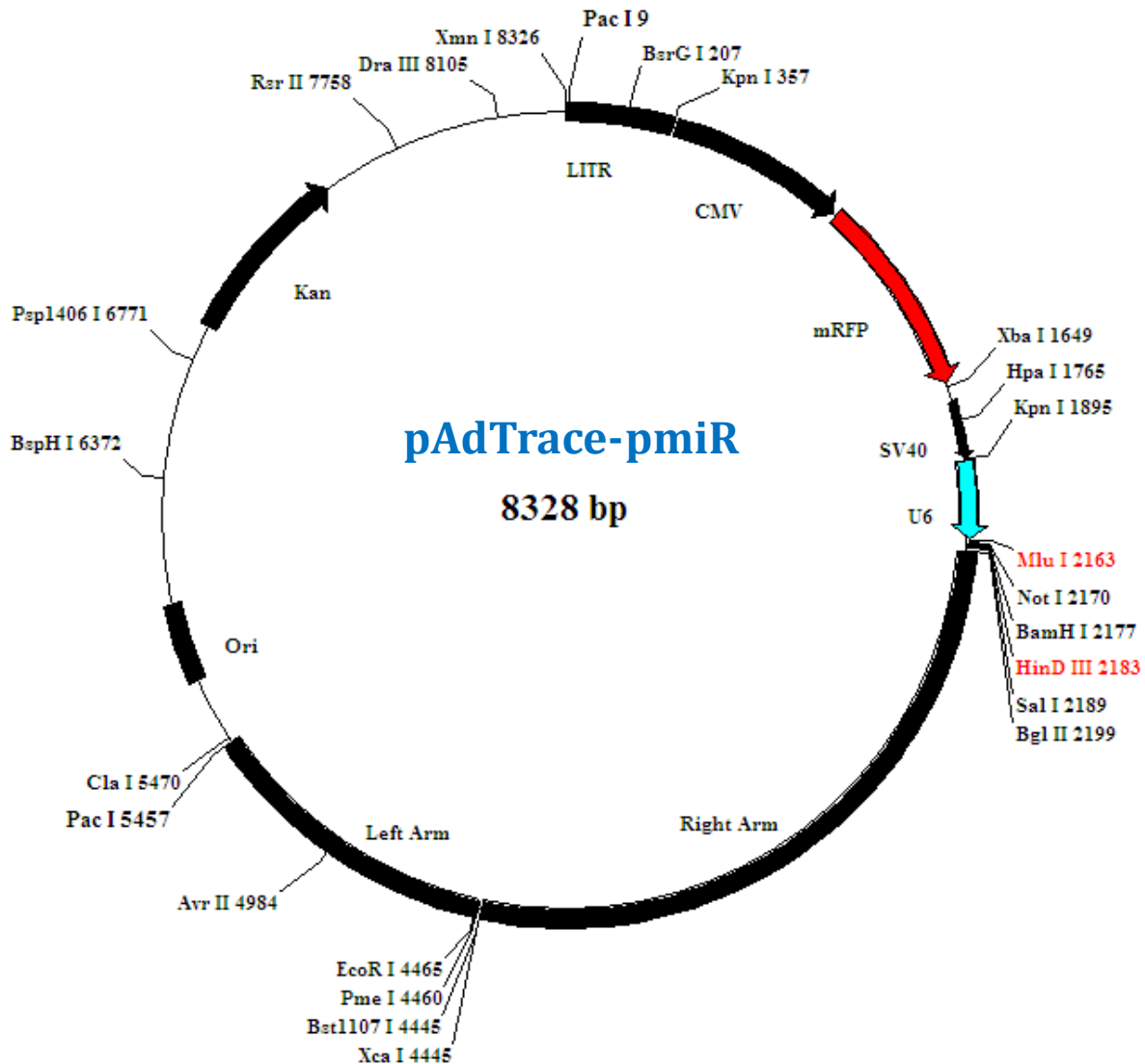


Vector: pAdTrace-pmiR (adenoviral shuttle vector for pre-miR, shRNA or anti-miR oligos)

Antibiotic Selection: Kan

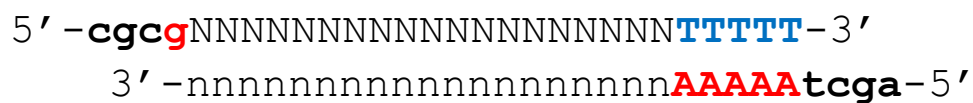
Creator(S): Qiang Wei & Shujuan Yan @ Molecular Oncology Laboratory of The University of Chicago Medical Center

Date of Construction: October, 2016



NOTE: XbaI (at 1649) is methylated!

Designing pre-miR, shRNA, or anti-miR oligo cassette (MluI/HindIII or XbaI)



pAdTrace-pmiR Vector Sequence

NNNTAATTAANNNTCCCTTCCAGCTCTCTGCCCTTTTGGATTGAAGCCAATATGATAATGAGGGGGTGGAGTTTGTGACGTGGCGCGG
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Unique enzymes in pAdTrace-pmiR:

BsrG I	T`GTAC,A	207				3749	3807	3850	3911
Xba I	T`CTAG,A	1649				3921	4157	4159	4201
Hpa I	GTT AAC	1765				4277	4282	4291	4619
Mlu I	A`CGCG,T	2163				4891	5005	5035	5210
Not I	GC`GGCC,GC	2170				5342	5363	5381	5492
BamH I	G`GATC,C	2177				5518	5535	5578	5585
HinD III	A`AGCT,T	2183				5606	5697	5725	5852
Sal I	G`TCGA,C	2189				5871	5992	6102	6237
Bgl II	A`GATC,T	2199				6246	6608	6699	6829
Bst1107 I	GTA TAC	4445				6952	7048	7151	7214
Xca I	GTA TAC	4445				7308	7372	7473	7476
Pme I	CTTT AAAC	4460				7716	7756	7761	7811
EcoR I	G`AATT,C	4465				7827	7853	7995	8134
Avr II	C`CTAG,G	4984				8249	8276	8304	
Cla I	AT`CG,AT	5470		Afl III	(4)	158	2163	4611	5652
BspH I	T`CATG,A	6372		Aha II	(13)	486	539	622	808
Psp1406 I	AA`CG,TT	6771				979	1426	1483	1534
Rsr II	CG`GWC,CG	7758				1633	3245	4198	6994
Dra III	CAC,NNN`GTG	8105				7242			
Xmn I	GAANN NNTTC	8326		Ahd I	(3)	1142	2809	6545	
Number of enzymes = 20				Alu I	(44)	25	930	1097	1214

The following enzymes do not cut in pAdTrace-pmiR:

Afl II	Age I	Asc I	Blp I	BsiC I		1781	2185	2322	2555		
BsiW I	BstB I	Bsu36 I	Eco72 I	EcoN I		2647	2927	3013	3063		
EcoR V	Esp I	Fse I	Nhe I	Nru I		3213	3555	3582	3652		
Paer7 I	Pml I	Pvu I	Sca I	Sfi I		3658	3861	4181	4238		
Spe I	Spl I	Srf I	Ssp I	Xho I		4325	4569	4784	5108		
						5594	5820	5910	5956		
						6213	6734	6863	6916		
pAdTrace-pmiR: sites sorted by name:						6942	6988	7079	7348		
Aat II	(5)	489	542	625	811	7806	7935	8153	8192		
		982									
Alw I	(25)	945	1653	2173	2184						
Acc I	(3)	2190	3506	4444		2660	2752	2951	3342		
Acc65 I	(2)	359	1897			3505	3883	5467	5474		
Aci I	(111)	88	106	126	151	6214	6300	6300	6397		
		233	243	294	422	6398	6798	6799	7062		
		450	462	476	643	7079	7109	7420	7487		
		734	767	871	892	7666					
		953	1067	1090	1114	AlwN I	(6)	2489	2647	2732	4453
		1189	1267	1336	1406			6068	6866		
		1471	1619	2169	2173	Apa I	(2)	3302	3608		
		2175	2277	2280	2283	ApaL I	(2)	3188	5966		
		2409	2472	2475	2478	Apo I	(6)	257	1816	3199	4465
		2487	2499	2503	2505			7907	7918		
		2537	2568	2572	2702	Ase I	(6)	5	371	1988	4940
		2791	2809	2937	3055			5459	6717		
		3308	3311	3396	3400	Asp718	(2)	359	1897		
		3417	3513	3593	3732	Ava I	(5)	1224	1416	2619	2799

		4874				3580	3583	3596	3653
Ava II	(7)	2803	2827	3852	3993	3656	3659	3749	3922
		4071	6683	7758		4041	4092	4160	4179
Avr II	(1)	4984				4201	4282	4490	5036
BamH I	(1)	2177				5039	5558	5576	5579
Ban I	(17)	359	829	1080	1338	5697	5852	5995	6060
		1425	1533	1632	1897	6063	6269	6597	7048
		2985	3406	4197	5101	7151	7203	7214	7304
		6493	6993	7241	7276	7309	7346	7387	7474
		8142				7477	7480	7716	7812
Ban II	(9)	1023	2324	2381	2537	7853	7867	8285	
		3302	3608	4327	7607				
		8180				Bsp120 I	(2)	3298	3604
Bbe I	(6)	1429	1537	1636	4201	Bsp1286 I	(2)	2294	7545
		6997	7245			BspH I	(1)	6372	
Bbs I	(2)	1383	4091			BspM I	(8)	2656	3518 3558 3878
Bbv I	(19)	1535	1790	2282	2285			4552	6900 7129 7510
		2477	2504	2564	2656	BspM II	(2)	4571	4798
		3591	3607	3667	4190	Bsr I	(19)	660	1158 2960 3640
		5050	6071	6074	6280			4755	5060 6059 6072
		7315	7357	7878				6186	6592 6710 6753
Bbv II	(2)	1382	4092					6825	6870 6951 7035
Bcl I	(2)	1659	7083			BsrB I	(5)	1406	5007 5585 7855
Bcn I	(18)	1532	2357	2621	2622			8249	
		2801	2802	3147	3539	BsrD I	(3)	3300	6606 7475
		3629	4038	4264	4876	BsrG I	(1)	207	
		4877	6033	6729	6850	BssH II	(6)	1607	2785 2787 4043
		7247	7407					4174	8306
Bfa I	(11)	364	956	1650	1851	BssS I	(5)	1035	4204 4311 5825
		4985	6147	6400	6735			7834	
		6801	6943	8256		Bst1107 I	(1)	4445	
Bgl I	(7)	454	576	647	2681	BstE II	(4)	1103	1274 3865 4754
		4732	6665	8325		BstN I	(19)	454	647 1133 1287
Bgl II	(1)	2199						2845	3022 3316 3361
Bpm I	(3)	2365	4993	6615				3441	3847 3966 4053
Bsa I	(5)	2429	2817	3793	4305			4119	4318 4350 5680
		6606						5801	5814 7629
BsaA I	(8)	704	1178	2027	3080	BstU I	(38)	88	231 233 294
		5291	6815	7546	8105			350	424 1246 1336
BsaB I	(3)	1664	2744	7101				1609	1890 2165 2175
BsaH I	(13)	486	539	622	808			2338	2505 2574 2787
		979	1426	1483	1534			2789	2791 3396 3911
		1633	3245	4198	6994			4045	4111 4159 4176
		7242						4246	4279 4516 5216
BsaJ I	(44)	724	961	973	1108			5383	5699 6280 6610
		1132	1168	1225	1285			7308	7609 7997 8289
		1381	1417	1486	1612			8306	8308
		1901	2173	2348	2355	BstX I	(2)	1505	3289
		2503	2619	2799	3021	BstY I	(14)	949	1646 2177 2199
		3033	3145	3302	3315			2653	6293 6304 6390
		3439	3440	3537	3965			6402	6791 6803 7055
		3981	4052	4133	4157			7413	7659
		4169	4187	4262	4787	Cac8 I	(50)	450	643 1609 2167
		4874	4875	4984	5812			2342	2409 2503 2537
		6847	7051	7405	7674			2541	2545 2572 2663
BsaW I	(8)	1643	3184	4571	4798			2787	2789 3011 3029
		5858	6005	6975	7273			3398	3746 3818 4045
BseR I	(5)	959	1283	3891	4207			4049	4176 4183 4286
		4776						4733	4895 5214 5583
Bsg I	(5)	1542	2571	3181	4236			5669	5706 6266 6657
		5161						6894	6918 6969 6986
BsiE I	(7)	2173	2819	4865	5568			7136	7322 7541 7607
		5992	7151	8138				7613	7641 7645 7686
BsiHKA I	(8)	2294	2324	3192	3952			7690	7744 8208 8251
		4327	5970	7355	7545			8265	8308
Bsm I	(4)	1753	1846	3274	4305	Cfr10 I	(10)	202	1629 3598 4094
BsmA I	(11)	797	2430	2454	2816			4400	4731 6625 7561
		2900	3237	3794	4304			7742	8206
		4897	6607	7085		Cla I	(1)	5470	
BsmB I	(2)	2901	3236			Csp6 I	(15)	208	360 582 607
BsmF I	(10)	539	690	858	1130			662	695 746 903
		1149	2816	3685	3838			1160	1412 1601 1898
		4422	7393					2017	3933 7547
BsoF I	(71)	1067	1115	1268	1332	Dde I	(9)	1150	2531 2640 3214
		1337	1472	1524	1527			3575	3671 5927 6336
		1619	1779	2170	2173			6502	
		2271	2274	2277	2280	Dpn I	(35)	951	1047 1443 1648
		2283	2466	2475	2478			1661	2179 2201 2655
		2487	2490	2493	2553			2747	2957 3337 3370
		2645	2935	3309	3312			3500	3551 3889 5469

		5473	6220	6295	6306		1618	1922	2172	2354	
		6314	6392	6404	6509		2798	3031	3300	3314	
		6793	6805	7057	7074		3380	3438	3606	3683	
		7085	7104	7415	7493		3964	4051	4117	4167	
		7574	7583	7661			4288	4331	4726	5135	
DpnII	(35)	949	1045	1441	1646		5667	5678	5696	6130	
		1659	2177	2199	2653		6588	6668	7150	7324	
		2745	2955	3335	3368		7715	7742	7955	8097	
		3498	3549	3887	5467	Hga I	(7)	889	1490	2352	3252
		5471	6218	6293	6304			4101	5762	6340	
		6312	6390	6402	6507	HgiA I	(8)	2294	2324	3192	3952
		6791	6803	7055	7072			4327	5970	7355	7545
		7083	7102	7413	7491	HgiE II	(2)	3590	6231		
		7572	7581	7659		Hha I	(60)	88	202	233	350
Dra I	(8)	1704	2069	2082	2708			1000	1012	1246	1336
		4460	4663	6411	6430			1428	1536	1609	1611
Dra III	(1)	8105						1635	2340	2661	2787
Drd I	(5)	1488	4137	5760	7269			2789	2791	2976	3396
		8060						3744	3989	4033	4045
Dsa I	(11)	724	961	1381	2173			4047	4061	4091	4111
		2348	2503	3302	3981			4176	4178	4200	4246
		4133	4157	7674				4281	4518	5027	5385
Eae I	(13)	283	1031	1472	1507			5529	5562	5832	5899
		2170	4049	4115	4329			5999	6173	6282	6675
		4724	7148	7322	7713			6768	6898	6996	7067
		7740						7236	7244	7308	7345
Eag I	(2)	2170	7148					7611	7871	8255	8263
Ear I	(4)	1910	5536	7586	7796			8289	8308	8310	8319
Eco47 III	(3)	2975	4090	5026		HinC II	(3)	1765	2191	2586	
Eco57 I	(10)	1118	1451	1475	1481	Hind II	(3)	1765	2191	2586	
		2467	2698	4104	6199	Hind III	(1)	2183			
		7387	7819			Hinf I	(21)	774	1290	1935	2192
EcoO109 I	(5)	1920	2827	3030	3993			2609	2729	2862	3150
		4287						3706	4258	4802	4816
EcoR I	(1)	4465						4838	5552	5627	6023
EcoR II	(19)	452	645	1131	1285			6540	7727	7861	8032
		2843	3020	3314	3359			8054			
		3439	3845	3964	4051	HinI I	(13)	486	539	622	808
		4117	4316	4348	5678			979	1426	1483	1534
		5799	5812	7627				1633	3245	4198	6994
Ehe I	(6)	1427	1535	1634	4199			7242			
		6995	7243			HinP I	(60)	86	200	231	348
Fnu4H I	(71)	1067	1115	1268	1332			998	1010	1244	1334
		1337	1472	1524	1527			1426	1534	1607	1609
		1619	1779	2170	2173			1633	2338	2659	2785
		2271	2274	2277	2280			2787	2789	2974	3394
		2283	2466	2475	2478			3742	3987	4031	4043
		2487	2490	2493	2553			4045	4059	4089	4109
		2645	2935	3309	3312			4174	4176	4198	4244
		3580	3583	3596	3653			4279	4516	5025	5383
		3656	3659	3749	3922			5527	5560	5830	5897
		4041	4092	4160	4179			5997	6171	6280	6673
		4201	4282	4490	5036			6766	6896	6994	7065
		5039	5558	5576	5579			7234	7242	7306	7343
		5697	5852	5995	6060			7609	7869	8253	8261
		6063	6269	6597	7048			8287	8306	8308	8317
		7151	7203	7214	7304	Hpa I	(1)	1765			
		7309	7346	7387	7474	Hpa II	(39)	203	1531	1630	1644
		7477	7480	7716	7812			2355	2620	2800	3145
		7853	7867	8285				3185	3435	3537	3599
Fok I	(20)	184	258	1125	1182			3627	4036	4095	4262
		1421	2551	2881	3080			4401	4572	4732	4799
		3376	3418	3652	4260			4875	5859	6006	6032
		6511	6692	6864	7047			6222	6626	6660	6727
		7109	7566	7591	7955			6849	6976	7147	7224
Fsp I	(3)	1011	6767	7344				7246	7274	7405	7495
Gdi II	(11)	1032	1473	2169	2171			7562	7743	8207	
		4116	4328	4725	7147	Hph I	(18)	120	739	1114	1285
		7149	7712	7739				1336	1557	2870	3860
Gsu I	(3)	2366	4994	6616				4031	4331	4427	4749
Hae I	(11)	285	966	1173	1395			5352	6389	6616	6790
		1509	3380	4051	5667			7421	8107		
		5678	6130	7324		Kas I	(6)	1425	1533	1632	4197
Hae II	(14)	1429	1537	1636	2977			6993	7241		
		3745	4092	4201	5028	Kpn I	(2)	363	1901		
		5530	5900	6997	7245	Mae I	(11)	364	956	1650	1851
		8256	8264					4985	6147	6400	6735
Hae III	(44)	285	448	641	966			6801	6943	8256	
		1033	1066	1117	1173	Mae II	(30)	81	113	187	486
		1360	1395	1474	1509			498	539	622	703

		2797	2803	2827	3030	Ava I	C`YCGR,G	5	Ava II	G`GWC,C	7
		3298	3299	3437	3604	Avr II	C`CTAG,G	1	BamH I	G`GATC,C	1
		3605	3681	3852	3962	Ban I	G`GYRC,C	17	Ban II	G,RCY`C	9
		3993	4071	4166	4287	Bbe I	G,CGC`C	6	Bbs I	GAAGAC 8/12	2
		5133	6587	6666	6683	Bbv I	GCAGC 13/17	19	Bbv II	GAAGAC 7/11	2
		7758	8096			Bcl I	T`GATC,A	2	Bcn I	CC,S`GG	18
Scrf I	(37)	454	647	1133	1287	Bfa I	C`TA,G	11	Bgl I	GCCN,NNN`NGGC	7
		1531	2356	2620	2621	Bgl II	A`GATC,T	1	Blp I	GC`TNA,GC	-
		2800	2801	2845	3022	Bpm I	CTGGAG 22/20	3	Bsa I	GGTCTC 7/11	5
		3146	3316	3361	3441	BsaA I	YAC GTR	8	BsaB I	GATNN NNATC	3
		3538	3628	3847	3966	BsaH I	GR`CG,YC	13	BsaJ I	C`CNNG,G	44
		4037	4053	4119	4263	BsaW I	W`CCGG,W	8	BseR I	GAGGAG 16/14	5
		4318	4350	4875	4876	Bsg I	GTGCAG 22/20	5	BsiC I	TT`CG,AA	-
		5680	5801	5814	6032	BsiE I	CG,RY`CG	7	BsiHKA I	G,WGCW`C	8
		6728	6849	7246	7406	BsiW I	C`GTAC,G	-	Bsm I	GAATG,C 7	4
		7629				BsmA I	GTCTC`/9	11	BsmB I	CGTCTC 7/11	2
Sec I	(44)	724	961	973	1108	BsmF I	GGGAC 15/19	10	BsoF I	GC`N,GC	71
		1132	1168	1225	1285	Bsp120 I	G`GGCC,C	2	Bsp1286 I	G,DGCH`C	2
		1381	1417	1486	1612	BspH I	T`CATG,A	1	BspM I	ACCTGC 10/14	8
		1901	2173	2348	2355	BspM II	T`CCGG,A	2	Bsr I	ACT,GG`	19
		2503	2619	2799	3021	BsrB I	GAG CGG	5	BsrD I	GCAATG, 8	3
		3033	3145	3302	3315	BsrG I	T`GTAC,A	1	BssH II	G`CGCG,C	6
		3439	3440	3537	3965	BssS I	C`TCGT,G	5	Bst1107 I	GTA TAC	1
		3981	4052	4133	4157	BstB I	TT`CG,AA	-	BstE II	G`GTNAC,C	4
		4169	4187	4262	4787	BstN I	CC`W,GG	19	BstU I	CG CG	38
		4874	4875	4984	5812	BstX I	CCAN,NNNN`NTGG	2	BstY I	R`GATC,Y	14
SfaN I	(16)	722	1817	3084	3104	Bsu36 I	CC`TNA,GG	-	Cac8 I	GCN NGC	50
		3889	4281	4362	5490	Cfr10 I	R`CCGG,Y	10	Cla I	AT`CG,AT	1
		5528	5748	7201	7456	Csp6 I	G`TA,C	15	Dde I	C`TNA,G	9
		7540	7604	7672	7879	Dpn I	GA TC	35	DpnII	`GATC,	35
Sfc I	(7)	1299	2463	2490	2920	Dra I	TTT AAA	8	Dra III	CAC,NNN`GTG	1
		3653	5917	6108		Drd I	GACNN,NN`NNGTC	5	Dsa I	C`CRYG,G	11
Sma I	(3)	2621	2801	4876		Eae I	Y`GGCC,R	13	Eag I	C`GGCC,G	2
SnaB I	(2)	704	5291			Ear I	CTCTTC 7/10	4	Eco47 III	AGC GCT	3
Sph I	(3)	2344	3820	7647		Eco57 I	CTGAAG 21/19	10	Eco72 I	CAC GTG	-
Stu I	(2)	1173	1395			EcoN I	CCTNN`N,NNAGG	-	Eco109 I	RG`GNC,CY	5
Sty I	(14)	724	961	1108	1168	EcoR I	G`AATT,C	1	EcoR II	`CCWGG,	19
		1381	1901	2348	3033	EcoR V	GAT ATC	-	Ehe I	GGC GCC	6
		4133	4169	4187	4984	Esp I	GC`TNA,GC	-	Fnu4H I	GC`N,GC	71
		7051	7674			Fok I	GGATG 14/18	20	Fse I	GG,CCGG`CC	-
Taq I	(16)	1042	1048	1258	2123	Fsp I	TGC GCA	3	Gdi II	`YGGC,CG	11
		2190	2195	3886	5094	Gsu I	CTGGAG 21/19	3	Hae I	WGG CCW	11
		5470	5752	7355	7511	Hae II	R,CGC`Y	14	Hae III	GG CC	44
		7535	7571	7733	8138	Hga I	GACGC 9/14	7	HgiA I	G,WGCW`C	8
Tfi I	(8)	1935	2609	3150	4258	HgiE II	ACCNNNNNNGGT -1/132		Hha I	G,CG`C	60
		4838	5627	7727	7861	Hinc II	GTY RAC	3	Hind II	GTY RAC	3
Tsp45 I	(23)	77	109	183	218	Hind III	A`AGCT,T	1	Hinf I	G`ANT,C	21
		1103	1274	1280	2027	HinI I	GR`CG,YC	13	Hinp I	G`CG,C	60
		2512	2859	3252	3865	Hpa I	GTT AAC	1	Hpa II	C`CG,G	39
		4014	4416	4736	4754	Hph I	GGTGA 12/11	18	Kas I	G`GCGC,C	6
		5116	5267	5357	5389	Kpn I	G,GTAC`C	2	Mae I	C`TA,G	11
		7362	7668	8278		Mae II	A`CG,T	30	Mae III	`GTNAC,	40
Tth111 I	(2)	2440	7360			Mbo I	`GATC,	35	Mbo II	GAAGA 12/11	17
Tth111 II	(9)	2559	2725	2764	3852	Mlu I	A`CGCG,T	1	Mme I	TCCRAC 25/23	6
		4623	6241	6250	6280	Mnl I	CCTC 10/10	67	Msc I	TGG CCA	4
		7678				Mse I	T`TA,A	36	Msl I	CAYNN NNRTG	5
Vsp I	(6)	5	371	1988	4940	Msp I	C`CG,G	39	MspAI I	CMG CKG	15
		5459	6717			Mun I	C`AATT,G	2	Nae I	GCC GGC	3
Xba I	(1)	1649				Nar I	GG`CG,CC	6	Nci I	CC`S,GG	18
Xca I	(1)	4445				Nco I	C`CATG,G	6	Nde I	CA`TA,TG	2
Xcm I	(3)	2733	4324	7058		NgoM I	G`CCGG,C	3	Nhe I	G`CTAG,C	-
Xho II	(14)	949	1646	2177	2199	Nla III	,CATG`	38	Nla IV	GGN NCC	40
		2653	6293	6304	6390	Not I	GC`GGCC,GC	1	Nru I	TCG CGA	-
		6402	6791	6803	7055	Nsi I	A,TGCA`T	2	Nsp7524 I	R`CATG,Y	8
		7413	7659			NspB II	CMG CKG	15	NspH I	R,CATG`Y	8
Xma I	(3)	2619	2799	4874		PaeR7 I	C`TCGA,G	-	Pal I	GG CC	44
Xma III	(2)	2170	7148			PflM I	CCAN,NNN`NTGG	2	Ple I	GAGTC 9/10	3
Xmn I	(1)	8326				Pme I	CTTT AAAC	1	Pml I	CAC GTG	-
						PpuM I	RG`GWC,CY	2	Psp1406 I	AA`CG,TT	1
						PspA I	C`CCGG,G	3	Pst I	C,TGCA`G	5
						Pvu I	CG,AT`CG	-	Pvu II	CAG CTG	7
						Rsa I	GT AC	15	Rsr II	CG`GWC,CG	1
						Sac I	G,AGCT`C	2	Sac II	CC,GC`GG	3
						Sal I	G`TCGA,C	1	Sap I	GCTCTTC 8/11	3
						Sau3A I	`GATC,	35	Sau96 I	G`GNC,C	30
						Sca I	AGT ACT	-	ScrF I	CC`N,GG	37
						Sec I	C`CNNG,G	44	SfaN I	GCATC 9/13	16
						Sfc I	C`TRYA,G	7	Sfi I	GGCCN,NNN`NGGCC	-
						Sma I	CCC GGG	3	SnaB I	TAC GTA	2
						Spe I	A`CTAG,T	-	Sph I	G,CATG`C	3
Site usage in pAdTrace-pmiR:											
Aat II	G,ACGT`C	5	Acc I	GT`MK,AC	3						
Acc65 I	G`GTAC,C	2	Aci I	C`CG,C	111						
Afl II	C`TTAA,G	-	Afl III	A`CRYG,T	4						
Age I	A`CCGG,T	-	Aha II	GR`CG,YC	13						
Ahd I	GACNN,N`NNGTC	3	Alu I	AG CT	44						
Alw I	GGATC 8/9	25	AlwN I	CAG,NNN`CTG	6						
Apa I	G,GGCC`C	2	ApaL I	G`TGCA,C	2						
Apo I	R`AATT,Y	6	Asc I	GG`CGCG,CC	-						
Ase I	AT`TA,AT	6	Asp178	G`GTAC,C	2						

Spl I	C`GTAC,G	-	Srf I	GCCC GGGC	-	Vsp I	AT`TA,AT	6	Xba I	T`CTAG,A	1
Ssp I	AAT ATT	-	Stu I	AGG CCT	2	Xca I	GTA TAC	1	Xcm I	CCANNNN,N`NNNTGG3	
Sty I	C`CWWG,G	14	Taq I	T`CG,A	16	Xho I	C`TCGA,G	-	Xho II	R`GATC,Y	14
Tfi I	G`AWT,C	8	Tsp45 I	`GTSAC,	23	Xma I	C`CCGG,G	3	Xma III	C`GGCC,G	2
Tth11 I	GACN`N,NGTC	2	Tth11 II	CAARCA 16/14	9						