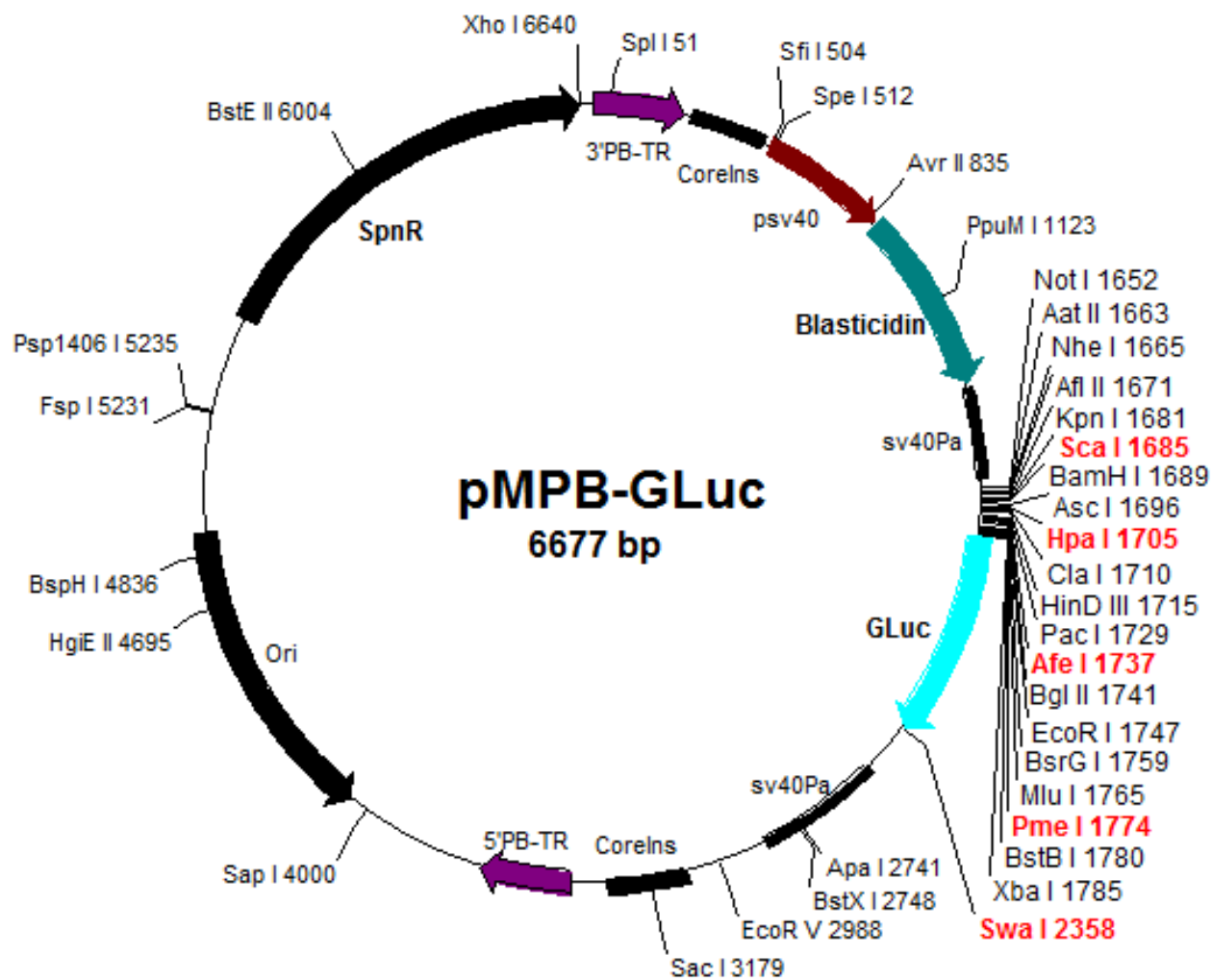


Vector: pMPB-GLuc (modified PiggyBac Gaussia luciferase reporter)

Antibiotic Selection: Spectinomycin-resistant

Creator(s): Chen Zhao, Molecular Oncology Lab of The University of Chicago Medical Center

Date of Construction: April, 2012



pMPB-GLuc Vector Sequence

(Spectinomycin or Blastacin-resistant)

CTGCAGAACACGCAGCTAGATTAAACCTAGAAAAGATAATCATATTGTGACGTACGTTAAAGATAATCATGCGTAAAATTGACGCATG
TGTTTTATCGGTCTGTATATCGAGGTTTATTTATTAATTTGAATAGATATTAAGTTTTATTATATTTACTTTACATACTAATAATA
AATTCAACAAACAATTTATTTATGTTTTATTTATTTATTTAAAAAACAACAACTCAAATTTCTTCTATAAAGTAACAAAACTTTT
ATGAGGGACAGCCCCCCCCAAAGCCCCCAGGGATGTAATTACGTCCCTCCCCCGTAGGGGGCAGCAGCGAGCCCGCCGGGGCTCC
GCTCCGGTCCGGCGCTCCCCCGCATCCCCGAGCCGGCAGCGTGCGGGGACAGCCCGGGCACGGGGAAGGTGGCACGGGATCGCTTT
CCTCTGAACGCTTCTCGCTGCTCTTTGAGCCTGCAGACACCTGGGGGATACGGGGAAAAGGCCTCCACGGCCAGACTAGTAAATGTG
TGTCAAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCATAGTCCCGCCCTAACTCCG
GGAAAGTCCCAGGCTCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCATAGTCCCGCCCTAACTCCG
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ATCACCAAGGTAGTCGGCAATAACCCTCGAGCCACCAATGACCAAAAATCCCTTAACGTGAGTTA

Unique enzymes in pMPB-GLuc:

Enzyme	Recognition Sequence	Count	1419	1485	1651	1655
BsiW I	C`GTAC,G	51	1721	1723	1925	1927
Spl I	C`GTAC,G	51	1953	2104	2113	2280
Sfi I	GGCCN,NNN`NGGCC	504	2855	2878	2900	2912
Spe I	A`CTAG,T	512	2933	3117	3150	3184
Avr II	C`CTAG,G	835	3392	3405	3554	3661
PpuM I	RG`GWC,CY	1123	3666	3714	3751	3806
Not I	GC`GGCC,GC	1652	3909	3965	3975	3999
Aat II	G,ACGT`C	1663	4042	4049	4070	4161
Nhe I	G`CTAG,C	1665	4189	4316	4335	4456
Afl II	C`TTAA,G	1671	4566	4701	4710	5072
Acc65 I	G`GTAC,C	1677	5163	5354	5400	5667
Asp718	G`GTAC,C	1677	5687	5855	5952	5964
Kpn I	G,GTAC`C	1681	6031	6094	6290	6293
Sca I	AGT ACT	1685	6371	6418		
BamH I	G`GATC,C	1689	Afl II (1)	1671		
Asc I	GG`CGCG,CC	1696	Afl III (4)	894	1390	1765
Hpa I	GTT AAC	1705	Aha II (3)	1461	1660	5898
Cla I	AT`CG,AT	1710	Ahd I (2)	2099	5009	
HinD III	A`AGCT,T	1715	Alu I (29)	16	799	853
Eco47 III	AGC GCT	1737		1066	1171	1535
Bgl II	A`GATC,T	1741		1949	1995	2543
EcoR I	G`AATT,C	1747	Alw I (19)	434	888	1278
BsrG I	T`GTAC,A	1759		1496	1685	1696
Mlu I	A`CGCG,T	1765		2304	2815	3319
Pme I	CTTT AAAC	1774		4764	4764	4861
BsiC I	TT`CG,AA	1780	AlwN I (2)	2011	4532	6332
BstB I	TT`CG,AA	1780	Apa I (1)	2741		
Xba I	T`CTAG,A	1785	ApaL I (3)	2039	4430	6119
Xmn I	GAANN NNTTC	2058	Apo I (7)	175	233	1570
EcoN I	CCTNN`N,NNAGG	2732		2353	2427	6587
Bsp120 I	G`GGCC,C	2737	Asc I (1)	1696		
Apa I	G,GGCC`C	2741	Ase I (6)	122	906	3652
BstX I	CCAN,NNNN`NTGG	2748		3946	5181	3887
EcoRV	GAT ATC	2988	Asp718 (1)	1677		
Sac I	G,AGCT`C	3179	Ava I (9)	339	377	403
Sap I	GCTCTTC 8/11	4000		2843	2869	2907
Ear I	CTCTTC 7/10	4000		6640		5736
HgiE II	ACCNNNNNNGGT -1/134695		Ava II (7)	355	1123	2892
BspH I	T`CATG,A	4836		5369	5643	6284
Fsp I	TGC GCA	5231	Avr II (1)	835		
Psp1406 I	AA`CG,TT	5235	BamH I (1)	1689		
BstE II	G`GTNAC,C	6004	Ban I (4)	1238	1677	3860
PaeR7 I	C`TCGA,G	6640	Ban II (6)	347	1228	2173
Xho I	C`TCGA,G	6640		2907	3179	2741
Number of enzymes = 44			Bbs I (2)	1049	1873	
			Bbv I (18)	25	337	340
				1075	1180	1544
				2806	4535	4538
				5438	5676	5761
				5821	6193	5805
			Bbv II (2)	1048	1872	
			Bcl I (2)	886	6042	
			Bcn I (19)	341	342	405
				858	859	1458
				1989	2563	2712
				2846	2909	2910
				4497	5193	5540
			Bfa I (18)	17	28	318
				836	1073	1605
				1739	1786	2462
				3289	3300	4611
				5199	6525	4864
			Bgl I (3)	504	5129	6476
			Bgl II (1)	1741		
			Blp I (2)	1359	6153	
			Bpm I (5)	1463	1520	1977
						5079

The following enzymes do not cut in pMPB-GLuc:

Enzyme	Recognition Sequence	Count
Age I	Bbe I	BsmB I
Bsu36 I	Ehe I	Fse I
Nar I	Nde I	PflM I
		Bsp1286 I
		Kas I
		SnaB I
		Bst1107 I
		Mun I
		Tth111 I

pMPB-GLuc: sites sorted by name:

Enzyme	Count	1663	1754	2134	315	336	348	370
Aat II	(1)	1663						
Acc I	(2)	1754	2134					
Acc65 I	(1)	1677						
Aci I	(74)	315	336	348	370			
		393	683	695	704			
		716	726	737	783			
		1083	1165	1232	1416			

Bsa I	(2)	6096				Dde I	(8)	795	1359	2143	3191
BsaA I	(5)	2557	5070					4391	4800	4966	6153
		895	1393	3026	3084	Dpn I	(39)	429	883	888	1198
		6601						1259	1273	1475	1491
BsaB I	(2)	1262	1827					1691	1743	1824	1912
BsaH I	(3)	1461	1660	5898				2019	2130	2200	2310
BsaJ I	(47)	289	290	339	340			2331	2364	2821	3314
		403	476	502	547			4684	4759	4770	4778
		619	742	777	835			4856	4868	4973	5314
		856	962	1267	1374			5332	5378	5861	6044
		1721	1795	1840	1885			6224	6234	6309	6327
		1906	1925	2005	2066			6555	6576	6614	
		2151	2173	2312	2561	DpnII	(39)	427	881	886	1196
		2709	2770	2843	2906			1257	1271	1473	1489
		2907	2956	2957	3424			1689	1741	1822	1910
		3535	3855	4276	5529			2017	2128	2198	2308
		5552	5735	5766	6073			2329	2362	2819	3312
		6137	6276	6618				4682	4757	4768	4776
BsaW I	(8)	352	2894	3562	3574			4854	4866	4971	5312
		4322	4469	5300	6310			5330	5376	5859	6042
BseR I	(2)	831	1391					6222	6232	6307	6325
Bsg I	(5)	1151	1985	2198	2268			6553	6574	6612	
		3666				Dra I	(5)	1774	2358	2591	4875
BsiC I	(1)	1780						4894			
BsiE I	(9)	1083	1199	1655	2131	Dra III	(4)	1369	5553	5981	6601
		3121	4032	4456	5379	Drd I	(3)	1051	3195	4224	
		6225				Dsa I	(12)	502	742	962	1721
BsiHKA I	(5)	1966	2043	3179	4434			1795	1885	1906	1925
		6123						2173	5552	5766	6137
BsiW I	(1)	51				Eae I	(12)	505	965	1080	1371
Bsm I	(3)	1600	2457	3261				1652	1837	1882	1888
BsmA I	(3)	982	2556	5071				3493	3955	5397	5931
BsmF I	(15)	281	291	410	529	Eag I	(2)	1080	1652		
		601	665	1136	1472	Ear I	(1)	4000			
		2012	2579	2662	2836	Eco47 III	(1)	1737			
		2955	2965	6400		Eco57 I	(3)	1060	4663	5989	
BsoF I	(65)	14	326	329	336	Eco72 I	(2)	895	1393		
		387	454	783	1064	EcoN I	(1)	2732			
		1083	1157	1160	1163	EcoO109 I	(2)	1123	2737		
		1166	1169	1333	1419	EcoR I	(1)	1747			
		1533	1652	1655	1950	EcoR II	(23)	289	475	547	602
		1953	2000	2075	2114			619	1266	2004	2066
		2225	2277	2280	2696			2150	2311	2317	2640
		2795	2862	2913	2920			2698	2770	2956	3534
		2923	3185	3304	3406			3701	3854	4142	4263
		3437	3440	3555	3667			4276	5496	6073	
		3714	3941	4022	4040	EcoR V	(1)	2988			
		4043	4161	4316	4459	Esp I	(2)	1359	6153		
		4524	4527	4733	5061	Fnu4H I	(65)	14	326	329	336
		5400	5427	5522	5665			387	454	783	1064
		5750	5794	5810	5965			1083	1157	1160	1163
		6032	6182	6291	6371			1166	1169	1333	1419
		6468						1533	1652	1655	1950
Bsp120 I	(1)	2737						1953	2000	2075	2114
BspH I	(1)	4836						2225	2277	2280	2696
BspM I	(2)	2269	6191					2795	2862	2913	2920
BspM II	(2)	3562	3574					2923	3185	3304	3406
Bsr I	(22)	721	1097	1121	1682			3437	3440	3555	3667
		1690	2224	2614	2724			3714	3941	4022	4040
		3545	3917	4523	4536			4043	4161	4316	4459
		4650	5056	5174	5217			4524	4527	4733	5061
		5484	5579	5644	6382			5400	5427	5522	5665
		6478	6500					5750	5794	5810	5965
BsrB I	(4)	350	2900	3808	4049			6032	6182	6291	6371
BsrD I	(4)	5070	5244	6193	6486			6468			
BsrG I	(1)	1759				Fok I	(20)	307	359	686	1015
BssH II	(3)	1696	3755	6568				1250	1483	2049	2560
BssS I	(2)	1138	4289					2887	2939	3441	3590
BstB I	(1)	1780						3722	4975	5156	5443
BstE II	(1)	6004						5575	5728	5972	6473
BstN I	(23)	291	477	549	604	Fsp I	(1)	5231			
		621	1268	2006	2068	Gai II	(11)	506	1079	1081	1370
		2152	2313	2319	2642			1651	1653	1836	1881
		2700	2772	2958	3536			3956	5396	5930	
		3703	3856	4144	4265	Gsu I	(5)	1464	1519	1976	5080
		4278	5498	6075				6095			
BstU I	(25)	1195	1485	1657	1698	Hae I	(11)	498	834	967	1845
		1723	1767	1902	1927			1890	3495	3531	4131
		3117	3223	3394	3554			4142	4594	6563	
		3757	3963	3965	4163	Hae II	(10)	364	1739	2890	3353
		4744	5074	5758	6031			3672	3994	4364	5911
		6096	6159	6452	6568			6341	6490		
		6570				Hae III	(30)	498	507	776	782
BstX I	(1)	2748						834	967	1082	1373
BstY I	(11)	881	1489	1689	1741			1654	1839	1845	1884
		1910	2308	4757	4768			1890	2317	2340	2739
		4854	4866	6325				3495	3531	3957	4131
Cac8 I	(43)	333	384	391	467			4142	4160	4594	5052
		562	581	634	653			5132	5399	5933	5967
		1059	1173	1465	1667			6497	6563		
		1698	1892	1997	2043	Hga I	(10)	89	1042	1468	2079
		2239	2303	2783	2859			3090	3253	4226	4804
		2866	2917	3164	3261			5552	5888		
		3348	3502	3753	3757	HgiA I	(5)	1966	2043	3179	4434
		3909	3938	4047	4133			6123			
		4170	4730	5121	5754	HgiE II	(1)	4695			
		5931	6036	6216	6385	Hha I	(37)	363	1063	1485	1698
		6491	6495	6570				1700	1738	2889	3225
Cfr10 I	(9)	382	1463	2340	2864			3352	3595	3671	3757
		3615	3639	5089	6440			3759	3900	3965	3993
		6493						4026	4296	4363	4463
Cla I	(1)	1710						4637	4746	5139	5232
Csp6 I	(9)	52	1678	1684	1760			5631	5681	5758	5910
		5490	5723	5936	5944			6098	6159	6186	6340
		6427						6434	6454	6489	6570

HinC II	(5)	6572				Nae I	(4)	384	1465	2866	6495
		900	1705	1755	2135	Nci I	(19)	340	341	404	405
		2638						857	858	1457	1939
Hind II	(5)	900	1705	1755	2135			1988	2562	2711	2844
		2638						2845	2908	2909	3748
Hind III	(1)	1715						4496	5192	5539	
Hinf I	(20)	988	1320	1409	1446	Nco I	(4)	742	962	1795	2173
		1782	1801	2100	2147	Ngm I	(4)	382	1463	2864	6493
		2512	2724	3110	3218	Nhe I	(1)	1665			
		3479	3951	4016	4091	Nla III	(27)	71	88	583	655
		4487	5004	5875	6088			746	966	1498	1646
HinI I	(3)	1461	1660	5898				1799	2177	2503	3040
HinP I	(37)	361	1061	1483	1696			3100	3263	3412	3476
		1698	1736	2887	3223			3500	3730	3774	4120
		3350	3593	3669	3755			4840	5331	5341	5419
		3757	3898	3963	3991			5455	5698	6654	
		4024	4294	4361	4461	Nla IV	(20)	346	553	625	1124
		4635	4744	5137	5230			1240	1679	1691	2170
		5629	5679	5756	5908			2339	2739	2904	3862
		6096	6157	6184	6338			4148	4187	4959	5053
		6432	6452	6487	6568			5094	5305	5950	6315
		6570				Not I	(1)	1652			
Hpa I	(1)	1705				Nru I	(2)	1195	1902		
Hpa II	(38)	340	353	358	383	Nsi I	(3)	585	657	3261	
		404	857	1456	1464	Nsp7524 I	(5)	84	579	651	3259
		1693	1939	1988	2341			4116			
		2561	2711	2844	2865	NspB II	(10)	1171	1723	1927	1955
		2890	2895	2908	3563			3661	3940	4458	4703
		3575	3616	3626	3640			5667	6290		
		3748	3834	4323	4470	NspH I	(5)	88	583	655	3263
		4496	4686	5090	5124			4120			
		5191	5301	5538	6311	PaeR7 I	(1)	6640			
		6441	6494			Pal I	(30)	498	507	776	782
Hph I	(11)	959	2357	3524	4853			834	967	1082	1373
		5080	5494	5552	5868			1654	1839	1845	1884
		6015	6101	6608				1890	2317	2340	2739
Kpn I	(1)	1681						3495	3531	3957	4131
Mae I	(18)	17	28	318	513			4142	4160	4594	5052
		836	1073	1605	1666			5132	5399	5933	5967
		1739	1786	2462	2930	Ple I	(3)	1809	2108	4495	
		3289	3300	4611	4864	Pme I	(1)	1774			
		5199	6525			Pml I	(2)	895	1393		
Mae II	(19)	50	54	304	894	PpuM I	(1)	1123			
		1392	1660	2245	2944	Psp1406 I	(1)	5235			
		3025	3083	3448	3465	PspA I	(5)	339	403	856	2843
		3682	4819	5235	5924			2907			
		6410	6600	6669		Pst I	(3)	6	471	2783	
Mae III	(24)	46	248	1544	2346	Pvu I	(4)	1199	2131	5379	6225
		2401	3079	3139	3742	Pvu II	(2)	1171	3940		
		4472	4535	4651	4934	Rsa I	(9)	53	1679	1685	1761
		5265	5323	5476	5541			5491	5724	5937	5945
		5672	5759	5803	5998			6428			
		6004	6106	6436	6674	Rsr II	(2)	355	2892		
Mbo I	(39)	427	881	886	1196	Sac I	(1)	3179			
		1257	1271	1473	1489	Sac II	(2)	1724	1928		
		1689	1741	1822	1910	Sal I	(2)	1753	2133		
		2017	2128	2198	2308	Sap I	(1)	4000			
		2329	2362	2819	3312	Sau3A I	(39)	427	881	886	1196
		4682	4757	4768	4776			1257	1271	1473	1489
		4854	4866	4971	5312			1689	1741	1822	1910
		5330	5376	5859	6042			2017	2128	2198	2308
		6222	6232	6307	6325			2329	2362	2819	3312
		6553	6574	6612				4682	4757	4768	4776
Mbo II	(15)	231	996	1053	1081			4854	4866	4971	5312
		1499	1877	2065	3383			5330	5376	5859	6042
		3988	4777	4850	6200			6222	6232	6307	6325
		6559	6562	6595				6553	6574	6612	
Mlu I	(1)	1765				Sau96 I	(14)	355	1123	2315	2338
Mme I	(3)	4330	4514	6562				2737	2738	2892	5051
Mnl I	(47)	103	258	318	446			5130	5147	5369	5643
		508	766	772	795			6284	6496		
		801	809	812	824	Sca I	(1)	1685			
		944	1005	1346	1347	ScrF I	(42)	291	340	341	404
		1369	1486	1835	1952			405	477	549	604
		2117	2237	2671	2804			621	857	858	1268
		2932	3176	3362	3389			1457	1939	1988	2006
		3419	3683	3965	4014			2068	2152	2313	2319
		4224	4297	4548	4948			2562	2642	2700	2711
		5029	5175	5381	5520			2772	2844	2845	2908
		5744	5841	5881	6289			2909	2958	3536	3703
Msc I	(3)	967	1890	3495				3748	3856	4144	4265
Mse I	(31)	22	57	122	138			4278	4496	5192	5498
		212	906	1672	1704			5539	6075		
		1727	1731	1773	2357	Sec I	(47)	289	290	339	340
		2583	2590	3067	3074			403	476	502	547
		3295	3508	3652	3887			619	742	777	835
		3946	4822	4874	4879			856	962	1267	1374
		4893	4946	5181	5220			1721	1795	1840	1885
		5837	6353	6666				1906	1925	2005	2066
Msl I	(5)	1833	2746	5261	5420			2151	2173	2312	2561
		6116						2709	2770	2843	2906
Msp I	(38)	340	353	358	383			2907	2956	2957	3424
		404	857	1456	1464			3535	3855	4276	5529
		1693	1939	1988	2341			5552	5735	5766	6073
		2561	2711	2844	2865			6137	6276	6618	
		2890	2895	2908	3563	SfaN I	(20)	380	591	663	1036
		3575	3616	3626	3640			1093	1225	1271	1571
		3748	3834	4323	4470			1836	1908	2428	2866
		4496	4686	5090	5124			3314	3369	3603	3701
		5191	5301	5538	6311			4212	5264	5457	5749
		6441	6494			Sfc I	(8)	2	467	1047	2779
MspA1 I	(10)	1171	1723	1927	1955			4381	4572	5250	6099
		3661	3940	4458	4703	Sfi I	(1)	504			
		5667	6290			Sma I	(5)	341	405	858	2845

Spe I	(1)	2909				BssS I	C`TCGT,G	2	Bst1107 I	GTA TAC	-
Sph I	(3)	512	655	3263		BstB I	TT`CG,AA	1	BstE II	G`GTNAC,C	1
Spl I	(1)	51				BstN I	CC`W,GG	23	BstU I	CG CG	25
Srf I	(2)	405	2845			BstX I	CCAN,NNNN`NTGG	1	BstY I	R`GATC,Y	11
Ssp I	(2)	2587	3247			Bsu36 I	CC`TNA,GG	-	Cac8 I	GCN NGC	43
Stu I	(2)	498	834			Cfr10 I	R`CCGG,Y	9	Clal I	AT`CG,AT	1
Sty I	(8)	742	835	962	1795	Csp6 I	G`TA,C	9	Dde I	C`TNA,G	8
		2173	5529	6276	6618	Dpn I	GA TC	39	DpnII	`GATC,	39
Taq I	(18)	108	1256	1407	1710	Dra I	TTT AAA	5	Dra III	CAC,NNN`GTG	4
		1754	1780	1915	2134	Drd I	GACNN,NN`NNGTC	3	Dsa I	C`CRYG,G	12
		2197	4216	5513	5773	Eae I	Y`GGCC,R	12	Eag I	C`GGCC,G	2
		5873	5904	5916	6210	Ear I	CTCTTC`7/10	1	Eco47 III	AGC GCT	1
		6225	6641			Eco57 I	CTGAAG`21/19	3	Eco72 I	CAC GTG	2
Tfi I	(12)	988	1320	1409	1446	EcoN I	CCTNN`N,NNAGG	1	EcoO109 I	RG`GNC,CY	2
		1782	2147	2724	3218	EcoR I	G`AATT,C	1	EcoR II	`CCWGG,	23
		3479	3951	4091	6088	EcoR V	GAT ATC	1	Ehe I	GGC GCC	-
Tsp45 I	(9)	46	2346	3079	3139	Esp I	GC`TNA,GC	2	Fnu4H I	GC`N,GC	65
		5265	5476	5541	6004	Fok I	GGATG`14/18	20	Fse I	GG,CCGG`CC	-
		6106				Fsp I	TGC GCA	1	Gdi II	`YGGC,CG	11
Tth111 II	(8)	198	1804	3174	4705	Gsu I	CTGGAG`21/19	5	Hae I	WGG CCW	11
		4714	4744	5761	5768	Hae II	R,GCGC`Y	10	Hae III	GG CC	30
Vsp I	(6)	122	906	3652	3887	Hga I	GACGC`9/14	10	HgaI A	G,WGCW`C	5
		3946	5181			HgiE II	ACCNNNNNNGGT`-1/131	1	Hha I	G,CG`C	37
Xba I	(1)	1785				Hinc II	GTY RAC	5	Hind II	GTY RAC	5
Xho I	(1)	6640				Hind III	A`AGCT,T	1	Hinf I	G`ANT,C	20
Xho II	(11)	881	1489	1689	1741	HinI I	GR`CG,YC	3	HinP I	G`CG,C	37
		1910	2308	4757	4768	Hpa I	GTT AAC	1	Hpa II	C`CG,G	38
		4854	4866	6325		Hph I	GGTGA`12/11	11	Kas I	G`GCGC,C	-
Xma I	(5)	339	403	856	2843	Kpn I	G,GTAC`C	1	Mae I	C`TA,G	18
		2907				Mae II	A`CG,T	19	Mae III	`GTNAC,	24
Xma III	(2)	1080	1652			Mbo I	`GATC,	39	Mbo II	GAAGA`12/11	15
Xmn I	(1)	2058				Mlu I	A`CGCG,T	1	Mme I	TCCRAC`25/23	3
						Mnl I	CCTC`10/10	47	Msc I	TGG CCA	3
						Mse I	T`TA,A	31	Msl I	CAYNN NNRTG	5
						Msp I	C`CG,G	38	MspAl I	CMG CKG	10
						Mun I	C`AATT,G	-	Nae I	GCC GGC	4
						Nar I	GG`CG,CC	-	Nci I	CC`s,GG	19
						Nco I	C`CATG,G	4	Nde I	CA`TA,TG	-
						NgoM I	G`CCGG,C	4	Nhe I	GC`TAG,C	1
						Nla III	,CATG`	27	Nla IV	GGN NCC	20
						Not I	GC`GGCC,GC	1	Nru I	TGC CGA	2
						Nsi I	A,TGCA`T	3	Nsp7524 I	R`CATG,Y	5
						NspB II	CMG CKG	10	NspH I	R,CATG`Y	5
						Paer7 I	C`TCGA,G	1	Pal I	GG CC	30
						Pf1M I	CCAN,NNN`NTGG	-	Ple I	GAGTC`9/10	3
						Pme I	CTTT AAAC	1	Pml I	CAC GTG	2
						PpuM I	RG`GWC,CY	1	Psp1406 I	AA`CG,TT	1
						PspA I	C`CCGG,G	5	Pst I	C,TGCA`G	3
						Pvu I	CG,AT`CG	4	Pvu II	CAG CTG	2
						Rsa I	GT AC	9	Rsr II	CG`GWC,CG	2
						Sac I	G,AGCT`C	1	Sac II	CC,GC`GG	2
						Sal I	G`TCGA,C	2	Sap I	GCTCTC`8/11	1
						Sau3A I	`GATC,	39	Sau96 I	G`GNC,C	14
						Sea I	AGT ACT	1	ScrF I	CC`N,GG	42
						Sec I	C`CNNG,G	47	SfaN I	GATC`9/13	20
						Sfc I	C`TRYA,G	8	Sfi I	GGCCN,NNN`NGGCC	1
						Sma I	CCC GGG	5	SnaB I	TAC GTA	-
						Spe I	A`CTAG,T	1	Sph I	G,CATG`C	3
						Spl I	C`GTAC,G	1	Srf I	GCCC GGGC	2
						Ssp I	AAT ATT	2	Stu I	AGG CCT	2
						Sty I	C`CWWG,G	8	Taq I	T`CG,A	18
						Tfi I	G`AWT,C	12	Tsp45 I	`GTSAC,	9
						Tth111 I	GACN`N,NGTC	-	Tth111 II	CAARCA`16/14	8
						Vsp I	AT`TA,AT	6	Xba I	T`CTAG,A	1
						Xca I	GTA TAC	-	Xcm I	CCANNN,N`NNNNTGG-	-
						Xho I	C`TCGA,G	1	Xho II	R`GATC,Y	11
						Xma I	C`CCGG,G	5	Xma III	C`GGCC,G	2

Site usage in pMPB-GLuc:

Aat II	G,ACGT`C	1	Acc I	GT`MK,AC	2
Acc65 I	G`GTAC,C	1	Aci I	C`CG,C	74
Afl II	C`TTAA,G	1	Afl III	A`CRYG,T	4
Age I	A`CCGG,T	-	Aha II	GR`CG,YC	3
Ahd I	GACNN,N`NNGTC	2	Alu I	AG CT	29
Alw I	GGATC`8/9	19	AlwN I	CAG,NNN`CTG	2
Apa I	G,GGCC`C	1	ApaL I	G`TGCA,C	3
Apo I	R`AATT,Y	7	Asc I	GG`CGCG,CC	1
Ase I	AT`TA,AT	6	Asp718	G`GTAC,C	1
Ava I	C`YCGR,G	9	Ava II	G`GWC,C	7
Avr II	C`CTAG,G	1	BamH I	G`GATC,C	1
Ban I	G`GYRC,C	4	Ban II	G,RGCY`C	6
Bbe I	G,CGGC`C	-	Bbs I	GAAGAC`8/12	2
Bbv I	GCAGC`13/17	18	Bbv II	GAAGAC`7/11	2
Bcl I	T`GATC,A	2	Bcn I	CC,S`GG	19
Bfa I	C`TA,G	18	Bgl I	GCCN,NNN`NGGC	3
Bgl II	A`GATC,T	1	Blp I	GC`TNA,GC	2
Bpm I	CTGGAG`22/20	5	Bsa I	GGTCTC`7/11	2
BsaA I	YAC GTR	5	BsaB I	GATNN NNATC	2
BsaH I	GR`CG,YC	3	BsaJ I	C`CNNG,G	47
BsaW I	W`CCGG,W	8	BseR I	GAGGAG`16/14	2
Bsg I	GTGCAG`22/20	5	BsiC I	TT`CG,AA	1
BsiE I	CG,RY`CG	9	BsiHKA I	G,WGCW`C	5
BsiW I	C`GTAC,G	1	Bsm I	GAATG,C`7	3
BsmA I	GTCTC`/9	3	BsmB I	CGTCTC`7/11	-
BsmF I	GGGAC`15/19	15	BsoF I	GC`N,GC	65
Bspl20 I	G`GGCC,C	1	Bsp1286 I	G,DGCH`C	-
BspH I	T`CATG,A	1	BspM I	ACCTGC`10/14	2
BspM II	T`CCGG,A	2	Bsr I	ACT,GG`	22
BsrB I	GAG CGG	4	BsrD I	GCAATG,`8	4
BsrG I	T`GTAC,A	1	BssH II	G`CGCG,C	3