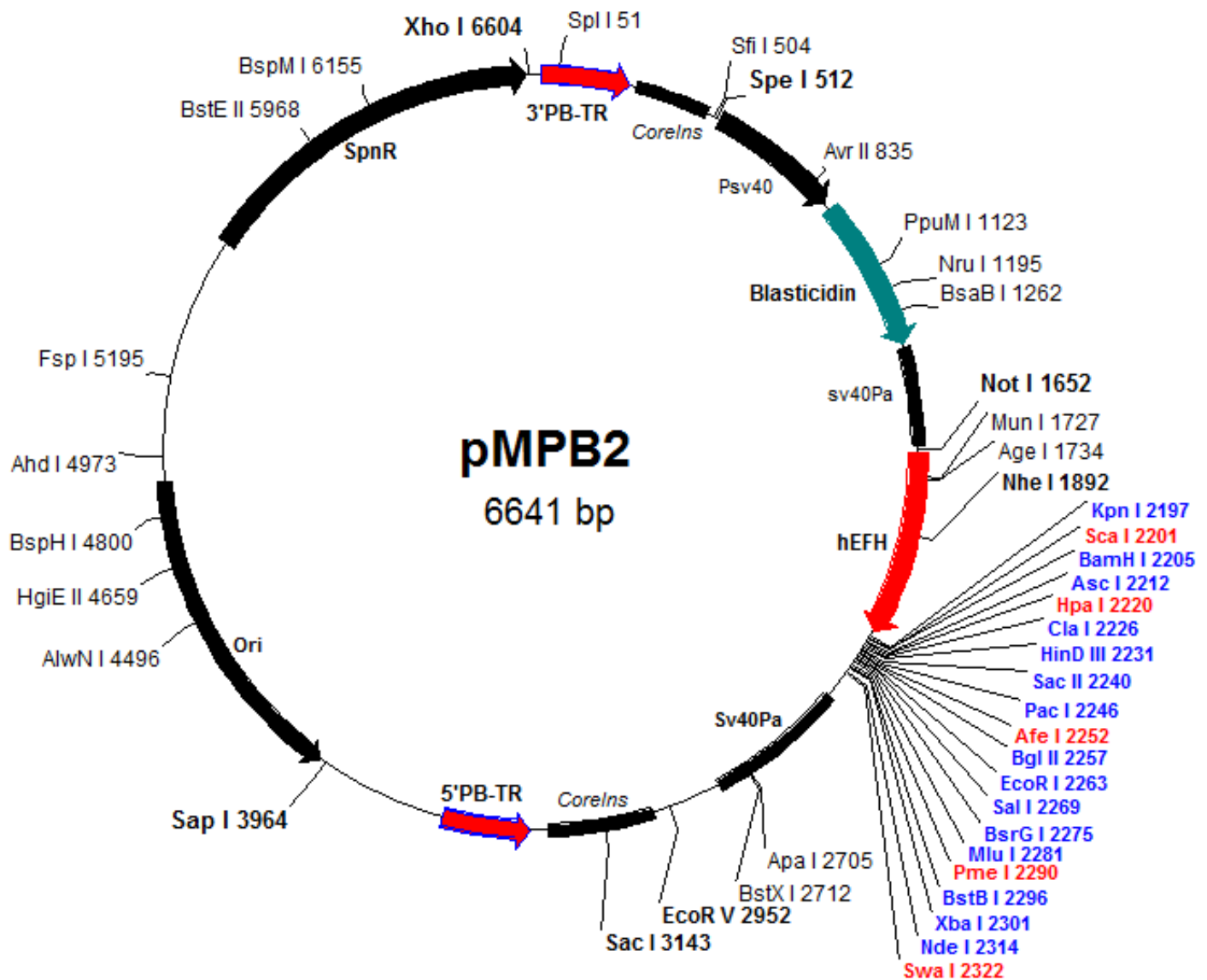


Vector: pMPB2 (MOLab PiggyBac-2 vector)

Antibiotic Selection: Spectinomycin or Blasticidin-resistant

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

Date of Construction: October, 2011



pMPB2 Vector Sequence

(Spectinomycin or Blastisin-resistant)

CTGCAGAACACGCAGCTAGATTAACTCTAGAAAAGATAATCATATTGTGACGTACGTTAAAGATAAATCATGCGTAAAAATTGACGCATG
TGTTTTATCGGTCTGTATATCGAGGTTTATTTATTAATTTGAATAGATATTAAGTTTTATTATATTTACTTTACATACTAATAATA
AATTCAACAAACAATTTATTTATGTTTTATTTATTTATTTAAAAAACAACAACTCAAAATTTCTTCTATAAAGTAACAAAACTTTT
ATGAGGGACAGCCCCCCCCAAAGCCCCCAGGGATGTAATTACGTCCCTCCCCCGCTAGGGGGCAGCAGCGAGCCCGCCGGGGCTCC
GCTCCGGTCCGGCGCTCCCCCGCATCCCCGAGCCGGCAGCGTGCGGGGACAGCCCCGGGCACGGGGAAGGTGGCACGGGATCGCTTT
CCTCTGAACGCTTCTCGCTGCTCTTTGAGCCTGCAGACACCTGGGGGGATACGGGGAAAAGGCCTCCACGGCCAGACTAGTAAATGTG
TGTCAAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCATAGTCCCGCCCTAACTCCG
CCCATCCCGCCCTAACTCCGCCCAGTTCCGCCCATTCTCCGCCCCATGGCTGACTAATTTTTTTTTTATTTATGAGAGGCCGAGGCC
GCCTCTGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTTTGCAAAAGCTCCCGGGAGCTTGTATA
TCCATTTTCGGATCTGATCAGCACGTGTTGACAATTAATCATCGGCATAGTATATCGGCATAGTATAATACGACAAGGTGAGGAACT
AAACCATGGCCAAGCCTTTGTCTCAAGAAGAATCCACCCTCATTGAAAGAGCAACGGCTACAATCAACAGCATCCCATCTCTGAAG
ACTACAGCGTCGCCAGCGCAGCTCTCTCTAGCGACGGCCGATCTTCACTGGTGTCAATGTATATCATTTTTACTGGGGACCTTGTG
CAGAACTCGTGGTGTGGCACTGCTGCTGCTGCGGCAGCTGGCAACCTGACTTGTATCGTTCGCGATCGGAAATGAGAACAGGGGCA
TCTTGAGCCCTGCGGACGGTGCCGACAGGTGCTTCTCGATCTGCATCTGGGATCAAAGCCATAGTGAAGGACAGTGTGACAGC
CGACGGCAGTTGGGATTCGTGAATTGCTGCCCTCTGGTTATGTGTGGGAGGGCTAAGCACTTCGTGGCCGAGGAGCAGGACTGACAC
GTGCTACGAGATTTGATTCCACCGCCGCTTCTATGAAAGGTTGGGCTTCGGAATCGTTTTCCGGGACCCGGCTGGATGATCCTC
CAGCGCGGGATCTCATGCTGGAGTTCTTCGCCACCCCAACTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATC
ACAAATTTACAAATAAAGCATTTTTTTCACTGCATTTCTAGTTGTGGTTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGCGCG
CCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGGAGGGGTTCGGCAATTGAACCGGTGC
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GATGAGCGAAATGTAGTGCTTACGTTGTCCCGCATTTGGTACAGCGCAGTAACCGGCAAAATCGCGCCGAAGGATGTGCTGCGGAC
TGGGCAATGGAGCGCCTGCCGGCCAGTATCAGCCCGTCATACTTGAAGCTAGACAGGCTTATCTTGGACAAGAAGAAGATCGCTTG
GCCTCGCGCGCAGATCAGTTGGAAGAATTTGTCCACTACGTGAAAGGCGAGATCACCAAGGTAGTCGGCAAAATAACCCTCGAGCCAC
CCAATGACCAAAAATCCCTTAACGTGAGTTA

Unique enzymes in pMPB2:

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
Not I	GC`GGCC,GC	1652
Mun I	C`AATT,G	1727
Age I	A`CCAG,T	1734
Nhe I	G`CTAG,C	1892
Bsu36 I	CC`TNA,GG	1941
Kas I	G`GCGC,C	2184
Nar I	GG`CG,CC	2185
Ehe I	GGC GCC	2186
Bbe I	G,GCGC`C	2188
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
Hpa I	GTT AAC	2221
Cla I	AT`CG,AT	2226
HinD III	A`AGCT,T	2231
Sac II	CC,GC`GG	2240
Pac I		2246
Afe I		2252
Eco47 III	AGC GCT	2253
Bgl II	A`GATC,T	2257
EcoR I	G`AATT,C	2263
Sal I	G`TCGA,C	2269
Acc I	GT`MK,AC	2270
BsrG I	T`GTAC,A	2275
Mlu I	A`CGCG,T	2281
Pme I	C`TTT AAAC	2290
BsiC I	TT`CG,AA	2296
BstB I	TT`CG,AA	2296
Xba I	T`CTAG,A	2301
SnaB I	TAC GTA	2309
Nde I	CA`TA,TG	2314
Swa I		2321
Bsp120 I	G`GGCC,C	2701
Apa I	G,GGCC`C	2705
BstX I	CCAN,NNNN`NTGG	2712
EcoR V	GAT ATC	2952
Sac I	G,AGCT`C	3143
Sap I	GCTCTTC 8/11	3964

Ear I	CTCTTC 7/10	3964
AlwN I	CAG,NNN`CTG	4496
HgiE II	ACCNNNNNNGGT -1/134659	
BspH I	T`CATG,A	4800
Ahd I	GACNN,N`NNGTC	4973
Fsp I	TGC GCA	5195
BstE II	G`GTNAC,C	5968
BspM I	ACCTGC 10/14	6155
Paer7 I	C`TCGA,G	6604
Xho I	C`TCGA,G	6604
Number of enzymes = 58		

The following enzymes do not cut in pMPB2:

Aat II	Afl II	BsmB I	Bsp1286 I	Bst1107 I
Fse I	Pf1M I	Tth111 I	Xca I	Xcm I

pMPB2: sites sorted by name:

Acc I	(1)	2270			
Acc65 I	(1)	2193			
Aci I	(77)	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	2237	2239	2819
		2842	2864	2876	2897
		3081	3114	3148	3356
		3369	3518	3625	3630
		3678	3715	3770	3873
		3929	3939	3963	4006
		4013	4034	4125	4153
		4280	4299	4420	4530
		4665	4674	5036	5127
		5318	5364	5631	5651
		5819	5916	5928	5995
		6058	6254	6257	6335
		6382			
Afl III	(4)	894	1390	2281	4080
Age I	(1)	1734			
Aha II	(3)	1461	2185	5862	
Ahd I	(1)	4973			
Alu I	(32)	16	799	853	863
		1066	1171	1535	1886
		1892	1896	2034	2175
		2233	2507	3141	3267
		3310	3745	3840	3904
		4022	4248	4338	4384
		4641	5162	5262	5325

		5572	6002	6116	6488		1683	2543	2626	2800
Alw I	(18)	434	888	1278	1469		2919	2929	6364	
		1496	2163	2201	2212	BsoF I	(61)	14	326	336
		2779	3283	4642	4728		387	454	783	1064
		4728	4825	4826	5290		1083	1157	1160	1163
		6267	6296				1166	1169	1333	1419
AlwN I	(1)	4496					1533	1652	1655	1873
Apa I	(1)	2705					1932	1947	1978	2660
ApaL I	(2)	4394	6083				2759	2826	2877	2884
Apo I	(6)	175	233	1570	2263		2887	3149	3268	3370
		2391	6551				3401	3404	3519	3631
Asc I	(1)	2212					3678	3905	3986	4004
Ase I	(6)	122	906	3616	3851		4007	4125	4280	4423
		3910	5145				4488	4491	4697	5025
Asp718	(1)	2193					5364	5391	5486	5629
Ava I	(11)	339	377	403	856		5714	5758	5774	5929
		1701	1803	2807	2833		5996	6146	6255	6335
		2871	5700	6604			6432			
Ava II	(7)	355	1123	2856	5111	Bsp120 I	(1)	2701		
		5333	5607	6248		BspH I	(1)	4800		
Avr II	(1)	835				BspM I	(1)	6155		
BamH I	(1)	2205				BspM II	(2)	3526	3538	
Ban I	(8)	1238	1662	1737	1993	Bsr I	(23)	721	1097	1121
		2184	2193	3824	4921		1790	2198	2206	2578
Ban II	(6)	347	1228	1908	2705		2688	3509	3881	4487
		2871	3143				4500	4614	5020	5138
Bbe I	(1)	2188					5181	5448	5543	5608
Bbs I	(1)	1049					6346	6442	6464	
Bbv I	(18)	25	337	340	398	BsrB I	(5)	350	1657	2864
		1075	1180	1544	2671		4013			
		2770	4499	4502	4708	BsrD I	(4)	5034	5208	6157
		5402	5640	5725	5769	BsrG I	(1)	2275		
		5785	6157			BssH II	(3)	2212	3719	6532
Bbv II	(1)	1048				Bsss I	(2)	1138	4253	
Bcl I	(2)	886	6006			BstB I	(1)	2296		
Bcn I	(18)	341	342	405	406	BstE II	(1)	5968		
		858	859	1458	2049	BstN I	(18)	291	477	549
		2527	2676	2809	2810		621	1268	2606	2664
		2873	2874	3713	4461		2736	2922	3500	3667
		5157	5504				3820	4108	4229	4242
Bfa I	(21)	17	28	318	513		5462	6039		
		836	1073	1605	1742	BstU I	(25)	1195	1485	1756
		1893	2019	2081	2255		1970	2214	2239	2283
		2302	2426	2894	3253		3081	3187	3358	3518
		3264	4575	4828	5163		3721	3927	3929	4127
		6489					4708	5038	5722	5995
Bgl I	(3)	504	5093	6440			6060	6123	6416	6532
Bgl II	(1)	2257					6534			
Blp I	(2)	1359	6117			BstX I	(1)	2712		
Bpm I	(4)	1463	1520	5043	6060	BstY I	(10)	881	1489	2167
Bsa I	(3)	2037	2521	5034			2257	4721	4732	4818
BsaA I	(6)	895	1393	2309	2990		4830	6289		
		3048	6565			Bsu36 I	(1)	1941		
BsaB I	(1)	1262				Cac8 I	(42)	333	384	391
BsaH I	(3)	1461	2185	5862			562	581	634	653
BsaJ I	(39)	289	290	339	340		1059	1173	1465	1894
		403	476	502	547		1908	1929	2092	2120
		619	742	777	835		2214	2747	2823	2830
		856	962	1267	1374		2881	3128	3225	3312
		1804	2068	2237	2525		3466	3717	3721	3873
		2673	2734	2807	2870		3902	4011	4097	4134
		2871	2920	2921	3388		4694	5085	5718	5895
		3499	3819	4240	5493		6000	6180	6349	6455
		5516	5699	5730	6037		6459	6534		
		6101	6240	6582		Cfr10 I	(12)	382	1463	1734
BsaW I	(10)	352	1659	1734	2858		2090	2181	2828	3579
		3526	3538	4286	4433		3603	5053	6404	6457
		5264	6274			Cla I	(1)	2226		
BseR I	(2)	831	1391			Csp6 I	(11)	52	1784	2194
Bsg I	(3)	1151	1852	3630			2276	2310	5454	5687
BsiC I	(1)	2296					5900	5908	6391	
BsiE I	(8)	1083	1199	1655	3085	Dde I	(10)	795	1359	1941
		3996	4420	5343	6189		2086	3155	4355	4764
BsiHKA I	(3)	3143	4398	6087			4930	6117		
BsiW I	(1)	51				Dpn I	(33)	429	883	888
Bsm I	(3)	1600	2421	3225			1259	1273	1475	1491
BsmA I	(4)	982	2038	2520	5035		2169	2207	2259	2328
BsmF I	(15)	281	291	410	529		2785	3278	4648	4723
		601	665	1136	1472		4734	4742	4820	4832

		4937	5278	5296	5342			5516	5852		
		5825	6008	6188	6198	HgiA I	(3)	3143	4398	6087	
		6273	6291	6519	6540	HgiE II	(1)	4659			
		6578				Hha I	(43)	363	1063	1485	1684
DpnII	(33)	427	881	886	1196			1756	1927	2064	2159
		1257	1271	1473	1489			2187	2214	2216	2254
		2167	2205	2257	2326			2853	3189	3316	3559
		2783	3276	4646	4721			3635	3721	3723	3864
		4732	4740	4818	4830			3929	3957	3990	4260
		4935	5276	5294	5340			4327	4427	4601	4710
		5823	6006	6186	6196			5103	5196	5595	5645
		6271	6289	6517	6538			5722	5874	6062	6123
		6576						6150	6304	6398	6418
Dra I	(6)	2030	2290	2322	2555			6453	6534	6536	
		4839	4858			HinC II	(4)	900	2221	2271	2602
Dra III	(4)	1369	5517	5945	6565	Hind II	(4)	900	2221	2271	2602
Drd I	(3)	1051	3159	4188		HinD III	(1)	2231			
Dsa I	(7)	502	742	962	2237	Hinf I	(19)	988	1320	1409	1446
		5516	5730	6101				1965	2084	2298	2476
Eae I	(9)	505	965	1080	1371			2688	3074	3182	3443
		1652	3457	3919	5361			3915	3980	4055	4451
		5895						4968	5839	6052	
Eag I	(2)	1080	1652			HinI I	(3)	1461	2185	5862	
Ear I	(1)	3964				HinP I	(43)	361	1061	1483	1682
Eco47 III	(1)	2253						1754	1925	2062	2157
Eco57 I	(4)	1060	1907	4627	5953			2185	2212	2214	2252
Eco72 I	(2)	895	1393					2851	3187	3314	3557
EcoN I	(3)	1745	1940	2696				3633	3719	3721	3862
EcoO109 I	(2)	1123	2701					3927	3955	3988	4258
EcoR I	(1)	2263						4325	4425	4599	4708
EcoR II	(18)	289	475	547	602			5101	5194	5593	5643
		619	1266	2604	2662			5720	5872	6060	6121
		2734	2920	3498	3665			6148	6302	6396	6416
		3818	4106	4227	4240			6451	6532	6534	
		5460	6037			Hpa I	(1)	2221			
EcoR V	(1)	2952				Hpa II	(42)	340	353	358	383
Ehe I	(1)	2186						404	857	1456	1464
Esp I	(2)	1359	6117					1660	1735	1959	2047
Fnu4H I	(61)	14	326	329	336			2059	2091	2182	2209
		387	454	783	1064			2525	2675	2808	2829
		1083	1157	1160	1163			2854	2859	2872	3527
		1166	1169	1333	1419			3539	3580	3590	3604
		1533	1652	1655	1873			3712	3798	4287	4434
		1932	1947	1978	2660			4460	4650	5054	5088
		2759	2826	2877	2884			5155	5265	5502	6275
		2887	3149	3268	3370			6405	6458		
		3401	3404	3519	3631	Hph I	(10)	959	3488	4817	5044
		3678	3905	3986	4004			5458	5516	5832	5979
		4007	4125	4280	4423			6065	6572		
		4488	4491	4697	5025	Kas I	(1)	2184			
		5364	5391	5486	5629	Kpn I	(1)	2197			
		5714	5758	5774	5929	Mae I	(21)	17	28	318	513
		5996	6146	6255	6335			836	1073	1605	1742
		6432						1893	2019	2081	2255
Fok I	(20)	307	359	686	1015			2302	2426	2894	3253
		1250	1483	1937	2524			3264	4575	4828	5163
		2851	2903	3405	3554			6489			
		3686	4939	5120	5407	Mae II	(20)	50	54	304	894
		5539	5692	5936	6437			1392	1849	2132	2308
Fsp I	(1)	5195						2908	2989	3047	3412
Gdi II	(9)	506	1079	1081	1370			3429	3646	4783	5199
		1651	1653	3920	5360			5888	6374	6564	6633
		5894				Mae III	(25)	46	248	1544	2161
Gsu I	(4)	1464	1519	5044	6059			2177	2365	3043	3103
Hae I	(9)	498	834	967	3459			3706	4436	4499	4615
		3495	4095	4106	4558			4898	5229	5287	5440
		6527						5505	5636	5723	5767
Hae II	(12)	364	2065	2188	2255			5962	5968	6070	6400
		2854	3317	3636	3958			6638			
		4328	5875	6305	6454	Mbo I	(33)	427	881	886	1196
Hae III	(26)	498	507	776	782			1257	1271	1473	1489
		834	967	1082	1373			2167	2205	2257	2326
		1654	1946	2051	2703			2783	3276	4646	4721
		3459	3495	3921	4095			4732	4740	4818	4830
		4106	4124	4558	5016			4935	5276	5294	5340
		5096	5363	5897	5931			5823	6006	6186	6196
		6461	6527					6271	6289	6517	6538
Hga I	(10)	89	1042	1468	1998			6576			
		3054	3217	4190	4768	Mbo II	(13)	231	996	1053	1081

		1499	3347	3952	4741	PaeR7 I	(1)	6604				
		4814	6164	6523	6526	Pal I	(26)	498	507	776	782	
		6559						834	967	1082	1373	
Mlu I	(1)	2281						1654	1946	2051	2703	
Mme I	(3)	4294	4478	6526				3459	3495	3921	4095	
Mnl I	(49)	103	258	318	446			4106	4124	4558	5016	
		508	766	772	795			5096	5363	5897	5931	
		801	809	812	824			6461	6527			
		944	1005	1346	1347	Ple I	(2)	1973	4459			
		1369	1486	1710	1799	Pme I	(1)	2290				
		1894	1936	1990	2006	Pml I	(2)	895	1393			
		2635	2768	2896	3140	PpuM I	(1)	1123				
		3326	3353	3383	3647	Psp1406 I	(2)	1849	5199			
		3929	3978	4188	4261	PspA I	(5)	339	403	856	2807	
		4512	4912	4993	5139			2871				
		5345	5484	5708	5805	Pst I	(3)	6	471	2747		
		5845	6253	6292	6537	Pvu I	(3)	1199	5343	6189		
		6612				Pvu II	(3)	1171	1886	3904		
Msc I	(2)	967	3459			Rsa I	(11)	53	1785	2195	2201	
Mse I	(31)	22	57	122	138			2277	2311	5455	5688	
		212	906	2029	2220			5901	5909	6392		
		2243	2247	2289	2321	Rsr II	(2)	355	2856			
		2547	2554	3031	3038	Sac I	(1)	3143				
		3259	3472	3616	3851	Sac II	(1)	2240				
		3910	4786	4838	4843	Sal I	(1)	2269				
		4857	4910	5145	5184	Sap I	(1)	3964				
		5801	6317	6630		Sau3A I	(33)	427	881	886	1196	
Msl I	(4)	2710	5225	5384	6080			1257	1271	1473	1489	
Msp I	(42)	340	353	358	383			2167	2205	2257	2326	
		404	857	1456	1464			2783	3276	4646	4721	
		1660	1735	1959	2047			4732	4740	4818	4830	
		2059	2091	2182	2209			4935	5276	5294	5340	
		2525	2675	2808	2829			5823	6006	6186	6196	
		2854	2859	2872	3527			6271	6289	6517	6538	
		3539	3580	3590	3604			6576				
		3712	3798	4287	4434	Sau96 I	(13)	355	1123	2049	2701	
		4460	4650	5054	5088			2702	2856	5015	5094	
		5155	5265	5502	6275			5111	5333	5607	6248	
		6405	6458					6460				
MspAl I	(9)	1171	1886	2239	3625	Sca I	(1)	2201				
		3904	4422	4667	5631	ScrF I	(36)	291	340	341	404	
		6254						405	477	549	604	
Mun I	(1)	1727						621	857	858	1268	
Nae I	(5)	384	1465	2092	2830			1457	2048	2526	2606	
		6459						2664	2675	2736	2808	
Nar I	(1)	2185						2809	2872	2873	2922	
Nci I	(18)	340	341	404	405			3500	3667	3712	3820	
		857	858	1457	2048			4108	4229	4242	4460	
		2526	2675	2808	2809			5156	5462	5503	6039	
		2872	2873	3712	4460	Sec I	(39)	289	290	339	340	
		5156	5503					403	476	502	547	
Nco I	(2)	742	962					619	742	777	835	
Nde I	(1)	2314						856	962	1267	1374	
NgOM I	(5)	382	1463	2090	2828			1804	2068	2237	2525	
		6457						2673	2734	2807	2870	
Nhe I	(1)	1892						2871	2920	2921	3388	
Nla III	(25)	71	88	583	655			3499	3819	4240	5493	
		746	966	1498	1646			5516	5699	5730	6037	
		2467	3004	3064	3227			6101	6240	6582		
		3376	3440	3464	3694	SfaN I	(19)	380	591	663	1036	
		3738	4084	4804	5295			1093	1225	1271	1571	
		5305	5383	5419	5662			1918	2392	2830	3278	
		6618						3333	3567	3665	4176	
Nla IV	(24)	346	553	625	1124			5228	5421	5713		
		1240	1664	1739	1791	Sfc I	(8)	2	467	1047	2743	
		1995	2074	2186	2195			4345	4536	5214	6063	
		2207	2703	2868	3826	Sfi I	(1)	504				
		4112	4151	4923	5017	Sma I	(5)	341	405	858	2809	
		5058	5269	5914	6279			2873				
Not I	(1)	1652				SnaB I	(1)	2309				
Nru I	(1)	1195				Spe I	(1)	512				
Nsi I	(3)	585	657	3225		Sph I	(3)	583	655	3227		
Nsp7524 I	(5)	84	579	651	3223	Spl I	(1)	51				
		4080				Srf I	(2)	405	2809			
NspB II	(9)	1171	1886	2239	3625	Ssp I	(2)	2551	3211			
		3904	4422	4667	5631	Stu I	(2)	498	834			
		6254				Sty I	(7)	742	835	962	2068	
NspH I	(5)	88	583	655	3227			5493	6240	6582		
		4084				Taq I	(17)	108	1256	1407	1899	

		2041	2226	2270	2296	BstB I	TT`CG,AA	1	BstE II	G`GTNAC,C	1
		4180	5477	5737	5837	BstN I	CC`W,GG	18	BstU I	CG CG	25
		5868	5880	6174	6189	BstX I	CCAN,NNN`NTGG	1	BstY I	R`GATC,Y	10
		6605				Bsu36 I	CC`TNA,GG	1	Cac8 I	GCN NGC	42
Tfi I	(11)	988	1320	1409	1446	Cfr10 I	R`CCGG,Y	12	Cla I	AT`CG,AT	1
		2298	2688	3182	3443	Csp6 I	G`TA,C	11	Dde I	C`TNA,G	10
		3915	4055	6052		Dpn I	GA TC	33	DpnII	`GATC,	33
Tsp45 I	(9)	46	2177	3043	3103	Dra I	TTT AAA	6	Dra III	CAC,NNN`GTG	4
		5229	5440	5505	5968	Drd I	GACNN,NN`NNGTC	3	Dsa I	C`CRYG,G	7
		6070				Eae I	Y`GGCC,R	9	Eag I	C`GGCC,G	2
Tth111 II	(8)	198	2108	3138	4669	Ear I	CTCTTC 7/10	1	Eco47 III	AGC GCT	1
		4678	4708	5725	5732	Eco57 I	CTGAAG 21/19	4	Eco72 I	CAC GTG	2
Vsp I	(6)	122	906	3616	3851	EcoN I	CCTNN`N,NNAGG	3	EcoO109 I	RG`GNC,CY	2
		3910	5145			EcoR I	G`AATT,C	1	EcoR II	`CCWGG,	18
Xba I	(1)	2301				EcoR V	GAT ATC	1	Ehe I	GGC GCC	1
Xho I	(1)	6604				Esp I	GC`TNA,GC	2	Fnu4H I	GC`N,GC	61
Xho II	(10)	881	1489	2167	2205	Fok I	GGATG 14/18	20	Fse I	GG,CCGG`CC	-
		2257	4721	4732	4818	Fsp I	TGT GCA	1	Gdi II	`YGGC,CG	9
Xma I	(5)	339	403	856	2807	Gsu I	CTGGAG 21/19	4	Hae I	WGG CCW	9
		2871				Hae II	R,GCCG`Y	12	Hae III	GG CC	26
Xma III	(2)	1080	1652			Hga I	GACGC 9/14	10	HgiA I	G,WGCW`C	3
						HgiE II	ACNNNNNNNGGT -1/131		Hha I	G,CG`C	43
		4830	6289			Hinc II	ATY RAC	4	Hind II	GTY RAC	4
						Hind III	A`AGCT,T	1	Hinf I	G`ANT,C	19
						HinI I	GR`CG,YC	3	HinP I	G`CG,C	43
						Hpa I	GTT AAC	1	Hpa II	C`CG,G	42
						Hph I	GGTGA 12/11	10	Kas I	G`CGCG,C	1
						Kpn I	G,GTAC`C	1	Mae I	C`TA,G	21
						Mae II	A`CG,T	20	Mae III	`GTNAC,	25
						Mbo I	`GATC,	33	Mbo II	GAAGA 12/11	13
						Mlu I	A`CGCG,T	1	Mme I	TCCRAC 25/23	3
						Mnl I	CCTC 10/10	49	Msc I	TGG CCA	2
						Mse I	T`TA,A	31	Msl I	CAYNN NNRTG	4
						Msp I	C`CG,G	42	MspAl I	CMG CKG	9
						Mun I	C`AATT,G	1	Nae I	GCC GGC	5
						Nar I	GG`CG,CC	1	Nci I	CC`S,GG	18
						Nco I	C`CATG,G	2	Nde I	CA`TA,TG	1
						NgoM I	G`CCGG,C	5	Nhe I	G`CTAG,C	1
						Nla III	,CATG`	25	Nla IV	GGN NCC	24
						Not I	GC`GGCC,GC	1	Nru I	TCG CGA	1
						Nsi I	A,TGCA`T	3	Nsp7524 I	R`CATG,Y	5
						NspB II	CMG CKG	9	NspH I	R,CATG`Y	5
						Paer7 I	C`TCGA,G	1	Pal I	GG CC	26
						PflM I	CCAN,NNN`NTGG	-	Ple I	GAGTC 9/10	2
						Pme I	CTTT AAAC	1	Pml I	CAC GTG	2
						PpuM I	RG`GWC,CY	1	Psp1406 I	AA`CG,TT	2
						PspA I	C`CCGG,G	5	Pst I	C,TGCA`G	3
						Pvu I	CG,AT`CG	3	Pvu II	CAG CTG	3
						Rsa I	GT AC	11	Rsr II	CG`GWC,CG	2
						Sac I	G,AGCT`C	1	Sac II	CC,GC`GG	1
						Sal I	G`TCGA,C	1	Sap I	GCTCTTC 8/11	1
						Sau3A I	`GATC,	33	Sau96 I	G`GNC,C	13
						Sca I	AGT ACT	1	ScrF I	CC`N,GG	36
						Sec I	C`CNNG,G	39	sfaN I	GCATC 9/13	19
						Sfc I	C`TRYA,G	8	sfi I	GGCCN,NNN`NGGCC	1
						Sma I	CCC GGG	5	SnaB I	TAC GTA	1
						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`CWVG,G	7	Taq I	T`CG,A	17
						Tfi I	G`AWT,C	11	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	CCANNNN,N`NNNTGG-	-
						Xho I	C`TCGA,G	1	Xho II	R`GATC,Y	10
						Xma I	C`CCGG,G	5	Xma III	C`GGCC,G	2

Site usage in pMPB2:

Aat II	G,ACGT`C	-	Acc I	GT`MK,AC	1
Acc65 I	G`GTAC,C	1	Aci I	C`CG,C	77
Afl II	C`TTAA,G	-	Afl III	A`CRYG,Y	4
Age I	A`CCGG,T	1	Aha II	GR`CG,TC	3
Ahd I	GACNN,N`NNGTC	1	Alu I	AG CT	32
Alw I	GGATC 8/9	18	AlwN I	CAG,NNN`CTG	1
Apa I	G,GGCC`C	1	Apal I	G`TGCA,C	2
Apo I	R`AATT,Y	6	Asc I	GG`CGCG,CC	1
Ase I	AT`TA,AT	6	Asp718	G`GTAC,C	1
Ava I	C`YCGR,G	11	Ava II	G`GWC,C	7
Avr II	C`CTAG,G	1	BamH I	G`GATC,C	1
Ban I	G`GYRC,C	8	Ban II	G,RGCY`C	6
Ebe I	G,GC GC`C	1	Bbs I	GAAGAC 8/12	1
Bbv I	GCAGC 13/17	18	Bbv II	GAAGAC 7/11	1
Bcl I	T`GATC,A	2	Bcn I	CC,S`GG	18
Bfa I	C`TA,G	21	Bgl I	GCCN,NNN`NGGC	3
Bgl II	A`GATC,T	1	Blp I	GC`TNA,GC	2
Bpm I	CTGGAG 22/20	4	Bsa I	GGTCTC 7/11	3
BsaA I	YAC GTR	6	BsaB I	GATNN NNATC	1
BsaH I	GR`CG,YC	3	BsaJ I	C`CNNG,G	39
BsaW I	W`CCGG,W	10	BseR I	GAGGAG 16/14	2
Bsg I	GTGCAG 22/20	3	BsIC I	TT`CG,AA	1
BsiE I	CG,RY`CG	8	BsiHKA I	G,WGCW`C	3
BsiW I	C`GTAC,G	1	Bsm I	GAATG,C 7	3
BsmA I	GTCTC`/9	4	BsmB I	CGTCTC 7/11	-
BsmF I	GGGAC 15/19	15	BsoF I	GC`N,GC	61
Bsp120 I	G`GGCC,C	1	Bsp1286 I	G,DGCH`C	-
BspH I	T`CATG,A	1	BspM I	ACCTGC 10/14	1
BspM II	T`CCGG,A	2	Bsr I	ACT,GG`	23
BsrB I	GAG CGG	5	BsrD I	GCAATG, 8	4
BsrG I	T`GTAC,A	1	BssH II	G`CGCG,C	3
Bsss I	C`TCGT,G	2	Bst1107 I	GTA TAC	-