

10 20 30 40 50 60

5' gaattctat ttttcgatttcaaattttccaaacttaaatatgattgaa tgcctgagaaaggtaata  
 ...  
 3' cttaagataaaagctaaagtttaaagggttgaatttataacttaacttacggactctttccattat

gaattctat ttttcgatttcaaattttccaaacttaaatatgattgaa tgcctgagaaaggtaata

70 80 90 100 110 120 130

gagatg ttttagtttattatgaagtattaggggcgtcttttaaat tcaatctatcaatttgtgaa  
 ctctacaaaatcaataaactttcataatccccgcagaaaatttaagttagatagttaaacactt

gagatg ttttagtttattatgaagtattaggggcgtcttttaaat tcaatctatcaatttgtgaa

140 150 160 170 180 190

atatattactcaaaacccaataaccattctaaaacttattcaaaatata tttgctttaaagagc  
 tataaatgagttttgggttatggtaagattttgaataagttttatataacgaaattttctcg

atatattactcaaaacccaataaccattctaaaacttattcaaaatata tttgctttaaagagc

200 210 220 230 240 250 260

**SfuI**  
**AsuII**  
**NspV**  
**BstBI**  
**Bpu14I**  
**Csp45I**  
**Bsp119I**  
**BspT104I**

atacatactaaaaaacaggcatctttcgaactatagcgcatagaatactacgg tgaatcaaaaa  
 tatgtatgattttttgtccgtagaaagcttgatatcgcgatcttatgatgccacttagttttt

atacatactaaaaaacaggcatctttcgaactatagcgcatagaatactacgg tgaatcaaaaa

270 280 290 300 310 320

caaataaaatttaggagggtatattcaagtatacaaaaaaactttagtg tggaggggatttagataa  
 gtttattttaaatcctccatataagttcatatgtttttttgaaatcacactcccctaaatctatt

caaataaaatttaggagggtatattcaagtatacaaaaaaactttagtg tggaggggatttagataa

330 340 350 360 370 380 390

aaagtattcgttatccttataaattaattcttaaacatgcaccaatgtatacattaaataatatt  
 tttcataagcaataggaatatttaattaagaatttgtagctgggttacatagtaatttattataa

aaagtattcgttatccttataaattaattcttaaacatgcaccaatgtatacattaaataatatt

400 410 420 430 440 450

atgtgaattaagtctatcaatttaatttattatggtactttatatttgattaataattgcaagtt  
 tacacttaattcagatagttaaattaataataacaatgaaatataaactaattattaacgttcaa

atgtgaattaagtctatcaatttaatttattatggtactttatatttgattaataattgcaagtt

460 470 480 490 500 510 520

EcoICRI  
 Ecl136II  
 Eco53kl

taaaatcataatttaatggttgaaaggccactatttctaattaacttaaggagttgtttatttgagc  
 attttagtattaaattacaactttccgggtgataagattaattgaattcctcaacaataaactcg

← His Gln Phe Ala Val Ile Arg Ile Leu Lys Leu Leu Gln Lys Asn Ser Ser

taaaatcataatttaatggttgaaaggccactatttctaattaacttaaggagttgtttatttgagc

530 540 550 560 570 580

Aval  
 Cfr9I  
 SstI XmaI  
 SacI BsoBI  
 FrlOI TspMI  
 BanII XmaCI  
 Eco24I Eco88I  
 EcoT38I Ama87I BmeT110I  
 Psp124BI BsiHKCI SmaI

tcggtaccggggataatcttgaaaggaggatgcctaaaaacgaagaacattaaaaacatatat  
 agccatgggcccctattagaactttcctccctacggatttttgcttcttgtaatttttgatatata

← Pro Val Arg Pro Tyr Asp Gln Phe Ser Pro His Arg Phe Val Phe Phe Met Leu Phe Met Tyr

tcggtaccggggataatcttgaaaggaggatgcctaaaaacgaagaacattaaaaacatatat

590 600 610 620 630 640 650

ttgcaccgtctaattggatttatgaaaaatcattttatcagtttgaaaattatgtattatgataag  
 aacgtggcagattacctaataacttttagtaaaatagtcaaacttttaatacataatactattc

← Lys Cys Arg Arg Ile Ser Lys His Phe Ile Met Lys Asp Thr Gln Phe Asn His Ile Ile Leu

ttgcaccgtctaattggatttatgaaaaatcattttatcagtttgaaaattatgtattatgataag

1 → TTTGAAA TTATGTATTATGATAAG



NcoI Bsp19I Smil Swal

Cry7Aa2\_Fw\_NcoI

TC CCATGGGTAATTTAAATAATTTAGGTGGATATGAAGATAGTAATAG

aaagaggaggaaaaacccatgggtaattttaataatTTAGGTGGATATGAAGATAGTAATAGAACA  
 tttctcctcctttttggtaccattaaatttattaaatccacctatacttctatcattatcctgt

1 Met Gly Asn Leu Asn Asn Leu Gly Gly Tyr Glu Asp Ser Asn Arg Thr  
 Cry7Aa2\_MB39\_NA311.1

Met Gly Asn Leu Asn Asn Leu Gly Gly Tyr Glu Asp Ser Asn Arg Thr

Phe Leu Leu Phe Phe Trp Pro Tyr Asn Leu Tyr Asn Leu His Ile His Leu Tyr Tyr Tyr Phe Met

1 AAAGAGGAGGAAAAACCCATGGGTAATTTAAATAATTTAGGTGGATATGAAGATAGTAATAGAACA



ttaaataatttctctcaattatcctactcaaaaagcattatcaccatcattaaaggatatgaacta  
 aatttattaagagagttaataggatgagtttttcgtaatagtggtagtaatttctatacttgat

20 Leu Asn Asn Ser Leu Asn Tyr Pro Thr Gln Lys Ala Leu Ser 30 Pro Ser Leu Lys Asp Met Asn Tyr  
 Cry7Aa2\_MB39\_NA311.1

Leu Asn Asn Ser Leu Asn Tyr Pro Thr Gln Lys Ala Leu Ser Pro Ser Leu Lys Asp Met Asn Tyr

1 TTAAATAATTCTCTCAATTATCCTACTCAAAAAGCATTATCACCATCATTAAAGGATATGAACTA



ccaggatTTTTTATCTATAACTGAGAGGGAACAACCTGAAGCACTCGCTAGTGGTAATACAGCTA  
 ggtcctaaaaaatagatatgactctcccttggacttcgtagcgatcaccattatgtcgat

40 Gln Asp Phe Leu Ser Ile Thr 45 Glu Arg Glu Gln 50 Pro Glu Ala Leu Ala 55 Ser Gly Asn Thr Ala  
 Cry7Aa2\_MB39\_NA311.1

Gln Asp Phe Leu Ser Ile Thr Glu Arg Glu Gln Pro Glu Ala Leu Ala Ser Gly Asn Thr Ala

1 CCAGGATTTTTTATCTATAACTGAGAGGGAACAACCTGAAGCACTCGCTAGTGGTAATACAGCTA

850 860 870 880 890 900 910

Adel  
Dralll

ttaatactgtagttagtggttacaggggctacactaagtgcggttaggtgtcccaggtgcaagtttt  
aattatgacatcaatcacaatgtccccgatgtgattcacgcaatccacaggggtccacgttcaaaa

60 Ile Asn Thr Val Val Ser Val Thr Gly Ala Thr Leu Ser Ala Leu Gly Val Pro Gly Ala Ser Phe

Cry7Aa2\_MB39\_NA311.1

Ile Asn Thr Val Val Ser Val Thr Gly Ala Thr Leu Ser Ala Leu Gly Val Pro Gly Ala Ser Phe

1

ttaatactgtagttagtggttacaggggctacactaagtgcggttaggtgtcccaggtgcaagtttt  
TTAATACTGTAGTTAGTGTTACAGGGGCTACACTAAGTGCGTTAGGTGTCCCAGGTGCAAGTTTT.

920 930 940 950 960 970

PceI AatI StuI SseBI Eco147I Ball Mlsl MscI MluNI Msp20I

atcactaactttttacctgaaaattgcaggcctttttatggccaaaagataaaaaatatttgggatga  
tagtgattgaaaatggacttttaacgtccggaaaataccgggttttctatttttataaacctact

85 Ile Thr Asn Phe Tyr Leu Lys Ile 90 Ala Gly Leu Leu Trp 95 Pro Lys Asp Lys Asn 100 Ile Trp Asp Glu

Cry7Aa2\_MB39\_NA311.1

Ile Thr Asn Phe Tyr Leu Lys Ile Ala Gly Leu Leu Trp Pro Lys Asp Lys Asn Ile Trp Asp Glu

1

atcactaactttttacctgaaaattgcaggcctttttatggccaaaagataaaaaatatttgggatga  
ATCACTAACTTTTACCTGAAAATTGCAGGCCTTTTATGGCCAAAAGATAAAAAATATTTGGGATGA.

980 990 1000 1010 1020 1030 1040

atztatgacagaagtagaaacacttattgatcaaaaaatagaagaatatgtaaggaataaagcga  
taaatactgtcttcacatcttgtgaataactagttttttatcttcttatacattccttatttcgct

105 Phe Met Thr Glu Val Glu Thr 110 Leu Ile Asp Gln Lys Ile 115 Glu Glu Tyr Val Arg Asn Lys Ala

Cry7Aa2\_MB39\_NA311.1

Phe Met Thr Glu Val Glu Thr Leu Ile Asp Gln Lys Ile Glu Glu Tyr Val Arg Asn Lys Ala

1

atztatgacagaagtagaaacacttattgatcaaaaaatagaagaatatgtaaggaataaagcga  
ATTTATGACAGAAGTAGAAACACTTATTGATCAAAAAATAGAAGAATATGTAAGGAATAAAGCGA

1050 1060 1070 1080 1090 1100

ttgcagaattaaatggattaggagcagccttagataaatatcaaaaagcacttgcagattggctg  
 aacgtcttaatttacctaatacctcgtcgggaatctatttatagtttttcgtgaacgtctaaccgac

125 130 135 140 145  
 Ile Ala Glu Leu Asn Gly Leu Gly Ala Ala Leu Asp Lys Tyr Gln Lys Ala Leu Ala Asp Trp Leu

Cry7Aa2\_MB39\_NA311.1

Ile Ala Glu Leu Asn Gly Leu Gly Ala Ala Leu Asp Lys Tyr Gln Lys Ala Leu Ala Asp Trp Leu

1 ▶ ttgcagaattaaatggattaggagcagccttagataaatatcaaaaagcacttgcagattggctg  
 TTGCAGAATTAAATGGATTAGGAGCAGCCTTAGATAAATATCAAAAAGCACTTGCAGATTGGCTG

1110 1120 1130 1140 1150 1160 1170

ggcaacaagatgatccagcagctatatttgctgtggcaactgaatttcgtataatagatttctt  
 ccgtttgttctactaggtcgtcgatataaacgacaccgttgacttaagcatattatctaagaga

150 155 160 165  
 Gly Lys Gln Asp Asp Pro Ala Ala Ile Phe Ala Val Ala Thr Glu Phe Arg Ile Ile Asp Ser Leu

Cry7Aa2\_MB39\_NA311.1

Gly Lys Gln Asp Asp Pro Ala Ala Ile Phe Ala Val Ala Thr Glu Phe Arg Ile Ile Asp Ser Leu

1 ▶ ggcaacaagatgatccagcagctatatttgctgtggcaactgaatttcgtataatagatttctt  
 GGCAACAAGATGATCCAGCAGCTATATTTGCTGTGGCAACTGAATTTTCGTATAATAGATTCTCT

1180 1190 1200 1210 1220 1230

ttttgaatttagtatgccttcatttaagggttactggatatgaaataccattactaacagtttacg  
 aaaacttaatcataggaagtaaatccaatgacctatactttatggtaatgattgtcaaatgc

170 175 180 185  
 Phe Glu Phe Ser Met Pro Ser Phe Lys Val Thr Gly Tyr Glu Ile Pro Leu Leu Thr Val Tyr

Cry7Aa2\_MB39\_NA311.1

Phe Glu Phe Ser Met Pro Ser Phe Lys Val Thr Gly Tyr Glu Ile Pro Leu Leu Thr Val Tyr

1 ▶ ttttgaatttagtatgccttcatttaagggttactggatatgaaataccattactaacagtttacg  
 TTTTGAATTTAGTATGCCTTCATTTAAGGTTACTGGATATGAAATACCATTACTAACAGTTTACG

1240 1250 1260 1270 1280 1290 1300

cacaagcggcaaaccttcacatctagctttattaagagatttactctttatggagataaatgggga  
 gtgttcgccgttgggaagtagatcgaaataattctctaagatgagaataacctctatttaccct

190 195 200 205 210  
 Ala Gln Ala Ala Asn Leu His Leu Ala Leu Leu Arg Asp Ser Thr Leu Tyr Gly Asp Lys Trp Gly

Cry7Aa2\_MB39\_NA311.1

Ala Gln Ala Ala Asn Leu His Leu Ala Leu Leu Arg Asp Ser Thr Leu Tyr Gly Asp Lys Trp Gly

1 ▶ cacaagcggcaaaccttcacatctagctttattaagagatttactctttatggagataaatgggga  
 CACAAGCGGCAAACCTTCATCTAGCTTTATTAAGAGATTCTACTCTTTATGGAGATAAATGGGGA

1310 1320 1330 1340 1350 1360

ttcactcagaacaacattgaggaaaattataatcgtcaaagaacatatttctgaatattcagg  
 aagtgagtccttgttgaactccttttaataattagcagttttcttggataaagacttataagtc

Phe Thr Gln Asn Asn Ile Glu Glu Asn Tyr Asn Arg Gln Lys Lys His Ile Ser Glu Tyr Ser Gly  
 Cry7Aa2\_MB39\_NA311.1

Phe Thr Gln Asn Asn Ile Glu Glu Asn Tyr Asn Arg Gln Lys Lys His Ile Ser Glu Tyr Ser Gly

1 ▶ ttcactcagaacaacattgaggaaaattataatcgtcaaagaacatatttctgaatattcagg  
 TTCACTCAGAACAACATTGAGGAAAATTATAATCGTCAAAGAACATATTTCTGAATATTCAGG

1370 1380 1390 1400 1410 1420 1430

ccattgtaccgagtggtataatagtggtccttagcagattgaacggttccacttatgaacaatgga  
 ggtaacatggctcaccatattatcaccagaatcgtctaacttgccaaggtgaatacttgttacct

His Cys Thr Glu Trp Tyr Asn Ser Gly Leu Ser Arg Leu Asn Gly Ser Thr Tyr Glu Gln Trp  
 Cry7Aa2\_MB39\_NA311.1

His Cys Thr Glu Trp Tyr Asn Ser Gly Leu Ser Arg Leu Asn Gly Ser Thr Tyr Glu Gln Trp

1 ▶ ccattgtaccgagtggtataatagtggtccttagcagattgaacggttccacttatgaacaatgga  
 CCATTGTACCGAGTGGTATAATAGTGGTCTTAGCAGATTGAACGGTTCCACTTATGAACAATGGA

1440 1450 1460 1470 1480 1490

taaattataatcgttttcgtagagaaatgatattaatggattagatcttgtcgcgtgtatttctt  
 attaatattagcaaaagcatctcttactataattaccataatctagaacagcgacataaagga

BglIII

Ile Asn Tyr Asn Arg Phe Arg Arg Glu Met Ile Leu Met Val Leu Asp Leu Val Ala Val Phe Pro  
 Cry7Aa2\_MB39\_NA311.1

Ile Asn Tyr Asn Arg Phe Arg Arg Glu Met Ile Leu Met Val Leu Asp Leu Val Ala Val Phe Pro

1 ▶ taaattataatcgttttcgtagagaaatgatattaatggattagatcttgtcgcgtgtatttctt  
 TAAATTATAATCGTTTTTCGTAGAGAAATGATATTAATGGTATTAGATCTTGTGCTGTATTTCCT

1500 1510 1520 1530 1540 1550 1560

atcatgaccctcgaaggatttcaatggaacaagtagcagttaacgagagaagtgtataccga  
 taagtactgggagcttcataagttaccttggttcatgctcaattgctcttccacatatggct

Ile His Asp Pro Arg Arg Tyr Ser Met Glu Thr Ser Thr Gln Leu Thr Arg Glu Val Tyr Thr Asp  
 Cry7Aa2\_MB39\_NA311.1

Ile His Asp Pro Arg Arg Tyr Ser Met Glu Thr Ser Thr Gln Leu Thr Arg Glu Val Tyr Thr Asp

1 ▶ atcatgaccctcgaaggatttcaatggaacaagtagcagttaacgagagaagtgtataccga  
 ATTCATGACCCTCGAAGGTATTCAATGGAACAAGTAGCAGTTAACGAGAGAAGTGTATACCGA

1570 1580 1590 1600 1610 1620

Cry7Aa2-seq-Fw

CAATTAGCAATCCAGATATAGG

tccagttatcttgtcaattagcaatccagatataggtccaagtttttctcagatggaaaatactg  
 aggtcaatagaacagttaatcgtaggtctatatccaggttcaaaaagagtctaccttttatgac

Pro Val Ile Leu Ser Ile Ser Asn Pro Asp Ile Gly Pro Ser Phe Ser Gln Met Glu Asn Thr

Cry7Aa2\_MB39\_NA311.1

Pro Val Ile Leu Ser Ile Ser Asn Pro Asp Ile Gly Pro Ser Phe Ser Gln Met Glu Asn Thr

1 tccagttatcttgtcaattagcaatccagatataggtccaagtttttctcagatggaaaatactg  
 3 TCCAGTTATCTTGTCAATTAGCAATCCAGATATAGGTCCAAGTTTTTCTCAGATGGAAAATACTG  
 AA-TACTG

1630 1640 1650 1660 1670 1680 1690

cgattagaacaccacaccttggttgattattagatgagctttatatatacatcaaaaataaaa  
 gctaactcttgtggtgtggaacaactaataaatctactcgaaatataatagtagttttatattt

Ala Ile Arg Thr Pro His Leu Val Asp Tyr Leu Asp Glu Leu Tyr Ile Tyr Thr Ser Lys Tyr Lys

Cry7Aa2\_MB39\_NA311.1

Ala Ile Arg Thr Pro His Leu Val Asp Tyr Leu Asp Glu Leu Tyr Ile Tyr Thr Ser Lys Tyr Lys

1 cgattagaacaccacaccttggttgattattagatgagctttatatatacatcaaaaataaaa  
 3 CGATTAGAACACCACACCTTGTGATTATTTAGATGAGCTTTATATATATACATCAAAATATAAA  
 CGATTAGAACACCACACCTTGTGATTATTTAGATGAGCTTTATATATATACATCAAAATATAAA

1700 1710 1720 1730 1740 1750

gcattttcacatgagattcaaccagacctatTTTTATTGGAGTGCACATAAGGTTAGCTTTAAAAA  
 cgtaaaagtgtactctaagttggtctggataaaataacctcacgtgtattccaatcgaaatTTTT

Ala Phe Ser His Glu Ile Gln Pro Asp Leu Phe Tyr Trp Ser Ala His Lys Val Ser Phe Lys Lys

Cry7Aa2\_MB39\_NA311.1

Ala Phe Ser His Glu Ile Gln Pro Asp Leu Phe Tyr Trp Ser Ala His Lys Val Ser Phe Lys Lys

1 gcattttcacatgagattcaaccagacctatTTTTATTGGAGTGCACATAAGGTTAGCTTTAAAAA  
 3 GCATTTTCACATGAGATTCAACCAGACCTATTTTATTGGAGTGCACATAAGGTTAGCTTTAAAAA  
 GCATTTTCACATGAGATTCAACCAGACCTATTTTATTGGAGTGCACATAAGGTTAGCTTTAAAAA

1760 1770 1780 1790 1800 1810

atcggagcaatccaatttatatacaacagg catatatgg taaaacaagtgg atatatttcat  
 tagcctcgttaggttaaataatggtgtcc gtataatacc atttgttcacc tatataaagta

365 370 375 380  
 Ser Glu Gln Ser Asn Leu Tyr Thr Thr Gly Ile Tyr Gly Lys Thr Ser Gly Tyr Ile Ser

Cry7Aa2\_MB39\_NA311.1

Ser Glu Gln Ser Asn Leu Tyr Thr Thr Gly Ile Tyr Gly Lys Thr Ser Gly Tyr Ile Ser

1 → atcggagcaatccaatttatatacaacagg catatatgg taaaacaagtgg atatatttcat  
 ATCGGAGCAATCCAATTTATATAACAACAGG G CATATATGG G TAAAACAAGTGG G AT T TATTTTCAT  
 3 → ATCGGAGCAATCCAATTTATATAACAACAGG CATATATGG TAAAACAAGTGG ATATATTTTCAT

1820 1830 1840 1850 1860 1870

caggagcatattcattt agaggggaatgatatc tatagaacattagcagctcca tcagttg t  
 gtcctcgtataagtaaa tctcccttactatag atatcttgtaatcgtcagagt agtcaac a

385 390 395 400  
 Ser Gly Ala Tyr Ser Phe Arg Gly Asn Asp Ile Tyr Arg Thr Leu Ala Ala Pro Ser Val Val

Cry7Aa2\_MB39\_NA311.1

Ser Gly Ala Tyr Ser Phe Arg Gly Asn Asp Ile Tyr Arg Thr Leu Ala Ala Pro Ser Val Val

1 → caggagcatattcattt agaggggaatgatatc tatagaacattagcagctcca tcagttg t  
 CAGGAGCATATTCATTT TAGAGGGAATG GAAT C C TATAGAACATT T GCAGCTCC C C TCAGTTG GA  
 3 → CAGGAGCATATTCATTT AGAGGGAATGATATC TATAGAACATTAGCAGCTCCA TCAGTTG T

1890 1900 1910 1920 1930

agtttatccg tatactc agaattatggtg tcgagcaagtt gagttttacggtgtaaaagg  
 tcaaataggc atatgag tcttaataccac agctcgttcaa ctcaaaatgccacattttcc

405 410 415 420  
 Val Tyr Pro Tyr Thr Gln Asn Tyr Gly Val Glu Gln Val Glu Phe Tyr Gly Val Lys Gly

Cry7Aa2\_MB39\_NA311.1

Val Tyr Pro Tyr Thr Gln Asn Tyr Gly Val Glu Gln Val Glu Phe Tyr Gly Val Lys Gly

1 → agtttatccg tatactc agaattatggtg tcgagcaagtt gagttttacggtgtaaaagg  
 AGTTTATCCG G TAA A C T C A A A A T T T G G G G G C C A A G C A A G T T T G A G T T T A C G G G  
 3 → AGTTTATCCG TATACTC AGAATTATGGTG TCGAGCAAGTT GAGTTTACGGTG TAAAAGG

1950 1960 1970 1980 1990 2000

acatgtacattatagaggagataacaaatatgatctgacgtatgattctattgatcaattacccc  
 tgtacatgtaatatctcctctattgtttatactagactgcatactaagataactagttaatgggg

425 430 435 440 445  
 His Val His Tyr Arg Gly Asp Asn Lys Tyr Asp Leu Thr Tyr Asp Ser Ile Asp Gln Leu Pro

Cry7Aa2\_MB39\_NA311.1

His Val His Tyr Arg Gly Asp Asn Lys Tyr Asp Leu Thr Tyr Asp Ser Ile Asp Gln Leu Pro

3 → acatgtacattatagaggagataacaaatatgatctgacgtatgattctattgatcaattacccc  
 ACATGTACATTATAGAGGAGATAACAAATATGATCTGACGTATGATTCTATTGATCAATTACCCC





Clal  
BshVI  
BanIII  
BseCI  
BspXI  
BspDI  
Bsa29I  
Bsu15I  
BsuTUI

cagacggagaaccaatacacgaaaaatacactcatcgattatgtcatgctacagctatatctaaa  
gtctgcctcttggttatgtgctttttatgtgagtagctaatacagtagatgctgatatagattt

Pro Asp Gly Glu Pro Ile His Glu Lys Tyr Thr His Arg Leu Cys His Ala Thr Ala Ile Ser Lys

Cry7Aa2\_MB39\_NA311.1

Pro Asp Gly Glu Pro Ile His Glu Lys Tyr Thr His Arg Leu Cys His Ala Thr Ala Ile Ser Lys



3 ► cagacggagaaccaatacacgaaaaatacactcatcgattatgtcatgctacagctatatctaaa  
CAGACGGAGAACCAATACACGAAAAATACACTCATCGATTATGTTCATGCTACAGCTATATCTAAA



tcaactccggattatgataatgctactatcccgatcttttcttggacgcatagaagtgcggagta  
agttgaggcctaatactattacgatgatagggttagaaaagaacctgcgtatcttcacgcctcat

Ser Thr Pro Asp Tyr Asp Asn Ala Thr Ile Pro Ile Phe Ser Trp Thr His Arg Ser Ala Glu Tyr

Cry7Aa2\_MB39\_NA311.1

Ser Thr Pro Asp Tyr Asp Asn Ala Thr Ile Pro Ile Phe Ser Trp Thr His Arg Ser Ala Glu Tyr



3 ► tcaactccggattatgataatgctactatcccgatcttttcttggacgcatagaagtgcggagta  
TCAACTCCGGATTATGATAATGCTACTATCCCGATCTTTTCTTGGACGCATAGAAGTGCGGAGTA  
4 ◀ TCAATTCGGATTATGATAATGCTACTTCCCGATCTTTTCTTGGACGCATAGAAGTGCGGAGTA



ttacaatagaatctatccaaacaaaatcacaaaattccagctgtaaaatgtataaactagatg  
aatgttatcttagataggttgttttagtggttttaaggctcgacatttttacatatttgatctac

Tyr Asn Arg Ile Tyr Pro Asn Lys Ile Thr Lys Ile Pro Ala Val Lys Met Tyr Lys Leu Asp

Cry7Aa2\_MB39\_NA311.1

Tyr Asn Arg Ile Tyr Pro Asn Lys Ile Thr Lys Ile Pro Ala Val Lys Met Tyr Lys Leu Asp



3 ► ttacaatagaatctatccaaacaaaatcacaaaattccagctgtaaaatgtataaactagatg  
TTACAATAGAATCTATCCAAACAAAATCACAAAATTCCAGCTGTAAAATGTATAAACTAGATG  
4 ◀ TTACAATAGAATCTATCCAAACAAAATCCAAAATTCCAGCTGTAAAATGTATAAACTAGATG

0 2210 2220 2230 2240 2250 2260

atccatctacagttgtcaaagggcctggatttacaggtggagatttagttaagagaggggagtaat  
 taggtagatgtcaacagtttcccggacctaaatgtccacctctaatcaattctctccctcatta

515 520 525 530  
 Asp Pro Ser Thr Val Lys Gly Pro Gly Phe Thr Gly Gly Asp Leu Val Lys Arg Gly Ser Asn  
**Cry7Aa2\_MB39\_NA311.1**

Asp Pro Ser Thr Val Val Lys Gly Pro Gly Phe Thr Gly Gly Asp Leu Val Lys Arg Gly Ser Asn



3 → atccatctacagttgtcaaagggcctggatttacaggtggagatttagttaagagaggggagtaat  
 ATCCATCTACAGTTGTCAAAGGGCCTGGATTTACAGGTGGAGATTTAGTTAAGAGAGGGGAGTAAT  
 4 ← ATCCATCTACAGTTGTCAAAGGGCCTGGATTTACAGGTGGAGATTTAGTTAAGAGAGGGGAGTAAT

2270 2280 2290 2300 2310 2320

ggttatataggagatataaaggctaccgtaaactcaccactttctcaaaattatcgtgtagagt  
 ccaatatatcctctatatttccgatggcatttgagtggtgaaagagtttaatagcacaatctca

535 540 545 550  
 Gly Tyr Ile Gly Asp Ile Lys Ala Thr Val Asn Ser Pro Leu Ser Gln Asn Tyr Arg Val Arg Val  
**Cry7Aa2\_MB39\_NA311.1**

Gly Tyr Ile Gly Asp Ile Lys Ala Thr Val Asn Ser Pro Leu Ser Gln Asn Tyr Arg Val Arg Val



3 → ggttatataggagatataaaggctaccgtaaactcaccactttctcaaaattatcgtgtagagt  
 GGTTATATAGGAGATATAAAGGCTACCGTAAACTCACCCTTTCTCAAATTATCGTGTTAGAGT  
 4 ← GGTTATATAGGAGATATAAAGGCTACCGTAAACTCACCCTTTCTCAAATTATCGTGTTAGAGT

0 2340 2350 2360 2370 2380 2390

tcgatacgccactaatgtttctggacaattcaacgtgtatattaatgataaagcaacgcttctaa  
 agctatgcggtgattacaaagacctgttaagttgcacatataattactatttcggtgcaagatt

555 560 565 570 575  
 Arg Tyr Ala Thr Asn Val Ser Gly Gln Phe Asn Val Tyr Ile Asn Asp Lys Ala Thr Leu Leu  
**Cry7Aa2\_MB39\_NA311.1**

Arg Tyr Ala Thr Asn Val Ser Gly Gln Phe Asn Val Tyr Ile Asn Asp Lys Ala Thr Leu Leu



3 → tcgatacgccactaatgtttctggacaattcaacgtgtatattaatgataaagcaacgcttctaa  
 TCGATACGCCACTAATGTTTCTGGACAATTCAACGTGTATATTAATGATAAAGCAACGCTTCTAA  
 4 ← TCGATACGCCACTAATGTTTCTGGACAATTCAACGTGTATATTAATGATAAAGCAACGCTTCTAA

2400 2410 2420 2430 2440 2450

gaaagtttcaaaatactgtagaacaataggtgaaggaaaagatttaacctatgattcatttggac  
ctttcaaagttttatgacatctttgttatccacttccttttctaattggataactaagtaaacct

Arg Lys Phe Gln Asn Thr Val Glu Thr Ile Gly Glu Gly Lys Asp Leu Thr Tyr Asp Ser Phe Gly  
Cry7Aa2\_MB39\_NA311.1

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



3 → gaaagtttcaaaatactgtagaacaataggtgaaggaaaagatttaacctatgattcatttggac  
4 ← GAAAGTTTCAAATACTGTAGAAACAATAGGTGAAGGAAAAGATTTAACCTATGATTCATTTGGA  
GAAAGTTTCAAATACTGTAGAAACAATAGGTGAAGGAAAAGATTTAACCTATGATTCATTTGGA

0 2470 2480 2490 2500 2510 2520

tatatagaatattctacgaccattcaatttccggatgagcatccaaaaatcactcttcatttaag  
atatactttataagatgctggttaaggttaaggcctactcgtaggtttttagtgagaagtaaatc

Tyr Ile Glu Tyr Ser Thr Thr Ile Gln Phe Pro Asp Glu His Pro Lys Ile Thr Leu His Leu Ser  
Cry7Aa2\_MB39\_NA311.1

Tyr Ile Glu Tyr Ser Thr Thr Ile Gln Phe Pro Asp Glu His Pro Lys Ile Thr Leu His Leu Ser



3 → tatatagaatattctacgaccattcaatttccggatgagcatccaaaaatcactcttcatttaag  
4 ← TATATAGAATATTCTACGACCATTCAATTTCCGGATGAGCATCCAAAAATCACTCTTCATTTAAG  
TATATAGAATATTCTACGACCATTCAATTTCCGGATGAGCATCCAAAAATCACTCTTCATTTAAG

2530 2540 2550 2560 2570 2580

tgatttgagtaacaattcatcattttatgtagattcaatcgaatttatccctgtagatgtaaatt  
actaaactcattgtaagtagtaaaatacatcctaagtagcttaaataggacatctacatttaa

Asp Leu Ser Asn Asn Ser Ser Phe Tyr Val Asp Ser Ile Glu Phe Ile Pro Val Asp Val Asn  
Cry7Aa2\_MB39\_NA311.1

Asp Leu Ser Asn Asn Ser Ser Phe Tyr Val Asp Ser Ile Glu Phe Ile Pro Val Asp Val Asn



3 → tgatttgagtaacaattcatcattttatgtagattcaatcgaatttatccctgtagatgtaaatt  
4 ← TGATTTGAGTAACAATTCATCATTTTATGTAGATTCAATCGAATTTATCCCTGTAGATGTA AATT  
TGATTTGAGTAACAATTCATCATTTTATGTAGATTCAATCGAATTTATCCCTGTAGATGTA AATT



atgatgaaaaagaaaaactagaaaaagcacagaaagccgtgaataccttgtttacagaggggaaga  
 tactactttttctttttgatctttttcgtgtcttttcggcacttatggaacaaatgtctcccttct

Tyr Asp Glu Lys Glu Lys Leu Glu Lys Ala Gln Lys Ala Val Asn Thr Leu Phe Thr Glu Gly Arg

Cry7Aa2\_MB39\_NA311.1

Tyr Asp Glu Lys Glu Lys Leu Glu Lys Ala Gln Lys Ala Val Asn Thr Leu Phe Thr Glu Gly Arg

3 → atgatgaaaaagaaaaactagaaaaagcacagaaagccgtgaataccttgtttacagaggggaaga  
 ATGATGAAAAAGAAAAACTAGAAAAAGCACAGAAAGCCGTGAATACCTTGTTTACAGAGGGGAAGA.  
 4 ← ATGATGAAAAAGAAAAACTAGAAAAAGCACAGAAAGCCGTGAATACCTTGTTTACAGAGGGGAAGA.



Csil  
 Mabl  
 SexAI\*

aatgcactccaaaaagacgtgacagattataaagtggaccaggtttcaatttttagtggattgtat  
 ttacgtgaggtttttctgcactgtctaatatttcacctggtccaaagttaaaatcacctaacata

Asn Ala Leu Gln Lys Asp Val Thr Asp Tyr Lys Val Asp Gln Val Ser Ile Leu Val Asp Cys Ile

Cry7Aa2\_MB39\_NA311.1

Asn Ala Leu Gln Lys Asp Val Thr Asp Tyr Lys Val Asp Gln Val Ser Ile Leu Val Asp Cys Ile

3 → aatgcactccaaaaagacgtgacagattataaagtggaccaggtttcaatttttagtggattgtat  
 AATGCACTCCAAAAAGACGTGACAGATTATAAAGTGGACCAGGTTTCAATTTTAGTGGATTGTAT.  
 4 ← AATGCACTCCAAAAAGACGTGACAGATTATAAAGTGGACCAGGTTTCAATTTTAGTGGATTGTAT.



atcaggggattttatatcccaatgagaaacgcgaactacaaaatctagtcaaatcgcaaaacgtt  
 tagtcccctaaatatagggttactctttgcgcttgatgttttagatcagtttatgcgttttgcaa

Ser Gly Asp Leu Tyr Pro Asn Glu Lys Arg Glu Leu Gln Asn Leu Val Lys Tyr Ala Lys Arg

Cry7Aa2\_MB39\_NA311.1

Ser Gly Asp Leu Tyr Pro Asn Glu Lys Arg Glu Leu Gln Asn Leu Val Lys Tyr Ala Lys Arg

3 → atcaggggattttatatcccaatgagaaacgcgaactacaaaatctagtcaaatcgcaaaacgtt  
 ATCAGGGGATTTATATCCCAATGAGAAACGCGA-CTACAA-TCTAGTCAA-TACGCAA-CGTT  
 4 ← ATCAGGGGATTTATATCCCAATGAGAAACGCGAACTACAAAATCTAGTCAAATACGCAAACGTT

2790 2800 2810 2820 2830 2840

tgagctattcccgtaatttacttctagatccaacattcgattctattaattcatctgaggagaat  
 actcgataagggcattaaatgaagatctaggttgtaagctaagataattaagtagactcctctta

Leu Ser Tyr Ser Arg Asn Leu Leu Leu Asp Pro Thr Phe Asp Ser Ile Asn Ser Ser Glu Asn  
 Cry7Aa2\_MB39\_NA311.1

Leu Ser Tyr Ser Arg Asn Leu Leu Leu Asp Pro Thr Phe Asp Ser Ile Asn Ser Ser Glu Glu Asn



3 → TGAGCTATTC~~CGTAATTTACTTCTAGATCCA~~CATTTCGATTC~~ATAAATTCATCTGAGGA~~AAA  
 4 ← TGAGCTATTC~~CGTAATTTACTTCTAGATCCA~~ACATTTCGATTCTATTAATTCATCTGAGGAGAAT

0 2860 2870 2880 2890 2900 2910

ggttggatggaagtaatggtattgtgattggaatggggattttgtattcaaaggtaactat  
 ccaaccataccttcattaccataacactaacctttaccctaaaacataagtttccattgataaa

Gly Trp Tyr Gly Ser Asn Gly Ile Val Ile Gly Asn Gly Asp Phe Val Phe Lys Gly Asn Tyr Leu  
 Cry7Aa2\_MB39\_NA311.1

Gly Trp Tyr Gly Ser Asn Gly Ile Val Ile Gly Asn Gly Asp Phe Val Phe Lys Gly Asn Tyr Leu



3 → GGTGG~~AATGGA~~ATAATGGTATTG~~GA~~ATTGGA~~AGGGGGATTTT~~TT~~TT~~CAAG  
 4 ← GGTGGTATGGAAGTAATGGTATTGTGATTGGAATGGGGATTTTGTATTCAAAGGTAACTATTT

2920 2930 2940 2950 2960 2970

aatTTTTcaggtaccaatgatacacaatatccaacatatctctaccaaaaaatagatgaatcca  
 ttaaaaaagtcgatggttactatgtggtataggttgtagagatggTTTTtacttaggt

Ile Phe Ser Gly Thr Asn Asp Thr Gln Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser  
 Cry7Aa2\_MB39\_NA311.1

Ile Phe Ser Gly Thr Asn Asp Thr Gln Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser



2 ← AATTTTTCAGGTACCAATGATACACAATATCCAACATATCTCTACCAAAAAATAGATGAATCCA  
 4 ← AATTTTTCAGGTACCAATGATACACAATATCCAACATATCTCTACCAAAAAATAGATGAATCCA

0 2990 3000 3010 3020 3030

aactcaaagaa tatacacgctataaactgaaaggTTTTATCGAAAGTAGTCAGGATT  
 TTGAGTTTCTT ATATGTGCGATATTTGACTTTCCAAAATAGCTTTCATCAGTCCTAA

775 780 785  
 Tyr Thr Arg Tyr Lys Leu Lys Gly Phe Ile Glu Ser Ser Gln Asp

Cry7Aa2\_MB39\_NA311.1

Lys Leu Lys Glu Tyr Thr Arg Tyr Lys Leu Lys Gly Phe Ile Glu Ser Ser Gln Asp

2 ← AACTCAAAGAAATTTCCCC-----CGTTAAAACTGAAAGGTTTTTACGAAAGTAGTCAGGATT  
 4 ← AACTCAAAGAA TATACACGCTATAAACTGAAAGGTTTTTATCGAAAGTAGTCAGGATT

3040 3050 3060 3070 3080 3090 3100

tagaagcttatgtgattcgctatgatgcaaaacatagaac attggatgTTTTCTGATAATCTATT  
 ATCTTCGAATACTAAGCGATACTACGTTTTGTATCTTG TAACCTACAAAGACTATTAGATAA

790 795 800 805 810  
 Leu Glu Ala Tyr Val Ile Arg Tyr Asp Ala Lys His Arg Thr Leu Asp Val Ser Asp Asn Leu Leu

Cry7Aa2\_MB39\_NA311.1

Leu Glu Ala Tyr Val Ile Arg Tyr Asp Ala Lys His Arg Thr Leu Asp Val Ser Asp Asn Leu Leu

2 ← TAGAAGCTTATGTGATTTCGCTATGATGCAAAACATAGAACCATTGGATGTTTTCTGATAATCTATT.  
 4 ← TAGAAGCTTATGTGATTTCGCTATGATGCAAAACATAGAAC ATTGGATGTTTTCTGATAATCTATT.

3110 3120 3130 3140 3150 3160

acc ggatatttctccctgagaatacatgtggagaaccaaatcgctgCGCGGCACAACAATACC T  
 TGG CCTATAAGAGGGACTCTTATGTACACCTCTTGGTTTAGCGACGCGCGTGTGTTATGG A

815 820 825 830  
 Pro Asp Ile Leu Pro Glu Asn Thr Cys Gly Glu Pro Asn Arg Cys Ala Ala Gln Gln Tyr Leu

Cry7Aa2\_MB39\_NA311.1

Pro Asp Ile Leu Pro Glu Asn Thr Cys Gly Glu Pro Asn Arg Cys Ala Ala Gln Gln Tyr Leu

2 ← ACCCGGATATTCTCCCTGAGAATACATGTGGAGAACCAATCGTTGCGCGGCACAACAATACCT  
 4 ← ACC GGATATTCTCCCTGAGAATACATGTGGAGAACCAATCGCTGCGCGGCACAACAATACC T

3170 3180 3190 3200 3210 3220

ggatgaaaatccaagttcagaatgtagttc gatgcaagatggaat tttgtctgattcgcattcat  
 cctacttttaggttcaagttcacatcaagctacgttctaccttaaaacagactaagcgtaagta

Asp Glu Asn Pro Ser Ser Glu Cys Ser Ser Met Gln Asp Gly Ile Leu Ser Asp Ser His Ser  
 Cry7Aa2\_MB39\_NA311.1

Asp Glu Asn Pro Ser Ser Glu Cys Ser Ser Met Gln Asp Gly Ile Leu Ser Asp Ser His Ser

2 ← ggatgaaaatccaagttcagaatgtagttc gatgcaagatggaat tttgtctgattcgcattcat  
 4 ← GGATGAAAATCCAAGTTCAGAATGTAGTTCGATGCAAGATGGAATTTTGTCTGATTTCGCATTCAT  
 GGATGAAAATCCAAGTTCAGAATGTAGTTCGATGCAAGATGGAATTTTGTCTGATTTCGCATTCAT

3230 3240 3250 3260 3270 3280 3290

tttctcttaatatagatacaggttctatcaatcacaatgagaat ttaggaat tgggtgttgttt  
 aaagagaattatctatgtccaagatagttagttactcttaaatccttaaacccacaacaaa

Phe Ser Leu Asn Ile Asp Thr Gly Ser Ile Asn His Asn Glu Asn Leu Gly Ile Trp Val Leu Phe  
 Cry7Aa2\_MB39\_NA311.1

Phe Ser Leu Asn Ile Asp Thr Gly Ser Ile Asn His Asn Glu Asn Leu Gly Ile Trp Val Leu Phe

2 ← tttctcttaatatagatacaggttctatcaatcacaatgagaat ttaggaat tgggtgttgttt  
 4 ← TTTCTCTTAATATAGATACAGGTTCTATCAATCACAATGAGAATTTAGGAATTTGGGTGTTGTTT  
 TTTCTCTTAATATAGATACAGGTTCTATCAATCACAATGAGAATTTAGGAATTTGGG

3300 3310 3320 3330 3340 3350

TestCry7Aa2 (David)

GCCCAGT

aaaat ttcgacattagaaggat atgcgaaat tggaaat ctagaagt gattgaagat ggcccagt  
 ttttaaagctgtaatcttctatacgtttaaacctttagatcttcaacttctaccgggtca

Lys Ile Ser Thr Leu Glu Gly Tyr Ala Lys Phe Gly Asn Leu Glu Val Ile Glu Asp Gly Pro Val  
 Cry7Aa2\_MB39\_NA311.1

Lys Ile Ser Thr Leu Glu Gly Tyr Ala Lys Phe Gly Asn Leu Glu Val Ile Glu Asp Gly Pro Val

gctgtaatcttctatacgc  
 Cry7Aa2-seq-Rv

2 ← aaaat ttcgacattagaaggat atgcgaaat tggaaat ctagaagt gattgaagat ggcccagt  
 AAAATTTTCGACATTAGAAGGATATGCGAAATTTGGAAATCTAGAAGTGATTGAAGATGGCCCAGT

160 3370 3380 3390 3400 3410 3420

PfIMI  
AccB71  
Van911

TestCry7Aa2 (David)

TATTGGAGAAGCATTAGC

tattggagaagcattagcccgtgtgaaacgccaagaaacgaagtggagaaacaagttagcccaac  
ataacctcttcgtaatcgggcacaccttgcggttctttgcttcacctctttgttcaatcgggttg

Ile Gly Glu Ala Leu Ala Arg Val Lys Arg Gln Glu Thr Lys Trp Arg Asn Lys Leu Ala Gln

Cry7Aa2\_MB39\_NA311.1

Ile Gly Glu Ala Leu Ala Arg Val Lys Arg Gln Glu Thr Lys Trp Arg Asn Lys Leu Ala Gln

2

tattggagaagcattagcccgtgtgaaacgccaagaaacgaagtggagaaacaagttagcccaac  
TATTGGAGAAGCATTAGCCC GTGTGAAACGCCAAGAAACGAAGTGGAGAAACAAGTTAGCCCAAC

3430 3440 3450 3460 3470 3480

tgacaacggaacacacaagcgatttatacacgagcaaaacaagcgtggataatctttttgCGAAT  
actgttgCctttgtgttcgctaataatgtgctcgtttgttcgCGacctattagaaaaacgCtta

Leu Thr Thr Glu Thr Gln Ala Ile Tyr Thr Arg Ala Lys Gln Ala Leu Asp Asn Leu Phe Ala Asn

Cry7Aa2\_MB39\_NA311.1

Leu Thr Thr Glu Thr Gln Ala Ile Tyr Thr Arg Ala Lys Gln Ala Leu Asp Asn Leu Phe Ala Asn

2

tgacaacggaacacacaagcgatttatacacgagcaaaacaagcgtggataatctttttgCGAAT  
TGACAACGGAACACACAAGCGATTTATACACGAGCAAAACAAGCCTGGATAATCTTTTTCGGAAT

3500 3510 3520 3530 3540 3550

gcacaagactctcacttaaaaagagatgTTacatttgcggaaattgcggctgcaagaaagattgt  
cgtgttctgagagtgaatttttcttacaatgtaaagcctttaacgCCgacgttctttctaaca

Ala Gln Asp Ser His Leu Lys Arg Asp Val Thr Phe Ala Glu Ile Ala Ala Ala Arg Lys Ile Val

Cry7Aa2\_MB39\_NA311.1

Ala Gln Asp Ser His Leu Lys Arg Asp Val Thr Phe Ala Glu Ile Ala Ala Ala Arg Lys Ile Val

2

gcacaagactctcacttaaaaagagatgTTacatttgcggaaattgcggctgcaagaaagattgt  
GCACAAGACTCTCACTTAAAAAGAGATGTTACATTTGCGGAAATTGCGGCTGCAAGAAAGATTGT



3560 3570 3580 3590 3600 3610

ccaatcaatacgcgaagcgtatatgtcatggttatctggtggtccagggtgtaaatcacccatttt  
 ggtagttatgcgcttcgcatatacagtagcaataagacaacaagggtccacatttagtgggataaa

Gln Ser Ile Arg Glu Ala Tyr Met Ser Trp Leu Ser Val Val Pro Gly Val Asn His Pro Ile

Cry7Aa2\_MB39\_NA311.1

Gln Ser Ile Arg Glu Ala Tyr Met Ser Trp Leu Ser Val Val Pro Gly Val Asn His Pro Ile

2

ccaatcaatacgcgaagcgtatatgtcatggttatctggtggtccagggtgtaaatcacccatttt  
 CCAATCAATACGCGAAGCGTATATGTCATGGTTATCTGTTGTTCCAGGTGTAATCACCCATTTT

3620 3630 3640 3650 3660 3670 3680

ttacagagttaagtgggcgagtacaacgagcatttcaattatatgatgtacgaaatgttgtgcggt  
 aatgtctcaattcaccgctcatgttgctcgtaaagttaataatactacatgctttacaacacgca

Phe Thr Glu Leu Ser Gly Arg Val Gln Arg Ala Phe Gln Leu Tyr Asp Val Arg Asn Val Val Arg

Cry7Aa2\_MB39\_NA311.1

Phe Thr Glu Leu Ser Gly Arg Val Gln Arg Ala Phe Gln Leu Tyr Asp Val Arg Asn Val Val Arg

2

ttacagagttaagtgggcgagtacaacgagcatttcaattatatgatgtacgaaatgttgtgcggt  
 TTACAGAGTTAAGTGGGCGAGTACAACGAGCATTTC AATTATATGATGTACGAAATGTTGTGCGT

3690 3700 3710 3720 3730 3740

aatggtcgattcctcaatggcttatccgattggattgtaacatctgacgtaaagggtacaagaaga  
 ttaccagctaaggagttaccgaataggctaacctaacattgtagactgcatttccatgttcttct

Asn Gly Arg Phe Leu Asn Gly Leu Ser Asp Trp Ile Val Thr Ser Asp Val Lys Val Gln Glu Glu

Cry7Aa2\_MB39\_NA311.1

Asn Gly Arg Phe Leu Asn Gly Leu Ser Asp Trp Ile Val Thr Ser Asp Val Lys Val Gln Glu Glu

2

aatggtcgattcctcaatggcttatccgattggattgtaacatctgacgtaaagggtacaagaaga  
 AATGGTCGATTCTCAATGGCTTATCCGATTGGATTGTAACATCTGACGTA AAGGTACAAGAAGA

3750 3760 3770 3780 3790 3800 3810

aatgggaataacgtattagttcttaacaattgggatgcacaagtattacaaaacgtaaaactct  
 ttacccttattgcataatcaagaattgtaaccctacgtgttcataatgttttgcattttgaga

Asn Gly Asn Asn Val Leu Val Leu Asn Asn Trp Asp Ala Gln Val Leu Gln Asn Val Lys Leu

Cry7Aa2\_MB39\_NA311.1

Asn Gly Asn Asn Val Leu Val Leu Asn Asn Trp Asp Ala Gln Val Leu Gln Asn Val Lys Leu

2

aatgggaataacgtattagttcttaacaattgggatgcacaagtattacaaaacgtaaaactct  
 AAATGGGAATAACGTATTAGTTCTTAACAATTGGGATGCACAAGTATTACAAAACGTA AACTCT



PteI  
Paul  
BsePI  
BssHII

atcaagaccgtgggtatatcttacatgtaacagcgcgcaagataggaattggggaaggatata  
tagttctggcaccatataagaatgtacattgtcgcgcttctatccttaacccttcctatata

1050 1055 1060 1065 1070  
Tyr Gln Asp Arg Gly Tyr Ile Leu His Val Thr Ala Arg Lys Ile Gly Ile Gly Glu Gly Tyr Ile

Cry7Aa2\_MB39\_NA311.1

Tyr Gln Asp Arg Gly Tyr Ile Leu His Val Thr Ala Arg Lys Ile Gly Ile Gly Glu Gly Tyr Ile

2 ←

atcaagaccgtgggtatatcttacatgtaacagcgcgcaagataggaattggggaaggatata  
ATCAAGACCGTGGGTATATCTTACATGTAACAGCGCGCAAGATAGGAATTGGGGAAGGATATATA



acgattacggatgaagaagggcatacagatcaattgagatttactgcatgtgaagagattgatgc  
tgctaatagcctacttcttcccgatgtctagttaactctaaatgacgtacacttctctaactacg

1075 1080 1085 1090  
Thr Ile Thr Asp Glu Glu Gly His Thr Asp Gln Leu Arg Phe Thr Ala Cys Glu Glu Ile Asp Ala

Cry7Aa2\_MB39\_NA311.1

Thr Ile Thr Asp Glu Glu Gly His Thr Asp Gln Leu Arg Phe Thr Ala Cys Glu Glu Ile Asp Ala

2 ←

acgattacggatgaagaagggcatacagatcaattgagatttactgcatgtgaagagattgatgc  
ACGATTACGGATGAAGAAGGGCATAACAGATCAATTGAGATTTACTGCATGTGAAGAGATTGATGC



NsiI  
Zsp2I  
EcoT22I  
Mph1103I

atctaatacggtttatatccggttatattacaaaagaactggaattcttcccagatacagagaaag  
tagattacgcaaatataggccaatataatgttttcttgaccttaagaagggtctatgtctctttc

1095 1100 1105 1110  
Ser Asn Ala Phe Ile Ser Gly Tyr Ile Thr Lys Glu Leu Glu Phe Phe Pro Asp Thr Glu Lys

Cry7Aa2\_MB39\_NA311.1

Ser Asn Ala Phe Ile Ser Gly Tyr Ile Thr Lys Glu Leu Glu Phe Phe Pro Asp Thr Glu Lys

2 ←

atctaatacggtttatatccggttatattacaaaagaactggaattcttcccagatacagagaaag  
ATCTAATGCGTTTATATCCGGTTATATTACAAAAGAAGCTGGAATTCTTCCCAGATACAGAGAAAG

110 4020 4030 4040 4050 4060 4070

tgcatatagaaataggcgaaacagaaggaatattcctggtagaaagtatagagttatTTTTgatg  
 acgtatatctttatccgctttgtcttcttataaggaccatctttcataatctcaataaaaactac

1115 1120 1125 1130 1135  
 Val His Ile Glu Ile Gly Glu Thr Glu Gly Ile Phe Leu Val Glu Ser Ile Glu Leu Phe Leu Met

Cry7Aa2\_MB39\_NA311.1

Val His Ile Glu Ile Gly Glu Thr Glu Gly Ile Phe Leu Val Glu Ser Ile Glu Leu Phe Leu Met

CATATCTCAATAAAAACTAC  
 Cry7Aa2\_His\_PstI\_Rv

2 ←  
 tgcatatagaaataggcgaaacagaaggaatattcctggtagaaagtatagagttatTTTTgatg  
 TGCATATAGAAATAGGCGAAACAGAAGGAATATTCCTGGTAGAAAGTATAGAGTTATTTTTGATG

4080 4090 4100 4110 4120 4130

gaagagctatgtcatcatcatcatcattaactgcaggcatgcaagcttggcactggccgctcg  
 ctctcgcatacagtagtagtagtagtaattgacgtccgtacgttcgaaccgtgaccggcagc

1140 1145  
 Glu Glu Leu Cys His His His His His His \*

Cry7Aa2\_MB39\_NA311.1

M13 fwd

1 5  
 His His His His His His \*

6xHis

Glu Glu Leu Cys His His His His His His \*

\* Thr Met Met Met Met Met Met Leu Gln Leu Cys Ala Leu Lys Ala Ser Ala Thr Thr

PstI PaeI BbuI SphI

CTTCTCGATACAGTAGTAGTAGTAGTAATTGACGTCC

Cry7Aa2\_His\_PstI\_Rv

2 ←  
 gaagagctatgtcatcatcatcatcattaactgcaggcatgcaagcttggcactggccgctcg  
 GAAGAGCTATGTCATCATCATCATCATCATTAACTGCAGGCATGCAAGCTTGGCACTGGCCGTCG

4140 4150 4160 4170 4180 4190 4200

ttttacaacgt cgtgactgggaaaaccctggcgttacccttaactcgccttgcagcacatcc  
 aaaatggttgc gactgacccttttgggaccgcaatgggttgaattagcggaaacgtcgtgtagg

M13 fwd

Lys Cys Arg Arg Ser Gln Ser Phe Gly Pro Thr Val Trp Ser Leu Arg Arg Ala Ala Cys Gly

2 ←  
 ttttacaacgt cgtgactgggaaaaccctggcgttacccttaactcgccttgcagcacatcc  
 TTT-ACAACGTT-CGTGACTGG

4210 4220 4230 4240 4250 4260

ccctttcgccagctggcgtaatagcgaagaggcccgcaccgatcgcccttcccaacagttgcgca  
 ++++++  
 gggaaagcggctcgaccgcattatcgcttctccgggctggctagcgggaagggttgtaacgcgt



Gly Lys Ala Leu Gln Arg Leu Leu Ser Ser Ala Arg Val Ser Arg Gly Glu Trp Cys Asn Arg Leu

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4270 4280 4290 4300 4310 4320 4330

gcctgaatggcgaatggcgccctgatgcggtatTTTTCTCCTTACGCATCTGTGCGGTATTTACAC  
 ++++++  
 cggacttaccgcttaccgcggaactacgccataaaagaggaatgctagacacgccataaagtgtg



Arg Phe Pro Ser His Arg Arg Ile Arg Tyr Lys Arg Arg Val Cys Arg His Pro Ile Glu Cys

gcctgaatggcgaatggcgccctgatgcggtatTTTTCTCCTTACGCATCTGTGCGGTATTTACAC

4340 4350 4360 4370 4380 4390

cgcatatggtgcaactctcagtacaatctgctctgatgccgcatagttaagccagccccgacaccc  
 ++++++  
 gcgatataccagctgagagtcattgtagacgagactacggcgtatcaattcggctcggggctgtggg



Arg Met

cgcatatggtgcaactctcagtacaatctgctctgatgccgcatagttaagccagccccgacaccc

4400 4410 4420 4430 4440 4450 4460

gccaacacccgctgacgcgccctgacgggcttgtctgctcccggcatccgcttacagacaagctg  
 ++++++  
 cggttgtggggcactgacgcgggactgcccgaacagacgagggcctagggcgaatgtctgttcgac

gccaacacccgctgacgcgccctgacgggcttgtctgctcccggcatccgcttacagacaagctg

4470 4480 4490 4500 4510 4520

tgaccgtctccgggagctgcatgtgtcagaggTTTTACCAGTCATCACCGAAACGCGGAGACGA  
 ++++++  
 actggcagaggccctcgacgtacacagcttccaaaagtggcagtagtggtttgcgcgctctgct

tgaccgtctccgggagctgcatgtgtcagaggTTTTACCAGTCATCACCGAAACGCGGAGACGA

4530 4540 4550 4560 4570 4580 4590

aagggcctcgtgatacgcctatTTTTATAGGTTAATGTCATGATAATAATGGTTTCTTAGACGTC  
 ++++++  
 tTCCCGGAGCACTATGCGGATAAAAATATCCAATTACAGTACTATTATTACCAAAGAATCTGCAG

Zral AatII

aagggcctcgtgatacgcctatTTTTATAGGTTAATGTCATGATAATAATGGTTTCTTAGACGTC

4600 4610 4620 4630 4640 4650

aggtggcacttttcggggaaatgtgcgcggaaccctatattgtttatTTTTCTAAATACATTCAA  
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+  
tccaccgtgaaaagccccctttacacgcgccttggggataaacaataaaaagatttatgtaagtt

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4660 4670 4680 4690 4700 4710 4720

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tatacataggcgagtactctgttattgggactatTTTACGAAGTTATTAGGTAGGAGGTTTCAACC

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4730 4740 4750 4760 4770 4780

agagtgagttttatgtcgcgaatatattaatgtttctgggtgaaccttatcaaatTTTTCGTTGATTTA  
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+  
tctcactcaaaatacagcgtttataattacaagaccacttgggaatagtttaaagcaactaat

agagtgagttttatgtcgcgaatatattaatgtttctgggtgaaccttatcaaatTTTTCGTTGATTTA

4790 4800 4810 4820 4830 4840 4850

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NruI  
BtuMI  
Bsp68I



AhII  
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SpeI

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**Pfi23II**

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← \* Ser Leu Leu Asp Lys Tyr Ala Ile Leu Arg Gly Ser Asn Leu Arg

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6550 6560 6570 6580 6590 6600

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← Arg Gln Ile Lys Ala Pro Gly Asn Lys Leu Asp Phe Met Thr Ser Leu Phe Leu Tyr Gly Ser Pro

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6610 6620 6630 6640 6650 6660 6670

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← Asp Leu Lys Ile Ala Ile Leu Ile His Asp Asn Leu Ile Lys Val Leu Glu Val Ser Asn Pro Glu

gtccaactttatagcaattagtatatggtcattttaaactctttaccaattcaacgctattaggtt

6680 6690 6700 6710 6720 6730

Psyl  
 PflFI  
 AspI  
 Tth111I

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← Lys Pro Asn Gln Gly Val Tyr Asp Pro His Glu Val Ile Asp Lys Ile His Ser Ser Tyr Lys

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6740 6750 6760 6770 6780 6790 6800

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← Met Leu Phe Leu Tyr Val Leu Tyr Lys Ser Gly Lys His Phe Tyr Ile Val  
 Glu Tyr Ile Gly Pro His Gln Lys Lys Val His Lys Ile Phe Gly Pro Phe Met →

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6810 6820 6830 6840 6850 6860

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← Arg Ser Ala Ser Gln Val Ile Cys Ile Tyr Asn Asp Leu Trp Lys Phe Cys His Asn Ser Trp Phe →

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6870 6880 6890 6900 6910 6920 6930

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Ile Tyr Asn Leu Phe Phe Ile Ser Arg Gln Ile Ser Pro Ser Ser Arg Leu Phe Ile Ser Leu



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6940 6950 6960 6970 6980 6990

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Phe Tyr His Lys Gly Val Phe Glu Pro Ser Arg Gly Thr Gly Leu \*



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Met Asp Asn Ser Ile



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Arg Leu Asn Leu Tyr Asn Gln Gly Glu Leu Leu Met Leu Gly Ile Leu Phe Thr Ala Ala Pro Ser



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Thr Asp Val Val Lys Asp Leu Gln Asp Lys Val Ile Ser Leu Gln Asp His Glu Val Ala Phe



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Leu Asn Thr Thr Ile Ser Asn Met Leu Thr Ala Val Gly Ile Gly Val Ala Ile Ile Thr Ala Val



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Phe Thr Ala Ala Phe Ala Tyr Val Thr Tyr Ser Asn Lys Arg Ala Lys Lys Asn Met Asp Glu Ala



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Ser Arg Lys Leu Glu Glu Ala Glu Ser Lys Val Ser Val Leu Glu Glu Lys Ser Ala Gln Leu



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Glu Arg Lys Ile Leu Glu Ala Glu Gln Leu Leu Ala Asp Ala Asn Ser Ile Ser Asn Val Gly Ser



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BamHI







8630 8640 8650 8660 8670 8680

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Leu Leu Phe Asn Gly Arg Lys \*  
 Tyr Tyr Leu Thr Gly Gly Asn Asn Ser Met Ser Arg Phe Phe Lys Phe Gly Lys Leu His Val Thr



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PspPPI  
 Psp5II  
 PpuMI

Lys Gly Asn Gly Asp Lys Leu Leu Asp Ile Leu Leu Thr Ala Ser Lys Lys Leu Lys Arg Ser



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1 5  
 Met Ser Ile Gln His Phe  
 signal sequence  
 AmpR

Leu Ala Pro Thr Gly Asn Leu Tyr Arg Gly Thr Leu Lys Lys Glu Glu Tyr Glu Tyr Ser Thr Phe



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10 15 20 25  
 Arg Val Ala Leu Ile Pro Phe Phe Ala Ala Phe Cys Leu Pro Val Phe Ala His Pro Glu Thr  
 signal sequence  
 AmpR

Arg Val Ala Leu Ile Pro Phe Phe Ala Ala Phe Cys Leu Pro Val Phe Ala His Pro Glu Thr  
 Pro Cys Arg Pro Tyr Ser Leu Phe Cys Gly Ile Leu Pro Ser Cys Phe Cys Ser Pro Arg Asn Ala



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Leu Val Lys Val Lys Asp Ala Glu Asp Gln Leu Gly Ala Arg Val Gly Tyr Ile Glu Leu Asp Leu

AmpR

Leu Val Lys Val Lys Asp Ala Glu Asp Gln Leu Gly Ala Arg Val Gly Tyr Ile Glu Leu Asp Leu  
 Gly Glu Ser Lys Arg Cys

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8950 8960 8970 8980 8990 9000 9010

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Asn Ser Gly Lys Ile Leu Glu Ser Phe Arg Pro Glu Glu Arg Phe Pro Met Met Ser Thr Phe Lys

AmpR

Asn Ser Gly Lys Ile Leu Glu Ser Phe Arg Pro Glu Glu Arg Phe Pro Met Met Ser Thr Phe Lys

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9020 9030 9040 9050 9060 9070

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Val Leu Leu Cys Gly Ala Val Leu Ser Arg Ile Asp Ala Gly Gln Glu Gln Leu Gly Arg Arg

AmpR

Val Leu Leu Cys Gly Ala Val Leu Ser Arg Ile Asp Ala Gly Gln Glu Gln Leu Gly Arg Arg

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9080 9090 9100 9110 9120 9130 9140

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Ile His Tyr Ser Gln Asn Asp Leu Val Glu Tyr Ser Pro Val Thr Glu Lys His Leu Thr Asp Gly

AmpR

Ile His Tyr Ser Gln Asn Asp Leu Val Glu Tyr Ser Pro Val Thr Glu Lys His Leu Thr Asp Gly

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115 Met Thr Val Arg Glu Leu 120 Cys Ser Ala Ala 125 Thr Met Ser Asp Asn Thr Ala Ala Asn Leu 135 Leu

AmpR

Met Thr Val Arg Glu Leu Cys Ser Ala Ala Ile Thr Met Ser Asp Asn Thr Ala Ala Asn Leu Leu

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140 Leu Thr Thr Ile Gly Gly Pro Lys Glu Leu Thr Ala Phe Leu His Asn Met Gly Asp His Val 155

AmpR

Leu Thr Thr Ile Gly Gly Pro Lys Glu Leu Thr Ala Phe Leu His Asn Met Gly Asp His Val

Thr Val

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9280 9290 9300 9310 9320 9330

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160 Thr Arg Leu Asp Arg Trp Glu Pro Glu Leu Asn Glu Ala Ile Pro Asn Asp Glu Arg Asp Thr Thr 175

AmpR

Thr Arg Leu Asp Arg Trp Glu Pro Glu Leu Asn Glu Ala Ile Pro Asn Asp Glu Arg Asp Thr Thr

Arg Arg Ser Arg Gln Ser Gly Ser Ser Phe Ser Ala Met Gly Phe Ser Ser Arg Ser Val Val

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180 Met Pro Val Ala Met Ala Thr Thr Leu Arg Lys Leu Leu Thr Gly Glu Leu Leu Thr Leu Ala Ser 200

AmpR

Met Pro Val Ala Met Ala Thr Thr Leu Arg Lys Leu Leu Thr Gly Glu Leu Leu Thr Leu Ala Ser

Ile Gly Thr Ala Ile Ala Val Val Asn Arg Leu Ser Asn Val Pro Ser Ser Ser Val Arg Ala Glu

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9410 9420 9430 9440 9450 9460

ccggcaacaattaatagactggatggaggcggataaagttgcaggaccacttctgcgctcggccc  
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Arg Gln Gln Leu Ile Asp Trp Met Glu Ala Asp Lys Val Ala Gly Pro Leu Leu Arg Ser Ala

AmpR

Arg Gln Gln Leu Ile Asp Trp Met Glu Ala Asp Lys Val Ala Gly Pro Leu Leu Arg Ser Ala

Arg Cys Cys Asn Ile Ser Gln Ile Ser Ala Ser Leu Thr Ala Pro Gly Ser Arg Arg Glu Ala Arg

ccggcaacaattaatagactggatggaggcggataaagttgcaggaccacttctgcgctcggccc

9470 9480 9490 9500 9510 9520 9530

BssAI  
 BsrFI  
 Cfr10I  
 Bse118I

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 aaggccgaccgaccaataacgactatcttagacctcggccactcgcaccagagcgccatagtaa

Leu Pro Ala Gly Trp Phe Ile Ala Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser Arg Gly Ile Ile

AmpR

Leu Pro Ala Gly Trp Phe Ile Ala Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser Arg Gly Ile Ile

Gly Ala Pro Gln Asn Ile Ala Ser Leu Asp Pro Ala Pro Ser Arg Pro Asp Arg Pro Ile Met

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9540 9550 9560 9570 9580 9590

Dril  
 AhdI  
 AspEI  
 BmeRI  
 Eam1105I

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 cgtcgtgaccccggtctaccattcgggagggcatagcatcaatagatgtgctgccctcagtcgg

Ala Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile Val Val Ile Tyr Thr Thr Gly Ser Gln Ala

AmpR

Ala Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile Val Val Ile Tyr Thr Thr Gly Ser Gln Ala

gcagcactggggccagatggtaagccctcccgatatcgtagttatctacacgacggggagtcaggc

9600 9610 9620 9630 9640 9650 9660

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Thr Met Asp Glu Arg Asn Arg Gln Ile Ala Glu Ile Gly Ala Ser Leu Ile Lys His Trp \*

AmpR

Thr Met Asp Glu Arg Asn Arg Gln Ile Ala Glu Ile Gly Ala Ser Leu Ile Lys His Trp \*



aactatggatgaacgaaatagacagatcgctgagataggtgcctcactgattaagcattggtaac

9670 9680 9690 9700 9710 9720

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9800 9810 9820 9830 9840 9850

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ori

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ori

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9930 9940 9950 9960 9970 9980

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ori

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Cail  
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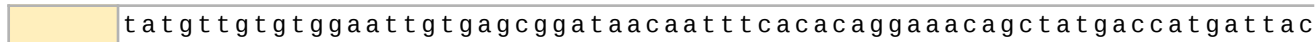
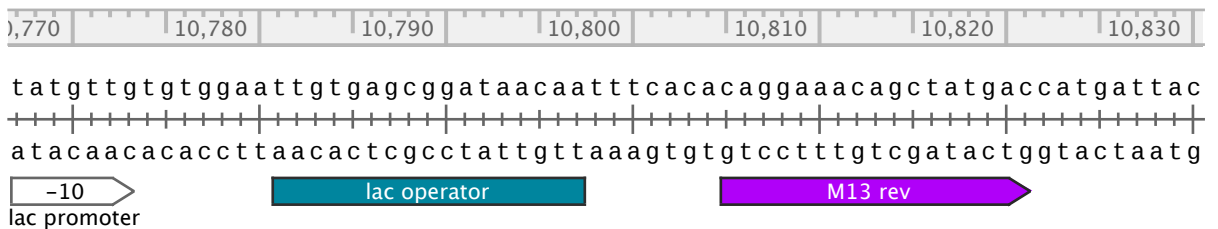
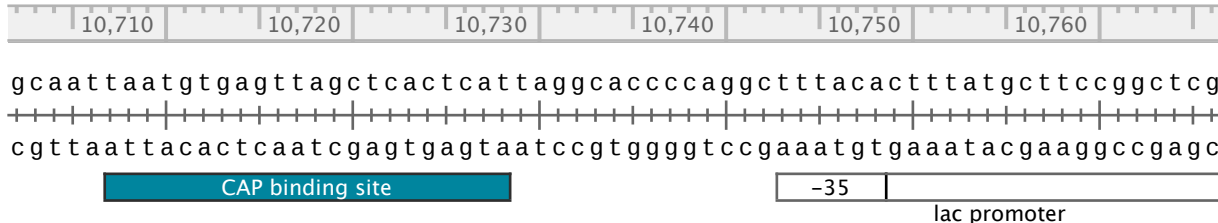
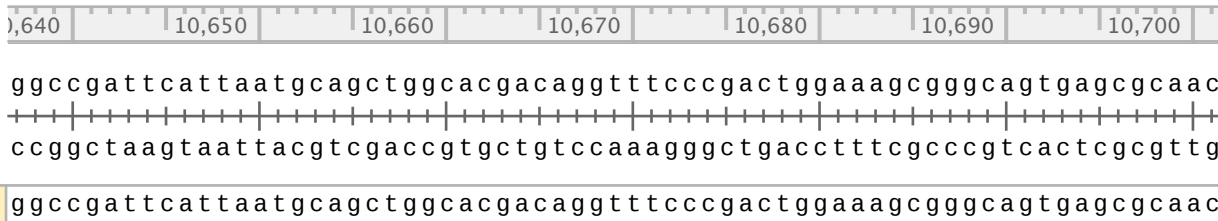
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**Original Sequence: pSTABr-Cry7Aa-like+His.dna**

- 1: PLM00084480+pJET-Cry7Aa-2+59 ▶  
1336 bases / Jan 22, 2018  
13 .. 1328 (11 mismatches, 12 gaps)
- 2: PLM00084481+pJET-Cry7Aa-2+67 ◀  
1251 bases / Jan 22, 2018  
2 .. 1188 (5 mismatches, 6 gaps)
- 3: PLM00155239+pSTAB2\_0\_-cry7Aa+His+cry7Aa-seq-Fw ▶  
1290 bases / Mar 26, 2019  
11 .. 1288 (9 mismatches, 8 gaps)
- 4: PLM00155242+pSTAB2\_0\_-cry7Aa+His+cry7Aa-seq-Rv ◀  
1219 bases / Apr 5, 2019  
3 .. 1218 (3 mismatches)