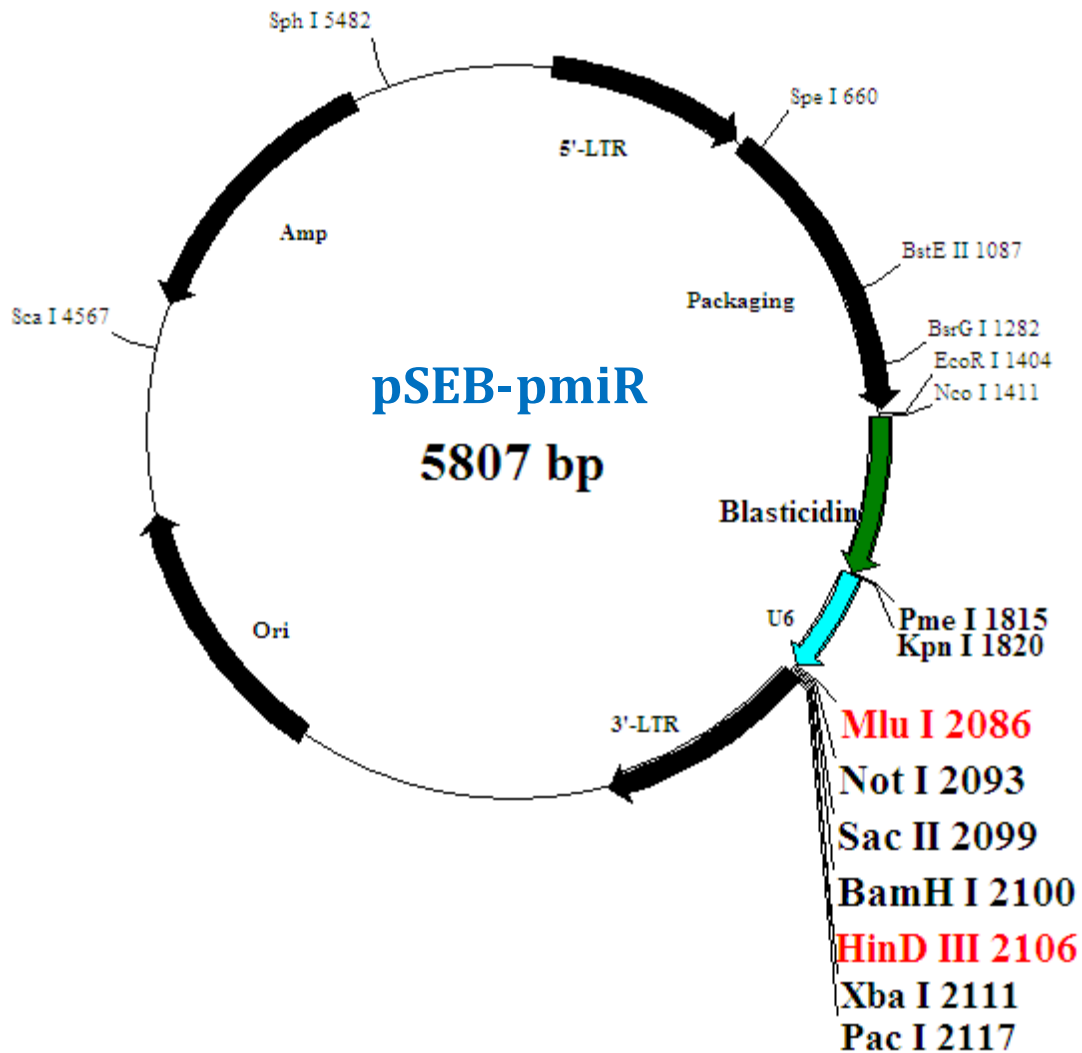


**Vector:** pSEB-pmiR (retroviral vector for pre-miR or Anti-miR Oligo cassette)

**Antibiotic Selection:** Amp

**Creator(S):** Qiang Wei, Molecular Oncology Lab of The University of Chicago Medical Center

**Date of Construction:** October, 2016



**Designing pre-miR or anti-miR Oligo Cassette (MluI/HindIII)**

5' - **cgcg**NNNNNNNNNNNNNNNNNNNNNNNNNNNN**TTTTT**-3'

3' - nnnnnnnnnnnnnnnnnnnnnnnnnnnnn**AAAAA**tcga-5'

## pSEB-pmiR Vector Sequence

TGAAAGACCCACCTGTAGGTTTGGCAAGCTAGCTTAAAGTAAACGCCATTTTGAAGGCATGGAAAATACATAACTGAGAATAGAGAAGTTA  
 GATCAAGGTTAGGAACAGAGACAGCAGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTCCCCGGCTCAGGGCCAAGAACAG  
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 CGGCGCCAGTCTCCGATAGACTGCGTCGCCGGGTACCCGATTTCCCAATAAAGCCTCTGCTGTTTGCATCCGAATCGTGGACTCGC  
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 CAACCCTGGGAGACGTCCAGGACTTTGGGGCCGTTTTTGTGGCCGACTGAGGAAGGGAGTTCGATGTGAATCCGACCCCGTCCAGGA  
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 TACC **aaggctcgggacaggaagaggcctatttc**ccatgattccttcatatttgcataatcagatacaaggctgttagagagataaattagaatt  
 aatttgactgtaaacacaaagataattagtagcaaaaatcgtgacgtagaaagtaataatttcttgggtagtttgcagttttaaataattatgtt  
 ttaaattgactatcatatcttaccgtaacttgaagatttctgatttcttgg **ctttatatacttctgtggaaggacgaaaACCGCTCGC**  
**CGCCGGATCC****AAGCTTCTAGATTAATTA**CGATAAAAATAAAAAGATTTTTATTTAGTCTCCAGAAAAGGGGGAAATGAAAGACCCCACT  
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 CCAGCTGAAGCCTATAGAGTACGAGCCATAGATAAAAATAAAGATTTTATTTAGTCTCCAGAAAAGGGGGGAA

Unique enzymes in pSEB-pmiR:

Spe I	A`CTAG,T	660	BsrG I	T`GTAC,A	1282
BstE II	G`GTNAC,C	1087	EcoR I	G`AATT,C	1404

Nco I	C`CATG,G	1411			Bcn I	(14)	164	399	400	571
Bbv II	GAAGAC 7/11	1497					724	2335	2570	2571
Bbs I	GAAGAC 8/12	1498					3575	4271	4622	5123
Bsg I	GTGCAG 22/20	1600					5158	5509		
Nru I	TCG CGA	1644			Bfa I	(13)	31	219	661	673
BsaB I	GATNN NNATC	1711					1394	1522	2113	2200
Pme I	CTTT AAAC	1815					2390	3689	3942	4277
BsaA I	YAC GTR	1950					5712			
Mlu I	A`CGCG,T	2086			Bgl I	(2)	4207	5325		
Not I	GC`GGCC,GC	2093			Bpm I	(3)	2137	4157	5775	
Sac II	CC,GC`GG	2099			Bsa I	(6)	476	530	1149	2625
BamH I	G`GATC,C	2100					2646	4148		
HinD III	A`AGCT,T	2106			BsaA I	(1)	1950			
Sca I	AGT ACT	4567			BsaB I	(1)	1711			
Sph I	G,CATG`C	5482			BsaH I	(8)	742	1398	4624	5006
Number of enzymes = 19							5310	5493	5607	5628

The following enzymes do not cut in pSEB-pmiR:

Acc I	Age I	Apa I	Avr II	Bcl I	BsaJ I	(32)	161	240	250	397
Bgl II	Blp I	BsiC I	BsiW I	Bsm I			461	497	546	547
Bsp120 I	Bsp1286 I	BspM I	BspM II	Bst1107 I			694	733	734	746
BstB I	BstX I	Cla I	Dra III	Eco72 I			747	1167	1236	1245
Esp I	Fse I	HinC II	Hind II	Hpa I			1265	1266	1411	1716
Mun I	Nsi I	PaeR7 I	PflM I	Pml I	BsaW I	(3)	3400	3547	4378	
Rsr II	Sal I	Sfi I	SnaB I	Spl I	BseR I	(4)	464	1293	1332	2634
Srf I	Stu I	Xca I	Xcm I	Xho I	Bsg I	(1)	1600			
pSEB-pmiR: sites sorted by name:					BsiE I	(10)	592	727	1532	1648
Aat II	(2)	745	5009				2096	3110	3534	4457
Acc65 I	(3)	401	1820	2572	BsiHKA I	(6)	338	2509	3512	4673
Aci I	(58)	197	203	566			4606	5353		
		688	727	860	BsmA I	(21)	107	475	531	609
		1042	1133	1199			734	832	949	1073
		1317	1355	1532			1132	1150	1328	1431
		1681	2092	2096			2154	2277	2624	2645
		2368	2374	2670			4149	4923	5076	5120
		2987	3043	3053	BsmB I	(7)	733	831	1072	1131
		3120	3127	3148			1329	5077	5119	
		3267	3394	3413	BsmF I	(10)	172	185	564	729
		3644	3779	3788			764	1205	1585	2343
		4241	4432	4478	BsoF I	(36)	727	901	917	920
		4643	4720	4829			925	928	1133	1513
		4975	5149	5188			1532	1606	1609	1612
		5224	5262	5275			1615	1618	1782	2093
		5358	5617				2096	3019	3100	3118
Afl II	(3)	35	1006	2204			3121	3239	3394	3537
Afl III	(2)	2086	3194				3602	3605	3811	4139
Aha II	(8)	742	1398	4624			4478	4505	4600	4829
		5310	5493	5607			5116	5225	5329	5402
Ahd I	(4)	1020	2617	2663			3914	4922	5027	5551
Alu I	(28)	30	34	336	BspH I	(4)	374	1030	1058	1546
		668	676	1515			1570	2545	2995	3601
		2108	2199	2203			3614	3728	4134	4252
		2826	2859	2954	Bsr I	(16)	4295	4562	4734	5440
		3136	3362	3452			1042	2886	3127	4928
		3755	4276	4376	BsrB I	(4)	4148	4322		
		5118	5137	5382	BsrD I	(2)	1282			
Alw I	(14)	453	1051	1357	BsrG I	(1)	317	368	2488	2539
		2096	2107	3756			317	368	2488	2539
		3842	3939	3940	BssH II	(4)	1587	3367	4751	5058
		4719	4725	4404	Bsss I	(4)	1087			
					BstE II	(1)	1087			
AlwN I	(2)	2328	3610		BstN I	(17)	241	548	735	748
ApaL I	(3)	3508	4754	5251			1169	1194	1217	1237
Apo I	(2)	872	1404				1267	1717	2412	2934
Asc I	(2)	368	2539				3222	3343	3356	5429
Ase I	(6)	1911	2118	2837			5706			
		3024	4259	2965	BstU I	(22)	317	319	370	903
Asp718	(3)	401	1820	2572			905	1135	1644	2088
Ava I	(5)	331	397	498			2098	2488	2490	2541
		2568		2502			3041	3043	3241	3822
Ava II	(13)	186	199	254			4152	4645	4977	5077
		690	1219	1572			5079	5182		
		2370	2425	4225	BstY I	(7)	2100	3835	3846	3932
		5702					3944	4712	4729	
BamH I	(1)	2100			Bsu36 I	(2)	781	1018		
Ban I	(14)	244	401	1142			32	319	370	
		1687	1820	2415	Cac8 I	(32)	28	586	631	650
		2938	4035	5309			582	1199	1508	1622
		5606	5627	5492			1199	1508	1622	2090
Ban II	(7)	338	351	1677			2197	2201	2490	2541
		2522	5559	5573			2987	3016	3125	3211
Bbe I	(5)	1401	5313	5496			3248	3808	4199	5212
		5631		5610			5360	5380	5384	5480
Bbs I	(1)	1498					5521	5569	5611	5641
Bbv I	(9)	931	939	1524			629	4167	5630	5639
		3613	3616	3822			402	658	1283	1821
		5127		4516			1940	2573	4566	5242
Bbv II	(1)	1497					5753			
					Dde I	(19)	75	167	208	476

		781	1018	1290	1808			2751	2772	3029	3094
		2244	2338	2379	2648			3169	3565	4082	5720
		2719	3469	3878	4044	HinI I	(8)	742	1398	4624	5006
		4584	5010	5245				5310	5493	5607	5628
Dpn I	(25)	94	459	1046	1178	HinP I	(36)	317	319	368	370
		1363	1647	1708	1722			646	903	922	1398
		2102	2264	3762	3837			1510	2488	2490	2539
		3848	3856	3934	3946			2541	2816	2976	3041
		4051	4392	4410	4456			3069	3102	3372	3439
		4714	4731	4767	5352			3539	3713	3822	4215
		5576						4308	4645	4977	5077
DpnII	(25)	92	457	1044	1176			5180	5310	5331	5464
		1361	1645	1706	1720			5493	5547	5607	5628
		2100	2262	3760	3835	Hpa II	(24)	163	398	569	630
		3846	3854	3932	3944			723	1401	2334	2569
		4049	4390	4408	4454			2912	3401	3548	3574
		4712	4729	4765	5350			3764	4168	4202	4269
		5574						4379	4621	5122	5156
Dra I	(6)	1815	1992	2005	3953			5508	5631	5640	5655
		3972	4664			Hph I	(13)	1157	1183	1401	3931
Drd I	(3)	1500	3302	5171				4158	4572	4780	4813
Dsa I	(4)	694	1411	2096	5512			5097	5106	5599	5644
Eae I	(11)	582	724	1109	1130			5725			
		1414	1529	2093	3033	Kas I	(5)	1397	5309	5492	5606
		4475	5509	5641				5627			
Eag I	(3)	724	1529	2093		Kpn I	(3)	405	1824	2576	
Ear I	(7)	1070	1311	1833	2816	Mae I	(13)	31	219	661	673
		3078	4882	5370				1394	1522	2113	2200
Eco47 III	(2)	923	5548					2390	3689	3942	4277
Eco57 I	(4)	1509	3741	4755	5759			5712			
EcoN I	(2)	784	1392			Mae II	(10)	742	1081	1122	1949
EcoO109 I	(7)	254	1219	1572	1843			1954	3897	4313	4686
		2425	5063	5517				5006	5448		
EcoR I	(1)	1404				Mae III	(20)	39	994	1022	1087
EcoR II	(17)	239	546	733	746			1231	1950	2029	2208
		1167	1192	1215	1235			2686	3550	3613	3729
		1265	1715	2410	2932			4012	4343	4401	4554
		3220	3341	3354	5427			4742	5130	5421	5441
		5704				Mbo I	(25)	92	457	1044	1176
EcoR V	(3)	140	2310	5695				1361	1645	1706	1720
Ehe I	(5)	1399	5311	5494	5608			2100	2262	3760	3835
		5629						3846	3854	3932	3944
Fnu4H I	(36)	727	901	917	920			4049	4390	4408	4454
		925	928	1133	1513			4712	4729	4765	5350
		1532	1606	1609	1612			5574			
		1615	1618	1782	2093	Mbo II	(15)	1086	1299	1445	1502
		2096	3019	3100	3118			1530	1849	2832	3066
		3121	3239	3394	3537			3855	3928	4683	4761
		3602	3605	3811	4139			4870	5358	5570	
		4478	4505	4600	4829	Mlu I	(1)	2086			
		5116	5225	5329	5402	Mme I	(6)	829	1106	2633	2685
Fok I	(11)	423	1140	1300	1464			3408	3592		
		1699	2593	4053	4234	Mnl I	(47)	167	216	368	387
		4521	5164	5408				432	460	484	506
Fsp I	(2)	4309	5332					510	566	776	872
Gdi II	(11)	723	725	1129	1528			1168	1271	1304	1310
		1530	2092	2094	3034			1313	1319	1349	1352
		4474	5510	5642				1367	1374	1390	1454
Gsu I	(3)	2138	4158	5776				1795	1796	1834	2387
Hae I	(6)	584	1111	1416	3209			2539	2558	2603	2630
		3220	3672					2654	2714	3043	3092
Hae II	(9)	925	1401	3072	3442			3302	3375	3626	4026
		5313	5496	5550	5610			4107	4253	4459	5054
		5631						5112	5372	5656	
Hae III	(29)	129	173	584	726	Msc I	(3)	584	1111	1416	
		762	774	987	1111	Mse I	(28)	36	1007	1119	1149
		1132	1197	1416	1531			1173	1814	1911	1991
		1845	2095	2299	2344			2004	2118	2122	2205
		3035	3209	3220	3238			2739	2837	2965	3024
		3672	4130	4210	4477			3900	3952	3957	3971
		5064	5362	5511	5519			4024	4259	4298	4663
		5643						5035	5216	5413	5683
Hga I	(10)	381	642	895	1491	Msl I	(2)	4339	4498		
		2552	3304	3882	4614	Msp I	(24)	163	398	569	630
		5172	5641					723	1401	2334	2569
HgiA I	(6)	338	2509	3512	4673			2912	3401	3548	3574
		4758	5255					3764	4168	4202	4269
HgiE II	(2)	3773	5253					4379	4621	5122	5156
Hha I	(36)	319	321	370	372			5508	5631	5640	5655
		648	905	924	1400	MspAl I	(11)	588	1620	2098	2670
		1512	2490	2492	2541			3018	3536	3781	4722
		2543	2818	2978	3043			5188	5382	5738	
		3071	3104	3374	3441	Nae I	(2)	631	5641		
		3541	3715	3824	4217	Nar I	(5)	1398	5310	5493	5607
		4310	4647	4979	5079			5628			
		5182	5312	5333	5466	Nci I	(14)	163	398	399	570
		5495	5549	5609	5630			723	2334	2569	2570
HinD III	(1)	2106						3574	4270	4621	5122
Hinf I	(16)	442	450	791	802			5157	5508		
		1437	1769	1858	2729	Nco I	(1)	1411			

Nde I	(2)	2019	5258		
NgoM I	(2)	629	5639		
Nhe I	(2)	30	2199		
Nla III	(18)	62	1205	1415	1858
		2231	2685	2852	3198
		3918	4409	4419	4497
		4533	4926	5031	5115
		5482	5555		
Nla IV	(33)	188	201	246	403
		521	552	692	761
		893	1144	1221	1399
		1573	1689	1822	2102
		2359	2372	2417	2574
		2940	3226	3265	4037
		4131	4172	4383	4973
		5311	5494	5518	5608
		5629			
Not I	(1)	2093			
Nru I	(1)	1644			
Nsp7524 I	(3)	3194	5111	5478	
NspB II	(11)	588	1620	2098	2670
		3018	3536	3781	4722
		5188	5382	5738	
NspH I	(3)	3198	5115	5482	
Pal I	(29)	129	173	584	726
		762	774	987	1111
		1132	1197	1416	1531
		1845	2095	2299	2344
		3035	3209	3220	3238
		3672	4130	4210	4477
		5064	5362	5511	5519
		5643			
Ple I	(3)	799	2737	3573	
Pme I	(1)	1815			
PpuM I	(4)	254	1219	1572	2425
Psp1406 I	(2)	4313	4686		
PspA I	(2)	397	2568		
Pst I	(3)	921	929	1105	
Pvu I	(3)	1648	4457	5353	
Pvu II	(4)	1620	3018	5382	5738
Rsa I	(9)	403	659	1284	1822
		1941	2574	4567	5243
		5754			
Sac I	(2)	338	2509		
Sac II	(1)	2099			
Sap I	(2)	2816	3078		
Sau3A I	(25)	92	457	1044	1176
		1361	1645	1706	1720
		2100	2262	3760	3835
		3846	3854	3932	3944
		4049	4390	4408	4454
		4712	4729	4765	5350
		5574			
Sau96 I	(27)	127	171	186	199
		254	551	690	760
		773	985	1196	1219
		1572	1843	2297	2342
		2357	2370	2425	4129
		4208	4225	4447	5063
		5360	5517	5702	
Sca I	(1)	4567			
ScrF I	(31)	163	241	398	399
		548	570	723	735
		748	1169	1194	1217
		1237	1267	1717	2334
		2412	2569	2570	2934
		3222	3343	3356	3574
		4270	4621	5122	5157
		5429	5508	5706	
Sec I	(32)	161	240	250	397
		461	497	546	547
		694	733	734	746
		747	1167	1236	1245
		1265	1266	1411	1716
		1824	2096	2332	2411
		2421	2568	2631	2933
		3354	5428	5506	5512
SfaN I	(20)	185	444	641	938
		1485	1542	1674	1720
		2356	2614	3290	4342
		4535	4782	5143	5235
		5273	5311	5627	5639
Sfc I	(10)	15	917	925	1101
		1496	2184	3459	3650
		4328	5746		
Sma I	(2)	399	2570		
Spe I	(1)	660			
Sph I	(1)	5482			
Ssp I	(2)	2737	4891		
Sty I	(7)	250	461	1245	1411

		1824	2421	2631	
Taq I	(9)	794	1038	1349	1360
		1705	2046	2732	3294
		4738			
Tfi I	(8)	442	802	1437	1769
		1858	2772	3029	3169
Tsp45 I	(7)	1022	1231	1950	4343
		4554	5130	5441	
Tth111 I	(4)	390	811	1217	2561
Tth111 II	(8)	146	422	613	632
		2316	3783	3792	3822
Vsp I	(6)	1911	2118	2837	2965
		3024	4259		
Xba I	(3)	218	2112	2389	
Xho II	(7)	2100	3835	3846	3932
		3944	4712	4729	
Xma I	(2)	397	2568		
Xma III	(3)	724	1529	2093	
Xmn I	(3)	2800	2838	4686	

Site usage in pSEB-pmiR:

Aat II	G,ACGT`C	2	Acc I	GT`MK,AC	-
Acc65 I	G`GTAC,C	3	Aci I	C`CG,C	58
Afl II	C`TTAA,G	3	Afl III	A`CRYG,T	2
Age I	A`CCGG,T	-	Aha II	GR`CG,YC	8
Ahd I	GACNN,N`NNGTC	4	Alu I	AG CT	28
Alw I	GGATC 8/9	14	AlwN I	CAG,NNN`CTG	2
Apa I	G,GGCC`C	-	ApaL I	G`TGCA,C	3
Apo I	R`AATT,Y	2	Asc I	GG`CGCG,CC	2
Ase I	AT`TA,AT	6	Asp718	G`GTAC,C	3
Ava I	C`YCGR,G	5	Ava II	G`GWC,C	13
Avr II	C`CTAG,G	-	BamH I	G`GATC,C	1
Ban I	G`GYRC,C	14	Ban II	G,RCGY`C	7
Bbe I	G,CGCC`C	5	Bbs I	GAAGAC 8/12	1
Bbv I	GCAGC 13/17	9	Bbv II	GAAGAC 7/11	1
Bcl I	T`GATC,A	-	Bcn I	CC,S`GG	14
Bfa I	C`TA,G	13	Bgl I	GCCN,NNN`NGGC	2
Bgl II	A`GATC,T	-	Bpl I	GC`TNA,GC	-
Bpm I	CTGGAG 22/20	3	Bsa I	GGTCTC 7/11	6
BsaA I	YAC GTR	1	BsaB I	GATNN NNATC	1
BsaH I	GR`CG,YC	8	BsaJ I	C`CNNG,G	32
BsaW I	W`CCGG,W	3	BseR I	GAGGAG 16/14	4
Bsg I	GTGCG 22/20	1	BsiC I	TT`CG,AA	-
BsiE I	CG,RY`CG	10	BsiHKA I	G,WGCW`C	6
BsiW I	C`GTAC,G	-	Bsm I	GAATG,C 7	-
BsmA I	GTCTC`/9	21	BsmB I	CGTCTC 7/11	7
BsmF I	GGGAC 15/19	10	BsoF I	GC`N,GC	36
Bsp120 I	G`GGCC,C	-	Bsp1286 I	G,DGCH`C	-
BspH I	T`CATG,A	4	BspM I	ACCTGC 10/14	-
BspM II	T`CCGG,A	4	Bsr I	ACT,GG`	16
BsrB I	GAG CGG	4	BsrD I	GCAATG, 8	2
BsrG I	T`GTAC,A	1	Bssh II	G`CGCG,C	4
BssS I	C`TCGT,G	4	Bst1107 I	GTA TAC	-
BstB I	TT`CG,AA	-	BstE II	G`GTNAC,C	1
BstN I	CC`W,GG	17	BstU I	CG CG	22
BstX I	CCAN,NNNN`NTGG	-	BstY I	R`GATC,Y	7
Bsu36 I	CC`TNA,GG	2	Cac8 I	GCN NGC	32
Cfr10 I	R`CCGG,Y	4	Cla I	AT`CG,AT	-
Csp6 I	G`TA,C	9	Dde I	C`TNA,G	19
Dpn I	GA TC	25	DpnII	`GATC,	25
Dra I	TTT AAA	6	Dra III	CAC,NNN`GTG	-
Drd I	GACNN,NN`NNGTC	3	Dsa I	C`CRYG,G	4
Eae I	Y`GGCC,R	11	Eag I	C`GGCC,G	3
Ear I	CTCTC 7/10	7	Eco47 III	AGC GCT	2
Eco57 I	CTGAAG 21/19	4	Eco72 I	CAC GTG	-
EcoN I	CCTNN`N,NNAGG	2	Eco109 I	RG`GNC,CY	7
EcoR I	G`AATT,C	1	EcoR II	`CCWGG,	17
EcoR V	GAT ATC	3	Ehe I	GGC GCC	5
Esp I	GC`TNA,GC	-	Fnu4H I	GC`N,GC	36
Fok I	GGATG 14/18	11	Fse I	GG,CCGG`CC	-
Fsp I	TGC GCA	2	Gdi II	`YGGC,CG	11
Gsu I	CTGGAG 21/19	3	Hae I	WGG CCW	6
Hae II	R,CGCC`Y	9	Hae III	GG CC	29
Hga I	GACGC 9/14	10	HgiA I	G,WGCW`C	6
HgiE II	ACNNNNNNGGT -1/132	-	Hha I	G,CG`C	36
HinC II	GTY RAC	-	Hind II	GTY RAC	-
Hind III	A`AGCT,T	1	Hinf I	G`ANT,C	16
HinI I	GR`CG,YC	8	HinP I	G`CG,C	36
Hpa I	GTT AAC	-	Hpa II	C`CG,G	24
Hph I	GGTGA 12/11	13	Kas I	G`GCGC,C	5
Kpn I	G,GTAC`C	3	Mae I	C`TA,G	13
Mae II	A`CG,T	10	Mae III	`GTNAC,	20
Mbo I	`GATC,	25	Mbo II	GAAGA 12/11	15
Mlu I	A`CGCG,T	1	Mme I	TCCRAC 25/23	6
Mnl I	CCTC 10/10	47	Msc I	TGG CCA	3
Mse I	T`TA,A	28	Msl I	CAYNN NNRTG	2
Msp I	C`CG,G	24	MspA1 I	CMG CKG	11
Mun I	C`AATT,G	-	Nae I	GCC GGC	2
Nar I	GG`CG,CC	5	Nci I	CC`S,GG	14

Nco I	C`CATG,G	1	Nde I	CA`TA,TG	2
NgoM I	G`CCGG,C	2	Nhe I	G`CTAG,C	2
Nla III	,CATG`	18	Nla IV	GGN NCC	33
Not I	GC`GGCC,GC	1	Nru I	TCG CGA	1
Nsi I	A,TGCA`T	-	Nsp7524 I	R`CATG,Y	3
NspB II	CMG CKG	11	NspH I	R,CATG`Y	3
PaeR7 I	C`TCGA,G	-	Pal I	GG CC	29
PflM I	CCAN,NNN`NTGG	-	Ple I	GAGTC 9/10	3
Pme I	CTTT AAAC	1	Pml I	CAC GTG	-
PpuM I	RG`GWC,CY	4	Psp1406 I	AA`CG,TT	2
PspA I	C`CCGG,G	2	Pst I	C,TGCA`G	3
Pvu I	CG,AT`CG	3	Pvu II	CAG CTG	4
Rsa I	GT AC	9	Rsr II	CG`GWC,CG	-
Sac I	G,AGCT`C	2	Sac II	CC,GC`GG	1
Sal I	G`TCGA,C	-	Sap I	GCTCTTC 8/11	2
Sau3A I	`GATC,	25	Sau96 I	G`GNC,C	27
Sca I	AGT ACT	1	ScrF I	CC`N,GG	31
Sec I	C`CNNG,G	32	SfaN I	GCATC 9/13	20
Sfc I	C`TRYA,G	10	Sfi I	GGCCN,NNN`NGGCC	-
Sma I	CCC GGG	2	SnaB I	TAC GTA	-
Spe I	A`CTAG,T	1	Sph I	G,CATG`C	1
Spl I	C`GTAC,G	-	Srf I	GCCC GGGC	-
Ssp I	AAT ATT	2	Stu I	AGG CCT	-
Sty I	C`CWWG,G	7	Taq I	T`CG,A	9
Tfi I	G`AWT,C	8	Tsp45 I	`GTSAC,	7
Tth11 I	GACN`N,NGTC	4	Tth11 II	CAARCA 16/14	8
Vsp I	AT`TA,AT	6	Xba I	T`CTAG,A	3
Xca I	GTA TAC	-	Xcm I	CCANNNN,N`NNNNTGG-	-
Xho I	C`TCGA,G	-	Xho II	R`GATC,Y	7
Xma I	C`CCGG,G	2	Xma III	C`GGCC,G	3