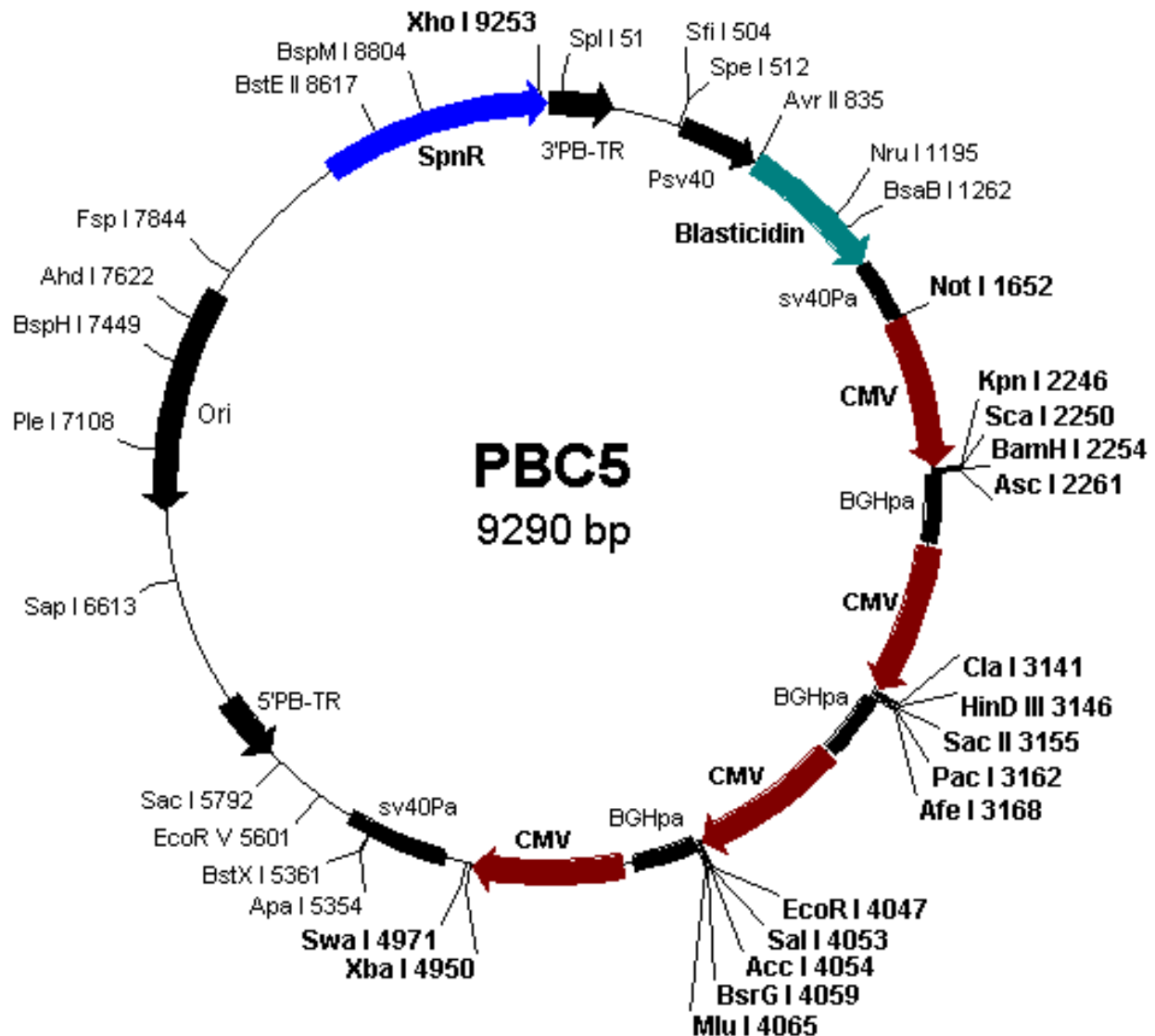


Vector: PBC5 (MOLab modified piggyBac vector with CMV promoter)

Antibiotic Selection: Spectinomycin or Blasticidin-resistant

Creator(s): Xian Chen & Palak Shah, Molecular Oncology Lab of The University of Chicago

Date of Construction: January, 2013



PBC5 Vector Sequence

(Spectinomycin or Blastisin-resistant)

CTGCAGAACACGCAGCTAGATTAACTCTAGAAAAGATAATCATATTGTGACGTACGTTAAAGATAAATCATGCGTAAAATTGACGCATG
TGTTTTATCGGTCTGTATATCGAGGTTTATTTATTAATTTGAATAGATATTAAGTTTTATTATATTTTACACTTACATACTAATAATA
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CCTCTGAACGTTCTCGCTGCTCTTTGAGCCTGCAGACACCTGGGGGATACGGGGAAAAGGCCTCCACGGCCAGACTAGTAAATGTG
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 GAGATCACCAAGGTAGTCGGCAAATAACC**CTCGAG**CCACCCA**TGA**CCAAAATCCCTTAACGTGAGTTA

Unique enzymes in PBC5:

			Asc I	GG`CGCG,CC	2261
			Cla I	AT`CG,AT	3141
BsiW I	C`GTAC,G	51	HinD III	A`AGCT,T	3146
Spl I	C`GTAC,G	51	Sac II	CC,GC`GG	3155
Sfi I	GGCCN,NNN`NGGCC	504	Pac I	TTA,AT`TAA	3162
Spe I	A`CTAG,T	512	Afe I	AGC GCT	3168
Avr II	C`CTAG,G	835	Eco47 III	AGC GCT	3168
PpuM I	RG`GWC,CY	1123	EcoR I	G`AATT,C	4047
Nru I	TCG CGA	1195	Sal I	G`TCGA,C	4053
BsaB I	GATNN NNATC	1262	Acc I	GT`MK,AC	4054
Not I	GC`GGCC,GC	1652	BsrG I	T`GTAC,A	4059
Acc65 I	G`GTAC,C	2242	Mlu I	A`CGCG,T	4065
Asp718	G`GTAC,C	2242	Xba I	T`CTAG,A	4950
Kpn I	G,GTAC`C	2246	Swa I	ATTT AAAT	4971
Sca I	AGT ACT	2250	EcoN I	CCTNN`N,NNAGG	5345
BamH I	G`GATC,C	2254	Bsp120 I	G`GGCC,C	5350

Apa I	G,GGCC`C	5354			2552	3130	3168	3459	
BstX I	CCAN,NNNN`NTGG	5361			4037	4356	4934	5428	
EcoR V	GAT ATC	5601			5932	7291	7377	7377	
Sac I	G,AGCT`C	5792			7474	7475	7939	8916	
Sap I	GCTCTTC 8/11	6613			8945				
Ear I	CTCTTC 7/10	6613			2548	3455	4352	7145	
Ple I	GAGTC 9/10	7108		AlwN I (4)	5354				
BspH I	T`CATG,A	7449		ApaL I (2)	7043	8732			
Ahd I	GACNN,N`NNGTC	7622		Apo I (6)	175	233	1570	4047	
Fsp I	TGC GCA	7844			5040	9200			
Psp1406 I	AA`CG,TT	7848		Asc I (1)	2261				
BstE II	G`GTNAC,C	8617		Ase I (6)	122	906	6265	6500	
BspM I	ACCTGC 10/14	8804			6559	7794			
PaeR7 I	C`TCGA,G	9253		Asp718 (1)	2242				
Xho I	C`TCGA,G	9253		Ava I (9)	339	377	403	856	
Number of enzymes = 45						5456	5482	5520	8349

The following enzymes do not cut in PBC5:

Afl II	Age I	Bbe I	Bgl II	BsiC I	Avr II (1)	835			
BsmB I	Bsp1286 I	Bst1107 I	BstB I	Bsu36 I	BamH I (1)	2254			
Ehe I	Fse I	Hpa I	Kas I	Mun I	Ban I (11)	1238	2116	2242	2364
Nar I	Nhe I	Pf1M I	Pme I	Tth111 I		3014	3271	3921	4168

PBC5: sites sorted by name:

Aat II	(16)	1776	1829	1912	2098	Ban II (8)	347	1228	2517	3424
		2674	2727	2810	2996		4321	5354	5520	5792
		3581	3634	3717	3903	Bbs I (4)	1049	2488	3395	4292
		4478	4531	4614	4800	Bbv I (18)	25	337	340	398
Acc I	(1)	4054					1075	1180	1544	5320
Acc65 I	(1)	2242					5419	7148	7151	7357
Aci I	(116)	315	336	348	370		8051	8289	8374	8418
		393	683	695	704	Bbv II (4)	1048	2487	3394	4291
		716	726	737	783	Bcl I (5)	886	2286	3193	4090
		1083	1165	1232	1416		8655			
		1419	1485	1651	1655	Bcn I (17)	341	342	405	406
		1709	1737	1749	1763		858	859	1458	5176
		1930	2021	2054	2158		5325	5458	5459	5522
		2179	2273	2282	2508		5523	6362	7110	7806
		2532	2607	2635	2647		8153			
		2661	2828	2919	2952	Bfa I (23)	17	28	318	513
		3056	3077	3152	3154		836	1073	1605	2308
		3180	3189	3415	3439		2552	3170	3215	3459
		3514	3542	3554	3568		4112	4356	4951	5075
		3735	3826	3859	3963		5543	5902	5913	7224
		3984	4077	4086	4312		7477	7812	9138	
		4336	4411	4439	4451	Bgl I (15)	504	1741	1863	1934
		4465	4632	4723	4756		2639	2761	2832	3546
		4860	4881	5468	5491		3668	3739	4443	4565
		5513	5525	5546	5730		4636	7742	9089	
		5763	5797	6005	6018	Blp I (2)	1359	8766		
		6167	6274	6279	6327	Bpm I (4)	1463	1520	7692	8709
		6364	6419	6522	6578	Bsa I (2)	5170	7683		
		6588	6612	6655	6662	BsaA I (10)	895	1393	1991	2889
		6683	6774	6802	6929		3796	4693	4958	5639
		6948	7069	7179	7314		5697	9214		
		7323	7685	7776	7967	BsaB I (1)	1262			
		8013	8280	8300	8468	BsaH I (18)	1461	1773	1826	1909
		8565	8577	8644	8707		2095	2671	2724	2807
		8903	8906	8984	9031		2993	3578	3631	3714
Afe I	(1)	3168					3900	4475	4528	4611
Afl III	(4)	894	1390	4065	6729		4797	8511		
Aha II	(18)	1461	1773	1826	1909	BsaJ I (44)	289	290	339	340
		2095	2671	2724	2807		403	476	502	547
		2993	3578	3631	3714		619	742	777	835
		3900	4475	4528	4611		856	962	1267	1374
		4797	8511				2011	2356	2909	3152
Ahd I	(1)	7622					3263	3816	4160	4713
Alu I	(31)	16	799	853	863		5174	5322	5383	5456
		1066	1171	1535	2217		5519	5520	5569	5570
		3115	3148	4022	4919		6037	6148	6468	6889
		5156	5790	5916	5959		8142	8165	8348	8379
		6394	6489	6553	6671	BsaW I (9)	352	2239	5507	6175
		6897	6987	7033	7290		6187	6935	7082	7913
		7811	7911	7974	8221		8923			
		8651	8765	9137		BseR I (2)	831	1391		
Alw I	(25)	434	888	1278	1469	Bsg I (2)	1151	6279		
		1496	2232	2250	2261	BsiE I (9)	1083	1199	1655	3180

		5734	6645	7069	7992			9108	9183		
		8838						382	1463	5477	6228
BsiHKA I	(3)	5792	7047	8736		Cfr10 I	(8)	6252	7702	9053	9106
BsiW I	(1)	51				Cla I	(1)	3141			
Bsm I	(3)	1600	5070	5874		Csp6 I	(34)	52	1869	1894	1949
BsmA I	(7)	982	2084	2982	3889			1982	2033	2190	2243
		4786	5169	7684				2249	2767	2792	2847
BsmF I	(26)	281	291	410	529			2880	2931	3088	3674
		601	665	1136	1472			3699	3754	3787	3838
		1826	1977	2145	2724			3995	4060	4571	4596
		2875	3043	3631	3782			4651	4684	4735	4892
		3950	4528	4679	4847			4959	8103	8336	8549
		5192	5275	5449	5568			8557	9040		
		5578	9013			Dde I	(13)	795	1359	2418	2527
BsoF I	(60)	14	326	329	336			3325	3434	4222	4331
		387	454	783	1064			5804	7004	7413	7579
		1083	1157	1160	1163			8766			
		1166	1169	1333	1419	Dpn I	(42)	429	883	888	1198
		1533	1652	1655	2273			1259	1273	1475	1491
		3180	4077	5309	5408			2238	2256	2288	2547
		5475	5526	5533	5536			3136	3174	3195	3454
		5798	5917	6019	6050			4043	4092	4351	4940
		6053	6168	6280	6327			4977	5434	5927	7297
		6554	6635	6653	6656			7372	7383	7391	7469
		6774	6929	7072	7137			7481	7586	7927	7945
		7140	7346	7674	8013			7991	8474	8657	8837
		8040	8135	8278	8363			8847	8922	8940	9168
		8407	8423	8578	8645			9189	9227		
		8795	8904	8984	9081	DpnII	(42)	427	881	886	1196
Bsp120 I	(1)	5350						1257	1271	1473	1489
BspH I	(1)	7449						2236	2254	2286	2545
BspM I	(1)	8804						3134	3172	3193	3452
BspM II	(2)	6175	6187					4041	4090	4349	4938
Bsr I	(25)	721	1097	1121	1947			4975	5432	5925	7295
		2247	2255	2845	3752			7370	7381	7389	7467
		4649	5227	5337	6158			7479	7584	7925	7943
		6530	7136	7149	7263			7989	8472	8655	8835
		7669	7787	7830	8097			8845	8920	8938	9166
		8192	8257	8995	9091			9187	9225		
		9113				Dra I	(4)	4971	5204	7488	7507
BsrB I	(4)	350	5513	6421	6662	Dra III	(4)	1369	8166	8594	9214
BsrD I	(4)	7683	7857	8806	9099	Drd I	(3)	1051	5808	6837	
BsrG I	(1)	4059				Dsa I	(11)	502	742	962	2011
BssH II	(3)	2261	6368	9181				2909	3152	3816	4713
BssS I	(2)	1138	6902					8165	8379	8750	
BstE II	(1)	8617				Eae I	(12)	505	965	1080	1371
BstN I	(32)	291	477	549	604			1652	2270	3177	4074
		621	1268	1741	1934			6106	6568	8010	8544
		2358	2543	2639	2832	Eag I	(3)	1080	1652	3177	
		3265	3450	3546	3739	Ear I	(1)	6613			
		4162	4347	4443	4636	Eco47 III	(1)	3168			
		5255	5313	5385	5571	Eco57 I	(3)	1060	7276	8602	
		6149	6316	6469	6757	Eco72 I	(2)	895	1393		
		6878	6891	8111	8688	EcoN I	(1)	5345			
BstU I	(26)	1195	1485	1711	2263	EcoO109 I	(2)	1123	5350		
		2609	3154	3516	4067	EcoR I	(1)	4047			
		4413	5730	5836	6007	EcoR II	(32)	289	475	547	602
		6167	6370	6576	6578			619	1266	1739	1932
		6776	7357	7687	8371			2356	2541	2637	2830
		8644	8709	8772	9065			3263	3448	3544	3737
		9181	9183					4160	4345	4441	4634
BstX I	(1)	5361						5253	5311	5383	5569
BstY I	(16)	881	1489	2236	2254			6147	6314	6467	6755
		2545	3134	3172	3452			6876	6889	8109	8686
		4041	4349	4938	7370	EcoR V	(1)	5601			
		7381	7467	7479	8938	Esp I	(2)	1359	8766		
Cac8 I	(54)	333	384	391	467	Fnu4H I	(60)	14	326	329	336
		562	581	634	653			387	454	783	1064
		1059	1173	1465	1737			1083	1157	1160	1163
		1930	2263	2316	2493			1166	1169	1333	1419
		2497	2635	2828	3223			1533	1652	1655	2273
		3400	3404	3542	3735			3180	4077	5309	5408
		4120	4297	4301	4439			5475	5526	5533	5536
		4632	5396	5472	5479			5798	5917	6019	6050
		5530	5777	5874	5961			6053	6168	6280	6327
		6115	6366	6370	6522			6554	6635	6653	6656
		6551	6660	6746	6783			6774	6929	7072	7137
		7343	7734	8367	8544			7140	7346	7674	8013
		8649	8829	8998	9104			8040	8135	8278	8363

		8407	8423	8578	8645	Hph I	(14)	959	2026	2924	3831
		8795	8904	8984	9081			4728	6137	7466	7693
Fok I	(22)	307	359	686	1015			8107	8165	8481	8628
		1250	1483	2517	3424			8714	9221		
		4321	5173	5500	5552	Kpn I	(1)	2246			
		6054	6203	6335	7588	Mae I	(23)	17	28	318	513
		7769	8056	8188	8341			836	1073	1605	2308
		8585	9086					2552	3170	3215	3459
Fsp I	(1)	7844						4112	4356	4951	5075
Gdi II	(13)	506	1079	1081	1370			5543	5902	5913	7224
		1651	1653	2269	3176			7477	7812	9138	
		3178	4073	6569	8009	Mae II	(42)	50	54	304	894
		8543						1392	1773	1785	1826
Gsu I	(4)	1464	1519	7693	8708			1909	1990	2095	2671
Hae I	(9)	498	834	967	6108			2683	2724	2807	2888
		6144	6744	6755	7207			2993	3578	3590	3631
		9176						3714	3795	3900	4475
Hae II	(10)	364	3170	5503	5966			4487	4528	4611	4692
		6285	6607	6977	8524			4797	4957	5557	5638
		8954	9103					5696	6061	6078	6295
Hae III	(35)	498	507	776	782			7432	7848	8537	9023
		834	967	1082	1373			9213	9282		
		1654	1735	1928	2272	Mae III	(35)	46	248	1544	1712
		2633	2826	3179	3540			1799	2148	2610	2697
		3733	4076	4437	4630			3046	3517	3604	3953
		5352	6108	6144	6570			4414	4501	4850	5014
		6744	6755	6773	7207			5692	5752	6355	7085
		7665	7745	8012	8546			7148	7264	7547	7878
		8580	9110	9176				7936	8089	8154	8285
Hga I	(13)	89	1042	1468	2176			8372	8416	8611	8617
		3074	3981	4878	5703			8719	9049	9287	
		5866	6839	7417	8165	Mbo I	(42)	427	881	886	1196
		8501						1257	1271	1473	1489
HgiA I	(3)	5792	7047	8736				2236	2254	2286	2545
HgiE II	(4)	2353	3260	4157	7308			3134	3172	3193	3452
Hha I	(37)	363	1063	1485	2263			4041	4090	4349	4938
		2265	3169	5502	5838			4975	5432	5925	7295
		5965	6208	6284	6370			7370	7381	7389	7467
		6372	6513	6578	6606			7479	7584	7925	7943
		6639	6909	6976	7076			7989	8472	8655	8835
		7250	7359	7752	7845			8845	8920	8938	9166
		8244	8294	8371	8523			9187	9225		
		8711	8772	8799	8953	Mbo II	(16)	231	996	1053	1081
		9047	9067	9102	9183			1499	2492	3399	4296
		9185						5996	6601	7390	7463
HinC II	(3)	900	4055	5251				8813	9172	9175	9208
Hind II	(3)	900	4055	5251		Mlu I	(1)	4065			
HinD III	(1)	3146				Mme I	(3)	6943	7127	9175	
Hinf I	(21)	988	1320	1409	1446	Mnl I	(62)	103	258	318	446
		2061	2959	3866	4763			508	766	772	795
		4947	5125	5337	5723			801	809	812	824
		5831	6092	6564	6629			944	1005	1346	1347
		6704	7100	7617	8488			1369	1486	2192	2302
		8701						2344	2390	2465	2522
HinI I	(18)	1461	1773	1826	1909			3090	3209	3251	3297
		2095	2671	2724	2807			3372	3429	3997	4106
		2993	3578	3631	3714			4148	4194	4269	4326
		3900	4475	4528	4611			4894	5284	5417	5545
		4797	8511					5789	5975	6002	6032
HinP I	(37)	361	1061	1483	2261			6296	6578	6627	6837
		2263	3167	5500	5836			6910	7161	7561	7642
		5963	6206	6282	6368			7788	7994	8133	8357
		6370	6511	6576	6604			8454	8494	8902	8941
		6637	6907	6974	7074			9186	9261		
		7248	7357	7750	7843	Msc I	(2)	967	6108		
		8242	8292	8369	8521	Mse I	(28)	22	57	122	138
		8709	8770	8797	8951			212	906	3158	3162
		9045	9065	9100	9181			4970	5196	5203	5680
		9183						5687	5908	6121	6265
Hpa II	(37)	340	353	358	383			6500	6559	7435	7487
		404	857	1456	1464			7492	7506	7559	7794
		2240	2258	3176	5174			7833	8450	8966	9279
		5324	5457	5478	5503	Msl I	(8)	2016	2914	3821	4718
		5508	5521	6176	6188			5359	7874	8033	8729
		6229	6239	6253	6361	Msp I	(37)	340	353	358	383
		6447	6936	7083	7109			404	857	1456	1464
		7299	7703	7737	7804			2240	2258	3176	5174
		7914	8151	8924	9054			5324	5457	5478	5503
		9107						5508	5521	6176	6188

		6229	6239	6253	6361	Sau3A I	(42)	427	881	886	1196
		6447	6936	7083	7109			1257	1271	1473	1489
		7299	7703	7737	7804			2236	2254	2286	2545
		7914	8151	8924	9054			3134	3172	3193	3452
		9107						4041	4090	4349	4938
MspA1 I	(11)	1171	2284	3154	3191			4975	5432	5925	7295
		4088	6274	6553	7071			7370	7381	7389	7467
		7316	8280	8903				7479	7584	7925	7943
Nae I	(4)	384	1465	5479	9108			7989	8472	8655	8835
Nci I	(17)	340	341	404	405			8845	8920	8938	9166
		857	858	1457	5175			9187	9225		
		5324	5457	5458	5521	Sau96 I	(20)	355	1123	1734	1927
		5522	6361	7109	7805			2632	2825	3539	3732
		8152						4436	4629	5350	5351
Nco I	(6)	742	962	2011	2909			5505	7664	7743	7760
		3816	4713					7982	8256	8897	9109
Nde I	(5)	1885	2783	3690	4587	Sca I	(1)	2250			
		4963				ScrF I	(49)	291	340	341	404
NgoM I	(4)	382	1463	5477	9106			405	477	549	604
Nla III	(36)	71	88	583	655			621	857	858	1268
		746	966	1498	1646			1457	1741	1934	2358
		1955	2015	2499	2853			2543	2639	2832	3265
		2913	3406	3760	3820			3450	3546	3739	4162
		4303	4657	4717	5116			4347	4443	4636	5175
		5653	5713	5876	6025			5255	5313	5324	5385
		6089	6113	6343	6387			5457	5458	5521	5522
		6733	7453	7944	7954			5571	6149	6316	6361
		8032	8068	8311	9267			6469	6757	6878	6891
Nla IV	(25)	346	553	625	1124			7109	7805	8111	8152
		1240	2118	2244	2256			8688			
		2366	3016	3273	3923	Sec I	(44)	289	290	339	340
		4170	4820	5352	5517			403	476	502	547
		6475	6761	6800	7572			619	742	777	835
		7666	7707	7918	8563			856	962	1267	1374
		8928						2011	2356	2909	3152
Not I	(1)	1652						3263	3816	4160	4713
Nru I	(1)	1195						5174	5322	5383	5456
Nsi I	(3)	585	657	5874				5519	5520	5569	5570
Nsp7524 I	(8)	84	579	651	2495			6037	6148	6468	6889
		3402	4299	5872	6729			8142	8165	8348	8379
NspB II	(11)	1171	2284	3154	3191			8686	8750	8889	9231
		4088	6274	6553	7071	SfaN I	(28)	380	591	663	1036
		7316	8280	8903				1093	1225	1271	1571
NspH I	(8)	88	583	655	2499			2009	2414	2496	2907
		3406	4303	5876	6733			3321	3403	3814	4218
Pac I	(1)	3162						4300	4711	5041	5479
PaeR7 I	(1)	9253						5927	5982	6216	6314
Pal I	(35)	498	507	776	782			6825	7877	8070	8362
		834	967	1082	1373	Sfc I	(8)	2	467	1047	5392
		1654	1735	1928	2272			6994	7185	7863	8712
		2633	2826	3179	3540	Sfi I	(1)	504			
		3733	4076	4437	4630	Sma I	(5)	341	405	858	5458
		5352	6108	6144	6570			5522			
		6744	6755	6773	7207	SnaB I	(5)	1991	2889	3796	4693
		7665	7745	8012	8546			4958			
		8580	9110	9176		Spe I	(1)	512			
Ple I	(1)	7108				Sph I	(6)	583	655	2499	3406
Pml I	(2)	895	1393					4303	5876		
PpuM I	(1)	1123				Spl I	(1)	51			
Psp1406 I	(1)	7848				Srf I	(2)	405	5458		
PspA I	(5)	339	403	856	5456	Ssp I	(2)	5200	5860		
		5520				Stu I	(2)	498	834		
Pst I	(3)	6	471	5396		Sty I	(10)	742	835	962	2011
Pvu I	(3)	1199	7992	8838				2909	3816	4713	8142
Pvu II	(2)	1171	6553					8889	9231		
Rsa I	(34)	53	1870	1895	1950	Swa I	(1)	4971			
		1983	2034	2191	2244	Taq I	(18)	108	1256	1407	2295
		2250	2768	2793	2848			3141	3202	4054	4099
		2881	2932	3089	3675			4945	6829	8126	8386
		3700	3755	3788	3839			8486	8517	8529	8823
		3996	4061	4572	4597			8838	9254		
		4652	4685	4736	4893	Tfi I	(11)	988	1320	1409	1446
		4960	8104	8337	8550			4947	5337	5831	6092
		8558	9041					6564	6704	8701	
Rsr II	(2)	355	5505			Tsp45 I	(8)	46	5692	5752	7878
Sac I	(1)	5792						8089	8154	8617	8719
Sac II	(1)	3155				Tth111 II	(11)	198	2318	3225	4061
Sal I	(1)	4053						4122	5787	7318	7327
Sap I	(1)	6613						7357	8374	8381	

Vsp I	(6)	122	906	6265	6500
		6559	7794		
Xba I	(1)	4950			
Xho I	(1)	9253			
Xho II	(16)	881	1489	2236	2254
		2545	3134	3172	3452
		4041	4349	4938	7370
		7381	7467	7479	8938
Xma I	(5)	339	403	856	5456
		5520			
Xma III	(3)	1080	1652	3177	

Site usage in PBC5:

Aat II	G,ACGT`C	16	Acc I	GT`MK,AC	1
Acc65 I	G`GTAC,C	1	Aci I	C`CG,C	116
Afe I	AGC GCT	1	Afl I II	C`TTAA,G	-
Afl III	A`CRYG,T	4	Age I	A`CCGG,T	-
Aha II	GR`CG,YC	18	Ahd I	GACNN,N`NNGTC	1
Alu I	AG CT	31	Alw I	GGATC 8/9	25
AlwN I	CAG,NNN`CTG	4	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	9
Ava II	G`GWC,C	7	Avr II	C`CTAG,G	1
BamH I	G`GATC,C	1	Ban I	G`GYRC,C	11
Ban II	G,RGCY`C	8	Bbe I	G,CGGC`C	-
Bbs I	GAAGAC 8/12	4	Bbv I	GCAGC 13/17	18
Bbv II	GAAGAC 7/11	4	Bcl I	T`GATC,A	5
Bcn I	CC,S`GG	17	Bfa I	C`TA,G	23
Bgl I	GCCN,NNN`NGGC	15	Bgl II	A`GATC,T	-
Blp I	GC`TNA,GC	2	Bpm I	CTGGAG 22/20	4
Bsa I	GGTCTC 7/11	2	BsaA I	YAC GTR	10
BsaB I	GATNN NNATC	1	BsaH I	GR`CG,YC	18
BsaJ I	C`CNNG,G	44	BsaW I	W`CCGG,W	9
BseR I	GAGGAG 16/14	2	Bsg I	GTGCA 22/20	2
BsiC I	TT`CG,AA	-	BsiE I	CG,R`Y`CG	9
BsiHKA I	G,WGCW`C	3	BsiW I	C`GTAC,G	1
Bsm I	GAATG,C 7	3	BsmA I	GTCTC`/9	7
BsmB I	CGTCTC 7/11	-	BsmF I	GGGAC 15/19	26
BsoF I	GC`N,GC	60	Bsp120 I	G`GGCC,C	1
Bspl286 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`	25	BsrB I	GAG CGG	4
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	-	BstB I	TT`CG,AA	-
BstE II	G`GTNAC,C	1	BstN I	CC`W,GG	32
BstU I	CG CG	26	BstX I	CCAN,NNNN`NTGG	1
BstY I	R`GATC,Y	16	Bsu36 I	CC`TNA,GG	-
Cac8 I	GCN NGC	54	Cfr10 I	R`CCGG,Y	8
Cla I	AT`CG,AT	1	Csp6 I	G`TA,C	34
Dde I	C`TNA,G	13	Dpn I	GA TC	42
DpnII	`GATC,	42	Dra I	TTT AAA	4

Dra III	CAC,NNN`GTG	4	Drd I	GACNN,NN`NNGTC	3
Dsa I	C`CRYG,G	11	Eae I	Y`GGCC,R	12
Eag I	C`GGCC,G	3	Ear I	CTCTTC 7/10	1
Eco47 III	AGC GCT	1	Eco57 I	CTGAAG 21/19	3
Eco72 I	CAC GTG	2	EcoN I	CCTNN`N,NNAGG	1
EcoO109 I	RG`GNC,CY	2	EcoR I	G`AATT,C	1
EcoR II	`CCWGG,	32	EcoR V	GAT ATC	1
Ehe I	GGC GCC	-	Esp I	GC`TNA,GC	2
Fnu4H I	GC`N,GC	60	Fok I	GGATG 14/18	22
Fse I	GG,CCGG`CC	-	Fsp I	TGC GCA	1
Gdi II	`YGGC,CG	13	Gsu I	CTGGAG 21/19	4
Hae I	WGG CCW	9	Hae II	R,GCGC`Y	10
Hae III	GG CC	35	Hga I	GACGC 9/14	13
HgiA I	G,WGCW`C	3	HgiE II	ACCCNNNNNNGGT -1/134	4
Hha I	G,CG`C	37	Hinc II	GTY RAC	3
Hind II	GTY RAC	3	Hind III	A`AGCT,T	1
Hinf I	G`ANT,C	21	HinI I	GR`CG,YC	18
HinP I	G`CG,C	37	Hpa I	GTT AAC	-
Hpa II	C`CG,G	37	Hph I	GGTGA 12/11	14
Kas I	G`GCGC,C	-	Kpn I	G,GTAC`C	1
Mae I	C`TA,G	23	Mae II	A`CG,T	42
Mae III	GTNAC,	35	Mbo I	`GATC,	42
Mbo II	GAAGA 12/11	16	Mlu I	A`CGCG,T	1
Mme I	TCCRAC 25/23	3	Mnl I	CCTC 10/10	62
Msc I	TGG CCA	2	Mse I	T`TA,A	28
Msl I	CAYNN NNRTG	8	Msp I	C`CG,G	37
MspAl I	CMG CKG	11	Mun I	C`AATT,G	-
Nae I	GCC GGC	4	Nar I	GG`CG,CC	4
Nci I	CC`S,GG	17	Nco I	C`CATG,G	6
Nde I	CA`TA,TG	5	Ngm I	G`CCGG,C	4
Nhe I	G`CTAG,C	-	Nla III	,CATG`	36
Nla IV	GGN NCC	25	Not I	GC`GGCC,GC	1
Nru I	TGC CGA	1	Nsi I	A,TGCA`T	3
Nsp7524 I	R`CATG,Y	8	NspB II	CMG CKG	11
NspH I	R,CATG`Y	8	Pac I	TTA,AT`TAA	1
PaeR7 I	C`TCGA,G	1	Pal I	GG CC	35
PflM I	CCAN,NNN`NTGG	-	Ple I	GAGTC 9/10	1
Pme I	CTTT AAAC	-	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	3	Pvu II	CAG CTG	2
Rsa I	GT AC	34	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,	42	Sau96 I	G`GNC,C	20
Sea I	AGT ACT	1	ScrF I	CC`N,GG	49
Sec I	C`CNNG,G	44	SfaN I	GCATC 9/13	28
Sfc I	C`TRYA,G	8	Sfi I	GGCCN,NNN`NGGCC	1
Sma I	CCC GGG	5	SnaB I	TAC GTA	5
Spe I	A`CTAG,T	1	Sph I	G,CATG`C	6
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	10	Swa I	ATTT AAAT	1
Taq I	T`CG,A	18	Tfi I	G`AWT,C	11
Tsp45 I	`GTSAC,	8	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	CCANNNN,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	3	Xmn I	GAANN NNTTC	-