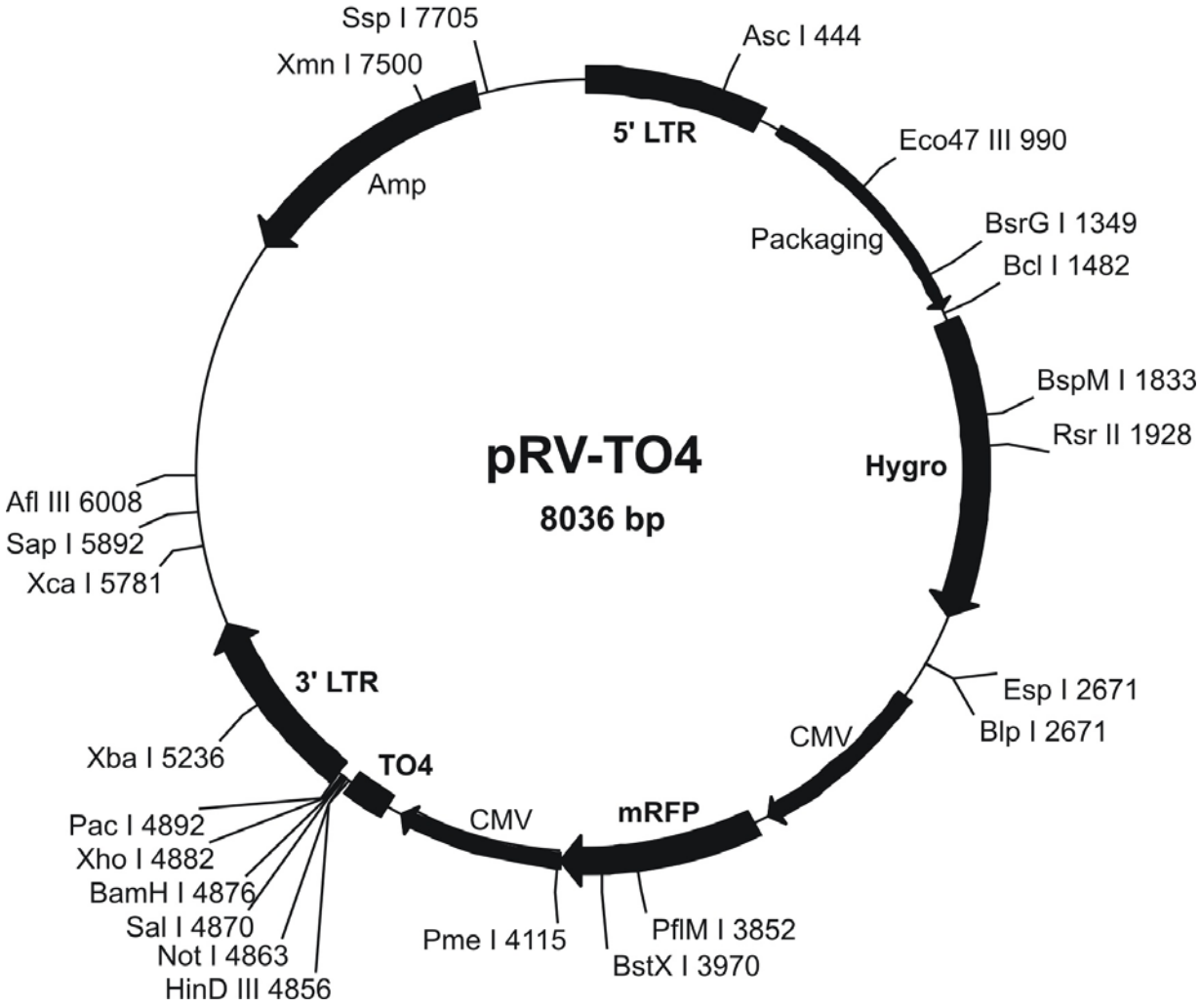
Name of Vector: pRV-TO4
Antibiotic Selection: Amp
Created by: Wei Jiang and Hong Yin
(He Lab @ The University of Chicago)
Date of Creation: February 2005



pRV-TO4 Full-length Sequence

TTTGAAAGAC CCCACCCGTA GGTGGCAAGC TAGCTTAAGT AACGCCACTT TGCAAGGCAT GGAAAAATAC
ATAACTGAGA ATAGAAAAGT TCAGATCAAG GTCAGGAACA AAGAAACAGC TGAATACCAA ACAGGATATC
TGTGGTAAGC GGTTCCTGCC CCGGCTCAGG GCCAAGAACA GATGAGACAG CTGAGTGATG GGCCAAACAG
GATATCTGTG GTAAGCAGTT CCTGCCCCGG CTCGGGGCCA AGAACAGATG GTCCCCAGAT GCGGTCCAGC
CCTCAGCAGT TTCTAGTGAA TCATCAGATG TTTCCAGGGT GCCCCAAGGA CCTGAAAATG ACCCTGTACC
TTATTTGAAC TAACCAATCA GTTCGCTTCT CGCTTCTGTT CGCGCGCTTC CGCTCTCCGA GCTCAATAAA
AGAGCCCACA ACCCCTCACT CGGCGCGCCA GTCTTCCGAT AGACTGCGTC GCCCGGGTAC CCGTATTCCC
AATAAAGCCT CTTGCTGTTT GCATCCGAAT CGTGGTCTCG CTGTTCCTTG GGAGGGTCTC CTCTGAGTGA
TTGACTACCC ACGACGGGGG TCTTTCATTT GGGGGCTCGT CCGGGATTTG GAGACCCCTG CCCAGGGACC
ACCGACCCAC CACCGGGAGG TAAGCTGGCC AGCAACTTAT CTGTGTCTGT CCGATTGTCT AGTGTCTATG
TTTGATGTTA TGCGCCTGCG TCTGTACTAG TTAGCTAACT AGCTCTGTAT CTGGCGGACC CGTGGTGGAA
CTGACGAGTT CTGAACACCC GGCCGCAACC CTGGGAGACG TCCCAGGGAC TTTGGGGGCC GTTTTTGTGG
CCCGACCTGA GGAAGGGAGT CGATGTGGAA TCCGACCCCG TCAGGATATG TGGTTCTGGT AGGAGACGAG
AACCTAAAAC AGTTCCCGCC TCCGTCTGAA TTTTTGCTTT CGGTTTGGAA CCGAAGCCGC GCGTCTTGTC
TGCTGCAGCG CTGCAGCATC GTTCTGTGTT GTCTCTGTCT GACTGTGTTT CTGTATTTGT CTGAAAATTA
GGGCCAGACT GTTACCACTC CCTTAAGTTT GACCTTAGGT CACTGGAAAG ATGTCGAGCG GATCGCTCAC
AACCAGTCGG TAGATGTCAA GAAGAGACGT TGGGTTACCT TCTGCTCTGC AGAATGGCCA ACCTTTAACG
TCGGATGGCC GCGAGACGGC ACCTTTAACC GAGACCTCAT CACCCAGGTT AAGATCAAGG TCTTTTCACC
TGGCCCGCAT GGACACCCAG ACCAGGTCCC CTACATCGTG ACCTGGGAAG CCTTGGCTTT TGACCCCCCT
CCCTGGGTCA AGCCCTTTGT ACACCCTAAG CCTCCGCCTC CTCTTCCTCC ATCCGCCCCG TCTCTCCCCC
TTGAACCTCC TCGTTCGACC CCGCCTCGAT CCTCCCTTTA TCCAGCCCTC ACTCCTTCTC TAGGCGCCGG
AATTCCGATC TGATCAGCTT GCCACAACCC GTACCAAAGA TGGATAGATC CGGAAAGCCT GAACTCACCG
CGACGTCTGT CGAGAAGTTT CTGATCGAAA AGTTCGACAG CGTCTCCGAC CTGATGCAGC TCTCGGAGGG
CGAAGAATCT CGTGCTTTCA GCTTCGATGT AGGAGGGCGT GGATATGTCC TGCGGGTAAA TAGCTGCGCC
GATGGTTTCT ACAAAGATCG TTATGTTTAT CGGCACTTTG CATCGGCCGC GCTCCCGATT CCGGAAGTGC
TTGACATTGG GGAATTCAGC GAGAGCCTGA CCTATTGCAT CTCCCGCCGT GCACAGGGTG TCACGTTGCA
AGACCTGCCT GAAACCGAAC TGCCCGCTGT TCTGCAGCCG GTCGCGGAGG CCATGGATGC GATCGCTGCG
GCCGATCTTA GCCAGACGAG CGGGTTCGGC CCATTCGGAC CGCAAGGAAT CGGTCAATAC ACTACATGGC
GTGATTTCAT ATGCGCGATT GCTGATCCCC ATGTGTATCA CTGGCAAACT GTGATGGACG ACACCGTCAG
TGCGTCCGTC GCGCAGGCTC TCGATGAGCT GATGCTTTGG GCCGAGGACT GCCCCGAAGT CCGGCACCTC
GTGCACGCGG ATTTCGGCTC CAACAATGTC CTGACGGACA ATGGCCGCAT AACAGCGGTC ATTGACTGGA
GCGAGGCGAT GTTCGGGGAT TCCCAATACG AGGTCGCCAA CATCTTCTTC TGGAGGCCGT GGTTGGCTTG
TATGGAGCAG CAGACGCGCT ACTTCGAGCG GAGGCATCCG GAGCTTGCAG GATCGCCGCG GCTCCGGGCG
TATATGCTCC GCATTGGTCT TGACCAACTC TATCAGAGCT TGGTTGACGG CAATTTCGAT GATGCAGCTT
GGGCGCAGGG TCGATGCGAC GCAATCGTCC GATCCGGAGC CGGGACTGTC GGGCGTACAC AAATCGCCCG
CAGAAGCGCG GCCGTCTGGA CCGATGGCTG TGTAGAAGTA CTCGCCGATA GTGGAAACCG ACGCCCCAGC
ACTCGTCCGA GGGCAAAGGA ATAGAGTAGA TGCCGACCGA ACAAGAGCTG ATTTCGAGAA CGCCTCAGCC
AGCAACTCGC GCGAGCCTAG CAAGGCAAAT GCGAGAGAAC GGCCTTACGC TTGGTGGCAC AGTTCTCGTC
CACAGTTCGC TAAGCTCGCT CGGCTGGGTC GCGGGAGGGC CGGTCGCAGT GATTCAGGCC CTTCTGGATT
GTGTTGGTCC CCAGGGCACG ATTGTCATGC CCACGCACTC GGGTGATCTG ACTGATCCCG CAGATTGGAG
ATCGCCGCCC GTGCCTGCCG ATTGGGTGC**aga tc**C
TAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATATATGGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGC
CTGGCTGACCGCCCAACGACCCCCGCCCATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAGGGACTTTCCA
TTGACGTCAATGGGTGGAGTATTTACGGTAAACTGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCT
ATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCAGTACATGACCTTATGGGACTTTCCTACTTGGCAGTACA
TCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACG
GGGATTTCCAAGTCTCCACCCCATTGACGTCAATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGT
AACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTGGTTTAGTGAACC
GTCAGATCCGCTAGaccatggcctcctccgaggacgtcatcaaggagttcatgcgcttcaaggtgcgcatggagggctccgt
gaacggccacgagttcgagatcgagggcgagggcgagggccgcccctacgagggcacccagaccgccaagctgaaggtgacc
aagggcggcccccctgcccttcgcctgggacatcctgtcccctcagttccagtacggctccaaggcctacgtgaagcaccccgccg
acatccccgactacttgaagctgtccttccccgagggcttcaagtgggagcgcgtgatgaacttcgaggacggcggcgtggtgac
cgtgacccaggactcctccctgcaggacggcgagttcatctacaaggtgaagctgcgcggcaccaacttcccctccgacggccc
cgtaatgcagaagaagaccatgggctgggaggcctccaccgagcggatgtaccccgaggacggcgccctgaagggcgagat
caagatgaggctgaagctgaaggacggcggccactacgacgccgaggtcaagaccacctacatggccaagaagcccgtgc
agctgcccggcgcctacaagaccgacatcaagctggacatcacctcccacaacgaggactacaccatcgtggaacagtacga
gcgcgccgagggccgccactccaccggcgcctaaggatc**t gtt taa ac**ATTGATTATTGACTAGTTATTA

ATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATATATGGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGCCT
GGCTGACCGCCCAACGACCCCCGCCCATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAGGGACTTTCCATT
GACGTCAATGGGTGGAGTATTTACGGTAAACTGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTAT
TGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCAGTACATGACCTTATGGGACTTTCCTACTTGGCAGTACATC
TACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGG
GATTTCCAAGTCTCCACCCCATTGACGTCAATGGGAGTTTGTTTTGGAACCAAAATCAACGGGACTTTCCAAAATGTCGTAA
CAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTCTCCCTATCAGTGAT
AGAGATCTCCCTATCAGTGATAGAGATCTCCCTATCAGTGATAGAGATCTCCCTATCAGTGATAGAGATCGAGCTGTTTAGT
GAACCGTCAGATCGCCTGGAGACGCCATCCACGCTGTTTTGACCTCCATAGA**AGAtctaagctt gcgg ccg cgt cga cgg atc cct cga gtt aat taa cgAT**AAAATA AAAGATTTTA TTTAGTCTCC AGAAAAAGGG GGGAATGAAA
GACCCCACCT GTAGGTTTGG CAAGCTAGCT TAAGTAACGC CATTTTGCAA GGCATGGAAA AATACATAAC
TGAGAATAGA GAAGTTCAGA TCAAGGTCAG GAACAGATGG AACAGCTGAA TATGGGCCAA ACAGGATATC
TGTGGTAAGC AGTTCCTGCC CCGGCTCAGG GCCAAGAACA GATGGAACAG CTGAATATGG GCCAAACAGG
ATATCTGTGG TAAGCAGTTC CTGCCCCGGC TCAGGGCCAA GAACAGATGG TCCCCAGATG CGGTCCAGCC
CTCAGCAGTT TCTAGAGAAC CATCAGATGT TTCCAGGGTG CCCCAAGGAC CTGAAATGAC CCTGTGCCTT
ATTTGAACTA ACCAATCAGT TCGCTTCTCG CTTCTGTTCG CGCGCTTCTG CTCCCCGAGC TCAATAAAAG
AGCCCACAAC CCCTCACTCG GGGCGCCAGT CCTCCGATTG ACTGAGTCGC CCGGGTACCC GTGTATCCAA
TAAACCCTCT TGCAGTTGCA TCCGACTTGT GGTCTCGCTG TTCCTTGGGA GGGTCTCCTC TGAGTGATTG
ACTACCCGTC AGCGGGGGTC TTTCATTTGG GGGCTCGTCC GGGATCGGGA GACCCCTGCC CAGGGACCAC
CGACCCACCA CCGGGAGGTA AGCTGGCTGC CTCGCGCGTT TCGGTGATGA CGGTGAAAAC CTCTGACACA
TGCAGCTCCC GGAGACGGTC ACAGCTTGTC TGTAAGCGGA TGCCGGGAGC AGACAAGCCC GTCAGGGCGC
GTCAGCGGGT GTTGGCGGGT GTCGGGGCGC AGCCATGACC CAGTCACGTA GCGATAGCGG AGTGTATACT
GGCTTAACTA TGCGGCATCA GAGCAGATTG TACTGAGAGT GCACCATATG CGGTGTGAAA TACCGCACAG
ATGCGTAAGG AGAAAATACC GCATCAGGCG CTCTTCCGCT TCCTCGCTCA CTGACTCGCT GCGCTCGGTC
GTTCGGCTGC GGCGAGCGGT ATCAGCTCAC TCAAAGGCGG TAATACGGTT ATCCACAGAA TCAGGGGATA
ACGCAGGAAA GAACATGTGA GCAAAAGGCC AGCAAAAGGC CAGGAACCGT AAAAAGGCCG CGTTGCTGGC
GTTTTTCCAT AGGCTCCGCC CCCCTGACGA GCATCACAAA AATCGACGCT CAAGTCAGAG GTGGCGAAAC
CCGACAGGAC TATAAAGATA CCAGGCGTTT CCCCCTGGAA GCTCCCTCGT GCGCTCTCCT GTTCCGACCC
TGCCGCTTAC CGGATACCTG TCCGCCTTTC TCCCTTCGGG AAGCGTGGCG CTTTCTCATA GCTCACGCTG
TAGGTATCTC AGTTCGGTGT AGGTCGTTCG CTCCAAGCTG GGCTGTGTGC ACGAACCCCC CGTTCAGCCC
GACCGCTGCG CCTTATCCGG TAACTATCGT CTTGAGTCCA ACCCGGTAAG ACACGACTTA TCGCCACTGG
CAGCAGCCAC TGGTAACAGG ATTAGCAGAG CGAGGTATGT AGGCGGTGCT ACAGAGTTCT TGAAGTGGTG
GCCTAACTAC GGCTACACTA GAAGGACAGT ATTTGGTATC TGCGCTCTGC TGAAGCCAGT TACCTTCGGA
AAAAGAGTTG GTAGCTCTTG ATCCGGCAAA CAAACCACCG CTGGTAGCGG TGGTTTTTTT GTTTGCAAGC
AGCAGATTAC GCGCAGAAAA AAAGGATCTC AAGAAGATCC TTTGATCTTT TCTACGGGGT CTGACGCTCA
GTGGAACGAA AACTCACGTT AAGGGATTTT GGTCATGAGA TTATCAAAAA GGATCTTCAC CTAGATCCTT
TTAAATTAAA AATGAAGTTT TAAATCAATC TAAAGTATAT ATGAGTAAAC TTGGTCTGAC AGTTACCAAT
GCTTAATCAG TGAGGCACCT ATCTCAGCGA TCTGTCTATT TCGTTCATCC ATAGTTGCCT GACTCCCCGT
CGTGTAGATA ACTACGATAC GGGAGGGCTT ACCATCTGGC CCCAGTGCTG CAATGATACC GCGAGACCCA
CGCTCACCGG CTCCAGATTT ATCAGCAATA AACCAGCCAG CCGGAAGGGC CGAGCGCAGA AGTGGTCCTG
CAACTTTATC CGCCTCCATC CAGTCTATTA ATTGTTGCCG GGAAGCTAGA GTAAGTAGTT CGCCAGTTAA
TAGTTTGCGC AACGTTGTTG CCATTGCTGC AGGCATCGTG GTGTCACGCT CGTCGTTTGG TATGGCTTCA
TTCAGCTCCG GTTCCCAACG ATCAAGGCGA GTTACATGAT CCCCCATGTT GTGCAAAAAA GCGGTTAGCT
CCTTCGGTCC TCCGATCGTT GTCAGAAGTA AGTTGGCCGC AGTGTTATCA CTCATGGTTA TGGCAGCACT
GCATAATTCT CTTACTGTCA TGCCATCCGT AAGATGCTTT TCTGTGACTG GTGAGTACTC AACCAAGTCA
TTCTGAGAAT AGTGTATGCG GCGACCGAGT TGCTCTTGCC CGGCGTCAAC ACGGGATAAT ACCGCGCCAC
ATAGCAGAAC TTTAAAAGTG CTCATCATTG GAAAACGTTC TTCGGGGCGA AAACTCTCAA GGATCTTACC
GCTGTTGAGA TCCAGTTCGA TGTAACCCAC TCGTGCACCC AACTGATCTT CAGCATCTTT TACTTTCACC
AGCGTTTCTG GGTGAGCAAA AACAGGAAGG CAAAATGCCG CAAAAAAGGG AATAAGGGCG ACACGGAAAT
GTTGAATACT CATACTCTTC CTTTTTCAAT ATTATTGAAG CATTTATCAG GGTTATTGTC TCATGAGCGG
ATACATATTT GAATGTATTT AGAAAAATAA ACAAATAGGG GTTCCGCGCA CATTTCCCCG AAAAGTGCCA
CCTGACGTCT AAGAAACCAT TATTATCATG ACATTAACCT ATAAAAATAG GCGTATCACG AGGCCCTTTC
GTCTTCAAGA ATTCATACCA GATCACCGAA AACTGTCCTC CAAATGTGTC CCCCTCACAC TCCCAAATTC
GCGGGCTTCT GCCTCTTAGA CCACTCTACC CTATTCCCCA CACTCACCGG AGCCAAAGCC GCGGCCCTTC
CGTTTCTTTG CT

Unique enzymes in pRV-TO4:

Asc I	GG`CGCG,CC	444
Eco47 III	AGC|GCT	990
BsrG I	T`GTAC,A	1349
Bcl I	T`GATC,A	1482
BspM I	ACCTGC 10/14	1833
Rsr II	CG`GWC,CG	1928
Blp I	GC`TNA,GC	2671
Esp I	GC`TNA,GC	2671
PflM I	CCAN,NNN`NTGG	3852
BstX I	CCAN,NNNN`NTGG	3970
Pme I	CTTT|AAAC	4115
HinD III	A`AGCT,T	4856
Not I	GC`GGCC,GC	4863
Sal I	G`TCGA,C	4870
BamH I	G`GATC,C	4876
PaeR7 I	C`TCGA,G	4882
Xho I	C`TCGA,G	4882
Pac I	TTA,AT`TAA	4892
Xba I	T`CTAG,A	5236
Bst1107 I	GTA|TAC	5781
Xca I	GTA|TAC	5781
Sap I	GCTCTTC 8/11	5892
Afl III	A`CRYG,T	6008
Xmn I	GAANN|NNTTC	7500
Ssp I	AAT|ATT	7705

Number of enzymes = 25

The following enzymes do not cut in pRV-TO4:

Age I	Apa I	Avr II	BsiC I	BsiW I
Bsm I	Bsp120 I	Bsp1286 I	BstB I	Cla I
Eco72 I	Fse I	Hpa I	Mlu I	Mun I
Nae I	NgoM I	Nru I	Nsi I	Pml I
Sfi I	Sph I	Spl I	Srf I	Xcm I

pRV-TO4: sites sorted by name:

Aat II	(12)	812	1547	2954	3007
		3090	3276	3447	4257
		4310	4393	4579	7823
Acc I	(2)	4871	5780		
Acc65 I	(2)	477	5419		
Aci I	(99)	150	272	401	755
		794	927	968	1109
		1200	1266	1365	1384
		1422	1539	1663	1728
		1795	1845	1865	1889
		1911	1931	2108	2146
		2156	2269	2297	2299
		2320	2449	2459	2692
		2789	2806	2887	2915
		2927	2941	3108	3199
		3232	3336	3357	3418
		3532	3555	3579	3654
		3732	3801	3871	3936
		4084	4190	4218	4230
		4244	4411	4502	4535
		4639	4660	4862	4866
		5215	5517	5681	5720
		5730	5772	5797	5835
		5848	5874	5891	5934
		5941	5962	6053	6081
		6208	6227	6348	6458
		6593	6602	6964	7055
		7246	7292	7413	7457
		7534	7643	7742	7789
		7956	8014	8016	
Afl II	(3)	35	1073	4974	
Afl III	(1)	6008			
Aha II	(21)	809	1465	1544	2512
		2951	3004	3087	3273
		3444	3891	3948	3999
		4098	4254	4307	4390
		4576	4819	5388	7438
		7820			
Ahd I	(5)	1087	3607	5464	5510
		6901			
Alu I	(44)	30	34	120	191
		412	655	735	743
		1488	1600	1632	1674
		2059	2284	2349	2378
		2568	2675	3395	3562
		3679	3796	3925	3991
		4021	4698	4788	4858
		4969	4973	5060	5135
		5354	5597	5650	5669
		5950	6176	6266	6312
		6569	7090	7190	7253
Alw I	(21)	1118	1424	1513	1980
		2298	2407	2780	2827
		3410	4113	4872	4883
		5554	6570	6656	6656
		6753	6754	7218	7533
		7539			
AlwN I	(4)	232	5100	5175	6424
ApaL I	(5)	1800	2102	5824	6322
		7568			
Apo I	(5)	939	1471	1763	7894
		7950			
Asc I	(1)	444			
Ase I	(2)	4139	7073		
Asp718	(2)	477	5419		
Ava I	(9)	242	473	2769	3689
		3881	4882	5349	5382
		5415			
Ava II	(15)	261	274	329	627
		757	1286	1928	2469
		2737	5204	5217	5272
		5569	7039	7261	
BamH I	(1)	4876			
Ban I	(15)	319	477	1209	1464
		2094	3294	3545	3803
		3890	3998	4097	5262
		5387	5419	6849	
Ban II	(8)	414	427	598	3488
		4700	5356	5369	5540
Bbe I	(5)	1468	3894	4002	4101
		5391			
Bbs I	(3)	445	3848	7879	
Bbv I	(13)	998	1006	1609	1867
		2260	2387	4000	5659
		5756	6427	6430	6636
		7330			
Bbv II	(3)	446	3847	7880	
Bcl I	(1)	1482			
Bcn I	(21)	163	239	475	476
		604	646	791	2307
		2423	3997	5107	5182
		5417	5418	5546	5588
		5655	5690	6389	7085
		7436			
Bfa I	(14)	31	294	690	728
		740	1461	2608	3421
		4132	4970	5237	6503
		6756	7091		
Bgl I	(7)	2919	3041	3112	4222
		4344	4415	7021	
Bgl II	(4)	4718	4739	4760	4850
Blp I	(1)	2671			
Bpm I	(5)	2188	2242	4834	4907
		6971			
Bsa I	(8)	531	552	606	1216
		5472	5493	5548	6962
BsaA I	(4)	3169	3643	4472	5762
BsaB I	(4)	4717	4738	4759	4780
BsaH I	(21)	809	1465	1544	2512
		2951	3004	3087	3273
		3444	3891	3948	3999
		4098	4254	4307	4390
		4576	4819	5388	7438
		7820			
BsaJ I	(48)	160	236	315	325
		473	537	622	623
		761	800	801	813
		814	1234	1303	1312
		1332	1333	1872	2073
		2228	2297	2528	2741
		2742	3189	3426	3438
		3573	3597	3633	3690
		3750	3846	3882	3951
		4077	4492	5104	5179
		5258	5268	5415	5478
		5564	5565	6168	8014
BsaW I	(8)	1520	1741	2278	2414
		6214	6361	7192	8001
BseR I	(6)	540	1360	1399	3424
		3748	5481		
Bsg I	(2)	2848	4007		
BsiE I	(13)	794	1728	1863	1884
		1893	2463	2558	2705
		4866	5924	6348	7271
		7420			
BsiHKA I	(9)	414	1804	2106	4700
		5356	5828	6326	7487
		7572			
BsmA I	(22)	180	530	551	607
		801	899	1016	1140
		1199	1217	1395	1587
		3262	4565	4811	4924
		5471	5492	5549	5652
		6963	7737		
BsmB I	(8)	800	898	1139	1198
		1396	1588	4810	5651
BsmF I	(18)	247	640	796	831
		1272	2437	2723	3004
		3155	3323	3595	3614
		4307	4458	4626	5190
		5582	7918		
BsoF I	(52)	794	968	984	987
		992	995	1200	1598
		1675	1728	1856	1887
		1890	2146	2249	2297
		2300	2376	2460	2806
		3532	3580	3733	3797
		3802	3937	3989	3992
		4084	4863	4866	5602
		5648	5745	5798	5914
		5932	5935	6053	6208
		6351	6416	6419	6625
		6953	7142	7292	7319
		7414	7643	8014	8017
BspH I	(3)	6728	7736	7841	
BspM I	(1)	1833			
BspM II	(4)	1520	1741	2278	2414
Bsr I	(19)	450	1097	1125	2005
		2170	3125	3623	4428
		5392	5756	5787	6415
		6428	6542	6948	7066
		7109	7376	7548	
BsrB I	(7)	403	1109	1911	2269
		3871	5941	7742	
BsrD I	(2)	6962	7136		
BsrG I	(1)	1349			
BssH II	(4)	393	444	4072	5335
BssS I	(6)	1620	2099	3500	6181
		7565	7872		
Bst1107 I	(1)	5781			
BstE II	(3)	1154	3568	3739	
BstN I	(22)	316	624	802	815
		1236	1261	1284	1304
		1334	2743	2919	3112
		3598	3752	4222	4415
		4813	5259	5566	6036
		6157	6170		
BstU I	(36)	393	395	446	970
		972	1202	1541	1730
		1865	1976	2042	2108

		2257	2299	2459	2600
		2602	2692	2889	3711
		3801	4074	4192	4868
		5335	5337	5609	5611
		5714	6055	6636	6966
		7459	7791	7956	8016
BstX I	(1)	3970			
BstY I	(15)	1517	2831	3414	4106
		4718	4739	4760	4850
		4876	6649	6660	6746
		6758	7526	7543	
Bsu36 I	(3)	848	1085	4102	
Cac8 I	(35)	28	32	395	446
		657	661	717	1266
		1490	1845	2046	2106
		2286	2449	2591	2604
		2677	2816	2915	3108
		4074	4218	4411	4860
		4967	4971	5337	5599
		5939	6025	6062	6622
		7013	7146	7958	
Cfr10 I	(4)	1858	2700	4094	6981
Csp6 I	(25)	347	478	725	1350
		1502	2436	2489	3047
		3072	3127	3160	3211
		3368	3625	3877	4066
		4350	4375	4430	4463
		4514	4671	5420	5815
		7380			
Dde I	(27)	76	166	192	283
		554	848	1085	1357
		1898	2585	2671	3615
		4102	4854	5015	5110
		5185	5226	5407	5495
		5818	6283	6692	6858
		7398	7824	7970	
Dpn I	(45)	96	1113	1245	1430
		1479	1484	1519	1565
		1698	1883	1896	1986
		2293	2413	2777	2786
		2802	2833	3416	3512
		3908	4108	4720	4741
		4762	4783	4808	4852
		4878	5035	5549	6576
		6651	6662	6670	6748
		6760	6865	7206	7224
		7270	7528	7545	7581
		7907			
DpnII	(45)	94	1111	1243	1428
		1477	1482	1517	1563
		1696	1881	1894	1984
		2291	2411	2775	2784
		2800	2831	3414	3510
		3906	4106	4718	4739
		4760	4781	4806	4850
		4876	5033	5547	6574
		6649	6660	6668	6746
		6758	6863	7204	7222
		7268	7526	7543	7579
		7905			
Dra I	(4)	4115	6767	6786	7478
Dra III	(2)	1808	2101		
Drd I	(5)	2024	2405	3953	5703
		6116			
Dsa I	(9)	761	1872	2228	2297
		3189	3426	3846	4492
		8014			
Eae I	(13)	657	791	1176	1197
		1725	1890	2143	2460
		3496	3937	3972	4863
		7289			
Eag I	(5)	791	1725	1890	2460
		4863			
Ear I	(4)	1137	1378	5892	7696
Eco47 III	(1)	990			
Eco57 I	(6)	3583	3916	3940	3946
		6555	7569		
EcoN I	(2)	851	1459		
EcoO109 I	(5)	329	1286	2718	5272
		7877			
EcoR I	(3)	1471	1763	7894	
EcoR II	(22)	314	622	800	813
		1234	1259	1282	1302
		1332	2741	2917	3110
		3596	3750	4220	4413
		4811	5257	5564	6034
		6155	6168		
EcoR V	(4)	138	214	5082	5157
Ehe I	(5)	1466	3892	4000	4099
		5389			
Esp I	(1)	2671			
Fnu4H I	(52)	794	968	984	987
		992	995	1200	1598
		1675	1728	1856	1887
		1890	2146	2249	2297
		2300	2376	2460	2806
		3532	3580	3733	3797
		3802	3937	3989	3992
		4084	4863	4866	5602
		5648	5745	5798	5914
		5932	5935	6053	6208
		6351	6416	6419	6625
		6953	7142	7292	7319
		7414	7643	8014	8017
Fok I	(14)	499	1207	1367	1889
		2262	3590	3647	3886
		4809	5440	5696	6867
		7048	7335		
Fsp I	(2)	3476	7123		
Gdi II	(15)	790	792	1196	1724
		1726	1889	1891	2142
		2459	2461	3497	3938
		4862	4864	7288	
Gsu I	(5)	2187	2241	4833	4908
		6972			
Hae I	(10)	659	1178	1871	3431
		3638	3860	3974	6023
		6034	6486		
Hae II	(8)	992	1468	3894	4002
		4101	5391	5886	6256
Hae III	(50)	172	203	248	659
		793	829	841	1054
		1178	1199	1264	1727
		1871	1892	1920	2072
		2145	2227	2462	2633
		2700	2719	2913	3106
		3431	3498	3531	3582
		3638	3825	3860	3939
		3974	4083	4216	4409
		4865	5071	5116	5146
		5191	6023	6034	6052
		6486	6944	7024	7291
		7878	8019		
Hga I	(17)	457	709	962	1571
		2023	2262	2407	2519
		3354	3955	4657	4826
		4858	5704	6118	6696
		7428			
HgiA I	(9)	414	1804	2106	4700
		5356	5828	6326	7487
		7572			
HgiE II	(2)	5826	6587		
Hha I	(42)	395	397	446	448
		715	972	991	1467
		1679	1732	1976	2044
		2259	2386	2459	2602
		3465	3477	3711	3801
		3893	4001	4074	4076
		4100	5337	5339	5390
		5611	5714	5744	5885
		5918	6188	6255	6355
		6529	6638	7031	7124
		7461	7793		
HinC II	(3)	2356	4872	7442	
Hind II	(3)	2356	4872	7442	
HinD III	(1)	4856			
Hinf I	(17)	299	518	858	869
		1616	1738	1938	2189
		2712	3239	3755	4542
		5409	5908	5983	6379
		6896			
HinI I	(21)	809	1465	1544	2512
		2951	3004	3087	3273
		3444	3891	3948	3999
		4098	4254	4307	4390
		4576	4819	5388	7438
		7820			
HinP I	(42)	393	395	444	446
		713	970	989	1465
		1677	1730	1974	2042
		2257	2384	2457	2600
		3463	3475	3709	3799
		3891	3999	4072	4074
		4098	5335	5337	5388
		5609	5712	5742	5883
		5916	6186	6253	6353
		6527	6636	7029	7122
		7459	7791		
Hpa II	(35)	162	238	474	602
		644	790	1468	1521
		1742	1859	2092	2279
		2305	2415	2421	2701
		3996	4095	5106	5181
		5416	5544	5586	5654
		5688	6215	6362	6388
		6578	6982	7016	7083
		7193	7435	8002	
Hph I	(19)	1224	1250	1529	2784
		3204	3579	3750	3801
		4022	4507	5629	5638
		6745	6972	7386	7594
		7627	7901	7992	
Kas I	(5)	1464	3890	3998	4097
		5387			
Kpn I	(2)	481	5423		
Mae I	(14)	31	294	690	728
		740	1461	2608	3421
		4132	4970	5237	6503
		6756	7091		
Mae II	(24)	809	1148	1189	1544
		1814	2951	2963	3004
		3087	3168	3273	3444
		3642	4254	4266	4307
		4390	4471	4576	5761
		6711	7127	7500	7820
Mae III	(26)	39	1061	1089	1154
		1298	1810	2890	2977
		3326	3568	3739	3745
		4193	4280	4629	4978
		5662	5757	6364	6427
		6543	6826	7157	7215
		7368	7556		
Mbo I	(45)	94	1111	1243	1428
		1477	1482	1517	1563
		1696	1881	1894	1984
		2291	2411	2775	2784
		2800	2831	3414	3510
		3906	4106	4718	4739
		4760	4781	4806	4850
		4876	5033	5547	6574
		6649	6660	6668	6746
		6758	6863	7204	7222
		7268	7526	7543	7579
		7905			
Mbo II	(16)	446	1153	1366	1624
		2207	2210	3849	3852
		4859	5880	6669	6742
		7497	7575	7684	7880
Mme I	(8)	896	1173	1610	2144
		3842	5480	6222	6406
Mnl I	(77)	291	444	508	536
		560	641	843	939
		1235	1338	1371	1377
		1380	1386	1416	1419
		1434	1441	1457	1600
		1637	1861	2068	2107
		2167	2194	2217	2265
		2523	2593	2689	3370
		3433	3441	3444	3475
		3508	3514	3520	3535
		3623	3685	3718	3768
		3825	3850	3870	3877
		3909	3946	4036	4041
		4072	4673	4849	4890
		5234	5386	5405	5450
		5477	5501	5583	5614
		5644	5906	6116	6189
		6440	6840	6921	7067

		7273	7868	7931	7947
		7976			
Msc I	(3)	659	1178	3974	
Mse I	(20)	36	1074	1186	1216
		1240	4114	4139	4888
		4892	4975	5789	6714
		6766	6771	6785	6838
		7073	7112	7477	7849
Msl I	(4)	3194	4497	7153	7312
Msp I	(35)	162	238	474	602
		644	790	1468	1521
		1742	1859	2092	2279
		2305	2415	2421	2701
		3996	4095	5106	5181
		5416	5544	5586	5654
		5688	6215	6362	6388
		6578	6982	7016	7083
		7193	7435	8002	
MspA1 I	(14)	120	191	1847	2156
		2299	3991	5060	5135
		5517	5720	6350	6595
		7536	8016		
Nar I	(5)	1465	3891	3999	4098
		5388			
Nci I	(21)	162	238	474	475
		603	645	790	2306
		2422	3996	5106	5181
		5416	5417	5545	5587
		5654	5689	6388	7084
		7435			
Nco I	(5)	1872	3189	3426	3846
		4492			
Nde I	(4)	1970	3063	4366	5831
Nhe I	(2)	30	4969		
Nla III	(26)	62	1272	1876	1959
		1994	2760	3133	3193
		3430	3463	3481	3850
		3973	4436	4496	5001
		5647	5752	6012	6732
		7223	7233	7311	7347
		7740	7845		
Nla IV	(42)	154	247	263	321
		479	628	759	828
		960	1211	1288	1466
		2096	2119	2303	2419
		2739	3296	3487	3547
		3583	3631	3805	3826
		3892	4000	4099	4599
		4878	5206	5264	5389
		5421	5570	6040	6079
		6851	6945	6986	7197
		7787	8006		
Not I	(1)	4863			
Nsp7524 I	(2)	5643	6008		
NspB II	(14)	120	191	1847	2156
		2299	3991	5060	5135
		5517	5720	6350	6595
		7536	8016		
NspH I	(2)	5647	6012		
Pac I	(1)	4892			
PaeR7 I	(1)	4882			
Pal I	(50)	172	203	248	659
		793	829	841	1054
		1178	1199	1264	1727
		1871	1892	1920	2072
		2145	2227	2462	2633
		2700	2719	2913	3106
		3431	3498	3531	3582
		3638	3825	3860	3939
		3974	4083	4216	4409
		4865	5071	5116	5146
		5191	6023	6034	6052
		6486	6944	7024	7291
		7878	8019		
PflM I	(1)	3852			
Ple I	(3)	866	5417	6387	
Pme I	(1)	4115			
PpuM I	(3)	329	1286	5272	
Psp1406 I	(2)	7127	7500		
PspA I	(2)	473	5415		
Pst I	(6)	988	996	1172	1857
		3768	7146		
Pvu I	(2)	1884	7271		
Pvu II	(5)	120	191	3991	5060
		5135			
Rsa I	(25)	348	479	726	1351
		1503	2437	2490	3048
		3073	3128	3161	3212
		3369	3626	3878	4067
		4351	4376	4431	4464
		4515	4672	5421	5816
		7381			
Rsr II	(1)	1928			
Sac I	(3)	414	4700	5356	
Sac II	(2)	2300	8017		
Sal I	(1)	4870			
Sap I	(1)	5892			
Sau3A I	(45)	94	1111	1243	1428
		1477	1482	1517	1563
		1696	1881	1894	1984
		2291	2411	2775	2784
		2800	2831	3414	3510
		3906	4106	4718	4739
		4760	4781	4806	4850
		4876	5033	5547	6574
		6649	6660	6668	6746
		6758	6863	7204	7222
		7268	7526	7543	7579
		7905			
Sau96 I	(42)	170	201	246	261
		274	329	627	757
		827	840	1052	1263
		1286	1919	1928	2070
		2469	2698	2718	2737
		2912	3105	3529	3581
		3824	4081	4215	4408
		5069	5114	5144	5189
		5204	5217	5272	5569
		6943	7022	7039	7261
		7877	8018		
Sca I	(2)	2490	7381		
ScrF I	(43)	162	238	316	474
		475	603	624	645
		790	802	815	1236
		1261	1284	1304	1334
		2306	2422	2743	2919
		3112	3598	3752	3996
		4222	4415	4813	5106
		5181	5259	5416	5417
		5545	5566	5587	5654
		5689	6036	6157	6170
		6388	7084	7435	
Sec I	(48)	160	236	315	325
		473	537	622	623
		761	800	801	813
		814	1234	1303	1312
		1332	1333	1872	2073
		2228	2297	2528	2741
		2742	3189	3426	3438
		3573	3597	3633	3690
		3750	3846	3882	3951
		4077	4492	5104	5179
		5258	5268	5415	5478
		5564	5565	6168	8014
SfaN I	(24)	260	520	1005	1585
		1729	1796	1868	2053
		2283	2363	2385	2541
		3187	4490	5203	5461
		5675	5808	5846	5884
		6104	7156	7349	7596
Sfc I	(9)	984	992	1168	1853
		3764	4954	6273	6464
		7142			
Sma I	(2)	475	5417		
SnaB I	(2)	3169	4472		
Spe I	(2)	727	4131		
Ssp I	(1)	7705			
Stu I	(2)	3638	3860		
Sty I	(12)	325	537	1312	1872
		3189	3426	3573	3633
		3846	4492	5268	5478
Taq I	(21)	861	1105	1416	1427
		1551	1566	1575	1635
		2052	2265	2367	2392
		2575	3507	3513	3723
		4784	4871	4883	6108
		7552			
Tfi I	(9)	299	518	869	1616
		1738	1938	2189	2712
		5983			
Tsp45 I	(10)	1089	1298	1810	3568
		3739	3745	5662	5757
		7157	7368		
Tth111 I	(7)	466	878	1284	1580
		2024	5408	5755	
Tth111 II	(10)	144	220	498	691
		1740	5088	5163	6597
		6606	6636		
Vsp I	(2)	4139	7073		
Xba I	(1)	5236			
Xca I	(1)	5781			
Xho I	(1)	4882			
Xho II	(15)	1517	2831	3414	4106
		4718	4739	4760	4850
		4876	6649	6660	6746
		6758	7526	7543	
Xma I	(2)	473	5415		
Xma III	(5)	791	1725	1890	2460
		4863			
Xmn I	(1)	7500			

Site usage in pRV-TO4:

Aat II	G,ACGT`C	12	Acc I	GT`MK,AC	2
Acc65 I	G`GTAC,C	2	Aci I	C`CG,C	99
Afl II	C`TTAA,G	3	Afl III	A`CRYG,T	1
Age I	A`CCGG,T	-	Aha II	GR`CG,YC	21
Ahd I	GACNN,N`NNGTC	5	Alu I	AG|CT	44
Alw I	GGATC 8/9	21	AlwN I	CAG,NNN`CTG	4
Apa I	G,GGCC`C	-	ApaL I	G`TGCA,C	5
Apo I	R`AATT,Y	5	Asc I	GG`CGCG,CC	1
Ase I	AT`TA,AT	2	Asp718	G`GTAC,C	2
Ava I	C`YCGR,G	9	Ava II	G`GWC,C	15
Avr II	C`CTAG,G	-	BamH I	G`GATC,C	1
Ban I	G`GYRC,C	15	Ban II	G,RGCY`C	8
Bbe I	G,GCGC`C	5	Bbs I	GAAGAC 8/12	3
Bbv I	GCAGC 13/17	13	Bbv II	GAAGAC 7/11	3
Bcl I	T`GATC,A	1	Bcn I	CC,S`GG	21
Bfa I	C`TA,G	14	Bgl I	GCCN,NNN`NGGC	7
Bgl II	A`GATC,T	4	Blp I	GC`TNA,GC	1
Bpm I	CTGGAG 22/20	5	Bsa I	GGTCTC 7/11	8
BsaA I	YAC|GTR	4	BsaB I	GATNN|NNATC	4
BsaH I	GR`CG,YC	21	BsaJ I	C`CNNG,G	48
BsaW I	W`CCGG,W	8	BseR I	GAGGAG 16/14	6
Bsg I	GTGCAG 22/20	2	BsiC I	TT`CG,AA	-
BsiE I	CG,RY`CG	13	BsiHKA I	G,WGCW`C	9
BsiW I	C`GTAC,G	-	Bsm I	GAATG,C 7	-
BsmA I	GTCTC`/9	22	BsmB I	CGTCTC 7/11	8
BsmF I	GGGAC 15/19	18	BsoF I	GC`N,GC	52
Bsp120 I	G`GGCC,C	-	Bsp1286 I	G,DGCH`C	-
BspH I	T`CATG,A	3	BspM I	ACCTGC 10/14	1
BspM II	T`CCGG,A	4	Bsr I	ACT,GG`	19
BsrB I	GAG|CGG	7	BsrD I	GCAATG, 8	2
BsrG I	T`GTAC,A	1	BssH II	G`CGCG,C	4
BssS I	C`TCGT,G	6	Bst1107 I	GTA|TAC	1
BstB I	TT`CG,AA	-	BstE II	G`GTNAC,C	3
BstN I	CC`W,GG	22	BstU I	CG|CG	36
BstX I	CCAN,NNNN`NTGG	1	BstY I	R`GATC,Y	15
Bsu36 I	CC`TNA,GG	3	Cac8 I	GCN|NGC	35
Cfr10 I	R`CCGG,Y	4	Cla I	AT`CG,AT	-
Csp6 I	G`TA,C	25	Dde I	C`TNA,G	27
Dpn I	GA|TC	45	DpnII	`GATC,	45
Dra I	TTT|AAA	4	Dra III	CAC,NNN`GTG	2
Drd I	GACNN,NN`NNGTC	5	Dsa I	C`CRYG,G	9
Eae I	Y`GGCC,R	13	Eag I	C`GGCC,G	5
Ear I	CTCTTC 7/10	4	Eco47 III	AGC|GCT	1
Eco57 I	CTGAAG 21/19	6	Eco72 I	CAC|GTG	-
EcoN I	CCTNN`N,NNAGG	2	EcoO109 I	RG`GNC,CY	5
EcoR I	G`AATT,C	3	EcoR II	`CCWGG,	22
EcoR V	GAT|ATC	4	Ehe I	GGC|GCC	5
Esp I	GC`TNA,GC	1	Fnu4H I	GC`N,GC	52
Fok I	GGATG 14/18	14	Fse I	GG,CCGG`CC	-
Fsp I	TGC|GCA	2	Gdi II	`YGGC,CG	15
Gsu I	CTGGAG 21/19	5	Hae I	WGG|CCW	10
Hae II	R,GCGC`Y	8	Hae III	GG|CC	50
Hga I	GACGC 9/14	17	HgiA I	G,WGCW`C	9
HgiE II	ACCNNNNNNGGT -1/132		Hha I	G,CG`C	42
HinC II	GTY|RAC	3	Hind II	GTY|RAC	3

HinD III	A`AGCT,T	1	Hinf I	G`ANT,C	17	Pml I	CAC|GTG	-	PpuM I	RG`GWC,CY	3
HinI I	GR`CG,YC	21	HinP I	G`CG,C	42	Psp1406 I	AA`CG,TT	2	PspA I	C`CCGG,G	2
Hpa I	GTT|AAC	-	Hpa II	C`CG,G	35	Pst I	C,TGCA`G	6	Pvu I	CG,AT`CG	2
Hph I	GGTGA 12/11	19	Kas I	G`GCGC,C	5	Pvu II	CAG|CTG	5	Rsa I	GT|AC	25
Kpn I	G,GTAC`C	2	Mae I	C`TA,G	14	Rsr II	CG`GWC,CG	1	Sac I	G,AGCT`C	3
Mae II	A`CG,T	24	Mae III	`GTNAC,	26	Sac II	CC,GC`GG	2	Sal I	G`TCGA,C	1
Mbo I	`GATC,	45	Mbo II	GAAGA 12/11	16	Sap I	GCTCTTC 8/11	1	Sau3A I	`GATC,	45
Mlu I	A`CGCG,T	-	Mme I	TCCRAC 25/23	8	Sau96 I	G`GNC,C	42	Sca I	AGT|ACT	2
Mnl I	CCTC 10/10	77	Msc I	TGG|CCA	3	ScrF I	CC`N,GG	43	Sec I	C`CNNG,G	48
Mse I	T`TA,A	20	Msl I	CAYNN|NNRTG	4	SfaN I	GCATC 9/13	24	Sfc I	C`TRYA,G	9
Msp I	C`CG,G	35	MspA1 I	CMG|CKG	14	Sfi I	GGCCN,NNN`NGGCC	-	Sma I	CCC|GGG	2
Mun I	C`AATT,G	-	Nae I	GCC|GGC	-	SnaB I	TAC|GTA	2	Spe I	A`CTAG,T	2
Nar I	GG`CG,CC	5	Nci I	CC`S,GG	21	Sph I	G,CATG`C	-	Spl I	C`GTAC,G	-
Nco I	C`CATG,G	5	Nde I	CA`TA,TG	4	Srf I	GCCC|GGGC	-	Ssp I	AAT|ATT	1
NgoM I	G`CCGG,C	-	Nhe I	G`CTAG,C	2	Stu I	AGG|CCT	2	Sty I	C`CWWG,G	12
Nla III	,CATG`	26	Nla IV	GGN|NCC	42	Taq I	T`CG,A	21	Tfi I	G`AWT,C	9
Not I	GC`GGCC,GC	1	Nru I	TCG|CGA	-	Tsp45 I	`GTSAC,	10	Tth111 I	GACN`N,NGTC	7
Nsi I	A,TGCA`T	-	Nsp7524 I	R`CATG,Y	2	Tth111 II	CAARCA 16/14	10	Vsp I	AT`TA,AT	2
NspB II	CMG|CKG	14	NspH I	R,CATG`Y	2	Xba I	T`CTAG,A	1	Xca I	GTA|TAC	1
Pac I	TTA,AT`TAA	1	PaeR7 I	C`TCGA,G	1	Xcm I	CCANNNN,N`NNNNTGG	-	Xho I	C`TCGA,G	1
Pal I	GG|CC	50	PflM I	CCAN,NNN`NTGG	1	Xho II	R`GATC,Y	15	Xma I	C`CCGG,G	2
Ple I	GAGTC 9/10	3	Pme I	CTTT|AAAC	1	Xma III	C`GGCC,G	5	Xmn I	GAANN|NNTTC	1