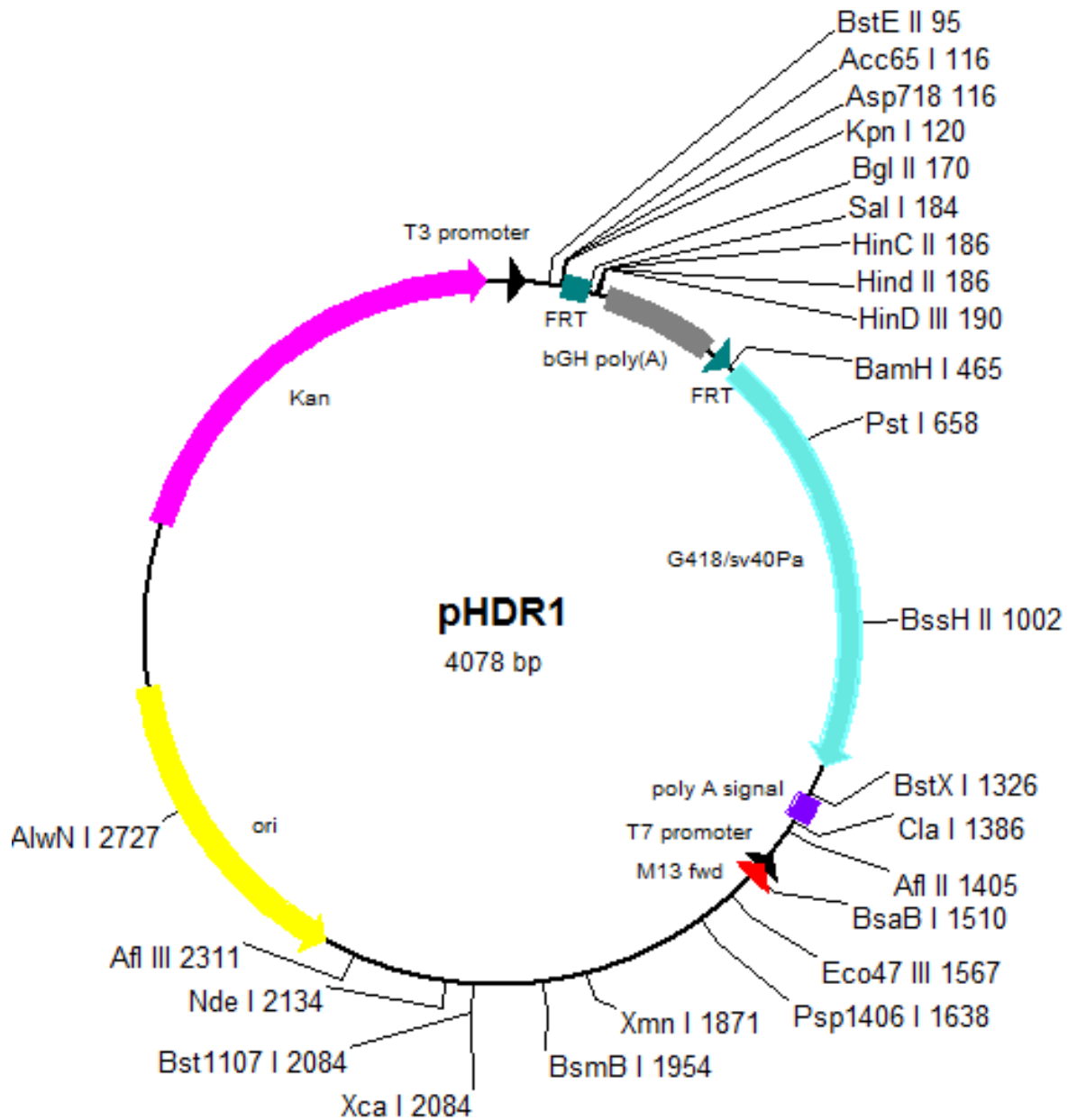


Vector: pHDR1

Antibiotic Selection: Kan

Creator(s): Li Li & Xue Hu, Molecular Oncology Lab of The University of Chicago Medical Center

Date of Construction: February, 2016



pHDR1 Full-Length Sequence

PmeI StuI FRT BGHpa FRT G418/SV40Pa

GGAAACAGCTATGACCATGATTACGCCAAGCTCGAAATTAACCTCACTAAAGGGAACAAAAGCTGGTACGAGGACAGGCTGGAGCCATGG
 CTGGTGACCgtttaaacAGGCCTggtaccGAAGTTCCTATTCCGAAGTTCCTATTCTCTAGAAAAGTATAGGAACTTCagatctTTAATTAA
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 GGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTCCGGCTGTCTAGCGCAGGGGCGCCCGTCTTTTTGTCAAGACCGACCTGTCC
 GGTGCCCTGAATGAAGTGCAGGACGAGGCAGCGGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGGCGAGCTGTGCTCGACGTTGTCA
 CTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCAGGGGAGGATCTCTGTCTACCTTGCTCCTGCCGAGAAAAGTATCCAT
 CATGGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCATTTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGT
 ACTCGGATGGAAGCCGGTCTTGTGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCCGCCAGGCTCAAGG
 CGCGCATGCCGACGGCGAGGATCTCGTCTGACCCATGGCGATGCCTGCTTGCCTGAATATCATGGTGGAAAATGGCCGCTTTTCTGGATT
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 ACCCATGGCGATGCTGCTTGGCGAATATCATGGTGGAAAATGGCCGCTTTTCTGGATTCACTGACTGTGGCCGGCTGGGTGTGGCGGACC
 GCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCTCGTCTTTACGGTATCGC
 CGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTCTTCTGACCTTTCGCTTCAAGaatt

Unique enzymes in pHDR1:

BstE II	G`GTNAC,C	95	Hind II	GTY RAC	186
Acc65 I	G`GTAC,C	116	HinD III	A`AGCT,T	190
Asp718	G`GTAC,C	116	BamH I	G`GATC,C	465
Kpn I	G,GTAC`C	120	Pst I	C,TGCA`G	658
Bgl II	A`GATC,T	170	BssH II	G`CGCG,C	1002
Sal I	G`TCGA,C	184	BstX I	CCAN,NNNN`NTGG	1326
HinC II	GTY RAC	186	Cla I	AT`CG,AT	1386

pHDR1 Vector

Afl II	C`TTAA,G	1405				3152	3393	3428	
BsaB I	GATNN NNATC	1510				Ban II	(2)	970	3759
Eco47 III	AGC GCT	1567				Bbe I	(2)	608	3397
Psp1406 I	AA`CG,TT	1638				Bbs I	(2)	397	4060
Xmn I	GAANN NNTTC	1871				Bbv I	(12)	678	720 1241 1913
BsmB I	CGTCTC 7/11	1954						1962	2059 2730 2733
Bst1107 I	GTA TAC	2084						2939	3467 3509 4030
Xca I	GTA TAC	2084				Bbv II	(2)	396	4061
Nde I	CA`TA,TG	2134				Bcn I	(9)	610	770 1504 1652
Afl III	A`CRYG,T	2311						1958	1993 2692 3399
AlwN I	CAG,NNN`CTG	2727						3559	
Number of enzymes = 25						Bfa I	(5)	150	217 445 2806

The following enzymes do not cut in pHDR1:

Aat II	Age I	Apa I	Apo I	Asc I		Bgl II	(1)	170	
Ase I	Ava I	Avr II	Bcl I	Bgl I		Bpm I	(2)	102	1840
Blp I	Bsa I	BseR I	Bsg I	BsiW I		BsaA I	(3)	909	2065 3698
Bsm I	Bsp120 I	BspM II	BsrG I	Bsu36 I		BsaB I	(1)	1510	
Dra III	Eco72 I	EcoN I	EcoO109 I	EcoR I		BsaH I	(3)	605	1307 3394
EcoR V	Esp I	Fse I	Hpa I	Mlu I		BsaJ I	(7)	87	265 768 1037
Mun I	Nhe I	Not I	Nru I	Nsi I				2471	3557 3826
PaeR7 I	PflM I	Pml I	PpuM I	PspA I		BsaW I	(4)	636	2517 2664 3425
Pvu I	Sac I	Sac II	Sca I	Sfi I		BsiC I	(2)	197	1287
Sma I	SnaB I	Spe I	Spl I	Srf I		BsiE I	(4)	514	2227 2651 3303
Ssp I	Vsp I	Xcm I	Xho I	Xma I		BsiHKA I	(6)	718	908 2131 2629
								3507	3697
						BsmA I	(2)	1955	3227
						BsmB I	(1)	1954	
						BsmF I	(4)	756	1288 1584 3545
						BsoF I	(45)	514	566 577 667
								672	709 750 837
								840	843 1079 1175
								1216	1230 1331 1524
								1605	1902 1905 1951
								2048	2101 2217 2235
								2238	2356 2511 2654
								2719	2722 2928 3303
								3355	3366 3456 3461
								3498	3539 3626 3629
								3632	3868 3964 4005
								4019	
						Bsp1286 I	(2)	908	3697
						BspH I	(2)	3031	3228
						BspM I	(5)	492	873 1323 3281
								3662	
						Bsr I	(12)	548	749 1490 1620
								1644	2059 2090 2718
								2731	2845 3337 3538
						BsrB I	(5)	1218	1272 2244 3226
								4007	
						BsrD I	(2)	838	3627
						BssH II	(1)	1002	
						BssS I	(3)	1197	2484 3986
						Bst1107 I	(1)	2084	
						BstB I	(2)	197	1287
						BstE II	(1)	95	
						BstN I	(7)	114	267 992 2339
								2460	2473 3781
						BstU I	(11)	671	972 1004 1843
								1912	1914 2017 2358
								2939	3460 3761
						BstX I	(1)	1326	
						BstY I	(11)	170	465 776 1022
								1505	2952 2963 3049
								3061	3565 3811

pHDR1: sites sorted by name:

Acc I	(2)	185	2083		
Acc65 I	(1)	116			
Aci I	(55)	469	514	577	671
		735	836	839	1079
		1119	1124	1174	1190
		1216	1272	1331	1602
		1605	1616	1772	1788
		1843	1899	1984	2023
		2033	2075	2100	2138
		2151	2177	2194	2237
		2244	2265	2356	2384
		2511	2530	2651	2761
		2896	2905	3224	3303
		3366	3460	3524	3625
		3628	3868	3908	3913
		3963	3979	4005	
Afl II	(1)	1405			
Afl III	(1)	2311			
Aha II	(3)	605	1307	3394	
Ahd I	(2)	3204	4064		
Alu I	(19)	9	31	64	192
		711	1169	1449	1836
		1893	1904	1953	1972
		2253	2479	2569	2615
		2872	3500	3958	
Alw I	(14)	461	472	783	850
		1029	1512	2873	2959
		2959	3056	3057	3572
		3639	3818		
AlwN I	(1)	2727			
ApaL I	(2)	2127	2625		
Asp718	(1)	116			
Ava II	(3)	1121	1598	3910	
BamH I	(1)	465			
Ban I	(7)	116	273	604	639

pHDR1 Vector

Cac8 I	(30)	225	402	406	499					1105	1330	1401	1490	
		685	904	970	976					1786	2326	2337	2355	
		1004	1008	1049	1053					2789	3302	3476	3867	
		1107	1528	1570	1788					3894				
		2242	2328	2365	2925				Hga I	(5)	1314	1848	2007	2421
		3288	3474	3693	3759						2999			
		3765	3793	3797	3838				HgiA I	(6)	718	908	2131	2629
		3842	3896								3507	3697		
Cfr10 I	(4)	924	1105	3713	3894				HgiE II	(3)	262	2129	2890	
Cla I	(1)	1386							Hha I	(25)	599	607	671	708
Csp6 I	(5)	68	117	910	2118						974	1004	1006	1234
		3699									1568	1914	2017	2047
Dde I	(7)	327	1268	1581	2121						2188	2221	2491	2558
		2586	2995	3161							2658	2832	2941	3388
Dpn I	(20)	172	467	778	856						3396	3460	3497	3763
		937	946	1024	1507						4023			
		2879	2954	2965	2973				HinC II	(1)	186			
		3051	3063	3168	3567				Hind II	(1)	186			
		3645	3726	3735	3813				HinD III	(1)	190			
DpnII	(20)	170	465	776	854				Hinf I	(12)	1090	1224	1276	1383
		935	944	1022	1505						1469	1867	2211	2286
		2877	2952	2963	2971						2682	3199	3879	4013
		3049	3061	3166	3565				HinI I	(3)	605	1307	3394	
		3643	3724	3733	3811				HinP I	(25)	597	605	669	706
Dra I	(4)	105	1394	3070	3089						972	1002	1004	1232
Drd I	(4)	632	2006	2419	3421						1566	1912	2015	2045
Dsa I	(3)	87	1037	3826							2186	2219	2489	2556
Eae I	(10)	511	685	1076	1103						2656	2830	2939	3386
		1328	1488	3300	3474						3394	3458	3495	3761
		3865	3892								4021			
Eag I	(2)	511	3300						Hpa II	(24)	510	587	609	637
Ear I	(5)	949	1159	2195	3738						768	858	925	1106
		3948									1503	1650	1957	1991
Eco47 III	(1)	1567									2518	2665	2691	2881
Eco57 I	(6)	152	750	1182	2858						3299	3376	3398	3426
		3539	3971								3557	3647	3714	3895
EcoR II	(7)	112	265	990	2337				Hph I	(6)	106	784	1932	1941
		2458	2471	3779							3048	3573		
Ehe I	(2)	606	3395						Kas I	(2)	604	3393		
Fnu4H I	(45)	514	566	577	667				Kpn I	(1)	120			
		672	709	750	837				Mae I	(5)	150	217	445	2806
		840	843	1079	1175						3059			
		1216	1230	1331	1524				Mae II	(7)	721	908	1638	2064
		1605	1902	1905	1951						3014	3510	3697	
		2048	2101	2217	2235				Mae III	(14)	95	725	1031	1645
		2238	2356	2511	2654						1668	1752	1965	2060
		2719	2722	2928	3303						2667	2730	2846	3129
		3355	3366	3456	3461						3514	3820		
		3498	3539	3626	3629				Mbo I	(20)	170	465	776	854
		3632	3868	3964	4005						935	944	1022	1505
		4019									2877	2952	2963	2971
Fok I	(11)	426	929	954	1532						3049	3061	3166	3565
		1594	1672	1858	1999						3643	3724	3733	3811
		3170	3718	3743					Mbo II	(11)	401	965	1175	1257
Fsp I	(2)	707	3496								2183	2972	3045	3754
Gdi II	(10)	510	512	1075	1102						3964	4046	4061	
		1327	1487	3299	3301				Mme I	(2)	2525	2709		
		3864	3891						Mnl I	(25)	53	65	211	253
Gsu I	(2)	101	1839								299	374	520	656
Hae I	(7)	112	687	1401	2326						1013	1205	1411	1640
		2337	2789	3476							1698	1737	1917	1947
Hae II	(5)	608	1569	2189	2559						2209	2419	2492	2743
		3397									3143	3309	3445	3802
Hae III	(17)	112	513	687	1078						3994			

pHDR1 Vector

Msc I	(2)	687	3476		
Mse I	(15)	39	104	176	180
		1393	1406	1558	1778
		1810	2092	3017	3069
		3074	3088	3141	
Msl I	(4)	1042	1324	1363	3831
Msp I	(24)	510	587	609	637
		768	858	925	1106
		1503	1650	1957	1991
		2518	2665	2691	2881
		3299	3376	3398	3426
		3557	3647	3714	3895
MspAl I	(6)	711	1904	2023	2653
		2898	3500		
Nae I	(2)	1107	3896		
Nar I	(2)	605	3394		
Nci I	(9)	609	769	1503	1651
		1957	1992	2691	3398
		3558			
Nco I	(3)	87	1037	3826	
Nde I	(1)	2134			
NgoM I	(2)	1105	3894		
Nla III	(21)	20	91	408	479
		824	1010	1041	1067
		1438	1658	1722	1785
		1950	2055	2315	3035
		3232	3613	3799	3830
		3856			
Nla IV	(12)	85	118	275	467
		606	641	1600	2343
		2382	3154	3395	3430
Nsp7524 I	(6)	404	1006	1654	1946
		2311	3795		
NspB II	(6)	711	1904	2023	2653
		2898	3500		
NspH I	(6)	408	1010	1658	1950
		2315	3799		
Pal I	(17)	112	513	687	1078
		1105	1330	1401	1490
		1786	2326	2337	2355
		2789	3302	3476	3867
		3894			
Fle I	(2)	1477	2690		
Pme I	(2)	105	1394		
Psp1406 I	(1)	1638			
Pst I	(1)	658			
Pvu II	(3)	711	1904	3500	
Rsa I	(5)	69	118	911	2119
		3700			
Rsr II	(2)	1121	3910		
Sal I	(1)	184			
Sap I	(5)	949	1159	2195	3738
		3948			
Sau3A I	(20)	170	465	776	854
		935	944	1022	1505
		2877	2952	2963	2971
		3049	3061	3166	3565
		3643	3724	3733	3811
Sau96 I	(4)	1121	1598	1785	3910
ScrF I	(16)	114	267	609	769
		992	1503	1651	1957
		1992	2339	2460	2473
		2691	3398	3558	3781
Sec I	(7)	87	265	768	1037

		2471	3557	3826	
SfaN I	(23)	323	564	819	903
		967	1035	1242	1511
		1519	1615	1693	1755
		1978	2111	2149	2187
		2407	3353	3608	3692
		3756	3824	4031	
Sfc I	(4)	654	1462	2576	2767
Sph I	(3)	408	1010	3799	
Stu I	(2)	112	1401		
Sty I	(3)	87	1037	3826	
Taq I	(17)	33	185	197	204
		718	874	898	934
		1096	1287	1386	2411
		3507	3663	3687	3723
		3885			
Tfi I	(7)	1090	1224	1383	1867
		2286	3879	4013	
Tsp45 I	(8)	95	725	1031	1752
		1965	2060	3514	3820
Tth111 I	(3)	723	2058	3512	
Tth111 II	(7)	227	1041	1773	2900
		2909	2939	3830	
Xba I	(2)	149	444		
Xca I	(1)	2084			
Xho II	(11)	170	465	776	1022
		1505	2952	2963	3049
		3061	3565	3811	
Xma III	(2)	511	3300		
Xmn I	(1)	1871			

Site usage in pHDR1:

Aat II	G,ACGT`C	-	Acc I	GT`MK,AC	2
Acc65 I	G`GTAC,C	1	Aci I	C`CG,C	55
Afl II	C`TTAA,G	1	Afl III	A`CRYG,T	1
Age I	A`CCGG,T	-	Aha II	GR`CG,YC	3
Ahd I	GACNN,N`NNGTC	2	Alu I	AG CT	19
Alw I	GGATC 8/9	14	AlwN I	CAG,NNN`CTG	1
Apa I	G,GGCC`C	-	ApaL I	G`TGCA,C	2
Apo I	R`AATT,Y	-	Asc I	GG`CGCG,CC	-
Ase I	AT`TA,AT	-	Asp718	G`GTAC,C	1
Ava I	C`YCGR,G	-	Ava II	G`GWC,C	3
Avr II	C`CTAG,G	-	BamH I	G`GATC,C	1
Ban I	G`GYRC,C	7	Ban II	G,RCY`C	2
Bbe I	G,CGCC`C	2	Bbs I	GAAGAC 8/12	2
Bbv I	GCAGC 13/17	12	Bbv II	GAAGAC 7/11	2
Bcl I	T`GATC,A	-	Bcn I	CC,S`GG	9
Bfa I	C`TA,G	5	Bgl I	GCCN,NNN`NGGC	-
Bgl II	A`GATC,T	1	Blp I	GC`TNA,GC	-
Bpm I	CTGGAG 22/20	2	Bsa I	GGTCTC 7/11	-
BsaA I	YAC GTR	3	BsaB I	GATNN NNATC	1
BsaH I	GR`CG,YC	3	BsaJ I	C`CNNG,G	7
BsaW I	W`CCGG,W	4	BseR I	GAGGAG 16/14	-
Bsg I	GTGCAG 22/20	-	BsiC I	TT`CG,AA	2
BsiE I	CG,RY`CG	4	BsiHKA I	G,WGCW`C	6
BsiW I	C`GTAC,G	-	Bsm I	GAATG,C 7	-
BsmA I	GTCTC`/9	2	BsmB I	CGTCTC 7/11	1
BsmF I	GGGAC 15/19	4	BsoF I	GC`N,GC	45
Bsp120 I	G`GGCC,C	-	Bsp1286 I	G,DGCH`C	2
BspH I	T`CATG,A	2	BspM I	ACCTGC 10/14	5
BspM II	T`CCGG,A	-	Bsr I	ACT,GG`	12
BsrB I	GAG CGG	5	BsrD I	GCAATG, 8	2
BsrG I	T`GTAC,A	-	BssH II	G`CGCG,C	1

pHDR1 Vector

BssS I	C`TCGT,G	3	Bst1107 I	GTA TAC	1	Msp I	C`CG,G	24	MspA1 I	CMG CKG	6
BstB I	TT`CG,AA	2	BstE II	G`GTNAC,C	1	Mun I	C`AATT,G	-	Nae I	GCC GGC	2
BstN I	CC`W,GG	7	BstU I	CG CG	11	Nar I	GG`CG,CC	2	Nci I	CC`S,GG	9
BstX I	CCAN,NNNN`NTGG	1	BstY I	R`GATC,Y	11	Nco I	C`CATG,G	3	Nde I	CA`TA,TG	1
Bsu36 I	CC`TNA,GG	-	Cac8 I	GCN NGC	30	Ngom I	G`CCGG,C	2	Nhe I	G`CTAG,C	-
Cfr10 I	R`CCGG,Y	4	Cla I	AT`CG,AT	1	Nla III	,CATG`	21	Nla IV	GGN NCC	12
Csp6 I	G`TA,C	5	Dde I	C`TNA,G	7	Not I	GC`GGCC,GC	-	Nru I	TCG CGA	-
Dpn I	GA TC	20	DpnII	`GATC,	20	Nsi I	A,TGCA`T	-	Nsp7524 I	R`CATG,Y	6
Dra I	TTT AAA	4	Dra III	CAC,NNN`GTG	-	NspB II	CMG CKG	6	NspH I	R,CATG`Y	6
Drd I	GACNN,NN`NNGTC	4	Dsa I	C`CRYG,G	3	FaeR7 I	C`TCGA,G	-	Pal I	GG CC	17
Eae I	Y`GGCC,R	10	Eag I	C`GGCC,G	2	PflM I	CCAN,NNN`NTGG	-	Ple I	GAGTC 9/10	2
Ear I	CTCTTC 7/10	5	Eco47 III	AGC GCT	1	Pme I	CTTT AAAC	2	Pml I	CAC GTG	-
Eco57 I	CTGAAG 21/19	6	Eco72 I	CAC GTG	-	PpuM I	RG`GWC,CY	-	Psp1406 I	AA`CG,TT	1
EcoN I	CCTNN`N,NNAGG	-	Eco0109 I	RG`GNC,CY	-	PspA I	C`CCGG,G	-	Pst I	C,TGCA`G	1
EcoR I	G`AATT,C	-	EcoR II	`CCWGG,	7	Pvu I	CG,AT`CG	-	Pvu II	CAG CTG	3
EcoR V	GAT ATC	-	Ehe I	GGC GCC	2	Rsa I	GT AC	5	Rsr II	CG`GWC,CG	2
Esp I	GC`TNA,GC	-	Fnu4H I	GC`N,GC	45	Sac I	G,AGCT`C	-	Sac II	CC,GC`GG	-
Fok I	GGATG 14/18	11	Fse I	GG,CCGG`CC	-	Sal I	G`TCGA,C	1	Sap I	GCTCTTC 8/11	5
Fsp I	TGC GCA	2	Gdi II	`YGGC,CG	10	Sau3A I	`GATC,	20	Sau96 I	G`GNC,C	4
Gsu I	CTGGAG 21/19	2	Hae I	WGG CCW	7	Sca I	AGT ACT	-	ScrF I	CC`N,GG	16
Hae II	R,GCGC`Y	5	Hae III	GG CC	17	Sec I	C`CNNG,G	7	SfaN I	GCATC 9/13	23
Hga I	GACGC 9/14	5	HgiA I	G,WGCW`C	6	Sfc I	C`TRYA,G	4	Sfi I	GGCCN,NNN`NGGCC	-
HgiE II	ACCNNNNNNGGT -1/133	-	Hha I	G,CG`C	25	Sma I	CCC GGG	-	SnaB I	TAC GTA	-
Hinc II	GTY RAC	1	Hind II	GTY RAC	1	Spe I	A`CTAG,T	-	Sph I	G,CATG`C	3
Hind III	A`AGCT,T	1	Hinf I	G`ANT,C	12	Spl I	C`GTAC,G	-	Srf I	GCCC GGGC	-
HinI I	GR`CG,YC	3	HinP I	G`CG,C	25	Ssp I	AAT ATT	-	Stu I	AGG CCT	2
Hpa I	GTT AAC	-	Hpa II	C`CG,G	24	Sty I	C`CWWG,G	3	Taq I	T`CG,A	17
Hph I	GGTGA 12/11	6	Kas I	G`GCGC,C	2	Tfi I	G`AWT,C	7	Tsp45 I	`GTSAC,	8
Kpn I	G,GTAC`C	1	Mae I	C`TA,G	5	Tth111 I	GACN`N,NGTC	3	Tth111 II	CAARCA 16/14	7
Mae II	A`CG,T	7	Mae III	`GTNAC,	14	Vsp I	AT`TA,AT	-	Xba I	T`CTAG,A	2
Mbo I	`GATC,	20	Mbo II	GAAGA 12/11	11	Xca I	GTA TAC	1	Xcm I	CCANNNN,N`NNNNTGG-	-
Mlu I	A`CGCG,T	-	Mme I	TCCRAC 25/23	2	Xho I	C`TCGA,G	-	Xho II	R`GATC,Y	11
Mnl I	CCTC 10/10	25	Msc I	TGG CCA	2	Xma I	C`CCGG,G	-	Xma III	C`GGCC,G	2
Mse I	T`TA,A	15	Msl I	CAYNN NNRTG	4						