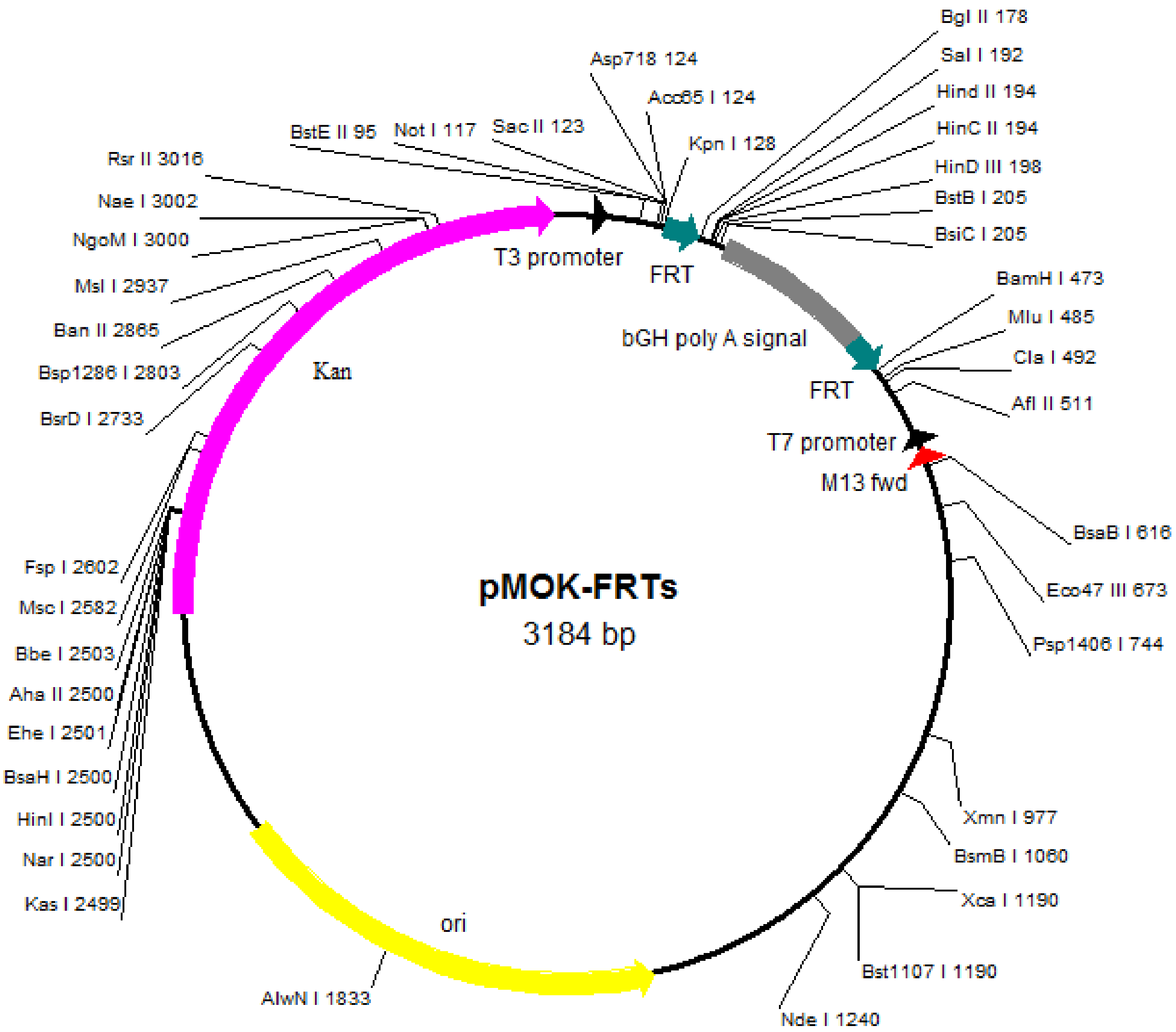
**Vector:** **pMOK-FRTs**

**Antibiotic Selection:** Kan

**Creator(s):** Li Li & Xue Hu, Molecular Oncology Lab of University of Chicago Medical Center

**Date of Construction:** December, 2015



# pMOK-FRTs Full-Length Sequence

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GGAAACAGCTATGACCATGATTACGCCAAGCTCGAAATTAACCCTCACTAAAGGGAACAAAAGCTGGTACGAGGACAGGCTG
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CCTATTCCGAAGTTCCTATTCTCTAGAAAGTATAGGAACTTCagatctTTAATTAAgtcgacAAGCTTttcgaaCCTCGACT
GTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCACTGTCC
TTTCCTAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAG
CAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGCTGGGGATGAAGTTCCTATTCCGAAGTTCCTATTCTCTAGAAAGTAT
AGGAACTTCggatccGATATCccggccACGCGTtgtacaCTCGAGactagtATCGATgtttaaacAGGCCTcttaagTGCCT
AATCGGACGAAAAAATGACCATGATTACGCCAAGCTCCAATTCGCCCTATAGTGAGTCGTATTACAATTCACTGGCCGTCGT
TTTACCCGGATCTGCATCGCAGGATGCTGCTGGCTACCCTGTGGAACACCTACATCTGTATTAACGAAGCGCTGGCATTGAC
CCTGAGTGATTTTTCTCTGGTCCCGCCGCATCCATACCGCCAGTTGTTTACCCTCACAACGTTCCAGTAACCGGGCATGTTC
ATCATCAGTAACCCGTATCGTGAGCATCCTCTCTCGTTTCATCGGTATCATTACCCCCATGAACAGAAATCCCCCTTACACG
GAGGCATCAGTGACCAAACAGGAAAAAACCGCCCTTAACATGGCCCGCTTTATCAGAAGCCAGACATTAACGCTTCTGGAGA
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CCTCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCCCGGAGACGGTCACAGCTTGTCTGTAAGCGGAT
GCCGGGAGCAGACAAGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCGCAGCCATGACCCAGTCACGTAGCG
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CCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTC
TCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAG
CCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCA
CTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAG
AAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAA
ACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGA
TCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCTT
CACCTAGATCCTTTTAAATTAAAAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTACCAA
TGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTCGTTCATCCATAGTTGCCTGACTCCCCGTCATTCAAATAT
GTATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAATATATGATTGAACAAGATGGATTGCACGCAGGTTCTCCG
GCCGCTTGGGTGGAGAGGCTATTCGGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGT
CAGCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTGCAAGACGAGGCAGCGCGGCT
ATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTGCTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTG
GGCGAAGTGCCGGGGCAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGC
GGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGATGGA
AGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCG
AGCATGCCCGACGGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAATGGCCGCTTTT
CTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGA
GCTTGGCGGCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGC
CTTCTTGACGAGTTCTTCTGACCTTTCGTCTTCAAGaatt
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Unique enzymes in pMOK-FRTs:

| | | |
|---|---|---|
| BstE II | G`GTNAC,C | 95 |
| Not I | GC`GGCC,GC | 117 |
| Sac II | CC,GC`GG | 123 |
| Acc65 I | G`GTAC,C | 124 |
| Asp718 | G`GTAC,C | 124 |
| Kpn I | G,GTAC`C | 128 |
| Bgl II | A`GATC,T | 178 |
| Sal I | G`TCGA,C | 192 |
| HinC II | GTY\|RAC | 194 |
| Hind II | GTY\|RAC | 194 |
| HinD III | A`AGCT,T | 198 |
| BsiC I | TT`CG,AA | 205 |
| BstB I | TT`CG,AA | 205 |
| BamH I | G`GATC,C | 473 |
| Mlu I | A`CGCG,T | 485 |
| Cla I | AT`CG,AT | 492 |
| Afl II | C`TTAA,G | 511 |
| BsaB I | GATNN\|NNATC | 616 |
| Eco47 III | AGC\|GCT | 673 |
| Psp1406 I | AA`CG,TT | 744 |
| Xmn I | GAANN\|NNTTC | 977 |
| BsmB I | CGTCTC 7/11 | 1060 |
| Bst1107 I | GTA\|TAC | 1190 |
| Xca I | GTA\|TAC | 1190 |
| Nde I | CA`TA,TG | 1240 |
| AlwN I | CAG,NNN`CTG | 1833 |
| Kas I | G`GCGC,C | 2499 |
| Aha II | GR`CG,YC | 2500 |
| BsaH I | GR`CG,YC | 2500 |
| HinI I | GR`CG,YC | 2500 |
| Nar I | GG`CG,CC | 2500 |

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Ehe I      GGC|GCC        2501
Bbe I      G,GCGC`C        2503
Msc I      TGG|CCA        2582
Fsp I      TGC|GCA        2602
BsrD I     GCAATG, 8       2733
Bsp1286 I   G,DGCH`C       2803
Ban II     G,RGCY`C       2865
Msl I      CAYNN|NNRTG     2937
NgoM I     G`CCGG,C       3000
Nae I      GCC|GGC        3002
Rsr II     CG`GWC,CG       3016
Number of enzymes = 42

The following enzymes do not cut in pMOK-FRTs:

Aat II     Age I      Apa I      Apo I      Asc I
Ase I      Ava I      Avr II     Bcl I      Bgl I
Blp I      Bsa I      BseR I     Bsg I      BsiW I
Bsm I      Bsp120 I    BspM II    BsrG I     BssH II
BstX I     Bsu36 I    Dra III    Eco72 I    EcoN I
EcoO109 I   EcoR I     EcoR V     Esp I      Fse I
Hpa I      Mun I      Nhe I      Nru I      Nsi I
PaeR7 I     PflM I     Pml I      PpuM I     PspA I
Pst I      Pvu I      Sac I      Sca I      Sfi I
Sma I      SnaB I     Spe I      Spl I      Srf I
Ssp I      Vsp I      Xcm I      Xho I      Xma I

pMOK-FRTs: sites sorted by name:

Acc I      (2)  193     1189
Acc65 I    (1)  124
Aci I      (44) 116     120     122     477
               708     711     722     878
               894     949     1005    1090
               1129    1139    1181    1206
               1244    1257    1283    1300
               1343    1350    1371    1462
               1490    1617    1636    1757
               1867    2002    2011    2330
               2409    2472    2566    2630
               2731    2734    2974    3014
               3019    3069    3085    3111
Afl II     (1)  511
Afl III    (2)  485     1417
Aha II     (1)  2500
Ahd I      (2)  2310    3170
Alu I      (17) 9       31      64      200
               555     942     999     1010
               1059    1078    1359    1585
               1675    1721    1978    2606
               3064
Alw I      (11) 469     480     618     1979
               2065    2065    2162    2163
               2678    2745    2924
AlwN I     (1)  1833
ApaL I     (2)  1233    1731
Asp718     (1)  124
Ava II     (2)  704     3016
BamH I     (1)  473
Ban I      (5)  124     281     2258    2499
               2534
Ban II     (1)  2865
Bbe I      (1)  2503
Bbs I      (2)  405     3166
Bbv I      (9)  1019    1068    1165    1836
               1839    2045    2573    2615
               3136
Bbv II     (2)  404     3167
Bcn I      (7)  610     758     1064    1099
               1798    2505    2665
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Bfa I      (5)  158     225     453     1912
               2165
Bgl II     (1)  178
Bpm I      (2)  102     946
BsaA I     (2)  1171    2804
BsaB I     (1)  616
BsaH I     (1)  2500
BsaJ I     (6)  87      120     273     1577
               2663    2932
BsaW I     (3)  1623    1770    2531
BsiC I     (1)  205
BsiE I     (4)  120     1333    1757    2409
BsiHKA I    (4)  1237    1735    2613    2803
BsmA I     (2)  1061    2333
BsmB I     (1)  1060
BsmF I     (2)  690     2651
BsoF I     (32) 117     120     630     711
               1008    1011    1057    1154
               1207    1323    1341    1344
               1462    1617    1760    1825
               1828    2034    2409    2461
               2472    2562    2567    2604
               2645    2732    2735    2738
               2974    3070    3111    3125
Bsp1286 I   (1)  2803
BspH I     (2)  2137    2334
BspM I     (2)  2387    2768
Bsr I      (10) 596     726     750     1165
               1196    1824    1837    1951
               2443    2644
BsrB I     (3)  1350    2332    3113
BsrD I     (1)  2733
BssS I     (2)  1590    3092
Bst1107 I   (1)  1190
BstB I     (1)  205
BstE II    (1)  95
BstN I     (5)  275     1445    1566    1579
               2887
BstU I     (10) 122     487     949     1018
               1020    1123    1464    2045
               2566    2867
BstY I     (9)  178     473     611     2058
               2069    2155    2167    2671
               2917
Cac8 I     (21) 114     233     410     414
               634     676     894     1348
               1434    1471    2031    2394
               2580    2799    2865    2871
               2899    2903    2944    2948
               3002
Cfr10 I    (2)  2819    3000
Cla I      (1)  492
Csp6 I     (4)  68      125     1224    2805
Dde I      (6)  335     687     1227    1692
               2101    2267
Dpn I      (15) 180     475     613     1985
               2060    2071    2079    2157
               2169    2274    2673    2751
               2832    2841    2919
DpnII      (15) 178     473     611     1983
               2058    2069    2077    2155
               2167    2272    2671    2749
               2830    2839    2917
Dra I      (4)  105     500     2176    2195
Drd I      (3)  1112    1525    2527
Dsa I      (3)  87      120     2932
Eae I      (6)  117     594     2406    2580
               2971    2998
Eag I      (2)  117     2406
Ear I      (3)  1301    2844    3054
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Eco47 III   (1)   673
Eco57 I     (4)   160     1964    2645    3077
EcoR II     (5)   273     1443    1564    1577
                  2885
Ehe I       (1)   2501
Fnu4H I     (32)  117     120     630     711
                  1008    1011    1057    1154
                  1207    1323    1341    1344
                  1462    1617    1760    1825
                  1828    2034    2409    2461
                  2472    2562    2567    2604
                  2645    2732    2735    2738
                  2974    3070    3111    3125
Fok I       (9)   434     638     700     778
                  964     1105    2276    2824
                  2849
Fsp I       (1)   2602
Gdi II      (7)   116     118     593     2405
                  2407    2970    2997
Gsu I       (2)   101     945
Hae I       (6)   112     507     1432    1443
                  1895    2582
Hae II      (4)   675     1295    1665    2503
Hae III     (13)  112     119     507     596
                  892     1432    1443    1461
                  1895    2408    2582    2973
                  3000
Hga I       (4)   954     1113    1527    2105
HgiA I      (4)   1237    1735    2613    2803
HgiE II     (3)   270     1235    1996
Hha I       (17)  674     1020    1123    1153
                  1294    1327    1597    1664
                  1764    1938    2047    2494
                  2502    2566    2603    2869
                  3129
HinC II     (1)   194
Hind II     (1)   194
HinD III    (1)   198
Hinf I      (8)   575     973     1317    1392
                  1788    2305    2985    3119
HinI I      (1)   2500
HinP I      (17)  672     1018    1121    1151
                  1292    1325    1595    1662
                  1762    1936    2045    2492
                  2500    2564    2601    2867
                  3127
Hpa II      (16)  609     756     1063    1097
                  1624    1771    1797    1987
                  2405    2482    2504    2532
                  2663    2753    2820    3001
Hph I       (5)   106     1038    1047    2154
                  2679
Kas I       (1)   2499
Kpn I       (1)   128
Mae I       (5)   158     225     453     1912
                  2165
Mae II      (5)   744     1170    2120    2616
                  2803
Mae III     (12)  95      751     774     858
                  1071    1166    1773    1836
                  1952    2235    2620    2926
Mbo I       (15)  178     473     611     1983
                  2058    2069    2077    2155
                  2167    2272    2671    2749
                  2830    2839    2917
Mbo II      (8)   409     1289    2078    2151
                  2860    3070    3152    3167
Mlu I       (1)   485
Mme I       (2)   1631    1815
Mnl I       (21)  53      65      219     261
                  307     382     517     746
                  804     843     1023    1053
                  1315    1525    1598    1849
                  2249    2415    2551    2908
                  3100
Msc I       (1)   2582
Mse I       (15)  39      104     184     188
                  499     512     664     884
                  916     1198    2123    2175
                  2180    2194    2247
Msl I       (1)   2937
Msp I       (16)  609     756     1063    1097
                  1624    1771    1797    1987
                  2405    2482    2504    2532
                  2663    2753    2820    3001
MspA1 I     (6)   122     1010    1129    1759
                  2004    2606
Nae I       (1)   3002
Nar I       (1)   2500
Nci I       (7)   609     757     1063    1098
                  1797    2504    2664
Nco I       (2)   87      2932
Nde I       (1)   1240
NgoM I      (1)   3000
Nla III     (16)  20      91      416     544
                  764     828     891     1056
                  1161    1421    2141    2338
                  2719    2905    2936    2962
Nla IV      (10)  85      126     283     475
                  706     1449    1488    2260
                  2501    2536
Not I       (1)   117
Nsp7524 I   (5)   412     760     1052    1417
                  2901
NspB II     (6)   122     1010    1129    1759
                  2004    2606
NspH I      (5)   416     764     1056    1421
                  2905
Pal I       (13)  112     119     507     596
                  892     1432    1443    1461
                  1895    2408    2582    2973
                  3000
Ple I       (2)   583     1796
Pme I       (2)   105     500
Psp1406 I   (1)   744
Pvu II      (2)   1010    2606
Rsa I       (4)   69      126     1225    2806
Rsr II      (1)   3016
Sac II      (1)   123
Sal I       (1)   192
Sap I       (3)   1301    2844    3054
Sau3A I     (15)  178     473     611     1983
                  2058    2069    2077    2155
                  2167    2272    2671    2749
                  2830    2839    2917
Sau96 I     (3)   704     891     3016
ScrF I      (12)  275     609     757     1063
                  1098    1445    1566    1579
                  1797    2504    2664    2887
Sec I       (6)   87      120     273     1577
                  2663    2932
SfaN I      (17)  331     617     625     721
                  799     861     1084    1217
                  1255    1293    1513    2459
                  2714    2798    2862    2930
                  3137
Sfc I       (3)   568     1682    1873
Sph I       (2)   416     2905
Stu I       (2)   112     507
Sty I       (2)   87      2932
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Taq I      (11)  33      193     205     212
                 492     1517    2613    2769
                 2793    2829    2991
Tfi I      (4)   973     1392    2985    3119
Tsp45 I    (6)   95      858     1071    1166
                 2620    2926
Tth111 I   (2)   1164    2618
Tth111 II  (6)   235     879     2006    2015
                 2045    2936
Xba I      (2)   157     452
Xca I      (1)   1190
Xho II     (9)   178     473     611     2058
                 2069    2155    2167    2671
                 2917
Xma III    (2)   117     2406
Xmn I      (1)   977
```

Site usage in pMOK-FRTs:

```
Aat II     G,ACGT`C         -    Acc I      GT`MK,AC         2
Acc65 I    G`GTAC,C         1    Aci I      C`CG,C           44
Afl II     C`TTAA,G         1    Afl III    A`CRYG,T         2
Age I      A`CCGG,T         -    Aha II     GR`CG,YC         1
Ahd I      GACNN,N`NNGTC    2    Alu I      AG|CT            17
Alw I      GGATC 8/9        11   AlwN I     CAG,NNN`CTG      1
Apa I      G,GGCC`C         -    ApaL I     G`TGCA,C         2
Apo I      R`AATT,Y         -    Asc I      GG`CGCG,CC       -
Ase I      AT`TA,AT         -    Asp718     G`GTAC,C         1
Ava I      C`YCGR,G         -    Ava II     G`GWC,C          2
Avr II     C`CTAG,G         -    BamH I     G`GATC,C         1
Ban I      G`GYRC,C         5    Ban II     G,RGCY`C         1
Bbe I      G,GCGC`C         1    Bbs I      GAAGAC 8/12      2
Bbv I      GCAGC 13/17      9    Bbv II     GAAGAC 7/11      2
Bcl I      T`GATC,A         -    Bcn I      CC,S`GG          7
Bfa I      C`TA,G           5    Bgl I      GCCN,NNN`NGGC    -
Bgl II     A`GATC,T         1    Blp I      GC`TNA,GC        -
Bpm I      CTGGAG 22/20     2    Bsa I      GGTCTC 7/11      -
BsaA I     YAC|GTR          2    BsaB I     GATNN|NNATC      1
BsaH I     GR`CG,YC         1    BsaJ I     C`CNNG,G         6
BsaW I     W`CCGG,W         3    BseR I     GAGGAG 16/14     -
Bsg I      GTGCAG 22/20     -    BsiC I     TT`CG,AA         1
BsiE I     CG,RY`CG         4    BsiHKA I   G,WGCW`C         4
BsiW I     C`GTAC,G         -    Bsm I      GAATG,C 7        -
BsmA I     GTCTC`/9         2    BsmB I     CGTCTC 7/11      1
BsmF I     GGGAC 15/19      2    BsoF I     GC`N,GC          32
Bsp120 I   G`GGCC,C         -    Bsp1286 I  G,DGCH`C         1
BspH I     T`CATG,A         2    BspM I     ACCTGC 10/14     2
BspM II    T`CCGG,A         -    Bsr I      ACT,GG`          10
BsrB I     GAG|CGG          3    BsrD I     GCAATG, 8        1
BsrG I     T`GTAC,A         -    BssH II    G`CGCG,C         -
BssS I     C`TCGT,G         2    Bst1107 I  GTA|TAC          1
BstB I     TT`CG,AA         1    BstE II    G`GTNAC,C        1
BstN I     CC`W,GG          5    BstU I     CG|CG            10
BstX I     CCAN,NNNN`NTGG   -    BstY I     R`GATC,Y         9
Bsu36 I    CC`TNA,GG        -    Cac8 I     GCN|NGC          21
Cfr10 I    R`CCGG,Y         2    Cla I      AT`CG,AT         1
Csp6 I     G`TA,C           4    Dde I      C`TNA,G          6
Dpn I      GA|TC            15   DpnII      `GATC,           15
Dra I      TTT|AAA          4    Dra III    CAC,NNN`GTG      -
Drd I      GACNN,NN`NNGTC   3    Dsa I      C`CRYG,G         3
Eae I      Y`GGCC,R         6    Eag I      C`GGCC,G         2
Ear I      CTCTTC 7/10      3    Eco47 III  AGC|GCT          1
Eco57 I    CTGAAG 21/19     4    Eco72 I    CAC|GTG          -
EcoN I     CCTNN`N,NNAGG    -    EcoO109 I  RG`GNC,CY        -
EcoR I     G`AATT,C         -    EcoR II    `CCWGG,          5
EcoR V     GAT|ATC          -    Ehe I      GGC|GCC          1
Esp I      GC`TNA,GC        -    Fnu4H I    GC`N,GC          32
Fok I      GGATG 14/18      9    Fse I      GG,CCGG`CC       -
Fsp I      TGC|GCA          1    Gdi II     `YGGC,CG         7
Gsu I      CTGGAG 21/19     2    Hae I      WGG|CCW          6
Hae II     R,GCGC`Y         4    Hae III    GG|CC            13
Hga I      GACGC 9/14       4    HgiA I     G,WGCW`C         4
HgiE II    ACCNNNNNNGGT -1/133   Hha I      G,CG`C           17
HinC II    GTY|RAC          1    Hind II    GTY|RAC          1
HinD III   A`AGCT,T         1    Hinf I     G`ANT,C          8
HinI I     GR`CG,YC         1    HinP I     G`CG,C           17
Hpa I      GTT|AAC          -    Hpa II     C`CG,G           16
Hph I      GGTGA 12/11      5    Kas I      G`GCGC,C         1
Kpn I      G,GTAC`C         1    Mae I      C`TA,G           5
Mae II     A`CG,T           5    Mae III    `GTNAC,          12
Mbo I      `GATC,           15   Mbo II     GAAGA 12/11      8
Mlu I      A`CGCG,T         1    Mme I      TCCRAC 25/23     2
Mnl I      CCTC 10/10       21   Msc I      TGG|CCA          1
Mse I      T`TA,A           15   Msl I      CAYNN|NNRTG      1
Msp I      C`CG,G           16   MspA1 I    CMG|CKG          6
Mun I      C`AATT,G         -    Nae I      GCC|GGC          1
Nar I      GG`CG,CC         1    Nci I      CC`S,GG          7
Nco I      C`CATG,G         2    Nde I      CA`TA,TG         1
NgoM I     G`CCGG,C         1    Nhe I      G`CTAG,C         -
Nla III    ,CATG`           16   Nla IV     GGN|NCC          10
Not I      GC`GGCC,GC       1    Nru I      TCG|CGA          -
Nsi I      A,TGCA`T         -    Nsp7524 I  R`CATG,Y         5
NspB II    CMG|CKG          6    NspH I     R,CATG`Y         5
PaeR7 I    C`TCGA,G         -    Pal I      GG|CC            13
PflM I     CCAN,NNN`NTGG    -    Ple I      GAGTC 9/10       2
Pme I      CTTT|AAAC        2    Pml I      CAC|GTG          -
PpuM I     RG`GWC,CY        -    Psp1406 I  AA`CG,TT         1
PspA I     C`CCGG,G         -    Pst I      C,TGCA`G         -
Pvu I      CG,AT`CG         -    Pvu II     CAG|CTG          2
Rsa I      GT|AC            4    Rsr II     CG`GWC,CG        1
Sac I      G,AGCT`C         -    Sac II     CC,GC`GG         1
Sal I      G`TCGA,C         1    Sap I      GCTCTTC 8/11     3
Sau3A I    `GATC,           15   Sau96 I    G`GNC,C          3
Sca I      AGT|ACT          -    ScrF I     CC`N,GG          12
Sec I      C`CNNG,G         6    SfaN I     GCATC 9/13       17
Sfc I      C`TRYA,G         3    Sfi I      GGCCN,NNN`NGGCC  -
Sma I      CCC|GGG          -    SnaB I     TAC|GTA          -
Spe I      A`CTAG,T         -    Sph I      G,CATG`C         2
Spl I      C`GTAC,G         -    Srf I      GCCC|GGGC        -
Ssp I      AAT|ATT          -    Stu I      AGG|CCT          2
Sty I      C`CWWG,G         2    Taq I      T`CG,A           11
Tfi I      G`AWT,C          4    Tsp45 I    `GTSAC,          6
Tth111 I   GACN`N,NGTC      2    Tth111 II  CAARCA 16/14     6
Vsp I      AT`TA,AT         -    Xba I      T`CTAG,A         2
Xca I      GTA|TAC          1    Xcm I      CCANNNN,N`NNNNTGG-
Xho I      C`TCGA,G         -    Xho II     R`GATC,Y         9
Xma I      C`CCGG,G         -    Xma III    C`GGCC,G         2
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