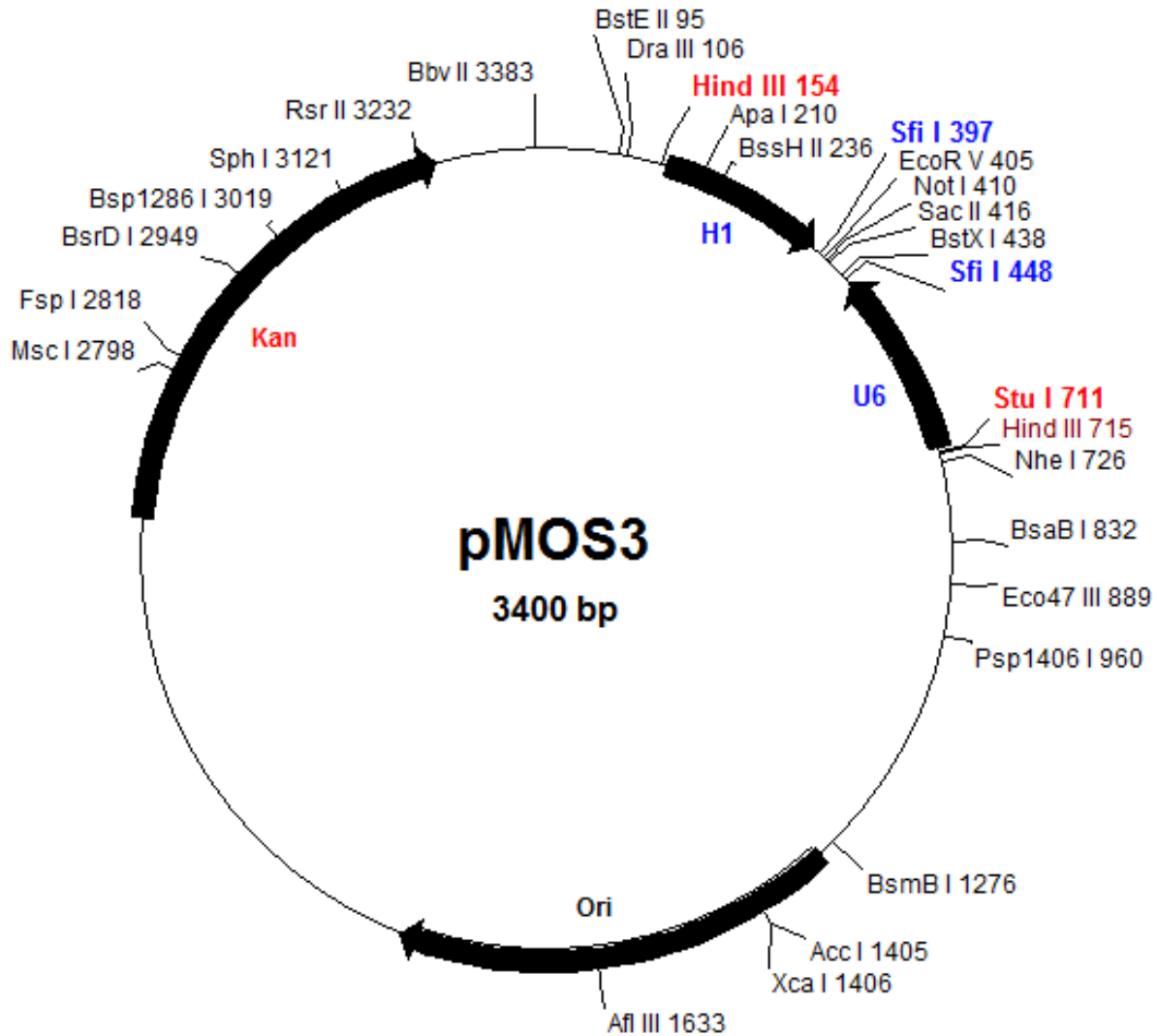


Vector: pMOS3 (for stepwise cloning of pMPBOS knockdown vector)

Antibiotic Selection: Kan

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

Date of Construction: March 2012



Sfi I Site Stuffer and siRNA Cassette Design:

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    EcoRV  Not I  M13Rev  BstX I
    H1>>> ggccaaaacGGCCgatatacGCGGCGCGggaaacagctatgaCCAtgaacgcTGGCCgttttggcc
           cgggttttgCCGGctatagcgcggcgccctttgtcgatactggtactgccaacggcaaaaaccgg <<<U6
    
```

Sfi I Digestion

5' -GGCCAAA	A (n19-27nt) TTTT	TGGCC-3'
3' -CCGGT	TTTT (n19-27nt) A	AAAACCGG-5'

pMOS3 Full-Length Sequence

GGAAACAGCTATGACCATGATTACGCCAAGCTCGAAATTAACCCCTACTAAAGGGAACAAAAGCTGGTACGAGGACAGGCTG
GAGCCATGGCTGGTACCACGTCGTGGAATGCCCTTC**GaattAATTC**AGCACCTGCACATGGGAC**GTCGAg****AAGCTT**agctta
attcgaacgctgacgtcatcaaccgctccaaggaatcgccggccagtgctactaggcgggaacaccagcgcgctgccc
cctggcaggaagatggctgtgagggacaggggagtgccgcccctgcaatatttgcctgctgctatgtgttctgggaaatcacc
ataaacgtgaaatgtctttggatttgggaatcttataagttctgtatgagaccacagatcgcccaaacggccgatatcGCCG
GCCCGgaaacagctatgaCCAtgacgcTggccgcttttggcctcctttccacaagatatataaagccaagaaatcgaatac
ttaaagttacggttaagcatatgatagtcctattttaaacaataattttaaactgcaaacctaccaagaaatattactttc
tacgtcacgtattttgtactaataatctttgttttacagtcaaattaatttctctctaacagccttgtatcgtat
atgcaaatatgaaggaatcatgggaaatagggcctcttctctgcccagcctt**AGGCCT**aaagcttggg**AAGCT**agctTGCCTAA
TCGGACGAAAAATGACCATGATTACGCCAAGCTCCAATTCGCCCTATAGTGAGTTCGTATTACAATTCAGTGGCCGTCGTTT
TACCCGGATCTGCATCGCAGGATGCTGCTGGCTACCCCTGTGGAACACCTACATCTGTATTAAACGAAGCGCTGGCATTGACCC
TGAGTGATTTTTCTCTGGTCCCGCCGCATCCATAACCGCCAGTTGTTTACCCCTCACAACTTCCAGTAACCGGGCATGTTTCAT
CATCAGTAACCCGTATCGTGAGCATCCTCTCTCGTTTTCATCGGTATCATTACCCCATGAACAGAAAATCCCCCTTACACGGA
GGCATCAGTGACCAAACAGGAAAAAACCGCCCTTAAACATGGCCCGCTTTTATCAGAAGCCAGACATTAACGCTTCTGGAGAAA
CTCAACGAGCTGGACCGGATGAACAGGCAGACATCTGTGAATCGCTTACGACCACGCTGATGAGCTTTACCGCAGCTGCC
TCGCGCTTTTCGGTGATGACGGTGAACCTCTGACACATGCAGCTCCCGGAGACGGTACAGCTTGTCTGTAAGCGGATGC
CGGGAGCAGACAAGCCCGTCAGGGCGCTCAGCGGTGTTGGCGGTGTCGGGGCGCAGCCATGACCCAGTACGTAAGCGGAT
AGCGGAGTGTATACTGGCTTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGTGTGAAATACCGCA
CAGATGCGTAAGGAGAAAATACCGCATCAGGCGCTTCCCGCTTCCCTCGCTCACTGACTCGCTGCGCTCGTTCGGCTG
CGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAATGTGAG
CAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCCGCTTGTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCA
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CTCGTGGCTCTCTCTGTTCCGACCCCTGCCGCTTACCGGATACTGTCCGCCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTC
ATAGCTCACGCTGTAGGTATCTCAGTTCCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTACGCC
CGACCGCTGCGCTTATCCGGTAACTATCGTCTTGTAGTCCAACCCGGTAAAGACACGACTTATCGCCACTGGCAGCAGCCACT
GGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAA
GGCAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAGAGTGGTGGTACTCTTGTATCCCGCAAACAAAC
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TTTTCTACGGGCTGACGCTCAGTGGAACGAAACTCACGTTAAGGGATTTTGGTTCATGAGATTATCAAAAAGGATCTTCA
CCTAGATCTTTTAAATTAATAATGAAGTTTTAAATCAATCTAAAATATATATGAGTAAACTTGGTCTGACAGTTACCAATG
CTTAATCAGTGAGGCACCTATCTCAGCGATCTGCTATTTTCGTTTCATCCATAGTTGCCCT**GAC**TCCC**GTC**ATTCAAATATGT
ATCCGCTCATGAGACAATAACCCCTGATAAATGCTTCAATAATAT**ATG**ATTGAACAAGATGGATTGCACGCAGGTTCTCCGGC
CGCTTGGGTGGAGAGGCTATTCGGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTTGTTCCGGCTGTCA
GCGCAGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCTGAATGAACTGCAAGACGAGGCAGCGCGGCTAT
CGTGGCTGGCCACGACGGGCTTCCCTTGCAGCTGTGCTCGACGTTGTCACTGAAGCGGGAAGGACTGGCTGCTATTGGG
CGAAGTGCCGGGGCAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGG
CTGCATACGCTTGATCCGGCTACCTGCCATTTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGATGGAAG
CCGGTCTTGTGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCCAGCCGAACCTGTTCCGCCAGGCTCAAGGCGAG
CATGCCCCAGGCGAGGATCTCGTCTGACCCATGGCGATGCCCTGCTTGGCCGAATATCATGGTGGAAAAATGGCCGCTTTTCT
GGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGC
TTGGCGCGAAATGGGCTGACCGCTTCTCGTGTCTTACGGTATCGCCGCTCCCGATTTCGACGCGCATCGCTTCTATCGCCT
TCTTGACGAGTTCTTCT**TGACCTTCT****GTCCTC**AAgaatt

Unique enzymes in pMOS3:

BstE II	G`GTNAC,C	95	BsmB I	CGTCTC 7/11	1276		
PflM I	CCAN,NNN`NTGG	106	Acc I	GT`MK,AC	1405		
Dra III	CAC,NNN`GTG	106	Bst1107 I	GTA TAC	1406		
Bsm I	GAATG,C 7	116	Xca I	GTA TAC	1406		
Bsg I	GTGCAG 22/20	120	Afl III	A`CRYG,T	1633		
Blp I	GC`TNA,GC	157	Msc I	TGG CCA	2798		
Esp I	GC`TNA,GC	157	Fsp I	TGC GCA	2818		
Bsp120 I	G`GGCC,C	206	BsrD I	GCAATG, 8	2949		
Apa I	G,GGCC`C	210	Bsp1286 I	G, DGCH`C	3019		
BssH II	G`CGCC,C	236	Sph I	G,CATG`C	3121		
Ssp I	AAT ATT	295	NgoM I	G`CCGG,C	3216		
Bsa I	GGTCTC 7/11	371	Nae I	GCC GGC	3218		
EcoR V	GAT ATC	405	Rsr II	CG`GWC,CG	3232		
Not I	GC`GGCC,GC	410	Bbs I	GAAGAC 8/12	3382		
Sac II	CC,GC`GG	416	Bbv II	GAAGAC 7/11	3383		
BstX I	CCAN,NNNN`NTGG	438	Number of enzymes = 38				
EcoO109 I	RG`GNC,CY	687	The following enzymes do not cut in pMOS3:				
Bsu36 I	CC`TNA,GG	706	Acc65 I	Afl II	Age I	Apo I	Asc I
Stu I	AGG CCT	711	Asp718	Ava I	Avr II	BamH I	Bcl I
Nhe I	G`CTAG,C	726	Bgl II	BseI I	BsiW I	BspM II	BsrG I
BsaB I	GATNN NNATC	832	Cla I	Eco72 I	EcoN I	EcoR I	Fse I
Eco47 III	AGC GCT	889	HinC II	Hind II	Hpa I	Kpn I	Mlu I
Psp1406 I	AA`CG,TT	960					

Mun I	Nru I	Nsi I	PaeR7 I	Pme I						
Pml I	PpuM I	PspA I	Pst I	Pvu I		2247	2610	2796	3015	
Sac I	Sal I	Sca I	Sma I	SnaB I		3081	3087	3115	3119	
Spe I	Spl I	Srf I	Xba I	Xcm I		3160	3164	3218		
					Cfr10 I	(2)	3035	3216		
pMOS3: sites sorted by name:					Csp6 I	(4)	68	591	1440	3021
					Dde I	(8)	157	706	713	903
							1443	1908	2317	2483
Aat II	(2)	149	181		Dpn I	(14)	387	829	2201	2276
Acc I	(1)	1405					2287	2295	2373	2385
Aci I	(46)	189	204	223			2490	2889	2967	3048
		413	415	924			3057	3135		
		938	1094	1110		DpnII	(14)	385	827	2199
		1221	1306	1345	409		2285	2293	2371	2383
		1397	1422	1460	927		2488	2887	2965	3046
		1499	1516	1559	1165		3055	3133		
		1587	1678	1706	1355	Dra I	(4)	528	541	2392
		1852	1973	2083	1473	Dra III	(1)	106		2411
		2227	2546	2625	1566	Drd I	(3)	1328	1741	2743
		2782	2846	2947	1833	Dsa I	(3)	87	413	3148
		3190	3230	3235	2218	Eae I	(9)	389	398	410
		3301	3327	3285	2688		810	2622	2796	3187
							3214			
Afl III	(1)	1633				Eag I	(3)	398	410	2622
Aha II	(4)	146	178	284	2716	Ear I	(4)	697	1517	3060
Ahd I	(2)	2526	3386			Eco47 III	(1)	889		3270
Alu I	(22)	9	31	64	156	Eco57 I	(3)	2180	2861	3293
		161	424	717	726	EcoO109 I	(1)	687		
		730	771	1158	1215	EcoR II	(5)	247	1659	1780
		1226	1275	1294	1575		3101			1793
		1801	1891	1937	2194	EcoR V	(1)	405		
		2822	3280			Ehe I	(2)	285	2717	
Alw I	(9)	834	2195	2281	2281	Esp I	(1)	157		
		2378	2379	2894	2961	Fnu4H I	(32)	410	413	846
		3140					1224	1227	1273	1370
AlwN I	(2)	134	2049				1423	1539	1557	1560
Apa I	(1)	210					1678	1833	1976	2041
Apal I	(2)	1449	1947				2044	2250	2625	2677
Ase I	(2)	123	620				2688	2778	2783	2820
Ava II	(2)	920	3232				2861	2948	2951	2954
Ban I	(4)	283	2474	2715	2750		3190	3286	3327	3341
Ban II	(2)	210	3081			Fok I	(8)	854	916	994
Bbe I	(2)	287	2719				1321	2492	3040	3065
Bbs I	(1)	3382								
Bbv I	(9)	1235	1284	1381	2052	Fsp I	(1)	2818		
		2055	2261	2789	2831	Gdi II	(11)	390	397	399
		3352					411	439	809	2621
Bbv II	(1)	3383					2623	3186	3213	
Bcn I	(7)	826	974	1280	1315	Gsu I	(2)	101	1161	
		2014	2721	2881		Hae I	(6)	451	711	1648
Bfa I	(4)	219	727	2128	2381		2111	2798		1659
Bgl I	(2)	397	448			Hae II	(5)	287	891	1511
Blp I	(1)	157					2719			1881
Bpm I	(2)	102	1162			Hae III	(18)	208	391	400
Bsa I	(1)	371					442	451	688	711
BsaA I	(3)	583	1387	3020			812	1108	1648	1659
BsaB I	(1)	832					1677	2111	2624	2798
BsaH I	(4)	146	178	284	2716	Hga I	(5)	443	1170	1329
BsaJ I	(7)	87	194	247	413		2321			1743
		1793	2879	3148		HgiA I	(4)	1453	1951	2829
BsaW I	(3)	1839	1986	2747		HgiE II	(2)	1451	2212	3019
Bsg I	(1)	120				Hha I	(21)	238	240	246
BsIC I	(2)	118	168				890	1236	1339	1369
BsIE I	(5)	401	413	1549	1973		1510	1543	1813	1880
		2625					1980	2154	2263	2710
BsiHKA I	(4)	1453	1951	2829	3019		2718	2782	2819	3085
Bsm I	(1)	116					3345			
BsmA I	(3)	372	1277	2549		HinD III	(2)	154	715	
BsmB I	(1)	1276				Hinf I	(11)	199	357	672
BsmF I	(4)	157	284	906	2867		1189	1533	1608	2004
BsoF I	(32)	410	413	846	927		2521	3201	3335	
		1224	1227	1273	1370	HinI I	(4)	146	178	284
		1423	1539	1557	1560	HinP I	(21)	236	238	244
		1678	1833	1976	2041		888	1234	1337	1367
		2044	2250	2625	2677		1508	1541	1811	1878
		2688	2778	2783	2820		1978	2152	2261	2708
		2861	2948	2951	2954		2716	2780	2817	3083
		3190	3286	3327	3341		3343			
Bsp120 I	(1)	206				Hpa II	(16)	825	972	1279
Bsp1286 I	(1)	3019					1840	1987	2013	2203
BspH I	(2)	2353	2550				2621	2698	2720	2748
BspM I	(3)	142	2603	2984			2879	2969	3036	3217
Bsr I	(11)	211	812	942	966	Hph I	(6)	106	318	1254
		1381	1412	2040	2053		2370	2895		1263
		2167	2659	2860		Kas I	(2)	283	2715	
BsrB I	(4)	191	1566	2548	3329	Mae I	(4)	219	727	2128
BsrD I	(1)	2949				Mae II	(11)	102	146	178
BssH II	(1)	236					577	582	960	1386
BssS I	(2)	1806	3308				2336	2832	3019	
Bst1107 I	(1)	1406				Mae III	(15)	95	214	499
BstB I	(2)	118	168				967	990	1074	1287
BstE II	(1)	95					1382	1989	2052	2168
BstN I	(5)	249	1661	1782	1795		2451	2836	3142	
		3103				Mbo I	(14)	385	827	2199
BstU I	(13)	204	238	240	409		2285	2293	2371	2383
		415	1165	1234	1236		2488	2887	2965	3046
		1339	1680	2261	2782		3055	3133		
		3083				Mbo II	(9)	267	685	1505
BstX I	(1)	438					2367	3076	3286	2294
BstY I	(7)	827	2274	2285	2371		3383			3368
		2383	2887	3133		Mne I	(2)	1847	2031	
Bsu36 I	(1)	706				Mnl I	(19)	53	65	261
Cac8 I	(23)	206	238	242	440		699	962	1020	1059
		728	732	850	892		1239	1269	1531	1741
		1110	1564	1650	1687					

		1814	2065	2465	2631		Age I	A`CCGG,T	-	Aha II	GR`CG,YC	4
		2767	3124	3316			Ahd I	GACNN,N`NNGTC	2	Alu I	AG CT	22
Msc I	(1)	2798					Alw I	GGATC 8/9	9	AlwN I	CAG,NNN`CTG	2
Mse I	(15)	39	123	163	527		Apa I	G,GGCC`C	1	AlpA I	G`TGCA,C	2
		540	620	880	1100		Apo I	R`AATT,Y	-	Asc I	GG`CGCG,CC	-
		1132	1414	2339	2391		Ase I	AT`TA,AT	2	Asp718	G`GTAC,C	-
		2396	2410	2463			AvA I	C`YCGR,G	-	AvA II	G`GWC,C	2
Msl I	(2)	333	3153				Avr II	C`CTAG,G	-	BamH I	G`GATC,C	-
Msp I	(16)	825	972	1279	1313		Ban I	G`GYRC,C	4	Ban II	G,RCY`C	2
		1840	1987	2013	2203		Bbe I	G,CGC`C	2	Bbs I	GAAGAC 8/12	1
		2621	2698	2720	2748		Bbv I	GCAGC 13/17	9	Bbv II	GAAGAC 7/11	1
		2879	2969	3036	3217		Bcl I	T`GATC,A	-	Bcn I	CC,S`GG	7
MspAl I	(6)	415	1226	1345	1975		Bfa I	C`TA,G	4	Bgl I	GCCN,NNN`NGCC	2
		2220	2822				Bgl II	A`GATC,T	-	Blp I	GC`TNA,GC	1
Nae I	(1)	3218					Bpm I	CTGGAG 22/20	2	Bsa I	GGTCTC 7/11	1
Nar I	(2)	284	2716				BsaA I	YAC GTR	3	BsaB I	GATNN NNATC	1
Nci I	(7)	825	973	1279	1314		BsaH I	GR`CG,YC	4	BsaJ I	C`CNNG,G	7
		2013	2720	2880			BsaW I	W`CCGG,W	3	BseR I	GAGGAG 16/14	-
Nco I	(2)	87	3148				Bsg I	GTGCAG 22/20	1	BsiC I	TT`CG,AA	2
Nde I	(2)	512	1456				BsiE I	CG,RY`CG	5	BsiHKA I	G,WGCW`C	4
Ngom I	(1)	3216					BsiW I	C`GTAC,G	-	Bsm I	GAATG,C 7	1
Nhe I	(1)	726					BsmA I	GTCTC`/9	3	BsmB I	CGTCTC 7/11	1
Nla III	(19)	20	91	143	304		BsmF I	GGGAC 15/19	4	BsoF I	GC`N,GC	32
		435	679	760	980		Bsp120 I	G`GGCC,C	1	Bsp1286 I	G,DGCH`C	1
		1044	1107	1272	1377		BspH I	T`CATG,A	2	BspM I	ACCTGC 10/14	3
		1637	2357	2554	2935		BspM II	T`CCGG,A	-	Bsr I	ACT,GG`	11
		3121	3152	3178			BsrB I	GAG CGG	4	BsrD I	GCAATG, 8	1
Nla IV	(9)	85	208	285	922		BarG I	T`GTAC,A	-	BssH II	G`CGCG,C	1
		1665	1704	2476	2717		BssS I	C`TCGT,G	2	Bst1107 I	GTA TAC	1
		2752					BstB I	TT`CG,AA	2	BstE II	G`GTNAC,C	1
Not I	(1)	410					BstN I	CC`W,GG	5	BstU I	CG CG	13
Nsp7524 I	(5)	300	976	1268	1633		BstX I	CCAN,MNNN`NTGG	1	BstY I	R`GATC,Y	7
		3117					Bsu36 I	CC`TNA,GG	1	Ca8 I	GCN NGC	23
NspB II	(6)	415	1226	1345	1975		Cfr10 I	R`CCGG,Y	2	ClA I	AT`CG,AT	-
		2220	2822				Csp6 I	G`TA,C	4	Dde I	C`TNA,G	8
NspH I	(5)	304	980	1272	1637		Dpn I	GA TC	14	DpnII	`GATC,	14
		3121					Dra I	TTT AAA	4	Dra III	CAC,NNN`GTG	1
Pal I	(18)	208	391	400	412		Drd I	GACNN,NN`NNGTC	3	Dsa I	C`CRYG,G	3
		442	451	688	711		Eae I	Y`GGCC,R	9	Eag I	C`GCC,G	3
		812	1108	1648	1659		Ear I	CTCTTC 7/10	4	Eco47 III	AGC GCT	1
		1677	2111	2624	2798		Eco57 I	CTGAAG 21/19	3	Eco72 I	CAC GTG	-
		3189	3216				EcoN I	CCTNN`N,NNAGG	-	Eco109 I	RG`GNC,CY	1
PflM I	(1)	106					EcoR I	G`AATT,C	-	EcoR II	`CCWGG,	5
Ple I	(2)	799	2012				EcoR V	GAT ATC	1	Ehe I	GGC GCC	2
Psp1406 I	(1)	960					Esp I	GC`TNA,GC	1	Fnu4H I	GC`N,GC	32
Pvu II	(2)	1226	2822				Fok I	GGATG 14/18	8	Fse I	GG,CCGG`CC	-
Rsa I	(4)	69	592	1441	3022		Fsp I	TGC GCA	1	Gdi II	`YGGC,CG	11
Rsr II	(1)	3232					Gsu I	CTGGAG 21/19	2	Hae I	WGG CCW	6
Sac II	(1)	416					Hae II	R,CGC`Y	5	Hae III	GG CC	18
Sap I	(3)	1517	3060	3270			Hga I	GAGCG 9/14	5	HgiA I	G,WGCW`C	4
Sau3A I	(14)	385	827	2199	2274		HgiE II	ACCNNNNNNGGT -1/132	-	Hha I	G,CG`C	21
		2285	2293	2371	2383		Hinc II	GTY RAC	-	Hind II	GTY RAC	-
		2488	2887	2965	3046		Hind III	A`AGCT,T	2	Hinf I	G`ANT,C	11
		3055	3133				HinI I	GR`CG,YC	4	HinP I	G`CG,C	21
Sau96 I	(6)	206	207	687	920		Hpa I	GTT AAC	-	Hpa II	C`CG,G	16
		1107	3232				Hph I	GGTGA 12/11	6	Kas I	G`GCGC,C	2
ScrF I	(12)	249	825	973	1279		Kpn I	G,GTAC`C	-	Mae I	C`TA,G	4
		1314	1661	1782	1795		Mae II	A`CG,T	11	Mae III	`GTNAC,	15
		2013	2720	2880	3103		Mbo I	`GATC,	14	Mbo II	GAAGA 12/11	9
Sec I	(7)	87	194	247	413		Mlu I	A`CCGG,T	-	Mme I	TCCRAC 25/23	2
		1793	2879	3148			Mnl I	CCTC 10/10	19	Msc I	TGG CCA	1
SfaN I	(16)	833	841	937	1015		Mse I	T`TA,A	15	Msl I	CAYNN NNRTG	2
		1077	1300	1433	1471		Msp I	C`CG,G	16	MspAl I	CMG CKG	6
		1509	1729	2675	2930		Mun I	C`AATT,G	-	Nae I	GCC GGC	1
		3014	3078	3146	3353		Nar I	GG`CG,CC	2	Nci I	CC`S,GG	7
Sfc I	(3)	784	1898	2089			Nco I	C`CATG,G	2	Nde I	CA`TA,TG	2
Sfi I	(2)	397	448				Ngom I	G`CCGG,C	1	Nhe I	G`CTAG,C	1
Sph I	(1)	3121					Nla III	,CATG`	19	Nla IV	GGN NCC	9
Ssp I	(1)	295					Not I	GC`GGCC,GC	1	Nru I	TCG CGA	-
Stu I	(1)	711					Nsi I	A,TGCA`T	-	Nsp7524 I	R`CATG,Y	5
Sty I	(3)	87	194	3148			NspB II	CMG CKG	6	NspH I	R,CATG`Y	5
Taq I	(11)	33	118	149	168		PaeR7 I	C`TCGA,G	-	Pal I	GG CC	18
		485	1733	2829	2985		PflM I	CCAN,NNN`NTGG	1	Ple I	GAGTC 9/10	2
		3009	3045	3207			Pme I	CTTT AAAC	-	Pml I	CAC GTG	-
Tfi I	(7)	199	357	672	1189		PpuM I	RG`GWC,CY	-	Psp1406 I	AA`CG,TT	1
		1608	3201	3335			PspA I	C`CCGG,G	-	Pst I	C,TGCA`G	-
Tsp45 I	(8)	95	214	578	1074		Pvu I	CG,AT`CG	-	Pvu II	CAG CTG	2
		1287	1382	2836	3142		Rsa I	GT AC	4	Rsr II	CG`GWC,CG	1
Tth111 I	(3)	101	1380	2834			Sac I	G,AGCT`C	-	Sac II	CC,GC`GG	1
Tth111 II	(5)	1095	2222	2231	2261		Sal I	G`TCGA,C	-	Sap I	GCTCTTC 8/11	3
		3152					Sau3A I	`GATC,	14	Sau96 I	G`GNC,C	6
Vsp I	(2)	123	620				Sca I	AGT ACT	-	ScrF I	CC`N,GG	12
Xca I	(1)	1406					Sec I	C`CNNG,G	7	SfaN I	GCATC 9/13	16
Xho II	(7)	827	2274	2285	2371		Sfc I	C`TRYA,G	3	Sfi I	GGCCN,NNN`NGGCC	2
		2383	2887	3133			Sma I	CCC GGG	-	SnaB I	TAC GTA	-
Xma III	(3)	398	410	2622			Spe I	A`CTAG,T	-	Sph I	G,CATG`C	1
Xmn I	(3)	114	124	1193			SpI I	C`GTAC,G	-	Srf I	GCCC GGCC	-
							Ssp I	AAT ATT	1	Stu I	AGG CCT	1
							Sty I	C`CWWG,G	3	Taq I	T`CG,A	11
							Tfi I	G`AWT,C	7	Tsp45 I	`GTSAC,	8
							Tth111 I	GACN`N,NGTC	3	Tth111 II	CAARCA 16/14	5
							Vsp I	AT`TA,AT	2	Xba I	T`CTAG,A	-
							Xca I	GTA TAC	1	Xcm I	CCANNNN,NNN`NTGG	-
							Xho I	C`TCGA,G	-	Xho II	R`GATC,Y	7
							Xma I	C`CCGG,G	-	Xma III	C`GGCC,G	3

Site usage in pMOS3:

Aat II	G,ACGT`C	2	Acc I	GT`MK,AC	1
Acc65 I	G`GTAC,C	-	Aci I	C`CG,C	
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Afl II	C`TTAA,G	-	Afl III	A`CRYG,T	1