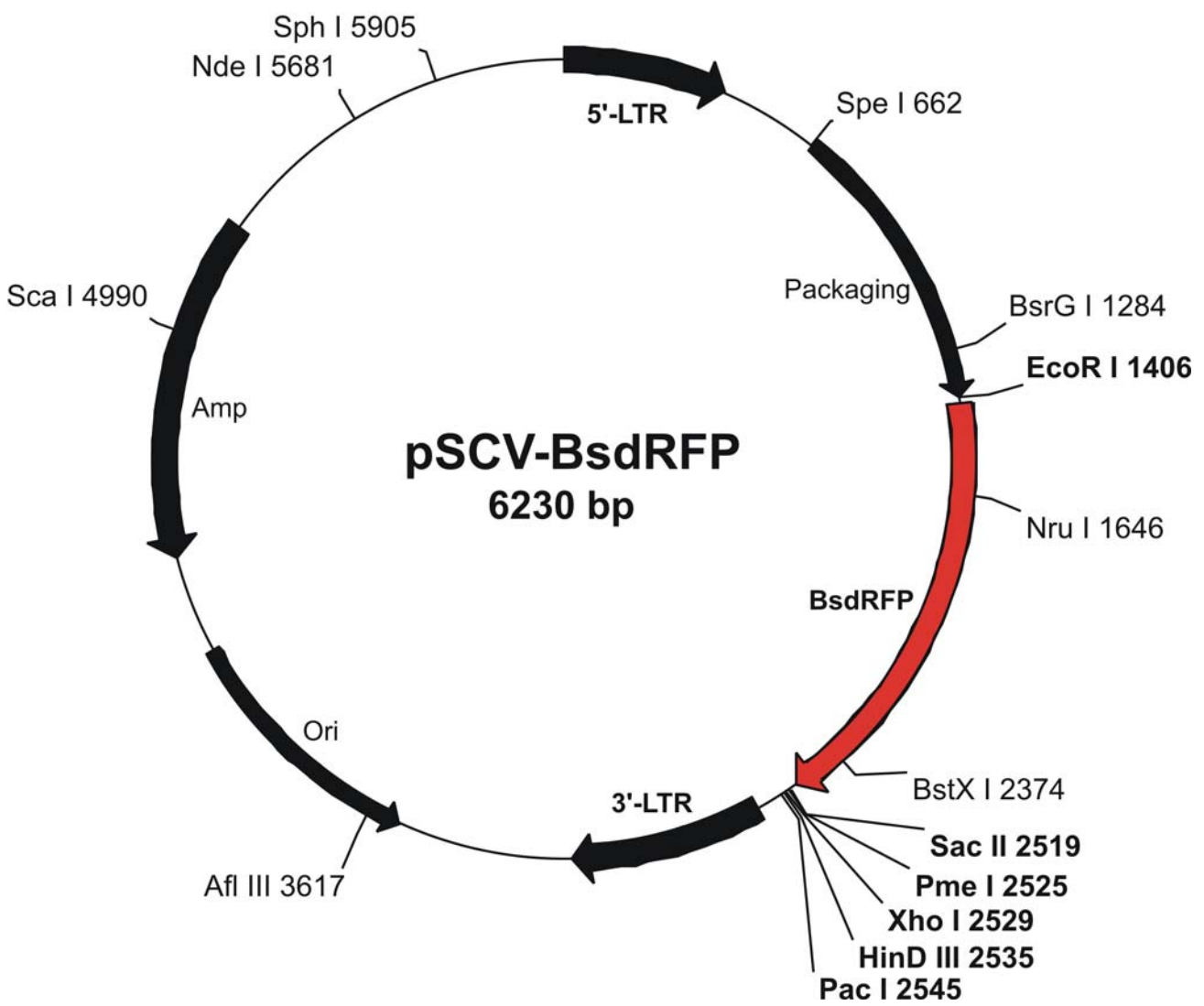


Name of Vector: pSCV-BsdRFP
Antibiotic Selection: Amp
Created by: Hong Yin
(He Lab @ The University of Chicago)
Date of Creation: April 2005



pSCV-BsdRFP Sequence

TGAAAGACCC CACCTGTAGG TTTGGCAAGC TAGCTTAAGT AACGCCATTT TGCAAGGCATGGAAAATACATAACTGAGAA
TAGAGAAGTT CAGATCAAGG TTAGGAACAG AGAGACAGCAGAATATGGGC CAAACAGGAT ATCTGTGGTAAGCAGTTCCCT
GCCCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGATGCGGTCCCGCCCTCAGCAGTTTCTAGAGAACCATCAGATGTTTTCCAGG
GTGCCCCAAGGACCTGAAATGACCCTGTGCCTTATTTGAACTAACCAATCAGTTCGCTTCTCGCTTCTGTTCGCGCGCTTCTGTCT
CCCCGAGCTC AATAAAAAGAG CCCACAACCCCTCACTCGGC GCGCCAGTCC TCCGATAGAC TCGCTCGCCCGGGTACCCGT
ATTCCCAATAAAAGCCTCTTG CTGTTTGCAT CCGAATCGTG GACTCGCTGA TCCTTGGGAG GGTCTCCTCAGATTGATTGA
CTGCCACCT CGGGGTCTT TCATTTGGAG GTTCCACCGA GATTTGGAGACCCCTGCCA GGGACCACCGACCCCCCGC
CGGGAGGTAA GCTGGCCAGC GGTCGTTTCGTGTCTGTCTC TGTCTTTGTG CGTGTTTGTG CCGCATCTAATGTTTGC
CTGCGTCTGTACTAGTTAGC TAACTAGCTC TGTATCTGGC GGACCCGTGG TGGAACTGAC GAGTCTGAACACCCGGCCG
CAACCTGGG AGACGTCCA GGGACTTTGG GGGCCGTTTT TGTGGCCGACCTGAGGAAG GGATCGATGTGGAATCCGA
CCCCGTAGG ATATGTGGTT CTGGTAGGAGACGAGAACCT AAAACAGTTC CCGCTCCGT CTGAATTTTGTCTTTCGGTT
TGAACCGAAGCCGCGCTC TTGTCTGCTG CAGCGCTGCA GCATCGTTCT GTGTTGTCTC TGTCTGACTGTGTTTCTGTA
TTTGTCTGAA AATTAGGGCC AGACTGTTAC CACTCCCTTA AGTTTGACCTTAGGTCAGT GAAAAGATGTCGAGCGGATCG
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TGGCCGCGAGACGGCACCTT TAACCGAGAC CTCATCACC AGGTTAAGAT CAAGGTCTTT TCACCTGGCCCGCATGGACA
CCAGACCAG GTCCCTACA TCGTGACCTG GGAAGCCTTG GCTTTTGACCCCTCCCTG GGTCAAGCCTTTGTACACC
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Unique enzymes in pSCV-BsdRFP:

Spe I	A`CTAG,T	662			2517	4179	4265	4265
BsrG I	T`GTAC,A	1284	AlwN I	(3)	159	2751	4033	
EcoR I	G`AATT,C	1406	ApaL I	(3)	3931	5177	5674	
Nru I	TCG CGA	1646	Apo I	(2)	874	1406		
BsaB I	GATNN NNATC	1713	Asc I	(2)	370	2962		
BsaA I	YAC GTR	2047	Ase I	(4)	3260	3388	3447	4682
Pf1M I	CCAN,NNN`NTGG	2256	Asp718	(2)	403	2995		
BstX I	CCAN,NNNN`NTGG	2374	Ava I	(8)	333	399	500	2093
Sac II	CC,GC`GG	2519			2285	2529	2925	2991
Pme I	CTTT AAAC	2525	Ava II	(13)	188	201	256	553
PaeR7 I	C`TCGA,G	2529			692	1221	1574	2780
Xho I	C`TCGA,G	2529			2793	2848	4648	4870
HinD III	A`AGCT,T	2535			6125			
Pac I	TTA,AT`TAA	2545	Ban I	(18)	246	403	1144	1399
Afl III	A`CRYG,T	3617			1689	1949	2207	2294
Sca I	AGT ACT	4990			2402	2501	2838	2995
Nde I	CA`TA,TG	5681			3361	4458	5732	5915
Sph I	G,CATG`C	5905			6029	6050		
Number of enzymes = 18			Ban II	(9)	340	353	1679	1811
					1892	2932	2945	5982

The following enzymes do not cut in pSCV-BsdRFP:

Acc I	Age I	Apa I	Avr II	BamH I	Bbe I	(8)	1403	2298	2406	2505
Bcl I	Bgl II	Blp I	BsiC I	BsiW I	Bbs I	(2)	5736	5919	6033	6054
Bsm I	Bsp120 I	BspM I	BspM I	BspM II	Bbv I	(10)	1500	2252		
Bst1107 I	BstB I	Cla I	Dra III	Eco72 I			933	941	1526	1631
Esp I	Fse I	HinC II	Hind II	Hpa I			2404	4036	4039	4245
Mlu I	Mun I	Not I	Nsi I	Pml I	Bbv II	(2)	4939	5550		
Rsr II	Sal I	Sfi I	SnaB I	Spl I	Bcn I	(15)	1499	2251		
							166	401	402	573
							726	2401	2758	2993
							2994	3998	4694	5045
							5546	5581	5932	

pSCV-BsdRFP: sites sorted by name:

Aat II	(3)	747	1851	5432						
Acc65 I	(2)	403	2995							
Aci I	(68)	199	205	568	590					
		690	729	862	903					
		1044	1135	1201	1300					
		1319	1357	1534	1616	Bgl I	(2)	4630	5748	
		1683	1821	1824	1936	Bpm I	(3)	2560	4580	6198
		1959	1983	2058	2136	Bsa I	(6)	478	532	1151
		2205	2275	2340	2488			3069	4571	
		2516	2518	2791	2797	BsaA I	(1)	2047		
		3093	3307	3410	3466	BsaB I	(1)	1713		
		3476	3500	3543	3550	BsaH I	(13)	744	1400	1848
		3571	3662	3690	3817			2352	2403	2502
		3836	3957	4067	4202			5429	5733	5916
		4211	4573	4664	4855			6051		
		4901	5022	5066	5143	BsaJ I	(41)	163	242	252
		5252	5351	5398	5572			463	499	548
		5611	5621	5647	5685			696	735	736
		5698	5724	5781	6040			749	1169	1238
								1267	1268	1413
Afl II	(3)	35	1008	2627				1842	1977	2001
Afl III	(1)	3617						2094	2154	2250
Aha II	(13)	744	1400	1848	2295			2355	2481	2516
		2352	2403	2502	5047			2834	2844	2991
		5429	5733	5916	6030			3356	3777	5851
		6051						5935		5929
Ahd I	(5)	1022	2011	3040	3086	BsaW I	(3)	3823	3970	4801
		4510				BseR I	(7)	466	1295	1334
Alu I	(34)	30	34	338	582			1830	2152	3057
		670	678	1517	1622	Bsg I	(2)	1602	2411	
		1966	2083	2200	2329	BsiE I	(9)	594	729	1534
		2395	2425	2537	2622			3533	3957	4880
		2626	2930	3249	3282			5776		5029
		3377	3441	3559	3785	BsiHKA I	(6)	340	2932	3935
		3875	3921	4178	4699			5181	5678	5096
		4799	4862	5541	5560	BsmA I	(21)	108	477	533
		5805	6161					736	834	951
Alw I	(13)	455	1053	1359	1729			1134	1152	1330

		2577	2700	3047	3068			3777	5850	6127	
		4572	5346	5499	5543	EcoR V	(3)	141	2733	6118	
		6215				Ehe I	(8)	1401	2296	2404	2503
BsmB I	(7)	735	833	1074	1133			5734	5917	6031	6052
		1331	5500	5542		Fnu4H I	(44)	729	903	919	922
BsmF I	(12)	174	187	566	731			927	930	1135	1515
		766	1207	1587	1999			1534	1608	1611	1614
		2018	2766	2779	5911			1617	1620	1784	1822
BsoF I	(44)	729	903	919	922			1936	1984	2137	2201
		927	930	1135	1515			2206	2341	2393	2396
		1534	1608	1611	1614			2488	3442	3523	3541
		1617	1620	1784	1822			3544	3662	3817	3960
		1936	1984	2137	2201			4025	4028	4234	4562
		2206	2341	2393	2396			4901	4928	5023	5252
		2488	3442	3523	3541			5539	5648	5752	5825
		3544	3662	3817	3960	Fok I	(14)	425	1142	1302	1466
		4025	4028	4234	4562			1701	1994	2051	2290
		4901	4928	5023	5252			3016	4476	4657	4944
		5539	5648	5752	5825			5587	5831		
BspH I	(4)	4337	5345	5450	5974	Fsp I	(3)	1880	4732	5755	
Bsr I	(17)	376	1032	1060	1548	Gdi II	(11)	725	727	1131	1530
		1572	2027	2968	3418			1532	1901	2342	3457
		4024	4037	4151	4557			4897	5933	6065	
		4675	4718	4985	5157	Gsu I	(3)	2561	4581	6199	
		5863				Hae I	(10)	586	1113	1418	1835
BsrB I	(5)	1044	2275	3309	3550			2042	2264	2378	3632
		5351						3643	4095		
BsrD I	(2)	4571	4745			Hae II	(12)	927	1403	2298	2406
BsrG I	(1)	1284						2505	3495	3865	5736
BssH II	(5)	319	370	2476	2911			5919	5973	6033	6054
		2962				Hae III	(37)	130	175	586	728
BssS I	(5)	1589	1904	3790	5174			764	776	989	1113
		5481						1134	1199	1418	1533
BstE II	(3)	1089	1972	2143				1835	1902	1935	1986
BstN I	(19)	243	550	737	750			2042	2229	2264	2343
		1171	1196	1219	1239			2378	2487	2722	2767
		1269	1719	2002	2156			3458	3632	3643	3661
		2835	3357	3645	3766			4095	4553	4633	4900
		3779	5852	6129				5487	5785	5934	5942
BstU I	(24)	319	321	372	905			6066			
		907	1137	1646	2115	Hga I	(11)	383	644	897	1493
		2205	2478	2518	2911			2359	2975	3727	4305
		2913	2964	3464	3466			5037	5595	6064	
		3664	4245	4575	5068	HgiA I	(6)	340	2932	3935	5096
		5400	5500	5502	5605			5181	5678		
BstX I	(1)	2374				HgiE II	(2)	4196	5676		
BstY I	(7)	2510	4258	4269	4355	Hha I	(45)	321	323	372	374
		4367	5135	5152				650	907	926	1402
Bsu36 I	(3)	783	1020	2506				1514	1869	1881	2115
Cac8 I	(32)	28	32	321	372			2205	2297	2405	2478
		584	588	633	652			2480	2504	2913	2915
		1201	1510	1624	2478			2964	2966	3241	3401
		2620	2624	2913	2964			3466	3494	3527	3797
		3410	3439	3548	3634			3864	3964	4138	4247
		3671	4231	4622	5635			4640	4733	5070	5402
		5783	5803	5807	5903			5502	5605	5735	5756
		5944	5992	6034	6064			5889	5918	5972	6032
Cfr10 I	(5)	631	2498	4590	6053			6053			
		6062				HinD III	(1)	2535			
Csp6 I	(10)	404	660	1285	2029	Hinf I	(16)	444	452	793	804
		2281	2470	2996	4989			1439	1771	2159	3152
		5665	6176					3174	3195	3452	3517
Dde I	(20)	75	169	210	478			3592	3988	4505	6143
		783	1020	1292	2019	HinI I	(13)	744	1400	1848	2295
		2506	2667	2761	2802			2352	2403	2502	5047
		3071	3142	3892	4301			5429	5733	5916	6030
		4467	5007	5433	5668			6051			
Dpn I	(27)	95	461	1048	1180	HinP I	(45)	319	321	370	372
		1365	1649	1710	1724			648	905	924	1400
		1916	2312	2512	2687			1512	1867	1879	2113
		4185	4260	4271	4279			2203	2295	2403	2476
		4357	4369	4474	4815			2478	2502	2911	2913
		4833	4879	5137	5154			2962	2964	3239	3399
		5190	5775	5999				3464	3492	3525	3795
DpnII	(27)	93	459	1046	1178			3862	3962	4136	4245
		1363	1647	1708	1722			4638	4731	5068	5400
		1914	2310	2510	2685			5500	5603	5733	5754
		4183	4258	4269	4277			5887	5916	5970	6030
		4355	4367	4472	4813			6051			
		4831	4877	5135	5152	Hpa II	(26)	165	400	571	632
		5188	5773	5997				725	1403	2400	2499
Dra I	(4)	2525	4376	4395	5087			2757	2992	3335	3824
Drd I	(4)	1502	2357	3725	5594			3971	3997	4187	4591
Dsa I	(5)	696	1413	2250	2516			4625	4692	4802	5044
		5935						5545	5579	5931	6054
Eae I	(13)	584	726	1111	1132			6063	6078		
		1416	1531	1900	2341	Hph I	(17)	1159	1185	1403	1983
		2376	3456	4898	5932			2154	2205	2426	4354
		6064						4581	4995	5203	5236
Eag I	(2)	726	1531					5520	5529	6022	6067
Ear I	(6)	1072	1313	3239	3501			6148			
		5305	5793			Kas I	(8)	1399	2294	2402	2501
Eco47 III	(2)	925	5971					5732	5915	6029	6050
Eco57 I	(8)	1511	1987	2320	2344	Kpn I	(2)	407	2999		
		2350	4164	5178	6182	Mae I	(13)	31	221	663	675
EcoN I	(2)	786	1394					1396	1524	1812	2623
EcoO109 I	(6)	256	1221	1574	2848			2813	4112	4365	4700
		5486	5940					6135			
EcoR I	(1)	1406				Mae II	(10)	744	1083	1124	1848
EcoR II	(19)	241	548	735	748			2046	4320	4736	5109
		1169	1194	1217	1237			5429	5871		
		1267	1717	2000	2154	Mae III	(21)	39	996	1024	1089
		2833	3355	3643	3764			1233	1972	2143	2149

Bfa I	C`TA,G	13	Bgl I	GCCN,NNN`NGGC	2	Hpa I	GTT AAC	-	Hpa II	C`CG,G	26
Bgl II	A`GATC,T	-	Blp I	GC`TNA,GC	-	Hph I	GGTGA 12/11	17	Kas I	G`GGCC,C	8
Bpm I	CTGGAG 22/20	3	Bsa I	GGTCTC 7/11	6	Kpn I	G,GTAC`C	2	Mae I	C`TA,G	13
Bsaa I	YAC GTR	1	BsaB I	GATNN NNATC	1	Mae II	A`CG,T	10	Mae III	`GTNAC,	21
Bsah I	GR`CG,YC	13	BsaJ I	C`CNNG,G	41	Mbo I	`GATC,	27	Mbo II	GAAGA 12/11	16
Bsaw I	W`CCGG,W	3	BseR I	GAGGAG 16/14	7	Mlu I	A`CGCG,T	-	Mme I	TCCRAC 25/23	7
Bsg I	GTGCAG 22/20	2	BsiC I	TT`CG,AA	-	Mnl I	CCTC 10/10	69	Msc I	TGG CCA	4
Bsie I	CG,RY`CG	9	BsiHKA I	G,WGCW`C	6	Mse I	T`TA,A	25	Msl I	CAYNN NNRTG	2
BsiW I	C`GTAC,G	-	Bsm I	GAATG,C 7	-	Msp I	C`CG,G	26	MspAl I	CMG CKG	12
BsmA I	GTCTC`/9	21	BsmB I	CGTCTC 7/11	7	Mun I	C`AATT,G	-	Nae I	GCC GGC	2
BsmF I	GGGAC 15/19	12	BsoF I	GC`N,GC	44	Nar I	GG`CG,CC	8	Nci I	CC`S,GG	15
Bsp120 I	G`GGCC,C	-	Bsp1286 I	G,DGCH`C	-	Nco I	C`CATG,G	2	Nde I	CA`TA,TG	1
BspH I	T`CATG,A	4	BspM I	ACCTGC 10/14	-	Ngm I	G`CCGG,C	2	Nhe I	G`CTAG,C	2
BspM II	T`CCGG,A	-	Bsr I	ACT,GG`	17	Nla III	,CATG`	21	Nla IV	GGN NCC	40
BsrB I	GAG CGG	5	BseD I	GCAATG, 8	2	Not I	GC`GGCC,GC	-	Nru I	TCG CGA	1
BsrG I	T`GTAC,A	1	BssH II	G`CGCG,C	5	Nsi I	A,TGCA`T	-	Nsp7524 I	R`CATG,Y	3
BssS I	C`TCGT,G	5	Bst1107 I	GTA TAC	-	NspB II	CMG CKG	12	NspH I	R,CATG`Y	3
BstB I	TT`CG,AA	-	BstE II	G`GTNAC,C	3	Pac I	TTA,AT`TAA	1	Paer7 I	C`TCGA,G	1
BstN I	CC`W,GG	19	BstU I	CG CG	24	Pal I	GG CC	37	Pf1M I	CCAN,NNN`NTGG	1
BstX I	CCAN,NNNN`NTGG	1	BstY I	R`GATC,Y	7	Ple I	GAGTC 9/10	3	Pme I	CTTT AAAC	1
Bsu36 I	CC`TNA,GG	3	Cac8 I	GCN NGC	32	Pml I	CAC GTG	-	PpuM I	RG`GWC,CY	4
Cfr10 I	R`CCGG,Y	5	Clal I	AT`CG,AT	-	Psp1406 I	AA`CG,TT	-	Pspa I	C`CCGG,G	2
Csp6 I	G`TA,C	10	Dde I	C`TNA,G	20	Pst I	C,TGCA`G	4	Pvu I	CG,AT`CG	3
Dpn I	GA TC	27	DpnII	`GATC,	27	Pvu II	CAG CTG	5	Rsa I	GT AC	10
Dra I	TTT AAA	4	Dra III	CAC,NNN`GTG	-	Rsr II	CG`GWC,CG	-	Sac I	G,AGCT`C	2
Drd I	GACNN,NN`NNGTC	4	Dsa I	C`CRYG,G	5	Sac II	CC,GC`GG	1	Sal I	G`TCGA,C	-
Eae I	Y`GGCC,R	13	Eag I	C`GGCC,G	2	Sap I	GCTCTTC 8/11	2	Sau3A I	`GATC,	27
Ear I	CTCTTC 7/10	6	Eco47 III	AGC GCT	2	Sau96 I	G`GNC,C	30	Sca I	AGT ACT	1
Eco57 I	CTGAAG 21/19	8	Eco72 I	CAC GTG	-	ScrF I	CC`N,GG	34	Sec I	C`CNNG,G	41
EcoN I	CCTNN`N,NNAGG	2	EcoO109 I	RG`GNC,CY	6	SfaN I	GCATC 9/13	20	Sfc I	C`TRYA,G	11
EcoR I	G`AATT,C	1	EcoR II	`CCWGG,	19	Sfi I	GGCCN,NNN`NGGCC	-	Sma I	CCC GGG	2
EcoRV	GAT ATC	3	Ehe I	GGC GCC	8	SnaB I	TAC GTA	-	Spe I	A`CTAG,T	1
Esp I	GC`TNA,GC	-	Fnu4H I	GC`N,GC	44	Sph I	G,CATG`C	1	SpI I	C`GTAC,G	-
Fok I	GGATG 14/18	14	Fse I	GG,CCGG`CC	-	Srf I	GCCC GGGC	-	Ssp I	AAT ATT	2
Fsp I	TGC GCA	3	Gdi II	`YGGC,CG	11	Stu I	AGG CCT	2	Sty I	C`CWG,G	9
Gsu I	CTGGAG 21/19	3	Hae I	WGG CCW	10	Taq I	T`CG,A	12	Tfi I	G`AWT,C	7
Hae II	R,CGCC`Y	12	Hae III	GG CC	37	Tsp45 I	`GTSAC,	9	Tth111 I	GACN`N,NGTC	4
Hga I	GACGC 9/14	11	HgiA I	G,WGCW`C	6	Tth111 II	CAARCA 16/14	8	Vsp I	AT`TA,AT	4
HgiE II	ACCNNNNNNGGT -1/132	-	Hha I	G,CG`C	45	Xba I	T`CTAG,A	3	Xca I	GTA TAC	-
Hinc II	GTY RAC	-	Hind II	GTY RAC	-	Xcm I	CCANNNN,N`NNNNTGG-	-	Xho I	C`TCGA,G	1
Hind III	A`AGCT,T	1	Hinf I	G`ANT,C	16	Xho II	R`GATC,Y	7	Xma I	C`CCGG,G	2
HinI I	GR`CG,YC	13	HinP I	G`CG,C	45	Xma III	C`GGCC,G	2	Xmn I	GAANN NNTTC	3