

Sequence_Listing
SEQUENCE LISTING

<110> Merial Limited
Audonnet, Jean-Christophe
Seetha, Jaganathan

<120> High Resolution Melt Genotyping of IBV, CSFV and NDV

<130> MER 12-208

<150> 61/738,688
<151> 2012-12-18

<160> 46

<170> PatentIn version 3.5

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<400> 3
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 ccatagctat gacagcacct cttcagggtta tggcttggtc taaggcaciaa ttctgtagtg 120
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 gtagcaagac tggraayagg ta 22

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Sequence_Listing

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<223> DNA of CSFV of LBK

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tgaagaactg gtgctagcaa gaaagcaggt caacaacttt caagggacag acaggtataa 120
tctaggtcca atagtcaata tgggtgctaag gaggctgaga gtcattgatga tgaccttgat 180
tgaggagagg gtatgagcgt ggttaacccg cgatctggac ccgctattag gactctattg 240
tagataacac tattttatttt tattttattta gatattacta tttgtttatt tattttattta 300
ttgaatgagt aagaactggt acaaactacc tcgtgttacc acactacact catttttaac 360
agcactt 367

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<220>
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tctaggtcca atagtcaata tgggtgctaag gaggctgaga gtcattgatga tgaccttgat 180
tgaggagagg gtatgagcgt ggttaacccg cgatctggac ccgctattag gactctattg 240
tagataacac tattttatttt tattttattta gatattacta tttgtttatt tattttattta 300
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<210> 12
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<220>
<223> PCR product of CSFV of Pestiffa

<400> 12
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atgaagaact ggtgttgga agaaaacaga tcaacaactt tcaagggaca gacaggtaca 120
acctaggccc aatagtcaac atggtgttaa ggaggctgag agtcattgat atgacgctga 180
tagggagagg ggcattgagc cgggtaaccc gggatctgaa cccgccagta ggaccctatt 240

Sequence_Listing

gtagataaca ctaatTTTTT tttttttttt tttttttttt ttagatatta ttattttattt 300
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 actcattttt aggggggggg 379

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 ggtacaatct aggcccaata gtcaacatgg tgtaaggag gctgagagtc atattattgc 180
 ccttattggg gaggggggta tgagcgcggg caaccggga tctggaccg ccagtaggac 240
 cctattgtag ataactactaa ttttttattt atttagatat tattatttat ttattttattt 300
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 tatgaagaac tgggtgttggc aagaaaacag atcaacaact ttcaaggagac agacagggtac 120
 aacctaggcc caatagtcaa catggtgtta aggaggctga gagtcatgat gatgacgctg 180
 atagggagag gggcatgagc gcgggtaacc cgggatctga acccgccagt aggaccctat 240
 ttagataac actaattttc ttttttcttt tttatttatt tagatattat tattttattta 300
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<400> 15
 ttagcaaga ctgggaatag gtacatcccc ggggaagggtc acaacatgca aggaagacat 60
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Sequence_Listing

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aacctaggcc caatagtcaa catggtgtta aggaggctga gagtcatgat gatgacgctg      180
ataggggagag gggcatgagc gcgggtaacc cgggatctga acccgccagt aggaccctat      240
tgtagataac actaattttc ttttttcttt tttatttatt tagatattat tatttattta      300
tttatttatt tattgaatga gtaagaactg gtataaacac ctcaagacca cactacactc      360
atttttaaca gcactttaa                                          379

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<220>
<223> PCR product of CSFV of YSC

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<400> 16
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aagaaaacag atcaacaact ttcaaggagc agacaggtac aacctaggcc caatagtcaa      120
catggtgtta aggaggctga gagtcatgat gatgacgctg ataggggagag gggcatgagc      180
gcgggtaacc cgggatctga acccgccagt aggaccctat tgtagacaac actaatcttt      240
tttttttttt tttttttttt tttttttttt tttttttaga tttttttttt tttttttttt      300
tttttttttt aaaaaagcaa aaactgggat aaaccccccc ccccccccc cccccttttt      360
tttttaaaaa aacttttagc                                          379

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<210> 17
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<220>
<223> forward primer 1 for NDV

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<400> 17
atgggcyyca gaycttctac                                          20

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<210> 18
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<212> DNA
<213> artificial sequence

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<220>
<223> reverse primer 1 for NDV

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<400> 18
ctgccactgc tagttgtgat aatcc                                          25

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<220>
<223> DNA of NDV strain clone30

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Sequence_Listing

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 actaacctgt cttgattatt tacagttagt ttacctgtct atcaagttag aaaaaacacg 120
 ggtagaagat tctggatccc gggtggcgcc ctccaggtgc aagatgggct ccagaccttc 180
 taccaagaac ccagcaccta tgatgctgac tatccgggtt gcgctggtac tgagttgcat 240
 ctgtccggca aactccattg atggcaggcc tcttgagct gcaggaattg tggttacagg 300
 agacaaagcc gtcaacatat acacctcatc ccagacagga tcaatcatag ttaagctcct 360
 cccgaatctg cccaaggata aggaggcatg tgcgaaagcc cccttgatg catacaacag 420
 gacattgacc actttgctca ccccccttgg tgactctatc cgtaggatac aagagtctgt 480
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 <223> DNA of NDV strain Mukteswar

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 aatgatctgt cttgattact tacagttagt ttccctgtct atcaaattag aaaaaacacg 120
 ggtagaagag ttcggatccc ggccggcgca ccaaaagcgc aagatgggct ccagatcttc 180
 taccaggatc ccagtacctc taatgctgac catacggatc acgctggcac tgagttatgt 240
 ccgtctgaca agttctcttg atggcaggcc tcttgagcc gcagggatcg tggtaacagg 300
 ggataaagca gttaacatat acacctcatc ccagacaggg tcaatcatag tcaagttact 360
 cccaaatatg cccaaggaca aagaggcatg tgcaaaagcc ccattggagg cttacaacag 420
 gacactgact actttgctta ccccccttgg tgattctatc cgcaggatac aagagtctgt 480
 gactacatcc ggaggaagga gacagagacg ctttataggt gccattattg gcag 534

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 <211> 534
 <212> DNA
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<220>
 <223> DNA of NDV strain B1

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 actaatctgt cttgattatt tacagttagt ttacctgtcc atcaagttag aaaaaacacg 120
 ggtagaagac tctggatccc gggtggcgcc ctccaggtgc aggatgggct ccagaccttt 180
 taccaagaac ccagcaccta tgatgctgac tatccgggtc gcgctggtat tgagttgcat 240
 ctgtccggca aactccattg atggcaggcc ttttgagct gcaggaattg tggttacagg 300
 agacaaagca gtcaacatat acacctcatc ccagacagga tcaatcatag ttaagctcct 360

Sequence_Listing

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cccgaatctg cccaaggata aggaggcatg tgcgaaagcc cccttgatg catacaacag      420
gacattgacc actttgctca ccccccttgg tgactctatc cgtaggatac aagagtctgt      480
gactacatct ggagggggga gacaggggcg ccttataggc gccattattg gcgg          534

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<210> 22
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<212> DNA
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<220>
<223> DNA of NDV strain VG/GA

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<400> 22
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actaatctgt cttgattatt tacagttagt ttacctgtcc atcaagttag aaaaaacacg     120
ggtagaagat tctggatccc ggttgccgcc ctccaggtgc aggatgggct ccagaccttc     180
taccaagaac ccagcaccta tgatgctgac tatccgggtc gcgctggtag tgagttgcat     240
ctgtccggca aactccattg atggcaggcc tcttgagct gcaggaattg tggttacagg     300
agacaaagca gtcaacatat acacctcatc ccagacagga tcaatcatag ttaagctcct     360
cccgaatctg cccaaggata aggaggcatg tgcgaaagcc cccttgatg catataacag      420
gacattgacc actttgctca ccccccttgg tgactctatc cgtagaatac aagagtctat      480
gactacatct ggagggggga gacaggggcg ccttataggc gccattattg gcgg          534

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<210> 23
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<220>
<223> DNA of NDV strain KBNP-C4152R2L

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actaatctgt cttgattatt tacagttagt ttacctgtct atcaagttag aaaaaacacg     120
cgtacgggta gaagagtctg gatcccgacc ggcacattca ggacgcaata tgggctccaa     180
actttctacc aggattccag cacctctgat gctgaccacc cggattacgc tgatattgag     240
ctgtatccgt ccgacaagct ctcttgacgg caggcctctt gcagctgcag gaattgtagt     300
aacaggagat aaggcagtca atgtatacac ctcgtctcag acaggggtcaa tcatagtcaa     360
gttgctcccg aatatgccc aaggataaaga ggcgtgtgca aaagcccat tagaggcata      420
taacagaaca ctgactactt tgctaactcc tcttggcgac tccatccgca agatccaagg     480
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Sequence_Listing

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<400> 24

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20 25 30

Asp Gly Arg Pro Leu Ala Ala Ala Gly Ile Val Val Thr Gly Asp Lys
35 40 45

Ala Val Asn Ile Tyr Thr Ser Ser Gln Thr Gly Ser Ile Ile Val Lys
50 55 60

Leu Leu Pro Asn Leu Pro Lys Asp Lys Glu Ala Cys Ala Lys Ala Pro
65 70 75 80

Leu Asp Ala Tyr Asn Arg Thr Leu Thr Thr Leu Leu Thr Pro Leu Gly
85 90 95

Asp Ser Ile Arg Arg Ile Gln Glu Ser Val Thr Thr Ser Gly Gly Gly
100 105 110

Arg Gln Gly Arg Leu Ile Gly Ala Ile Ile Gly Gly Val Ala Leu Gly
115 120 125

Val Ala Thr Ala Ala Gln Ile Thr Ala Ala Ala Ala Leu Ile Gln Ala
130 135 140

Lys Gln Asn Ala Ala Asn Ile Leu Arg Leu Lys Glu Ser Ile Ala Ala
145 150 155 160

Thr Asn Glu Ala Val His Glu Val Thr Asp Gly Leu Ser Gln Leu Ala
165 170 175

Val Ala Val Gly Lys Met Gln Gln Phe Val Asn Asp Gln Phe Asn Lys
180 185 190

Thr Ala Gln Glu Leu Asp Cys Ile Lys Ile Ala Gln Gln Val Gly Val
195 200 205

Glu Leu Asn Leu Tyr Leu Thr Glu Leu Thr Thr Val Phe Gly Pro Gln
210 215 220

Ile Thr Ser Pro Ala Leu Asn Lys Leu Thr Ile Gln Ala Leu Tyr Asn
225 230 235 240

Leu Ala Gly Gly Asn Met Asp Tyr Leu Leu Thr Lys Leu Gly Val Gly
245 250 255

Sequence_Listing

Asn Asn Gln Leu Ser Ser Leu Ile Gly Ser Gly Leu Ile Thr Gly Asn
 260 265 270
 Pro Ile Leu Tyr Asp Ser Gln Thr Gln Leu Leu Gly Ile Gln Val Thr
 275 280 285
 Leu Pro Ser Val Gly Asn Leu Asn Asn Met Arg Ala Thr Tyr Leu Glu
 290 295 300
 Thr Leu Ser Val Ser Thr Thr Lys Gly Phe Ala Ser Ala Leu Val Pro
 305 310 315 320
 Lys Val Val Thr Gln Val Gly Ser Val Ile Glu Glu Leu Asp Thr Ser
 325 330 335
 Tyr Cys Ile Glu Thr Asp Leu Asp Leu Tyr Cys Thr Arg Ile Val Thr
 340 345 350
 Phe Pro Met Ser Pro Gly Ile Tyr Ser Cys Leu Ser Gly Asn Thr Ser
 355 360 365
 Ala Cys Met Tyr Ser Lys Thr Glu Gly Ala Leu Thr Thr Pro Tyr Met
 370 375 380
 Thr Ile Lys Gly Ser Val Ile Ala Asn Cys Lys Met Thr Thr Cys Arg
 385 390 395 400
 Cys Val Asn Pro Pro Gly Ile Ile Ser Gln Asn Tyr Gly Glu Ala Val
 405 410 415
 Ser Leu Ile Asp Lys Gln Ser Cys Asn Val Leu Ser Leu Gly Gly Ile
 420 425 430
 Thr Leu Arg Leu Ser Gly Glu Phe Asp Val Thr Tyr Gln Lys Asn Ile
 435 440 445
 Ser Ile Gln Asp Ser Gln Val Ile Ile Thr Gly Asn Leu Asp Ile Ser
 450 455 460
 Thr Glu Leu Gly Asn Val Asn Asn Ser Ile Ser Asn Ala Leu Asn Lys
 465 470 475 480
 Leu Glu Glu Ser Asn Arg Lys Leu Asp Lys Val Asn Val Lys Leu Thr
 485 490 495
 Ser Thr Ser Ala Leu Ile Thr Tyr Ile Val Leu Thr Ile Ile Ser Leu
 500 505 510
 Val Phe Gly Ile Leu Ser Leu Ile Leu Ala Cys Tyr Leu Met Tyr Lys
 515 520 525

Sequence_Listing

Gln Lys Ala Gln Gln Lys Thr Leu Leu Trp Leu Gly Asn Asn Thr Leu
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Asp Gln Met Arg Ala Thr Thr Lys Met
545 550

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<220>
<223> protein of NDV strain Mukteswar

<400> 25

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Ile Arg Ile Thr Leu Ala Leu Ser Tyr Val Arg Leu Thr Ser Ser Leu
20 25 30

Asp Gly Arg Pro Leu Ala Ala Ala Gly Ile Val Val Thr Gly Asp Lys
35 40 45

Ala Val Asn Ile Tyr Thr Ser Ser Gln Thr Gly Ser Ile Ile Val Lys
50 55 60

Leu Leu Pro Asn Met Pro Lys Asp Lys Glu Ala Cys Ala Lys Ala Pro
65 70 75 80

Leu Glu Ala Tyr Asn Arg Thr Leu Thr Thr Leu Leu Thr Pro Leu Gly
85 90 95

Asp Ser Ile Arg Arg Ile Gln Glu Ser Val Thr Thr Ser Gly Gly Arg
100 105 110

Arg Gln Arg Arg Phe Ile Gly Ala Ile Ile Gly Ser Val Ala Leu Gly
115 120 125

Val Ala Thr Ala Ala Gln Ile Thr Ala Ala Ser Ala Leu Ile Gln Ala
130 135 140

Asn Gln Asn Ala Ala Asn Ile Leu Arg Leu Lys Glu Ser Ile Ala Ala
145 150 155 160

Thr Asn Glu Ala Val His Glu Val Thr Gly Gly Leu Ser Gln Leu Ala
165 170 175

Val Ala Val Gly Lys Met Gln Gln Phe Val Asn Asp Gln Phe Asn Asn
180 185 190

Sequence_Listing

Thr Ala Gln Glu Leu Asp Cys Ile Lys Ile Thr Gln Gln Val Gly Val
195 200 205

Glu Leu Asn Leu Tyr Leu Thr Glu Leu Thr Thr Val Phe Gly Pro Gln
210 215 220

Ile Thr Ser Pro Ala Leu Thr Gln Leu Thr Val Gln Ala Leu Tyr Asn
225 230 235 240

Leu Ala Gly Gly Asn Val Asp Tyr Leu Leu Thr Lys Leu Gly Val Gly
245 250 255

Asn Asn Gln Leu Ser Ser Leu Ile Gly Ser Gly Leu Ile Thr Gly Asn
260 265 270

Pro Ile Phe Tyr Asp Ser Gln Thr Gln Leu Leu Gly Ile Gln Val Thr
275 280 285

Leu Pro Ser Val Gly Asn Leu Asn Asn Met Arg Ala Thr Tyr Leu Glu
290 295 300

Thr Leu Ser Val Ser Thr Thr Lys Gly Phe Ala Ser Ala Leu Val Pro
305 310 315 320

Lys Val Ala Thr Gln Val Gly Ser Val Ile Glu Glu Leu Asp Thr Ser
325 330 335

Tyr Cys Ile Glu Ala Asp Leu Asp Leu Tyr Cys Thr Arg Ile Val Thr
340 345 350

Phe Pro Met Ser Pro Gly Ile Tyr Ser Cys Leu Ser Gly Asn Thr Ser
355 360 365

Ala Cys Met Tyr Ser Lys Thr Glu Gly Ala Leu Thr Thr Pro Tyr Met
370 375 380

Thr Leu Lys Gly Ser Val Val Ala Asn Cys Gln Met Thr Thr Cys Arg
385 390 395 400

Cys Ala Asp Pro Pro Gly Ile Ile Ser Gln Asn Tyr Gly Glu Ala Val
405 410 415

Ser Leu Ile Asp Lys His Ser Cys Asn Val Val Ser Leu Asp Gly Ile
420 425 430

Thr Leu Arg Leu Ser Gly Glu Phe Asp Ala Thr Tyr Gln Lys Asn Ile
435 440 445

Ser Ile Leu Asp Ser Gln Val Leu Val Thr Gly Asn Leu Asp Ile Ser
450 455 460

Sequence_Listing

Thr Glu Leu Gly Asn Val Asn His Ser Ile Ser Asn Ala Leu Asp Lys
465 470 475 480

Leu Glu Glu Ser Asn Ser Lys Leu Asp Glu Val Asn Val Arg Leu Thr
485 490 495

Ser Thr Ser Ala Leu Ile Thr Tyr Ile Val Leu Thr Val Ile Ser Leu
500 505 510

Val Leu Gly Met Leu Ser Leu Val Leu Ala Cys Tyr Leu Met Tyr Lys
515 520 525

Gln Lys Ala Gln Arg Lys Thr Leu Leu Trp Leu Gly Asn Asn Thr Leu
530 535 540

Asp Gln Met Arg Ala Thr Thr Lys Met
545 550

<210> 26
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<213> artificial sequence

<220>
<223> protein of NDV strain B1

<400> 26

Met Gly Ser Arg Pro Phe Thr Lys Asn Pro Ala Pro Met Met Leu Thr
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Ile Arg Val Ala Leu Val Leu Ser Cys Ile Cys Pro Ala Asn Ser Ile
20 25 30

Asp Gly Arg Pro Phe Ala Ala Ala Gly Ile Val Val Thr Gly Asp Lys
35 40 45

Ala Val Asn Ile Tyr Thr Ser Ser Gln Thr Gly Ser Ile Ile Val Lys
50 55 60

Leu Leu Pro Asn Leu Pro Lys Asp Lys Glu Ala Cys Ala Lys Ala Pro
65 70 75 80

Leu Asp Ala Tyr Asn Arg Thr Leu Thr Thr Leu Leu Thr Pro Leu Gly
85 90 95

Asp Ser Ile Arg Arg Ile Gln Glu Ser Val Thr Thr Ser Gly Gly Gly
100 105 110

Arg Gln Gly Arg Leu Ile Gly Ala Ile Ile Gly Gly Val Ala Leu Gly
115 120 125

Val Ala Thr Ala Ala Gln Ile Thr Ala Ala Ala Ala Leu Ile Gln Ala
130 135 140

Sequence_Listing

Lys Gln Asn Ala Ala Asn Ile Leu Arg Leu Lys Glu Ser Ile Ala Ala
 145 150 155 160
 Thr Asn Glu Ala Val His Glu Val Thr Asp Gly Leu Ser Gln Leu Ala
 165 170 175
 Val Ala Val Gly Lys Met Gln Gln Phe Val Asn Asp Gln Phe Asn Lys
 180 185 190
 Thr Ala Gln Glu Leu Asp Cys Ile Lys Ile Ala Gln Gln Val Gly Val
 195 200 205
 Glu Leu Asn Leu Tyr Leu Thr Glu Leu Thr Thr Val Phe Gly Pro Gln
 210 215 220
 Ile Thr Ser Pro Ala Leu Asn Lys Leu Thr Ile Gln Ala Leu Tyr Asn
 225 230 235 240
 Leu Ala Gly Gly Asn Met Asp Tyr Leu Leu Thr Lys Leu Gly Ile Gly
 245 250 255
 Asn Asn Gln Leu Ser Ser Leu Ile Gly Ser Gly Leu Ile Thr Gly Asn
 260 265 270
 Pro Ile Leu Tyr Asp Ser Gln Thr Gln Leu Leu Gly Ile Gln Val Thr
 275 280 285
 Leu Pro Ser Val Gly Asn Leu Asn Asn Met Arg Ala Thr Tyr Leu Glu
 290 295 300
 Thr Leu Ser Val Ser Thr Thr Arg Gly Phe Ala Ser Ala Leu Val Pro
 305 310 315 320
 Lys Val Val Thr Gln Val Gly Ser Val Ile Glu Glu Leu Asp Thr Ser
 325 330 335
 Tyr Cys Ile Glu Thr Asp Leu Asp Leu Tyr Cys Thr Arg Ile Val Thr
 340 345 350
 Phe Pro Met Ser Pro Gly Ile Tyr Ser Cys Leu Ser Gly Asn Thr Ser
 355 360 365
 Ala Cys Met Tyr Ser Lys Thr Glu Gly Ala Leu Thr Thr Pro Tyr Met
 370 375 380
 Thr Ile Lys Gly Ser Val Ile Ala Asn Cys Lys Met Thr Thr Cys Arg
 385 390 395 400
 Cys Val Asn Pro Pro Gly Ile Ile Ser Gln Asn Tyr Gly Glu Ala Val
 405 410 415

Sequence_Listing

Ser Leu Ile Asp Lys Gln Ser Cys Asn Val Leu Ser Leu Gly Gly Ile
420 425 430

Thr Leu Arg Leu Ser Gly Glu Phe Asp Val Thr Tyr Gln Lys Asn Ile
435 440 445

Ser Ile Gln Asp Ser Gln Val Ile Ile Thr Gly Asn Leu Asp Ile Ser
450 455 460

Thr Glu Leu Gly Asn Val Asn Asn Ser Ile Ser Asn Ala Leu Asn Lys
465 470 475 480

Leu Glu Glu Ser Asn Arg Lys Leu Asp Lys Val Asn Val Lys Leu Thr
485 490 495

Ser Thr Ser Ala Leu Ile Thr Tyr Ile Val Leu Thr Ile Ile Ser Leu
500 505 510

Val Phe Gly Ile Leu Ser Leu Ile Leu Ala Cys Tyr Leu Met Tyr Lys
515 520 525

Gln Lys Ala Gln Gln Lys Thr Leu Leu Trp Leu Gly Asn Asn Thr Leu
530 535 540

Asp Gln Met Arg Ala Thr Thr Lys Met
545 550

<210> 27
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<213> artificial sequence

<220>
<223> protein of NDV strain VG/GA

<400> 27

Met Gly Ser Arg Pro Ser Thr Lys Asn Pro Ala Pro Met Met Leu Thr
1 5 10 15

Ile Arg Val Ala Leu Val Leu Ser Cys Ile Cys Pro Ala Asn Ser Ile
20 25 30

Asp Gly Arg Pro Leu Ala Ala Ala Gly Ile Val Val Thr Gly Asp Lys
35 40 45

Ala Val Asn Ile Tyr Thr Ser Ser Gln Thr Gly Ser Ile Ile Val Lys
50 55 60

Leu Leu Pro Asn Leu Pro Lys Asp Lys Glu Ala Cys Ala Lys Ala Pro
65 70 75 80

Sequence_Listing

Leu Asp Ala Tyr Asn Arg Thr Leu Thr Thr Leu Leu Thr Pro Leu Gly
 85 90 95
 Asp Ser Ile Arg Arg Ile Gln Glu Ser Met Thr Thr Ser Gly Gly Gly
 100 105 110
 Arg Gln Gly Arg Leu Ile Gly Ala Ile Ile Gly Gly Val Ala Leu Gly
 115 120 125
 Val Ala Thr Ala Ala Gln Met Ala Ala Ala Ala Ala Leu Ile Gln Ala
 130 135 140
 Lys Gln Asn Ala Ala Asn Ile Leu Arg Leu Lys Glu Ser Ile Ala Ala
 145 150 155 160
 Thr Asn Glu Ala Val His Glu Val Thr Asp Gly Leu Ser Gln Leu Ala
 165 170 175
 Val Ala Val Gly Lys Met Gln Gln Phe Val Asn Asp Gln Phe Asn Lys
 180 185 190
 Thr Ala Gln Glu Leu Asp Cys Ile Lys Ile Ala Gln Gln Val Gly Val
 195 200 205
 Glu Leu Asn Leu Tyr Leu Thr Glu Leu Thr Thr Val Phe Gly Pro Gln
 210 215 220
 Ile Thr Ser Pro Ala Leu Asn Lys Leu Thr Ile Gln Ala Leu Tyr Asn
 225 230 235 240
 Leu Ala Gly Gly Asn Met Asp Tyr Leu Leu Thr Lys Leu Gly Ile Gly
 245 250 255
 Asn Asn Gln Leu Ser Ser Leu Ile Gly Ser Gly Leu Ile Thr Gly Asn
 260 265 270
 Pro Ile Leu Tyr Asp Ser Gln Thr Gln Leu Leu Gly Ile Gln Val Thr
 275 280 285
 Leu Pro Ser Val Gly Asn Leu Asn Asn Met Arg Ala Thr Tyr Leu Glu
 290 295 300
 Thr Leu Ser Val Ser Thr Thr Arg Gly Phe Ala Ser Ala Leu Val Pro
 305 310 315 320
 Lys Val Val Thr Gln Val Gly Ser Val Ile Glu Glu Leu Asp Thr Ser
 325 330 335
 Tyr Cys Ile Glu Thr Asp Leu Asp Leu Tyr Cys Thr Arg Ile Val Thr
 340 345 350

Sequence_Listing

Phe Pro Met Ser Pro Gly Ile Tyr Ser Cys Leu Ser Gly Asn Thr Ser
355 360 365

Ala Cys Met Tyr Ser Lys Thr Glu Gly Ala Leu Thr Thr Pro Tyr Met
370 375 380

Thr Ile Lys Gly Ser Val Ile Ala Asn Cys Lys Met Thr Thr Cys Arg
385 390 395 400

Cys Val Asn Pro Pro Gly Ile Ile Ser Gln Asn Tyr Gly Glu Ala Val
405 410 415

Ser Leu Ile Asp Lys Gln Ser Cys Asn Val Leu Ser Leu Gly Gly Ile
420 425 430

Thr Leu Arg Leu Ser Gly Glu Phe Asp Val Thr Tyr Gln Lys Asn Ile
435 440 445

Ser Ile Gln Asp Ser Gln Val Ile Ile Thr Gly Asn Leu Asp Ile Ser
450 455 460

Thr Glu Leu Gly Asn Val Asn Asn Ser Ile Ser Asn Ala Leu Asn Lys
465 470 475 480

Leu Glu Glu Ser Asn Arg Lys Leu Asp Lys Val Asn Val Lys Leu Thr
485 490 495

Ser Thr Ser Ala Leu Ile Thr Tyr Ile Val Leu Thr Ile Ile Ser Leu
500 505 510

Val Phe Gly Ile Leu Ser Leu Ile Leu Ala Cys Tyr Leu Met Tyr Lys
515 520 525

Gln Lys Ala Gln Gln Lys Thr Leu Leu Trp Leu Gly Asn Asn Thr Leu
530 535 540

Asp Gln Met Arg Ala Thr Thr Lys Met
545 550

<210> 28
<211> 553
<212> PRT
<213> artificial sequence

<220>
<223> protein of NDV strain KBNP

<400> 28

Met Gly Ser Lys Leu Ser Thr Arg Ile Pro Ala Pro Leu Met Leu Thr
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Thr Arg Ile Thr Leu Ile Leu Ser Cys Ile Arg Pro Thr Ser Ser Leu
20 25 30

Sequence_Listing

Asp Gly Arg Pro Leu Ala Ala Ala Gly Ile Val Val Thr Gly Asp Lys
 35 40 45
 Ala Val Asn Val Tyr Thr Ser Ser Gln Thr Gly Ser Ile Ile Val Lys
 50 55 60
 Leu Leu Pro Asn Met Pro Arg Asp Lys Glu Ala Cys Ala Lys Ala Pro
 65 70 75 80
 Leu Glu Ala Tyr Asn Arg Thr Leu Thr Thr Leu Leu Thr Pro Leu Gly
 85 90 95
 Asp Ser Ile Arg Lys Ile Gln Gly Ser Val Ser Thr Ser Gly Gly Gly
 100 105 110
 Arg Gln Ala Arg Leu Ile Gly Ala Val Ile Gly Ser Val Ala Leu Gly
 115 120 125
 Val Ala Thr Ala Ala Gln Ile Thr Ala Ala Ala Ala Leu Ile Gln Ala
 130 135 140
 Asn Gln Asn Ala Ala Asn Ile Leu Arg Leu Lys Glu Ser Ile Ala Ala
 145 150 155 160
 Thr Asn Glu Ala Val His Glu Val Thr Asp Gly Leu Ser Gln Leu Ser
 165 170 175
 Val Ala Val Gly Lys Met Gln Gln Phe Val Asn Asp Gln Phe Asn Asn
 180 185 190
 Thr Ala Arg Glu Leu Asp Cys Ile Lys Ile Thr Gln Gln Val Gly Val
 195 200 205
 Glu Leu Asn Leu Tyr Leu Thr Glu Leu Thr Thr Val Phe Gly Pro Gln
 210 215 220
 Ile Thr Ser Pro Ala Leu Thr Gln Leu Thr Ile Gln Ala Leu Tyr Asn
 225 230 235 240
 Leu Ala Gly Gly Asn Met Asn Tyr Leu Leu Thr Lys Leu Gly Ile Gly
 245 250 255
 Asn Asn Gln Leu Ser Ser Leu Ile Gly Ser Gly Leu Ile Thr Gly Tyr
 260 265 270
 Pro Ile Leu Tyr Asp Ser Gln Thr Gln Leu Leu Gly Ile Gln Val Asn
 275 280 285
 Leu Pro Ser Val Gly Asn Leu Asn Asn Met Arg Ala Thr Tyr Leu Glu
 290 295 300

Sequence_Listing

Thr Leu Ser Val Ser Thr Thr Lys Gly Tyr Ala Ser Ala Leu Val Pro
 305 310 315 320
 Lys Val Val Thr Gln Val Gly Ser Val Ile Glu Glu Leu Asp Thr Ser
 325 330 335
 Tyr Cys Ile Glu Ser Asp Leu Asp Leu Tyr Cys Thr Arg Ile Val Thr
 340 345 350
 Phe Pro Met Ser Pro Gly Ile Tyr Ser Cys Leu Ser Gly Asn Thr Ser
 355 360 365
 Ala Cys Met Tyr Ser Lys Thr Glu Gly Ala Leu Thr Thr Pro Tyr Met
 370 375 380
 Ala Leu Lys Gly Ser Val Ile Ala Asn Cys Lys Ile Thr Thr Cys Arg
 385 390 395 400
 Cys Thr Asp Pro Pro Gly Ile Ile Ser Gln Asn Tyr Gly Glu Ala Val
 405 410 415
 Ser Leu Ile Asp Arg His Ser Cys Asn Val Leu Ser Leu Asp Gly Ile
 420 425 430
 Thr Leu Arg Leu Ser Gly Glu Phe Asp Ala Thr Tyr Gln Lys Asn Ile
 435 440 445
 Ser Ile Leu Asp Ser Gln Val Ile Val Thr Gly Asn Leu Asp Ile Ser
 450 455 460
 Thr Glu Leu Gly Asn Val Asn Asn Ser Ile Ser Asn Ala Leu Asp Ser
 465 470 475 480
 Leu Ala Glu Ser Asn Ser Lys Leu Glu Lys Ile Asn Val Arg Leu Thr
 485 490 495
 Ser Thr Ser Ala Leu Ile Thr Tyr Ile Val Leu Thr Val Ile Ser Leu
 500 505 510
 Val Phe Gly Ala Phe Ser Leu Gly Leu Ala Cys Tyr Leu Met Tyr Lys
 515 520 525
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 Asp Gln Met Arg Ala Thr Thr Arg Ala
 545 550

<210> 29

<211> 16

Sequence_Listing

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<212> DNA
<213> artificial sequence

<220>
<223> forward primer for IB-QX for IBV

<400> 29
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16

<210> 30
<211> 22
<212> DNA
<213> artificial sequence

<220>
<223> reverse primer for IB-QX for IBV

<400> 30
cacgtggaat catgcctggt at
22

<210> 31
<211> 25
<212> DNA
<213> artificial sequence

<220>
<223> forward primer 2 for NDV

<220>
<221> misc_feature
<222> (17)..(17)
<223> N is inosine

<400> 31
ctgccactgc tagttgngat aatcc
25

<210> 32
<211> 22
<212> DNA
<213> artificial sequence

<220>
<223> reverse primer 2 for NDV

<220>
<221> misc_feature
<222> (10)..(10)
<223> N is inosine

<220>
<221> misc_feature
<222> (19)..(19)
<223> N is inosine

<400> 32
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<210> 33
<211> 6
<212> PRT
<213> artificial sequence

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Sequence_Listing

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<223> F fusion of NDV cleavage site motif 1

<400> 33

Arg Arg Arg Lys Arg Phe
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<210> 34

<211> 6

<212> PRT

<213> artificial sequence

<220>

<223> F fusion of NDV cleavage site motif 2

<400> 34

Gly Arg Gln Gly Arg Leu
1 5

<210> 35

<211> 6

<212> PRT

<213> artificial sequence

<220>

<223> F fusion of NDV cleavage site motif 3

<400> 35

Gly Lys Gln Gly Arg Leu
1 5

<210> 36

<211> 1611

<212> DNA

<213> artificial sequence

<220>

<223> DNA of M5365

<400> 36

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catttacaag gaggtgctta tgcaatagtt aacagttctt catattataa taacgcaggt	180
ggttcctctg aatgcactgc tgggtattatt aaggatgttt ataattcttag cgcagcttct	240
atatctatga cagcaccacc tacgggtatg tcatgggtctg tttcacaatt ttgtacagca	300
cactgtaact tctctgactt tacagtgttt gtcacacatt gttttaaaag tggtcgcgga	360
cagtgtcctt taacaggcct aataccacag aattacattc gcattctctgc tatgagaaat	420
ggttctctct tttataattt aacagttagt gcgtctaaat accctaattt taaatctttt	480
caatgtgtta ataatgccac atctgtgtat ttaaagtgtg accttgtttt ctcttctaac	540
atgactactg atgttacagc agcgggtgtg tatttttaaag caggtggacc tgttacttac	600
agtgttatga agcagtttca ggtcttagct tattttgtta atggcactgt acaagaagtt	660

Sequence_Listing						
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cgaaggagt	taaatcactc	gggcgttaac	caattcactt	ttactaatgt	aagtaaagcc	840
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ggtaatataa	ttttaattgg	ccattttctca	gtcagtctgt	gtataaagca	agtgatttta	960
tgtatgggtc	ttatcccccc	tagttgttct	tttagaccag	aaaccattac	cagtggtttg	1020
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tctgtcttca	gtagtaaggc	aacgtgttgt	tatgcctact	cttataatgg	cccaagggca	1140
tgtaaagggt	tttattcagg	tgaattaagt	acgagttttg	aatgtggatt	gctggtttat	1200
gttactaaga	gtgatggctc	tcgtatacag	actagaacgg	agcccttagt	attaacgcaa	1260
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ggccaagggt	ttattactaa	tgtgactgat	tctgctgcta	atTTTtagtta	tttagcagat	1380
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tctggtggca	atatagttgg	tattcttact	tctagaaatg	aaacagggtc	tgaacagggt	1560
gagaaccagt	tttatgttaa	gttaaccaat	agctcacatc	gtcgcaggcg	t	1611

<210> 37
 <211> 1593
 <212> DNA
 <213> artificial sequence

<220>
 <223> DNA of V9/04

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tcattatcag	catgcactgt tggattattt aaggatgtgt ttaattctac agcggcttct	240
atttctatga	tagcaccgca attaggtagt tcgtgggtcca aggcacaaat ttgtacggca	300
cactgtaatt	tctcggatgt tacagttttt gtcacacatt gttatagtag tggtagtggg	360
tcttgccta	taacaggcat gattccacag aatcatattc gtatttctgc catgaaaaat	420
ggttatttat	tttataattt aacagttagt gtatctaagt accctacttt taaatccttt	480
caatgtgtta	ataatcaaac atccgtctac cttaatggag accttgttta cacttctaac	540
acgaccactg	ctgttacatc aacgggtggg gattttaaag caagtggacc tgggtacttac	600
agtggtagta	agcagtttca ggccttaact tatttgtaa tggcactgta ccagaggtat	660
tttggcgatg	accccctaga gggtgctagc atgtcatata atactggcaa ttttcagaag	720
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Sequence_Listing						
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ctcgtttctc	agcgggtttc	ggatatgtgg	aagggtttta	atgtatgggt	cttaccgccc	960
caaagtgtat	ttttagtcca	gaaaccatta	ataatggggt	tatggtttaa	ttcactttct	1020
atttcatttg	cttatgggcc	tcttcagggt	ggatgcaagc	aatctgtttt	tcaaggtaga	1080
gcaacgtggt	gttttgctta	ttcatataat	ggccctcacg	catgtaaagg	tgtttacagt	1140
ggtgagttat	ctaagttttt	tgaatgtgga	ttgttggttt	atgttactaa	gagtgatggc	1200
tcgcgataac	aaacagccac	tgaaccacca	gtcataactc	aacacaacta	taataatatt	1260
acattggata	agtgtgttga	gtataacata	tatggcaaaa	caggccaagg	ttttattact	1320
aatgtaacta	actctgctgc	tagttataat	tatttagcag	attcaggatt	ggctatctta	1380
gatacatctg	gtgccataga	catctttggt	gtacaagggt	ctcatgggtc	taattattat	1440
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<210> 38
 <211> 1710
 <212> DNA
 <213> artificial sequence

<220>
 <223> DNA of THA50151

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ggttcctctg	aatgcactgc tgggtattatt aaggatgttt ataatcttag cgcagctgct 240
atatctatga	cagcaccacc tacagggtatg tcatgggtctg cttcacaatt ttgtacagca 300
cactgtaact	tttctgattt tacagtgttt gttacacatt gttttaaaag tgggtcatgga 360
cattgtcctt	taacagggtc aataccaagg aattacattc gcatctctgc tatgagaaat 420
ggctttcttt	tttataattt aacagttagt gtatctaaat accctaattt taaatctctt 480
caatgtgtta	ataatgccac atctgtgtat ttaaattggg accttggttt ctcttctaac 540
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agtgttatga	aacagtttaa gggtctggct tactttgtta atgggtactgt gcaagatgta 660
atcctgtgcg	atgacacacc tagaggtttg ctagcctgtc aatataacac tggcaatttt 720
tcagatggct	tttatccttt tactaatagt actttagtta gggaaaagtt cattgtctat 780
cgcgaaagta	gtgttaatac tactctggcg ttaactaatt tcacttttac taatgtaagt 840
aatgcacagc	ctaatagtgg tgggtgttcat acttttcatt tatatcaaac gcaaacagct 900

Sequence_Listing							
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ggttt	gtggt	ttaattcctt	gtcagtttct	cttacttatg	gaccctaca	gggagggtgt	1080
aagcaatctg	tcttttagtgg	tagggcaacg	tgttgttatg	cctactctta	taatggccca		1140
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gtttatgtta	ctatgagtgc	tggctctcgt	atacagacta	gaacggagcc	cttagtatta		1260
acgcaacaca	attataataa	tattacttta	gataagtgtg	ttgactataa	tatatatggc		1320
agagtaggcc	aagggtttat	tactaatgtg	actgattctg	ctgctaattt	tagttattta		1380
gcagatgggtg	ggtttagctat	tttagatact	tcgggtgcca	tagatgtttt	tgttgtacag		1440
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gtagtgtctg	gtggaatat	agttggcttt	ctcacttctc	gtaatgaaac	tggttctcag		1560
cctattgaga	accaatttta	tgttaaactc	actaatgtaa	gtcgtcgtca	cagacgttcc		1620
attagtga	aaatgttacaag	ctgtccatac	gtaagttatg	gcaggttttg	tatacaacct		1680
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<210> 39
 <211> 1710
 <212> DNA
 <213> artificial sequence

<220>
 <223> DNA of THA40151

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atatctatga	cagcaccacc tacagggtatg
cactgtaact	tttctgattt tacagtgttt
cattgtcctt	taacagggtct aataccaaag
ggctcttctt	tttataat
caatgtgtta	ataatgccac atctgtgtat
atgactactg	atgttacatc agcgggtgtg
agtgttatga	aacagtttaa gggtctggct
atcctgtgtg	atgacacacc tagaggtttg
tcagatggct	tttatccttt tactaatagt
cgcgaaagta	gtgttaatac tactctggcg
aatgcacagc	ctaatagtgg tgggtgttcat

Sequence_Listing				
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gattttatgt	atgggtctta	tcaccctagt	tgttctttta gaccggaac cattaacagt	1020
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aagcaatctg	tcttttagtgg	tagggcaacg	tgttgttatg cctactctta	taatggccca 1140
agggcatgta	aagggtgttta	ttcagggtgaa	ttaagcacga gttttgaatg	tggattgctg 1200
gtttatgtta	ctatgagtgc	tggctctcgt	atacagacta gaacggagcc	cttagtatta 1260
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agagtaggcc	aagggttttat	tactaatgtg	actgattctg ctgctaattt	tagttattta 1380
gcagatgggtg	ggtttagctat	tttagatact	tcgggtgcca tagatgtttt	tgttgtacag 1440
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gtagtgtctg	gtggaatat	agttggcttt	ctcacttctc gtaatgaaac	tggttctcag 1560
cctattgaga	accaat	tttta	actc actaatgtaa gtcgtcgtca	cagacgttcc 1620
attagtga	aaa atgttacaag	ctgtccatac	gtaagttatg gcaggttttg	tatacaacct 1680
gatggctcta	ttaagcaaat	agtaccgcaa		1710

<210> 40
 <211> 1710
 <212> DNA
 <213> artificial sequence

<220>
 <223> DNA of THA20151

<400> 40	
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atatctatga	cagcaccacc tacagggtatg
cactgtaact	tttctgattt tacagtgttt
cattgtcctt	taacagggtct aataccaaag
ggctcttctt	tttataat
caatgtgtta	ataatgccac atctgtgtat
atgactactg	atgttacatc agcgggtgtg
agtgttatga	aacagtttaa gggtctggct
atcctgtgtg	atgacacacc tagaggtttg
tcagatggct	tttatccttt tactaatagt
cgcgaaagta	gtgttaatac tactctggcg
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Sequence_Listing							
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ggttt	gtggt	ttaattcctt	gtcagtttct	cttacttatg	gaccctaca	gggagggtgt	1080
aagcaatctg	tcttttagtgg	tagggcaacg	tgttgttatg	cctactctta	taatggccca		1140
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gcagatgggtg	ggtttagctat	tttagatact	tcgggtgcca	tagatgtttt	tgttgtacag		1440
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gtagtgtctg	gtggtaatat	agttggcttt	ctcacttctc	gtaatgaaac	tggttctcag		1560
cctattgaga	accaatttta	tgttaaactc	actaatgtaa	gtcgtcgtca	cagacgttcc		1620
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gatggctcta	ttaagcaa	aat	agtaccgcaa				1710

<210> 41
 <211> 1710
 <212> DNA
 <213> artificial sequence

<220>
 <223> DNA of THA90151

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ggttcctctg	aatgcactgc	tgggtattatt	aaggatgttt	ataatcttag	cgcagctgct		240
atatctatga	cagcaccacc	tatagggtatg	tcattggtctg	cttcacaatt	ttgtacagca		300
cactgtaact	tttctgattt	tacagtgttt	gttacacatt	gtttttaaag	tgggtcatgga		360
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ggctcttctt	tttataat	tt	aacagttagt	gtatctaaat	accctaattt	taaatctctt	480
caatgtgtta	ataatgccac	atctgtgtat	ttaaattggtg	accttgtttt	ctcttctaac		540
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Sequence_Listing																
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aagcaatctg	tcttt	agtg	g	taggg	caacg	tg	ttgt	t	atg	cctact	c	taatgg	ccca	1140		
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<212>	DNA
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<220>
<223> DNA of THA60151

<400>	42						
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cactgtaact	tttctgattt	tacagtgttt	gttacacatt	gttttaaaag	tggtcatgga		360
cattgtcctt	taacaggtct	aataccaaag	aattacattc	gcacatctgc	tatgagaaat		420
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caatgtgtta	ataatgccac	atctgtgtat	ttaaatggtg	accttgtttt	ctcttctaac		540
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aatgcacagc	ctaatagtgg	tggtgttcac	acttttcatt	tatatcaaac	gcaaacagct		900

Sequence_Listing							
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aagcaatctg	tcttttagtgg	tagggcaacg	tgttgttatg	cctactctta	taatggccca		1140
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gtttatgtta	ctatgagtgc	tggctctcgt	atacagacta	gaacggagcc	cttagtatta		1260
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<210> 43
 <211> 1657
 <212> DNA
 <213> artificial sequence

<220>
 <223> DNA of AF193423

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gggtcttgtc	ctataacagg catgattcca
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tataatatta	tgaaagaatt taaggttctt
gtaattttgt	gcgataattc ccccaagggt
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Sequence_Listing						
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tgtaagcaat	ctgttttttag	tggttaaggca	acgtgttggt	atgcctactc	ttataatggc	1140
ccaagggcat	gtaaagggtg	ttattcaggt	gaattaagca	tgaattttga	atgtggattg	1200
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<210> 44
 <211> 1643
 <212> DNA
 <213> artificial sequence

<220>
 <223> DNA of AY043312

<400> 44	
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cctttaggcc	tccaaatgga
120	
tggtcatctgc	aaggggggtgc
ttatgcagta	gtgaattcta
ctaatacaca	taataatgcc
180	
ggttctgcaa	gtgggtgcac
tgttggtggt	attaaggacg
tctataatca	aagtgcggct
240	
tccatagcta	tgacagcacc
tcttcagggt	atggccttgg
ctaagtcaca	atttttagt
300	
gcacactgta	acttttctga
aattacagtt	tttgtcacac
attgttatag	tagtggtaca
360	
gggtcttgtc	ctataacagg
catgattgca	cgtgatcata
ttcgtatttc	tgcaatgaaa
420	
aatggttctt	tattttataa
tttaacagtt	agcgtatcta
aataccctaa	ttttaagtct
480	
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cacatctggt	tatttaaagt
gtgatcttgt	ttttacttcc
540	
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gtcagcaggt	gtgtatttta
aagcaggtgg	acctgtaaat
600	
tatagtatta	tgaaagaatt
taaggttctt	gcttactttg
ttaatggtac	agcacaagat
660	
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ccccaaagggt	ttgctagcct
gtcaatataa	cactggcaat
720	
ttttcggatg	gcttttatcc
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ttagggaaaa	gttcattgtc
780	
tatcgcaaaa	gtagtgttaa
tactactctg	gcgttaacta
atttcacttt	tactaatgta
840	
agtaatgcac	agcctaatag
tggtgggtgt	catacttttc
atttatatca	aacacaaaca
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ttttaatttg	tcatttctga
gtcagtttgt	gtataaggca
960	

Sequence_Listing

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cagggcagct atggtcttaa ttattacaag gttaatcctt gtgaagatgt taaccaacag 1500
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<210> 45
<211> 5
<212> PRT
<213> artificial sequence

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<220>
<223> F fusion cleavage motif 4
<400> 45

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Arg Arg Gln Lys Arg
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<210> 46
<211> 5
<212> PRT
<213> artificial sequence

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<220>
<223> F fusion cleavage motif 5
<400> 46

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Gly Arg Gln Ala Arg
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