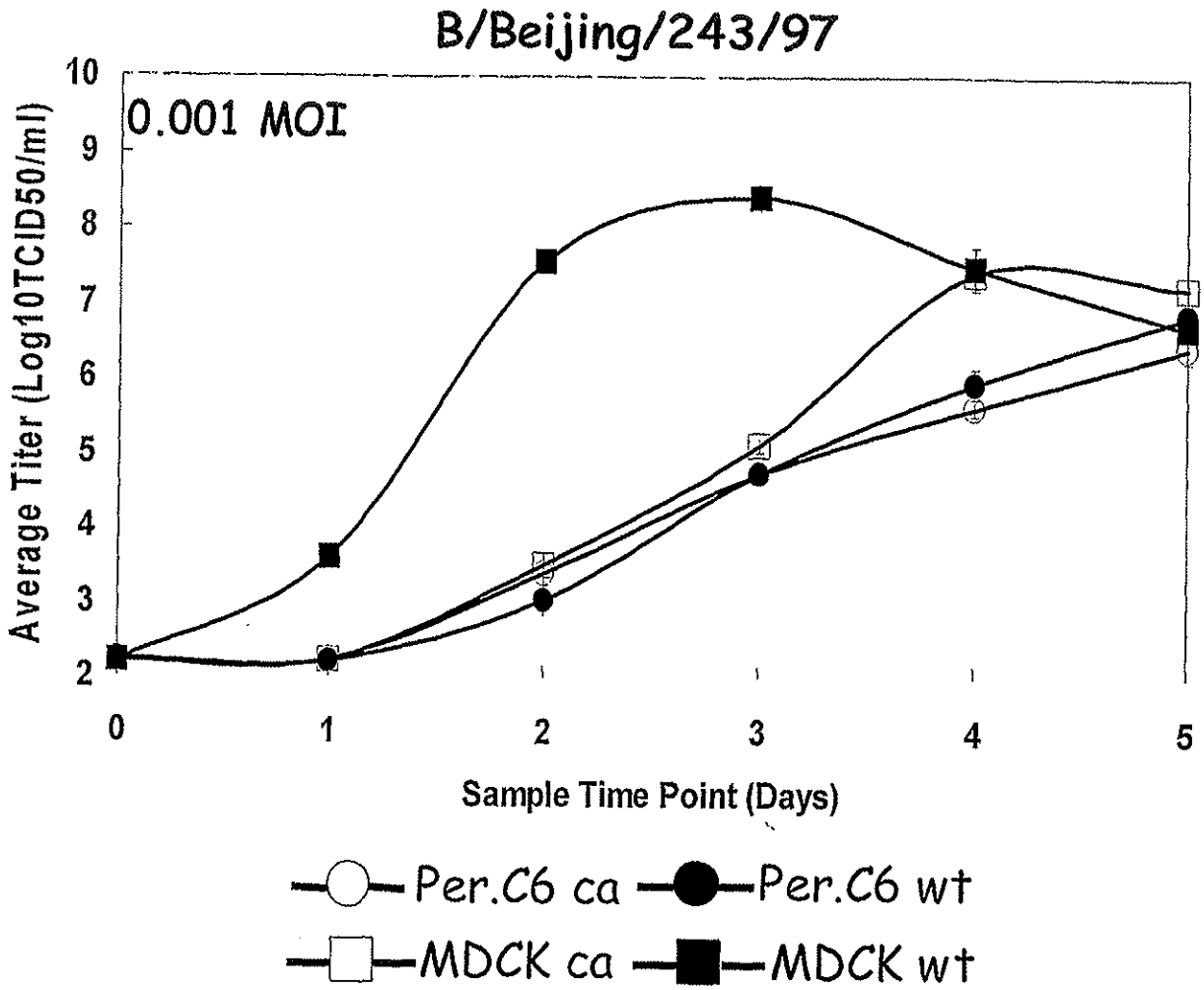

B/Beijing/243/97
0.001 MOI
Average Titer (Log10TCID50/ml)
10
9
8
7
6
5
4
3
2
0
1
2
3
4
5
Sample Time Point (Days)
Per.C6 ca
Per.C6 wt
MDCK ca
MDCK wt

Fig. 1

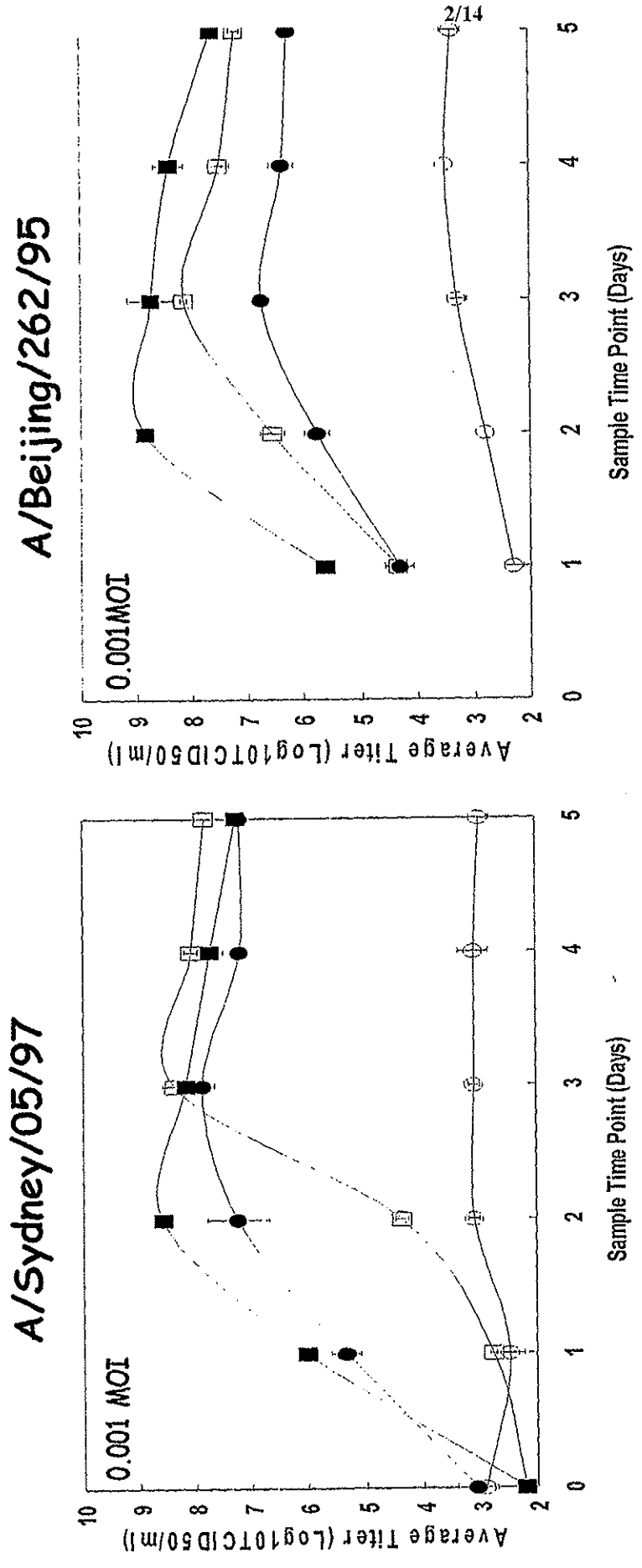

A/Sydney/05/97
A/Beijing/262/95
0.001 MOI
0.001MOI
Average Titer (Log10TCID50/ml)
Sample Time Point (Days)
Per.C6 ca
Per.C6 wt
MDCK ca
MDCK wt

Fig. 2

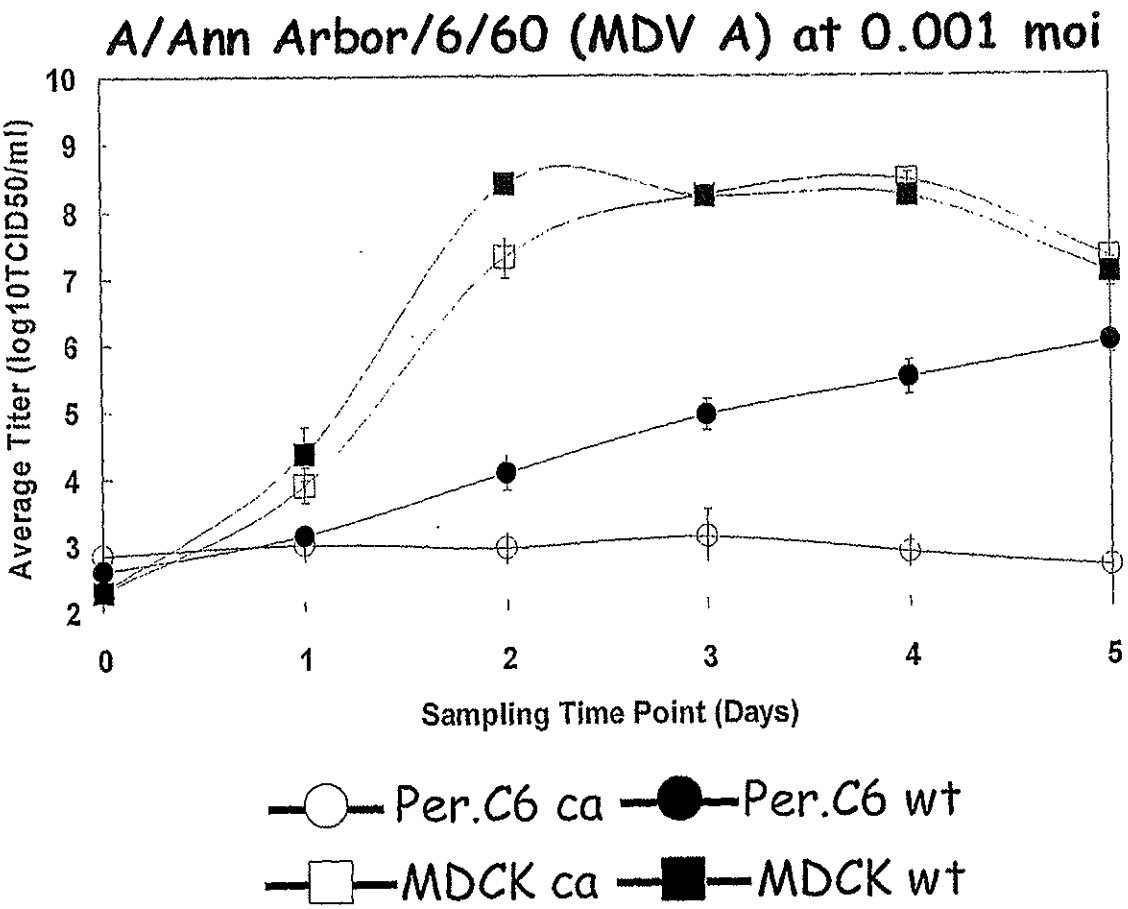

A/Ann Arbor/6/60 (MDV A) at 0.001 moi
Average Titer (log10TCID50/ml)
10
9
8
7
6
5
4
3
2
0
1
2
3
4
5
Sampling Time Point (Days)
Per.C6 ca
Per.C6 wt
MDCK ca
MDCK wt

Fig. 3

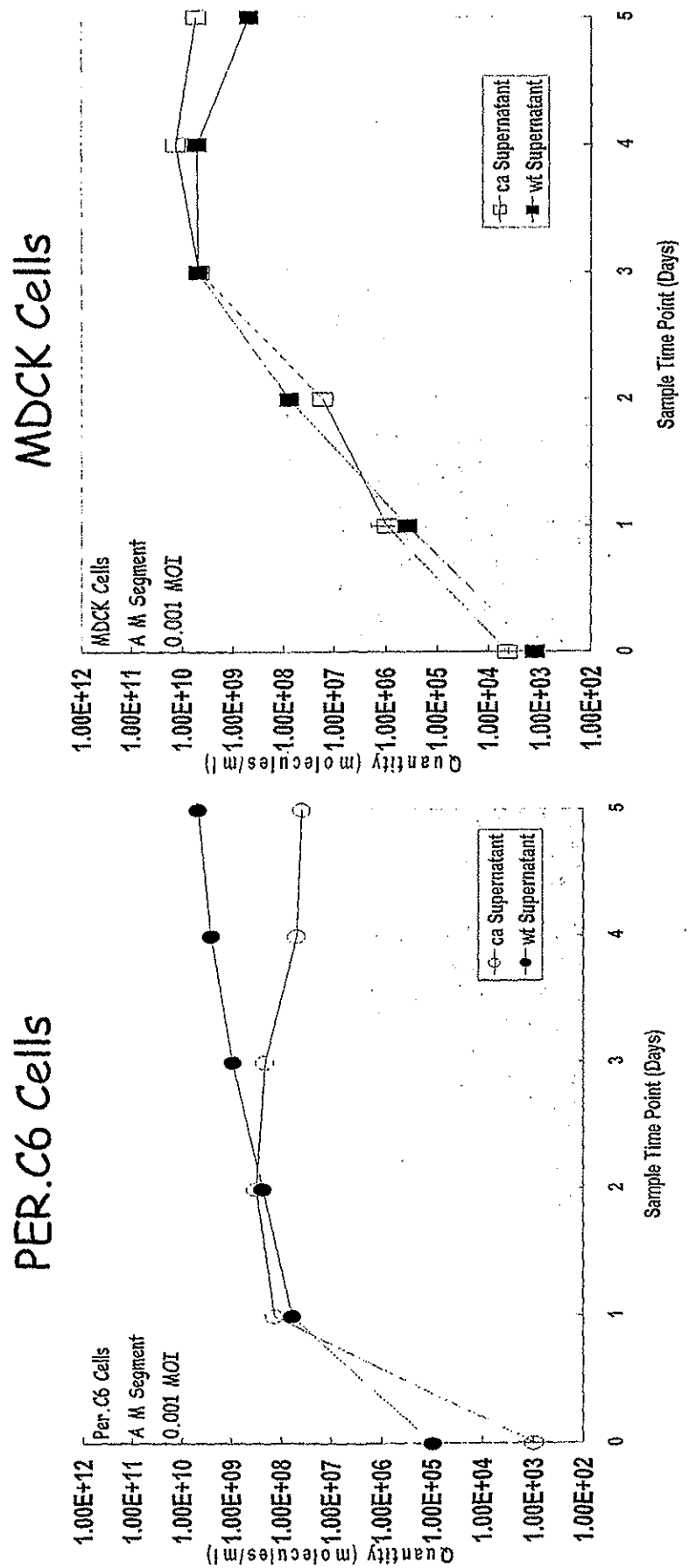
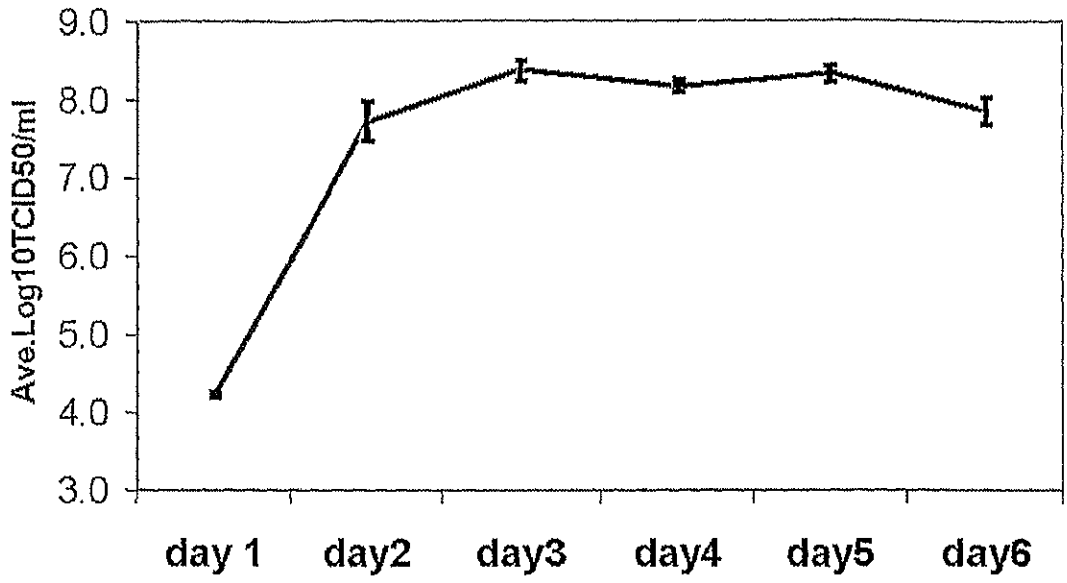

PER.C6 Cells
Per.C6 Cells
A M Segment
0.001 MOI
Quantity (molecules/ml)
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1.00E+11
1.00E+10
1.00E+09
1.00E+08
1.00E+07
1.00E+06
1.00E+05
1.00E+04
1.00E+03
1.00E+02
0
1
2
3
4
5
Sample Time Point (Days)
ca Supernatant
wt Supernatant
MDCK Cells
MDCK Cells
A M Segment
0.001 MOI
Quantity (molecules/ml)
Sample Time Point (Days)
ca Supernatant
wt Supernatant

Fig. 4



Replication of ca A/Vietnam/1203/2004 (H5N1) in MDCK cells

Fig. 5

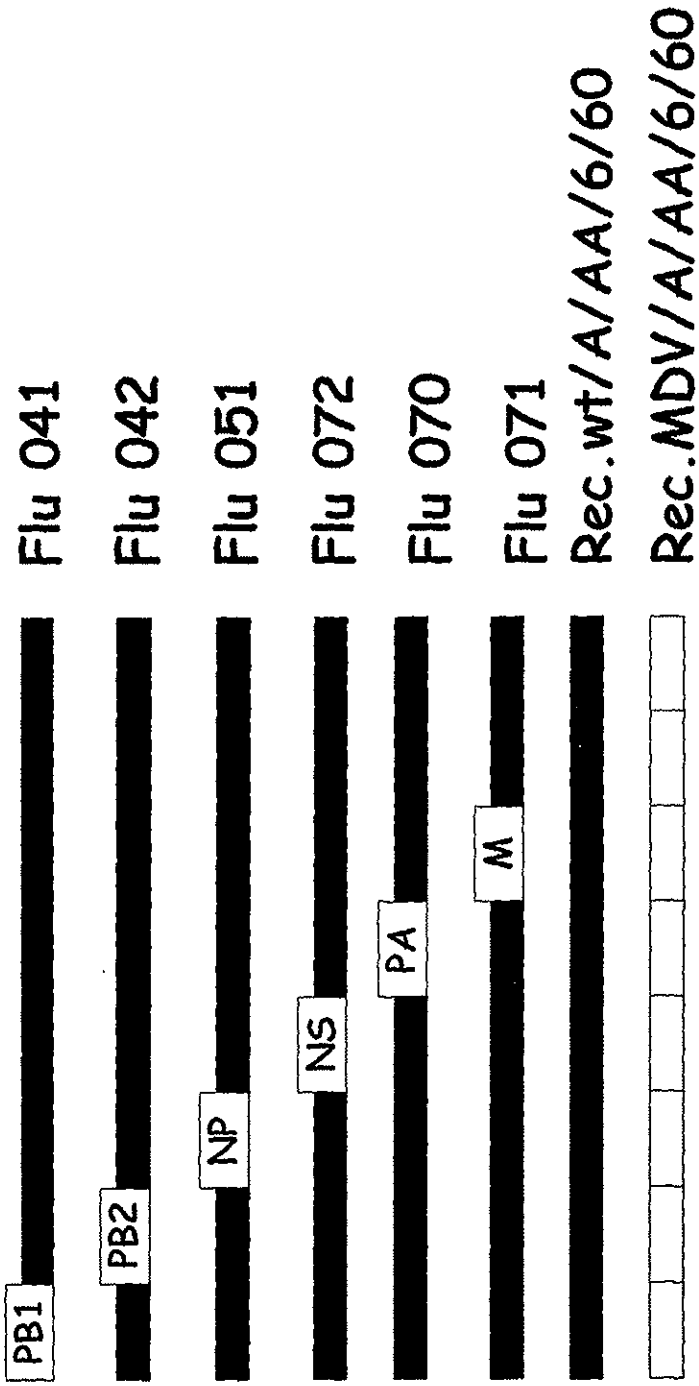

Flu 041
Flu 042
Flu 051
Flu 072
Flu 070
Flu 071
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Rec.MDV/A/AA/6/60
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NP
NS
PA
M

Fig. 6

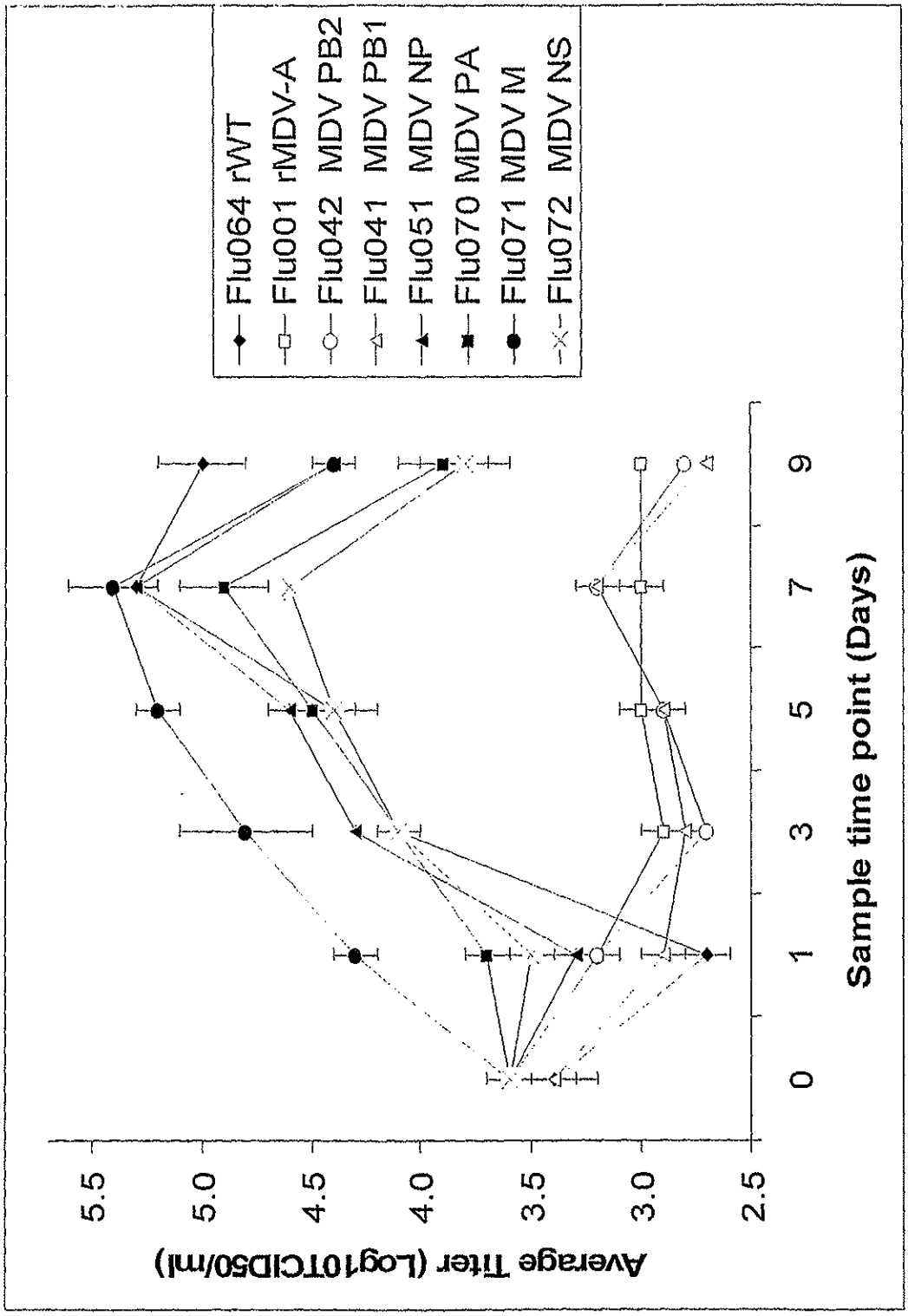

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Flu001 rMDV-A
Flu042 MDV PB2
Flu041 MDV PB1
Flu051 MDV NP
Flu070 MDV PA
Flu071 MDV M
Flu072 MDV NS
Average Titer (Log10TCID50/ml)
5.5
5.0
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3.5
3.0
2.5
0
1
3
5
7
9
Sample time point (Days)

Fig. 7

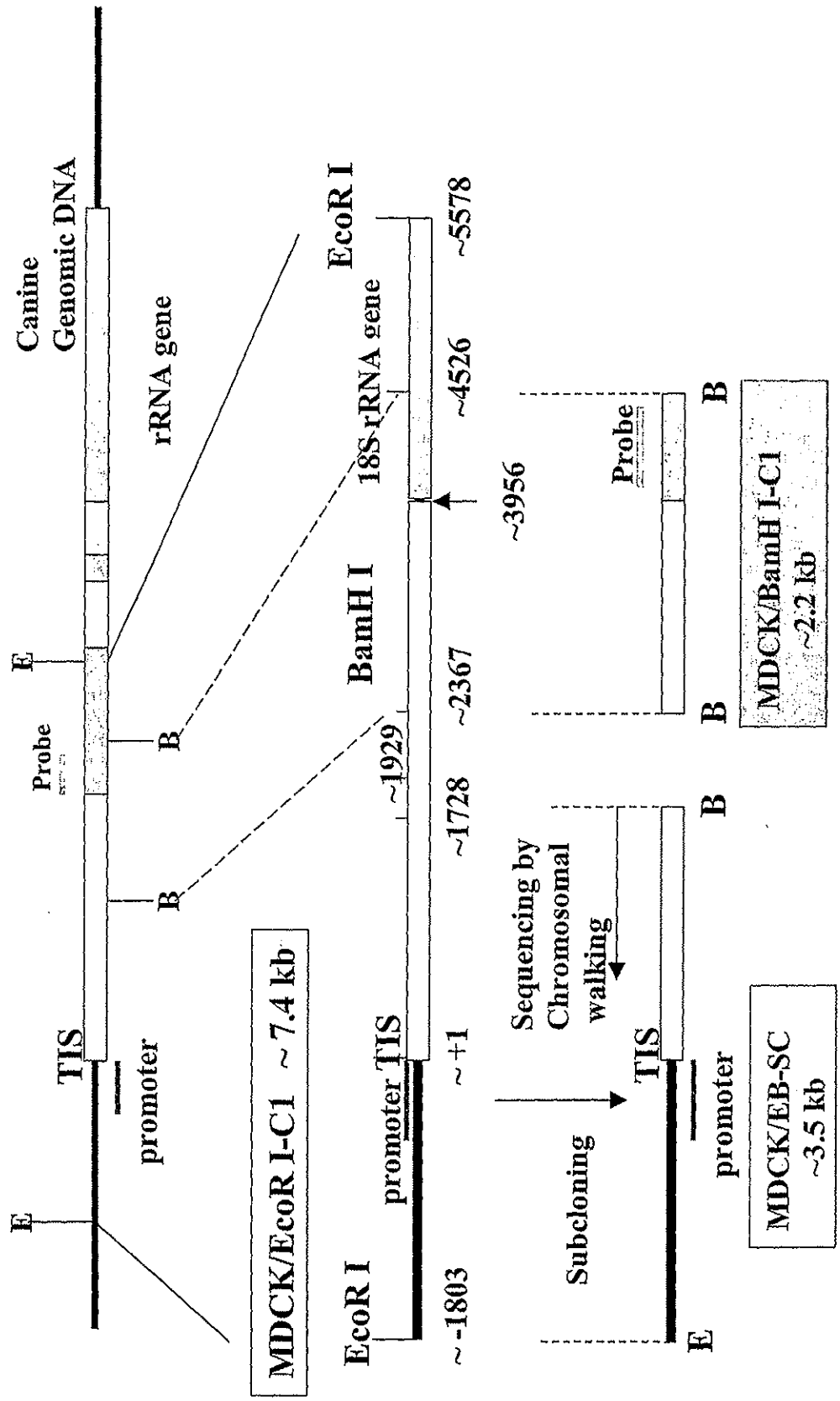

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rRNA gene
E
E
Probe
B
B
TIS
promoter
MDCK/EcoR I-C1 ~ 7.4 kb
EcoR I
promoter TIS
BamH I
EcoR I
18S-rRNA gene
~-1803
~+1
~1728
~1929
~2367
~3956
~4526
~5578
Sequencing by Chromosomal walking
Subcloning
TIS
promoter
E
B
B
Probe
B
B
MDCK/BamH I-C1 ~2.2 kb
MDCK/EB-SC ~3.5 kb

Fig. 8

(SEQ ID NO:1)

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Fig. 9A

(SEQ ID NO:1 continued)

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Fig. 9B

(SEQ ID NO:1 continued)

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Fig. 9C

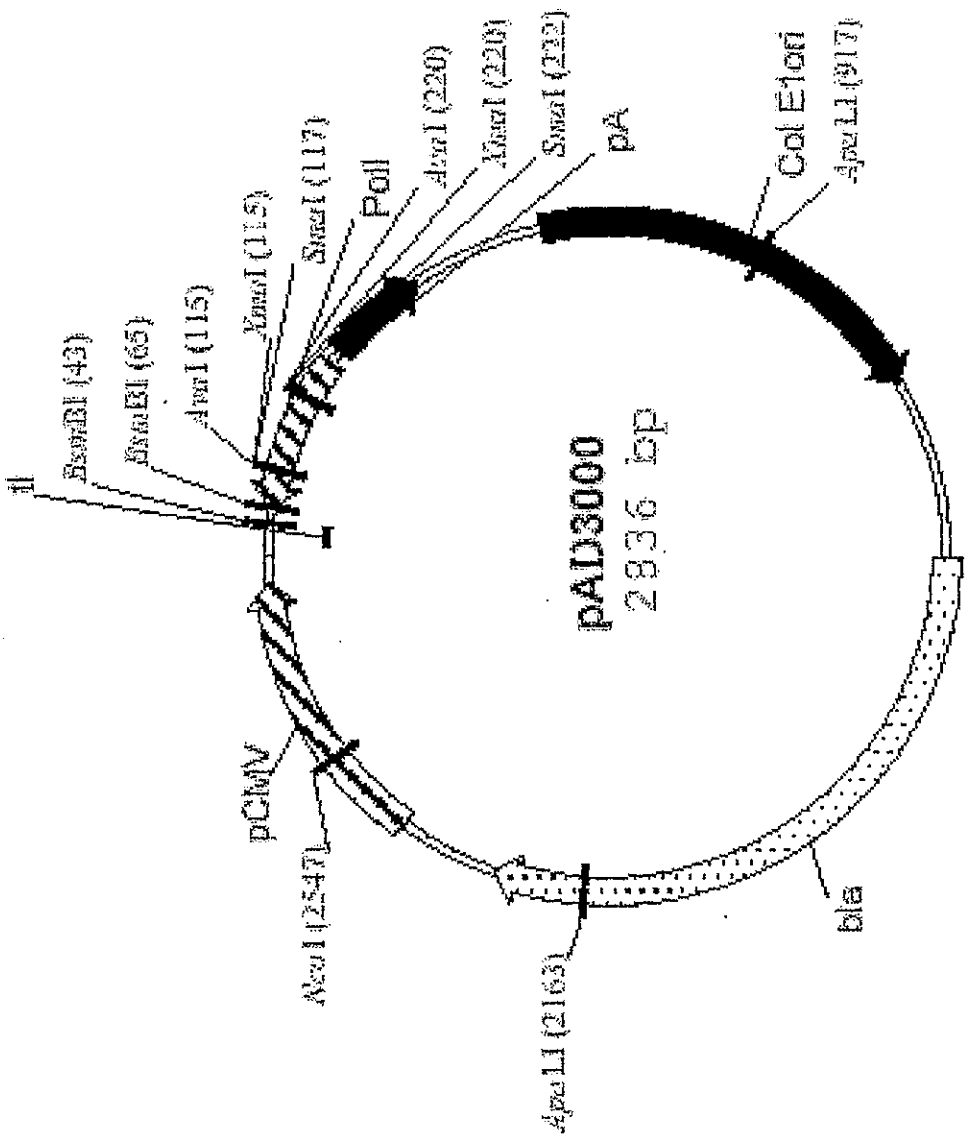

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BsmBI (65)
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Fig. 10

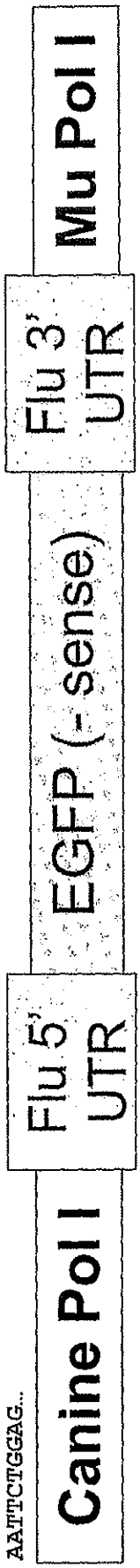

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Flu 5' UTR
EGFP (- sense)
Flu 3' UTR
Mu Pol I
1-1802
1-1803, or
1-1804

Fig. 11

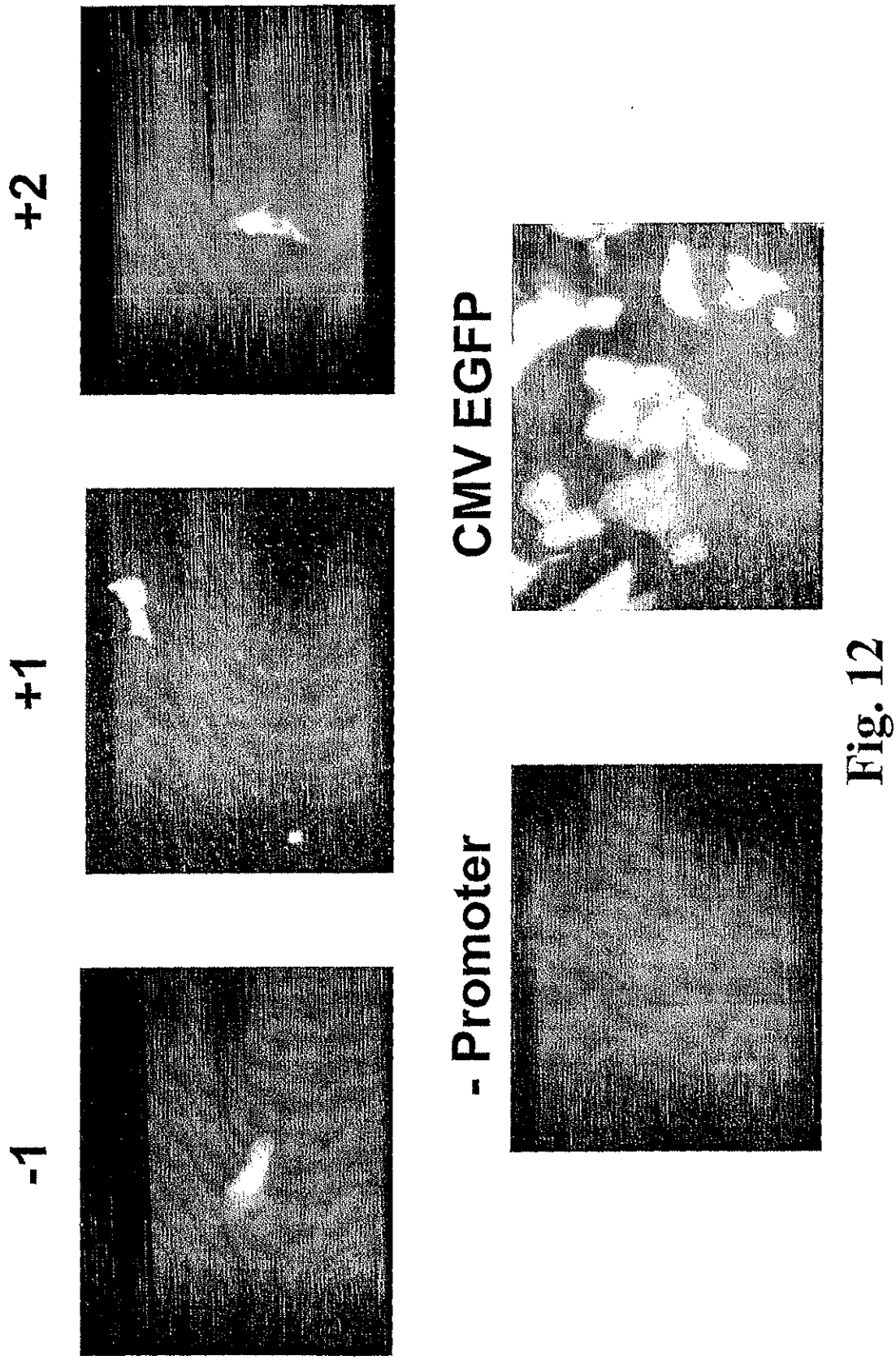


Fig. 12

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Duke, Gregory
Kemble, George
Young, James
Wang, Zhaoti

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<210> 11
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<212> DNA
<213> Canis familiaris

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ggggtggggg ggcgccgtgg ggcaggtttt ggggacagtt ggccgtgtca cggtcccggg 240

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gggtgggggt gggggggcgc cgtggggcag gttttgggga cagttggccg tgtcacggtc 180

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cgag 244

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<211> 190
<212> DNA
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cttgcccgag 190

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<213> Canis familiaris

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ttttcttgcc cgag 134

<210> 16
<211> 106
<212> DNA
<213> Canis familiaris

<400> 16
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ctgtggctgg tccccgccgg caggcgcggt tattttcttg cccgag 106

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<212> DNA
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cggttatttt cttgcccgag 80

<210> 18
<211> 217
<212> DNA
<213> Canis familiaris

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gtccccgccg gcaggcgcgg ttatttttctt gcccgag 217

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<211> 56
<212> DNA
<213> Canis familiaris

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