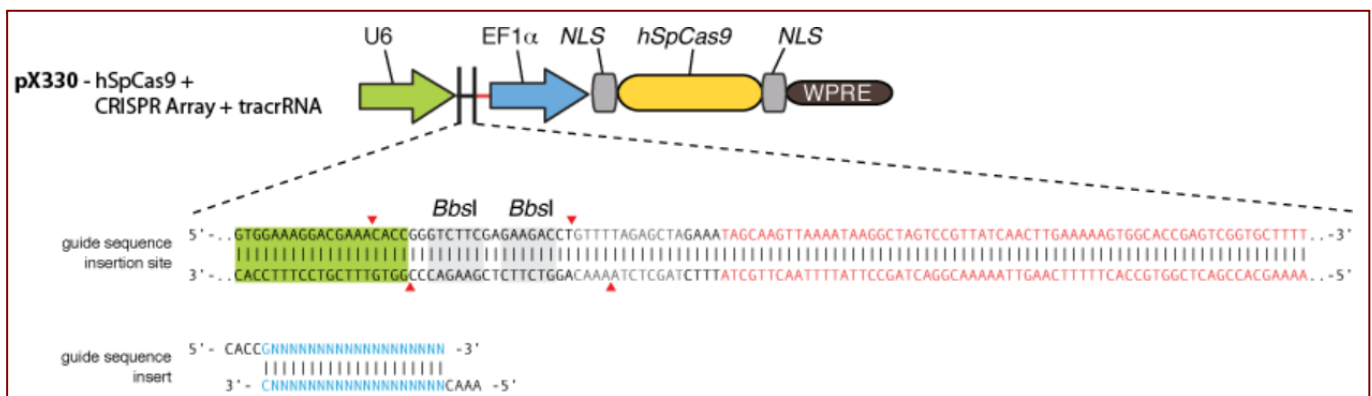
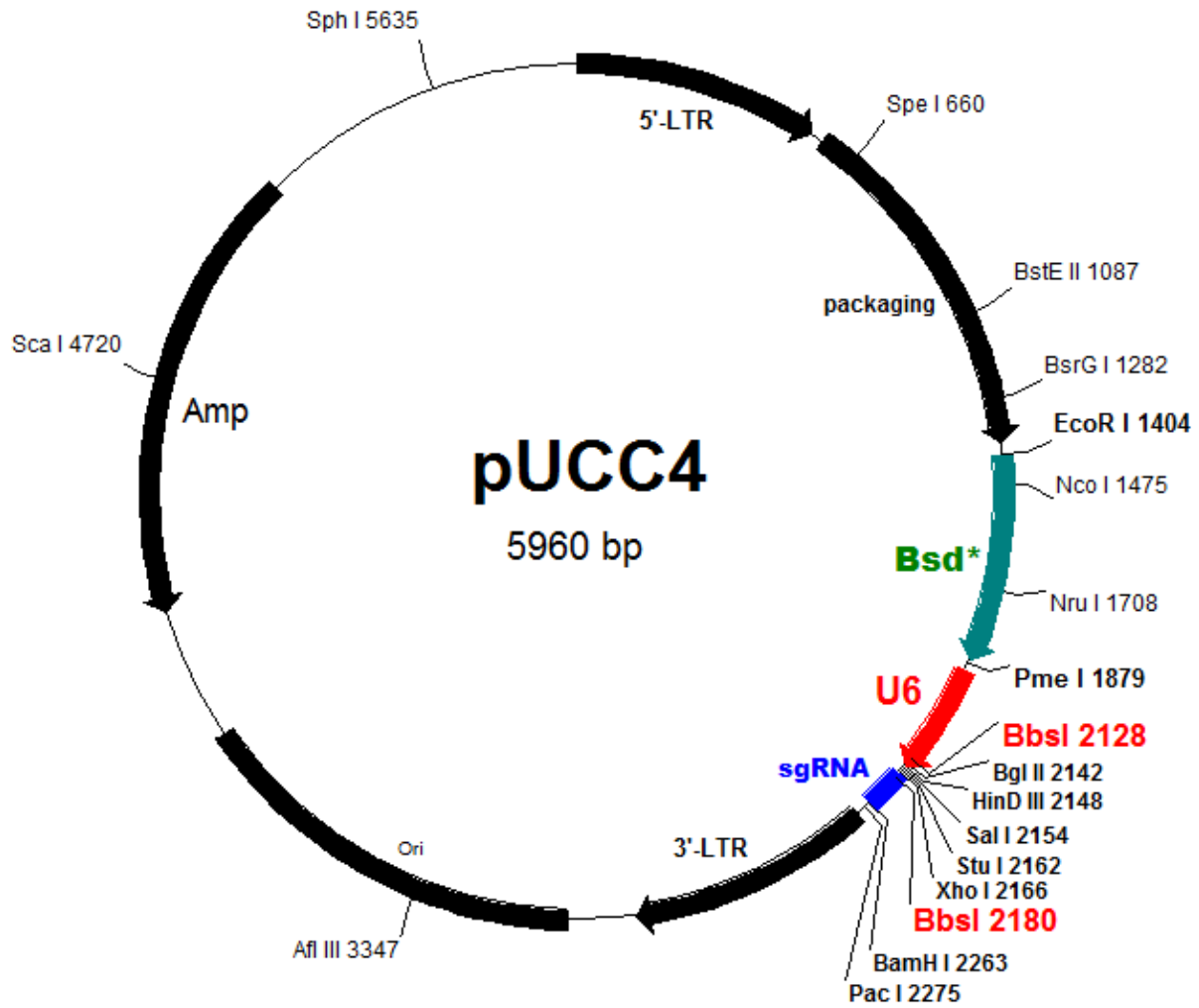


Vector: pUCC4 (UCMOLab/Universal CRISPR/Cas9 vector 4)

Antibiotic Selection: Amp/Blasticidin

Creator(s): Hongmei Zhang, DDS, PhD, Molecular Oncology Lab of The University of Chicago

Date of Construction: July, 2013



pUCC4 Full-Length Sequence

TGAAAGACCCACCTGTAGGTTTGGCAAGCTAGCTTAAGTAACGCCATTTTGC AAGCATTGCAAGCAGTGGAAAATACATAACTGAGAATAGAGAAGTGTAGATCAAGGTTAGGAA
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Unique enzymes in pUCC4:

Spe I	A`CTAG,T	660
BstE II	G`GTNAC,C	1087
BsrG I	T`GTAC,A	1282
EcoR I	G`AATT,C	1404
Nco I	C`CATG,G	1475
Bsg I	GTGCAG 22/20	1664
Nru I	TCG CGA	1708
BsaB I	GATNN NNATC	1775
Pme I	CTTT AAAC	1879
BsaA I	YAC GTR	1993
Bgl II	A`GATC,T	2142
HinD III	A`AGCT,T	2148
Sal I	G`TCGA,C	2154
Acc I	GT`MK,AC	2155

Stu I	AGG CCT	2162
PaeR7 I	C`TCGA,G	2166
Xho I	C`TCGA,G	2166
BamH I	G`GATC,C	2263
Pac I	TTA,AT`TAA	2275
Afl III	A`CRYG,T	3347
Sca I	AGT ACT	4720
Sph I	G,CATG`C	5635
Number of enzymes = 22		

The following enzymes do not cut in pUCC4:

Age I	Apa I	Avr II	Bcl I	Blp I
BsiC I	BsiW I	Bsm I	Bsp120 I	Bsp1286 I
BspM I	BspM II	Bst1107 I	BstB I	BstX I
Cla I	Dra III	Eco72 I	Esp I	Fse I

Hpa I	Mlu I	Mun I	Not I	Nsi I	747	1167	1236	1245
PflM I	Pml I	Rsr II	Sac II	Sfi I	1265	1266	1475	1780
SnaB I	Spl I	Srf I	Swa I	Xca I	2485	2564	2574	2721
pUCC4: sites sorted by name:					2784	3086	3507	5581
					5659	5665		
				BsaW I	(3)	3553	3700	4531
Aat II	(2)	745	5162	BseR I	(4)	464	1293	1332
Acc I	(1)	2155		Bsg I	(1)	1664		2787
Acc65 I	(2)	401	2725	BsiE I	(9)	592	727	1596
Aci I	(55)	197	203			3263	3687	4610
		688	727			5506		4759
		1042	1133	BsiHKA I	(6)	338	2662	3665
		1317	1355			4911	5408	
		1745	2521	BsmA I	(21)	107	475	531
		3037	3140			734	832	949
		3230	3273			1132	1150	1328
		3392	3420			2307	2430	2777
		3687	3797			4302	5076	5229
		4303	4394			5945		5273
		4752	4796	BsmB I	(7)	733	831	1072
		5081	5128			1329	5230	5272
		5351	5377	BsmF I	(10)	172	185	564
		5454	5511			764	1205	1649
Afe I	(2)	923	5701			2509	5641	2496
Afl II	(3)	35	1006	BsoF I	(34)	727	901	917
Afl III	(1)	3347				925	928	1133
Aha II	(8)	742	1398			1596	1670	1673
		5463	5646			1679	1682	1846
Ahd I	(4)	1020	2770			3253	3271	3274
Alu I	(29)	30	34			3547	3690	3755
		668	676			3964	4292	4631
		2150	2189			4753	4982	5269
		2660	2979			5482	5555	5378
		3171	3289			BspH I	(4)	4067
		3651	3908			Bsr I	(16)	374
		4592	5271				1030	1058
		5891					1634	3148
Alw I	(14)	453	1051				3767	4287
		2259	2270				4448	4715
		3995	4092			BsrB I	(4)	1042
		4872	4878			BsrD I	(2)	4301
AlwN I	(2)	2481	3763			BsrG I	(1)	1282
Apal I	(3)	3661	4907			BssH II	(4)	317
Apo I	(2)	872	1404			BssS I	(4)	1651
Asc I	(2)	368	2692			BstE II	(1)	1087
Ase I	(7)	1419	1954			BstN I	(17)	241
		3118	3177				1169	548
Asp718	(2)	401	2725				1267	1194
Ava I	(6)	331	397				3375	1217
		2655	2721				5859	1781
		186	199			BstU I	(20)	317
		690	1219				905	319
		2523	2578				1135	370
		5855					1708	903
BamH I	(1)	2263				BstY I	(8)	2142
Ban I	(14)	244	401				2263	3988
		1751	2241			Bsu36 I	(2)	781
		3091	4188			Cac8 I	(31)	28
		5759	5780				582	319
Ban II	(7)	338	351				586	631
		2675	5712				1199	650
Bbe I	(5)	1401	5466				1572	650
		5784					1686	650
Bbs I	(2)	2128	2180				1686	650
Bbv I	(9)	931	939				2354	650
		3766	3769				2643	650
		5280					3394	650
Bbv II	(2)	2129	2179				5130	650
Bcn I	(15)	164	399				5230	650
		724	2133				2142	650
		2724	3728				4085	650
		5276	5311				4085	650
Bfa I	(14)	31	219				1018	650
		1394	1586				781	650
		2353	2543				1872	650
		4430	5865				2532	650
Bgl I	(2)	4360	5478				4031	650
Bgl II	(1)	2142					5398	650
Bpm I	(3)	2290	4310				94	650
Bsa I	(6)	476	530				1363	650
		2799	4301				1711	650
BsaA I	(1)	1993					2265	650
BsaB I	(1)	1775					4001	650
BsaH I	(8)	742	1398				4204	650
		5463	5646				4867	650
BsaJ I	(30)	161	240				5505	650
		461	497				92	650
		694	733				457	650
			734				1709	650
			746				2263	650
							3999	650
							4007	650
							4202	650
							4607	650
							5503	650
							5729	650
							92	650
							1361	650
							2142	650
							3988	650
							4097	650
							4607	650
							5503	650
							5727	650

Dra I	(6)	1879	2035	2048	4106	Hpa II	(25)	163	398	569	630
		4125	4817					723	1401	2131	2487
Drd I	(3)	1564	3455	5324				2722	3065	3554	3701
Dsa I	(3)	694	1475	5665				3727	3917	4321	4355
Eae I	(10)	582	724	1109	1130			4422	4532	4774	5275
		1478	1593	3186	4628			5309	5661	5784	5793
		5662	5794					5808			
Eag I	(2)	724	1593			Hph I	(13)	1157	1183	1472	4084
Ear I	(6)	1070	1311	2969	3231			4311	4725	4933	4966
		5035	5523					5250	5259	5752	5797
Eco47 III	(2)	923	5701					5878			
Eco57 I	(3)	3894	4908	5912		Kas I	(5)	1397	5462	5645	5759
EcoN I	(2)	784	1392					5780			
EcoO109 I	(7)	254	1219	1636	1886	Kpn I	(2)	405	2729		
		2578	5216	5670		Mae I	(14)	31	219	661	673
EcoR I	(1)	1404						1394	1586	2190	2215
EcoR II	(17)	239	546	733	746			2353	2543	3842	4095
		1167	1192	1215	1235			4430	5865		
		1265	1779	2563	3085	Mae II	(10)	742	1081	1122	1992
		3373	3494	3507	5580			1997	4050	4466	4839
		5857						5159	5601		
EcoR V	(3)	140	2463	5848		Mae III	(20)	39	994	1022	1087
Ehe I	(5)	1399	5464	5647	5761			1231	1993	2072	2361
		5782						2839	3703	3766	3882
Fnu4H I	(34)	727	901	917	920			4165	4496	4554	4707
		925	928	1133	1577			4895	5283	5574	5594
		1596	1670	1673	1676	Mbo I	(26)	92	457	1044	1176
		1679	1682	1846	3172			1361	1709	1770	1784
		3253	3271	3274	3392			2142	2263	2415	3913
		3547	3690	3755	3758			3988	3999	4007	4085
		3964	4292	4631	4658			4097	4202	4543	4561
		4753	4982	5269	5378			4607	4865	4882	4918
		5482	5555					5503	5727		
Fok I	(11)	423	1140	1300	1528	Mbo II	(15)	1086	1299	1509	1594
		1763	2746	4206	4387			2129	2184	2985	3219
		4674	5317	5561				4008	4081	4836	4914
Fsp I	(2)	4462	5485					5023	5511	5723	
Gdi II	(9)	723	725	1129	1592	Mme I	(6)	829	1106	2786	2838
		1594	3187	4627	5663			3561	3745		
		5795				Mnl I	(50)	167	216	368	387
Gsu I	(3)	2291	4311	5929				432	460	484	506
Hae I	(7)	584	1111	1480	2162			510	566	776	872
		3362	3373	3825				1168	1271	1304	1310
Hae II	(9)	925	1401	3225	3595			1313	1319	1349	1352
		5466	5649	5703	5763			1367	1374	1390	1457
		5784						1518	1548	1859	1860
Hae III	(29)	129	173	584	726			1877	2172	2540	2692
		762	774	987	1111			2711	2756	2783	2807
		1132	1197	1480	1595			2867	3196	3245	3455
		1888	2162	2452	2497			3528	3779	4179	4260
		3188	3362	3373	3391			4406	4612	5207	5265
		3825	4283	4363	4630			5525	5809		
		5217	5515	5664	5672	Msc I	(3)	584	1111	1480	
		5796				Mse I	(30)	36	1007	1119	1149
Hga I	(10)	381	642	895	1555			1173	1419	1878	1954
		2705	3457	4035	4767			2034	2047	2204	2271
		5325	5794					2275	2358	2892	2990
HgiA I	(6)	338	2662	3665	4826			3118	3177	4053	4105
		4911	5408					4110	4124	4177	4412
HgiE II	(2)	3926	5406					4451	4816	5188	5369
Hha I	(36)	319	321	370	372			5566	5836		
		648	905	924	1400	Msl I	(2)	4492	4651		
		1576	2643	2645	2694	Msp I	(25)	163	398	569	630
		2696	2971	3131	3196			723	1401	2131	2487
		3224	3257	3527	3594			2722	3065	3554	3701
		3694	3868	3977	4370			3727	3917	4321	4355
		4463	4800	5132	5232			4422	4532	4774	5275
		5335	5465	5486	5619			5309	5661	5784	5793
		5648	5702	5762	5783			5808			
HinC II	(2)	1413	2156			MspA1 I	(10)	588	1684	2823	3171
Hind II	(2)	1413	2156					3689	3934	4875	5341
HinD III	(1)	2148						5535	5891		
Hinf I	(17)	442	450	791	802	Nae I	(2)	631	5794		
		1501	1833	1901	2247	Nar I	(5)	1398	5463	5646	5760
		2882	2904	2925	3182			5781			
		3247	3322	3718	4235	Nci I	(15)	163	398	399	570
		5873						723	2132	2487	2722
HinI I	(8)	742	1398	4777	5159			2723	3727	4423	4774
		5463	5646	5760	5781			5275	5310	5661	
HinP I	(36)	317	319	368	370	Nco I	(1)	1475			
		646	903	922	1398	Nde I	(2)	2062	5411		
		1574	2641	2643	2692	Ngom I	(2)	629	5792		
		2694	2969	3129	3194	Nhe I	(2)	30	2352		
		3222	3255	3525	3592	Nla III	(18)	62	1205	1479	1901
		3692	3866	3975	4368			2384	2838	3005	3351
		4461	4798	5130	5230			4071	4562	4572	4650
		5333	5463	5484	5617			4686	5079	5184	5268
		5646	5700	5760	5781			5635	5708		

Nla IV	(33)	188	201	246	403		1901	2925	3182	3322	
		521	552	692	761	Tsp45 I	(7)	1022	1231	1993	4496
		893	1144	1221	1399			4707	5283	5594	
		1637	1753	2243	2265	Tth111 I	(4)	390	811	1217	2714
		2512	2525	2570	2727	Tth111 II	(8)	146	422	613	632
		3093	3379	3418	4190			2469	3936	3945	3975
		4284	4325	4536	5126	Vsp I	(7)	1419	1954	2271	2990
		5464	5647	5671	5761			3118	3177	4412	
		5782				Xba I	(2)	218	2542		
Nru I	(1)	1708				Xho I	(1)	2166			
Nsp7524 I	(3)	3347	5264	5631		Xho II	(8)	2142	2263	3988	3999
NspB II	(10)	588	1684	2823	3171			4085	4097	4865	4882
		3689	3934	4875	5341	Xma I	(2)	397	2721		
		5535	5891			Xma III	(2)	724	1593		
NspH I	(3)	3351	5268	5635		Xmn I	(3)	2953	2991	4839	
Pac I	(1)	2275									
PaeR7 I	(1)	2166									
Pal I	(29)	129	173	584	726						

Site usage in pUCC4:

Aat II	G,ACGT`C	2	Acc I	GT`MK,AC	1
Acc65 I	G`GTAC,C	2	Aci I	C`CG,C	55
Afe I	AGC GCT	2	Afl II	C`TTAA,G	3
Afl III	A`CRYG,T	1	Age I	A`CCGG,T	-
Aha II	GR`CG,YC	8	Ahd I	GACNN,N`NNGTC	4
Alu I	AG CT	29	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	7
Asp718	G`GTAC,C	2	Ava I	C`YCGR,G	6
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,RCY`C	7	Bbe I	G,GGCC`C	5
Bbs I	GAAGAC 8/12	2	Bbv I	GCAGC 13/17	9
Bbv II	GAAGAC 7/11	2	Bcl I	T`GATC,A	-
Bcn I	CC,S`GG	15	Bfa I	C`TA,G	14
Bgl I	GCCN,NNN`NGGC	2	Bgl II	A`GATC,T	1
Blp 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	30	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	9
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	34	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,Y	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	20	BstX I	CCAN,NNNN`NTGG	-
BstY I	R`GATC,Y	8	Bsu36 I	CC`TNA,GG	2
Cac8 I	GCN NGC	31	Cfr10 I	R`CCGG,Y	4
Cla I	AT`CG,AT	-	Csp6 I	G`TA,C	8
Dde I	C`TNA,G	21	Dpn I	GA TC	26
DpnII	`GATC,	26	Dra I	TTT AAA	6
Dra III	CAC,NNN`GTG	3	Drd I	GACNN,MN`NNGTC	3
Dsa I	C`CRYG,G	3	Eae I	Y`GGCC,R	10
Eag I	C`GGCC,G	2	Ear I	CTCTCT 7/10	6
Eco47 III	AGC GCT	2	Eco57 I	CTGAAG 21/19	3
Eco72 I	CAC GTG	-	EcoN I	CCTNN`N,NNAGG	2
EcoO109 I	RG`GNC,CY	7	EcoR I	G`AATT,C	1
EcoR II	`CCWGG,	17	EcoRV	GAT ATC	3
Ehe I	GGC GCC	5	Esp I	GC`TNA,GC	-
Fnu4H I	GC`N,GC	34	Fok I	GGATG 14/18	11
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,GGCC`Y	9
Hae III	GG CC	29	Hga I	GACGC 9/14	10
HgiA I	G,WGCW`C	6	HgiE II	ACCNNNNNNGGT -1/132	-
Hha I	G,CG`C	36	HinC II	GTY RAC	2
Hind II	GTY RAC	2	HinD III	A`AGCT,T	1
Hinf I	G`ANT,C	17	HinI I	GR`CG,YC	8
HinP I	G`CG,C	36	Hpa I	GTT AAC	-
Hpa II	C`CG,G	25	Hph I	GGTGA 12/11	13
Kas I	G`CGCG,C	5	Kpn I	G,GTAC`C	2
Mae I	C`TA,G	14	Mae II	A`CG,T	10
Mae III	`GTNAC,	20	Mbo I	`GATC,	26
Mbo II	GAAGA 12/11	15	Mlu I	A`CGCG,T	50
Mme I	TCCRAC 25/23	6	Mnl I	CCTC 10/10	-
Msc I	TGG CCA	3	Mse I	T`TA,A	30
Msl I	CAYNN NNRTG	2	Msp I	C`CG,G	25
MspAl I	CMG CKG	10	Mun I	C`AATT,G	-
Nae I	GCC GGC	2	Nar I	GG`CG,CC	5
Nci I	CC`S,GG	15	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	-
Nru I	TCG CGA	1	Nsi I	A,TGCA`T	-
Nsp7524 I	R`CATG,Y	3	NspB II	CMG CKG	10
NspH I	R,CATG`Y	3	Pac I	TTA,AT`TAA	1
PaeR7 I	C`TCGA,G	1	Pal I	GG CC	29
Pf1M I	CCAN,NNN`NTGG	-	Ple I	GAGTC 9/10	4
Pme I	CTTT AAAC	1	Pml I	CAC GTG	4
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	8	Rsr II	CG`GWC,CG	-

Sac I	G,AGCT`C	2	Sac II	CC,GC`GG	-	Ssp I	AAT ATT	2	Stu I	AGG CCT	1
Sal I	G`TCGA,C	1	Sap I	GCTCTTC 8/11	2	Sty I	C`CWWG,G	6	Swa I	ATTT AAAT	-
Sau3A I	`GATC,	26	Sau96 I	G`GNC,C	27	Taq I	T`CG,A	12	Tfi I	G`AWT,C	8
Sca I	AGT ACT	1	ScrF I	CC`N,GG	32	Tsp45 I	`GTSAC,	7	Tth111 I	GACN`N,NGTC	4
Sec I	C`CNRG,G	30	SfaN I	GCATC 9/13	20	Tth111 II	CAARCA 16/14	8	Vsp I	AT`TA,AT	7
Sfc I	C`TRYA,G	10	Sfi I	GGCCN,NNN`NGGCC	-	Xba I	T`CTAG,A	2	Xca I	GTA TAC	-
Sma I	CCC GGG	2	SnaB I	TAC GTA	-	Xcm I	CCANNNN,N`NNNTGG-	-	Xho I	C`TCGA,G	1
Spe I	A`CTAG,T	1	Sph I	G,CATG`C	1	Xho II	R`GATC,Y	8	Xma I	C`CCGG,G	2
Spl I	C`GTAC,G	-	Srf I	GCCC GGGC	-	Xma III	C`GGCC,G	2	Xmn I	GAANN NNTTC	3