

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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Sequence_Listing

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tctaggtcca atagtcaata tgggtgctaag gaggctgaga gtcattgatga tgaccttgat 180
tgaggagagg gtatgagcgt ggttaacccg cgatctggac ccgctattag gactctattg 240
tagataacac tattttatttt tttttattta gatattacta tttgtttatt tttttattta 300
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agcactt 367

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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 tttttattta gatattacta tttgtttatt tttttattta 300
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acctaggccc aatagtcaac atggtgttaa ggaggctgag agtcattgat atgacgctga 180
tagggagagg ggcattgagc cgggtaaccc gggatctgaa cccgccagta ggaccctatt 240

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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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 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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 catttttaac agcacttta 379

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

<400> 15
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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 tttttattta      300
tttatttatt tattgaatga gtaagaactg gtataaacac ctcaagacca cactacactc      360
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<210> 16
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<212> DNA
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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 agacaggtag 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 aaactggtag 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
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<210> 18
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<212> DNA
<213> artificial sequence

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<220>
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<400> 18
ctgccactgc tagttgtgat aatcc                                          25

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<220>
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Sequence_Listing

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 ggtagaagat tctggatccc gggttgccgc 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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 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
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 <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 gggttgccgc 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

cccgaatctg	cccaaggata	aggaggcatg	tgcgaaagcc	cccttg gatg	catacaacag	420
gacattgacc	actttgtctca	cccccccttg	tgactctatc	cgtaggatac	aagagtctgt	480
gactacatct	ggagggggga	gacagggggcg	ccttataggc	gccattattg	gcgg	534

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

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tgcgctccgc	ccactcaccc
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tacagttagt	ttacctgtcc
atcaagttag	aaaaaacacg
	120
ggtagaagat	tctggatccc
ggttggcgcc	ctccaggtgc
aggatgggct	ccagaccttc
	180
taccaagaac	ccagcaccta
tgatgctgac	tatccgggtc
gcgctggtag	tgagttgcat
	240
ctgtccggca	aactccattg
atggcaggcc	tcttgacgct
gcaggaattg	tggttacagg
	300
agacaaagca	gtcaacatat
acacctcatc	ccagacagga
tcaatcatag	ttaagctcct
	360
cccgaatctg	cccaaggata
aggaggcatg	tgcgaaagcc
cccttg gatg	catataacag
	420
gacattgacc	actttgtctca
cccccccttg	tgactctatc
cgtagaatac	aagagtctat
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gacagggggcg	ccttataggc
gccattattg	gcgg
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 <212> DNA
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tacagttagt	ttacctgtct
atcaagttag	aaaaaacacg
	120
cgtaggggta	gaagagtctg
gatccccgacc	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	aatatgcccc
gggataaaga	ggcgtgtgca
aaagcccat	tagaggcata
	420
taacagaaca	ctgactactt
tgctaactcc	tcttggcgac
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Sequence_Listing

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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
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<213> artificial sequence

<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

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<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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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
<211> 553
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<213> artificial sequence

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<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

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Sequence_Listing

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 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
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 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
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<212> PRT
<213> artificial sequence

<220>
<223> protein of NDV strain KBNP

<400> 28

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Sequence_Listing

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 Ala Val Asn Val Tyr Thr Ser Ser Gln Thr Gly Ser Ile Ile Val Lys
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 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
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 Thr Asn Glu Ala Val His Glu Val Thr Asp Gly Leu Ser Gln Leu Ser
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 Val Ala Val Gly Lys Met Gln Gln Phe Val Asn Asp Gln Phe Asn Asn
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 195 200 205
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 260 265 270
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 275 280 285
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Sequence_Listing

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 325 330 335
 Tyr Cys Ile Glu Ser Asp Leu Asp Leu Tyr Cys Thr Arg Ile Val Thr
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 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
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 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
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 Val Phe Gly Ala Phe Ser Leu Gly Leu Ala Cys Tyr Leu Met Tyr Lys
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<211> 16

Sequence_Listing

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<212> DNA
<213> artificial sequence

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<223> reverse primer for IB-QX for IBV

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<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
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<210> 32
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<212> DNA
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<220>
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<210> 33
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Sequence_Listing

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<211> 6

<212> PRT

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<220>

<223> F fusion of NDV cleavage site motif 2

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<211> 6

<212> PRT

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<223> F fusion of NDV cleavage site motif 3

<400> 35

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<210> 36

<211> 1611

<212> DNA

<213> artificial sequence

<220>

<223> DNA of M5365

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cactgtaact tctctgactt tacagtgttt gtcacacatt gttttaaaag tggtcgcgga	360
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Sequence_Listing						
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<220>
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Sequence_Listing									
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acgcaacaca	attata	ataa	tatt	act	ttta	gata	ag	t	1320
g	gc	gc	gc	gc	gc	gc	gc	gc	
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gcagat	gg	t	a	g	c	t	a	t	1440
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ggcat	c	t	a	t	a	t	a	t	1500
g	t	c	t	a	a	t	a	t	
gtag	t	g	t	c	t	a	a	t	1560
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cctatt	g	a	a	a	a	a	a	a	1680
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g	t	a	a	g	t	t	a	t	
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Sequence_Listing							
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 <212> DNA
 <213> artificial sequence

<220>
 <223> DNA of THA90151

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		120
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aatagttctg	tatattataa	taacgcaggt
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		240
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		360
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aacagttagt	gtatctaaat	accctaattt
taaatctctt		
		480
caatgtgtta	ataatgccac	atctgtgtat
ttaaagtgtg	accttgtttt	ctcttcta
		540
atgactactg	atgttacatc	agcgggtgtg
tatttttaaag	caggtggacc	tggtatttat
		600
agtgttatga	aacagtttaa	ggttctggct
tactttgtta	atggtactgt	gcaagatgta
		660
atcctgtgtg	atgacacacc	tagaggtttg
ctagcctgtc	aatataacac	tggcaatttt
		720
tcagatggct	tttatccttt	tactaatagt
acttttagtta	gggaaaagtt	cattgtctat
		780
cgcgaaagta	gtgttaatac	tactctggcg
ttaactaatt	tcacttttac	taatgtaagt
		840
aatgcacagc	ctaatagtgg	tgggtgttcat
acttttcatt	tatatcaa	ac
		900

Sequence_Listing							
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ggttt	gtggt	ttaattcctt	gtcagtttct	cttacttatg	gaccctaca	gggaggggtg	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
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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
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<210> 42
 <211> 1710
 <212> DNA
 <213> artificial sequence

<220>
 <223> DNA of THA60151

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catttacaag	gaggtgctta tgcagtagtt aatagttctg tatattataa taacgcaggt 180
ggttcctctg	aatgcactgc tgggtattatt aaggatgttt ataactcttag cgcagctgct 240
atatctatga	cagcaccacc tatagggtatg tcatgggtctg cttcacaatt ttgtacagca 300
cactgtaact	tttctgattt tacagtgttt gttacacatt gttttaaaag tgggtcatgga 360
cattgtcctt	taacaggtct aataccaaag aattacattc gcatctctgc tatgagaaat 420
ggctctcttt	tttataat
aatagttagt	gtatctaaat accctaattt taaatctctt 480
caatgtgtta	ataatgccac atctgtgtat ttaaattggtg accttgtttt ctcttctaac 540
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agtgttatga	aacagtttaa gggtctggct tactttgtta atgggtactgt gcaagatgta 660
atcctgtgtg	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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gattttatgt	atgggtctta	tcaccctagt	tgttctttta	gaccggaac	cattaacagt		1020
ggttt	gtggt	ttaattcctt	gtcagtttct	cttacttatg	gaccctaca	gggagggtgt	1080
aagcaatctg	tcttttagtgg	tagggcaacg	tgttgttatg	cctactctta	taatggccca		1140
agggcatgta	aagggtgttta	ttcagggtgaa	ttaagcacga	gttttgaatg	tggattgctg		1200
gtttatgtta	ctatgagtgc	tggctctcgt	atacagacta	gaacggagcc	cttagtatta		1260
acgcaacaca	attataataa	tattacttta	gataagtgtg	ttgactataa	tatatatggc		1320
agagtaggcc	aagggttttat	tactaatgtg	actgattctg	ctgctaattt	tagttattta		1380
gcagatgggtg	ggtttagctat	tttagatact	tcgggtgcca	tagatgtttt	tgttgtacag		1440
ggcatctatg	gtcttaatta	ttacaagggt	aatccttgtg	aagatgttaa	ccaacagttt		1500
gtagtgtctg	gtggtaatat	agttggcttt	ctcacttctc	gtaatgaaac	tggttctcag		1560
cctattgaga	accaatttta	tgttaaactc	actaatgtaa	gtcgtcgtca	cagacgttcc		1620
attagtga	aaa	atgttacaag	ctgtccatac	gtaagttatg	gcaggttttg	tatacaacct	1680
gatggctcta	ttaagcaaat	agtaccgcaa					1710

<210> 43
 <211> 1657
 <212> DNA
 <213> artificial sequence

<220>
 <223> DNA of AF193423

<400> 43	
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tctatagcta	tgacagcacc tcttcagggt
gcacactgta	acttttctga aattacagtt
gggtcttgtc	ctataacagg catgattcca
aatggttctt	tattttataa tttaacagtt
tttcaatgtg	ttaacaactt cacatctgtt
aacaaaacta	ctgatgttac gtcagcaggt
tataatatta	tgaaagaatt taaggttctt
gtaattttgt	gcgataattc ccccaagggt
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	aacacaaaca
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	180
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	300
	360
	420
	480
	540
	600
	660
	720
	780
	840
	900

Sequence_Listing

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agtggtttgt ggtttaattc cttgtcagtt tctcttactt atggaccctt acagggaggg	1080
tgtaagcaat ctgttttttag tggtaaggca acgtgttggt atgcctactc ttataatggc	1140
ccaagggcat gtaaagggtgt ttattcaggt gaattaagca tgaattttga atgtggattg	1200
ctggtttatg ttactaagag tcatggctct cgtatacaga ctagaacgga gcccttagta	1260
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tctattggcc aaaacgtaac aacttgccct tatgtta	1657

<210> 44
 <211> 1643
 <212> DNA
 <213> artificial sequence

<220>
 <223> DNA of AY043312

<400> 44	
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ggttctgcaa gtgggtgcac tgttggtgtt attaaggacg tctataatca aagtgcggct	240
tccatagcta tgacagcacc tcttcagggt atggccttggc ctaagtcaca attttgtagt	300
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gggtcttgtc ctataacagg catgattgca cgtgatcata ttcgtatttc tgcaatgaaa	420
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tttcaatgtg ttaacaactt cacatctggt tatttaaattg gtgatcttgt ttttacttcc	540
aacaaaacta ctgatgttac gtcagcaggt gtgtatttta aagcagggtg acctgtaaat	600
tatagtatta tgaaagaatt taaggttctt gcttactttg ttaatggtac agcacaagat	660
gtaattttgt gtgacaattc cccaagggt ttgctagcct gtcaatataa cactggcaat	720
ttttcggatg gcttttatcc ttttactaat agtacttttag ttagggaaaa gttcattgtc	780
tatcgcgaaa gtagtgttaa tactactctg gcgttaacta atttcacttt tactaatgta	840
agtaatgcac agcctaatag tgggtggtgt catacttttc atttatatca aacacaaaca	900
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Sequence_Listing

```

agtgatttta tgtatgggtc ttaccaccct agttgttctt ttagaccaga aaccattaat 1020
agtggtttgt ggtttaattc cttgtcagtt tctcttactt acggaccctt acagggaggg 1080
tgtaagcaat ctgtcttttag tggtaaggca acgtgttggt atgcctactc ttataatggc 1140
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ctggtttatg ttactaagag tgatggctct cgtatacaga ctagaacgga gcccttagta 1260
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tttgtagtgt ctggtggcaa tatagttggc attcttactt ctagaaatga aacaggttct 1560
gaacagggtg agaaccagtt ttatgttaag ttagccaata gctcacatcg tcgcaggcgt 1620
tctattggcc aaaatgtaac aag 1643

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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
1      5

```

```

<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
1      5

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