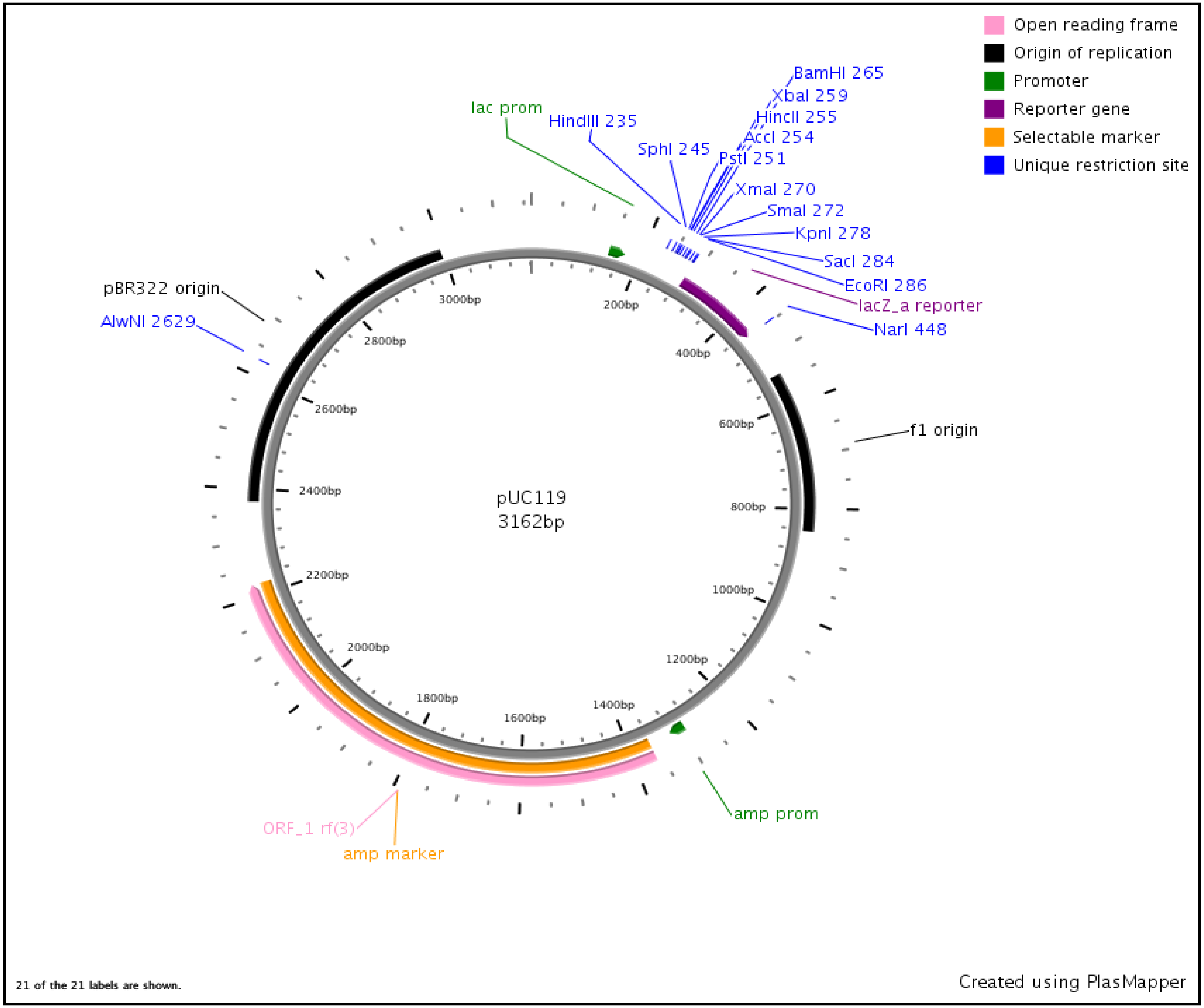
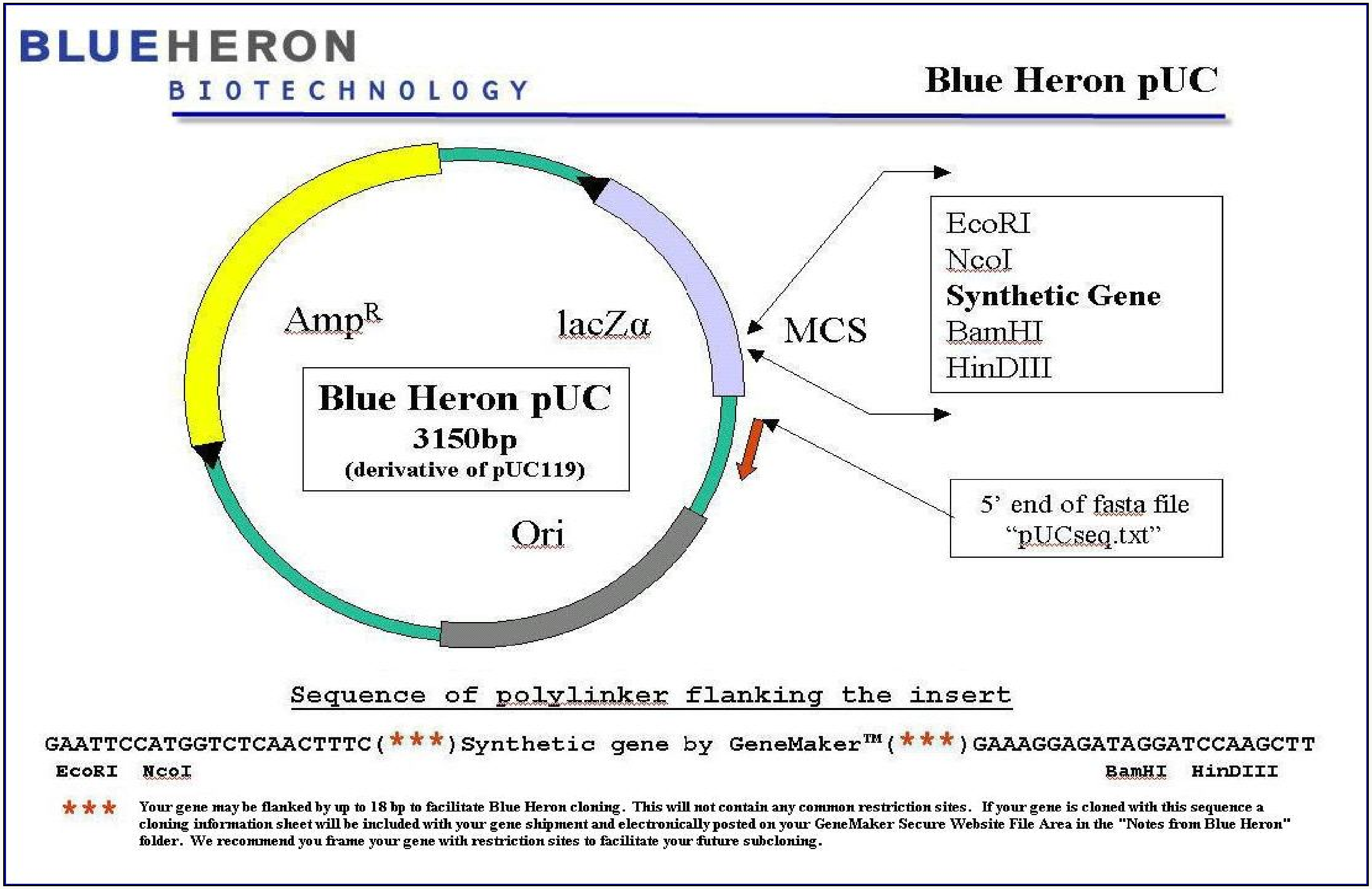
Blue Heron pUC119



Blue Heron Bio pUC (3150 bp) (pUC119 derivative) polylinker amp resistant bi-directional	You may download the [Blue Heron Bio pUC map]() which shows the sequence of the adaptors, and/or the [Blue Heron Bio pUC sequence]() file. Blue Heron Bio may flank your gene with up to 50 bp unique sequence to facilitate Blue Heron Bio cloning. Your gene and any unique flanking sequence is designed by Blue Heron Bio to to be fused non-directionally into the Blue Heron Bio adaptors between the CTTTC and GAAAG "sticky ends". If a unique flanking sequence is used, a cloning information sheet will be posted in your File Area: Notes from Blue Heron folder and included with your packing slip when your gene is shipped. This unique flanking sequence will not contain common restriction sites.	M13/pUC Forward 23-Base Sequencing Primer: 5'-CCCAG TCACG ACGTT GTAAA ACG-3' M13/pUC Reverse 23-Base Sequencing Primer: 5'-AGCGG ATAAC AATTT CACAC AGG-3'



Sequence of polylinker flanking the insert

GAATTCCATGGTCTCAACTTTC(***)Synthetic gene by GeneMaker™(***)GAAAGGAGATAGGATCCAAGCTT

EcoRI NcoI BamHI HinDIII

*** Your gene may be flanked by up to 18 bp to facilitate Blue Heron cloning. This will not contain any common restriction sites. If your gene is cloned with this sequence a cloning information sheet will be included with your gene shipment and electronically posted on your GeneMaker Secure Website File Area in the "Notes from Blue Heron" folder. We recommend you frame your gene with restriction sites to facilitate your future subcloning.

Blue Heron pUC119 DNA Sequence

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   1 agcgcccaat acgcaaaccg cctctccccg cgcgttggcc gattcattaa tgcagctggc acgacaggtt tcccgactgg aaagcgggca gtgagcgcaa
 101 cgcaattaat gtgagttagc tcactcatta ggcaccccag gctttacact ttatgcttcc ggctcgtatg ttgtgtggaa ttgtgagcgg ataacaattt
 201 cacacaggaa acagctatga ccatgattac gccaagcttg catgcctgca ggtcgactct agaggatccc cgggtaccga gctcgaattc actggccgtc
 301 gttttacaac gtcgtgactg ggaaaaccct ggcgttaccc aacttaatcg ccttgcagca catccccctt tcgccagctg gcgtaatagc gaagaggccc
 401 gcaccgatcg cccttcccaa cagttgcgca gcctgaatgg cgaatggcgc ctgatgcggt attttctcct tacgcatctg tgcggtattt cacaccgcat
 501 acgtcaaagc aaccatagta cgcgccctgt agcggcgcat taagcgcggc gggtgtggtg gttacgcgca gcgtgaccgc tacacttgcc agcgccctag
 601 cgcccgctcc tttcgctttc ttcccttcct ttctcgccac gttcgccggc tttccccgtc aagctctaaa tcgggggctc cctttagggt tccgatttag
 701 tgctttacgg cacctcgacc ccaaaaaact tgatttgggt gatggttcac gtagtgggcc atcgccctga tagacggttt ttcgcccttt gacgttggag
 801 tccacgttct ttaatagtgg actcttgttc caaactggaa caacactcaa ccctatctcg ggctattctt ttgatttata agggattttg ccgatttcgg
 901 cctattggtt aaaaaatgag ctgatttaac aaaaatttaa cgcgaatttt aacaaaatat taacgtttac aattttatgg tgcactctca gtacaatctg
1001 ctctgatgcc gcatagttaa gccagccccg acacccgcca acacccgctg acgcgccctg acgggcttgt ctgctcccgg catccgctta cagacaagct
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1201 atgtcatgat aataatggtt tcttagacgt caggtggcac ttttcgggga aatgtgcgcg gaacccctat ttgtttattt ttctaaatac attcaaatat
1301 gtatccgctc atgagacaat aaccctgata aatgcttcaa taatattgaa aaaggaagag tatgagtatt caacatttcc gtgtcgccct tattcccttt
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1501 tggatctcaa cagcggtaag atccttgaga gttttcgccc cgaagaacgt tttccaatga tgagcacttt taaagttctg ctatgtggcg cggtattatc
1601 ccgtattgac gccgggcaag agcaactcgg tcgccgcata cactattctc agaatgactt ggttgagtac tcaccagtca cagaaaagca tcttacggat
1701 ggcatgacag taagagaatt atgcagtgct gccataacca tgagtgataa cactgcggcc aacttacttc tgacaacgat cggaggaccg aaggagctaa
1801 ccgctttttt gcacaacatg ggggatcatg taactcgcct tgatcgttgg gaaccggagc tgaatgaagc cataccaaac gacgagcgtg acaccacgat
1901 gcctgtagca atggcaacaa cgttgcgcaa actattaact ggcgaactac ttactctagc ttcccggcaa caattaatag actggatgga ggcggataaa
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2101 tggggccaga tggtaagccc tcccgtatcg tagttatcta cacgacgggg agtcaggcaa ctatggatga acgaaataga cagatcgctg agataggtgc
2201 ctcactgatt aagcattggt aactgtcaga ccaagtttac tcatatatac tttagattga tttaaaactt catttttaat ttaaaaggat ctaggtgaag
2301 atcctttttg ataatctcat gaccaaaatc ccttaacgtg agttttcgtt ccactgagcg tcagaccccg tagaaaagat caaaggatct tcttgagatc
2401 cttttttct gcgcgtaatc tgctgcttgc aaacaaaaaa accaccgcta ccagcggtgg tttgtttgcc ggatcaagag ctaccaactc tttttccgaa
2501 ggtaactggc ttcagcagag cgcagatacc aaatactgtc cttctagtgt agccgtagtt aggccaccac ttcaagaact ctgtagcacc gcctacatac
2601 ctcgctctgc taatcctgtt accagtggct gctgccagtg gcgataagtc gtgtcttacc gggttggact caagacgata gttaccggat aaggcgcagc
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2801 gcttcccgaa gggagaaagg cggacaggta tccggtaagc ggcagggtcg gaacaggaga gcgcacgagg gagcttccag ggggaaacgc ctggtatctt
2901 tatagtcctg tcgggtttcg ccacctctga cttgagcgtc gatttttgtg atgctcgtca gggggcgga gcctatggaa aaacgccagc aacgcggcct
3001 ttttacggtt cctggccttt tgctggcctt ttgctcacat gttctttcct gcgttatccc ctgattctgt ggataaccgt attaccgcct ttgagtgagc
3101 tgataccgct cgccgcagcc gaacgaccga gcgcagcgag tcagtgagcg aggaagcgga ag
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Blue Heron pUC119 Restriction Map

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RESTRICTION MAP: ALL ENZYMES

====================================================================
Enzyme      Cuts    [ --------- Base 5' to Cleave Sites ---------- ]
====================================================================

AatII          1      1230

AccI           1       253

AclI           3       963  1547  1920

AcyI           3       447  1227  1609

AflII          0

AflIII         1      3037

AgeI           0

AhaIII         3      1571  2263  2282

AluI          18        55   119   214   236   281   377   663   920
                      1098  1117  1796  1859  1959  2480  2737  2783
                      2873  3099

AlwNI          1      2628

ApaBI          0

ApaI           0

ApaLI          3       980  1477  2723

ApoI           3       285   933   944

AscI           0

AsuI           7       396   756  1169  1785  2007  2024  2103
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AsuII          0

AvaI           2       269   857

AvaII          2      1785  2007

AvrII          0

BalI           0

BamHI          1       264

BclI           0

BetI           3      1853  2684  2831

BglI           2       437  2031

BglII          0

BsaAI          1       750

BsaBI          0

BseMII         2      1001  1662

BsePI          0

BsiYI          9        34   531   857   858  1111  2559  2838  3004  3022

Bsp1407I       0

BspHI          3      1204  1309  2317

BspLU11I       1      3037

BspMII         0

BstEII         0

BstXI          0

Cac8I         17        57    86   238   242   246   375   379   399
                       590   604   647  1023  2036  2427  2987  3024  3110

CauII          7       270   271  1077  1112  1613  1964  2660

Cfr10I         2       645  2064

CfrI           3        36   293  1756
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ClaI            0

CviJI          52        38    55   119   141   162   214   236   281
                        295   377   397   431   649   663   677   758
                        862   900   920  1021  1025  1065  1098  1117
                       1171  1758  1796  1859  1869  1959  2025  2034
                       2038  2064  2105  2117  2480  2509  2552  2563
                       2628  2707  2732  2737  2783  2873  2971  2997
                       3015  3026  3099  3118

CviRI          13        52   240   248   355   982  1120  1479  1723
                       1811  2004  2094  2429  2725

DdeI            6       987  1222  1648  2188  2354  2763

DpnI           15       266   407  1468  1504  1521  1779  1825  1843
                       2184  2289  2301  2379  2387  2398  2473

DraII           1      1169

DraIII          1       753

DrdI            3       797  1066  2935

DsaI            0

Eam1105I        1      2149

Eco47III        0

EcoNI           0

EcoRI           1       285

EcoRII          5       136   327  2876  2889  3010

EcoRV           0

EspI            0

Fnu4HI         22        53   356   429   533   547   569  1009  1118
                       1405  1634  1729  1756  2095  2423  2629  2632
                       2697  2840  2995  3113  3116  3134

FnuDII         14        30    32   522   546   566   942  1053  1156
                       1158  1258  1590  2083  2413  2994

FseI            0
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HaeI           3      2563  3015  3026

HaeII          5         5   450   595   603  2797

HaeIII        13        38   295   397   758   900  1171  1758  2025
                      2105  2563  2997  3015  3026

HgiAI          5       283   984  1481  1566  2727

HgiCI          5       131   273   446   709  2196

HgiJII         2       283   679

HhaI          23         4    32    97   428   449   524   537   546
                       568   594   602  1055  1158  1258  1590  1927
                      2020  2413  2522  2696  2796  2863  3133

HincII         1       254

HindIII        1       234

HinfI          8        41   255   798   820  2150  2667  3063  3138

HpaI           0

HpaII         14       159   270   646  1077  1111  1612  1854  1964
                      2031  2065  2469  2659  2685  2832

KpnI           1       277

MaeI           5       259   597  1956  2291  2544

MaeII         11       309   501   639   749   792   804   963  1227
                      1547  1920  2336

MaeIII        13       313   333   560   572  1100  1488  1676  1829
                      1887  2218  2501  2617  2680

MboI          15       264   405  1466  1502  1519  1777  1823  1841
                      2182  2287  2299  2377  2385  2396  2471

McrI           5       408  1631  1780  2703  3127

MfeI           0

MluI           0

MseI          20        47   106   344   540   811   909   926   937
                       949   960  1017  1198  1570  1935  1974  2209
                      2262  2276  2281  2333
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MslI           3      1378  1737  1896

MstI           2       427  1926

MwoI          17        10    94   138   237   407   437   446   453
                       541   543   585   612   642  2031  2419  2991  3105

NaeI           1       647

NarI           1       447

NcoI           0

NdeI           0

NheI           0

NlaIII        11       225   244  1124  1208  1313  1706  1742  1820
                      1830  2321  3041

NlaIV         14       133   266   275   448   678   690   711  1262
                      1852  2063  2104  2198  2970  3009

NotI           0

NruI           0

NspBII         6        55   377  1047  1513  2454  2699

NspI           3       244  1124  3041

PacI           0

PflMI          0

PmaCI          0

PmeI           0

PpuMI          0

PshAI          0

PstI           1       250

PvuI           2       408  1780

PvuII          2        55   377
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RsaI           4       275   519   992  1668

RsrII          0

SacI           1       283

SacII          0

SalI           1       252

SanDI          0

SauI           0

ScaI           1      1668

ScrFI         12       138   270   271   329  1077  1112  1613  1964
                      2660  2878  2891  3012

SduI           6       283   679   984  1481  1566  2727

SecI           5       136   268   269   327  2877

SexAI          0

SfeI           5       246   527  1903  2581  2772

SfiI           0

SgfI           0

SgrAI          0

SmaI           1       271

SmlI           4      1524  2392  2669  2931

SnaBI          0

SpeI           0

SphI           1       244

SplI           0

SrfI           0

Sse8387I       1       250

Sse8647I       0
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SspI           2       958  1344

StuI           0

StyI           0

SwaI           0

TaqI           5       253   283   715  1495  2939

TatI           2       990  1666

TfiI           2        41  3063

TseI          13        52   355   428   568  1117  1728  2094  2422
                      2628  2631  2696  3115  3133

Tsp45I         5       313   572  1100  1676  1887

Tsp4CI         9       422   776  1106  1141  1709  2224  2537  3007  3078

TspEI         10       103   178   195   285   933   944   970  1716
                      1971  2277

TspRI         10        95   296  1730  1757  2104  2209  2358  2629
                      2642  3148

Tth111I        0

VspI           3        47   106  1974

XbaI           1       258

XcmI           0

XhoI           0

XhoII          7       264  1502  1519  2287  2299  2385  2396

XmaIII         0

XmnI           1      1549

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