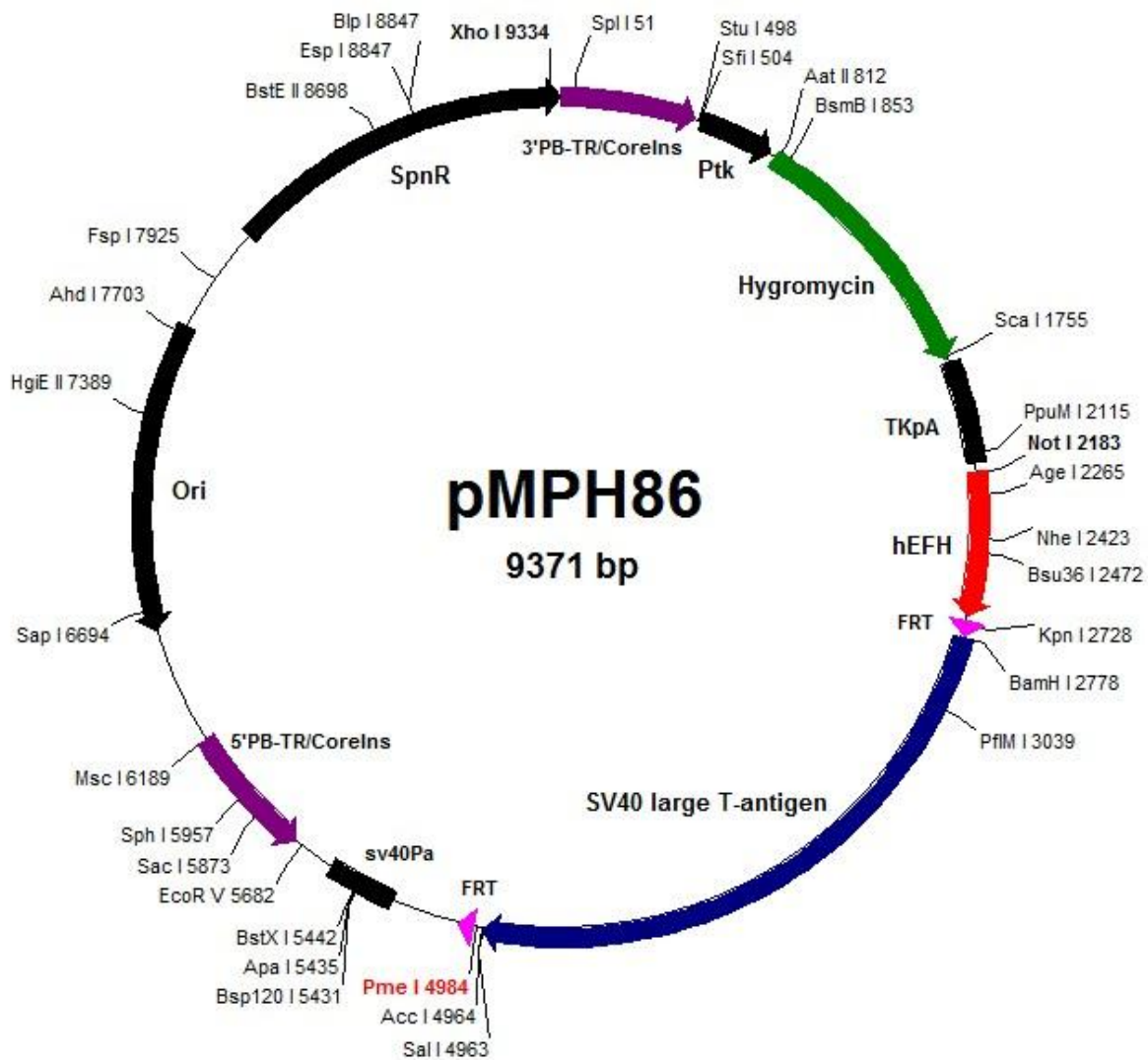


Vector: pMPH 86 (immortalization piggyBac vector-hygromycin resistance)

Antibiotic Selection: Spectinomycin-resistant

Creator(s): Ning Wang, Molecular Oncology Lab of The University of Chicago Medical Center

Date of Construction: May 2012



pMPH86 Vector Sequence (Spectinomycin-resistant)

CTGCAGAACACGCAGCTAGATTAAACCTAGAAAAGATAATCATATTGTGACGTACGTTAAAGATAATCATGCGTAAAATTGACGCATG
TGTTTTATCGGTCTGTATATCGAGGTTTATTTATTAATTTGAATAGATATTAAGTTTTATTATATTTACACTTACATACTAATAATA
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Unique enzymes in pMPH86:

					6659	6669	6693	6736
BsiW I	C`GTAC,G	51			6743	6764	6855	6883
Spl I	C`GTAC,G	51			7010	7029	7150	7260
Stu I	AGG CCT	498			7395	7404	7766	7857
Sfi I	GGCCN,NNN`NGGCC	504			8048	8094	8361	8381
Aat II	G,ACGT`C	812			8549	8646	8658	8725
BsmB I	CGTCTC 7/11	853			8788	8984	8987	9065
Sca I	AGT ACT	1755			9112			
Xcm I	CCANNNN,N`NNNNTGG2096			Afl III (3)	699	4975	6810	
PpuM I	RG`GWC,CY	2115		Age I (1)	2265			
Not I	GC`GGCC,GC	2183		Aha II (4)	809	1777	2716	8592
Age I	A`CCGG,T	2265		Ahd I (1)	7703			
Nhe I	G`CTAG,C	2423		Alu I (42)	16	865	897	939
Bsu36 I	CC`TNA,GG	2472			1324	1549	1614	1643
Kas I	G`GCGC,C	2715			2417	2423	2427	2565
Nar I	GG`CG,CC	2716			2706	2819	3285	3439
Ehe I	GGC GCC	2717			3596	3819	4092	4122
Bbe I	G,GCGC`C	2719			4163	4173	4927	5237
Acc65 I	G`GTAC,C	2724			5871	5997	6040	6475
Asp718	G`GTAC,C	2724			6570	6634	6752	6978
Kpn I	G,GTAC`C	2728			7068	7114	7371	7892
BamH I	G`GATC,C	2778			7992	8055	8302	8732
Pf1M I	CCAN,NNN`NTGG	3039		Alw I (19)	8846	9218		
Asc I	GG`CGCG,CC	4906			434	762	1245	1563
Cla I	AT`CG,AT	4920			1672	2694	2774	2785
Eco47 III	AGC GCT	4947			3493	5509	6013	7372
Bgl II	A`GATC,T	4951			7458	7458	7555	7556
Sal I	G`TCGA,C	4963			8020	8997	9026	
Acc I	GT`MK,AC	4964		AlwN I (3)	2079	3924	7226	
Pme I	CTTT AAAC	4984		Apa I (1)	5435			
Xmn I	GAANN NNTTC	4996		ApaL I (4)	1065	1367	7124	8813
Bsp120 I	G`GGCC,C	5431		Apo I (8)	175	233	635	1028
Apa I	G,GGCC`C	5435			3663	4957	5121	9281
BstX I	CCAN,NNNN`NTGG	5442		Asc I (1)	4906			
EcoR V	GAT ATC	5682		Ase I (7)	122	3406	4255	6346
Sac I	G,AGCT`C	5873			6581	6640	7875	
Sph I	G,CATG`C	5957		Asp718 (1)	2724			
Msc I	TGG CCA	6189		Ava I (11)	339	377	403	770
Sap I	GCTCTTC 8/11	6694			2232	2334	5537	5563
HgiE II	ACCNNNNNNGGT -1/137389				5601	8430	9334	
Ahd I	GACNN,N`NNGTC	7703		Ava II (14)	355	669	676	1193
Fsp I	TGC GCA	7925			1734	1939	2115	2825
BstE II	G`GTNAC,C	8698			4059	5586	7841	8063
Blp I	GC`TNA,GC	8847			8337	8978		
Esp I	GC`TNA,GC	8847		BamH I (1)	2778			
PaeR7 I	C`TCGA,G	9334		Ban I (8)	1359	2193	2268	2524
Xho I	C`TCGA,G	9334			2715	2724	6554	7651
Number of enzymes = 46				Ban II (6)	347	2053	2439	5435

The following enzymes do not cut in pMPH86:

Afl II	Avr II	Bsp1286 I	Bst1107 I	
Eco72 I				
Fse I	Nru I	Pml I	SnaB I	Spe
I				

pMPH86: sites sorted by name:

Aat II	(1)	812						
Acc I	(1)	4964						
Acc65 I	(1)	2724						
Aci I	(93)	315	336	348	370			
		393	555	612	662			
		667	738	762	804			
		928	993	1060	1110			
		1130	1154	1176	1196			
		1373	1411	1421	1534			
		1562	1564	1585	1714			
		1724	1864	1930	1997			
		2070	2182	2186	2287			
		2324	2404	2460	2463			
		2478	2509	2516	2543			
		3827	4931	4933	5549			
		5572	5594	5606	5627			
		5811	5844	5878	6086			
		6099	6248	6355	6360			
		6408	6445	6500	6603			
						Bfa I (24)		
						Bgl I (3)		
						Bgl II (1)		
						Blp I (1)		
						Bpm I (6)		
						Bsa I (4)		
						BsaA I (3)		
						BsaB I (2)		
						BsaH I (4)		

BsaJ I	(51)	289	290	339	340	BstU I	(38)	545	667	701	806
		403	476	502	529			995	1130	1241	1307
		562	672	770	1137			1373	1522	1564	1724
		1338	1493	1562	1793			1866	1930	1999	2287
		1942	1943	2045	2046			2456	2501	4908	4933
		2098	2121	2335	2599			4977	5811	5917	6088
		2782	2851	3187	4141			6248	6451	6657	6659
		4349	4784	4931	5255			6857	7438	7768	8452
		5403	5464	5537	5600			8725	8790	8853	9146
		5601	5650	5651	6118			9262	9264		
		6229	6549	6970	8223	BstX I	(1)	5442			
		8246	8429	8460	8767	BstY I	(10)	766	2698	2778	3497
		8831	8970	9312				4951	7451	7462	7548
BsaW I	(14)	352	1006	1543	1679			7560	9019		
		1852	2190	2265	5588	Bsu36 I	(1)	2472			
		6256	6268	7016	7163	Cac8 I	(49)	333	384	391	467
		7994	9004					543	553	759	1110
BseR I	(2)	2935	3145					1311	1371	1551	1714
Bsg I	(3)	2383	3271	6360				1950	1997	2053	2075
BsiC I	(2)	639	4990					2425	2439	2460	2623
BsiE I	(11)	993	1128	1149	1158			2651	3254	4396	4908
		1728	2186	5815	6726			5477	5553	5560	5611
		7150	8073	8919				5858	5955	6042	6196
BsiHKA I	(5)	1069	1371	5873	7128			6447	6451	6603	6632
		8817						6741	6827	6864	7424
BsiW I	(1)	51						7815	8448	8625	8730
Bsm I	(3)	3074	5151	5955				8910	9079	9185	9189
BsmA I	(6)	852	1839	1968	2569			9264			
		5250	7765			Cfr10 I	(12)	382	1123	2265	2489
BsmB I	(1)	853						2621	2712	5558	6309
BsmF I	(17)	281	291	410	545			6333	7783	9134	9187
		655	1702	1925	2101						
		2122	2214	4766	5273	Cl a I	(1)	4920			
		5356	5530	5649	5659	Csp6 I	(19)	52	1701	1754	2315
		9094						2725	2957	3430	3656
BsoF I	(72)	14	326	329	336			3671	3728	4022	4373
		387	454	663	731			4526	4970	8184	8417
		762	863	940	993	Dde I	(17)	8630	8638	9121	
		1121	1152	1155	1411			1163	2472	2566	2617
		1514	1562	1565	1641			3025	3098	3210	4307
		1725	2056	2071	2183			4540	4668	4751	4804
		2186	2404	2463	2478			5885	7085	7494	7660
		2509	2817	3286	3754			8847			
		4090	4093	5390	5489	Dpn I	(37)	429	768	830	963
		5556	5607	5614	5617			1148	1161	1251	1558
		5879	5998	6100	6131			1678	2700	2780	3499
		6134	6249	6361	6408			3883	4828	4953	5058
		6635	6716	6734	6737			5515	6008	7378	7453
		6855	7010	7153	7218			7464	7472	7550	7562
		7221	7427	7755	8094			7667	8008	8026	8072
		8121	8216	8359	8444			8555	8738	8918	8928
		8488	8504	8659	8726			9003	9021	9249	9270
		8876	8985	9065	9162	DpnII	(37)	9308			
Bsp120 I	(1)	5431						427	766	828	961
BspH I	(2)	4823	7530					1146	1159	1249	1556
BspM I	(2)	1098	8885					1676	2698	2778	3497
BspM II	(5)	1006	1543	1679	6256			3881	4826	4951	5056
		6268						5513	6006	7376	7451
Bsr I	(24)	1270	1435	2095	2300			7462	7470	7548	7560
		2321	4049	4182	4219			7665	8006	8024	8070
		5308	5418	6239	6611			8553	8736	8916	8926
		7217	7230	7344	7750			9001	9019	9247	9268
		7868	7911	8178	8273	Dra I	(14)	9306			
		8338	9076	9172	9194			2561	2797	2887	3691
BsrB I	(7)	350	1176	1534	2188			4009	4055	4126	4441
		5594	6502	6743				4871	4984	5052	5285
BsrD I	(8)	782	3619	4445	4498			7569	7588		
		7764	7938	8887	9180	Dra III	(5)	1073	1366	8247	8675
								9295			
BsrG I	(3)	2956	4021	4969		Drd I	(4)	1289	1670	5889	6918
BssH II	(3)	4906	6449	9262		Dsa I	(12)	502	529	1137	1493
BssS I	(3)	885	1364	6983				1562	2098	2121	2782
BstB I	(2)	639	4990					4931	8246	8460	8831
BstE II	(1)	8698				Eae I	(10)	505	990	1155	1408
BstN I	(24)	291	477	674	1944			1725	2183	6187	6649
		2047	2852	3529	3590			8091	8625		
		4263	4351	4452	4701	Eag I	(4)	990	1155	1725	2183
		5336	5394	5466	5652	Ear I	(2)	3162	6694		
		6230	6397	6550	6838	Eco47 III	(1)	4947			
		6959	6972	8192	8769	Eco57 I	(5)	2438	3185	4226	7357

		8683						8604	8792	8853	8880
EcoN I	(5)	2276	2471	2914	4145			9034	9128	9148	9183
		5426						9264	9266		
EcoO109 I	(4)	2076	2115	4799	5431	HinC II	(6)	752	1621	3865	4915
EcoR I	(3)	635	1028	4957				4965	5332		
EcoR II	(24)	289	475	672	1942	Hind II	(6)	752	1621	3865	4915
		2045	2850	3527	3588			4965	5332		
		4261	4349	4450	4699	HinD III	(3)	3594	4120	4925	
		5334	5392	5464	5650	Hinf I	(26)	881	1003	1203	1454
		6228	6395	6548	6836			2496	2615	2808	3029
		6957	6970	8190	8767			3138	3221	3987	4224
EcoR V	(1)	5682						4749	4773	5206	5418
Ehe I	(1)	2717						5804	5912	6173	6645
Esp I	(1)	8847						6710	6785	7181	7698
Fnu4H I	(72)	14	326	329	336			8569	8782		
		387	454	663	731	HinI I	(4)	809	1777	2716	8592
		762	863	940	993	HinP I	(50)	361	665	942	995
		1121	1152	1155	1411			1239	1307	1522	1649
		1514	1562	1565	1641			1722	1866	2213	2285
		1725	2056	2071	2183			2456	2593	2688	2716
		2186	2404	2463	2478			4906	4908	4946	5581
		2509	2817	3286	3754			5917	6044	6287	6363
		4090	4093	5390	5489			6449	6451	6592	6657
		5556	5607	5614	5617			6685	6718	6988	7055
		5879	5998	6100	6131			7155	7329	7438	7831
		6134	6249	6361	6408			7924	8323	8373	8450
		6635	6716	6734	6737			8602	8790	8851	8878
		6855	7010	7153	7218			9032	9126	9146	9181
		7221	7427	7755	8094			9262	9264		
		8121	8216	8359	8444	Hpa I	(2)	3865	4915		
		8488	8504	8659	8726	Hpa II	(48)	340	353	358	383
		8876	8985	9065	9162			404	564	771	1007
Fok I	(26)	307	359	510	1154			1124	1357	1544	1570
		1527	2468	2893	3030			1680	1686	1853	2191
		3665	3908	3956	4215			2266	2490	2578	2590
		4299	5254	5581	5633			2622	2713	5255	5405
		6135	6284	6416	7669			5538	5559	5584	5589
		7850	8137	8269	8422			5602	6257	6269	6310
		8666	9167					6320	6334	6442	6528
Fsp I	(1)	7925						7017	7164	7190	7380
Gdi II	(13)	506	989	991	1154			7784	7818	7885	7995
		1156	1407	1724	1726			8232	9005	9135	9188
		2182	2184	6650	8090	Hph I	(13)	706	794	2048	4353
		8624						6218	7547	7774	8188
Gsu I	(6)	1452	1506	3969	4236			8246	8562	8709	8795
		7774	8789					9302			
Hae I	(10)	498	708	1136	4398	Kas I	(1)	2715			
		6189	6225	6825	6836	Kpn I	(1)	2728			
		7288	9257			Mae I	(24)	17	28	318	513
Hae II	(12)	364	2596	2719	4949			2273	2424	2550	2612
		5584	6047	6366	6688			2758	2832	3115	3493
		7058	8605	9035	9184			3850	4164	4949	5023
Hae III	(37)	498	507	534	708			5156	5624	5983	5994
		992	1136	1157	1185			7305	7558	7893	9219
		1337	1410	1492	1727	Mae II	(20)	50	54	304	809
		1987	2044	2077	2095			1079	2062	2380	2663
		2185	2477	2582	4398			5638	5719	5777	6142
		4427	4800	5433	6189			6159	6376	7513	7929
		6225	6651	6825	6836			8618	9104	9294	9363
		6854	7288	7746	7826	Mae III	(29)	46	248	695	1075
		8093	8627	8661	9191			2692	2708	3323	3599
		9257						4358	5095	5773	5833
Hga I	(16)	89	609	706	738			6436	7166	7229	7345
		836	1288	1527	1672			7628	7959	8017	8170
		1784	2529	5784	5947			8235	8366	8453	8497
		6920	7498	8246	8582			8692	8698	8800	9130
HgiA I	(5)	1069	1371	5873	7128			9368			
		8817				Mbo I	(37)	427	766	828	961
HgiE II	(1)	7389						1146	1159	1249	1556
Hha I	(50)	363	667	944	997			1676	2698	2778	3497
		1241	1309	1524	1651			3881	4826	4951	5056
		1724	1868	2215	2287			5513	6006	7376	7451
		2458	2595	2690	2718			7462	7470	7548	7560
		4908	4910	4948	5583			7665	8006	8024	8070
		5919	6046	6289	6365			8553	8736	8916	8926
		6451	6453	6594	6659			9001	9019	9247	9268
		6687	6720	6990	7057			9306			
		7157	7331	7440	7833	Mbo II	(27)	231	578	889	1472
		7926	8325	8375	8452			1475	1997	2939	2950

		2981	3113	3178	3191		1568	1684	1861	1941	
		3572	3947	4703	4733		1986	2096	2116	2117	
		4747	4757	5003	6077		2195	2270	2322	2526	
		6682	7471	7544	8894		2605	2717	2726	2780	
		9253	9256	9289			4801	5433	5598	6556	
Mlu I	(2)	699	4975				6842	6881	7653	7747	
Mme I	(6)	875	1409	3056	7024		7788	7999	8644	9009	
		7208	9256			Not I	(1)	2183			
Mnl I	(65)	103	258	318	446	Nsi I	(2)	4017	5955		
		508	718	865	902	Nsp7524 I	(4)	84	581	5953	6810
		1126	1333	1372	1432	NspB II	(12)	1112	1421	1564	2417
		1459	1482	1530	1788		4092	4933	6355	6634	
		1815	2241	2330	2425		7152	7397	8361	8984	
		2467	2521	2537	2798	NspH I	(4)	88	585	5957	6814
		2874	2913	3000	3074	PaeR7 I	(1)	9334			
		3119	3165	3509	3563	Pal I	(37)	498	507	534	708
		4193	4212	4812	4819		992	1136	1157	1185	
		4848	4887	4896	4896		1337	1410	1492	1727	
		5365	5498	5626	5870		1987	2044	2077	2095	
		6056	6083	6113	6377		2185	2477	2582	4398	
		6659	6708	6918	6991		4427	4800	5433	6189	
		7242	7642	7723	7869		6225	6651	6825	6836	
		8075	8214	8438	8535		6854	7288	7746	7826	
		8575	8983	9022	9267		8093	8627	8661	9191	
		9342					9257				
Msc I	(1)	6189				PflM I	(1)	3039			
Mse I	(56)	22	57	122	138	Ple I	(4)	2504	3229	4232	7189
		212	691	742	2560	Pme I	(1)	4984			
		2796	2886	3076	3406	PpuM I	(1)	2115			
		3444	3460	3537	3553	Psp1406 I	(2)	2380	7929		
		3690	3700	3846	3864	PspA I	(5)	339	403	770	5537
		3877	4008	4054	4125		5601				
		4132	4255	4272	4297	Pst I	(6)	6	471	732	1122
		4440	4518	4633	4870		4396	5477			
		4914	4937	4941	4983	Pvu I	(3)	1149	8073	8919	
		5051	5277	5284	5761	Pvu II	(3)	2417	4092	6634	
		5768	5989	6202	6346	Rsa I	(19)	53	1702	1755	2316
		6581	6640	7516	7568		2726	2958	3431	3657	
		7573	7587	7640	7875		3672	3729	4023	4374	
		7914	8531	9047	9360		4527	4971	8185	8418	
Msl I	(5)	528	5440	7955	8114		8631	8639	9122		
		8810				Rsr II	(3)	355	1193	5586	
Msp I	(48)	340	353	358	383	Sac I	(1)	5873			
		404	564	771	1007	Sac II	(2)	1565	4934		
		1124	1357	1544	1570	Sal I	(1)	4963			
		1680	1686	1853	2191	Sap I	(1)	6694			
		2266	2490	2578	2590	Sau3A I	(37)	427	766	828	961
		2622	2713	5255	5405		1146	1159	1249	1556	
		5538	5559	5584	5589		1676	2698	2778	3497	
		5602	6257	6269	6310		3881	4826	4951	5056	
		6320	6334	6442	6528		5513	6006	7376	7451	
		7017	7164	7190	7380		7462	7470	7548	7560	
		7784	7818	7885	7995		7665	8006	8024	8070	
		8232	9005	9135	9188		8553	8736	8916	8926	
MspAl I	(12)	1112	1421	1564	2417		9001	9019	9247	9268	
		4092	4933	6355	6634		9306				
		7152	7397	8361	8984	Sau96 I	(29)	355	533	669	676
Mun I	(2)	2258	4063				1184	1193	1335	1734	
Nae I	(4)	384	2623	5560	9189		1939	1985	2043	2076	
Nar I	(1)	2716					2094	2115	2580	2825	
Nci I	(20)	340	341	404	405		4059	4426	4799	5431	
		564	771	772	1571		5432	5586	7745	7824	
		1687	2579	5256	5405		7841	8063	8337	8978	
		5538	5539	5602	5603		9190				
		6442	7190	7886	8233	Sca I	(1)	1755			
Nco I	(3)	1137	2121	2782		ScrF I	(44)	291	340	341	404
Nde I	(3)	1235	3789	5044			405	477	564	674	
NgoM I	(4)	382	2621	5558	9187		771	772	1571	1687	
Nhe I	(1)	2423					1944	2047	2579	2852	
Nla III	(33)	71	88	585	1141		3529	3590	4263	4351	
		1224	1259	2125	2786		4452	4701	5256	5336	
		3228	3549	3735	4019		5394	5405	5466	5538	
		4367	4745	4761	4827		5539	5602	5603	5652	
		5197	5734	5794	5957		6230	6397	6442	6550	
		6106	6170	6194	6424		6838	6959	6972	7190	
		6468	6814	7534	8025		7886	8192	8233	8769	
		8035	8113	8149	8392	Sec I	(51)	289	290	339	340
		9348					403	476	502	529	
Nla IV	(32)	346	671	1361	1384		562	672	770	1137	

		1338	1493	1562	1793	Bpm I	CTGGAG 22/20	6	Bsa I	GGTCTC 7/11	4
		1942	1943	2045	2046	BsaA I	YAC GTR	3	BsaB I	GATNN NNATC	2
		2098	2121	2335	2599	BsaH I	GR`CG,YC	4	BsaJ I	C`CNNG,G	51
		2782	2851	3187	4141	BsaW I	W`CCGG,W	14	BseI I	GAGGAG 16/14	2
		4349	4784	4931	5255	Bsg I	GTGCAG 22/20	3	BsiC I	TT`CG,AA	2
		5403	5464	5537	5600	BsiE I	CG,RY`CG	11	BsiHKA I	G,WGWC`C	5
		5601	5650	5651	6118	BsiW I	C`GTAC,G	1	Bsm I	GAATG,C 7	3
		6229	6549	6970	8223	BsmA I	GTCTC`/9	6	BsmB I	CGTCTC 7/11	1
		8246	8429	8460	8767	BsmF I	GGGAC 15/19	17	BsoF I	GC`N,GC	72
		8831	8970	9312		Bsp120 I	G`GGCC,C	1	Bsp1286 I	G,DGHC`C	-
						BspH I	T`CATG,A	2	BspM I	ACCTGC 10/14	2
						BspM II	T`CCGG,A	5	Bsr I	ACT,GG`	24
						BsrB I	GAG CGG	7	BsrD I	GCAATG, 8	8
SfaN I	(22)	380	641	850	994	BsrG I	T`GTAC,A	3	Bssh II	G`CGCG,C	3
		1061	1133	1318	1548	BssS I	C`TCGT,G	3	Bst1107 I	GTA TAC	-
		1628	1650	2449	3009	BstB I	TT`CG,AA	2	BstE II	G`GTNAC,C	1
		5122	5560	6008	6063	BstN I	CC`W,GG	24	BstU I	CG CG	38
		6297	6395	6906	7958	BstX I	CCAN,NNNN`NTGG	1	BstY I	R`GATC,Y	10
		8151	8443			Bsu36 I	CC`TNA,GG	1	Cac8 I	GCN NGC	49
						Cfr10 I	R`CCGG,Y	12	Cla I	AT`CG,AT	1
Sfc I	(11)	2	467	728	1118	Csp6 I	G`TA,C	19	Dde I	C`TNA,G	17
		3916	4392	5473	7075	Dpn I	GA TC	37	DpnII	`GATC,	37
		7266	7944	8793		Dra I	TTT AAA	14	Dra III	CAC,NNN`GTG	5
Sfi I	(1)	504				Drd I	GACNN,NN`NNGTC	4	Dsa I	C`CRYG,G	12
Sma I	(5)	341	405	772	5539	Eae I	Y`GGCC,R	10	Eag I	C`GGCC,G	4
		5603				Ear I	CTCTCT 7/10	2	Eco47 III	AGC GCT	1
Sph I	(1)	5957				Eco57 I	CTGAAG 21/19	5	Eco72 I	CAC GTG	-
Spl I	(1)	51				EcoN I	CCNN`N,NNAGG	5	EcoO109 I	RG`GNC,CY	4
Srf I	(2)	405	5539			EcoR I	G`AATT,C	3	EcoR II	`CCWGG,	24
Ssp I	(6)	2861	3318	3471	4342	EcoR V	GAT ATC	1	Ehe I	GGC GCC	1
		5281	5941			Esp I	GC`TNA,GC	1	Fnu4H I	GC`N,GC	72
Stu I	(1)	498				Fok I	GGATG 14/18	26	Fse I	GG,CCGG`CC	-
Sty I	(10)	1137	2121	2599	2782	Fsp I	TGC GCA	1	Gdi II	`YGGC,CG	13
		3187	4141	4784	8223	Gsu I	CTGCAG 21/19	6	Hae I	WGC CCW	10
Taq I	(26)	108	639	711	816	Hae II	R,GCGC`Y	12	Hae III	GG CC	37
		831	840	900	1317	Hga I	GACGC 9/14	16	HgiA I	G,WGWC`C	5
		1530	1632	1657	1960	HgiE II	ACCNNNNNNGGT -1/131		Hha I	G,CG`C	50
		2430	2572	4920	4964	Hinc II	GTY RAC	6	Hind II	GTY RAC	6
		4990	6910	8207	8467	Hind III	A`AGCT,T	3	Hinf I	G`ANT,C	26
		8567	8598	8610	8904	HinI I	GR`CG,YC	4	HinP I	G`CG,C	50
		8919	9335			Hpa I	GT AAC	2	Hpa II	C`CG,G	48
Tfi I	(14)	881	1003	1203	1454	Hph I	GGTGA 12/11	13	Kas I	G`GCGC,C	1
		2808	3029	3987	4773	Kpn I	G,GTAC`C	1	Mae I	C`TA,G	24
		5418	5912	6173	6645	Mae II	A`CG,T	20	Mae III	`GTNAC,	29
		6785	8782			Mbo I	`GATC,	37	Mbo II	GAAGA 12/11	27
Tsp45 I	(12)	46	695	1075	2708	Mlu I	A`CGCG,T	2	Mme I	TCCRAC 25/23	6
		4358	5773	5833	7959	Mnl I	CCTC 10/10	65	Msc I	TGG CCA	1
		8170	8235	8698	8800	Mse I	T`TA,A	56	Msl I	CAYNN NNRTG	5
Tth111 I	(3)	845	1289	2113	3242	Msp I	C`CG,G	48	MspAl I	CMG CKG	12
Tth111 II	(16)	198	1005	2639	3947	Mun I	C`AATT,G	2	Nae I	GCC GGC	4
		3637	3883	3898	3947	Nar I	GG`CG,CC	1	Nci I	CC`S,GG	20
		3960	4090	5868	7399	Nco I	C`CATG,G	3	Nde I	CA`TA,TG	3
Vsp I	(7)	7408	7438	8455	8462	NgoM I	G`CCGG,C	4	Nhe I	G`CTAG,C	1
		6581	6640	7875	6346	Nla III	,CATG`	33	Nla IV	GGN NCC	32
Xba I	(2)	2757	5022			Not I	GC`GGCC,GC	1	Nru I	TCG CGA	-
Xcm I	(1)	2096				Nsi I	A,TGCA`T	2	Nsp7524 I	R`CATG,Y	4
Xho I	(1)	9334				NspB II	CMG CKG	12	NspH I	R,CATG`Y	4
Xho II	(10)	766	2698	2778	3497	Paer7 I	C`TCGA,G	1	Pal I	GG CC	37
		4951	7451	7462	7548	PflM I	CCAN,NNN`NTGG	1	Ple I	GAGTC 9/10	4
		7560	9019			Pme I	C TTT AAAC	1	Pml I	CAC GTG	-
Xma I	(5)	339	403	770	5537	PpuM I	RG`GWC,CY	1	Psp1406 I	AA`CG,TT	2
		5601				PspA I	C`CCGG,G	5	Pst I	C,TGCA`G	6
Xma III	(4)	990	1155	1725	2183	Pvu I	CG,AT`CG	3	Pvu II	CAG CTG	3
Xmn I	(1)	4996				Rsa I	GT AC	19	Rsr II	CG`GWC,CG	3
						Sac I	G,AGCT`C	1	Sac II	CC,GC`GG	2
						Sal I	G`TCGA,C	1	Sap I	GCTCTC 8/11	1
						Sau3A I	`GATC,	37	Sau96 I	G`GNC,C	29
						Sca I	AGT ACT	1	ScrF I	CC`N,GG	44
						Sec I	C`CNNG,G	51	SfaN I	GCATC 9/13	22
						Sfc I	C`TRYA,G	11	Sfi I	GGCCN,NNN`NGGCC	1
						Sma I	CCC GGG	5	SnaB I	TAC GTA	-
						Spe I	A`CTAG,T	-	Sph I	G,CATG`C	1
						Spl I	C`GTAC,G	1	Srf I	GCCC GGGC	2
						Ssp I	AAT ATT	6	Stu I	AGG CCT	1
						Sty I	C`CWWG,G	10	Taq I	T`CG,A	26
						Tfi I	G`AWT,C	14	Tsp45 I	`GTSAC,	12
						Tth111 I	GACN`N,NGTC	3	Tth111 II	CAARCA 16/14	16
						Vsp I	AT`TA,AT	7	Xba I	T`CTAG,A	2
						Xca I	GTA TAC	-	Xcm I	CCANNN,N`NNNNTGG1	1
						Xho I	C`TCGA,G	5	Xho II	R`GATC,Y	10
						Xma I	C`CCGG,G	5	Xma III	C`GGCC,G	4

Site usage in pMPH86:

Aat II	G,ACGT`C	1	Acc I	GT`MK,AC	1
Acc65 I	G`GTAC,C	1	Aci I	C`CG,C	93
Afl II	C`TTAA,G	-	Afl III	A`CRYG,T	3
Age I	A`CCGG,T	1	Aha II	GR`CG,YC	4
Ahd I	GACNN,N`NNGTC	1	Alu I	AG CT	42
Alw I	GGATC 8/9	19	AlwN I	CAG,NNN`CTG	3
Apa I	G,GGCC`C	1	ApaL I	G`TGCA,C	4
Apo I	R`AATT,Y	8	Asc I	GG`CGCG,CC	1
Ase I	AT`TA,AT	7	Asp718	G`GTAC,C	1
Ava I	C`YCGR,G	11	Ava II	G`GWC,C	14
Avr II	C`CTAG,G	-	BamH I	G`GATC,C	1
Ban I	G`GYRC,C	8	Ban II	G,RCGY`C	6
Bbe I	G,GCGC`C	1	Bbs I	GAAGAC 8/12	3
Bbv I	GCAGC 13/17	23	Bbv II	GAAGAC 7/11	3
Bcl I	T`GATC,A	2	Bcn I	CC,S`GG	20
Bfa I	C`TA,G	24	Bgl I	GCCN,NNN`NGGC	3
Bgl II	A`GATC,T	1	Blp I	GC`TNA,GC	1