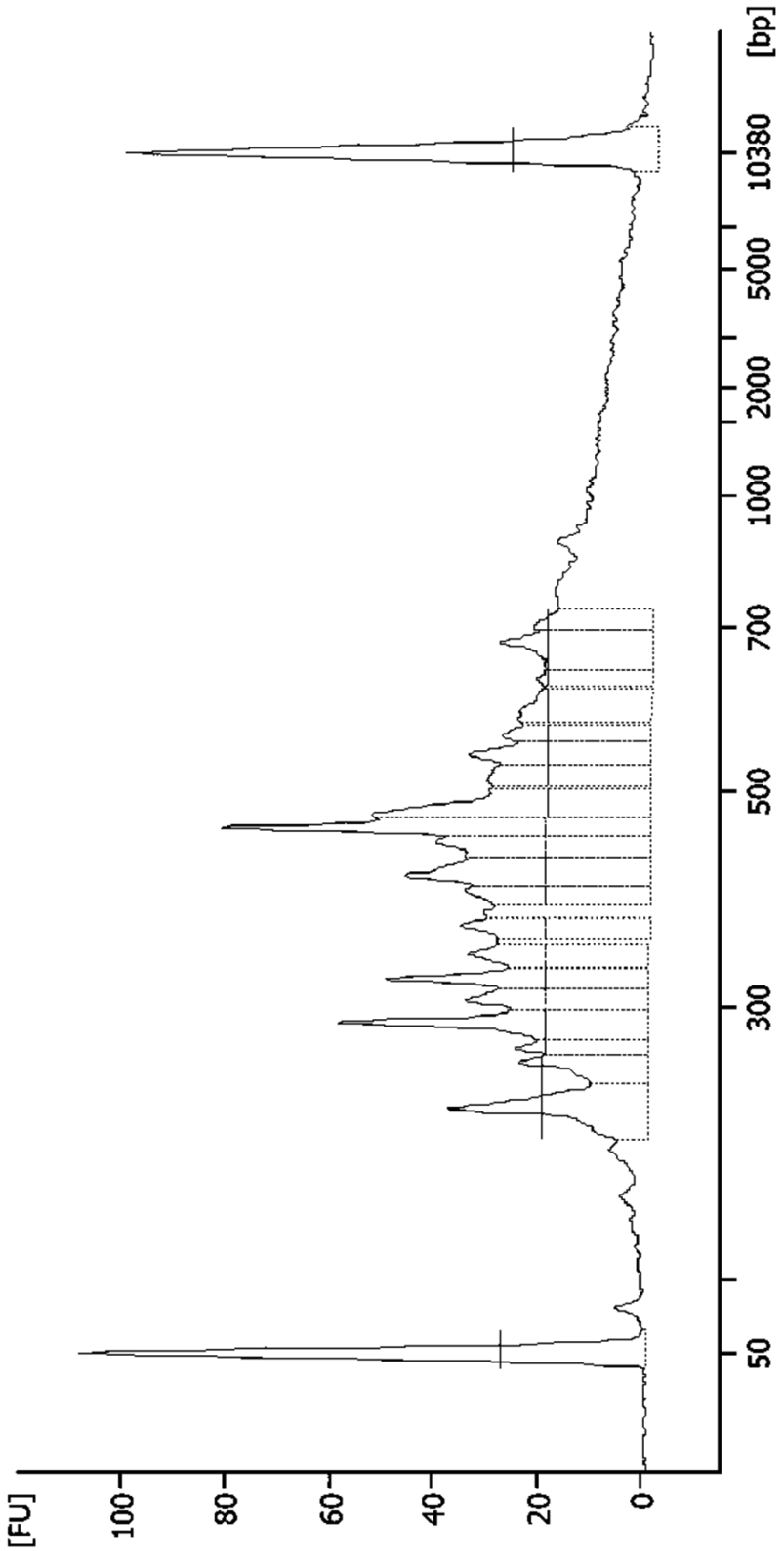


Fig. 112

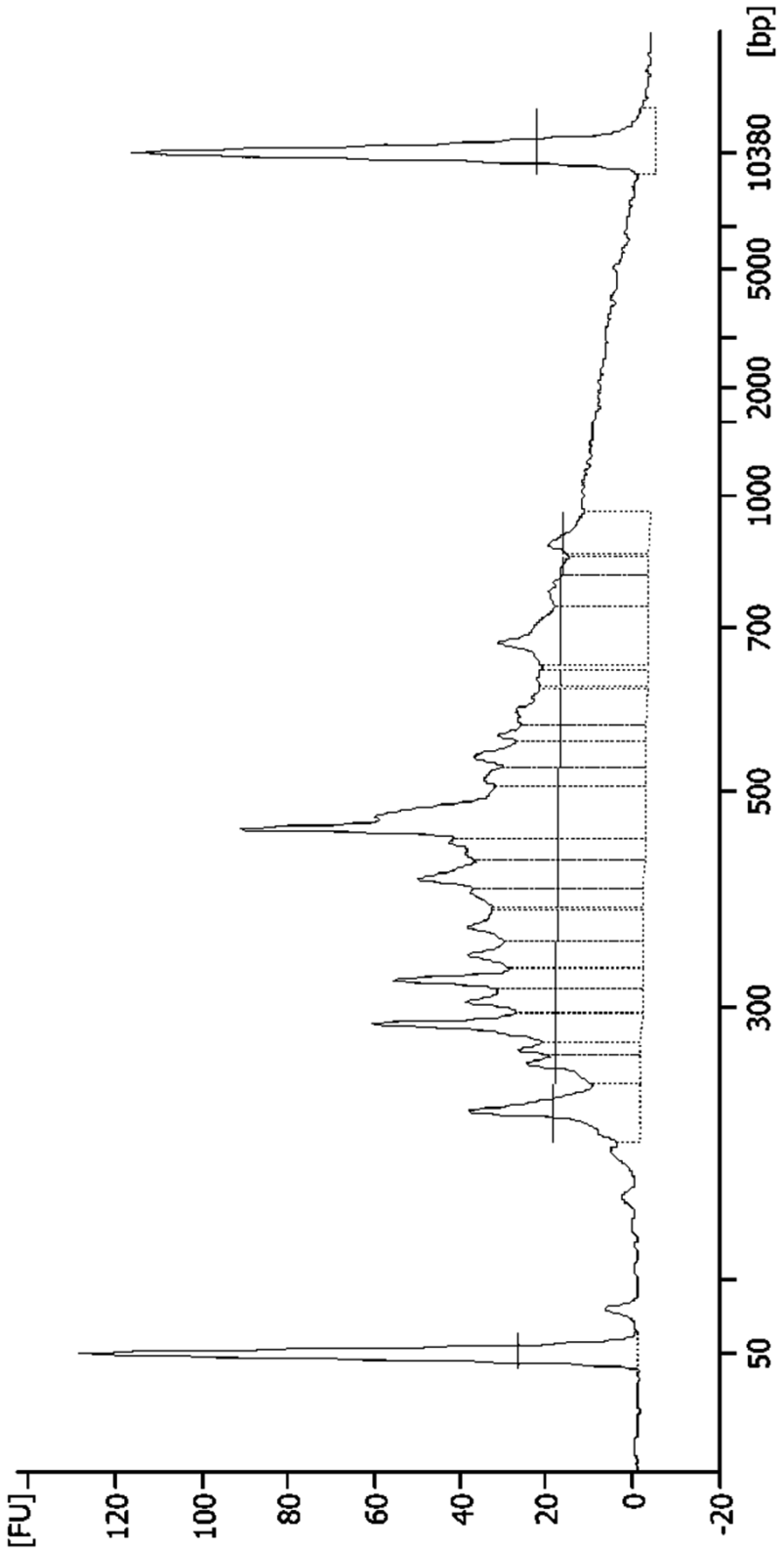


Fig. 113

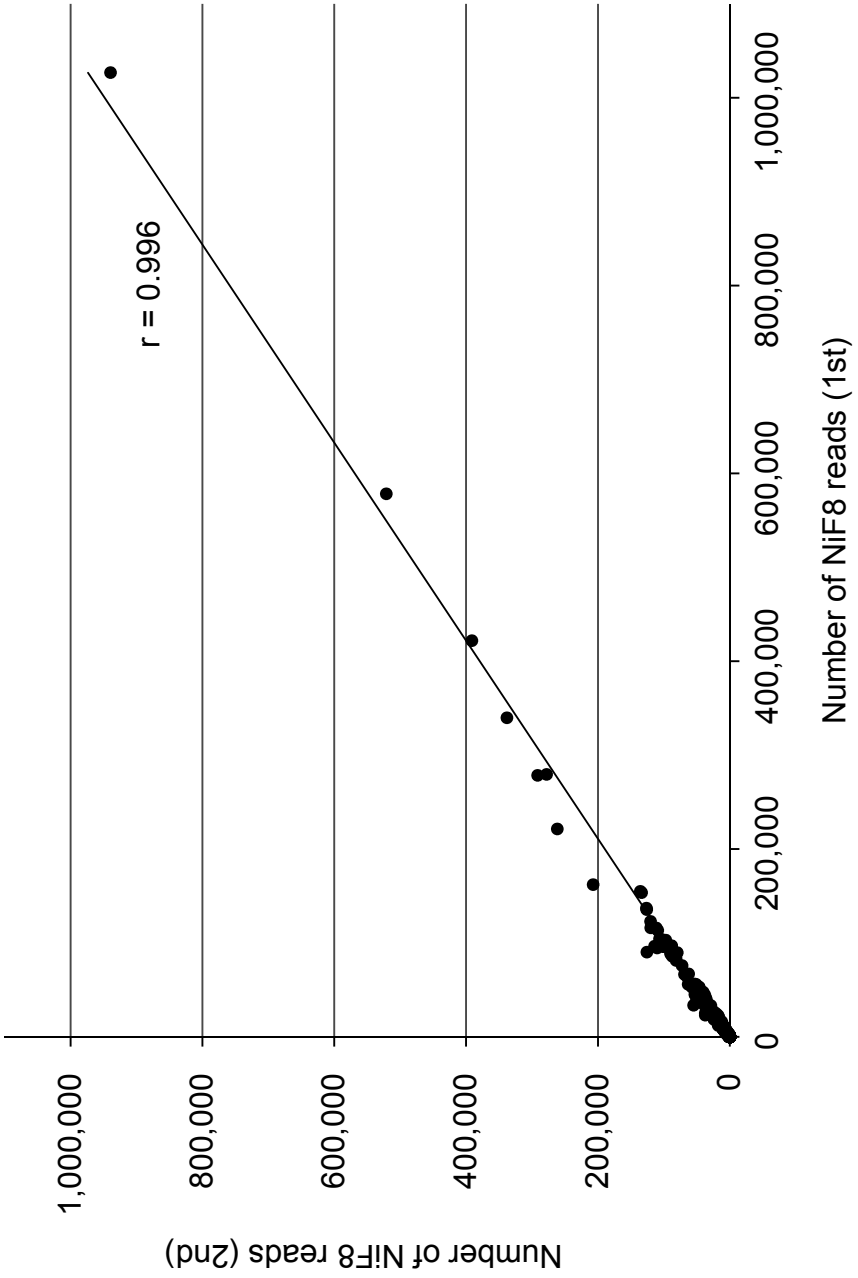

r = 0.996
Number of NiF8 reads (1st)
Number of NiF8 reads (2nd)
0
200,000
400,000
600,000
800,000
1,000,000

Fig. 114

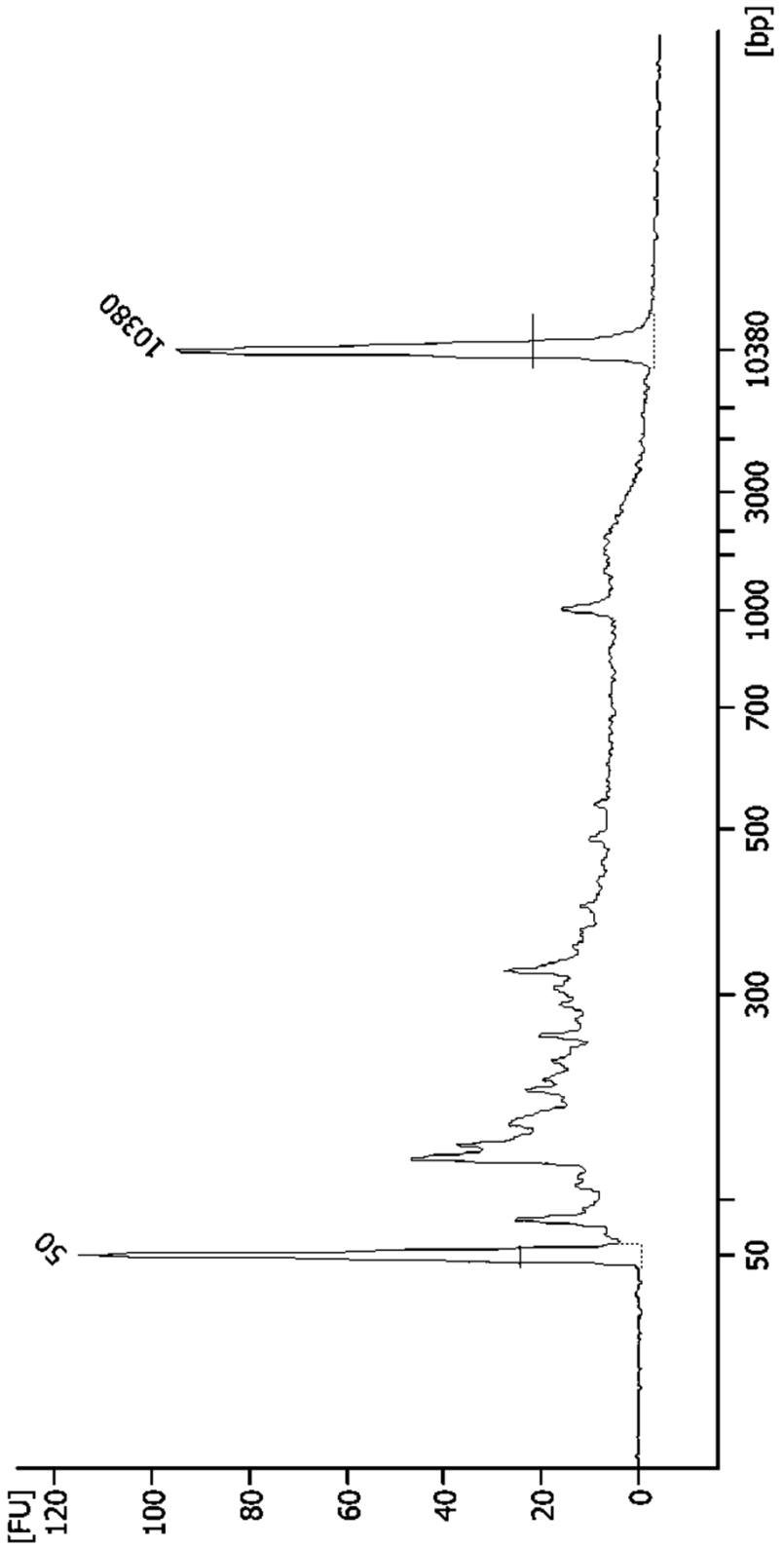

[FU]
120
100
80
60
40
20
0
50
300
500
700
1000
3000
10380
[bp]
50
10380

Fig. 115

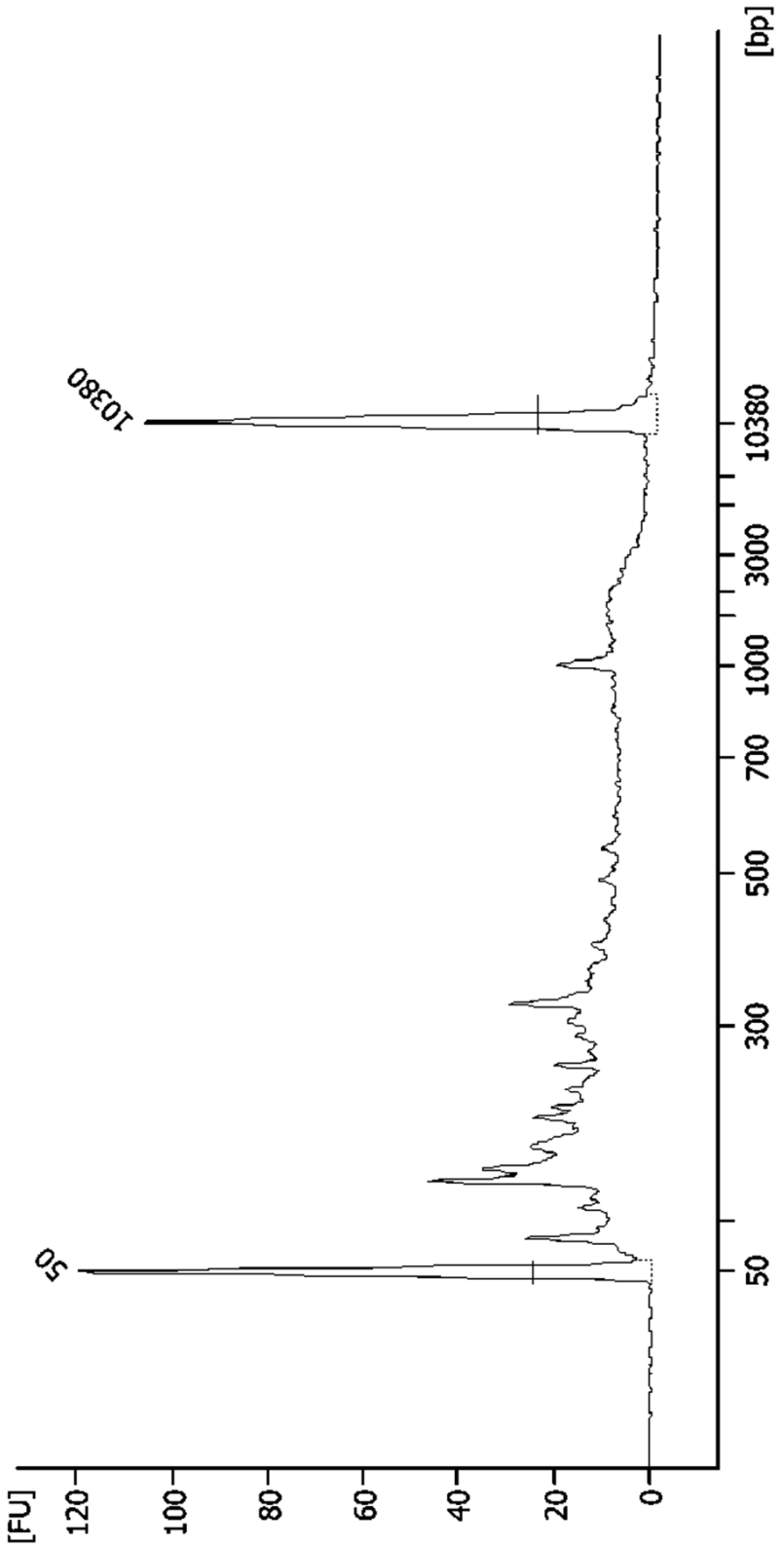

[FU]
120
100
80
60
40
20
0
50
10380
50
300
500
700
1000
3000
10380
[bp]

Fig. 116

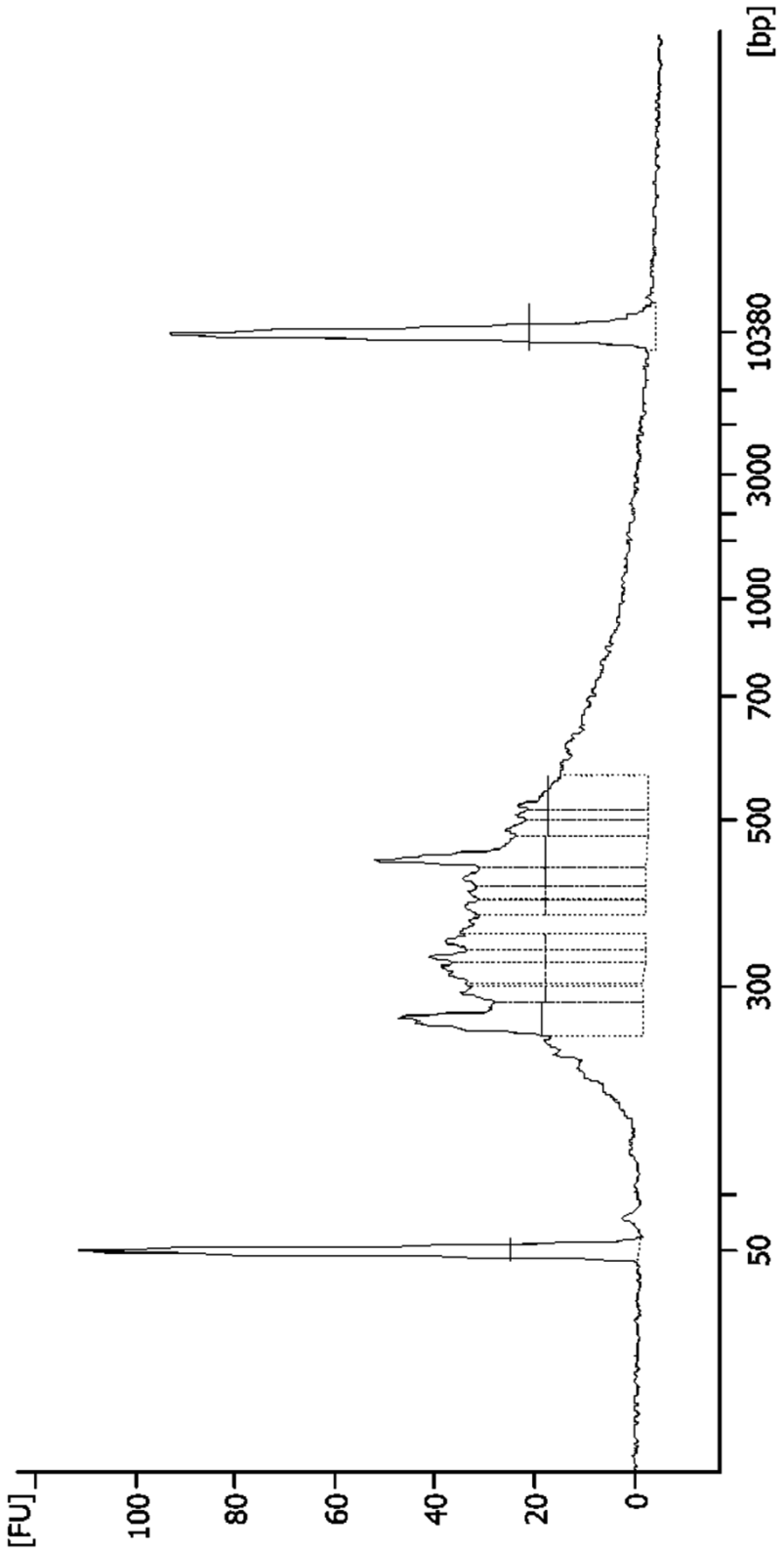


Fig. 117

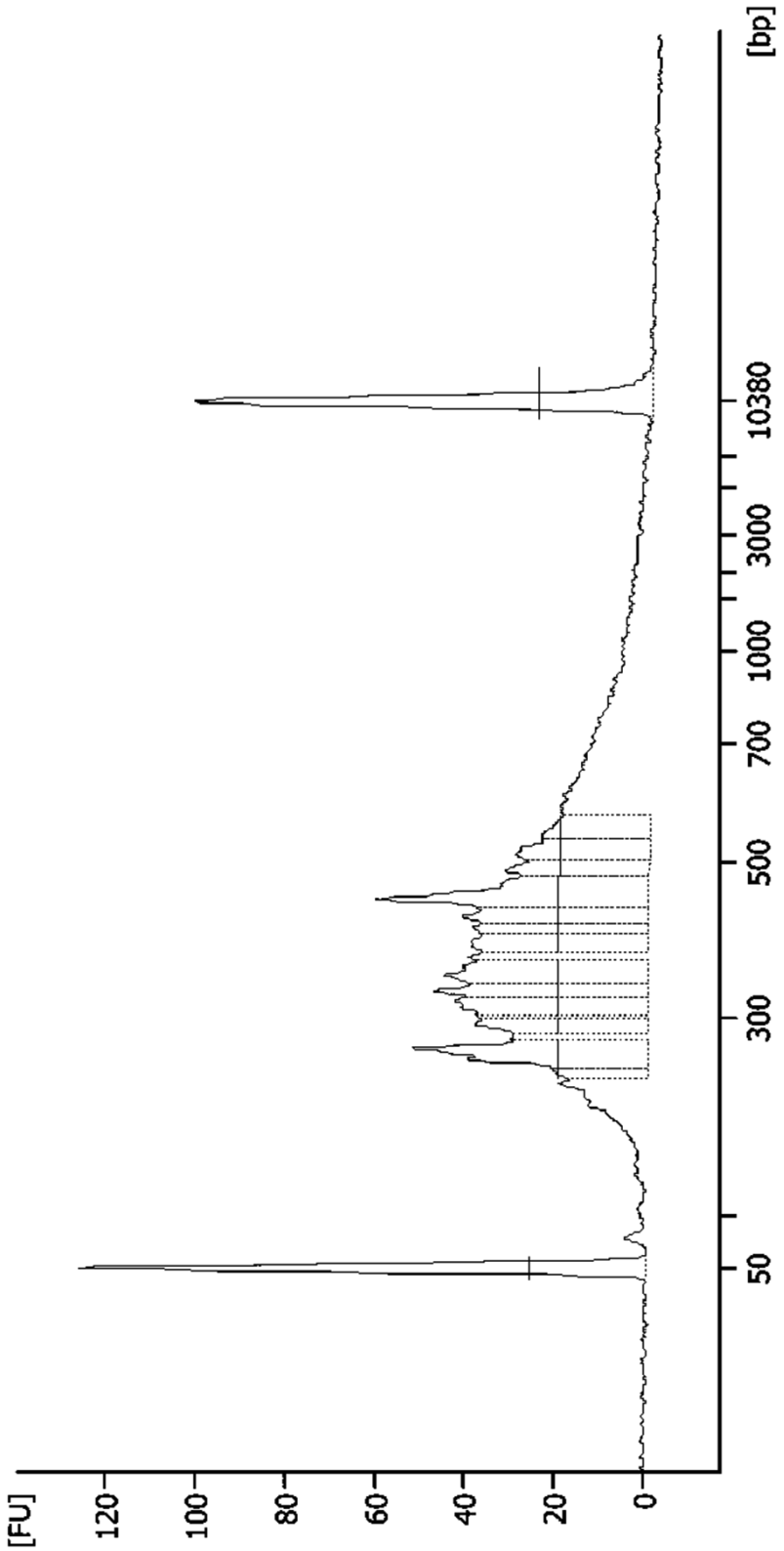


Fig. 118

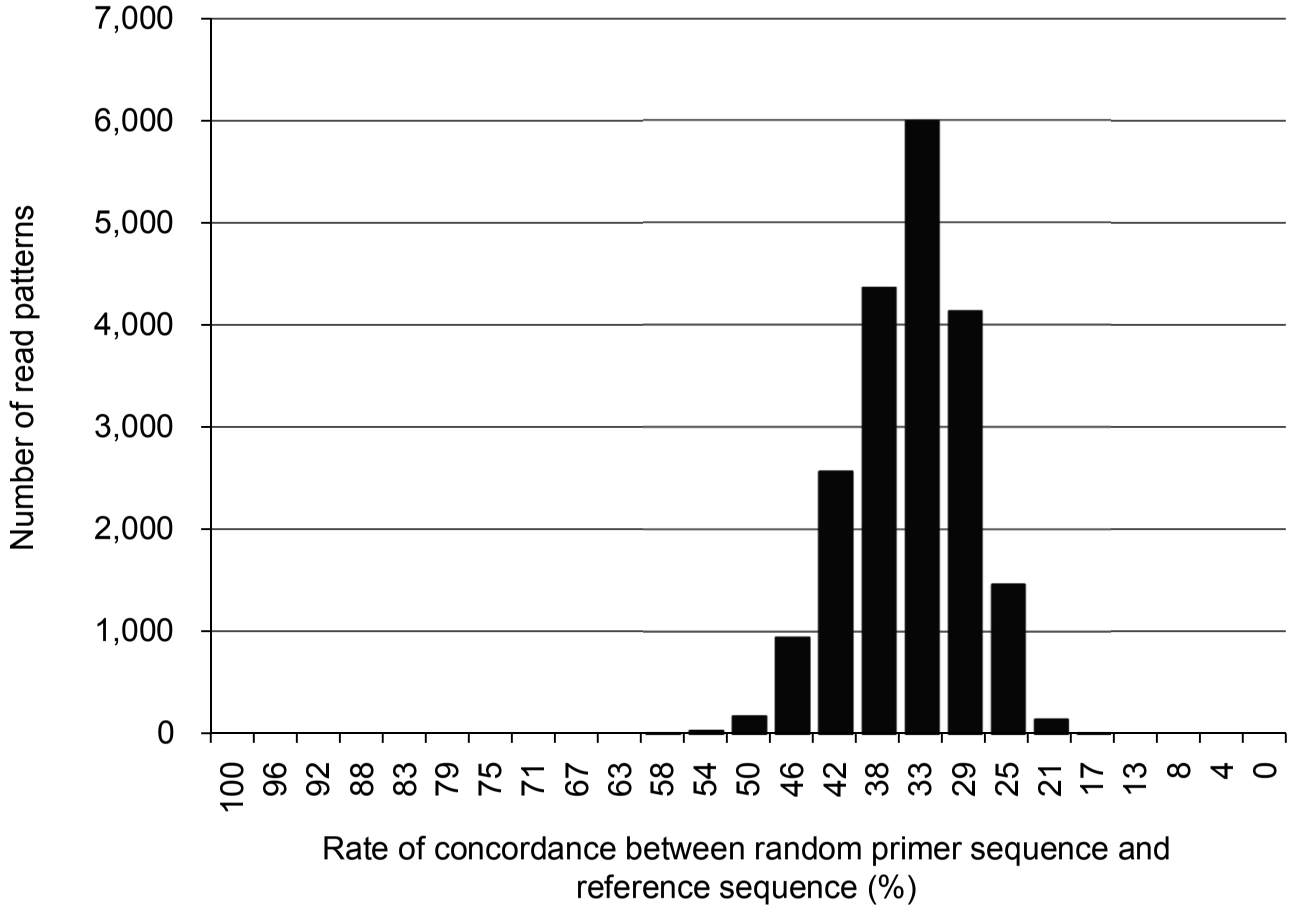
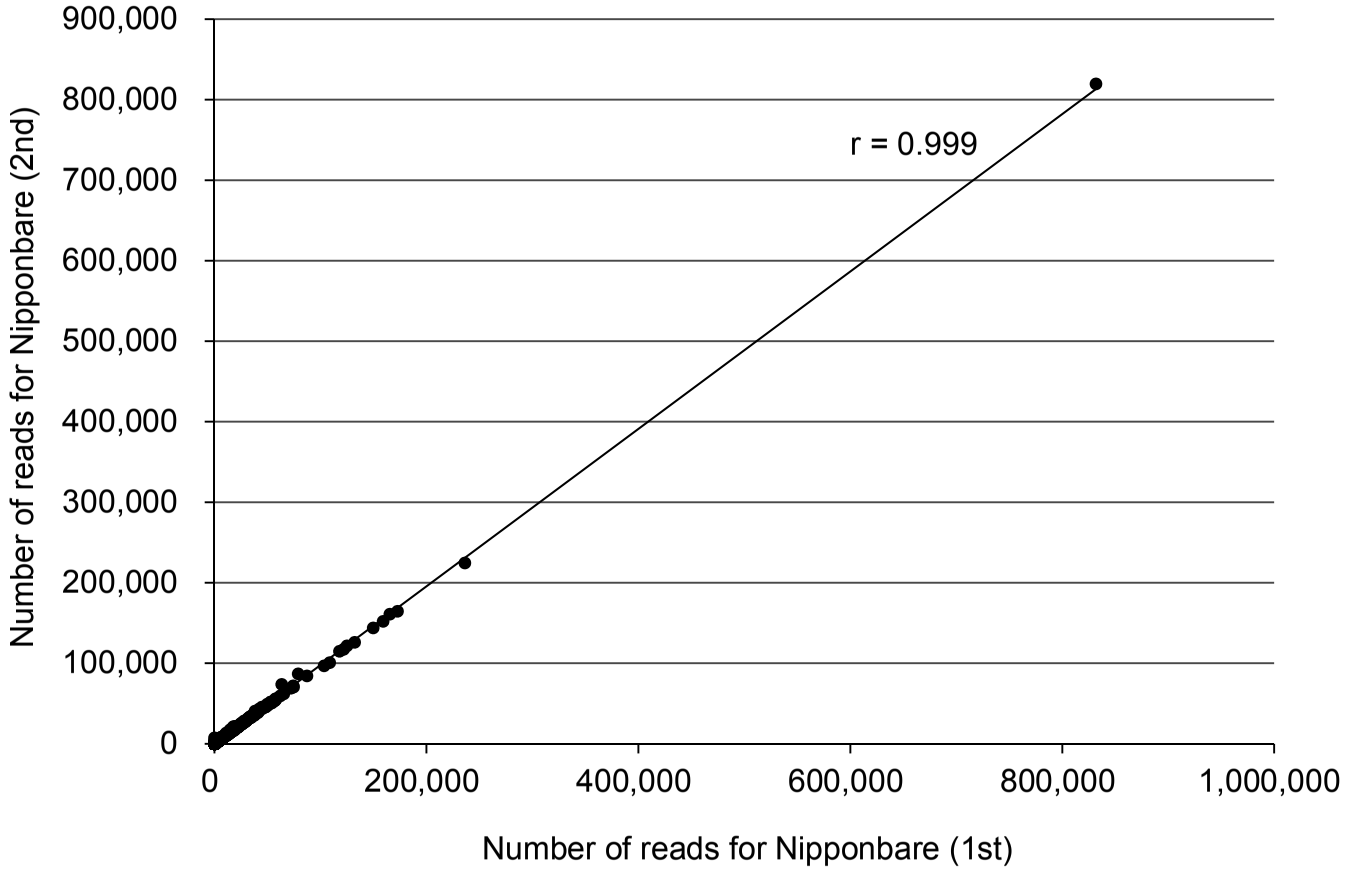

7,000
6,000
5,000
4,000
3,000
2,000
1,000
0
Number of read patterns
100
96
92
88
83
79
75
71
67
63
58
54
50
46
42
38
33
29
25
21
17
13
8
4
0
Rate of concordance between random primer sequence and reference sequence (%)

Fig. 119


900,000
800,000
700,000
600,000
500,000
400,000
300,000
200,000
100,000
0
Number of reads for Nipponbare (2nd)
r = 0.999
0
200,000
400,000
600,000
800,000
1,000,000
Number of reads for Nipponbare (1st)