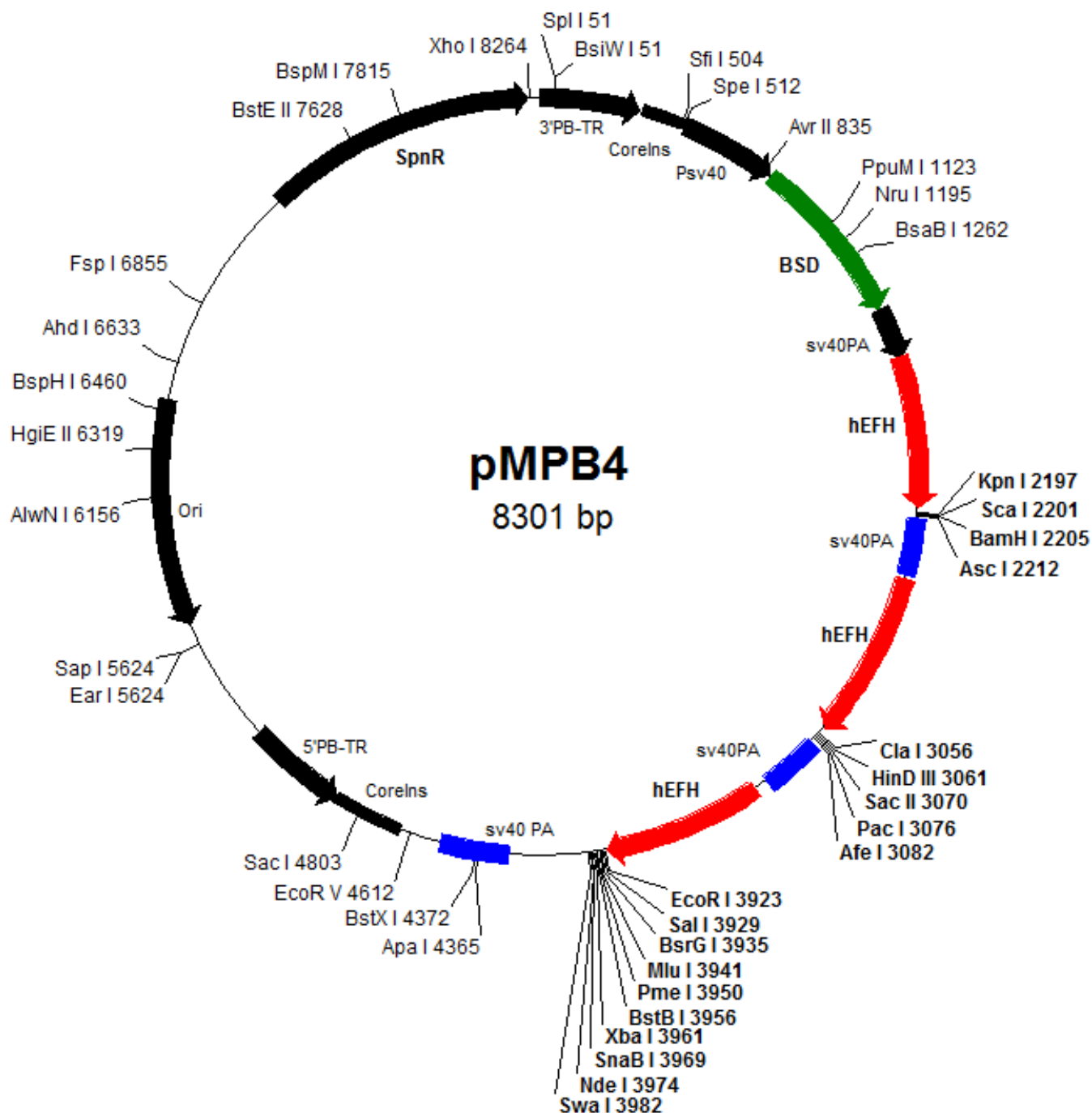


Vector: pMPB4 (modified PiggyBac vector; three expression cassettes)

Antibiotic Selection: Spectinomycin or Blastisin-resistant

Creator(s): Xiang (Sean) Chen, MD, PhD, Molecular Oncology Lab of The University of Chicago

Date of Construction: February, 2012



pMPB4 Vector Sequence (aka pMPB2b)

(Spectinomycin or Blastacin-resistant)

CTGCAGAACACGCAGCTAGATTAAACCTAGAAAAGATAATCAATTTGTGACGTACGTTAAAGATAATCATGCGTAAAATTTGACGCATG
TGTTTTATCGGTCTGTATATCGAGGTTTATTTATTAATTTGAATAGATATTAAGTTTTATTATATTTTACACTTACATACTAATAATA
AATTCAACAAACAATTTATTTATGTTTTATTTATTTATTTAAAAAACAACAAAACTCAAAATTTCTTCTATAAAAGTAACAAAAAC
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TCTTGAGCCCTGCGGACGGTGCAGACAGGTGCTTCTCGATCTGCATCTGGGATCAAAGCCATAGTGAAGGACAGTGATGGACAGC
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GTGCTACGAGATTTGATTCCACCGCCGCCTTCTATGAAAGGTTGGGCTTCGGAATCGTTTTCCGGGACGCCGGCTGGATGATCCTC
CAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCACCCCAACTTGTATTATGCAGCTTATAATGGTTACAAATAAAGCAATAGCATC
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 GGCAGCACTGCATAAATCTCTTACTGTGATGCCATCCGTAAGATGCTTTTCTGTGACTGGT**GAGTGTACCAGCCAGGACAGAAATGC**
CTCGACTTCGCTGCTACCCAAGGTTGCCGGGTGACGCACACCGTGGAAACGGATGAAGGCACGAACCCAGTGGACATAAGCCTGTTT
GGTTTCGTAAGCTGTAATGCAAGTAGCGTATG**CGCTCACGCAACTGGTCCAGAACCTTGACCCGAACGCAGCGGTGGTAACGGCGCAGT**
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TCGCTTGGCCTCGCGCGCAGATCAGTTGGAAGAATTTGTCCACTACGTGAAAGGCGAGATACCAAGGTAGTCGGCAAATAACCCTC****
GAGCCACCATGA**CCAAAATCCCTTAACGTGAGTTA**

Unique enzymes in pMPB4:

BsiW I	C`GTAC,G	51
Spl I	C`GTAC,G	51
Sfi I	GGCCN,NNN`NGGCC	504
Spe I	A`CTAG,T	512
Avr II	C`CTAG,G	835
Bbv II	GAAGAC 7/11	1048
Bbs I	GAAGAC 8/12	1049
PpuM I	RG`GWC,CY	1123
Nru I	TCG CGA	1195
BsaB I	GATNN NNATC	1262
Acc65 I	G`GTAC,C	2193
Asp718	G`GTAC,C	2193
Kpn I	G,GTAC`C	2197
Sca I	AGT ACT	2201
BamH I	G`GATC,C	2205
Asc I	GG`CGCG,CC	2212
Cla I	AT`CG,AT	3056
Hind III	A`AGCT,T	3061
Sac II	CC,GC`GG	3070
Eco47 III	AGC GCT	3083
EcoR I	G`AATT,C	3923
Sal I	G`TCGA,C	3929
Acc I	GT`MK,AC	3930
BsrG I	T`GTAC,A	3935
Mlu I	A`CCGG,T	3941
Pme I	CTTT AAAC	3950
BsiC I	TT`CG,AA	3956
BstB I	TT`CG,AA	3956
Xba I	T`CTAG,A	3961
SnaB I	TAC GTA	3969
Nde I	CA`TA,TG	3974
Bsp120 I	G`GGCC,C	4361
Apa I	G,GGCC`C	4365
BstX I	CCAN,NNNN`NTGG	4372
EcoR V	GAT ATC	4612
Sac I	G,AGCT`C	4803
Sap I	GCTCTC 8/11	5624

Ear I	CTCTC 7/10	5624
AlwN I	CAG,NNN`CTG	6156
HgiE II	ACCNNNNNGGT -1/136319	
BspH I	T`CATG,A	6460
Ahd I	GACNN,N`NNGTC	6633
Fsp I	TGC GCA	6855
BstE II	G`GTNAC,C	7628
BspM I	ACCTGC 10/14	7815
Paer7 I	C`TCGA,G	8264
Xho I	C`TCGA,G	8264
Number of enzymes = 47		

The following enzymes do not cut in pMPB4:

Aat II	Afl II	Bgl II	BsmB I	Bsp1286 I
Bst1107 I	Fse I	Hpa I	Pf1M I	Tth111 I

pMPB4: sites sorted by name:

Acc I	(1)	3930			
Acc65 I	(1)	2193			
Aci I	(106)	315	336	348	370
		393	683	695	704
		716	726	737	783
		1083	1165	1232	1416
		1419	1485	1651	1655
		1756	1793	1873	1929
		1932	1947	1978	1985
		2012	2278	2281	2347
		2513	2517	2618	2655
		2735	2791	2794	2809
		2840	2847	2874	3067
		3069	3091	3146	3149
		3215	3381	3385	3486
		3523	3603	3659	3662
		3677	3708	3715	3742
		4479	4502	4524	4536
		4557	4741	4774	4808
		5016	5029	5178	5285

		5290	5338	5375	5430			6924	7934		
		5533	5589	5599	5623	BseR I	(4)	831	1391	2253	3121
		5666	5673	5694	5785	Bsg I	(5)	1151	1852	2714	3582
		5813	5940	5959	6080			5290			
		6190	6325	6334	6696	BsiC I	(1)	3956			
		6787	6978	7024	7291	BsiE I	(10)	1083	1199	1655	2517
		7311	7479	7576	7588			3385	4745	5656	6080
		7655	7718	7914	7917			7003	7849		
		7995	8042			BsiHKA I	(3)	4803	6058	7747	
Afl III	(6)	894	1390	2252	3120	BsiW I	(1)	51			
		3941	5740			Bsm I	(5)	1600	2462	3330	4081
Age I	(3)	1734	2596	3464				4885			
Aha II	(7)	1461	2185	2323	3047	BsmA I	(6)	982	2038	2900	3768
		3191	3915	7522				4180	6695		
Ahd I	(1)	6633				BsmF I	(19)	281	291	410	529
Alu I	(44)	16	799	853	863			601	665	1136	1472
		1066	1171	1535	1886			1683	2334	2545	3202
		1892	1896	2034	2175			3413	4203	4286	4460
		2397	2748	2754	2758			4579	4589	8024	
		2896	3037	3063	3265	BsoF I	(77)	14	326	329	336
		3616	3622	3626	3764			387	454	783	1064
		3905	4167	4801	4927			1083	1157	1160	1163
		4970	5405	5500	5564			1166	1169	1333	1419
		5682	5908	5998	6044			1533	1652	1655	1873
		6301	6822	6922	6985			1932	1947	1978	2281
		7232	7662	7776	8148			2395	2514	2517	2735
Alw I	(25)	434	888	1278	1469			2794	2809	2840	3149
		1496	2163	2201	2212			3263	3382	3385	3603
		2331	2358	3025	3083			3662	3677	3708	4320
		3199	3226	3893	4439			4419	4486	4537	4544
		4943	6302	6388	6388			4547	4809	4928	5030
		6485	6486	6950	7927			5061	5064	5179	5291
		7956						5338	5565	5646	5664
AlwN I	(1)	6156						5667	5785	5940	6083
Apa I	(1)	4365						6148	6151	6357	6685
ApaL I	(2)	6054	7743					7024	7051	7146	7289
Apo I	(8)	175	233	1570	2432			7374	7418	7434	7589
		3300	3923	4051	8211			7656	7806	7915	7995
Asc I	(1)	2212						8092			
Ase I	(6)	122	906	5276	5511	Bsp120 I	(1)	4361			
		5570	6805			BspH I	(1)	6460			
Asp718	(1)	2193				BspM I	(1)	7815			
Ava I	(15)	339	377	403	856	BspM II	(2)	5186	5198		
		1701	1803	2563	2665	Bar I	(27)	721	1097	1121	1769
		3431	3533	4467	4493			1790	2198	2206	2631
		4531	7360	8264				2652	3499	3520	4238
Ava II	(7)	355	1123	4516	6771			4348	5169	5541	6147
		6993	7267	7908				6160	6274	6680	6798
Avr II	(1)	835						6841	7108	7203	7268
BamH I	(1)	2205						8006	8102	8124	
Ban I	(16)	1238	1662	1737	1993	BsrB I	(7)	350	1657	2519	3387
		2184	2193	2524	2599			4524	5432	5673	
		2855	3046	3392	3467	BsrD I	(4)	6694	6868	7817	8110
		3723	3914	5484	6581	BsrG I	(1)	3935			
Ban II	(8)	347	1228	1908	2770	BssH II	(3)	2212	5379	8192	
		3638	4365	4531	4803	BssS I	(2)	1138	5913		
Bbe I	(3)	2188	3050	3918		BstB I	(1)	3956			
Bbs I	(1)	1049				BstE II	(1)	7628			
Bbv I	(20)	25	337	340	398	BstN I	(18)	291	477	549	604
		1075	1180	1544	2406			621	1268	4266	4324
		3274	4331	4430	6159			4396	4582	5160	5327
		6162	6368	7062	7300			5480	5768	5889	5902
		7385	7429	7445	7817			7122	7699		
Bbv II	(1)	1048				BstU I	(33)	1195	1485	1756	1925
Bcl I	(2)	886	7666					1970	2214	2347	2618
Bcn I	(22)	341	342	405	406			2787	2832	3069	3215
		858	859	1458	2049			3486	3655	3700	3943
		2320	2911	3188	3779			4741	4847	5018	5178
		4187	4336	4469	4470			5381	5587	5589	5787
		4533	4534	5373	6121			6368	6698	7382	7655
		6817	7164					7720	7783	8076	8192
Bfa I	(31)	17	28	318	513			8194			
		836	1073	1605	1742	BstX I	(1)	4372			
		1893	2019	2081	2467	BstY I	(14)	881	1489	2167	2205
		2604	2755	2881	2943			2351	3029	3087	3219
		3085	3335	3472	3623			3897	6381	6392	6478
		3749	3811	3962	4086			6490	7949		
		4554	4913	4924	6235	Bsu36 I	(3)	1941	2803	3671	
		6488	6823	8149		Cac8 I	(54)	333	384	391	467
Bgl I	(3)	504	6753	8100				562	581	634	653
Blp I	(2)	1359	7777					1059	1173	1465	1894
Bpm I	(8)	1463	1520	2325	2382			1908	1929	2092	2120
		3193	3250	6703	7720			2214	2327	2756	2770
Bsa I	(5)	2037	2899	3767	4181			2791	2954	2982	3195
		6694						3624	3638	3659	3822
BsaA I	(8)	895	1393	2255	3123			3850	4407	4483	4490
		3969	4650	4708	8225			4541	4788	4885	4972
BsaB I	(1)	1262						5126	5377	5381	5533
BsaH I	(7)	1461	2185	2323	3047			5562	5671	5757	5794
		3191	3915	7522				6354	6745	7378	7555
BsaJ I	(45)	289	290	339	340			7660	7840	8009	8115
		403	476	502	547			8119	8194		
		619	742	777	835						
		856	962	1267	1374	Cfr10 I	(22)	382	1463	1734	1958
		1804	2068	2236	2666			2090	2181	2325	2596
		2930	3067	3104	3534			2820	2952	3043	3193
		3798	4185	4333	4394			3464	3688	3820	3911
		4467	4530	4531	4580			4488	5239	5263	6713
		4581	5048	5159	5479			8064	8117		
		5900	7153	7176	7359	Cla I	(1)	3056			
		7390	7697	7761	7900	Csp6 I	(13)	52	1784	2194	2200
		8242						2646	3514	3936	3970
BsaW I	(14)	352	1659	1734	2521			7114	7347	7560	7568
		2596	3389	3464	4518			8051			
		5186	5198	5946	6093	Dde I	(16)	795	1359	1941	2035
								2086	2803	2897	2948

		3671	3765	3816	4815							
		6015	6424	6590	7777	HgiE II	(1)	6319				
Dpn I	(39)	429	883	888	1198	Hha I	(57)	363	1063	1485	1684	
		1259	1273	1475	1491			1756	1927	2064	2159	
		2169	2207	2337	2353			2187	2214	2216	2347	
		3031	3089	3205	3221			2546	2618	2789	2926	
		3899	3988	4445	4938			3021	3049	3084	3215	
		6308	6383	6394	6402			3414	3486	3657	3794	
		6480	6492	6597	6938			3889	3917	4513	4849	
		6956	7002	7485	7668			4976	5219	5295	5381	
		7848	7858	7933	7951			5383	5524	5589	5617	
		8179	8200	8238				5650	5920	5987	6087	
DpnII	(39)	427	881	886	1196			6261	6370	6763	6856	
		1257	1271	1473	1489			7255	7305	7382	7534	
		2167	2205	2335	2351			7722	7783	7810	7964	
		3029	3087	3203	3219			8058	8078	8113	8194	
		3897	3986	4443	4936	HinC II	(3)	900	3931	4262		
		6306	6381	6392	6400	Hind II	(3)	900	3931	4262		
		6478	6490	6595	6936	HinD III	(1)	3061				
		6954	7000	7483	7666	Hinf I	(27)	988	1320	1409	1446	
		7846	7856	7931	7949			1965	2084	2271	2308	
		8177	8198	8236				2827	2946	3139	3176	
Dra I	(8)	2030	2892	3760	3950			3695	3814	3958	4136	
		3982	4215	6499	6518			4348	4734	4842	5103	
Dra III	(6)	1369	2231	3099	7177			5575	5640	5715	6111	
		7605	8225					6628	7499	7712		
Drd I	(3)	1051	4819	5848				1461	2185	2323	3047	
Dsa I	(7)	502	742	962	3067	HinI I	(7)	3191	3915	7522		
		7176	7390	7761				361	1061	1483	1682	
Eae I	(13)	505	965	1080	1371	HinP I	(57)	1754	1925	2062	2157	
		1652	2233	2514	3101			2185	2212	2214	2345	
		3382	5117	5579	7021			2544	2616	2787	2924	
		7555						3019	3047	3082	3213	
Eag I	(4)	1080	1652	2514	3382			3412	3484	3655	3792	
Ear I	(1)	5624						3887	3915	4511	4847	
Eco47 III	(1)	3083						4974	5217	5293	5379	
Eco57 I	(6)	1060	1907	2769	3637			5381	5522	5587	5615	
		6287	7613					5648	5918	5985	6085	
Eco72 I	(4)	895	1393	2255	3123			6259	6368	6761	6854	
EcoN I	(7)	1745	1940	2607	2802			7253	7303	7380	7532	
		3475	3670	4356				7720	7781	7808	7962	
EcoO109 I	(2)	1123	4361					8056	8076	8111	8192	
EcoR I	(1)	3923						8194				
EcoR II	(18)	289	475	547	602	Hpa II	(60)	340	353	358	383	
		619	1266	4264	4322			404	857	1456	1464	
		4394	4580	5158	5325			1660	1735	1959	2047	
		5478	5766	5887	5900			2059	2091	2182	2209	
		7120	7697					2318	2326	2522	2597	
EcoR V	(1)	4612						2821	2909	2921	2953	
Ehe I	(3)	2186	3048	3916				3044	3186	3194	3390	
Esp I	(2)	1359	7777					3465	3689	3777	3789	
Fnu4H I	(77)	14	326	329	336			3821	3912	4185	4335	
		387	454	783	1064			4468	4489	4514	4519	
		1083	1157	1160	1163			4532	5187	5199	5240	
		1166	1169	1333	1419			5250	5264	5372	5458	
		1533	1652	1655	1873			5947	6094	6120	6310	
		1932	1947	1978	2281			6714	6748	6815	6925	
		2395	2514	2517	2735			7162	7935	8065	8118	
		2794	2809	2840	3149	Hph I	(10)	959	5148	6477	6704	
		3263	3382	3385	3603			7118	7176	7492	7639	
		3662	3677	3708	4320			7725	8232			
		4419	4486	4537	4544	Kas I	(3)	2184	3046	3914		
		4547	4809	4928	5030	Kpn I	(1)	2197				
		5061	5064	5179	5291	Mae I	(31)	17	28	318	513	
		5338	5565	5646	5664			836	1073	1605	1742	
		5667	5785	5940	6083			1893	2019	2081	2467	
		6148	6151	6357	6685			2604	2755	2881	2943	
		7024	7051	7146	7289			3085	3335	3472	3623	
		7374	7418	7434	7589			3749	3811	3962	4086	
		7656	7806	7915	7995			4554	4913	4924	6235	
		8092						6488	6823	8149		
Fok I	(24)	307	359	686	1015	Mae II	(26)	50	54	304	894	
		1250	1483	1937	2345			1392	1849	2132	2254	
		2799	3213	3667	4184			2711	2994	3122	3579	
		4511	4563	5065	5214			3862	3968	4568	4649	
		5346	6599	6780	7067			4707	5072	5089	5306	
		7199	7352	7596	8097			6443	6859	7548	8034	
Fsp I	(1)	6855						8224	8293			
Gdi II	(15)	506	1079	1081	1370	Mae III	(31)	46	248	1544	2161	
		1651	1653	2232	2513			2177	2406	3023	3039	
		2515	3100	3381	3383			3274	3891	3907	4025	
		5580	7020	7554				4703	4763	5366	6096	
Gsu I	(8)	1464	1519	2326	2381			6159	6275	6558	6889	
		3194	3249	6704	7719			6947	7100	7165	7296	
Hae I	(9)	498	834	967	5119			7383	7427	7622	7628	
		5155	5755	5766	6218			7730	8060	8298		
		8187				Mbo I	(39)	427	881	886	1196	
Hae II	(16)	364	2065	2188	2927			1257	1271	1473	1489	
		3050	3085	3795	3918			2167	2205	2335	2351	
		4514	4977	5296	5618			3029	3087	3203	3219	
		5988	7535	7965	8114			3897	3986	4443	4936	
Hae III	(34)	498	507	776	782			6306	6381	6392	6400	
		834	967	1082	1373			6478	6490	6595	6936	
		1654	1946	2051	2235			6954	7000	7483	7666	
		2516	2808	2913	3103			7846	7856	7931	7949	
		3384	3676	3781	4363			8177	8198	8236		
		5119	5155	5581	5755	Mbo II	(15)	231	996	1053	1081	
		5766	5784	6218	6676			1499	2361	3229	5007	
		6756	7023	7557	7591			5612	6401	6474	7824	
		8121	8187					8183	8186	8219		
Hga I	(14)	89	1042	1468	1998	Mlu I	(1)	3941				
		2330	2860	3198	3728	Mme I	(3)	5954	6138	8186		
		4714	4877	5850	6428	Mnl I	(65)	103	258	318	446	
		7176	7512					508	766	772	795	
HgiA I	(3)	4803	6058	7747				801	809	812	824	

Apa I	G,GGCC`C	1	ApaL I	G`TGCA,C	2	Hga I	GACGC 9/14	14	HgiA I	G,WGCW`C	3
Apo I	R`AATT,Y	8	Asc I	GG`CGCG,CC	1	HgiE II	ACCNNNNNNGGT -1/131	1	Hha I	G,CG`C	57
Ase I	AT`TA,AT	6	Asp718	G`GTAC,C	1	HinC II	GTY RAC	3	Hind II	GTY RAC	3
Ava I	C`YCGR,G	15	Ava II	G`GWC,C	7	HinD III	A`AGCT,T	1	Hinf I	G`ANT,C	27
Avr II	C`CTAG,G	1	BamH I	G`GATC,C	1	HinI I	GR`CG,YC	7	HinP I	G`CG,C	57
Ban I	G`GYRC,C	16	Ban II	G,RCGY`C	8	Hpa I	GTT AAC	-	Hpa II	C`CG,G	60
Bbe I	G,CGCC`C	3	Bbs I	GAAGAC 8/12	1	Hph I	GGTGA 12/11	10	Kas I	G`GCGC,C	3
Bbv I	GCAGC 13/17	20	Bbv II	GAAGAC 7/11	1	Kpn I	G,GTAC`C	1	Mae I	C`TA,G	31
Bcl I	T`GATC,A	2	Bcn I	CC,S`GG	22	Mae II	A`CG,T	26	Mae III	`GTNAC,	31
Bfa I	C`TA,G	31	Bgl I	GCCN,NNN`NGGC	3	Mbo I	`GATC,	39	Mbo II	GAAGA 12/11	15
Bgl II	A`GATC,T	-	Blp I	GC`TNA,GC	2	Mlu I	A`CGCG,T	1	Mme I	TCCRAC 25/23	3
Bpm I	CTGGAG 22/20	8	Bsa I	GGTCTC 7/11	5	Mnl I	CCTC 10/10	65	Msc I	TGG CCA	2
BsaA I	YAC GTR	8	BsaB I	GATNN NNATC	1	Mse I	T`TA,A	32	Msl I	CAYNN NNRTG	4
BsaH I	GR`CG,YC	7	BsaJ I	C`CNNG,G	45	Msp I	C`CG,G	60	MspAl I	CMG CKG	11
BsaW I	W`CCGG,W	14	BseR I	GAGGAG 16/14	4	Mun I	C`AATT,G	3	Nae I	GCC GGC	9
Bsg I	GTGCAG 22/20	5	BsiC I	TT`CG,AA	1	Nar I	GG`CG,CC	3	Nci I	CC`S,GG	22
BsiE I	CG,RY`CG	10	BsiHKA I	G,WGCW`C	3	Nco I	C`CATG,G	2	Nde I	CA`TA,TG	1
BsiW I	C`GTAC,G	1	Bsm I	GAATG,C 7	5	NgoM I	G`CCGG,C	9	Nhe I	G`CTAG,C	3
BsmA I	GTCTC`/9	6	BsmB I	CGTCTC 7/11	-	Nla III	,CATG`	29	Nla IV	GGN NCC	36
BsmF I	GGGAC 15/19	19	BsoF I	GC`N,GC	77	Not I	GC`GGCC,GC	3	Nru I	TCG CGA	1
Bspl20 I	G`GGCC,C	1	Bsp1286 I	G,DGCH`C	-	Nsi I	A,TGCA`T	3	Nsp7524 I	R`CATG,Y	5
BspH I	T`CATG,A	1	BspM I	ACCTGC 10/14	1	NspB II	CMG CKG	11	NspH I	R,CATG`Y	5
BspM II	T`CCGG,A	2	Bsr I	ACT,GG`	27	Paer7 I	C`TCGA,G	1	Pal I	GG CC	34
BsrB I	GAG CGG	7	BsrD I	GCAATG, 8	4	Pf1M I	CCAN,NNN`NTGG	-	Ple I	GAGTC 9/10	4
BsrG I	T`GTAC,A	1	BssH II	G`CGCG,C	3	Pme I	CTTT AAAC	1	Pml I	CAC GTG	4
Bsss I	C`TCGT,G	2	Bst1107 I	GTA TAC	-	PpuM I	RG`GWC,CY	1	Psp1406 I	AA`CG,TT	4
BstB I	TT`CG,AA	1	BstE II	G`GTNAC,C	1	PspA I	C`CCGG,G	5	Pst I	C,TGCA`G	3
BstN I	CC`W,GG	18	BstU I	CG CG	33	Pvu I	CG,AT`CG	3	Pvu II	CAG CTG	5
BstX I	CCAN,NNNN`NTGG	1	BstY I	R`GATC,Y	14	Rsa I	GT AC	13	Rsr II	CG`GWC,CG	2
Bsu36 I	CC`TNA,GG	3	Cac8 I	GCN NGC	54	Sac I	G,AGCT`C	1	Sac II	CC,GC`GG	1
Cfr10 I	R`CCGG,Y	22	Cla I	AT`CG,AT	1	Sal I	G`TCGA,C	1	Sap I	GCTCTTC 8/11	1
Csp6 I	G`TA,C	13	Dde I	C`TNA,G	16	Sau3A I	`GATC,	39	Sau96 I	G`GNC,C	15
Dpn I	GA TC	39	DpnII	`GATC,	39	Sca I	AGT ACT	1	ScrF I	CC`N,GG	40
Dra I	TTT AAA	8	Dra III	CAC,NNN`GTG	6	Sec I	C`CNNG,G	45	SfaN I	GCATC 9/13	23
Drd I	GACNN,NN`NNGTC	3	Dsa I	C`CRYG,G	7	Sfc I	C`TRYA,G	8	Sfi I	GGCCN,NNN`NGGCC	1
Eae I	Y`GGCC,R	13	Eag I	C`GGCC,G	4	Sma I	CCC GGG	5	SnaB I	TAC GTA	1
Ear I	CTCTTC 7/10	1	Eco47 III	AGC GCT	1	Spe I	A`CTAG,T	1	Sph I	G,CATG`C	3
Eco57 I	CTGAAG 21/19	6	Eco72 I	CAC GTG	4	Spl I	C`GTAC,G	1	Srf I	GCCC GGGC	2
EcoN I	CCTNN`N,NNAGG	7	Eco109 I	RG`GNC,CY	2	Ssp I	AAT ATT	2	Stu I	AGG CCT	2
EcoR I	G`AATT,C	1	EcoR II	`CCWGG,	18	Sty I	C`CWGG,G	9	Taq I	T`CG,A	23
EcoR V	GAT ATC	1	Ehe I	GGC GCC	3	Tfi I	G`AWT,C	15	Tsp45 I	`GTSAC,	11
Esp I	GC`TNA,GC	2	Fnu4H I	GC`N,GC	77	Tth111 I	GACN`N,NGTC	-	Tth111 II	CAARCA 16/14	10
Fok I	GGATG 14/18	24	Fse I	GG,CCGG`CC	-	Vsp I	AT`TA,AT	6	Xba I	T`CTAG,A	1
Fsp I	TGC GCA	1	Gdi II	`YGGC,CG	15	Xca I	GTA TAC	-	Xcm I	CCANNNN,N`NNNNTGG-	1
Gsu I	CTGGAG 21/19	8	Hae I	WGG CCW	9	Xho I	C`TCGA,G	1	Xho II	R`GATC,Y	14
Hae II	R,CGGC`Y	16	Hae III	GG CC	34	Xma I	C`CCGG,G	5	Xma III	C`GGCC,G	4