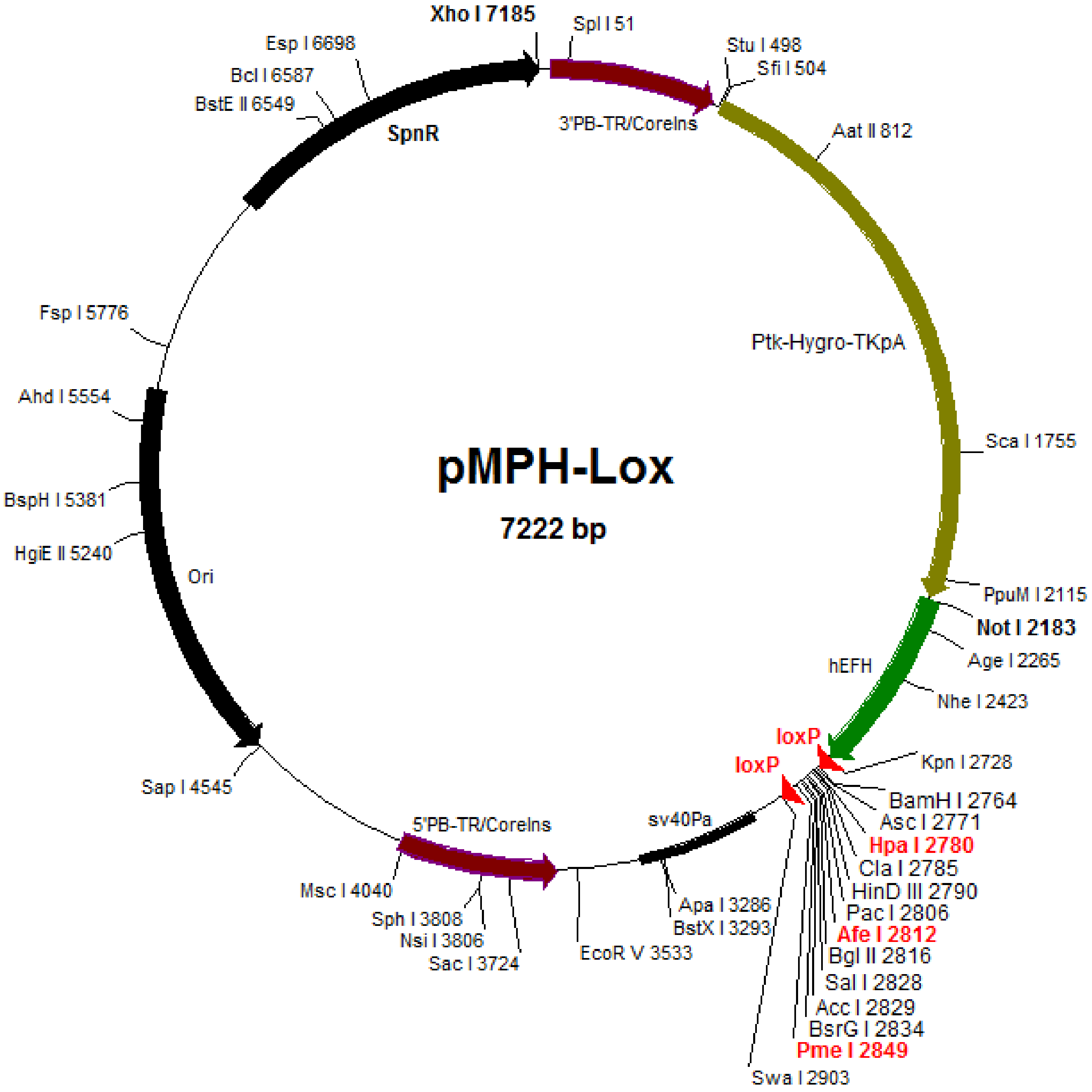
Vector: **pMPH-Lox** (MOLab *piggyBac LoxP* hygromycin-resistance vector)

Antibiotic Selection: **Spectinomycin-resistant**

Creator(s): Ning Wang & Bosi Zhang, Molecular Oncology Lab of The University of Chicago

Date of Construction: April, 2012



pMPH-Lox Vector Sequence

(Spectinomycin-resistant)

```
CTGCAGAACACGCAGCTAGATTAACCCTAGAAAGATAATCATATTGTGACGTACGTTAAAGATAATCATGCGTAAAATTGACGCATG
TGTTTTATCGGTCTGTATATCGAGGTTTATTTATTAATTTGAATAGATATTAAGTTTTATTATATTTACACTTACATACTAATAATA
AATTCAACAAACAATTTATTTATGTTTATTTATTTATTAAAAAAAAACAAAAACTCAAAATTTCTTCTATAAAGTAACAAAACTTTT
ATGAGGGACAGCCCCCCCCCAAAGCCCCCAGGGATGTAATTACGTCCCTCCCCCGCTAGGGGGCAGCAGCGAGCCGCCCGGGGCTCC
GCTCCGGTCCGGCGCTCCCCCCGCATCCCCGAGCCGGCAGCGTGCGGGGACAGCCCGGGCACGGGGAAGGTGGCACGGGATCGCTTT
CCTCTGAACGCTTCTCGCTGCTCTTTGAGCCTGCAGACACCTGGGGGGATACGGGGAAAAGGCCTCCACGGCCAGACTAGactgctt
catccccgtggcccgttgctcgcgtttgctggcggtgtccccggaagaaatatatttgcatgtctttagttctatgatgacacaaac
cccgcccagcgtcttgtcattggcgaattcgaacacgcagatgcagtcggggcggcgcggtcccaggtccacttcgcatattaaggt
gacgcgtgtggcctcgaacaccgagcgaccctgcagcgacccgcttaacagcgtcaacagcgtGCCGCAGATCCCGGGCAATGAGAT
ATGAAAAAGCCTGAACTCACCGCGACGTCTGTCGAGAAGTTTCTGATCGAAAAGTTCGACAGCGTCTCCGACCTGATGCAGCTCTCG
GAGGGCGAAGAATCTCGTGCTTTCAGCTTCGATGTAGGAGGGCGTGGATATGTCCTGCGGGTAAATAGCTGCGCCGATGGTTTCTAC
AAAGATCGTTATGTTTATCGGCACTTTGCATCGGCCGCGCTCCCGATTCCGGAAGTGCTTGACATTGGGGAATTCAGCGAGAGCCTG
ACCTATTGCATCTCCCGCCGTGCACAGGGTGTCACGTTGCAAGACCTGCCTGAAACCGAACTGCCCGCTGTTCTGCAGCCGGTCGCG
GAGGCCATGGATGCGATCGCTGCGGCCGATCTTAGCCAGACGAGCGGGTTCGGCCCATTCGGACCGCAAGGAATCGGTCAATACACT
ACATGGCGTGATTTCATATGCGCGATTGCTGATCCCCATGTGTATCACTGGCAAACTGTGATGGACGACACCGTCAGTGCGTCCGTC
GCGCAGGCTCTCGATGAGCTGATGCTTTGGGCCGAGGACTGCCCCGAAGTCCGGCACCTCGTGCACGCGGATTTCGGCTCCAACAAT
GTCCTGACGGACAATGGCCGCATAACAGCGGTCATTGACTGGAGCGAGGCGATGTTCGGGGATTCCCAATACGAGGTCGCCAACATC
TTCTTCTGGAGGCCGTGGTTGGCTTGTATGGAGCAGCAGACGCGCTACTTCGAGCGGAGGCATCCGGAGCTTGCAGGATCGCCGCGG
CTCCGGGCGTATATGCTCCGCATTGGTCTTGACCAACTCTATCAGAGCTTGGTTGACGGCAATTTCGATGATGCAGCTTGGGCGCAG
GGTCGATGCGACGCAATCGTCCGATCCGGAGCCGGGACTGTCGGGCGTACACAAATCGCCCGCAGAAGCGCGGCCGTCTGGACCGAT
GGCTGTGTAGAAGTACTCGCCGATAGTGGAAACCGACGCCCCAGCACTCGTCCGAGGGCAAAGGAATAGgggagatgggggaggcta
actgaaacacggaaggagacaataccggaaggaacccgcgctatgacggcaataaaaagacagaataaaacgcacgggtgttgggtc
gtttgttcataaacgcggggttcggtcccagggctggcactctgtcgataccccaccgagaccccattggggccaatacgcccgcgt
ttcttccttttccccaccccaccccccaagttcgggtgaaggcccagggctcgcagccaacgtcggggcggcaggccctgccatagc
cactggccccgtgggttagggacggggtcccccatggggaatggtttatggttcgtgggggttattattttgggcgttgcgtggggt
ctggtGCGGCCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCCACAGTCCCCGAGAAGTTGGGGGGAGGGGTCGGCAATTG
AACCGGTGCCTAGAGAAGGTGGCGCGGGGTAAACTGGGAAAGTGATGTCGTGTACTGGCTCCGCCTTTTTCCCGAGGGTGGGGGAGA
ACCGTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTAGCTTCGAGGGG
CTCGCATCTCTCCTTCACGCGCCCGCCGCCCTACCTGAGGCCGCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCCTCCCGCCTGTG
GTGCCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACCGGGCCTTTGTCCGGCGCTCCCTTGGAGCCTAC
CTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCCTGCTTGCTCAACTCTACGTCTTTGTTTCGTTTTCTGTTCTGCGCCGTTACA
GATCCAAGCTGTGACCGGCGCCTACGGTACCATAACTTCGTATAGCATACATTATACGAAGTTATGGATCCGGCGCGCCGTTAACAT
CGATAAGCTTCCGCGGTTAATTAAAGCGCTagatctGAATTCGTCGACTGTACAACGCGTGTTTAAACTTCGAAATAACTTCGTATA
GCATACATTATACGAAGTTATCATATGATTTAAATGATCTAACTAACTAAACTTGTTTATTGCANCTTATAATGGTTACAAATAAAG
CAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTCATCAATGTATCTTATCA
TGTCTGGAATGACTCAAATGATGTCAATTAGTCTATCAGAAGCTCATCTGGTCTCCCTTCCGGGGGACAAGACATCCCTGTTTAATA
TTTAAACAGCAGTGTTCCCAAACTGGGTTCTTATATCCCTTGCTCTGGTCAACCAGGTTGCAGGGTTTCCTGTCCTCACAGGAACGA
AGTCCCTAAAGAAACAGTGGCAGCCAGGTTTAGCCCCGGAATTGACTGGATTCCTTTTTTAGGGCCCATTGGTATGGCTTTTTCCCC
GTATCCCCCCAGGTGTCTGCAGGCTCAAAGAGCAGCGAGAAGCGTTCAGAGGAAAGCGATCCCGTGCCACCTTCCCCGTGCCCGGGC
TGTCCCCGCACGCTGCCGGCTCGGGGATGCGGGGGGAGCGCCGGACCGGAGCGGAGCCCCGGGCGGCTCGCTGCTGCCCCCTAGCGG
GGGAGGGACGTAATTACATCCCTGGGGGCTTTGGGGGGGGGCTGTCCCTGATATCTATAACAAGAAAATATATATATAATAAGTTAT
CACGTAAGTAGAACATGAAATAACAATATAATTATCGTATGAGTTAAATCTTAAAAGTCACGTAAAAGATAATCATGCGTCATTTTG
ACTCACGCGGTCGTTATAGTTCAAAATCAGTGACACTTACCGCATTGACAAGCACGCCTCACGGGAGCTCCAAGCGGCGACTGAGAT
GTCCTAAATGCACAGCGACGGATTCGCGCTATTTAGAAAGAGAGAGCAATATTTCAAGAATGCATGCGTCAATTTTACGCAGACTAT
CTTTCTAGGGTTAATCTAGCTGCATCAGGATCATATCGTCGGGTCTTTTTTCATCGCCCAAGCTGGCGCTATCTGGGCATCGGGGAG
GAAGAAGCCCGTGCCTTTTCCCGCGAGGTTGAAGCGGCATGGAAAGAGTTTGCCGAGGATGACTGCTGCTGCATTGACGTTGAGCGA
AAACGCACGTTTACCATGATGATTCGGGAAGGTGTGGCCATGCACGCCTTTAACGGTGAACTGTTCGTTCAGGCCACCTGGGATACC
AGTTCGTCGCGGCTTTTCCGGACACAGTTCCGGATGGTCAGCCCGAAGCGCATCAGCAACCCGAACAATACCGGCGACAGCCGGAAC
TGCCGTGCCGGTGTGCAGATTAATGACAGCGGTGCGGCGCTGGGATATTACGTCAGCGAGGACGGGTATCCTGGCTGGATGCCGCAG
AAATGGACATGGATACCCCGTGAGTTACCCGGCGGGCGCGCTTGGCGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATC
CGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTG
CGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTT
TGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAA
AGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTA
AAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAA
ACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGAT
ACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCT
CCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAA
GACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGT
```

```
GGTGGCCTAACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTA
GCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTC
AAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGATTATCAA
AAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTT
ACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTCGTTCATCCATAGTTGCCTGACTCCCCGTCGTGTAGATAA
CTACGATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGAGACCCACGCTCACCGGCTCCAGATTTATCAGCAA
TAAACCAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGGTCCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGGAAG
CTAGAGTAAGTAGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTCACGCTCGTCGTTTGGTA
TGGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGTTACATGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTC
CTCCGATCGTTGTCAGAAGTAAGTTGGCCGCAGTGTTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACTGTCATGCCAT
CCGTAAGATGCTTTTCTGTGACTGGTGAGTGTACCAGCCAGGACAGAAATGCCTCGACTTCGCTGCTACCCAAGGTTGCCGGGTGAC
GCACACCGTGGAAACGGATGAAGGCACGAACCCAGTGGACATAAGCCTGTTCGGTTCGTAAGCTGTAATGCAAGTAGCGTATGCGCT
CACGCAACTGGTCCAGAACCTTGACCGAACGCAGCGGTGGTAACGGCGCAGTGGCGGTTTTCATGGCTTGTTATGACTGTTTTTTTG
GGGTACAGTCTATGCCTCGGGCATCCAAGCAGCAAGCGCGTTACGCCGTGGGTCGATGTTTGATGTTATGGAGCAGCAACGATGTTA
CGCAGCAGGGCAGTCGCCCTAAAACAAAGTTAAACATTATGAGGGAAGCGGTGATCGCCGAAGTATCGACTCAACTATCAGAGGTAG
TTGGCGTCATCGAGCGCCATCTCGAACCGACGTTGCTGGCCGTACATTTGTACGGCTCCGCAGTGGATGGCGGCCTGAAGCCACACA
GTGATATTGATTTGCTGGTTACGGTGACCGTAAGGCTTGATGAAACAACGCGGCGAGCTTTGATCAACGACCTTTTGGAAACTTCGG
CTTCCCCTGGAGAGAGCGAGATTCTCCGCGCTGTAGAAGTCACCATTGTTGTGCACGACGACATCATTCCGTGGCGTTATCCAGCTA
AGCGCGAACTGCAATTTGGAGAATGGCAGCGCAATGACATTCTTGCAGGTATCTTCGAGCCAGCCACGATCGACATTGATCTGGCTA
TCTTGCTGACAAAAGCAAGAGAACATAGCGTTGCCTTGGTAGGTCCAGCGGCGGAGGAACTCTTTGATCCGGTTCCTGAACAGGATC
TATTTGAGGCGCTAAATGAAACCTTAACGCTATGGAACTCGCCGCCCGACTGGGCTGGCGATGAGCGAAATGTAGTGCTTACGTTGT
CCCGCATTTGGTACAGCGCAGTAACCGGCAAAATCGCGCCGAAGGATGTCGCTGCCGACTGGGCAATGGAGCGCCTGCCGGCCCAGT
ATCAGCCCGTCATACTTGAAGCTAGACAGGCTTATCTTGGACAAGAAGAAGATCGCTTGGCCTCGCGCGCAGATCAGTTGGAAGAAT
TTGTCCACTACGTGAAAGGCGAGATCACCAAGGTAGTCGGCAAATAACCCTCGAGCCACCCATGACCAAAATCCCTTAACGTGAGTT
A
```

Unique enzymes in pMPH-Lox:

```
BsiW I       C`GTAC,G        51
Spl I        C`GTAC,G        51
Stu I        AGG|CCT         498
Sfi I        GGCCN,NNN`NGGCC 504
Aat II       G,ACGT`C        812
BsmB I       CGTCTC 7/11     853
Sca I        AGT|ACT         1755
Xcm I        CCANNNN,N`NNNNTGG2096
PpuM I       RG`GWC,CY       2115
Not I        GC`GGCC,GC      2183
Mun I        C`AATT,G        2258
Age I        A`CCGG,T        2265
Nhe I        G`CTAG,C        2423
Bsu36 I      CC`TNA,GG       2472
Kas I        G`GCGC,C        2715
Nar I        GG`CG,CC        2716
Ehe I        GGC|GCC         2717
Bbe I        G,GCGC`C        2719
Acc65 I      G`GTAC,C        2724
Asp718       G`GTAC,C        2724
Kpn I        G,GTAC`C        2728
BamH I       G`GATC,C        2764
Asc I        GG`CGCG,CC      2771
Hpa I        GTT|AAC         2780
Cla I        AT`CG,AT        2785
HinD III     A`AGCT,T        2790
Pac I        TTA,AT`TAA      2806
Afe I        AGC|GCT         2812
Eco47 III    AGC|GCT         2812
Bgl II       A`GATC,T        2816
Sal I        G`TCGA,C        2828
Acc I        GT`MK,AC        2829
BsrG I       T`GTAC,A        2834
Pme I        CTTT|AAAC       2849
Swa I        ATTT|AAAT       2903
Bsp120 I     G`GGCC,C        3282
Apa I        G,GGCC`C        3286
BstX I       CCAN,NNNN`NTGG  3293
EcoR V       GAT|ATC         3533
Sac I        G,AGCT`C        3724
Nsi I        A,TGCA`T        3806
Sph I        G,CATG`C        3808
Msc I        TGG|CCA         4040
Sap I        GCTCTTC 8/11    4545
Ear I        CTCTTC 7/10     4545
HgiE II      ACCNNNNNNGGT -1/135240
BspH I       T`CATG,A        5381
Ahd I        GACNN,N`NNGTC   5554
Fsp I        TGC|GCA         5776
BstE II      G`GTNAC,C       6549
Bcl I        T`GATC,A        6587
Blp I        GC`TNA,GC       6698
Esp I        GC`TNA,GC       6698
PaeR7 I      C`TCGA,G        7185
Xho I        C`TCGA,G        7185
Number of enzymes = 55
```

The following enzymes do not cut in pMPH-Lox:

```
Afl II       Avr II       Bbs I        Bbv II       BsaB I
BseR I       Bsp1286 I    Bst1107 I    Eco72 I      Fse I
Nru I        PflM I       Pml I        SnaB I       Spe I
```

pMPH-Lox: sites sorted by name:

```
Aat II       (1)   812
Acc I        (1)   2829
Acc65 I      (1)   2724
Aci I        (92)  315      336      348      370
                   393      555      612      662
                   667      738      762      804
                   928      993      1060     1110
                   1130     1154     1176     1196
                   1373     1411     1421     1534
                   1562     1564     1585     1714
                   1724     1864     1930     1997
                   2070     2182     2186     2287
                   2324     2404     2460     2463
                   2478     2509     2516     2543
                   2796     2798     3400     3423
                   3445     3457     3478     3662
                   3695     3729     3937     3950
                   4099     4206     4211     4259
                   4296     4351     4454     4510
                   4520     4544     4587     4594
                   4615     4706     4734     4861
                   4880     5001     5111     5246
                   5255     5617     5708     5899
                   5945     6212     6232     6400
                   6497     6509     6576     6639
                   6835     6838     6916     6963
Afe I        (1)   2812
Afl III      (3)   699      2840     4661
Age I        (1)   2265
Aha II       (4)   809      1777     2716     6443
Ahd I        (1)   5554
Alu I        (33)  16       865      897      939
                   1324     1549     1614     1643
                   2417     2423     2427     2565
                   2706     2792     3088     3722
                   3848     3891     4326     4421
```

		4485	4603	4829	4919
		4965	5222	5743	5843
		5906	6153	6583	6697
		7069			
Alw I	(18)	434	762	1245	1563
		1672	2694	2760	2771
		3360	3864	5223	5309
		5309	5406	5407	5871
		6848	6877		
AlwN I	(2)	2079	5077		
Apa I	(1)	3286			
ApaL I	(4)	1065	1367	4975	6664
Apo I	(7)	175	233	635	1028
		2822	2972	7132	
Asc I	(1)	2771			
Ase I	(5)	122	4197	4432	4491
		5726			
Asp718	(1)	2724			
Ava I	(11)	339	377	403	770
		2232	2334	3388	3414
		3452	6281	7185	
Ava II	(12)	355	669	676	1193
		1734	1939	2115	3437
		5692	5914	6188	6829
BamH I	(1)	2764			
Ban I	(8)	1359	2193	2268	2524
		2715	2724	4405	5502
Ban II	(6)	347	2053	2439	3286
		3452	3724		
Bbe I	(1)	2719			
Bbv I	(21)	25	337	340	398
		742	874	1132	1525
		1652	2067	3252	3351
		5080	5083	5289	5983
		6221	6306	6350	6366
		6738			
Bcl I	(1)	6587			
Bcn I	(20)	341	342	405	406
		565	772	773	1572
		1688	2580	3108	3257
		3390	3391	3454	3455
		4294	5042	5738	6085
Bfa I	(17)	17	28	318	513
		2273	2424	2550	2612
		2814	3007	3475	3834
		3845	5156	5409	5744
		7070			
Bgl I	(3)	504	5674	7021	
Bgl II	(1)	2816			
Blp I	(1)	6698			
Bpm I	(4)	1453	1507	5624	6641
Bsa I	(4)	1967	2568	3102	5615
BsaA I	(3)	3571	3629	7146	
BsaH I	(4)	809	1777	2716	6443
BsaJ I	(45)	289	290	339	340
		403	476	502	529
		562	672	770	1137
		1338	1493	1562	1793
		1942	1943	2045	2046
		2098	2121	2335	2599
		2796	3106	3254	3315
		3388	3451	3452	3501
		3502	3969	4080	4400
		4821	6074	6097	6280
		6311	6618	6682	6821
		7163			
BsaW I	(14)	352	1006	1543	1679
		1852	2190	2265	3439
		4107	4119	4867	5014
		5845	6855		
Bsg I	(2)	2383	4211		
BsiC I	(2)	639	2855		
BsiE I	(11)	993	1128	1149	1158
		1728	2186	3666	4577
		5001	5924	6770	
BsiHKA I	(5)	1069	1371	3724	4979
		6668			
BsiW I	(1)	51			
Bsm I	(2)	3002	3806		
BsmA I	(6)	852	1839	1968	2569
		3101	5616		
BsmB I	(1)	853			
BsmF I	(16)	281	291	410	545
		655	1702	1925	2101
		2122	2214	3124	3207
		3381	3500	3510	6945
BsoF I	(67)	14	326	329	336
		387	454	663	731
		762	863	940	993
		1121	1152	1155	1411
		1514	1562	1565	1641
		1725	2056	2071	2183
		2186	2404	2463	2478
		2509	3241	3340	3407
		3458	3465	3468	3730
		3849	3951	3982	3985
		4100	4212	4259	4486
		4567	4585	4588	4706
		4861	5004	5069	5072
		5278	5606	5945	5972
		6067	6210	6295	6339
		6355	6510	6577	6727
		6836	6916	7013	
Bsp120 I	(1)	3282			
BspH I	(1)	5381			
BspM I	(2)	1098	6736		
BspM II	(5)	1006	1543	1679	4107
		4119			
Bsr I	(21)	1270	1435	2095	2300
		2321	3159	3269	4090
		4462	5068	5081	5195
		5601	5719	5762	6029
		6124	6189	6927	7023
		7045			
BsrB I	(7)	350	1176	1534	2188
		3445	4353	4594	
BsrD I	(5)	782	5615	5789	6738
		7031			
BsrG I	(1)	2834			
BssH II	(3)	2771	4300	7113	
BssS I	(3)	885	1364	4834	
BstB I	(2)	639	2855		
BstE II	(1)	6549			
BstN I	(17)	291	477	674	1944
		2047	3187	3245	3317
		3503	4081	4248	4401
		4689	4810	4823	6043
		6620			
BstU I	(38)	545	667	701	806
		995	1130	1241	1307
		1373	1522	1564	1724
		1866	1930	1999	2287
		2456	2501	2773	2798
		2842	3662	3768	3939
		4099	4302	4508	4510
		4708	5289	5619	6303
		6576	6641	6704	6997
		7113	7115		
BstX I	(1)	3293			
BstY I	(9)	766	2698	2764	2816
		5302	5313	5399	5411
		6870			
Bsu36 I	(1)	2472			
Cac8 I	(47)	333	384	391	467
		543	553	759	1110
		1311	1371	1551	1714
		1950	1997	2053	2075
		2425	2439	2460	2623
		2651	2773	3328	3404
		3411	3462	3709	3806
		3893	4047	4298	4302
		4454	4483	4592	4678
		4715	5275	5666	6299
		6476	6581	6761	6930
		7036	7040	7115	
Cfr10 I	(12)	382	1123	2265	2489
		2621	2712	3409	4160
		4184	5634	6985	7038
Cla I	(1)	2785			
Csp6 I	(11)	52	1701	1754	2315
		2725	2835	6035	6268
		6481	6489	6972	
Dde I	(9)	1163	2472	2566	2617
		3736	4936	5345	5511
		6698			
Dpn I	(34)	429	768	830	963
		1148	1161	1251	1558
		1678	2700	2766	2818
		2909	3366	3859	5229
		5304	5315	5323	5401
		5413	5518	5859	5877
		5923	6406	6589	6769
		6779	6854	6872	7100
		7121	7159		
DpnII	(34)	427	766	828	961
		1146	1159	1249	1556
		1676	2698	2764	2816
		2907	3364	3857	5227
		5302	5313	5321	5399
		5411	5516	5857	5875

		5921	6404	6587	6767
		6777	6852	6870	7098
		7119	7157		
Dra I	(6)	2561	2849	2903	3136
		5420	5439		
Dra III	(5)	1073	1366	6098	6526
		7146			
Drd I	(4)	1289	1670	3740	4769
Dsa I	(11)	502	529	1137	1493
		1562	2098	2121	2796
		6097	6311	6682	
Eae I	(10)	505	990	1155	1408
		1725	2183	4038	4500
		5942	6476		
Eag I	(4)	990	1155	1725	2183
Ear I	(1)	4545			
Eco47 III	(1)	2812			
Eco57 I	(3)	2438	5208	6534	
EcoN I	(3)	2276	2471	3277	
EcoO109 I	(3)	2076	2115	3282	
EcoR I	(3)	635	1028	2822	
EcoR II	(17)	289	475	672	1942
		2045	3185	3243	3315
		3501	4079	4246	4399
		4687	4808	4821	6041
		6618			
EcoR V	(1)	3533			
Ehe I	(1)	2717			
Esp I	(1)	6698			
Fnu4H I	(67)	14	326	329	336
		387	454	663	731
		762	863	940	993
		1121	1152	1155	1411
		1514	1562	1565	1641
		1725	2056	2071	2183
		2186	2404	2463	2478
		2509	3241	3340	3407
		3458	3465	3468	3730
		3849	3951	3982	3985
		4100	4212	4259	4486
		4567	4585	4588	4706
		4861	5004	5069	5072
		5278	5606	5945	5972
		6067	6210	6295	6339
		6355	6510	6577	6727
		6836	6916	7013	
Fok I	(19)	307	359	510	1154
		1527	2468	3105	3432
		3484	3986	4135	4267
		5520	5701	5988	6120
		6273	6517	7018	
Fsp I	(1)	5776			
Gdi II	(13)	506	989	991	1154
		1156	1407	1724	1726
		2182	2184	4501	5941
		6475			
Gsu I	(4)	1452	1506	5625	6640
Hae I	(9)	498	708	1136	4040
		4076	4676	4687	5139
		7108			
Hae II	(12)	364	2596	2719	2814
		3435	3898	4217	4539
		4909	6456	6886	7035
Hae III	(34)	498	507	534	708
		992	1136	1157	1185
		1337	1410	1492	1727
		1987	2044	2077	2095
		2185	2477	2582	3284
		4040	4076	4502	4676
		4687	4705	5139	5597
		5677	5944	6478	6512
		7042	7108		
Hga I	(16)	89	609	706	738
		836	1288	1527	1672
		1784	2529	3635	3798
		4771	5349	6097	6433
HgiA I	(5)	1069	1371	3724	4979
		6668			
HgiE II	(1)	5240			
Hha I	(50)	363	667	944	997
		1241	1309	1524	1651
		1724	1868	2215	2287
		2458	2595	2690	2718
		2773	2775	2813	3434
		3770	3897	4140	4216
		4302	4304	4445	4510
		4538	4571	4841	4908
		5008	5182	5291	5684
		5777	6176	6226	6303
		6455	6643	6704	6731
		6885	6979	6999	7034
		7115	7117		
HinC II	(5)	752	1621	2780	2830
		3183			
Hind II	(5)	752	1621	2780	2830
		3183			
HinD III	(1)	2790			
Hinf I	(18)	881	1003	1203	1454
		2496	2615	3057	3269
		3655	3763	4024	4496
		4561	4636	5032	5549
		6420	6633		
HinI I	(4)	809	1777	2716	6443
HinP I	(50)	361	665	942	995
		1239	1307	1522	1649
		1722	1866	2213	2285
		2456	2593	2688	2716
		2771	2773	2811	3432
		3768	3895	4138	4214
		4300	4302	4443	4508
		4536	4569	4839	4906
		5006	5180	5289	5682
		5775	6174	6224	6301
		6453	6641	6702	6729
		6883	6977	6997	7032
		7113	7115		
Hpa I	(1)	2780			
Hpa II	(49)	340	353	358	383
		404	564	771	1007
		1124	1357	1544	1570
		1680	1686	1853	2191
		2266	2490	2578	2590
		2622	2713	2768	3106
		3256	3389	3410	3435
		3440	3453	4108	4120
		4161	4171	4185	4293
		4379	4868	5015	5041
		5231	5635	5669	5736
		5846	6083	6856	6986
		7039			
Hph I	(12)	706	794	2048	4069
		5398	5625	6039	6097
		6413	6560	6646	7153
Kas I	(1)	2715			
Kpn I	(1)	2728			
Mae I	(17)	17	28	318	513
		2273	2424	2550	2612
		2814	3007	3475	3834
		3845	5156	5409	5744
		7070			
Mae II	(20)	50	54	304	809
		1079	2062	2380	2663
		3489	3570	3628	3993
		4010	4227	5364	5780
		6469	6955	7145	7214
Mae III	(26)	46	248	695	1075
		2692	2708	2946	3624
		3684	4287	5017	5080
		5196	5479	5810	5868
		6021	6086	6217	6304
		6348	6543	6549	6651
		6981	7219		
Mbo I	(34)	427	766	828	961
		1146	1159	1249	1556
		1676	2698	2764	2816
		2907	3364	3857	5227
		5302	5313	5321	5399
		5411	5516	5857	5875
		5921	6404	6587	6767
		6777	6852	6870	7098
		7119	7157		
Mbo II	(14)	231	578	889	1472
		1475	1997	3928	4533
		5322	5395	6745	7104
		7107	7140		
Mlu I	(2)	699	2840		
Mme I	(5)	875	1409	4875	5059
		7107			
Mnl I	(48)	103	258	318	446
		508	718	865	902
		1126	1333	1372	1432
		1459	1482	1530	1788
		1815	2241	2330	2425
		2467	2521	2537	3216
		3349	3477	3721	3907
		3934	3964	4228	4510
		4559	4769	4842	5093
		5493	5574	5720	5926
		6065	6289	6386	6426
		6834	6873	7118	7193

```
Msc I       (1)   4040
Mse I       (32)  22       57       122      138
                  212      691      742      2560
                  2779     2802     2806     2848
                  2902     3128     3135     3612
                  3619     3840     4053     4197
                  4432     4491     5367     5419
                  5424     5438     5491     5726
                  5765     6382     6898     7211
Msl I       (5)   528      3291     5806     5965
                  6661
Msp I       (49)  340      353      358      383
                  404      564      771      1007
                  1124     1357     1544     1570
                  1680     1686     1853     2191
                  2266     2490     2578     2590
                  2622     2713     2768     3106
                  3256     3389     3410     3435
                  3440     3453     4108     4120
                  4161     4171     4185     4293
                  4379     4868     5015     5041
                  5231     5635     5669     5736
                  5846     6083     6856     6986
                  7039
MspA1 I     (11)  1112     1421     1564     2417
                  2798     4206     4485     5003
                  5248     6212     6835
Mun I       (1)   2258
Nae I       (4)   384      2623     3411     7040
Nar I       (1)   2716
Nci I       (20)  340      341      404      405
                  564      771      772      1571
                  1687     2579     3107     3256
                  3389     3390     3453     3454
                  4293     5041     5737     6084
Nco I       (2)   1137     2121
Nde I       (2)   1235     2895
NgoM I      (4)   382      2621     3409     7038
Nhe I       (1)   2423
Nla III     (24)  71       88       585      1141
                  1224     1259     2125     3048
                  3585     3645     3808     3957
                  4021     4045     4275     4319
                  4665     5385     5876     5886
                  5964     6000     6243     7199
Nla IV      (31)  346      671      1361     1384
                  1568     1684     1861     1941
                  1986     2096     2116     2117
                  2195     2270     2322     2526
                  2605     2717     2726     2766
                  3284     3449     4407     4693
                  4732     5504     5598     5639
                  5850     6495     6860
Not I       (1)   2183
Nsi I       (1)   3806
Nsp7524 I   (4)   84       581      3804     4661
NspB II     (11)  1112     1421     1564     2417
                  2798     4206     4485     5003
                  5248     6212     6835
NspH I      (4)   88       585      3808     4665
Pac I       (1)   2806
PaeR7 I     (1)   7185
Pal I       (34)  498      507      534      708
                  992      1136     1157     1185
                  1337     1410     1492     1727
                  1987     2044     2077     2095
                  2185     2477     2582     3284
                  4040     4076     4502     4676
                  4687     4705     5139     5597
                  5677     5944     6478     6512
                  7042     7108
Ple I       (2)   2504     5040
Pme I       (1)   2849
PpuM I      (1)   2115
Psp1406 I   (2)   2380     5780
PspA I      (5)   339      403      770      3388
                  3452
Pst I       (5)   6        471      732      1122
                  3328
Pvu I       (3)   1149     5924     6770
Pvu II      (2)   2417     4485
Rsa I       (11)  53       1702     1755     2316
                  2726     2836     6036     6269
                  6482     6490     6973
Rsr II      (3)   355      1193     3437
Sac I       (1)   3724
Sac II      (2)   1565     2799
Sal I       (1)   2828
Sap I       (1)   4545
Sau3A I     (34)  427      766      828      961
                  1146     1159     1249     1556
                  1676     2698     2764     2816
                  2907     3364     3857     5227
                  5302     5313     5321     5399
                  5411     5516     5857     5875
                  5921     6404     6587     6767
                  6777     6852     6870     7098
                  7119     7157
Sau96 I     (25)  355      533      669      676
                  1184     1193     1335     1734
                  1939     1985     2043     2076
                  2094     2115     2580     3282
                  3283     3437     5596     5675
                  5692     5914     6188     6829
                  7041
Sca I       (1)   1755
ScrF I      (37)  291      340      341      404
                  405      477      564      674
                  771      772      1571     1687
                  1944     2047     2579     3107
                  3187     3245     3256     3317
                  3389     3390     3453     3454
                  3503     4081     4248     4293
                  4401     4689     4810     4823
                  5041     5737     6043     6084
                  6620
Sec I       (45)  289      290      339      340
                  403      476      502      529
                  562      672      770      1137
                  1338     1493     1562     1793
                  1942     1943     2045     2046
                  2098     2121     2335     2599
                  2796     3106     3254     3315
                  3388     3451     3452     3501
                  3502     3969     4080     4400
                  4821     6074     6097     6280
                  6311     6618     6682     6821
                  7163
SfaN I      (21)  380      641      850      994
                  1061     1133     1318     1548
                  1628     1650     2449     2973
                  3411     3859     3914     4148
                  4246     4757     5809     6002
                  6294
Sfc I       (9)   2        467      728      1118
                  3324     4926     5117     5795
                  6644
Sfi I       (1)   504
Sma I       (5)   341      405      772      3390
                  3454
Sph I       (1)   3808
Spl I       (1)   51
Srf I       (2)   405      3390
Ssp I       (2)   3132     3792
Stu I       (1)   498
Sty I       (6)   1137     2121     2599     6074
                  6821     7163
Swa I       (1)   2903
Taq I       (26)  108      639      711      816
                  831      840      900      1317
                  1530     1632     1657     1960
                  2430     2572     2785     2829
                  2855     4761     6058     6318
                  6418     6449     6461     6755
                  6770     7186
Tfi I       (10)  881      1003     1203     1454
                  3269     3763     4024     4496
                  4636     6633
Tsp45 I     (11)  46       695      1075     2708
                  3624     3684     5810     6021
                  6086     6549     6651
Tth111 I    (3)   845      1289     2113
Tth111 II   (9)   198      1005     2639     3719
                  5250     5259     5289     6306
                  6313
Vsp I       (5)   122      4197     4432     4491
                  5726
Xcm I       (1)   2096
Xho I       (1)   7185
Xho II      (9)   766      2698     2764     2816
                  5302     5313     5399     5411
                  6870
Xma I       (5)   339      403      770      3388
                  3452
Xma III     (4)   990      1155     1725     2183
```

Site usage in pMPH-Lox:

```
Aat II     G,ACGT`C        1     Acc I      GT`MK,AC        1
Acc65 I    G`GTAC,C        1     Aci I      C`CG,C          92
```

<table>
<tr><td>Afe I</td><td>AGC|GCT</td><td>1</td><td>Afl II</td><td>C`TTAA,G</td><td>-</td></tr>
<tr><td>Afl III</td><td>A`CRYG,T</td><td>3</td><td>Age I</td><td>A`CCGG,T</td><td>1</td></tr>
<tr><td>Aha II</td><td>GR`CG,YC</td><td>4</td><td>Ahd I</td><td>GACNN,N`NNGTC</td><td>1</td></tr>
<tr><td>Alu I</td><td>AG|CT</td><td>33</td><td>Alw I</td><td>GGATC 8/9</td><td>18</td></tr>
<tr><td>AlwN I</td><td>CAG,NNN`CTG</td><td>2</td><td>Apa I</td><td>G,GGCC`C</td><td>1</td></tr>
<tr><td>ApaL I</td><td>G`TGCA,C</td><td>4</td><td>Apo I</td><td>R`AATT,Y</td><td>7</td></tr>
<tr><td>Asc I</td><td>GG`CGCG,CC</td><td>1</td><td>Ase I</td><td>AT`TA,AT</td><td>5</td></tr>
<tr><td>Asp718</td><td>G`GTAC,C</td><td>1</td><td>Ava I</td><td>C`YCGR,G</td><td>11</td></tr>
<tr><td>Ava II</td><td>G`GWC,C</td><td>12</td><td>Avr II</td><td>C`CTAG,G</td><td>-</td></tr>
<tr><td>BamH I</td><td>G`GATC,C</td><td>1</td><td>Ban I</td><td>G`GYRC,C</td><td>8</td></tr>
<tr><td>Ban II</td><td>G,RGCY`C</td><td>6</td><td>Bbe I</td><td>G,GCGC`C</td><td>1</td></tr>
<tr><td>Bbs I</td><td>GAAGAC 8/12</td><td>-</td><td>Bbv I</td><td>GCAGC 13/17</td><td>21</td></tr>
<tr><td>Bbv II</td><td>GAAGAC 7/11</td><td>-</td><td>Bcl I</td><td>T`GATC,A</td><td>1</td></tr>
<tr><td>Bcn I</td><td>CC,S`GG</td><td>20</td><td>Bfa I</td><td>C`TA,G</td><td>17</td></tr>
<tr><td>Bgl I</td><td>GCCN,NNN`NGGC</td><td>3</td><td>Bgl II</td><td>A`GATC,T</td><td>1</td></tr>
<tr><td>Blp I</td><td>GC`TNA,GC</td><td>1</td><td>Bpm I</td><td>CTGGAG 22/20</td><td>4</td></tr>
<tr><td>Bsa I</td><td>GGTCTC 7/11</td><td>4</td><td>BsaA I</td><td>YAC|GTR</td><td>3</td></tr>
<tr><td>BsaB I</td><td>GATNN|NNATC</td><td>-</td><td>BsaH I</td><td>GR`CG,YC</td><td>4</td></tr>
<tr><td>BsaJ I</td><td>C`CNNG,G</td><td>45</td><td>BsaW I</td><td>W`CCGG,W</td><td>14</td></tr>
<tr><td>BseR I</td><td>GAGGAG 16/14</td><td>-</td><td>Bsg I</td><td>GTGCAG 22/20</td><td>2</td></tr>
<tr><td>BsiC I</td><td>TT`CG,AA</td><td>2</td><td>BsiE I</td><td>CG,RY`CG</td><td>11</td></tr>
<tr><td>BsiHKA I</td><td>G,WGCW`C</td><td>5</td><td>BsiW I</td><td>C`GTAC,G</td><td>1</td></tr>
<tr><td>Bsm I</td><td>GAATG,C 7</td><td>2</td><td>BsmA I</td><td>GTCTC`/9</td><td>6</td></tr>
<tr><td>BsmB I</td><td>CGTCTC 7/11</td><td>1</td><td>BsmF I</td><td>GGGAC 15/19</td><td>16</td></tr>
<tr><td>BsoF I</td><td>GC`N,GC</td><td>67</td><td>Bsp120 I</td><td>G`GGCC,C</td><td>1</td></tr>
<tr><td>Bsp1286 I</td><td>G,DGCH`C</td><td>-</td><td>BspH I</td><td>T`CATG,A</td><td>1</td></tr>
<tr><td>BspM I</td><td>ACCTGC 10/14</td><td>2</td><td>BspM II</td><td>T`CCGG,A</td><td>5</td></tr>
<tr><td>Bsr I</td><td>ACT,GG`</td><td>21</td><td>BsrB I</td><td>GAG|CGG</td><td>7</td></tr>
<tr><td>BsrD I</td><td>GCAATG, 8</td><td>5</td><td>BsrG I</td><td>T`GTAC,A</td><td>1</td></tr>
<tr><td>BssH II</td><td>G`CGCG,C</td><td>3</td><td>BssS I</td><td>C`TCGT,G</td><td>3</td></tr>
<tr><td>Bst1107 I</td><td>GTA|TAC</td><td>-</td><td>BstB I</td><td>TT`CG,AA</td><td>2</td></tr>
<tr><td>BstE II</td><td>G`GTNAC,C</td><td>1</td><td>BstN I</td><td>CC`W,GG</td><td>17</td></tr>
<tr><td>BstU I</td><td>CG|CG</td><td>38</td><td>BstX I</td><td>CCAN,NNNN`NTGG</td><td>1</td></tr>
<tr><td>BstY I</td><td>R`GATC,Y</td><td>9</td><td>Bsu36 I</td><td>CC`TNA,GG</td><td>1</td></tr>
<tr><td>Cac8 I</td><td>GCN|NGC</td><td>47</td><td>Cfr10 I</td><td>R`CCGG,Y</td><td>12</td></tr>
<tr><td>Cla I</td><td>AT`CG,AT</td><td>1</td><td>Csp6 I</td><td>G`TA,C</td><td>11</td></tr>
<tr><td>Dde I</td><td>C`TNA,G</td><td>9</td><td>Dpn I</td><td>GA|TC</td><td>34</td></tr>
<tr><td>DpnII</td><td>`GATC,</td><td>34</td><td>Dra I</td><td>TTT|AAA</td><td>6</td></tr>
<tr><td>Dra III</td><td>CAC,NNN`GTG</td><td>5</td><td>Drd I</td><td>GACNN,NN`NNGTC</td><td>4</td></tr>
<tr><td>Dsa I</td><td>C`CRYG,G</td><td>11</td><td>Eae I</td><td>Y`GGCC,R</td><td>10</td></tr>
<tr><td>Eag I</td><td>C`GGCC,G</td><td>4</td><td>Ear I</td><td>CTCTTC 7/10</td><td>1</td></tr>
<tr><td>Eco47 III</td><td>AGC|GCT</td><td>1</td><td>Eco57 I</td><td>CTGAAG 21/19</td><td>3</td></tr>
<tr><td>Eco72 I</td><td>CAC|GTG</td><td>-</td><td>EcoN I</td><td>CCTNN`N,NNAGG</td><td>3</td></tr>
<tr><td>EcoO109 I</td><td>RG`GNC,CY</td><td>3</td><td>EcoR I</td><td>G`AATT,C</td><td>3</td></tr>
<tr><td>EcoR II</td><td>`CCWGG,</td><td>17</td><td>EcoR V</td><td>GAT|ATC</td><td>1</td></tr>
<tr><td>Ehe I</td><td>GGC|GCC</td><td>1</td><td>Esp I</td><td>GC`TNA,GC</td><td>1</td></tr>
<tr><td>Fnu4H I</td><td>GC`N,GC</td><td>67</td><td>Fok I</td><td>GGATG 14/18</td><td>19</td></tr>
<tr><td>Fse I</td><td>GG,CCGG`CC</td><td>-</td><td>Fsp I</td><td>TGC|GCA</td><td>1</td></tr>
<tr><td>Gdi II</td><td>`YGGC,CG</td><td>13</td><td>Gsu I</td><td>CTGGAG 21/19</td><td>4</td></tr>
<tr><td>Hae I</td><td>WGG|CCW</td><td>9</td><td>Hae II</td><td>R,GCGC`Y</td><td>12</td></tr>
</table>

<table>
<tr><td>Hae III</td><td>GG|CC</td><td>34</td><td>Hga I</td><td>GACGC 9/14</td><td>16</td></tr>
<tr><td>HgiA I</td><td>G,WGCW`C</td><td>5</td><td>HgiE II</td><td>ACCNNNNNNGGT -1/13</td><td>1</td></tr>
<tr><td>Hha I</td><td>G,CG`C</td><td>50</td><td>HinC II</td><td>GTY|RAC</td><td>5</td></tr>
<tr><td>Hind II</td><td>GTY|RAC</td><td>5</td><td>HinD III</td><td>A`AGCT,T</td><td>1</td></tr>
<tr><td>Hinf I</td><td>G`ANT,C</td><td>18</td><td>HinI I</td><td>GR`CG,YC</td><td>4</td></tr>
<tr><td>HinP I</td><td>G`CG,C</td><td>50</td><td>Hpa I</td><td>GTT|AAC</td><td>1</td></tr>
<tr><td>Hpa II</td><td>C`CG,G</td><td>49</td><td>Hph I</td><td>GGTGA 12/11</td><td>12</td></tr>
<tr><td>Kas I</td><td>G`GCGC,C</td><td>1</td><td>Kpn I</td><td>G,GTAC`C</td><td>1</td></tr>
<tr><td>Mae I</td><td>C`TA,G</td><td>17</td><td>Mae II</td><td>A`CG,T</td><td>20</td></tr>
<tr><td>Mae III</td><td>`GTNAC,</td><td>26</td><td>Mbo I</td><td>`GATC,</td><td>34</td></tr>
<tr><td>Mbo II</td><td>GAAGA 12/11</td><td>14</td><td>Mlu I</td><td>A`CGCG,T</td><td>2</td></tr>
<tr><td>Mme I</td><td>TCCRAC 25/23</td><td>5</td><td>Mnl I</td><td>CCTC 10/10</td><td>48</td></tr>
<tr><td>Msc I</td><td>TGG|CCA</td><td>1</td><td>Mse I</td><td>T`TA,A</td><td>32</td></tr>
<tr><td>Msl I</td><td>CAYNN|NNRTG</td><td>5</td><td>Msp I</td><td>C`CG,G</td><td>49</td></tr>
<tr><td>MspA1 I</td><td>CMG|CKG</td><td>11</td><td>Mun I</td><td>C`AATT,G</td><td>1</td></tr>
<tr><td>Nae I</td><td>GCC|GGC</td><td>4</td><td>Nar I</td><td>GG`CG,CC</td><td>1</td></tr>
<tr><td>Nci I</td><td>CC`S,GG</td><td>20</td><td>Nco I</td><td>C`CATG,G</td><td>2</td></tr>
<tr><td>Nde I</td><td>CA`TA,TG</td><td>2</td><td>NgoM I</td><td>G`CCGG,C</td><td>4</td></tr>
<tr><td>Nhe I</td><td>G`CTAG,C</td><td>1</td><td>Nla III</td><td>,CATG`</td><td>24</td></tr>
<tr><td>Nla IV</td><td>GGN|NCC</td><td>31</td><td>Not I</td><td>GC`GGCC,GC</td><td>1</td></tr>
<tr><td>Nru I</td><td>TCG|CGA</td><td>-</td><td>Nsi I</td><td>A,TGCA`T</td><td>1</td></tr>
<tr><td>Nsp7524 I</td><td>R`CATG,Y</td><td>4</td><td>NspB II</td><td>CMG|CKG</td><td>11</td></tr>
<tr><td>NspH I</td><td>R,CATG`Y</td><td>4</td><td>Pac I</td><td>TTA,AT`TAA</td><td>1</td></tr>
<tr><td>PaeR7 I</td><td>C`TCGA,G</td><td>1</td><td>Pal I</td><td>GG|CC</td><td>34</td></tr>
<tr><td>PflM I</td><td>CCAN,NNN`NTGG</td><td>-</td><td>Ple I</td><td>GAGTC 9/10</td><td>2</td></tr>
<tr><td>Pme I</td><td>CTTT|AAAC</td><td>1</td><td>Pml I</td><td>CAC|GTG</td><td>-</td></tr>
<tr><td>PpuM I</td><td>RG`GWC,CY</td><td>1</td><td>Psp1406 I</td><td>AA`CG,TT</td><td>2</td></tr>
<tr><td>PspA I</td><td>C`CCGG,G</td><td>5</td><td>Pst I</td><td>C,TGCA`G</td><td>5</td></tr>
<tr><td>Pvu I</td><td>CG,AT`CG</td><td>3</td><td>Pvu II</td><td>CAG|CTG</td><td>2</td></tr>
<tr><td>Rsa I</td><td>GT|AC</td><td>11</td><td>Rsr II</td><td>CG`GWC,CG</td><td>3</td></tr>
<tr><td>Sac I</td><td>G,AGCT`C</td><td>1</td><td>Sac II</td><td>CC,GC`GG</td><td>2</td></tr>
<tr><td>Sal I</td><td>G`TCGA,C</td><td>1</td><td>Sap I</td><td>GCTCTTC 8/11</td><td>1</td></tr>
<tr><td>Sau3A I</td><td>`GATC,</td><td>34</td><td>Sau96 I</td><td>G`GNC,C</td><td>25</td></tr>
<tr><td>Sca I</td><td>AGT|ACT</td><td>1</td><td>ScrF I</td><td>CC`N,GG</td><td>37</td></tr>
<tr><td>Sec I</td><td>C`CNNG,G</td><td>45</td><td>SfaN I</td><td>GCATC 9/13</td><td>21</td></tr>
<tr><td>Sfc I</td><td>C`TRYA,G</td><td>9</td><td>Sfi I</td><td>GGCCN,NNN`NGGCC</td><td>1</td></tr>
<tr><td>Sma I</td><td>CCC|GGG</td><td>5</td><td>SnaB I</td><td>TAC|GTA</td><td>-</td></tr>
<tr><td>Spe I</td><td>A`CTAG,T</td><td>-</td><td>Sph I</td><td>G,CATG`C</td><td>1</td></tr>
<tr><td>Spl I</td><td>C`GTAC,G</td><td>1</td><td>Srf I</td><td>GCCC|GGGC</td><td>2</td></tr>
<tr><td>Ssp I</td><td>AAT|ATT</td><td>2</td><td>Stu I</td><td>AGG|CCT</td><td>1</td></tr>
<tr><td>Sty I</td><td>C`CWWG,G</td><td>6</td><td>Swa I</td><td>ATTT|AAAT</td><td>1</td></tr>
<tr><td>Taq I</td><td>T`CG,A</td><td>26</td><td>Tfi I</td><td>G`AWT,C</td><td>10</td></tr>
<tr><td>Tsp45 I</td><td>`GTSAC,</td><td>11</td><td>Tth111 I</td><td>GACN`N,NGTC</td><td>3</td></tr>
<tr><td>Tth111 II</td><td>CAARCA 16/14</td><td>9</td><td>Vsp I</td><td>AT`TA,AT</td><td>5</td></tr>
<tr><td>Xba I</td><td>T`CTAG,A</td><td>-</td><td>Xca I</td><td>GTA|TAC</td><td>-</td></tr>
<tr><td>Xcm I</td><td>CCANNNNN,N`NNNNTGG</td><td>1</td><td>Xho I</td><td>C`TCGA,G</td><td>1</td></tr>
<tr><td>Xho II</td><td>R`GATC,Y</td><td>9</td><td>Xma I</td><td>C`CCGG,G</td><td>5</td></tr>
<tr><td>Xma III</td><td>C`GGCC,G</td><td>4</td><td>Xmn I</td><td>GAANN|NNTTC</td><td>-</td></tr>
</table>