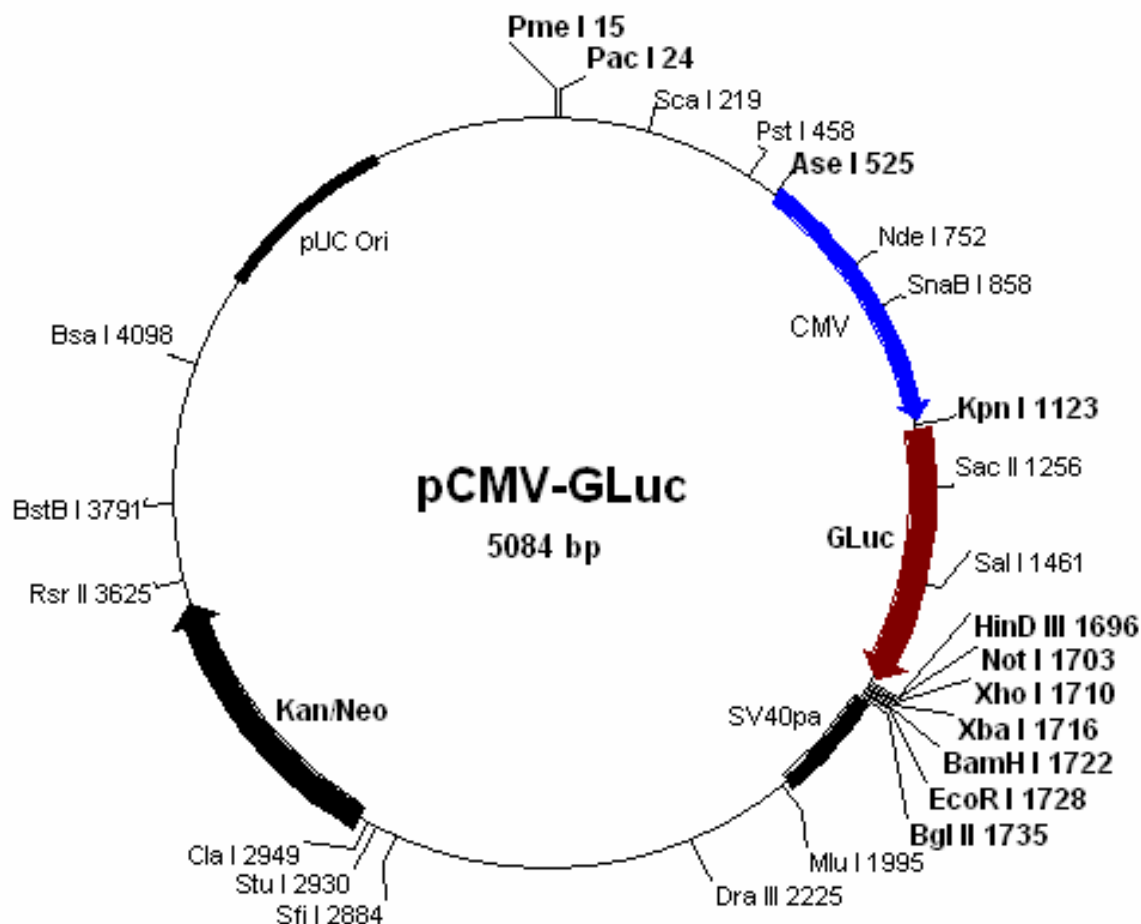


**Vector:** pCMV-GLuc (Gaussia Luciferase N-terminal tag vector)

**Antibiotic Selection:** Kan

**Creator(s):** Jinyong Luo and Ni Tang, Molecular Oncology Lab of The University of Chicago

**Date of Construction:** Dec, 2006



**GLuc C-terminal fusion linker site:**

3'-end GLuc      4xGly+Ser      *Hind* III      *Not* I      *Xho* I      *Xba* I      *Bam*HI  
.....  
GGT GGT GAC gga ggc ggc gga tca gaa gct tgc ggc cgc ctc gag tct aga gga

*Eco*RI      *Bgl* II  
tcc gaa ttc tag atc t  
**Stop**

*Xba*I (methylated)

# pCMV-GLuc Full-length Sequence and Restriction Sites

TAGTTATTATGTTTAAacttaattaagtgcacgagtggggttacatcgaactggatctcaacagcggtaagatccttgagagtttctg  
ccccgaagaacggttttccaatgatgagcacttttaagttctgctatgtggcgcgggtattatcccgtgtgacgcggggcaagagca  
actcggtcgcccatacactattctcagaatgacttgggtgagtagtaccagtcacagaaaagcatcttacggatggcatgacagt  
aagagaattatgcagtgctgccataaccatgagtgataaacactgcccgaacttacttctgacaacgatcggaggaccgaaggagct  
aaccgcttttttgcaacaatgggggatcatgtaactgccttgatcgttgggaaccggagctgaatgaagccataccaaacgacga  
gcgtgacaccacgatgcctgcagcaatggcaacaacggttgcgcaaacattactggaactacttactctagcttcccggcaaca  
ATTAATAGTAATCAATTACGGGGTCATTAGTTTCATAGCCCATATATGGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGCTG  
GCTGACCCGCCAACGACCCCCGCCATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAGGGACTTTCATTGACGTC  
AATGGGTGGAGTATTTACGGTAAACTGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACGTCAATG  
ACGGTAAATGGCCCGCTGGCATTATGCCAGTACATGACCTTATGGGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCG  
CTATTACCATGGTGTATGCGGTTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTTGACTCACGGGGATTTCCAAGTCTCCACCCCA  
TTGACGTCAATGGGAGTTTTGTTTTGGCACAAAATCAACGGGACTTTCAAAATGTGCTAACAACCTCCGCCCCATTGACGCCAAATGG  
GCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTGGTTTTAGTGAACCGTCAGATCCgctagagatcggtaggATGG  
AGTCAAAGTT CTGTTTGCCC TGATCTGCAT CGCTGTGGCC GAGGCCAAGC CCACCGAGAA CAACGAAGAC TTCAACATCG  
TGGCCGTGGC CAGCAACTTC GCGACCACGG ATCTCGATGC TGACCCGCGG AAGTTGCCCG GCAAGAAGCT GCCGCTGGAG  
GTGCTCAAAG AGATGGAAGC CAATGCCCGG AAAGCTGGCT GCACCAGGGG CTGTCTGATC TGCCTGTCCC ACATCAAGTG  
CACGCCAAG ATGAAGAAGT TCATCCCAGG ACGCTGCCAC ACCTACGAAG GCGACAAAGA GTCCGCACAG GCGGCATAG  
GCGAGGCGAT CGTCGACATT CCTGAGATT CTGGGTTCAA GGACTTGGAG CCCATGGAG AGTTCATCGC ACAGGTCGAT  
CTGTGTGTGG ACTGCACAAC TGGCTGCCTC AAAGGGCTG CCAACGTGCA GTGTTCTGAC CTGCTCAAGA AGTGGCTGCC  
GCAACGCTGT GCGACCTTG CCAGCAAGT CCAGGGCCAG GTGGACAAGA TCAAGGGGGC CGTGGTGAC gga ggc  
ggc gga tca gaa gtt tgc ggc ctc cgc ctc gag tct aga gga tcc gaa ttc lagatct  
atccgatccaccggannnnnTAACGTATCATAATCAGCCATACCAGATTTGTAGAGTTTTACTTGTCTTTAAAAAACCTCCCACAC  
CTCCCCCTGAACCTGAAACATAAAAATGAATGCAATTGTTGTTGTTAACTTGTATTATGCAGCTTATAATGGTTACAAATAAAGCAAT  
AGCATCACAAATTTACAAATAAAGCATTTTTTTCACTGCATTCTAGTTGTGGTTTTGTCCAAACTCATCAATGTATCTTAACGCGTA  
AATTGTAAGCGTTAATATTTTTGTTAAAAATTCGCGTTAAATTTTTGTTAAATCAGCTCATTTTTTAAACCAATAGGCCGAAATCGGCAA  
AATCCCTTATAAATCAAAAAGATAGACCGAGATAGGGTTGAGTGTGTTCCAGTTTTGGAACAAGAGTCCACTATTAAGAACGTGGA  
CTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCACTACGTGAACCATCACCTAATCAAGTTTTTTGGGGTTCGAG  
GTGCCGTAAAGCACTAAATCGGAACCTAAAGGGAGCCCCGATTTAGAGCTTGACGGGGAAAGCCGGCGAACGTGGCGAGAAAGGA  
AGGGAAGAAAGCGAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTACGCTGCGCGTAACCACCACACCCGCCGCGCTTAA  
TGCGCCGCTACAGGGCGCTCAGGTGGCACTTTTCGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAA  
TATGTATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGTCCCTGAGGCGGAAAGAACCAGCTG  
TGGAATGTGTGTAGTTAGGGTGTGGAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCA  
ACCAGGTGTGGAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCATAGTCCCCGCC  
CTAACTCCGCCCATCCCCCCCCCTAACTCCGCCAGTTCGCCCCATTCTCCGCCCATGGCTGACTAATTTTTTTTTTATTTATGCAGAG  
GCCGAGGCCGCTCGGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTTTGCAAAGATCGATCAAGA  
GACAGGATGAGGATCGTTTTCGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTCCGGCTA  
TGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTGAGCGCAGGGGCGCCCGGTTCTTTTTGTCAAGC  
CGACCTGTCCGGTGCCCTGAATGAACTGCAAGACGAGGCGAGCGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCAGCTGT  
GCTCGACGTTGTACTGAAGCGGGAAGGGACTGGCTGCTATTGGCGAAGTCCCGGGCAGGATCTCCTGTCTCATCTCACCTTGTCTC  
TGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGCTGCATACGCTTGTATCCGGCTACCTGCCCATTCGACCACCAAGCGAA  
ACATCGCATCGAGCGAGCAGTACTCGGATGGAAGCCGGTCTTGTGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCC  
AGCCGAACGTGTTCCGCCAGGCTCAAGGCGAGCATGCCCCGAGCGAGGATCTCGTCTGACCCATGGCGATGCTGCTTGGCGAATAT  
CATGGTGGAAAATGGCCGCTTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTAC  
CCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCTCTGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCAT  
CGCCTTCTATCGCCTTCTTTCGACGAGTCTTCTGAGCGGGACTCTGGGGTTGAAATGACCGACCAAGCGACGCCAACCTGCCATCA  
CGAGATTTTCGATTCCACCGCCGCTTCTATGAAAGTTGGGCTTCGGAATCGTTTTCCGGGACCGGCTGGATGATCTCCAGCGC  
GGGATCTCATGCTGGAGTCTTTCGCCACCCCTAGGGGGAGGCTAACTGAAACACGGAAGGAGACAATACCGGAAGGAACCCGCGCT  
ATGACGGCAATAAAAAGACAGAATAAAAACGCACGGTGTGGGTGCTTTGTTTCATAAACCGGGGTTCCGGTCCCAGGGCTGGCACTCT  
GTGATACCCACCGAGACCCATTGGGGCCAATACGCCCGCTTTCTTCTTTTCCCCACCCACCCCAAGTTCCGGGTGAAGGC  
CCAGGGCTCGCAGCAACGTGCGGGCGGCAGGCCCTGCCATAGCCTCAGGTTACTCATATATACTTTAGATTGATTTAAAACCTTCAT  
TTTTAATTTAAAAGGATCTAGGTGAAGATCTTTTTGATAATCTCATGACCAAAAATCCCTTAACTGAGTTTTTCGTTCCACTGAGCG  
TCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAAACAAAAAACCCCG  
CTACCAGCGGTGGTTTTGTTTGGCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAAGTGGCTTCAGCAGAGCGCAGATACCAAAT  
ACTGTCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCTACATACCTCGCTCTGCTAATCCTGTTA  
CCAGTGGCTGCTGCCAGTGGCGATAAGTCTGTCTTACCAGGTTGGACTCAAGACGATAGTTACCAGGATAAGGCGCAGCGGTGGGC  
TGAACGGGGGTTCTGTGCACACAGCCAGCTTGGAGCGCAACGACCTACACCGAATGAGATACTACAGCGTGGATGATGAGAAAGC  
GCCACGCTCCCGAAGGTAAGGCGGACAGGATCCGGTAAAGCGGCGAGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGG  
GCAACGCTTGGTATCTTTAATAGTCTGCTGGGTTTTCCGCCACCTCTGACTTGGCGTCAATTTTTGTGATGCTCGTCAGGGGGCGG  
AGCCTATGGA AAAACGCCAGCAACGCGCCTTTTTACGGTTCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCTGCGTTA  
TCCCCTGATTCTGTGGATAACCGTATTACCGCCATGCAT

**Unique enzymes in pCMV-GLuc:**

Pme I	CTTT AAAC	15
Pac I	TTA,AT`TAA	24
Sca I	AGT ACT	219
EcoN I	CCTNN`N,NNAGG	339
Pst I	C, TGCA`G	458
Ase I	AT`TA,AT	525
Vsp I	AT`TA,AT	525
Nde I	CA`TA,TG	752
SnaB I	TAC GTA	858
Acc65 I	G`GTAC,C	1119
Asp718	G`GTAC,C	1119
Kpn I	G,GTAC`C	1123
Bbv II	GAAGAC 7/11	1200
Bbs I	GAAGAC 8/12	1201
Nru I	TCG CGA	1230
Sac II	CC,GC`GG	1256
Ahd I	GACNN,N`NNGTC	1427
Sal I	G`TCGA,C	1461
Acc I	GT`MK,AC	1462
Hind III	A`AGCT,T	1696
Not I	GC`GGCC,GC	1703
Ava I	C`YCGR,G	1710
Paer7 I	C`TCGA,G	1710
Xho I	C`TCGA,G	1710
BamH I	G`GATC,C	1722
EcoR I	G`AATT,C	1728
Bgl II	A`GATC,T	1735
PflM I	CCAN,NNN`NTGG	1754
BstX I	CCAN,NNNN`NTGG	1755
Bcl I	T`GATC,A	1766
Mun I	C`AATT,G	1859
Hpa I	GTT AAC	1872
Mlu I	A`CGCG,T	1995
Dra III	CAC,NNN`GTG	2225
Sfi I	GGCCN,NNN`NGGCC	2884
BseR I	GAGGAG 16/14	2927
Stu I	AGG CCT	2930
Cla I	AT`CG,AT	2949
Kas I	G`GCGC,C	3108
Nar I	GG`CG,CC	3109
Ehe I	GGC GCC	3110
Bbe I	G,GCGC`C	3112
Tth111 I	GACN`N,NGTC	3227
Rsr II	CG`GWC,CG	3625
BsiC I	TT`CG,AA	3791
BstB I	TT`CG,AA	3791
Bsa I	GGTCTC 7/11	4098
EcoO109 I	RG`GNC,CY	4207

Number of enzymes = 48

Ase I	(1)	525		
Asp718	(1)	1119		
Ava I	(1)	1710		
Ava II	(3)	336	3625	4070
Avr II	(2)	2931	3946	
BamH I	(1)	1722		
Ban I	(5)	983	1119	2262 3108
		3143		
Ban II	(4)	1501	2300	3474 4184
Bbe I	(1)	3112		
Bbs I	(1)	1201		
Bbv I	(7)	468	1897	3182 3224
		3745	4198	4698
Bbv II	(1)	1200		
Bcl I	(1)	1766		
Bcn I	(8)	165	516	1268 1317
		3114	3274	3887 4651
Bfa I	(10)	507	1110	1717 1733
		1958	2376	2932 3947
		4281	4534	
Bgl I	(4)	608	730	801 2884
Bgl II	(1)	1735		
Bpm I	(3)	1305	3892	3949
Bsa I	(1)	4098		
BsaA I	(3)	858	2225	3413
BsaB I	(3)	1155	1771	2968
BsaH I	(8)	160	640	693 776
		962	3109	3811 3890
BsaJ I	(25)	878	1123	1168 1213
		1234	1253	1333 1394
		1479	1501	1640 2643
		2715	2838	2873 2882
		2931	3272	3541 3946
		4073	4074	4176 4177
		4867		
BsaW I	(6)	404	1750	3140 3984
		4674	4821	
BseR I	(1)	2927		
Bsg I	(3)	1313	1526	1596
BsiC I	(1)	3791		
BsiE I	(6)	182	331	1459 1706
		3018	4693	
BsiHKA I	(7)	32	117	1294 1371
		3222	3412	4717
Bsm I	(2)	1860	1953	
BsmA I	(5)	951	2534	2952 3971
		4099		
BsmF I	(11)	693	844	1012 1340
		2625	2697	2761 3260
		3792	3901	4056
BsoF I	(43)	185	280	307 457
		1278	1281	1328 1403
		1442	1553	1605 1608
		1685	1703	1706 1886
		2405	2427	2441 2879
		3018	3070	3081 3171
		3176	3213	3254 3341
		3344	3347	3583 3679
		3720	3734	3848 4187
		4202	4413	4619 4622
		4687	4830	4985
Bsp1286 I	(2)	117	3412	
BspH I	(2)	2535	4307	
BspM I	(4)	1597	2996	3377 3827
Bsr I	(12)	54	226	493 814
		1552	2139	2817 3052
		3253	4499	4613 4626
BsrB I	(4)	2369	2533	3722 3776
BsrD I	(2)	466	3342	
BssS I	(4)	31	3701	3827 4854
BstB I	(1)	3791		
BstN I	(16)	608	801	1334 1396
		1480	1641	1647 2645
		2700	2717	3496 4075
		4178	4868	4881 5002
BstU I	(18)	141	578	1230 1255
		1997	2033	2409 2429
		2453	2484	3175 3476
		3914	3998	4061 4130
		4403	4984	
BstX I	(1)	1755		
BstY I	(14)	53	70	1103 1238
		1636	1722	1735 3280
		3526	3918	4277 4289
		4375	4386	
Bsu36 I	(2)	2589	4221	
Cac8 I	(34)	454	604	797 1220
		1325	1371	1567 1631
		1700	2328	2371 2385
		2658	2677	2730 2749
		3003	3189	3408 3474
		3480	3508	3512 3553
		3557	3611	3894 4081
		4128	4184	4206 4417
		4977	5014	
Cfr10 I	(5)	1668	2326	3428 3609
		3892		
Cla I	(1)	2949		
Csp6 I	(9)	218	736	761 816
		849	900	1057 1120
		3414		
Dde I	(8)	199	1471	2589 2891
		3772	4221	4344 4753
Dpn I	(35)	55	72	330 376

**The following enzymes do not cut in pCMV-GLuc:**

Afl II	Age I	Apa I	Asc I	Blp I
BsiW I	BsmB I	Bsp120 I	BspM II	BsrG I
BssH II	Bst1107 I	BstE II	Eco47 III	Eco72 I
EcoR V	Esp I	Fse I	Nhe I	Pml I
PpuM I	PspA I	Sac I	Sma I	Spe I
Spl I	Srf I	Xca I	Xcm I	Xma I

**pCMV-GLuc: sites sorted by name:**

Aat II	(4)	643	696	779	965
Acc I	(1)	1462			
Acc65 I	(1)	1119			
Aci I	(69)	64	141	185	306
		352	576	604	616
		630	797	888	921
		1025	1046	1107	1253
		1255	1281	1432	1441
		1608	1684	1687	1702
		1706	2369	2396	2424
		2427	2441	2484	2531
		2594	2779	2791	2800
		2812	2822	2833	2879
		3018	3081	3175	3239
		3340	3343	3583	3623
		3628	3678	3694	3720
		3776	3845	3848	3914
		3996	4061	4128	4201
		4435	4444	4579	4689
		4810	4829	4956	4984
		5075			
Afl III	(2)	1995	5027		
Aha II	(8)	160	640	693	776
		962	3109	3811	3890
Ahd I	(1)	1427			
Alu I	(18)	347	410	510	1084
		1277	1323	1698	1888
		2055	2312	2607	2895
		3215	3673	4470	4727
		4773	4863		
Alw I	(21)	60	66	381	1099
		1245	1632	1696	1718
		1729	1740	2976	3287
		3354	3533	3898	3925
		4284	4285	4382	4382
		4468			
AlwN I	(3)	1339	4210	4618	
ApaL I	(3)	28	1367	4713	
Apo I	(4)	1728	1923	2027	2038



		3439	3448	3526	3902
		3918	4277	4289	4367
		4375	4386	4461	
Sau96 I	(11)	336	601	794	1643
		1666	2216	3625	4070
		4116	4174	4207	
Sca I	(1)	219			
ScrF I	(24)	164	515	608	801
		1267	1316	1334	1396
		1480	1641	1647	2645
		2700	2717	3113	3273
		3496	3886	4075	4178
		4650	4868	4881	5002
Sec I	(25)	878	1123	1168	1213
		1234	1253	1333	1394
		1479	1501	1640	2643
		2715	2838	2873	2882
		2931	3272	3541	3946
		4073	4074	4176	4177
		4867			
SfaN I	(15)	247	440	876	1164
		1236	1924	2687	2759
		3068	3323	3407	3471
		3539	3746	4931	
Sfc I	(4)	454	2444	4571	4762
Sfi I	(1)	2884			
SnaB I	(1)	858			
Sph I	(3)	2679	2751	3514	
Ssp I	(2)	2017	2570		
Stu I	(1)	2930			
Sty I	(7)	878	1123	1501	2838
		2931	3541	3946	
Taq I	(16)	46	1243	1462	1525
		1711	2258	2949	3222
		3378	3402	3438	3600
		3791	3836	4091	4929
Tfi I	(6)	1475	3594	3728	3838
		3875	5053		
Tsp45 I	(6)	227	438	1674	2398
		3229	3535		
Tth111 I	(1)	3227			
Tth111 II	(5)	1132	3545	4405	4435
		4444			
Vsp I	(1)	525			
Xba I	(2)	1716	1732		
Xho I	(1)	1710			
Xho II	(14)	53	70	1103	1238
		1636	1722	1735	3280
		3526	3918	4277	4289
		4375	4386		
Xma III	(2)	1703	3015		
Xmn I	(2)	100	1386		

### Site usage in pCMV-GLuc:

Aat II	G,ACGT`C	4	Acc I	GT`MK,AC	1
Acc65 I	G`GTAC,C	1	Aci I	C`CG,C	69
Afl II	C`TTAA,G	-	Afl III	A`CRYG,T	2
Age I	A`CCGG,T	-	Aha II	GR`CG,YC	8
Ahd I	GACNN,N`NNGTC	1	Alu I	AG CT	18
Alw I	GGATC 8/9	21	AlwN I	CAG,NNN`CTG	3
Apa I	G,GGCC`C	-	ApaL I	G`TGCA,C	3
Apo I	R`AATT,Y	4	Asc I	GG`CGCG,CC	-
Ase I	AT`TA,AT	1	Asp718	G`GTAC,C	1
Ava I	C`YCGR,G	1	Ava II	G`GWC,C	3
Avr II	C`CTAG,G	2	BamH I	G`GATC,C	1
Ban I	G`GYRC,C	5	Ban II	G,RCGY`C	4
Bbe I	G,CGGC`C	1	Bbs I	GAAGAC 8/12	1
Bbv I	GCAGC 13/17	7	Bbv II	GAAGAC 7/11	1
Bcl I	T`GATC,A	1	Bcn I	CC,S`GG	8
Bfa I	C`TA,G	10	Bgl I	GCCN,NNN`NGGC	4
Bgl II	A`GATC,T	1	Blp I	GC`TNA,GC	-
Bpm I	CTGGAG 22/20	3	Bsa I	GGTCTC 7/11	1
BsaA I	YAC GTR	3	BsaB I	GATNN NNAATC	3
BsaH I	GR`CG,YC	8	BsaJ I	C`CNNG,G	25
BsaW I	W`CCGG,W	6	BseR I	GAGGAG 16/14	1

Bsg I	GTGCAG 22/20	3	BsiC I	TT`CG,AA	1
BsiE I	CG,RY`CG	6	BsiHKA I	G,WGCW`C	7
BsiW I	C`GTAC,G	-	Bsm I	GAATG,C 7	2
BsmA I	GTCTC`9	5	BsmB I	CGTCTC 7/11	-
BsmF I	GGGAC 15/19	11	BsoF I	GC`N,GC	43
Bsp120 I	G`GGCC,C	-	Bsp1286 I	G,DGCH`C	2
BspH I	T`CATG,A	2	BspM I	ACCTGC 10/14	4
BspM II	T`CCGG,A	-	Bsr I	ACT,GG`	12
BsrB I	GAG CGG	4	BsrD I	GCAATG, 8	2
BsrG I	T`GTAC,A	-	Bssh II	G`CGCG,C	-
BssS I	C`TCGT,G	4	Bst1107 I	GTA TAC	-
BstB I	TT`CG,AA	1	BstE II	G`GTNAC,C	-
BstN I	CC`W,GG	16	BstU I	CG CG	18
BstX I	G`CAN,NNNN`NTGG	1	BstY I	R`GATC,Y	14
Bsu36 I	CC`TNA,GG	2	Cac8 I	GCN NGC	34
Cfr10 I	R`CCGG,Y	5	Cla I	AT`CG,AT	1
Csp6 I	G`TA,C	9	Dde I	C`TNA,G	8
Dpn I	GA TC	35	DpnII	`GATC,	35
Dra I	TTT AAA	5	Dra III	CAC,NNN`GTG	1
Drd I	GACNN,NN`NNGTC	3	Dsa I	C`CRYG,G	8
Eae I	Y`GGCC,R	9	Eag I	C`GGCC,G	2
Ear I	CTCTTC 7/10	3	Eco47 III	AGC GCT	-
Eco57 I	CTGAAG 21/19	3	Eco72 I	CAC GTG	-
EcoN I	CCTNN`N,NNAGG	1	Eco109 I	RG`GNC,CY	1
EcoR I	G`AATT,C	1	EcoR II	`CCGGG,	16
EcoR V	GAT ATC	-	Ehe I	GGC GCC	1
Esp I	GC`TNA,GC	-	Fnu4H I	GC`N,GC	43
Fok I	GGATG 14/18	7	Fse I	GG,CCGG`CC	-
Fsp I	TGC GCA	2	Gdi II	`YGGC,CG	9
Gsu I	CTGGAG 21/19	3	Hae I	WGG CCW	7
Hae II	R,CGCG`Y	4	Hae III	GG CC	27
Hga I	GACCG 9/14	8	HgiA I	G,WGCW`C	7
HgiE II	ACCCNNNNNGGT -1/132	-	Hha I	G,CG`C	22
Hinc II	GTY RAC	3	Hind II	GTY RAC	3
Hind III	A`AGCT,T	1	Hinf I	G`ANT,C	15
HinI I	GR`CG,YC	8	HinP I	G`CG,C	22
Hpa I	GTT AAC	1	Hpa II	C`CG,C	23
Hph I	GGTGA 12/11	7	Kas I	G`CGCG,C	1
Kpn I	G,GTAC`C	1	Mae I	C`TA,G	10
Mae II	A`CG,T	17	Mae III	`GTNAC,	17
Mbo I	`GATC,	35	Mbo II	GAAGA 12/11	12
Mlu I	A`CGCG,T	1	Mme I	TCCRAC 25/23	3
Mnl I	CCTC 10/10	32	Msc I	TGG CCA	2
Mse I	T`TA,A	20	Msl I	CAYNN NNRTG	5
Msp I	C`CG,G	23	MspA I	CMG CKG	7
Mun I	C`AATT,G	1	Nae I	GCC GGC	3
Nar I	GG`CG,CC	1	Nci I	CC`S,GG	8
Nco I	C`CATG,G	5	Nde I	CA`TA,TG	1
Ngom I	G`CCGG,C	3	Nhe I	G`CTAG,C	-
Nla III	,CATG`	21	Nla IV	GGN NCC	19
Not I	GC`GGCC,GC	1	Nru I	TCG CGA	1
Nsi I	A,TGCA`T	3	Nsp7524 I	R`CATG,Y	4
NspB II	CMG CKG	7	NspH I	R,CATG`Y	4
Pac I	TTA,AT`TAA	1	Paer7 I	C`TCGA,G	1
Pal I	GG CC	27	Pf1M I	CCAN,NNN`NTGG	1
Ple I	GAGTC 9/10	5	Pme I	CTTT AAAC	1
Pml I	CAC GTG	-	PpuM I	RG`GWC,CY	-
Psp1406 I	AA`CG,TT	2	PspA I	C`CCGG,G	-
Pst I	C,TGCA`G	1	Pvu I	CG,AT`CG	2
Pvu II	CAG CTG	2	Rsa I	GT AC	9
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	GCTCTC 8/11	2	Sau3A I	`GATC,	35
Sau96 I	G`GNC,C	11	Sca I	AGT ACT	1
ScrF I	CC`N,GG	24	Sec I	C`CNNG,G	25
SfaN I	GCATC 9/13	15	Sfc I	C`TRYA,G	4
Sfi I	GCCCN,NNN`NGGCC	1	Sma I	CCC GGG	-
SnaB I	TAC GTA	1	Spe I	A`CTAG,T	-
Sph I	G,CATG`C	3	Spl I	C`GTAC,G	-
Srf I	GCCC GGGC	-	Ssp I	AAT ATT	2
Stu I	AGG CCT	1	Sty I	C`CWWG,G	7
Taq I	T`CG,A	16	Tfi I	G`AWT,C	6
Tsp45 I	`GTSAC,	6	Tth111 I	GACN`N,NGTC	1
Tth111 II	CAARCA 16/14	5	Vsp I	AT`TA,AT	1
Xba I	T`CTAG,A	2	Xca I	GTA TAC	-
Xcm I	CCANNNN,N`NNNNTGG-	3	Xho I	C`TCGA,G	1
Xho II	R`GATC,Y	14	Xma I	C`CCGG,G	-
Xma III	C`GGCC,G	2	Xmn I	GAANN NNTTC	2