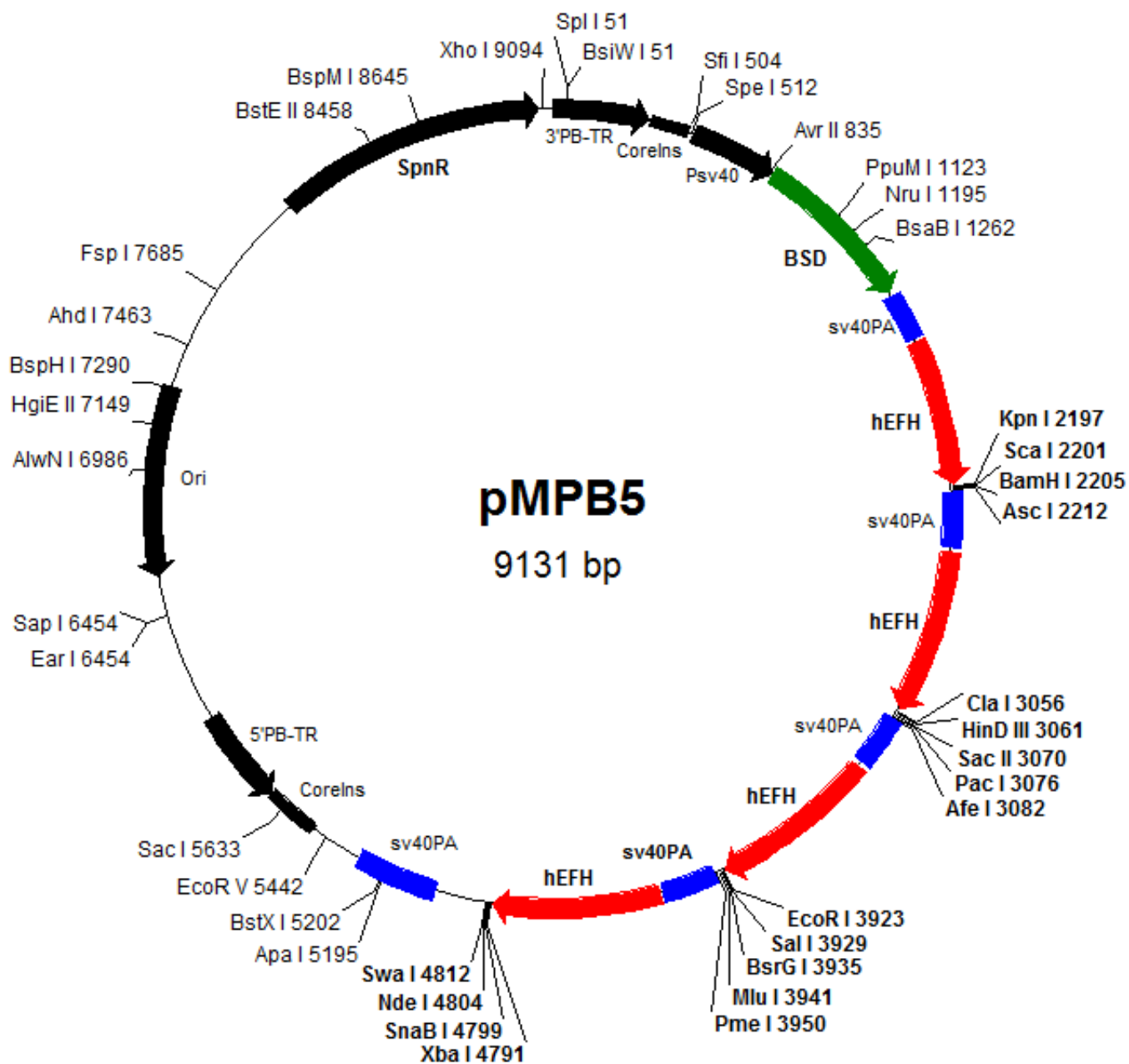


**Vector:** pMPB5 (modified PiggyBac vector; four expression cassettes)

**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



# pMPB5 Vector Sequence (aka, pMPB2c) (Spectinomycin or Blastacin-resistant)

CTGCAGAACACGCAGCTAGATTAACTCTAGAAAAGATAATCAATTTGTGACGTACGTTAAAGATAATCATGCGTAAAATTGACGCATG  
TGTTTTTATCGGTCTGTATATCGAGGTTTATTTTATTAATTTGAATAGATATTAAGTTTTTATTATATTTTACACTTACATACTAATAATA  
AATTCAACAAACAATTTATTTATGTTTTATTTATTTATTTAAAAAACAACAAAACTCAAAATTTCTTCTATAAAAGTAACAAAAACTTTT  
ATGAGGGACAGCCCCCCCCAAAGCCCCAGGGATGTAATTACGTCCCTCCCCCGCTAGGGGGCAGCAGCGAGCCCGCCGGGGCTCC  
GCTCCGGTCCGGCGCTCCCCCGCATCCCCGAGCCGGCAGCGTGCGGGGACAGCCGGGCACGGGGAAGGTGGCACGGGATCGCTTT  
CCTCTGAACGCTTCTCGCTGCTCTTTGAGCCTGCAGACACCTGGGGGGATACGGGGAAAAGGCCTCCACGGCCAGACTAGTAAATGTG  
TGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCAGGTGT  
GGAAAGTCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCATAGTCCCGCCCTAACTCCG  
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 CACTACGTGAAAGGCGAGATCACCAAGGTAGTCGGCAATAACCCTCGAGCCACCCAATGACCAAAAATCCCTTAACGTGAGTTA

**Unique enzymes in pMPB5**

BsiW I	C`GTAC,G	51	Eco47 III	AGC GCT	3083
Spl I	C`GTAC,G	51	EcoR I	G`AATT,C	3923
Sfi I	GGCCN,NNN`NGGCC	504	Sal I	G`TCGA,C	3929
Spe I	A`CTAG,T	512	Acc I	GT`MK,AC	3930
Avr II	C`CTAG,G	835	BsrG I	T`GTAC,A	3935
Bbv II	GAAGAC 7/11	1048	Mlu I	A`CGCG,T	3941
Bbs I	GAAGAC 8/12	1049	Pme I	CTT AAAC	3950
PpuM I	RG`GWC,CY	1123	Xba I	T`CTAG,A	4791
Nru I	TCG CGA	1195	SnaB I	TAC GTA	4799
BsaB I	GATNN NNATC	1262	Nde I	CA`TA,TG	4804
Acc65 I	G`GTAC,C	2193	Bsp120 I	G`GGCC,C	5191
Asp718	G`GTAC,C	2193	Apa I	G,GGCC`C	5195
Kpn I	G,GTAC`C	2197	BstX I	CCAN,NNNN`NTGG	5202
Sca I	AGT ACT	2201	EcoR V	GAT ATC	5442
BamH I	G`GATC,C	2205	Sac I	G,AGCT`C	5633
Asc I	GG`CGCG,CC	2212	Sap I	GCTCTC 8/11	6454
Cla I	AT`CG,AT	3056	Ear I	CTCTC 7/10	6454
HinD III	A`AGCT,T	3061	AlwN I	CAG,NNN`CTG	6986
Sac II	CC,GC`GG	3070	HgiE II	ACCNNNNNGGT -1/137149	
			BspH I	T`CATG,A	7290
			Ahd I	GACNN,N`NNGTC	7463

Fsp I	TGC GCA	7685				9094			
BstE II	G`GTNAC,C	8458				355	1123	5346	7601
BspM I	ACCTGC 10/14	8645				7823	8097	8738	
Paer7 I	C`TCGA,G	9094				835			
Xho I	C`TCGA,G	9094				2205			
Number of enzymes = 45						1238	1662	1737	1993

**The following enzymes do not cut in pMPB5**

Aat II	Afl II	Bgl II	BsiC I	BsmB I					
Bsp1286 I	Bst1107 I	BstB I	Fse I	Hpa I	Ban II	(9)	347	1228	1908
PflM I	Tth111 I	Xca I	Xcm I	Xmn I		(20)	1238	1662	1737

**pMPB5: sites sorted by name:**

Acc I	(1)	3930							
Acc65 I	(1)	2193							
Aci I	(120)	315	336	348	370				
		393	683	695	704				
		716	726	737	783	Bbv II	(1)	1048	
		1083	1165	1232	1416	Bcl I	(2)	886	8496
		1419	1485	1651	1655	Bcn I	(24)	341	342
		1756	1793	1873	1929			858	859
		1932	1947	1978	1985			2320	2911
		2012	2278	2281	2347			4056	4647
		2513	2517	2618	2655			5299	5300
		2735	2791	2794	2809			6203	6951
		2840	2847	2874	3067	Bfa I	(36)	17	28
		3069	3091	3146	3149			836	1073
		3215	3381	3385	3486			1893	2019
		3523	3603	3659	3662			2604	2755
		3677	3708	3715	3742			3085	3335
		4014	4017	4083	4249			3749	3811
		4253	4354	4391	4471			4491	4617
		4527	4530	4545	4576			4916	5384
		4583	4610	5309	5332			7065	7318
		5354	5366	5387	5571	Bgl I	(3)	504	7583
		5604	5638	5846	5859	Blp I	(2)	1359	8607
		6008	6115	6120	6168	Bpm I	(10)	1463	1520
		6205	6260	6363	6419			3193	3250
		6429	6453	6496	6503			7533	8550
		6524	6615	6643	6770	Bsa I	(6)	2037	2899
		6789	6910	7020	7155			5011	7524
		7164	7526	7617	7808	BsaA I	(9)	895	1393
		7854	8121	8141	8309			3991	4799
		8406	8418	8485	8548			9055	
		8744	8747	8825	8872	BsaB I	(1)	1262	
Afl III	(7)	894	1390	2252	3120	BsaH I	(9)	1461	2185
		3941	3988	6570				3191	3915
								8352	
Age I	(4)	1734	2596	3464	4332	BsaJ I	(48)	289	290
Aha II	(9)	1461	2185	2323	3047			403	476
		3191	3915	4059	4783			619	742
		8352						856	962
Ahd I	(1)	7463						1804	2068
Alu I	(50)	16	799	853	863			2930	3067
		1066	1171	1535	1886			3798	3972
		1892	1896	2034	2175			5015	5163
		2397	2748	2754	2758			5360	5361
		2896	3037	3063	3265			5878	5989
		3616	3622	3626	3764			7983	8006
		3905	4133	4484	4490			8527	8591
		4494	4632	4773	4997	BsaW I	(16)	352	1659
		5631	5757	5800	6235			2596	3389
		6330	6394	6512	6738			4332	5348
		6828	6874	7131	7652			6776	6923
		7752	7815	8062	8492	BseR I	(5)	831	1391
		8606	8978					3989	
Alw I	(28)	434	888	1278	1469	Bsg I	(6)	1151	1852
		1496	2163	2201	2212			4450	6120
		2331	2358	3025	3083	BsiE I	(11)	1083	1199
		3199	3226	3893	4067			3385	4253
		4094	4761	5269	5773			6910	7833
		7132	7218	7218	7315			5633	6888
		7316	7780	8757	8786	BsiHKA I	(3)	1600	2462
AlwN I	(1)	6986				BsiW I	(1)	51	5715
Apa I	(1)	5195				Bsm I	(6)	4911	5715
ApaL I	(2)	6884	8573			BsmA I	(7)	982	2038
Apo I	(9)	175	233	1570	2432			4636	5010
		3300	3923	4168	4881	BsmF I	(21)	281	291
		9041						601	665
Asc I	(1)	2212						1683	2334
Ase I	(6)	122	906	6106	6341			3413	4070
		6400	7635					5116	5290
Asp718	(1)	2193						8854	
Ava I	(17)	339	377	403	856	BsoF I	(85)	14	326
		1701	1803	2563	2665			387	454
		3431	3533	4299	4401			1083	1157
		5297	5323	5361	8190				

		1166	1169	1333	1419			7254	7420	8607		
		1533	1652	1655	1873	Dpn I	(42)	429	883	888	1198	
		1932	1947	1978	2281			1259	1273	1475	1491	
		2395	2514	2517	2735			2169	2207	2337	2353	
		2794	2809	2840	3149			3031	3089	3205	3221	
		3263	3382	3385	3603			3899	4073	4089	4767	
		3662	3677	3708	4017			4818	5275	5768	7138	
		4131	4250	4253	4471			7213	7224	7232	7310	
		4530	4545	4576	5150			7322	7427	7768	7786	
		5249	5316	5367	5374			7832	8315	8498	8678	
		5377	5639	5758	5860			8688	8763	8781	9009	
		5891	5894	6009	6121			9030	9068			
		6168	6395	6476	6494	DpnII	(42)	427	881	886	1196	
		6497	6615	6770	6913			1257	1271	1473	1489	
		6978	6981	7187	7515			2167	2205	2335	2351	
		7854	7881	7976	8119			3029	3087	3203	3219	
		8204	8248	8264	8419			3897	4071	4087	4765	
		8486	8636	8745	8825			4816	5273	5766	7136	
		8922						7211	7222	7230	7308	
Bsp120 I	(1)	5191						7320	7425	7766	7784	
BspH I	(1)	7290						7830	8313	8496	8676	
BspM I	(1)	8645						8686	8761	8779	9007	
BspM II	(2)	6016	6028					9028	9066			
Bsr I	(29)	721	1097	1121	1769	Dra I	(9)	2030	2892	3760	3950	
		1790	2198	2206	2631			4628	4812	5045	7329	
		2652	3499	3520	4367			7348				
		4388	5068	5178	5999	Dra III	(7)	1369	2231	3099	3967	
		6371	6977	6990	7104			8007	8435	9055		
		7510	7628	7671	7938	Drd I	(3)	1051	5649	6678		
		8033	8098	8836	8932	Dsa I	(7)	502	742	962	3067	
		8954						8006	8220	8591		
BsrB I	(8)	350	1657	2519	3387	Eae I	(15)	505	965	1080	1371	
		4255	5354	6262	6503			1652	2233	2514	3101	
BsrD I	(4)	7524	7698	8647	8940			3382	3969	4250	5947	
BsrG I	(1)	3935						6409	7851	8385		
BssH II	(3)	2212	6209	9022		Eag I	(5)	1080	1652	2514	3382	
BssS I	(2)	1138	6743					4250				
BstE II	(1)	8458				Ear I	(1)	6454				
BstN I	(18)	291	477	549	604	Eco47 III	(1)	3083				
		621	1268	5096	5154	Eco57 I	(7)	1060	1907	2769	3637	
		5226	5412	5990	6157			4505	7117	8443		
		6310	6598	6719	6732	Eco72 I	(5)	895	1393	2255	3123	
		7952	8529					3991				
BstU I	(37)	1195	1485	1756	1925	EcoN I	(9)	1745	1940	2607	2802	
		1970	2214	2347	2618			3475	3670	4343	4538	
		2787	2832	3069	3215			5186				
		3486	3655	3700	3943	EcoO109 I	(2)	1123	5191			
		4083	4354	4523	4568	EcoR I	(1)	3923				
		5571	5677	5848	6008	EcoR II	(18)	289	475	547	602	
		6211	6417	6419	6617			619	1266	5094	5152	
		7198	7528	8212	8485			5224	5410	5988	6155	
		8550	8613	8906	9022			6308	6596	6717	6730	
		9024						7950	8527			
BstX I	(1)	5202				EcoR V	(1)	5442				
BstY I	(16)	881	1489	2167	2205	Ehe I	(4)	2186	3048	3916	4784	
		2351	3029	3087	3219	Esp I	(2)	1359	8607			
		3897	4087	4765	7211	Fnu4H I	(85)	14	326	329	336	
		7222	7308	7320	8779			387	454	783	1064	
Bsu36 I	(4)	1941	2803	3671	4539			1083	1157	1160	1163	
Cac8 I	(60)	333	384	391	467			1166	1169	1333	1419	
		562	581	634	653			1533	1652	1655	1873	
		1059	1173	1465	1894			1932	1947	1978	2281	
		1908	1929	2092	2120			2395	2514	2517	2735	
		2214	2327	2756	2770			2794	2809	2840	3149	
		2791	2954	2982	3195			3263	3382	3385	3603	
		3624	3638	3659	3822			3662	3677	3708	4017	
		3850	4063	4492	4506			4131	4250	4253	4471	
		4527	4690	4718	5237			4530	4545	4576	5150	
		5313	5320	5371	5618			5249	5316	5367	5374	
		5715	5802	5956	6207			5377	5639	5758	5860	
		6211	6363	6392	6501			5891	5894	6009	6121	
		6587	6624	7184	7575			6168	6395	6476	6494	
		8208	8385	8490	8670			6497	6615	6770	6913	
		8839	8945	8949	9024			6978	6981	7187	7515	
Cfr10 I	(27)	382	1463	1734	1958			7854	7881	7976	8119	
		2090	2181	2325	2596			8204	8248	8264	8419	
		2820	2952	3043	3193			8486	8636	8745	8825	
		3464	3688	3820	3911			8922				
		4061	4332	4556	4688	Fok I	(26)	307	359	686	1015	
		4779	5318	6069	6093			1250	1483	1937	2345	
		7543	8894	8947				2799	3213	3667	4081	
Cla I	(1)	3056						4535	5014	5341	5393	
Csp6 I	(14)	52	1784	2194	2200			5895	6044	6176	7429	
		2646	3514	3936	4382			7610	7897	8029	8182	
		4800	7944	8177	8390			8426	8927			
		8398	8881			Fsp I	(1)	7685				
Dde I	(19)	795	1359	1941	2035	Gdi II	(18)	506	1079	1081	1370	
		2086	2803	2897	2948			1651	1653	2232	2513	
		3671	3765	3816	4539			2515	3100	3381	3383	
		4633	4684	5645	6845			3968	4249	4251	6410	

		7850	8384					7755	7992	8765	8895	
Gsu I	(10)	1464	1519	2326	2381			8948				
		3194	3249	4062	4117		Hph I	(10)	959	5978	7307	7534
		7534	8549						7948	8006	8322	8469
Hae I	(9)	498	834	967	5949				8555	9062		
		5985	6585	6596	7048		Kas I	(4)	2184	3046	3914	4782
		9017					Kpn I	(1)	2197			
Hae II	(18)	364	2065	2188	2927		Mae I	(36)	17	28	318	513
		3050	3085	3795	3918				836	1073	1605	1742
		4663	4786	5344	5807				1893	2019	2081	2467
		6126	6448	6818	8365				2604	2755	2881	2943
		8795	8944						3085	3335	3472	3623
Hae III	(38)	498	507	776	782				3749	3811	4203	4340
		834	967	1082	1373				4491	4617	4679	4792
		1654	1946	2051	2235				4916	5384	5743	5754
		2516	2808	2913	3103				7065	7318	7653	8979
		3384	3676	3781	3971		Mae II	(29)	50	54	304	894
		4252	4544	4649	5193				1392	1849	2132	2254
		5949	5985	6411	6585				2711	2994	3122	3579
		6596	6614	7048	7506				3862	3990	4447	4730
		7586	7853	8387	8421				4798	5398	5479	5537
		8951	9017						5902	5919	6136	7273
Hga I	(16)	89	1042	1468	1998				7689	8378	8864	9054
		2330	2860	3198	3728				9123			
		4066	4596	5544	5707		Mae III	(34)	46	248	1544	2161
		6680	7258	8006	8342				2177	2406	3023	3039
HgiA I	(3)	5633	6888	8577					3274	3891	3907	4142
HgiE II	(1)	7149							4759	4775	4855	5533
Hha I	(64)	363	1063	1485	1684				5593	6196	6926	6989
		1756	1927	2064	2159				7105	7388	7719	7777
		2187	2214	2216	2347				7930	7995	8126	8213
		2546	2618	2789	2926				8257	8452	8458	8560
		3021	3049	3084	3215				8890	9128		
		3414	3486	3657	3794		Mbo I	(42)	427	881	886	1196
		3889	3917	4083	4282				1257	1271	1473	1489
		4354	4525	4662	4757				2167	2205	2335	2351
		4785	5343	5679	5806				3029	3087	3203	3219
		6049	6125	6211	6213				3897	4071	4087	4765
		6354	6419	6447	6480				4816	5273	5766	7136
		6750	6817	6917	7091				7211	7222	7230	7308
		7200	7593	7686	8085				7320	7425	7766	7784
		8135	8212	8364	8552				7830	8313	8496	8676
		8613	8640	8794	8888				8686	8761	8779	9007
		8908	8943	9024	9026				9028	9066		
HinC II	(3)	900	3931	5092			Mbo II	(16)	231	996	1053	1081
Hind II	(3)	900	3931	5092					1499	2361	3229	4097
HinD III	(1)	3061							5837	6442	7231	7304
Hinf I	(30)	988	1320	1409	1446				8654	9013	9016	9049
		1965	2084	2271	2308		Mlu I	(1)	3941			
		2827	2946	3139	3176		Mme I	(3)	6784	6968	9016	
		3695	3814	4007	4044		Mnl I	(73)	103	258	318	446
		4563	4682	4966	5178				508	766	772	795
		5564	5672	5933	6405				801	809	812	824
		6470	6545	6941	7458				944	1005	1346	1347
		8329	8542						1369	1486	1710	1799
HinI I	(9)	1461	2185	2323	3047				1894	1936	1990	2006
		3191	3915	4059	4783				2231	2348	2572	2661
		8352							2756	2798	2852	2868
HinP I	(64)	361	1061	1483	1682				3099	3216	3440	3529
		1754	1925	2062	2157				3624	3666	3720	3736
		2185	2212	2214	2345				3967	4084	4308	4397
		2544	2616	2787	2924				4492	4534	4588	4604
		3019	3047	3082	3213				5125	5258	5386	5630
		3412	3484	3655	3792				5816	5843	5873	6137
		3887	3915	4081	4280				6419	6468	6678	6751
		4352	4523	4660	4755				7002	7402	7483	7629
		4783	5341	5677	5804				7835	7974	8198	8295
		6047	6123	6209	6211				8335	8743	8782	9027
		6352	6417	6445	6478				9102			
		6748	6815	6915	7089		Msc I	(2)	967	5949		
		7198	7591	7684	8083		Mse I	(33)	22	57	122	138
		8133	8210	8362	8550				212	906	2029	2891
		8611	8638	8792	8886				3073	3077	3759	3949
		8906	8941	9022	9024				4627	4811	5037	5044
Hpa II	(69)	340	353	358	383				5521	5528	5749	5962
		404	857	1456	1464				6106	6341	6400	7276
		1660	1735	1959	2047				7328	7333	7347	7400
		2059	2091	2182	2209				7635	7674	8291	8807
		2318	2326	2522	2597				9120			
		2821	2909	2921	2953		Msl I	(4)	5200	7715	7874	8570
		3044	3186	3194	3390		Msp I	(69)	340	353	358	383
		3465	3689	3777	3789				404	857	1456	1464
		3821	3912	4054	4062				1660	1735	1959	2047
		4258	4333	4557	4645				2059	2091	2182	2209
		4657	4689	4780	5015				2318	2326	2522	2597
		5165	5298	5319	5344				2821	2909	2921	2953
		5349	5362	6017	6029				3044	3186	3194	3390
		6070	6080	6094	6202				3465	3689	3777	3789
		6288	6777	6924	6950				3821	3912	4054	4062
		7140	7544	7578	7645				4258	4333	4557	4645

		4657	4689	4780	5015		Sap I	(1)	6454			
		5165	5298	5319	5344		Sau3A I	(42)	427	881	886	1196
		5349	5362	6017	6029				1257	1271	1473	1489
		6070	6080	6094	6202				2167	2205	2335	2351
		6288	6777	6924	6950				3029	3087	3203	3219
		7140	7544	7578	7645				3897	4071	4087	4765
		7755	7992	8765	8895				4816	5273	5766	7136
		8948							7211	7222	7230	7308
MspAl I	(12)	1171	1886	2748	3069				7320	7425	7766	7784
		3616	4484	6115	6394				7830	8313	8496	8676
		6912	7157	8121	8744				8686	8761	8779	9007
Mun I	(4)	1727	2589	3457	4325				9028	9066		
Nae I	(11)	384	1465	2092	2327		Sau96 I	(16)	355	1123	2049	2911
		2954	3195	3822	4063				3779	4647	5191	5192
		4690	5320	8949					5346	7505	7584	7601
Nar I	(4)	2185	3047	3915	4783				7823	8097	8738	8950
Nci I	(24)	340	341	404	405		Sca I	(1)	2201			
		857	858	1457	2048		ScrF I	(42)	291	340	341	404
		2319	2910	3187	3778				405	477	549	604
		4055	4646	5016	5165				621	857	858	1268
		5298	5299	5362	5363				1457	2048	2319	2910
		6202	6950	7646	7993				3187	3778	4055	4646
Nco I	(2)	742	962						5016	5096	5154	5165
Nde I	(1)	4804							5226	5298	5299	5362
Ngom I	(11)	382	1463	2090	2325				5363	5412	5990	6157
		2952	3193	3820	4061				6202	6310	6598	6719
		4688	5318	8947					6732	6950	7646	7952
Nhe I	(4)	1892	2754	3622	4490				7993	8529		
Nla III	(31)	71	88	583	655		Sec I	(48)	289	290	339	340
		746	966	1498	1646				403	476	502	547
		2360	2508	3228	3376				619	742	777	835
		4096	4244	4957	5494				856	962	1267	1374
		5554	5717	5866	5930				1804	2068	2236	2666
		5954	6184	6228	6574				2930	3067	3104	3534
		7294	7785	7795	7873				3798	3972	4402	4666
		7909	8152	9108					5015	5163	5224	5297
Nla IV	(42)	346	553	625	1124				5360	5361	5410	5411
		1240	1664	1739	1791				5878	5989	6309	6730
		1995	2074	2186	2195				7983	8006	8189	8220
		2207	2526	2601	2653				8527	8591	8730	9072
		2857	2936	3048	3394		SfaN I	(26)	380	591	663	1036
		3469	3521	3725	3804				1093	1225	1271	1571
		3916	4262	4337	4389				1918	2433	2780	3301
		4593	4672	4784	5193				3648	3949	4169	4516
		5358	6316	6602	6641				4882	5320	5768	5823
		7413	7507	7548	7759				6057	6155	6666	7718
		8404	8769						7911	8203		
Not I	(4)	1652	2514	3382	4250		Sfc I	(8)	2	467	1047	5233
Nru I	(1)	1195							6835	7026	7704	8553
Nsi I	(3)	585	657	5715			Sfi I	(1)	504			
Nsp7524 I	(5)	84	579	651	5713		Sma I	(5)	341	405	858	5299
		6570							5363			
NspB II	(12)	1171	1886	2748	3069		SnaB I	(1)	4799			
		3616	4484	6115	6394		Spe I	(1)	512			
		6912	7157	8121	8744		Sph I	(3)	583	655	5717	
NspH I	(5)	88	583	655	5717		Spl I	(1)	51			
		6574					Srf I	(2)	405	5299		
PaeR7 I	(1)	9094					Ssp I	(2)	5041	5701		
Pal I	(38)	498	507	776	782		Stu I	(2)	498	834		
		834	967	1082	1373		Sty I	(10)	742	835	962	2068
		1654	1946	2051	2235				2930	3798	4666	7983
		2516	2808	2913	3103				8730	9072		
		3384	3676	3781	3971		Taq I	(26)	108	1256	1407	1899
		4252	4544	4649	5193				2041	2269	2761	2903
		5949	5985	6411	6585				3056	3137	3629	3771
		6596	6614	7048	7506				3930	3956	4005	4497
		7586	7853	8387	8421				4639	6670	7967	8227
		8951	9017						8327	8358	8370	8664
Ple I	(5)	1973	2835	3703	4571				8679	9095		
		6949					Tfi I	(16)	988	1320	1409	1446
Pme I	(1)	3950							2271	2308	3139	3176
Pml I	(5)	895	1393	2255	3123				4007	4044	5178	5672
		3991							5933	6405	6545	8542
PpuM I	(1)	1123					Tsp45 I	(12)	46	2177	3039	3907
Psp1406 I	(5)	1849	2711	3579	4447				4775	5533	5593	7719
		7689							7930	7995	8458	8560
PspA I	(5)	339	403	856	5297		Tth111 II	(11)	198	2108	2970	3838
		5361							4706	5628	7159	7168
Pst I	(3)	6	471	5237					7198	8215	8222	
Pvu I	(3)	1199	7833	8679			Vsp I	(6)	122	906	6106	6341
Pvu II	(6)	1171	1886	2748	3616				6400	7635		
		4484	6394				Xba I	(1)	4791			
Rsa I	(14)	53	1785	2195	2201		Xho I	(1)	9094			
		2647	3515	3937	4383		Xho II	(16)	881	1489	2167	2205
		4801	7945	8178	8391				2351	3029	3087	3219
		8399	8882						3897	4087	4765	7211
Rsr II	(2)	355	5346						7222	7308	7320	8779
Sac I	(1)	5633					Xma I	(5)	339	403	856	5297
Sac II	(1)	3070							5361			
Sal I	(1)	3929					Xma III	(5)	1080	1652	2514	3382

## Site usage in pMPB5

Aat II	G,ACGT`C	-	Acc I	GT`MK,AC	1	Esp I	GC`TNA,GC	2	Fnu4H I	GC`N,GC	85
Acc65 I	G`GTAC,C	1	Aci I	C`CG,C	120	Fok I	GGATG 14/18	26	Fse I	GG,CCGG`CC	-
Afl II	C`TTAA,G	-	Afl III	A`CRYG,T	7	Fsp I	TGC GCA	1	Gdi II	`YGGC,CG	18
Age I	A`CCGG,T	4	Aha II	GR`CG,YC	9	Gsu I	CTGGAG 21/19	10	Hae I	WGG CCW	9
Ahd I	GACNN,N`NNGTC	1	Alu I	AG CT	50	Hae II	R,CGCG`Y	18	Hae III	GG CC	38
Alw I	GGATC 8/9	28	AlwN I	CAG,NNN`CTG	1	Hga I	GACGC 9/14	16	Hga I	G,WGCW`C	3
Apa I	G,GGCC`C	1	ApaL I	G`TGCA,C	2	HgiE II	ACNNNNNNNGGT -1/131	-	Hha I	G,CG`C	64
Apo I	R`AATT,Y	9	Asc I	GG`CGCG,CC	1	Hinc II	GTY RAC	3	Hind II	GTY RAC	3
Ase I	AT`TA,AT	6	Asp718	G`GTAC,C	1	Hind III	A`AGCT,T	1	Hinf I	G`ANT,C	30
Ava I	C`YCGR,G	17	Ava II	G`GWC,C	7	HinI I	GR`CG,YC	9	HinP I	G`CG,C	64
Avr II	C`CTAG,G	1	BamH I	G`GATC,C	1	Hpa I	GT AAC	-	Hpa II	C`CG,G	69
Ban I	G`GYRC,C	20	Ban II	G,RCGY`C	9	Hph I	GGTGA 12/11	10	Kas I	G`GCGC,C	4
Bbe I	G,CGCG`C	4	Bbs I	GAAGAC 8/12	1	Kpn I	G,GTAC`C	1	Mae I	C`TA,G	36
Bbv I	GCAGC 13/17	21	Bbv II	GAAGAC 7/11	1	Mae II	A`CG,T	29	Mae III	`GTNAC,	34
Bcl I	T`GATC,A	2	Bcn I	CC,S`GG	24	Mbo I	`GATC,	42	Mbo II	GAAGA 12/11	16
Bfa I	C`TA,G	36	Bgl I	GCCN,NNN`NGGC	3	Mlu I	A`CGCG,T	1	Mme I	TCCRAC 25/23	3
Bgl II	A`GATC,T	-	Blp I	GC`TNA,GC	2	Mnl I	CCTC 10/10	73	Msc I	TGG CCA	2
Bpm I	CTGGAG 22/20	10	Bsa I	GGTCTC 7/11	6	Mse I	T`TA,A	33	Msl I	CAYN NNRTG	4
BsaA I	YAC GTR	9	BsaB I	GATNN NNATC	1	Msp I	C`CG,G	69	MspAl I	CMG CKG	12
BsaH I	GR`CG,YC	9	BsaJ I	C`CNNG,G	48	Mun I	C`AATT,G	4	Nae I	GCC GGC	11
BsaW I	W`CCGG,W	16	BseR I	GAGGAG 16/14	5	Nar I	GG`CG,CC	4	Nci I	CC`S,GG	24
Bsg I	GTGCG 22/20	6	BseC I	TT`CG,AA	-	Nco I	C`CATG,G	2	Nde I	CA`TA,TG	1
BsiE I	CG,RY`CG	11	BsiHKA I	G,WGCW`C	3	Ngo I	G`CCGG,C	11	Nhe I	G`CTAG,C	4
BsiW I	C`GTAC,G	1	Bsm I	GAATG,C 7	6	Nla III	,CATG`	31	Nla IV	GGN NCC	42
BsmA I	GTCTC`/9	7	BsmB I	CGTCTC 7/11	-	Not I	GC`GGCC,GC	4	Nru I	TCG CGA	1
BsmF I	GGGAC 15/19	21	BsoF I	GC`N,GC	85	Nsi I	A,TGCA`T	3	Nsp7524 I	R`CATG,Y	5
Bsp120 I	G`GGCC,C	1	Bsp1286 I	G,DGCH`C	-	NspB II	CMG CKG	12	NspH I	R,CATG`Y	5
BspH I	T`CATG,A	1	BspM I	ACCTGC 10/14	1	Paer7 I	C`TCGA,G	1	Pal I	GG CC	38
BspM II	T`CCGG,A	2	Bsr I	ACT,GG`	29	PflM I	CCAN,NNN`NTGG	-	Ple I	GAGTC 9/10	5
BsrB I	GAG CGG	8	BsrD I	GCAATG, 8	4	Pme I	CTTT AAAC	1	Pml I	CAC GTG	5
BsrG I	T`GTAC,A	1	BssH II	G`CGCG,C	3	PpuM I	RG`GWC,CY	1	Psp1406 I	AA`CG,TT	5
Bsss I	C`TCGT,G	2	Bst1107 I	GTA TAC	-	PspA I	C`CCGG,G	5	Pst I	C,TGCA`G	3
BstB I	TT`CG,AA	-	BstE II	G`GTNAC,C	37	Pvu I	CG,AT`CG	3	Pvu II	CAG CTG	6
BstN I	CC`W,GG	18	BstU I	CG CG	1	Rsa I	GT AC	14	Rsr II	CG`GWC,CG	2
BstX I	CCAN,NNNN`NTGG	1	BstY I	R`GATC,Y	16	Sac I	G,AGCT`C	1	Sac II	CC,GC`GG	1
Bsu36 I	CC`TNA,GG	4	Cac8 I	GCN NGC	60	Sal I	G`TCGA,C	1	Sap I	GCTCTTC 8/11	1
Cfr10 I	R`CCGG,Y	27	Cla I	AT`CG,AT	1	Sau3A I	`GATC,	42	Sau96 I	G`GNC,C	16
Csp6 I	G`TA,C	14	Dde I	C`TNA,G	19	Sca I	AGT ACT	1	ScrF I	CC`N,GG	42
Dpn I	GA TC	42	DpnII	`GATC,	42	Sec I	C`CNNG,G	48	SfaN I	GCATC 9/13	26
Dra I	TTT AAA	9	Dra III	CAC,NNN`GTG	7	Sfc I	C`TRYA,G	8	Sfi I	GCCCN,NNN`NGGCC	1
Drd I	GACNN,NN`NNGTC	3	Dsa I	C`CRYG,G	7	Sma I	CCC GGG	5	SnaB I	TAC GTA	1
Eae I	Y`GGCC,R	15	Eag I	C`GGCC,G	5	Spe I	A`CTAG,T	1	Sph I	G,CATG`C	3
Ear I	CTCTTC 7/10	1	Eco47 III	AGC GCT	1	Spl I	C`GTAC,G	1	Srf I	GCCC GGGC	2
Eco57 I	CTGAAG 21/19	7	Eco72 I	CAC GTG	5	Ssp I	AAT ATT	2	Stu I	AGG CCT	2
EcoN I	CCTNN`N,NNAGG	9	Eco109 I	RG`GNC,CY	2	Sty I	C`CWWG,G	10	Taq I	T`CG,A	26
EcoR I	G`AATT,C	1	EcoR II	`CCWGG,	18	Tfi I	G`AWT,C	16	Tsp45 I	`GTSAC,	12
EcoR V	GAT ATC	1	Ehe I	GGC GCC	4	Tth111 I	GACN`N,NGTC	-	Tth111 II	CAARCA 16/14	11
						Vsp I	AT`TA,AT	6	Xba I	T`CTAG,A	1
						Xca I	GTA TAC	-	Xcm I	CCAMNNN,N`NNNNTGG-	-
						Xho I	C`TCGA,G	1	Xho II	R`GATC,Y	16
						Xma I	C`CCGG,G	5	Xma III	C`GGCC,G	5