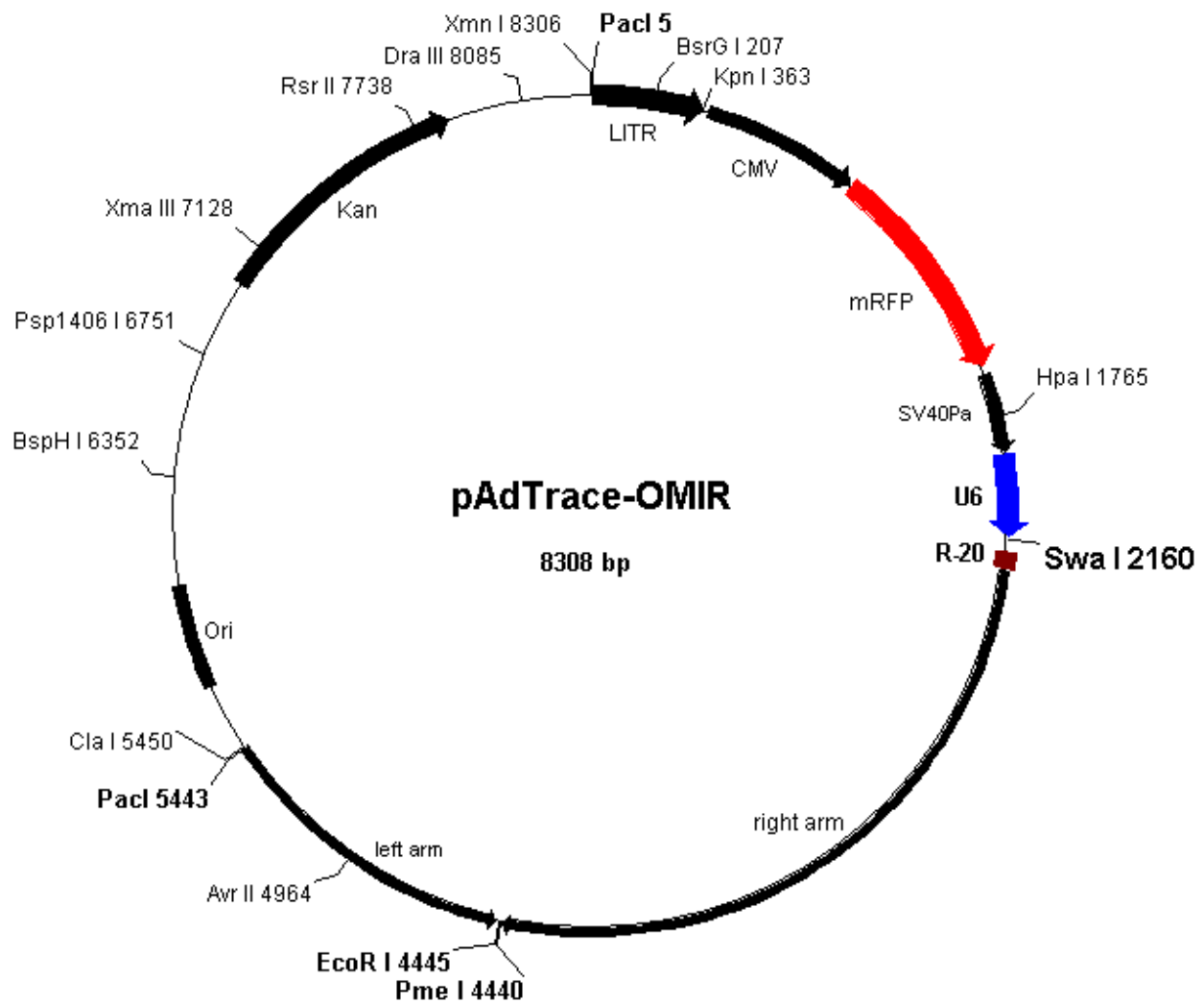


Vector: pAdTrace-OMIR (adeno shuttle vector for one-step mature miRNA expression)

Antibiotic Selection: Kan

Creator(s): Xian Chen, Molecular Oncology Laboratory of The University of Chicago

Date of Construction: June, 2013



Forward (5p) Oligo:

5' -tgtggaaggaaggaATTTxxxxxxx-5p tttttaaggcgggcaggaagagg-3'

Reverse (3p) Oligo:

5' -atcttgtggaaggaCGAACACCyyyyyyyy-3p ttttttAAATCGCCACATAGGTTTCGT-3'

3p Reverse-Complement

5' -ACGAACCTATGTGGCGATTTaaaaap3-yyyyyyyyGGTGTTTCGtcctttccacaagat-3'

pAdTrace-OMIR Full-Length Sequence

NNNTAATTAANNNTCCCTTCCAGCTCTCTGCCCTTTTGGATTGAAGCCAATATGATAATGAGGGGGTGGAGTTTGTGACGTGGCGCGGGCGTGGGAACGGGGC
GGGTGACGTAGTAGTGTGGCGGAAGTGTGATGTTGCAAGTGTGGCGGAACACATGTAAGCGACGGATGTGGCAAAAGTGACGTTTTTGGTGTGCGCCGGTGTACAC
AGGAAGTGAACAATTTTCGCCCGGTTTTAGCGCGATGTTGTAGTAATTTGGCGTAACCGAGTAAGATTTGGCCATTTTCGCCGGAAAACTGAATAAGAGGAAGTG
AAATCTGAATAATTTTGTGTACTCATAGCGCGTAANNNGgtaccTAGTTATTAATAGTAATCAATACGGGGTCATTAGTTCATAGCCCATATATGGATTCGCC
GTTACATAACTTACGGTAAATGGCCCGCTGGCTGACCGCCAAACGACCCCGCCATTTGACGTAATAAGCAGTATGTTCCCATAGTAACGCCAATAGGGACTT
TCCATTGACGTCAATGGGTGGAGTATTTACGGTAAACTGCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCTTATTGACGTCAATGACGGTAA
ATGGCCCGCTGGCATTATGCCAGTACATGACCTTATGGGACTTTCCTACTTGGCAGTACATCTACGTATTAGTTCATCCTATTACCATGGTGTATGCGGTTTTGC
CAGTACATCAATGGCGGTGGATAGCGGTTTTGACTACGGGGATTTCCAAGTCTCCACCCATTTGACGTCAATGGGAGTTTGGTTTGGCACAAAATCAACGGGACT
TTCCAAAATGTCGTAACAACCTCCGCCATTTGACGCAAAATGGCGCCAAAGCGTGTGACGTTGGGGTGTGTTTAAAGCAGAGTGGTTTAGTGAACCTGAGTAAAG
CTAGaccATGgctcctccgaggacgtcatcaaggagttcatgcgcttcaaggtgcgcatggagggtcctcgtaacggccacagagttcgagatcgagggcgagggc
gagggccgcccctacgagggcaccagaccgccaagctgaaggtgaccaaagggcgcccccctgccttcgctgggacatcctgtcccctcagttccagtagcgct
ccaaggtcactgtagaagcaccggcagacatccccgactactgaagctgcctcccaggggctcaagtgaggcgctgtaacttcgagagcggcggtgct
ggtagcctgacccaagactcctcctcaggaagcggcgttcatctacaaggtgaaagtcgagcggcaccactcccctcagcggccccctgagcaagaag
acatgggtggagggcctccaccgagcggatgtaccggaggaagcgccctgaagggcgagatcaagatgaggctgaagctgaaggacggcgggcactacgacg
ccgaggtcaagaccactacatggccaagaagccgctgacgtgcccggcgcctacaagaccgacatcaagctggacatcacctcccacaacgagagactacacat
cgtggaacagtagcagggcgccagggcgccactccaccggcggcAATCCACCGGATCTAGATAACTGATCATAATCAGCCATACCACATTTGTAGAGGTTTTAC
TTCGTTTAAAACCTCCACACCTCCCCCTGAACCTGAAACATAAAATGAATGTAATGTTTAACTGTTTAACTGTTTATGTAACTGTTTATGTAACTGTTTAAAG
CAATAGCATCACAATTTCAACAATAAAGCATTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTCATCAATGTATCTTAAACGGGAAACaaggtcgggcagg
aagagggcctatttcccagatcttccatatttgcatacacagaaggtgttagagagataattagaattaatttgaactgtaaacacaaagatattagtaga
aaatcgtgacgtagaagtaataatttctgggtagtttcagttttaaattatgttttaaattgactatcatatgcttaccgtaacttgaagatatttccat
ttctgctttatatabatcttgtggaaggaaggaaATTTAAAATGCCACATAGGTTCTCGTGATTGATCTNNNTAAGGGTGGGAAGAATATAAAGTGGGGCTCT
TATGTAGTTTTGTATCTGTTTTGACAGCAGCCGCCCATGAGCACCACCTCGTTTGTGGAAGCATTGTGAGCTCATATTTGACAACCGGCATGCCCCATGG
GCCGGGTGGCGTCAAGATGTGATGGGCTCCAGCATGATGGTCCGCCCGCTCCGCCGAACTACTACTACCTGACCTACGAGACCGTGTCTGGAACCGCGTTGG
AGACTGCAGCTCCGCCCGCTTCCAGCGCTGCAGCCAGCCCGCGGGATTGTGACTTTGCTTTCCTGAGCCGCTGCAAGCAGTGCAGCTCCCGTTC
ATCCGCCCGCATCAAGTGTGACGGCTTTTGGCAACTTTGATGTTTTCAGCGGAACTTAATGTCTGTTTTCGACAGCTGTGGATGTCGCGCAGCAGGTT
TCTGCCCTGAAGGCTTCTCCCTCCCAATGCGGTTTAAAACATAAAATAAAGCAGACTCTGTTTGGATTGGATCAAGCAAGTGTCTTGTCTCTTTATTTAG
GGTTTTGCGCGCGGTTAGGCCCGGGACAGCGGCTCCGGTCTGGTGGTGTAGGGTCCGTGTATTTTTTCCAGGACGTGGTAAAGGTGACTCTGGATGTCAGATACAT
GGCATAGCCCGCTCTCGGGTGGAGGTAGCACCAGTGCAGAGCTTTCATGCTCGGGGTGGTGTGTAGATGATCCAGTCTGACGAGGAGCGCTGGCGGTGGTGC
CTAAAATGTCTTTTCAGTAGGCTGATTGCCAGGGGCAACCATAAATGATGTTTACAAAAGCGGTTAAGCTGGGATGGGTGCATACCTGGGGATAGATGAGAT
GCATCTGGACTGTATTTTTAGGTTGGCTATGTTCCAGCCATATCCCTCCGGGATTCATGTTGTGCAAGCAACCCAGCAGTGTATCCGGTGCATTTGGGAAA
TTTTGCATGTAGCTTAGAAGAAATGCGTGGAAAGAACTTGGAGAGCCCTTGTGACCTCCAAGATTTTCCATGCATTCTGCATATGATGGCAATGGGCCACGG
CGCGCGCTGGCCGAAGATATTTCTGGGATCACTAACGTCATAGTTGTGTTCCAGGATGAGATCGTCACTAGGCTTTTTTACAAAGCAGCGGGGGAGGGTGGCCAG
ACTGGGTATAATGTTTCCATCCGGCCAGGGCGTAGTTACCTTACCTTGTGACTTTGACCTTTGAGCTTTGAGTTGAGTTGAGTTGAGTTGAGTTGAGTTGAGTT
GATGAAGAAAACGGTTTCCGGGTTAGGGAGATCAGCTGGGAAAGAAAGCAGGTTCCCTGAGCAGCTGCAGCTTACCAGCAGCGGTTGGCCCGTAAATCACACTAT
ACCGGTTGCAACTGTGATTTAGAGAGCTGCAGCTGCCGTCATCCCTGAGCAGGGGGCCACTTCGTTAAGCATGTCCTGACTGCGATGTTTTCCCTGACCAAAAT
CCGCGAGAAGGGCTCGCCGCCAGCAGTATGCAAGTCTTTTGAAGGAAGCAAAAGTTTTCACCGTTTTCAGACCGTCCGCCCTAGGCATGCTTTTTGAGCGTTGACC
AAGCATTCCAGCGGTCCACAGCTCGTCCCTGCTACCGCATCTGCATCCAGTCTCCCTGTTTCGCGGTTGGGGGCTTTCGCTTACGCGGATGACCGGATA
TCCGTGCTCGTCCAGACGGCCAGGGTCTATGTTTCCAGCGCGCAGGGTCCCTCGTACGCTAGTCTGGGTACCGGTTAAGCGGTTAAGCGGTGTCGCTCCGGGCT
GGCCAGGTTGCGCTTGGAGTGGTCTGCTGGTGTGAGCGCTGCCGTTTCCGCCCTCGCGTGGCCAGGTAGCATTGACCATGGTGTCTATGTCAGCCCT
TCCGCGCGTGGCCCTTGGCGCGAGCTTCCCTTGGAGAGGCGCCGCAAGGGGCAAGTGCAGACTTTTGGAGGCGTAGAGCTTGGGCGGAGAAATACCGAT
CCGGGATAGGACTCCGCGCCAGGGCCGCGAGCGTCTCGCATCCACGAGCCAGTCCAGCAGTGGCTGAGCTGCGCCCTCGGGTCAAAAACCGGTTTTCCCCTAT
TTTTGATCGTTTTTCCCTGTTTCCATGAGCCGTTGTCACGCTCGGTGACGAAAAGGCTGTCCTGTCCTCCCGTATACAGCTNNNGTTTAAACGAAATCTNNN
TATAAATGCAAGTGTCTCAAAAAATCAGGCAAGCTCCGCAAAAAGAAAGCACATCGTAGTCACTCATGCAAGATAAAGGCAGGTAAGCTCCGGAACC
ACCACAGAAAAAGACACCATTTTTCTCTCAAAATGTTCTCGGGTTTCTGCATAAAACAAAAATAAATAACAAAAAACATTTAAACATTAGAAGCTGTCTTAC
AACAGAAAAAACCTTATAAGCATAAGACGGACTACGGCATTGCCGCTGACGTTAAAAAACCTGGTCAACCGGTTTAAAGAACCCACAGCAGCTCCCTCG
GTATGTTCCGGATCATAATGTAAGACTCGTAAACACATCAGTTTATTACCGTCACTCCGTTTCCAGCTTAAAGAAAGCAGGTAAGTCCGAGGAAATACCCGAGG
CGTAGAGACAACATTACAGCCCAATAGGAGGTATAACAAAATTAATAGGAGAGAAAACACATAAACACCTGAAAAACCTCCTGCCTAGGCAAAATAGCACCT
CCCGTCCAGAACACATACAGCGCTTACAGCGGCAGCCTAACATGATACGCTTACCAGTAAAAAAGAAAACCTATTAAAAAAACACACTCGACACGGCACCAGC
TCAATCAGTCAAGTGTAAAAAGGGCAAAGTGCAGAGCGAGTATATATAGGACTAAAAAATGACGTAAACCGTTAAAGTCCAAAAAACACCCAGAAAACCGCAC
GCAACCTACGCCAGAAAACGAAAGCAAAAACCCCACTTCCCTCAATCGTCACTCCGTTTCCAGCTTAAAGTACGTTCCCTTAAAGAAAATACAATT
CCCAACACATACAAGTTACTCCGCCATAAACCTACGTCAACCGCCCGTTCCACGCCCCGCGCCAGTCAAAACTCCACCCCTCATATCATATTGGTTCA
ATCCAAAATAGGATATATTATGATGATNNNTAATTAAGatcGATcGATcNNNCGTGTGAAATACCCGACAGATGCGTAAGGAGAAAAATCCCGCATCAGCGCTCT
TCCGCTTCCCTCGCTACTGACTCGCTCGCTCGGTCGGTTCGGCTCGCGGAGCGGTATCAGCTCACTCAAAGCGGTAATACGGTTTCCAGAAATACCGGATAC
ACGAGGAAAGAACATCTGTAGCAAAAAGCCAGCAAAAAGCCAGGAAACCTGAAAGAGCCGCTGCTGCGTTTTTCCATAGGCTTCCGCCCTTACAGCATCA
CAAAAATCGACGCTCAAGTCAAGGTTGGGAAAACCCGACAGGACTATAAAGATACAGGCGTTTTCCCTGGAAGCTCCTCGTGGCTCTCCTGTTCCGACCCCTG
CCGTTACCGGATACCTGTCCGCTTCTCCTCCCTCGGGAAGCCTGGCGCTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCCGTTAGGTGTGCTCCTCAAGC
TGGGCTGTGTGACGAAACCCCGTTACGCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGAAGTCCAAAGCCGTTAAGCAGCAGCTATCAGCCACTGCGC
ACGAGGATAACAGGATTAGCAGAGCAGGATGATGAGCGGTTTATGAGGTTCTGAAAGTGGTGGCTAACACTAGGCTACACTAGAAGGAACTATTTGGGATC
TGCGCTGTGTAAGCCAGTTACCTTGGAAAAAGAGTGGTAGCTCTTGTACCGGAAACAACAACCCCGCTGGTAGCGGTGGTTTTTTTTGTGTTGCAAGCAGCAGA
TTACCGCGCAGAAAAAAGGATCTCAAGAAGATCTTTGATCTTTTACGGGTTCTGACGCTCAGTGGAAACGAAAACCTACGTTAAGGGATTTTGGTCAATGAGAT
ATCAAAAAGGATCTTCCACTAGATCTTTAAAATAAAAATGAAAGTTTAAATCAATCTAAAGTATATAGTAATACTGGTTCAGAGTTACCAATGCTTAATC
AGTAGGCACTTCTCAGGACTCTGCTATTTCGTTTCTTCCATGATGTTGCTGACTCCCGCTGTGTAGATAACTTACGATACGGAGGGTACCATCTGGCCCA
GTGCTGCAATGATACCGGAGACCCAGCCTCACGGCTCCAGATTTATCAGCAATAAACCAGCCAGCCGGAAGGGCCAGCGCAGAGTGGTCTGCACTTTATC
CGCTCCATCCAGTCTATTAATGTTGCCGGGAAGCTAGAGTAAGTAGTTGCCAGTAAATAGTTTGGCACAAGTGTGNNNNNAAAAAGGATCTTCACTTAGA
TCCTTTTCACTGAAAGCCAGTCCGAGAAACGGTGTGACCCCGGATGAAATGTCAGCTACTGGGCTATCTGGACAAGGAAAACCGCAAGCGAAAAGAGAAAGCA
GGTAGCTGCAATGGCTGGCTAGCT
CCCTGCAAGTAACTGGATGGCTTTCTCGCCGCAAGGATCTGATGGCGCAGGGGATCAAGCTCTGATCAAGAGACAGGATGAGGATCGTTCGCATGATTGAA
AAGATTGGATTGACACGAGGTTCTCGGCCGCTGGGTGGAGAGGCTATTGGCTATGACTGGGCACACAGCAATCGGCTGCTCTATGCGCCGCTGTTCGGGT
GTACGCGCAGGGGCGCGGTTCTTTTCAAGACCAGCTTCCGCTGAAATGAACTGCAAGACGAGGAGCGGCTTCTGTGGCTGGCCAGCACGGGCG
GTTCTTGGCAGCTGTGCTFCAGGTTGTCACCTGAGCGGGAAGGACTGGCTGTGTTTGGGCGAAGTGGCGGAGGATCTCCTGTCATCTACCTTGTCTCTG
CCGAGAAAGTATCCATCATGGCTGATGCAATGCGCGGCTGCATACGCTTGTATCCGGCTACCTGCCCCATTGACCCAAAGCGAAACATCGCATCGAGCGAGCAG
TACTCGGATGGAAGCCGGTCTTGTGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCCAGCGAAGTGTTCGCCAGGCTCAAGGCGAGCATGCCCGAG
GGCGAGGATCTGCTGTGACCCATGGCGATGCCTGCTTCCGAATATCATGGTGGAAAATGGCCGCTTTTTTGGATTATCGACTGTGGCCGGCTGGGTGTGGCG
ACCGCTATCAGGACATAGCTTGGTACCCTGATATTGCTGAAGAGCTTGGCGCGAAATGGGCTGACCGCTTCTCGTGTCTTACGGTATCGCCGCTCCGATTC

GCAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCCTTCTGAATTTTGTAAAAATTTTGTAAATCAGCTCATTTTTTAAACCAATAGGCCGAAATCGGCAACAT
 CCCTTATAAATCAAAGAATAGACCGCGATAGGGTGTAGTGTGTTCAGTTTGGAAACAAGAGTCCACTATTAAAGAAGCTGGACTCCAACGTCAAAGGGCGAAAA
 ACCGCTCTATCAGGGCGATGGCCACTACGTGAACCATCACCCAAATCAAGTTTTCGCGTTCGAGGTGCCGTAAGCTCTAAATCGGAACCCCTAAAGGGAGCCCC
 GATTTAGAGCTTGACGGGAAAGCGCGCAACGTGGCGAGAAAGGAAGGAAGGCGAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTACAGCTGCG
 CGTAACCACCACACCCGCGCGCTTAATGCGCCGNNNNNNN

Unique enzymes in pAdTrace-OMIR:

BsrG I	T`GTAC,A	207				5800	5890	5936	6193
Acc65 I	G`GTAC,C	359				6714	6843	6896	6922
Asp718	G`GTAC,C	359				6968	7059	7328	7786
Kpn I	G,GTAC`C	363			Alw I (24)	7915	8133	8172	2640
Xba I	T`CTAG,A	1649				945	1653	2192	2640
Hpa I	GTT AAC	1765				2732	2931	3322	3485
Swa I	ATTT AAAT	2160				3863	5447	5454	6194
Bst1107 I	GTA TAC	4425			AlwN I (6)	6280	6280	6377	6378
Xca I	GTA TAC	4425				6778	6779	7042	7059
Pme I	CTTT AAAC	4440				7089	7400	7467	7646
EcoR I	G`AATT,C	4445			Apa I (2)	2469	2627	2712	4433
Avr II	C`CTAG,G	4964			ApaL I (2)	6048	6846		
Cla I	AT`CG,AT	5450			Apo I (7)	3282	3588		
BspH I	T`CATG,A	6352				3168	5946		
Psp1406 I	AA`CG,TT	6751			Ase I (6)	257	1816	2155	3179
Eag I	C`GGCC,G	7128				4445	7887	7898	
Xma III	C`GGCC,G	7128				5	371	1982	4920
Rsr II	CG`GWC,CG	7738			Ava I (5)	5439	6697		
Dra III	CAC,NNN`GTG	8085			Asp718 (1)	359			
Xmn I	GAANN NNTTC	8306				1224	1416	2599	2779
Number of enzymes = 20						4854			
					Ava II (7)	2783	2807	3832	3973
						4051	6663	7738	
					Avr II (1)	4964			
					Ban I (16)	359	829	1080	1338
						1425	1533	1632	2965
						3386	4177	5081	6473
						6973	7221	7256	8122
					Ban II (9)	1023	2304	2361	2517
						3282	3588	4307	7587
						8160			
					Bbe I (6)	1429	1537	1636	4181
						6977	7225		
					Bbs I (2)	1383	4071		
					Bbv I (19)	1535	1790	2262	2265
						2457	2484	2544	2636
						3571	3587	3647	4170
						5030	6051	6054	6260
						7295	7337	7858	
					Bbv II (2)	1382	4072		
					Bcl I (2)	1659	7063		
					Bcn I (18)	1532	2337	2601	2602
						2781	2782	3127	3519
						3609	4018	4244	4856
						4857	6013	6709	6830
						7227	7387		
					Bfa I (11)	364	956	1650	1851
						4965	6127	6380	6715
						6781	6923	8236	
					Bgl I (7)	454	576	647	2661
						4712	6645	8305	
					Bpm I (3)	2345	4973	6595	
					Bsa I (5)	2409	2797	3773	4285
						6586			
					BsaA I (8)	704	1178	2021	3060
						5271	6795	7526	8085
					BsaB I (3)	1664	2724	7081	
					BsaH I (13)	486	539	622	808
						979	1426	1483	1534
						1633	3225	4178	6974
						7222			
					BsaJ I (42)	724	961	973	1108
						1132	1168	1225	1285
						1381	1417	1486	1612
						2328	2335	2483	2599
						2779	3001	3013	3125
						3282	3295	3419	3420
						3517	3945	3961	4032
						4113	4137	4149	4167
						4242	4767	4854	4855
						4964	5792	6827	7031
						7385	7654		
					BsaW I (8)	1643	3164	4551	4778
						5838	5985	6955	7253
					BseR I (5)	959	1283	3871	4187
						4756			
					Bsg I (5)	1542	2551	3161	4216
						5141			
					BsiE I (6)	2799	4845	5548	5972
						7131	8118		

The following enzymes do not cut in pAdTrace-OMIR:

Afl II	Age I	Asc I	BamH I	Bgl II					
Blp I	BsiC I	BsiW I	BstB I	Bsu36 I	Ban II (9)				
Eco72 I	EcoN I	EcoR V	Esp I	Fse I					
Hind III	Mlu I	Nhe I	Not I	Nru I					
PaeR7 I	Pml I	Pvu I	Sal I	Sca I	Bbe I (6)				
Sfi I	Spe I	Spl I	Srf I	Ssp I					

pAdTrace-OMIR: sites sorted by name:

Aat II	(5)	489	542	625	811				
		982							
Acc I	(2)	3486	4424						
Acc65 I	(1)	359							
Aci I	(108)	88	106	126	151				
		233	243	294	422				
		450	462	476	643				
		734	767	871	892				
		953	1067	1090	1114				
		1189	1267	1336	1406				
		1471	1619	2257	2260				
		2263	2389	2452	2455				
		2458	2467	2479	2483				
		2485	2517	2548	2552				
		2682	2771	2789	2917				
		3035	3288	3291	3376				
		3380	3397	3493	3573				
		3712	3729	3787	3830				
		3891	3901	4137	4139				
		4181	4257	4262	4271				
		4599	4871	4985	5015				
		5190	5322	5343	5361				
		5472	5498	5515	5558				
		5565	5586	5677	5705				
		5832	5851	5972	6082				
		6217	6226	6588	6679				
		6809	6932	7028	7131				
		7194	7288	7352	7453				
		7456	7696	7736	7741				
		7791	7807	7833	7975				
		8114	8229	8256	8284				
Afe I	(3)	2955	4070	5006					
Afl III	(3)	158	4591	5632					
Aha II	(13)	486	539	622	808				
		979	1426	1483	1534				
		1633	3225	4178	6974				
		7222							
Ahd I	(3)	1142	2789	6525					
Alu I	(43)	25	930	1097	1214				
		1331	1460	1526	1556				
		1781	2302	2535	2627				
		2907	2993	3043	3193				
		3535	3562	3632	3638				
		3841	4161	4218	4305				
		4549	4764	5088	5574				

BsiHKA I	(8)	2274	2304	3172	3932			3913	7527			
		4307	5950	7335	7525	Dde I	(9)	1150	2511	2620	3194	
Bsm I	(4)	1753	1846	3254	4285			3555	3651	5907	6316	
BsmA I	(11)	797	2410	2434	2796			6482				
		2880	3217	3774	4284	Dpn I	(34)	951	1047	1443	1648	
		4877	6587	7065				1661	2187	2635	2727	
BsmB I	(2)	2881	3216					2937	3317	3350	3480	
BsmF I	(10)	539	690	858	1130			3531	3869	5449	5453	
		1149	2796	3665	3818			6200	6275	6286	6294	
		4402	7373					6372	6384	6489	6773	
BsoF I	(69)	1067	1115	1268	1332			6785	7037	7054	7065	
		1337	1472	1524	1527			7084	7395	7473	7554	
		1619	1779	2251	2254			7563	7641			
		2257	2260	2263	2446	DpnII	(34)	949	1045	1441	1646	
		2455	2458	2467	2470			1659	2185	2633	2725	
		2473	2533	2625	2915			2935	3315	3348	3478	
		3289	3292	3560	3563			3529	3867	5447	5451	
		3576	3633	3636	3639			6198	6273	6284	6292	
		3729	3902	4021	4072			6370	6382	6487	6771	
		4140	4159	4181	4262			6783	7035	7052	7063	
		4470	5016	5019	5538			7082	7393	7471	7552	
		5556	5559	5677	5832			7561	7639			
		5975	6040	6043	6249	Dra I	(9)	1704	2063	2076	2160	
		6577	7028	7131	7183			2688	4440	4643	6391	
		7194	7284	7289	7326			6410				
		7367	7454	7457	7460	Dra III	(1)	8085				
		7696	7792	7833	7847	Drd I	(5)	1488	4117	5740	7249	
		8265						8040				
Bsp120 I	(2)	3278	3584			Dsa I	(10)	724	961	1381	2328	
Bsp1286 I	(2)	2274	7525					2483	3282	3961	4113	
BspH I	(1)	6352						4137	7654			
BspM I	(8)	2636	3498	3538	3858	Eae I	(12)	283	1031	1472	1507	
		4532	6880	7109	7490			4029	4095	4309	4704	
BspM II	(2)	4551	4778					7128	7302	7693	7720	
Bsr I	(19)	660	1158	2940	3620	Eag I	(1)	7128				
		4735	5040	6039	6052	Ear I	(4)	1904	5516	7566	7776	
		6166	6572	6690	6733	Eco47 III	(3)	2955	4070	5006		
		6805	6850	6931	7015	Eco57 I	(10)	1118	1451	1475	1481	
		7165	7366	7999				2447	2678	4084	6179	
BsrB I	(5)	1406	4987	5565	7835			7367	7799			
		8229				EcoO109 I	(5)	1914	2807	3010	3973	
BsrD I	(3)	3280	6586	7455				4267				
BsrG I	(1)	207				EcoR I	(1)	4445				
BssH II	(6)	1607	2765	2767	4023	EcoR II	(19)	452	645	1131	1285	
		4154	8286					2823	3000	3294	3339	
BssS I	(5)	1035	4184	4291	5805			3419	3825	3944	4031	
		7814						4097	4296	4328	5658	
Bst1107 I	(1)	4425						5779	5792	7607		
BstE II	(4)	1103	1274	3845	4734	Ehe I	(6)	1427	1535	1634	4179	
BstN I	(19)	454	647	1133	1287			6975	7223			
		2825	3002	3296	3341	Fnu4H I	(69)	1067	1115	1268	1332	
		3421	3827	3946	4033			1337	1472	1524	1527	
		4099	4298	4330	5660			1619	1779	2251	2254	
		5781	5794	7609				2257	2260	2263	2446	
BstU I	(36)	88	231	233	294			2455	2458	2467	2470	
		350	424	1246	1336			2473	2533	2625	2915	
		1609	1890	2318	2485			3289	3292	3560	3563	
		2554	2767	2769	2771			3576	3633	3636	3639	
		3376	3891	4025	4091			3729	3902	4021	4072	
		4139	4156	4226	4259			4140	4159	4181	4262	
		4496	5196	5363	5679			4470	5016	5019	5538	
		6260	6590	7288	7589			5556	5559	5677	5832	
		7977	8269	8286	8288			5975	6040	6043	6249	
BstX I	(2)	1505	3269					6577	7028	7131	7183	
BstY I	(13)	949	1646	2185	2633			7194	7284	7289	7326	
		6273	6284	6370	6382			7367	7454	7457	7460	
		6771	6783	7035	7393			7696	7792	7833	7847	
		7639						8265				
Cac8 I	(49)	450	643	1609	2322	Fok I	(20)	184	258	1125	1182	
		2389	2483	2517	2521			1421	2531	2861	3060	
		2525	2552	2643	2767			3356	3398	3632	4240	
		2769	2991	3009	3378			6491	6672	6844	7027	
		3726	3798	4025	4029			7089	7546	7571	7935	
		4156	4163	4266	4713	Fsp I	(3)	1011	6747	7324		
		4875	5194	5563	5649	Gdi II	(9)	1032	1473	4096	4308	
		5686	6246	6637	6874			4705	7127	7129	7692	
		6898	6949	6966	7116			7719				
		7302	7521	7587	7593	Gsu I	(3)	2346	4974	6596		
		7621	7625	7666	7670	Hae I	(11)	285	966	1173	1395	
		7724	8188	8231	8245			1509	3360	4031	5647	
		8288						5658	6110	7304		
Cfr10 I	(10)	202	1629	3578	4074	Hae II	(14)	1429	1537	1636	2957	
		4380	4711	6605	7541			3725	4072	4181	5008	
		7722	8186					5510	5880	6977	7225	
								8236	8244			
Cla I	(1)	5450				Hae III	(43)	285	448	641	966	
Csp6 I	(14)	208	360	582	607			1033	1066	1117	1173	
		662	695	746	903			1360	1395	1474	1509	
		1160	1412	1601	2011							

		1618	1916	2334	2778			2839	3232	3430	3845
		3011	3280	3294	3360			3994	4396	4716	4734
		3418	3586	3663	3944			5096	5154	5247	5266
		4031	4097	4147	4268			5271	5315	5337	5369
		4311	4706	5115	5647			5988	6051	6167	6450
		5658	5676	6110	6568			7342	7648	8258	8270
		6648	7130	7304	7695	Mbo I	(34)	949	1045	1441	1646
		7722	7935	8077				1659	2185	2633	2725
Hga I	(7)	889	1490	2332	3232			2935	3315	3348	3478
		4081	5742	6320				3529	3867	5447	5451
HgiA I	(8)	2274	2304	3172	3932			6198	6273	6284	6292
		4307	5950	7335	7525			6370	6382	6487	6771
HgiE II	(2)	3570	6211					6783	7035	7052	7063
Hha I	(60)	88	202	233	350			7082	7393	7471	7552
		1000	1012	1246	1336			7561	7639		
		1428	1536	1609	1611	Mbo II	(16)	1384	1387	1920	3223
		1635	2320	2641	2767			3313	3514	3551	4072
		2769	2771	2956	3376			5504	6293	6366	6767
		3724	3969	4013	4025			7582	7792	7874	8224
		4027	4041	4071	4091	Mme I	(6)	1377	2417	2612	5846
		4156	4158	4180	4226			6030	8061		
		4261	4498	5007	5365	Mnl I	(67)	56	304	905	968
		5509	5542	5812	5879			976	979	1010	1043
		5979	6153	6262	6655			1049	1055	1070	1158
		6748	6878	6976	7047			1220	1253	1303	1360
		7216	7224	7288	7325			1385	1405	1412	1444
		7591	7851	8235	8243			1481	1571	1576	1607
		8269	8288	8290	8299			1681	1720	1729	1905
HinC II	(2)	1765	2566					2458	2677	2682	2797
Hind II	(2)	1765	2566					2881	3131	3246	3376
Hinf I	(20)	774	1290	1929	2589			3445	3891	3985	4038
		2709	2842	3130	3686			4143	4165	4168	4180
		4238	4782	4796	4818			4200	4373	4501	4776
		5532	5607	6003	6520			4899	4966	4990	5248
		7707	7841	8012	8034			5395	5530	5740	5813
HinI I	(13)	486	539	622	808			6064	6464	6545	6691
		979	1426	1483	1534			6987	7073	7137	7273
		1633	3225	4178	6974			7630	7822	8113	
		7222						285	1509	4031	7304
HinP I	(60)	86	200	231	348	Msc I	(4)	5	9	371	1703
		998	1010	1244	1334	Mse I	(36)	1764	1885	1982	2062
		1426	1534	1607	1609			2075	2159	2608	2687
		1633	2318	2639	2765			3039	3624	3672	4439
		2767	2769	2954	3374			4642	4745	4920	5059
		3722	3967	4011	4023			5162	5285	5439	5443
		4025	4039	4069	4089			6338	6390	6395	6409
		4154	4156	4178	4224			6462	6697	6736	7895
		4259	4496	5005	5363			7907	7924	8022	8292
		5507	5540	5810	5877	Msl I	(5)	729	3267	3332	4526
		5977	6151	6260	6653			7659			
		6746	6876	6974	7045	Msp I	(39)	203	1531	1630	1644
		7214	7222	7286	7323			2335	2600	2780	3125
		7589	7849	8233	8241			3165	3415	3517	3579
		8267	8286	8288	8297			3607	4016	4075	4242
Hpa I	(1)	1765						4381	4552	4712	4779
Hpa II	(39)	203	1531	1630	1644			4855	5839	5986	6012
		2335	2600	2780	3125			6202	6606	6640	6707
		3165	3415	3517	3579			6829	6956	7127	7204
		3607	4016	4075	4242			7226	7254	7385	7475
		4381	4552	4712	4779			7542	7723	8187	
		4855	5839	5986	6012	MspAl I	(14)	1526	2469	2485	2627
		6202	6606	6640	6707			2789	3535	3562	3638
		6829	6956	7127	7204			4139	5015	5974	6219
		7226	7254	7385	7475			6968	7328		
		7542	7723	8187				1752	2583		
Hph I	(18)	120	739	1114	1285	Mun I	(2)	4713	7724	8188	
		1336	1557	2850	3840	Nae I	(3)	1426	1534	1633	4178
		4011	4311	4407	4729	Nar I	(6)	6974	7222		
		5332	6369	6596	6770			1531	2336	2600	2601
		7401	8087					2780	2781	3126	3518
Kas I	(6)	1425	1533	1632	4177			3608	4017	4243	4855
		6973	7221					4856	6012	6708	6829
		363						7226	7386		
Kpn I	(1)	364	956	1650	1851			724	961	1381	2328
Mae I	(11)	4965	6127	6380	6715	Nco I	(6)	4113	7654		
		6781	6923	8236				598	2090		
Mae II	(30)	81	113	187	486	Nde I	(2)	4711	7722	8186	
		498	539	622	703	NgoM I	(3)	162	668	728	965
		808	979	1177	2020	Nla III	(38)	998	1016	1385	1508
		2025	2829	3059	3324			1929	2270	2324	2332
		5153	5265	5270	5336			2864	2914	3137	3190
		5368	6335	6751	6794			3254	3485	3680	3695
		7338	7525	8029	8041			3800	3955	4117	4344
		8084	8194					4378	4525	4531	4595
Mae III	(40)	77	109	183	218			4711	4777	5636	6356
		266	337	425	512			6915	7096	7441	7627
		861	1103	1274	1280			7658	7684		
		1790	2021	2100	2492	Nla IV	(38)	361	831	1022	1082

		1118	1166	1340	1361		5508	5728	7181	7436	
		1427	1535	1634	2360		7520	7584	7652	7859	
		2784	2808	2967	3280	Sfc I	(7)	1299	2443	2470	2900
		3388	3409	3552	3586			3633	5897	6088	
		3662	3834	3974	4179	Sma I	(3)	2601	2781	4856	
		4269	4556	5083	5664	SnaB I	(2)	704	5271		
		5703	6475	6569	6610	Sph I	(3)	2324	3800	7627	
		6975	7223	7258	8124	Stu I	(2)	1173	1395		
		8145	8157			Sty I	(13)	724	961	1108	1168
Nsi I	(2)	3078	3256					1381	2328	3013	4113
Nsp7524 I	(8)	158	2320	3676	3691			4149	4167	4964	7031
		3796	4591	5632	7623			7654			
NspB II	(14)	1526	2469	2485	2627	Swa I	(1)	2160			
		2789	3535	3562	3638	Taq I	(14)	1042	1048	1258	2117
		4139	5015	5974	6219			3866	5074	5450	5732
		6968	7328					7335	7491	7515	7551
NspH I	(8)	162	2324	3680	3695			7713	8118		
		3800	4595	5636	7627	Tfi I	(8)	1929	2589	3130	4238
Pac I	(2)	9	5443					4818	5607	7707	7841
Pal I	(43)	285	448	641	966	Tsp45 I	(23)	77	109	183	218
		1033	1066	1117	1173			1103	1274	1280	2021
		1360	1395	1474	1509			2492	2839	3232	3845
		1618	1916	2334	2778			3994	4396	4716	4734
		3011	3280	3294	3360			5096	5247	5337	5369
		3418	3586	3663	3944			7342	7648	8258	
		4031	4097	4147	4268	Tth111 I	(2)	2420	7340		
		4311	4706	5115	5647	Tth111 II	(9)	2539	2705	2744	3832
		5658	5676	6110	6568			4603	6221	6230	6260
		6648	7130	7304	7695			7658			
		7722	7935	8077		Vsp I	(6)	5	371	1982	4920
PflM I	(2)	1387	2830					5439	6697		
Ple I	(3)	4790	6011	8020		Xba I	(1)	1649			
Pme I	(1)	4440				Xca I	(1)	4425			
PpuM I	(2)	2807	3973			Xcm I	(3)	2713	4304	7038	
Psp1406 I	(1)	6751				Xho II	(13)	949	1646	2185	2633
PspA I	(3)	2599	2779	4854				6273	6284	6370	6382
Pst I	(5)	1303	2447	2474	2904			6771	6783	7035	7393
		3637						7639			
Pvu II	(7)	1526	2627	3535	3562	Xma I	(3)	2599	2779	4854	
		3638	6968	7328		Xma III	(1)	7128			
Rsa I	(14)	209	361	583	608	Xmn I	(1)	8306			
		663	696	747	904						
		1161	1413	1602	2012						
		3914	7528								

Site usage in pAdTrace-OMIR:

Rsr II	(1)	7738				Aat II	G,ACGT`C	5	Acc I	GT`MK,AC	2
Sac I	(2)	2304	4307			Acc65 I	G`GTAC,C	1	Aci I	C`CG,C	108
Sac II	(2)	2486	4140			Afe I	AGC GCT	3	Afl II	C`TTAA,G	-
Sap I	(3)	5516	7566	7776		Afl III	A`CRYG,T	3	Age I	A`CCGG,T	-
Sau3A I	(34)	949	1045	1441	1646	Aha II	GR`CG,YC	13	Ahd I	GACNN,N`NNGTC	3
		1659	2185	2633	2725	Alu I	AG CT	43	Alw I	GGATC 8/9	24
		2935	3315	3348	3478	AlwN I	CAG,NNN`CTG	6	Apa I	G,GGCC`C	2
		3529	3867	5447	5451	Apal I	G`TGCA,C	2	Apo I	R`AATT,Y	7
		6198	6273	6284	6292	Asc I	GG`CGCG,CC	-	Ase I	AT`TA,AT	6
		6370	6382	6487	6771	Asp718	G`GTAC,C	1	Ava I	C`YCGR,G	5
		6783	7035	7052	7063	Ava II	G`GWC,C	7	Avr II	C`CTAG,G	1
		7082	7393	7471	7552	BamH I	G`GATC,C	-	Ban I	G`GYRC,C	16
		7561	7639			Ban II	G,RCGY`C	9	Bbe I	G,CGCC`C	6
		447	640	1064	1116	Bbs I	GAAGAC 8/12	2	Bbv I	GCAGC 13/17	19
Sau96 I	(30)	1359	1616	1914	2332	Bbv II	GAAGAC 7/11	2	Bcl I	T`GATC,A	2
		2777	2783	2807	3010	Bcn I	CC,S`GG	18	Bfa I	C`TA,G	11
		3278	3279	3417	3584	Bgl I	GCCN,NNN`NGGC	7	Bgl II	A`GATC,T	-
		3585	3661	3832	3942	Blp I	GC`TNA,GC	-	Bpm I	CTGGAG 22/20	3
		3973	4051	4146	4267	Bsa I	GGTCTC 7/11	5	BsaA I	YAC GTR	8
		5113	6567	6646	6663	BsaB I	GATNN NNATC	3	BsaH I	GR`CG,YC	13
		7738	8076			BsaJ I	C`CNNG,G	42	BsaW I	W`CCGG,W	8
		454	647	1133	1287	BseI I	GAGGAG 16/14	5	Bsg I	GTGCAG 22/20	5
ScrF I	(37)	1531	2336	2600	2601	BsiC I	TT`CG,AA	-	BsIE I	CG,RY`CG	6
		2780	2781	2825	3002	BsiHKA I	G,WGCW`C	8	BsiW I	C`GTAC,G	-
		3126	3296	3341	3421	Bsm I	GAATG,C 7	4	BsmA I	GTCTC`/9	11
		3518	3608	3827	3946	BsmB I	CGTCTC 7/11	2	BsmF I	GGGAC 15/19	10
		4017	4033	4099	4243	BsoF I	GC`N,GC	69	Bsp120 I	G`GGCC,C	2
		4298	4330	4855	4856	Bsp1286 I	G,DGCH`C	2	BspH I	T`CATG,A	1
		5660	5781	5794	6012	BspM I	ACCTGC 10/14	8	BspM II	T`CCGG,A	2
		6708	6829	7226	7386	Bsr I	ACT,GG`	19	Bsrf I	GAG CGG	5
		7609				BsrD I	GCAATG, 8	3	Bsrg I	T`GTAC,A	1
Sec I	(42)	724	961	973	1108	BssH II	G`CGCG,C	6	Bsss I	C`TCGT,G	5
		1132	1168	1225	1285	Bst1107 I	GTA TAC	1	BstB I	TT`CG,AA	-
		1381	1417	1486	1612	BstE II	G`GTNAC,C	4	BstN I	CC`W,GG	19
		2328	2335	2483	2599	BstU I	CG G	36	BstX I	CCAN,NNNN`NTGG	2
		2779	3001	3013	3125	BstY I	R`GATC,Y	13	Bsu36 I	CC`TNA,GG	-
		3282	3295	3419	3420	Cac8 I	GCN NGC	49	Cfr10 I	R`CCGG,Y	10
		3517	3945	3961	4032	Cla I	AT`CG,AT	1	Csp6 I	G`TA,C	14
		4113	4137	4149	4167	Dde I	C`TNA,G	9	Dpn I	GA TC	34
		4242	4767	4854	4855	DpnII	`GATC,	34	Dra I	TTT AAA	9
		4964	5792	6827	7031	Dra III	CAC,NNN`GTG	1	Drd I	GACNN,NN`NNGTC	5
		7385	7654			Dsa I	C`CRYG,G	10	Eae I	Y`GGCC,R	12
SfaN I	(16)	722	1817	3064	3084	Eag I	C`GGCC,G	1	Ear I	CTCTTC 7/10	4
		3869	4261	4342	5470	Eco47 III	AGC GCT	3	Eco57 I	CTGAAG 21/19	10
						Eco72 I	CAC GTG	-	EcoN I	CCTNN`N,NNAGG	-
						Eco0109 I	RG`GNC,CY	5	EcoR I	G`AATT,C	1
						EcoR II	`CCWGG,	19	EcoR V	GAT ATC	-
						Ehe I	GGC GCC	6	Esp I	GC`TNA,GC	-
						Fnu4H I	GC`N,GC	69	Fok I	GGATG 14/18	20
						Fse I	GG,CCGG`CC	-	Fsp I	TGC GCA	3
						Gdi II	`YGGC,CG	9	Gsu I	CTGGAG 21/19	3
						Hae I	WGG CCW	11	Hae II	R,GGCC`Y	14

Hae III	GG CC	43	Hga I	GACGC 9/14	7	PflM I	CCAN,NNN`NTGG	2	Ple I	GAGTC 9/10	3
HgiA I	G,WGCW`C	8	HgiE II	ACCNNNNNNGGT -1/132		Pme I	CTTT AAAC	1	Pml I	CAC GTG	-
Hha I	G,CG`C	60	HinC II	GTY RAC	2	PpuM I	RG`GWC,CY	2	Psp1406 I	AA`CG,TT	1
Hind II	GTY RAC	2	Hind III	A`AGCT,T	-	PspA I	C`CCGG,G	3	Pst I	C,TGCA`G	5
Hinf I	G`ANT,C	20	HinI I	GR`CG,YC	13	Pvu I	CG,AT`CG	-	Pvu II	CAG CTG	7
HinP I	G`CG,C	60	Hpa I	GTT AAC	1	Rsa I	GT AC	14	Rsr II	CG`GWC,CG	1
Hpa II	C`CG,G	39	Hph I	GGTGA 12/11	18	Sac I	G,AGCT`C	2	Sac II	CG,GC`GG	2
Kas I	G`GCGC,C	6	Kpn I	G,GTAC`C	1	Sal I	G`TCGA,C	-	Sap I	GCCTTTC 8/11	3
Mae I	C`TA,G	11	Mae II	A`CG,T	30	Sau3A I	`GATC,	34	Sau96 I	G`GNC,C	30
Mae III	`GTNAC,	40	Mbo I	`GATC,	34	Sca I	AGT ACT	-	ScrF I	CC`N,GG	37
Mbo II	GAAGA 12/11	16	Mlu I	A`CGCG,T	-	Sec I	C`CNNG,G	42	SfaN I	GCATC 9/13	16
Mme I	TCCRAC 25/23	6	Mnl I	CCTC 10/10	67	Sfc I	C`TRYA,G	7	Sfi I	GGCCN,NNN`NGGCC	-
Msc I	TGG CCA	4	Mse I	T`TA,A	36	Sma I	CCC GGG	3	SnaB I	TAC GTA	2
Msl I	CAYNN NNRTG	5	Msp I	C`CG,G	39	Spe I	A`CTAG,T	-	Sph I	G,CATG`C	3
MspAl I	CMG CKG	14	Mun I	C`AATT,G	2	Spl I	C`GTAC,G	-	Srf I	GCCC GGGC	-
Nae I	GCC GGC	3	Nar I	GG`CG,CC	6	Ssp I	AAT ATT	-	Stu I	AGG CCT	2
Nci I	CC`S,GG	18	Nco I	C`CATG,G	6	Sty I	C`CWWG,G	13	Swa I	ATTT AAAT	1
Nde I	CA`TA,TG	2	NgoM I	G`CCGG,C	3	Taq I	T`CG,A	14	Tfi I	G`AWT,C	8
Nhe I	G`CTAG,C	-	Nla III	,CATG`	38	Tsp45 I	`GTSAC,	23	Tth111 I	GACN`N,NGTC	2
Nla IV	GGN NCC	38	Not I	GC`GGCC,GC	-	Tth111 II	CAARCA 16/14	9	Vsp I	AT`TA,AT	6
Nru I	TCG CGA	-	Nsi I	A,TGCA`T	2	Xba I	T`CTAG,A	1	Xca I	GTA TAC	1
Nsp7524 I	R`CATG,Y	8	NspB II	CMG CKG	14	Xcm I	CCANNNN,N`NNNNTGG3		Xho I	C`TCGA,G	-
NspH I	R,CATG`Y	8	Pac I	TTA,AT`TAA	2	Xho II	R`GATC,Y	13	Xma I	C`CCGG,G	3
PaeR7 I	C`TCGA,G	-	Pal I	GG CC	43	Xma III	C`GGCC,G	1	Xmn I	GAANN NNTTC	1