

pTagGFP-mito vector

Table of restriction sites

Enzyme Name	Sequence	Count	Cutting Position				
AatI	AGG!CCT	1	2602				
AatII	GACGT!C	4	126	179	262	448	
Acc65I	G!GTACC	0					
AccI	GT!MKAC	0					
AccII	CG!CG	20	61	663	665	794	1031
			1349	1430	1705	2081	2101
			2125	2156	2847	3148	3586
			3670	3733	3802	4075	4656
AccIII	T!CCGGA	0					
AciI	G!CGG	31	371	404	529	624	648
			710	794	1031	1223	1226
			1424	2041	2068	2156	2266
			2847	2911	3012	3015	3295
			3350	3448	3586	3733	3873
			4116	4361	4482	4501	4628
			4656				
AciI	C!CGC	41	59	87	99	113	280
			508	590	613	661	921
			1029	1068	1206	1319	1335
			1347	1428	2096	2099	2113
			2203	2451	2463	2472	2484
			2494	2505	2551	2690	2753
			3255	3300	3366	3392	3517
			3520	3668	3800	4107	4251
			4747				
AcyI	GR!CGYC	9	123	176	259	445	610
			812	2781	3483	3562	
AfaI	GT!AC	11	220	245	300	333	384
			541	1021	1132	1156	1414
			3087				
AflI	G!GWCC	3	1332	3297	3742		
AflIII	C!TTAAG	1	1663				
AflIII	A!CRYGT	2	1151	4699			
AgeI	A!CCGGT	1	693				
AhaI	CC!SGG	5	645	2785	2945	3558	4322
AhaII	GR!CGYC	9	123	176	259	445	610
			812	2781	3483	3562	
AhaIII	TTT!AAA	3	1483	3925	3944		
AluI	AG!CT	21	567	723	756	828	861
			1077	1125	1136	1236	1410
			1560	1727	1984	2279	2567
			2887	3345	4142	4399	4445
			4535				
Alw44I	G!TGCAC	2	769	4385			
AlwI	GGATCNNNN!	8	695	2649	2960	3206	3598
			3957	4055	4141		
AlwI	!NNNNNGATCC	8	581	666	682	1281	3025
			3569	3956	4053		
AlwNI	CAGNNN!CTG	3	1382	3882	4290		
AocI	CC!TNAGG	2	2261	3893			
AocII	GDGCH!C	15	743	773	872	935	1265
			1312	1364	1972	2727	2820
			2894	3084	3146	3856	4389
Aor51HI	AGC!GCT	0					
AosI	TGC!GCA	1	2883				
AosII	GR!CGYC	9	123	176	259	445	610

			812	2781	3483	3562	
ApaI	GGGCC!C	0					
ApaLI	G!TGCAC	2	769	4385			
ApoI	R!AATTY	3	1595	1699	1710		
ApyI	CC!WGG	20	91	284	873	883	985
			1006	1060	1114	1186	1267
			1366	2317	2372	2389	3168
			3747	3850	4540	4553	4674
AquI	C!YCGRG	2	928	970			
AscI	GG!CGCGCC	0					
AseI	AT!TAAT	1	8				
AsnI	AT!TAAT	1	8				
Asp700I	GAANN!NNTTC	1	949				
Asp718I	G!GTACC	0					
AspHI	GWGCW!C	7	773	935	1312	1364	2894
			3084	4389			
AspI	GACN!NNGTC	1	2899				
AsuI	G!GNCC	14	84	277	642	875	1116
			1276	1332	1344	1888	3297
			3742	3788	3846	3879	
AsuII	TT!CGAA	1	3463				
AvaI	C!YCGRG	2	928	970			
AvaII	G!GWCC	3	1332	3297	3742		
AvaIII	ATGCA!T	3	2353	2425	4756		
AviII	TGC!GCA	1	2883				
AvrI	!CYCGRG	2	927	969			
AvrII	C!CTAGG	2	2603	3618			
AxyI	CC!TNAGG	2	2261	3893			
BalI	TGG!CCA	1	2863				
BamHI	G!GATCC	1	687				
BanI	G!GYRCC	4	466	1934	2780	2815	
BanII	GRGCY!C	3	1972	3146	3856		
BanIII	AT!CGAT	1	2621				
BbeI	GGCGC!C	1	2784				
BbiII/AcyI	GR!CGYC	9	123	176	259	445	610
			812	2781	3483	3562	
BbrPI	CAC!GTG	0					
BbsI	!GTCTTC	0					
BbsI	!GAAGAC	0					
BbvI	GCAGCNNNNNNNN!	7	1245	1569	2854	2896	3417
			3870	4370			
BbvI	!NNNNNNNNNNNGCTGC	12	602	605	608	848	1372
			2063	2728	2912	3005	4071
			4277	4280			
BbvII	GAAGACNN!	0					
BbvII	!NNNNNNGTCTTC	0					
BcefI	ACGGCNNNNNNNNNN!	11	777	789	837	918	1029
			1119	1197	1290	1413	3207
			3694				
BcefI	!NNNNNNNNNNNGCCGT	3	1923	2741	4200		
BcgI	!GCANNNNNNTCG	0					
BcgI	!CGANNNNNNTGC	0					
BclI	T!GATCA	0					
BcnI	CC!SGG	5	645	2785	2945	3558	4322
BfaI	C!TAG	8	593	1436	1630	2048	2604
			3619	3953	4206		
BfrI	C!TTAAG	1	1663				
BglI	GCCNNNN!NGGC	4	91	213	284	2556	
BglII	A!GATCT	0					

BinI	!NNNNNGATCC	8	581 3569	666 3956	682 4053	1281	3025
BinI	GGATCNNNN!	8	695 3957	2649 4055	2960 4141	3206	3598
BlnI	C!CTAGG	2	2603	3618			
BmyI	GDGCH!C	15	743 1312 2894	773 1364 3084	872 1972 3146	935 2727 3856	1265 2820 4389
BpmI	!CTCCAG	1	3578				
BpmI	!CTGGAG	5	828	1125	1185	1365	3599
Bpu1102I	GC!TNAGC	0					
BsaAI	YAC!GTR	3	341	1897	3085		
BsaBI	GATNN!NNATC	3	1291	1443	2640		
BsaHI	GR!CGYC	9	123 812	176 2781	259 3483	445 3562	610
BsaI	GGTCTCN!	0					
BsaI	!NNNNNGAGACC	1	3770				
BsaJI	C!CNNGG	24	361 1058 2315 2603 3746	871 1113 2387 2944 3848	881 1265 2510 3213 3849	971 1266 2545 3618 4539	1029 1395 2554 3745
BseAI	T!CCGGA	0					
BsePI	!GCGCGC	1	662				
BsgI	!GTGCAG	1	1230				
BsgI	!CTGCAC	1	845				
BsiEI	CGRY!CG	4	698	1428	2690	4365	
BsiWI	C!GTACG	0					
BsiYI	CCNNNNN!NNGG	26	50 1035 2119 3619 3837 4684	681 1125 2511 3620 3868	710 1341 2762 3751 4221	872 1401 3306 3786 4500	1005 1793 3587 3836 4666
BslI	CCNNNNN!NNGG	26	50 1035 2119 3619 3837 4684	681 1125 2511 3620 3868	710 1341 2762 3751 4221	872 1401 3306 3786 4500	1005 1793 3587 3836 4666
BsmAI	!GTCTC	1	429				
BsmAI	!GAGAC	4	2210	2628	3647	3775	
BsmI	GAATGCN!	1	1532				
BsmI	G!CATTC	1	1625				
Bsp1286I	GDGCH!C	15	743 1312 2894	773 1364 3084	872 1972 3146	935 2727 3856	1265 2820 4389
BspDI	AT!CGAT	1	2621				
BspEI	T!CCGGA	0					
BspHI	T!CATGA	2	2207	3979			
BspMI	ACCTGCNNNN!	2	3049	3499			
BspMI	!NNNNNNNNGCAGGT	1	2668				
BspMII	T!CCGGA	0					
BspWI	GCNNNNN!NNGC	42	91 401 753 911 2008 2348	213 618 794 920 2038 2420	245 621 800 1142 2065 2471	284 635 854 1334 2107 2550	377 657 867 1385 2109 2556

			2772	2856	2879	3018	3024
			3141	3224	3491	3678	3882
			4081	4653			
BsrFI	R!CCGGY	7	693	730	853	1998	3100
			3281	3564			
BsrI	ACTGGN!	3	2725	2926	4172		
BsrI	C!CAGT	7	296	655	909	1810	2488
			4284	4297			
BssHII	G!CGCGC	1	663				
Bst1107I	GTA!TAC	0					
BstBI	TT!CGAA	1	3463				
BstEII	G!GTNACC	1	885				
BstI	G!GATCC	1	687				
BstNI	CC!WGG	20	91	284	873	883	985
			1006	1060	1114	1186	1267
			1366	2317	2372	2389	3168
			3747	3850	4540	4553	4674
BstPI	G!GTNACC	1	885				
BstUI	CG!CG	20	61	663	665	794	1031
			1349	1430	1705	2081	2101
			2125	2156	2847	3148	3586
			3670	3733	3802	4075	4656
BstXI	CCANNNNN!NTGG	0					
BstYI	R!GATCY	10	586	671	687	2952	3198
			3590	3949	3961	4047	4058
Bsu36I	CC!TNAGG	2	2261	3893			
CbiI	TT!CGAA	1	3463				
CcrI	C!TCGAG	0					
CelII	GC!TNAGC	0					
CfoI	GCG!C	26	665	667	794	964	992
			1381	2047	2055	2081	2103
			2112	2125	2156	2775	2783
			2847	2884	3150	3410	3586
			3672	4075	4184	4358	4458
			4525				
Cfr10I	R!CCGGY	7	693	730	853	1998	3100
			3281	3564			
Cfr13I	G!GNCC	14	84	277	642	875	1116
			1276	1332	1344	1888	3297
			3742	3788	3846	3879	
Cfr9I	C!CCGGG	0					
CfrI	Y!GGCCR	7	774	1238	1425	2687	2861
			3252	3279			
ClaI	AT!CGAT	1	2621				
CpoI	CG!GWCCG	1	3297				
Csp45I	TT!CGAA	1	3463				
CspI	CG!GSCCG	1	642				
CviJI	RG!CY	95	43	85	94	278	567
			629	638	643	651	723
			756	776	828	861	876
			977	1077	1118	1125	1136
			1145	1174	1184	1236	1240
			1277	1345	1410	1427	1450
			1560	1727	1747	1889	1970
			1984	1998	2279	2320	2392
			2515	2544	2550	2559	2567
			2590	2602	2608	2689	2706
			2714	2741	2766	2850	2859
			2863	2887	2925	3001	3018

			3037	3100	3144	3154	3171
			3254	3281	3285	3322	3345
			3361	3541	3568	3629	3751
			3790	3847	3854	3861	3880
			3891	4142	4171	4214	4225
			4290	4369	4394	4399	4445
			4535	4633	4659	4677	4688
CvnI	CC!TNAGG	2	2261	3893			
DdeI	C!TNAG	8	1306	1313	2261	2563	3444
			3893	4016	4425		
DpnI	GA!TC	23	588	673	689	751	835
			1288	1440	2620	2624	2643
			2954	3032	3113	3122	3200
			3576	3592	3951	3963	4041
			4049	4060	4135		
DpnII	!GATC	23	586	671	687	749	833
			1286	1438	2618	2622	2641
			2952	3030	3111	3120	3198
			3574	3590	3949	3961	4039
			4047	4058	4133		
DraI	TTT!AAA	3	1483	3925	3944		
DraII	RG!GNCCY	1	3879				
DraIII	CACNNN!GTG	3	1152	1359	1897		
DrdI	GACNNNN!NNGTC	3	1852	2808	4597		
DsaI	C!CRYGG	5	361	1029	1395	2510	3213
DsaV	!CCNGG	25	89	282	643	871	881
			983	1004	1058	1112	1184
			1265	1364	2315	2370	2387
			2783	2943	3166	3556	3745
			3848	4320	4538	4551	4672
EaeI	Y!GGCCR	7	774	1238	1425	2687	2861
			3252	3279			
EagI	C!GGCCG	2	1425	2687			
Eam1105I	GACNNN!NNGTC	0					
EarI	!CTCTTC	1	999				
EarI	!GAAGAG	3	2252	3129	3339		
Ecl136II	GAG!CTC	0					
EclXI	C!GGCCG	2	1425	2687			
Eco105I	TAC!GTA	1	341				
Eco31I	GGTCTCN!	0					
Eco31I	!NNNNNGAGACC	1	3770				
Eco47I	G!GWCC	3	1332	3297	3742		
Eco47III	AGC!GCT	0					
Eco52I	C!GGCCG	2	1425	2687			
Eco57I	!CTGAAG	3	1077	2905	3337		
Eco57I	!CTTCAG	2	1373	4171			
Eco81I	CC!TNAGG	2	2261	3893			
EcoNI	CCTNN!NNNAGG	1	1003				
EcoO109I	RG!GNCCY	1	3879				
EcoO65I	G!GTNACC	1	885				
EcoRI	G!AATTC	0					
EcoRII	!CCWGG	20	89	282	871	881	983
			1004	1058	1112	1184	1265
			1364	2315	2370	2387	3166
			3745	3848	4538	4551	4672
EcoRV	GAT!ATC	0					
EcoT14I	C!CWGG	5	361	2510	2603	3213	3618
EcoT22I	ATGCA!T	3	2353	2425	4756		
EcoT38I	GRGCY!C	3	1972	3146	3856		

EheI	GGC!GCC	1	2782					
Esp3I	CGTCTCN!	0						
Esp3I	!NNNNNGAGACG	0						
EspI	GC!TNAGC	0						
FbaI	T!GATCA	0						
FinI	!GTCCC	4	2311	2383	2447	3742		
FinI	!GGGAC	6	161	312	480	2917	3449	
			3558					
Fnu4HI	GC!NGC	43	613	616	619	622	649	
			661	795	862	1032	1224	
			1227	1234	1386	1425	1428	
			1558	2077	2099	2113	2551	
			2690	2742	2753	2843	2848	
			2885	2926	3013	3016	3019	
			3255	3351	3392	3406	3520	
			3859	3874	4085	4291	4294	
			4359	4502	4657			
FokI	GGATGNNNNNNNN!	4	2648	3105	3130	3584		
FokI	!NNNNNNNNNNNNNCATCC	5	892	967	982	1096	2454	
FspI	TGC!GCA	1	2883					
GdiII	!NNNNNYGGCCG	5	1232	1419	2681	3246	3273	
GdiII	CGGCCRN!	3	780	1431	2693			
GsuI	!CTCCAG	1	3578					
GsuI	!CTGGAG	5	828	1125	1185	1365	3599	
HaeI	WGG!CCW	6	1174	2602	2863	4225	4677	
			4688					
HaeII	RGCGC!Y	6	965	1382	2048	2056	2784	
			4459					
HaeIII	GG!CC	29	85	278	643	776	876	
			1118	1174	1184	1240	1277	
			1345	1427	1747	1889	2544	
			2550	2559	2602	2689	2863	
			3254	3281	3790	3847	3880	
			4225	4659	4677	4688		
HapII	C!CGG	20	645	694	731	854	1999	
			2686	2763	2785	2813	2944	
			3034	3101	3282	3557	3565	
			3657	4131	4321	4347	4494	
HgaI	GACGCNNNNN!	5	527	618	820	3491	3570	
HgaI	!NNNNNNNNNNGCGTC	3	2114	4009	4587			
HgiAI	GWGCW!C	7	773	935	1312	1364	2894	
			3084	4389				
HgiEII	!ACNNNNNNNGGT	1	4111					
HhaI	GCG!C	26	665	667	794	964	992	
			1381	2047	2055	2081	2103	
			2112	2125	2156	2775	2783	
			2847	2884	3150	3410	3586	
			3672	4075	4184	4358	4458	
			4525					
Hin1I	GR!CGYC	9	123	176	259	445	610	
			812	2781	3483	3562		
HinP1I	G!CGC	26	663	665	792	962	990	
			1379	2045	2053	2079	2101	
			2110	2123	2154	2773	2781	
			2845	2882	3148	3408	3584	
			3670	4073	4182	4356	4456	
			4523					
HincII	GTY!RAC	1	1544					
HindIII	A!AGCTT	0						

HinfI	G!ANTC	13	411 2256 3547	1369 3266 4329	1432 3400 4725	1824 3452	1846 3510
HpaI	GTT!AAC	1	1544				
HpaII	C!CGG	20	645 2686 3034 3657	694 2763 3101 4131	731 2785 3282 4321	854 2813 3557 4347	1999 2944 3565 4494
HphI	GGTGANNNNNNN!	7	377 3852	897 3968	1050	1074	1203
HphI	!NNNNNNNTCACC	2	1898	2959			
KasI	G!GCGCC	1	2780				
KpnI	GGTAC!C	0					
Ksp632I	CTCTTCN!	1	1006				
Ksp632I	!NNNNGAAGAG	3	2248	3125	3335		
KspI	CCGC!GG	1	1032				
MaeI	C!TAG	8	593 3619	1436 3953	1630 4206	2048	2604
MaeII	A!CGT	17	123 445 1853 3865	135 767 1896 3998	176 1151 2006	259 1259 2897	340 1841 3084
MaeIII	!GTNAC	13	62 2070 4163	149 2082 4279	498 2901 4342	885 3207	1569 3897
MamI	GATNN!NNATC	3	1291	1443	2640		
MboI	!GATC	23	586 1286 2952 3574 4047	671 1438 3030 3590 4058	687 2618 3111 3949 4133	749 2622 3120 3961	833 2641 3198 4039
MboII	GAAGANNNNNNN!	6	951 3971	2037	2265	3142	3352
MboII	!NNNNNNNTCTTC	6	945 4042	993	3432	3599	3799
McrI	!CGRYCG	4	694	1424	2686	4361	
MfeI	!CAATTG	1	1530				
MflI	R!GATCY	10	586 3590	671 3949	687 3961	2952 4047	3198 4058
MluI	A!CGCGT	0					
MmeI	!TCCRAC	1	1848				
MmeI	!GTYGGA	2	4324	4508			
MnlI	CCTCNNNNNNN!	11	904 2570 4596	1009 3382	1500 3588	1509 3902	2564 4272
MnlI	!NNNNNNNGAGG	25	541 1028 1334 2539 2695	710 1040 1459 2576 2831	791 1091 1924 2579 3188	797 1181 2255 2591 3618	965 1211 2533 2631 4521
MroI	T!CCGGA	0					
MscI	TGG!CCA	1	2863				
MseI	T!TAA	15	8 1696 2105	1482 1708 3924	1543 1719 3938	1664 1736 3943	1685 1834 3995
MspI	C!CGG	20	645 2686 3034 3657	694 2763 3101 4131	731 2785 3282 4321	854 2813 3557 4347	1999 2944 3565 4494

MstI	TGC!GCA	1	2883					
MstII	CC!TNAGG	2	2261	3893				
MunI	C!AATTG	1	1531					
MvaI	CC!WGG	20	91	284	873	883	985	
			1006	1060	1114	1186	1267	
			1366	2317	2372	2389	3168	
			3747	3850	4540	4553	4674	
MvnI	CG!CG	20	61	663	665	794	1031	
			1349	1430	1705	2081	2101	
			2125	2156	2847	3148	3586	
			3670	3733	3802	4075	4656	
NaeI	GCC!GGC	4	732	2000	3283	3566		
NarI	GG!CGCC	1	2781					
NciI	CC!SGG	5	645	2785	2945	3558	4322	
NcoI	C!CATGG	3	361	2510	3213			
NdeI	CA!TATG	1	235					
NdeII	!GATC	23	586	671	687	749	833	
			1286	1438	2618	2622	2641	
			2952	3030	3111	3120	3198	
			3574	3590	3949	3961	4039	
			4047	4058	4133			
NgoMI	G!CCGGC	4	730	1998	3281	3564		
NheI	G!CTAGC	1	592					
NlaIII	CATG!	22	305	365	600	708	939	
			969	1164	1359	1404	2211	
			2351	2423	2514	2655	3000	
			3186	3217	3243	3599	3983	
			4703	4754				
NlaIV	GGN!NCC	17	468	652	689	1278	1936	
			1957	1969	2160	2321	2393	
			2782	2817	3665	3744	3789	
			4632	4671				
NotI	GC!GGCCGC	1	1425					
NruI	TCG!CGA	0						
NsiI	ATGCA!T	3	2353	2425	4756			
Nsp(7524)I	RCATG!Y	5	600	2351	2423	3186	4703	
Nsp(7524)V	TT!CGAA	1	3463					
NspBII	CMG!CKG	7	615	1031	1236	2279	2887	
			4116	4361				
NspII	GDGCH!C	15	743	773	872	935	1265	
			1312	1364	1972	2727	2820	
			2894	3084	3146	3856	4389	
NspIII	C!YCGRG	2	928	970				
NspIV	G!GNCC	14	84	277	642	875	1116	
			1276	1332	1344	1888	3297	
			3742	3788	3846	3879		
NunII	GG!CGCC	1	2781					
PacI	TTAAT!TAA	0						
Paer71	C!TCGAG	0						
PalI	GG!CC	29	85	278	643	776	876	
			1118	1174	1184	1240	1277	
			1345	1427	1747	1889	2544	
			2550	2559	2602	2689	2863	
			3254	3281	3790	3847	3880	
			4225	4659	4677	4688		
PflMI	CCANNNN!NTGG	3	681	1125	1401			
PleI	GAGTCNNNN!	3	1377	1832	2264			
PleI	!NNNNNGACTC	5	405	1426	1840	3446	4323	
PmaCI	CAC!GTG	0						

PmeI	GTTT!AAAC	0						
PmlI	CAC!GTG	0						
PpuMI	RG!GWCCY	0						
PshAI	GACNN!NNGTC	0						
PstI	CTGCA!G	0						
PvuI	CGAT!CG	0						
PvuII	CAG!CTG	3	1236	2279	2887			
RmaI	C!TAG	8	593	1436	1630	2048	2604	
			3619	3953	4206			
RsaI	GT!AC	11	220	245	300	333	384	
			541	1021	1132	1156	1414	
			3087					
RsrI	G!AATTC	0						
RsrII	CG!GWCCG	1	3297					
SacI	GAGCT!C	0						
SacII	CCGC!GG	1	1032					
SalI	G!TCGAC	0						
Sau3AI	!GATC	23	586	671	687	749	833	
			1286	1438	2618	2622	2641	
			2952	3030	3111	3120	3198	
			3574	3590	3949	3961	4039	
			4047	4058	4133			
Sau96I	G!GNCC	14	84	277	642	875	1116	
			1276	1332	1344	1888	3297	
			3742	3788	3846	3879		
SauI	CC!TNAGG	2	2261	3893				
ScaI	AGT!ACT	0						
ScrFI	CC!NGG	25	91	284	645	873	883	
			985	1006	1060	1114	1186	
			1267	1366	2317	2372	2389	
			2785	2945	3168	3558	3747	
			3850	4322	4540	4553	4674	
SduI	GDGCH!C	15	743	773	872	935	1265	
			1312	1364	1972	2727	2820	
			2894	3084	3146	3856	4389	
SecI	C!CNNGG	24	361	871	881	971	1029	
			1058	1113	1265	1266	1395	
			2315	2387	2510	2545	2554	
			2603	2944	3213	3618	3745	
			3746	3848	3849	4539		
SexI	!CTCGAG	0						
SfaNI	GCATCNNNNN!	9	743	914	1079	1597	2360	
			2432	3080	3144	3419		
SfaNI	!NNNNNNNNNGATGC	5	358	2739	2994	3210	4602	
SfcI	C!TRYAG	3	2116	4243	4434			
SfiI	GGCCNNNN!NGGCC	1	2556					
SfuI	TT!CGAA	1	3463					
SgrAI	CR!CCGGYG	0						
SinI	G!GWCC	3	1332	3297	3742			
SmaI	CCC!GGG	0						
SnaBI	TAC!GTA	1	341					
SnaI	!GTATAC	0						
SnoI	G!TGCAC	2	769	4385				
SpeI	A!CTAGT	0						
SphI	GCATG!C	3	2351	2423	3186			
SpI	C!GTACG	0						
SrfI	GCCC!GGGC	0						
Sse8387I	CCTGCA!GG	0						
SspI	AAT!ATT	2	1689	2242				

SstI	GAGCT!C	0						
SstII	CCGC!GG	1	1032					
SstIII	!ACGT	17	122	134	175	258	339	
			444	766	1150	1258	1840	
			1852	1895	2005	2896	3083	
			3864	3997				
StuI	AGG!CCT	1	2602					
StyI	C!CWWGG	5	361	2510	2603	3213	3618	
StySJI	!GAGNNNNNNGTRC	0						
StySJI	!GYACNNNNNNNCTC	0						
SwaI	ATTT!AAAT	0						
TaqI	T!CGA	15	752	1046	1073	1217	1930	
			2621	2894	3050	3074	3110	
			3272	3463	3508	3763	4601	
TaqII	GACCGANNNNNNNNNN!	3	1801	2818	3486			
TaqII	!NNNNNNNNNTCGGTC	1	3730					
TaqII	CACCCANNNNNNNNNN!	1	1408					
TaqII	!NNNNNNNNNTGGGTG	3	173	2685	3277			
TfiI	G!AWTC	5	3266	3400	3510	3547	4725	
ThaI	CG!CG	20	61	663	665	794	1031	
			1349	1430	1705	2081	2101	
			2125	2156	2847	3148	3586	
			3670	3733	3802	4075	4656	
Tsp45I	!GTSAC	4	885	2070	2901	3207		
TspEI	!AATT	10	19	1531	1595	1673	1699	
			1710	2357	2429	2521	3939	
Tth111I	GACN!NNGTC	1	2899					
Tth111II	CAARCANNNNNNNNNN!	1	4108					
Tth111III	!NNNNNNNNNTGYTTG	3	3216	4076	4115			
TthHB8I	T!CGA	15	752	1046	1073	1217	1930	
			2621	2894	3050	3074	3110	
			3272	3463	3508	3763	4601	
Van91I	CCANNNN!NTGG	3	681	1125	1401			
VspI	AT!TAAT	1	8					
XbaI	T!CTAGA	1	1435					
XcmI	!CCANNNNNNNNNTCG	1	3056					
XcyI	C!CCGGG	0						
XhoI	C!TCGAG	0						
XhoII	R!GATCY	10	586	671	687	2952	3198	
			3590	3949	3961	4047	4058	
XmaI	C!CCGGG	0						
XmaIII	C!GGCCG	2	1425	2687				
XmnI	GAANN!NNTTC	1	949					
XorII	CGAT!CG	0						