

Sun Feb 20, 2022 17:23 PST_NCre.apeMap

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      10      20      30      40      50      60      70      80      90     100
      *      *      *      *      *      *      *      *      *      *
      9 MwoI      41 HhaI
      8 AluI      18 Cac8I      34 BsiEI      67 BsiEI      84 NlaIII
1 TTGAGTGAGCTGATACCGCTCGCCGCGAGCCGAACGACCGAGCGCAGCGAGTCAGTGAGCGAGGAAGCGGTCGCTGAGGCTTGACATGATTGGTGCGTATG 100
      |||||
      HSP70A
      L S E L I P L A A A E R P S A A S Q * A R K R S L R L D M I G A Y V
      110      120      130      140      150      160      170      180      190     200
      *      *      *      *      *      *      *      *      *      *
      190 HhaI
      189 SfoI
      189 NlaIV
      178 AcyI
      189 NarI
      175 AccII
      189 KasI
      174 HhaI
      189 HaeII
      189 BbeI
      163 AccII
      173 AccII
      189 AcyI
      199 HaeIII
      162 BsiYI
      172 HhaI
      112 BfmI
      132 MwoI
      152 Hpy188III
      172 Cac8I
      182 Hpy188III
      197 BceAI
      110 AluI
      128 Cac8I
      149 AluI
      160 HaeIII
      172 BssHII
      189 AccBII
      200 Cac8I
167 TTTGATGAAGCTACAGGACTGATTGGCGGGCTATGAGGGCGGGGAAGCTCTGGAAGGGCGCGGATGGGCGCGCGCGCTCCAGAAGGCCATACGG 200
      |||||
      HSP70A
      C M K L Q D * F G G L * G R G K L W K G R D G A R G V Q K A P Y G
      210      220      230      240      250      260      270      280      290     300
      *      *      *      *      *      *      *      *      *      *
      210 NlaIV
      210 AccBII
      204 Cac8I
      202 MspAI
      219 HpaII
      233 AccII
      246 BstEII
      272 SduI
      201 BsiYI
      218 BsaWI
      230 Cac8I
      244 HpyCH4III
      272 BsiHKAI
      287 AccII
167 CCGCTGGCGGCACCCATCCGGTATAAAGCCCGCGACCCCGAAGCGGTGACCTCCACTTTCAGCGACAAACGAGCACTTATACATACGCGACTATTCCTGC 300
      |||||
      HSP70A
      P L A A P I R Y K S P R P R T V T S T F S D K R A L I H T R L F C
      310      320      330      340      350      360      370      380      390     400
      *      *      *      *      *      *      *      *      *      *
      346 NlaIII
      345 SphI
      325 SmlI
      345 NspI
      354 HhaI
      325 AflII
      345 MwoI
      354 Cac8I
      323 AluI
      345 Cac8I
      355 AccII
      321 MaeI
      344 HpyCH4V
      356 HhaI
      320 NheI
      341 Cac8I
      354 BssHII
      320 Cac8I
      330 DpnI
      340 AluI
      350 HpaII
      319 AluI
      329 XhoII
      339 HindIII
      353 AscI
      368 HhaI
167 CGCTATACATAACCACTCAGCTAGCTTAAGATCCCATCAAGCTTGCGATGCCGGCGCGCCAGAAGGAGCGCAGCCAAACAGGATGATGTTTGATGGGGT 400
      |||||
      HSP70A
      R Y T * P L S * L K I P S S L H A G R A R R S A A K P G * C L M G Y
      410      420      430      440      450      460      470      480      490     500
      *      *      *      *      *      *      *      *      *      *
      453 HhaI
      452 SfoI
      452 NlaIV
      452 NarI
      452 KasI
      452 HaeII
      479 MwoI
      475 HpyCH4V
      497 Hpy188III
      423 Hpy188III
      423 BsaWI
      452 BbeI
      473 NlaIII
      491 SduI
      412 HpyCH4V
      424 HpaII
      452 AcyI
      461 Cac8I
      472 SphI
      490 NlaIV
      405 SduI
      423 AccIII
      452 AccBII
      472 NspI
      481 BsiYI
      491 BseSI
      405 BsiHKAI
      417 BsiYI
      437 HaeIII
      449 MaeI
      460 HpyCH4V
      472 Cac8I
      490 AccBII
167 ATTTGAGCACTTGCAACCCCTTATCCGGAAGCCCTCGGCCCAAGGGTAGGGCGCAATGCAAGCAGTTCGCATGCAGCCCTGGAGCGGTGCCCTCCT 500
      |||||
      HSP70A
      L S T C N P Y P E A P W P T K A R R Q C K Q F A C S P W S G A L L
      510      520      530      540      550      560      570      580      590     600
      *      *      *      *      *      *      *      *      *      *
      586 MwoI
      586 Cac8I
      515 NlaIV
      515 DraII
      580 Hpy99I
      578 SalI
      509 HaeIII
      578 Hpy8I
      578 HincII
      507 HpaII
      507 BsiYI
      568 HaeIII
      579 TaqI
      598 DpnI
      506 Cfr10I
      517 HaeIII
      561 MseI
      578 AccI
      592 HpaII
167 GATAAACCGCGCAGGGGGCCTATGTTCTTTACTTTTTACAAGAGAAGTCAACATCTTAAATGGCCAGGTGAGTCGACGAGCAAGCCCGCGGAT 600
      |||||
      HSP70A
      I N R P G G L C S L L F Y K R S H S T S * N G Q V S R R A S P A D
      610      620      630      640      650      660      670      680      690     700
      *      *      *      *      *      *      *      *      *      *
      646 Hpy99I
      645 TaqI
      644 SalI
      644 Hpy8I
      614 HpyCH4V
      633 Cac8I
      644 HincII
      662 BseRI
      611 Cac8I
      628 MwoI
      644 AccI
      660 NlaIV
      677 SmlI
      698 Hpy99I
      607 Cac8I
      627 HpyCH4V
      |||
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001 CAGGCAGCGTCTTGCGAGATTGTGACTTGCACGCCCGCCGATTTGTCTCGACGAAGGCTTTTGCGTCTCTGTCCGTCTGAACGATCTAACCCCTCGGT 700
Int-1 Rbc S2
Q A A C L Q I * L A T P A L C R R R L L A P L S L S Q A A S N P A S
* * * * *
710 720 730 740 750 760 770 780 790 800
* * * * *
734 NlaIII
733 StyI
729 RsaI
728 NlaIV
728 KpnI 738 EcoRV 752 RsrII 787 HpaII
728 AccBII 751 HpaII 782 NlaIV
709 BsiYI 724 TaqI 733 NcoI 750 BsaWI 781 PpuMI
702 BceAI 714 HpyCH4V 728 Acc65I 743 AccII 781 DraII 798 EcoRV
701 CGCCGTTTCCATTTCGAGGAGATTTCGAGGTACCCATGGATATCGCGTCTTCGGTCCGCCGAAGAAGAAGCGGAAGGTGGAGGACCCCGGTGGCAGAGAT 800
M D I A S S G P P K K K R K V E D P G G R D
1
NCre_Chlamydomonas
A S S G P P K K K R K V E D P G G R
1
SV40_NLS
P F P F A G D S R Y P W I S R P P V R R R R S G R W R T P V A E I
* * * * *
810 820 830 840 850 860 870 880 890 900
* * * * *
852 AcyI
822 SduI 851 Hpy99I
822 Hpy8I 850 TaqI
822 BsiHKAI 849 SalI 897 AccII
822 BseSI 849 Hpy8I 890 NlaIII
813 BseRI 823 HpyCH4V 849 HincII 871 TspGWI 889 NspI 899 BsiEI
807 TaqI 822 ApaII 849 AccI 864 Tth111I 889 BspLU11I
803 NlaIII 819 HpyCH4III 837 HpaII 848 Hpy99I 863 Hpy99I 889 AflIII
801 ATCATGTGCAACCTCTCACCGTGACACGAGAACCTTCGGGCTCTGCCGCTGACGCCACGAGCGACGAGGTCCGTAAGAACCTGATGGACATGTTCCGCG 900
I M S N L L T V H Q N L P A L P V D A T S D E V R K N L M D M F R D
23
NCre_Chlamydomonas
S C R T S S P C T R T F R L C P S T P R A T R S V R T * W T C S A
* * * * *
910 920 930 940 950 960 970 980 990 1000
* * * * *
918 SduI 959 HaeIII 973 AluI
918 BsiHKAI 970 Cac8I 983 HpaII
916 Cac8I 942 TspGWI 955 NlaIII 969 HpyCH4V 982 BsaWI
901 ACCGCCAGGCGTTCAGCGAGCACACCTGGAAGATGCTGCTGCTCCGTGTGCGGCTCATGGGCCGCTTGGTGCAAGCTGACACAACCGGAAGTGGTTCCAGC 1000
R Q A F S E H T W K M L L S V C R S W A A W C K L N N R K W F P A
57
NCre_Chlamydomonas
T A R R S A S T P G R C C C P C A A H G P L G A S * T T G S G F Q P
* * * * *
1010 1020 1030 1040 1050 1060 1070 1080 1090 1100
* * * * *
1043 BsiYI 1091 NlaIII
1042 AvaI 1090 NspI
1037 Cac8I 1085 MwoI
1036 HpyCH4V 1084 AluI
1012 MaeII 1035 PstI 1083 PvuII
1011 BtrI 1035 BfmI 1049 Cac8I 1083 MspAI
1005 AvaI 1016 HhaI 1028 MwoI 1040 HaeIII 1064 DpnI 1080 HaeIII 1096 HpyCH4V
1001 CGAACCCGAGGACGTGCGGACTACCTGCTGTATCTGACGGCCCGAGGGCTGGCGGTGAAGACGATCCAGCAGCACCTGGGCGAGCTGAACATGCTGCAT 1100
E P E D V R D Y L L Y L Q A R G L A V K T I Q Q H L G Q L N M L H
90
NCre_Chlamydomonas
N P R T C A T T C C I C R P E G W R * R R S S S T W A S * T C C I
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1110 1120 1130 1140 1150 1160 1170 1180 1190 1200
* * * * *
1111 Cac8I 1183 HpaII
1110 HaeIII 1183 BsiYI
1106 MspAI 1182 NgoMIV
1102 MwoI 1156 MwoI 1182 NaeI
1102 BglI 1120 HaeIII 1137 BceAI 1154 HhaI 1174 MaeII 1182 Cfr10I
1102 BglI 1120 HaeIII 1137 BceAI 1154 HhaI 1174 MaeII 1182 Cfr10I 1199 Cac8I
1101 CGCCGAGCGGCTGCCTCGGCCCTCCGACAGCAATGCCGTGTCGTTGGTGATGCGGCCGATTCGCAAGGAGAAGCTGGATGCCGGCGAGAGGGCGAAGC 1200
R S G L P R P S D S N A V S L V M R R I R K E N V D A G E R A K Q
123
NCre_Chlamydomonas
A A A A C L G P P T A M P C R W * C A A F A R R T W M P A R G R S
* * * * *
1210 1220 1230 1240 1250 1260 1270 1280 1290 1300
* * * * *
1213 TaqI 1228 TaqI 1238 HhaI 1262 MspAI 1286 HaeIII
1206 MaeI 1219 RsaI 1237 FspI 1258 RsrII 1277 BsiYI
1201 AAGCACTAGCGTTCGACGCTACCGACTTCGACAGGTGCGCAGCCTGATGGAGAAGCTCGGACCGCTGCCAGGACATCCGCAATCTGGCCTTCCTGGGCAT 1300
A L A F E R T D F D Q V R S L M E N S D R C Q D I R N L A F L G I
157

NCre_Chlamydomonas																																																																					
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1310	1320	1330	1340	1350	1360	1370	1380	1390	1400																																																												
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										1378 Cac8I																																																											
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										1369 BceAI																																																											
										1363 MwoI	1373 CfrI																																																										
										1336 MwoI	1336 BsiYI																																																										
										1311 MaeII	1331 DpnI																																																										
										1309 AfIIII	1326 MwoI	1336 BsiYI																																																									
1301	A Y N T L L R I A E I A R I R V K D I S R T D G G R M L I H I G R																																																																				
190	CGCCTACAACCGTTGCTGCGCATCGCCGAGATCGCCCGCATATTAGGGTCAAGGACATCTCGCGCACTGACGGCGGCCGCGATGCTGATCCACATAGGCCGG																																																																				
NCre_Chlamydomonas																																																																					
P T T R C C A S P R S P A L G S R T S R A L T A A A C * S T * A G																																																																					
1410	1420	1430	1440	1450	1460	1470	1480	1490	1500																																																												
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										1422 Cac8I																																																											
										1421 HpyCH4V																																																											
										1420 PstI																																																											
										1475 DpnI																																																											
										1420 BfmI	1436 HaeIII																																																										
										1417 MwoI	1427 Hpy99I	1439 BsiYI																																																									
										1415 SduI	1425 AcyI	1435 DraII																																																									
										1415 BsiHKAI	1429 Hpy188III																																																										
1402	BstXI									1460 MwoI	1474 XhoII	1486 HpaII																																																									
1401	ACCAAGACGCTGGTGAGCACTGCAGGCGTCGAGAAGGCCCTTAGCCTGGCGGTGACGAAGCTCGTGGAGCGCTGGATCTCCGTGTCCGGCGTTGCCGATG																																																																				
T K T L V S T A G V E K A L S L G V T K L V E R W I S V S G V A D D																																																																					
223	T K T L V S T A G V E K A L S L G V T K L V E R W I S V S G V A D D																																																																				
NCre_Chlamydomonas																																																																					
P R R W * A L Q A S R R P L A W A * R S S W S A G S P C P A L P M																																																																					
1510	1520	1530	1540	1550	1560	1570	1580	1590	1600																																																												
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										1571 Hpy8I																																																											
										1571 AccI																																																											
										1567 AluI																																																											
										1526 BsiWI	1566 PvuII																																																										
										1524 AccII	1566 MspAII	1579 HhaI																																																									
										1522 MwoI	1548 HhaI	1564 Cac8I	1578 AccII	1597 TaqI																																																							
1501	ACCCAACTACTCTTCTGCGGGTACGCAAGAAGGGGTGGCTGCGCCAGTGCACACCGACCCAGCTGTCTACACGCGCCCTGGAGGGCATCTTCGA																																																																				
P N N Y L F C R V R K N G V A A P S A T S Q L S T R A L E G I F E																																																																					
257	P N N Y L F C R V R K N G V A A P S A T S Q L S T R A L E G I F E																																																																				
NCre_Chlamydomonas																																																																					
T P T T T S S A A Y A R T G W L R P V R P A S C L H A P W R A S S R																																																																					
1610	1620	1630	1640	1650	1660	1670	1680	1690	1700																																																												
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										1692 AccII																																																											
										1663 HpaII	1691 HhaI																																																										
										1662 Hpy188III	1690 AccII																																																										
										1662 BsaWI	1689 HhaI																																																										
										1662 AccIII	1689 Cac8I																																																										
										1673 HpyCH4V	1689 BssHII																																																										
1601	GCGCACCCACCGGTGATCTACGGGGCGAAGAGACACAGCGGGCAGCGTTACCTCGCGTGGTCCGGACACTCTGCACGGGTGGTGCTGCGCGCATATG																																																																				
A T H R L I Y G A K D D S G Q R Y L A W S G H S A R V G A A R D M																																																																					
290	A T H R L I Y G A K D D S G Q R Y L A W S G H S A R V G A A R D M																																																																				
NCre_Chlamydomonas																																																																					
R P T G * S T G R K T T A A S V T S R G P D T L H G L V L R A I W																																																																					
1710	1720	1730	1740	1750	1760	1770	1780	1790	1800																																																												
*	*	*	*	*	*	*	*	*	*																																																												
										1738 HpaII																																																											
										1738 BsiYI	1800 NlaIV																																																										
										1737 NgoMIV	1800 NarI																																																										
										1737 NaeI	1800 KasI																																																										
										1737 Cfr10I	1800 HaeII																																																										
										1707 Cac8I	1736 HaeIII	1778 HpaII	1800 BbeI																																																								
										1706 AccII	1727 DpnI	1737 Cac8I	1778 BsiYI	1800 AcyI																																																							
AccBII	1705 HhaI	1722 HpaII	1733 Cac8I			1760 MslI	1777 Hpy188III			1800																																																											
										1704 AccII	1720 PfoI	1732 HpyCH4V	1755 Hpy8I	1777 BsaWI	1798 HpaII																																																						
										1701 Cac8I	1718 DpnI	1730 NlaIII	1753 MaeII	1777 AccIII	1797 Cfr10I																																																						
1701	GCTCGCGCGGGCGTGTGATCCCCGAGATCATGCAGGCGCGGCTGGACCAACGTGAACATTGTGATGAACATACATCCGGAACCTGGAGCTCGGAGACCG																																																																				
A R A G V S I P E I M Q A G G W T N V N I V M N Y I R N L D S E T G																																																																					
323	A R A G V S I P E I M Q A G G W T N V N I V M N Y I R N L D S E T G																																																																				
NCre_Chlamydomonas																																																																					
L A R A C R S R R S C R P A A G P T * T L * * T T S G T W T R R P																																																																					

1813 Cac8I 1842 PstI 1855 NdeI 1892 DpnI
1805 NlaIII 1842 BfmI 1848 CfrI 1883 HhaI
1804 StyI 1837 DpnI 1848 BsiEI 1882 HaeII
1804 NcoI 1814 EcoNI 1836 XhoII 1847 NotI 1868 TspGWI
1801 HhaI 1811 BsiYI 1825 BceAI 1836 BglII 1868 TspGWI 1882 HaeII
1801 GCGCCATGGTCCGCTGCTGGAGGACGGCGACTAAAGATCTCTGCAGCGGCCCATATGATTCGCTCCGTGTAATGGAGGCGCTCGTTGATCTGAGC 1900
A M V R L L E D G D *
357
Ncre_Chlamydomonas Rbcs2 3'UTR
Rbc S2 3'UTR
A P W S A C W R T A T K D L C S G R H M I P L R V N G G A R * S E P
1910 1920 1930 1940 1950 1960 1970 1980 1990 2000
* * * * * * * * * *
1964 AluI 1999 MaeII
1960 BlnI 1998 BsaAI
1959 AluI 1982 DpnI 1997 AflIII
1916 BceAI 1941 SmlI
1901 CTGCCCCCTGACGACGGCGGTGGATGGAAGATACTGCTCTCAAGTGCTGAAGCGGTAGCTTAGCTCCCGTTTCGTGCTGATCAGTCTTTTCAACAC 2000
Rbcs2 3'UTR
Rbc S2 3'UTR
C P L T N G G G W K I L L S S A E A V A * L P V S C * S V F F N T
2010 2020 2030 2040 2050 2060 2070 2080 2090 2100
* * * * * * * * * *
2075 MwoI
2075 Cac8I
2069 XcmI
2069 StyI
2069 NcoI
2069 BsiYI
2096 AccII
2011 BseRI 2023 TspEI 2046 TspGWI 2058 HaeIII 2070 NlaIII 2095 HhaI
2001 GTAAAAAGCGGAGGAGTTTTCGAATTTTGTGGTTGTAAACGATCCTCCGTTGATTGTCCTCTTCTCCATGGGCGGGCTGGGCGTATTTGAAGCGCGA 2100
Rbcs2 3'UTR
Rbc S2 3'UTR
* K A E E F C N F V G C N D P P L I L A S F S M G G L G V F E A R
2110 2120 2130 2140 2150 2160 2170 2180 2190 2200
* * * * * * * * * *
2170 NlaIII
2169 SphI
2169 NspI
2169 Cac8I
2168 HpyCH4V
2164 MwoI
2163 HaeII
2161 HpaII 2172 HpyCH4V
2112 HhaI 2126 BsiYI 2141 Cac8I 2153 BceAI 2164 HhaI 2190 TaqI
2101 ATGTCTTCTTGGCTATGACACTTCCAGCAAAAGGTAGGGCGGGCTGCGAGACGGCTTCCCGGCGCTGCATGCAACACCGATGATGCTTCGACCCCCCG 2200
beta2-tubulin promoter
M S F L R Y D T S S K R * G G L R D G F P A L H A T P M M L R P P E
2210 2220 2230 2240 2250 2260 2270 2280 2290 2300
* * * * * * * * * *
2223 HhaI 2254 DraI
2222 HaeII 2248 HhaI
2218 NlaIII 2247 HaeII
2216 HpyCH4V 2244 Cac8I 2255 MseI 2276 HpyCH4V 2294 AluI
2202 AluI 2214 MwoI 2234 BsiYI 2247 Eco47III 2266 HaeIII 2291 Cac8I
2201 AAGCTCTTCGGGGCTGCATGGGCGCTCCGATGCCGCTCCAGGGCGAGCGCTGTTTAAATAGCCAGGCCCGCGATTGCAAAAGACATTATAGCGAGTACC 2300
beta2-tubulin promoter
A P S G L H G R S D A A P G R A L F K * P G P R L Q R H Y S E L P
2310 2320 2330 2340 2350 2360 2370 2380 2390 2400
* * * * * * * * * *
2378 SfoI
2378 NlaIV
2378 NarI
2378 Kasi
2378 HaeII
2378 BbeI
2378 AcyI
2378 AccBI
2322 DpnI 2344 MwoI 2368 BsiYI 2379 HhaI
2319 MaeI 2343 HaeIII 2359 DpnI 2370 MwoI
2301 AAAGCCATATTCAAACACCTAGATCACTACCTTCTACACAGGCCACTCGAGCTTGTGATCGCACTCCGCTAAGGGGCGCCTCTTCTCTTCGTTCA 2400
beta2-tubulin promoter
K P Y S N T * I T T T S T Q A T R A C D R T P L R G R L F L F V S
2410 2420 2430 2440 2450 2460 2470 2480 2490 2500
* * * * * * * * * *
2445 HpyCH4III
2443 BsiEI 2475 Cac8I 2493 TspEI
2442 TaqI 2471 Cac8I 2492 EcoRI
2416 NlaIII 2440 Hpy188III 2470 AccII 2492 ApoI
2401 GTCACAACCCGCAACATGACACAAGAATCCCTGTTACTTCTCGACCGATTGATTCGGATGATTCTCTACGCGAGCTCGGAAACGACCAGGAATTCGG 2500

[illegible]

[illegible]

[illegible]

196
 <----->
 AmpR
 S C R * L R Y G R A Y H L A P V L Q * Y R E T H A H R L Q I Y Q Q
 4110 4120 4130 4140 4150 4160 4170 4180 4190 4200
 * * * * * * * * * * * * * * * *
 4114 HpaII
 4113 MwoI 4173 TspEI 4189 MaeI
 4113 BglI 4127 HhaI 4171 MseI 4187 AluI
 4109 Cac8I 4121 HaeIII 4142 HpyCH4V 4170 VspI 4181 HpaII
 | | | | | | | | | |
 4101 ATAAACCAGCCAGCCGGAAGGCGGAGCCGAGAAAGTGGTCCTGCAACTTTATCCGCTCCCATCCAGTCTATTAATTGTTCCGGGAAGCTAGAGTAAGTA 4200
 F W G A P L A S R L L P G A V K D A E M W D I L Q Q R S A L T L L
 162
 <----->
 AmpR
 * T S Q P E G P S A E V V L Q L Y P P P S S L L I V A G K L E * V
 4210 4220 4230 4240 4250 4260 4270 4280 4290 4300
 * * * * * * * * * * * * * * * *
 4225 MaeII 4293 NlaIV
 4224 AclI 4291 HpaII
 4219 FspI 4247 MslI 4290 BsaWI
 4210 MseI 4220 HhaI 4240 BfmI 4264 Hpy99I 4287 AluI
 | | | | | | | | | |
 4201 GTTCGCCAGTTAATAGTTTGCAGCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTACAGCTCGTCGTTTGGTATGGCTTCATTACGCTCCGGTCCCA 4300
 E G T L L K R L T T A M A V P M T T D R E D N P I A E N L E P E W
 129
 <----->
 AmpR
 V R Q L I V C A T L L P L L Q A S W C H A R R L V W L H S A P V P N
 4310 4320 4330 4340 4350 4360 4370 4380 4390 4400
 * * * * * * * * * * * * * * * *
 4328 NlaIII 4367 DpnI
 4321 DpnI 4366 PvuI 4388 HaeIII
 4303 DpnI 4318 NlaIII 4335 HpyCH4V 4350 AluI 4366 BsiEI 4387 CfrI
 | | | | | | | | | |
 4301 ACGATCAAGCGAGTTACATGATCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCTCCGATCGTTGTGAGAAGTAAGTTGGCCGAGTGTTA 4400
 R D L R T V H D G M N H L F A T L E K P G G I T T L L L N A A T N D
 96
 <----->
 AmpR
 D Q G E L H D P P C C A K K R L A P S V L R S L S E V S W P Q C Y
 4410 4420 4430 4440 4450 4460 4470 4480 4490 4500
 * * * * * * * * * * * * * * * *
 4449 TspGWI 4478 RsaI
 4406 NlaIII 4428 TspEI 4442 NlaIII 4477 TatI
 4406 MslI 4423 HpyCH4V 4437 HpyCH4III 4477 ScaI
 | | | | | | | | | |
 4401 TCACTCATGGTTATGGCAGCACTGCATAATTCTTACTGTGATGCCATCCGTAAGATGCTTTTCTGTGAGTGAGTACTCAACCAAGTCATTCTGAG 4500
 S M T I A A S C L E R V T M G D T L H K E T V P S Y E V L D N Q S
 62
 <----->
 AmpR
 H S W L W Q H C I I L L L S C H P * D A F L * L V S T Q P S H S E
 4510 4520 4530 4540 4550 4560 4570 4580 4590 4600
 * * * * * * * * * * * * * * * *
 4581 SduI 4598 MaeII
 4581 BsiHKA I 4597 AclI
 4515 BsiEI 4535 AclI 4557 HhaI 4575 MseI 4594 XmnI
 4533 HpaII 4556 AccII 4574 DraI 4577 ScaI
 | | | | | | | | | |
 4501 AATAGTGTATGCGCGACCGAGTTGCTCTTGCCCGCGTCAATACGGGATAATACCGCGCACATAGCAGAACTTTAAAGTGCTCATCTGGAAGAACG 4600
 Y H I R R G L Q E Q G A D I R S L V A G C L L V K F T S M
 29
 <----->
 AmpR
 N S V C G D R V A L A R R Q Y G I I P R H I A E L * K C S S L E N V
 4610 4620 4630 4640 4650 4660 4670 4680 4690 4700
 * * * * * * * * * * * * * * * *
 4667 HpyCH4V
 4666 SduI
 4666 Hpy8I
 4625 DpnI 4642 DpnI 4666 BsiHKA I
 4624 XhoII 4641 XhoII 4666 BseI
 4619 SmlI 4632 MspAI I 4650 TaqI 4666 ApaI 4678 DpnI
 | | | | | | | | | |
 4601 TTCTTCGGGGCGAAACTCTCAAGGATCTTACCGCTGTGTGATCCAGTTCGATGTAACCCACTCGTGACCCCACTGATCTTCAGCATCTTTTACTTTC 4700
 L R G E N S Q G S Y R C * D P V R C N P L V H P T D L Q H L L S
 4710 4720 4730 4740 4750 4760 4770 4780 4790 4800
 * * * * * * * * * * * * * * * *
 4766 TspGWI
 4765 MslI
 | |
 4701 ACCAGCGTTTCTGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAGGGAATAAGGGCGACACGGAAATGTTGAATACTCATACTCTTCCTTTTC 4800
 P A F L G E Q K Q E G K M P Q K R E * G R H G N V E Y S Y S S F F
 4810 4820 4830 4840 4850 4860 4870 4880 4890 4900
 * * * * * * * * * * * * * * * *
 4835 NlaIII
 4834 Hpy188III 4853 MaeII
 4801 SspI 4834 BspHI 4850 MseI 4895 DpnI
 | | | | | | | | | |
 4801 AATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCTGAGCGTCAGACccccgtgaaaaagatcaa 4900
 pUCori

