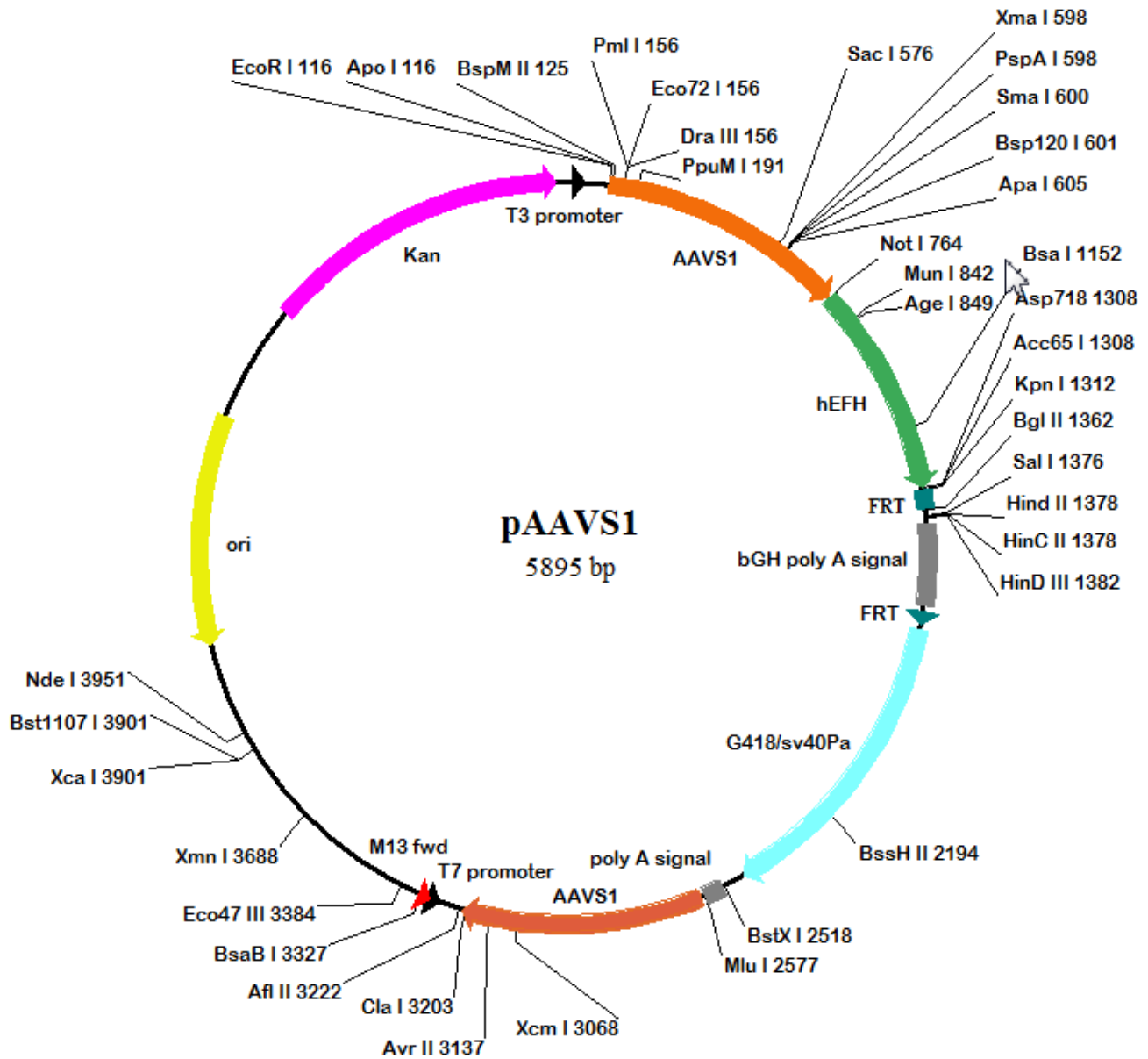


Vector: pHDR-AAVS1

Antibiotic Selection: Kan

Creator(s): Li Li & Xue Hu, Molecular Oncology Lab of The University of Chicago Medical Center

Date of Construction: February, 2016



pHDR-AAVS1 Full-Length Sequence



GGAACAGCTATGACCATGATACGCCAAGCTCGAAATTAACCTCACTAAAGGGAACAAAAGCTGGTACGAGGACAGGCTGGAGCCATGG
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pHDR-AAVS1 Vector

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Unique enzymes in pHDR-AAVS1:

			Aci I	(71)	171	333	763	767
					770	871	908	988
Apo I	R`AATT,Y	116			1044	1047	1062	1093
EcoR I	G`AATT,C	116			1100	1127	1661	1706
BspM II	T`CCGG,A	125			1769	1863	1927	2028
Dra III	CAC,NNN`GTG	156			2031	2271	2311	2316
Eco72 I	CAC GTG	156			2366	2382	2408	2464
Pml I	CAC GTG	156			2523	2870	3160	3419
PpuM I	RG`GWC,CY	191			3422	3433	3589	3605
Sac I	G,AGCT`C	576			3660	3716	3801	3840
PspA I	C`CCGG,G	598			3850	3892	3917	3955
Xma I	C`CCGG,G	598			3968	3994	4011	4054
Sma I	CCC GGG	600			4061	4082	4173	4201
Bsp120 I	G`GGCC,C	601			4328	4347	4468	4578
Apa I	G,GGCC`C	605			4713	4722	5041	5120
Not I	GC`GGCC,GC	764			5183	5277	5341	5442
Mun I	C`AATT,G	842			5445	5685	5725	5730
Age I	A`CCGG,T	849			5780	5796	5822	
Bsa I	GGTCTC 7/11	1152						
Acc65 I	G`GTAC,C	1308	Afl II	(1)	3222			
Asp718	G`GTAC,C	1308	Afl III	(2)	2577	4128		
Kpn I	G,GTAC`C	1312	Age I	(1)	849			
Bgl II	A`GATC,T	1362	Aha II	(4)	1300	1797	2499	5211
Sal I	G`TCGA,C	1376	Ahd I	(2)	5021	5881		
HinC II	GTY RAC	1378	Alu I	(31)	9	31	64	495
Hind II	GTY RAC	1378			531	574	579	661
Hind III	A`AGCT,T	1382			1001	1007	1011	1149
BssH II	G`CGCG,C	2194			1290	1384	1903	2361
BstX I	CCAN,NNNN`NTGG	2518			2859	2908	3266	3653
Mlu I	A`CGCG,T	2577			3710	3721	3770	3789
Xcm I	CCANNNN,N`NNNNTGG3068				4070	4296	4386	4432
Avr II	C`CTAG,G	3137			4689	5317	5775	
Cla I	AT`CG,AT	3203	Alw I	(22)	169	180	640	651
Afl II	C`TTAA,G	3222			1278	1653	1664	1975
BsaB I	GATNN NNATC	3327			2042	2221	2751	2762
Eco47 III	AGC GCT	3384			2888	3329	4690	4776
Xmn I	GAANN NNTTC	3688			4776	4873	4874	5389
Bst1107 I	GTA TAC	3901			5456	5635		
Xca I	GTA TAC	3901	AlwN I	(2)	2854	4544		
Nde I	CA`TA,TG	3951	Apa I	(1)	605			
Number of enzymes = 38			ApaL I	(2)	3944	4442		
			Apo I	(1)	116			
			Asp718	(1)	1308			
The following enzymes do not cut in pAAVS1:			Ava I	(4)	598	656	816	918
			Ava II	(7)	191	565	665	2313
Aat II	Asc I	Ase I	Bcl I	Bgl I		2966	3415	5727
BsiW I	Bsm I	BsrG I	EcoR V	Fse I	Avr II	(1)	3137	
Hpa I	Nru I	Nsi I	PaeR7 I	Pvu I	BamH I	(4)	173	644
Sac II	Sca I	Sfi I	SnaB I	Spe I	Ban I	(11)	777	852
Spl I	Srf I	Ssp I	Vsp I	Xho I		1308	1465	1796
						4969	5210	5245
pAAVS1: sites sorted by name:			Ban II	(5)	576	605	1023	2162
					5576			
Acc I	(2)	1377	3900	Bbe I	(3)	1303	1800	5214
Acc65 I	(1)	1308		Bbs I	(3)	576	1589	5877

pHDR-AAVS1 Vector

Bbv I	(14)	504	1870	1912	2433	BstB I	(2)	1389	2479		
		2917	3730	3779	3876	BstE II	(2)	95	466		
		4547	4550	4756	5284	BstN I	(16)	401	438	561	641
		5326	5847					682	1459	2184	2696
Bbv II	(3)	577	1588	5878				2760	2897	3072	3150
Bcn I	(14)	201	600	601	1164			4156	4277	4290	5598
		1802	1962	2815	3321	BstU I	(16)	871	1040	1085	1863
		3469	3775	3810	4509			2164	2196	2579	2870
		5216	5376					3660	3729	3731	3834
Bfa I	(16)	518	528	580	750			4175	4756	5277	5578
		857	1008	1134	1196	BstX I	(1)	2518			
		1342	1409	1637	2622	BstY I	(15)	173	644	1282	1362
		2999	3138	4623	4876			1657	1968	2214	2755
Bgl II	(1)	1362						3322	4769	4780	4866
Blp I	(2)	405	575					4878	5382	5628	
Bpm I	(4)	102	623	2717	3657	Bsu36 I	(2)	1056	2605		
Bsa I	(1)	1152				Cac8 I	(37)	354	529	1009	1023
BsaA I	(4)	156	2101	3882	5515			1044	1207	1235	1417
BsaB I	(1)	3327						1594	1598	1691	1877
BsaH I	(4)	1300	1797	2499	5211			2096	2162	2168	2196
BsaJ I	(17)	87	399	560	598			2200	2241	2245	2299
		640	680	681	919			3345	3387	3605	4059
		1183	1457	1960	2229			4145	4182	4742	5105
		2759	3137	4288	5374			5291	5510	5576	5582
		5643						5610	5614	5655	5659
BsaW I	(7)	125	774	849	1828			5713			
		4334	4481	5242		Cfr10 I	(9)	686	849	1073	1205
BseR I	(4)	200	2603	2942	3103			1296	2116	2297	5530
Bsg I	(2)	133	967					5711			
BsiC I	(2)	1389	2479			Cla I	(1)	3203			
BsiE I	(5)	767	1706	4044	4468	Csp6 I	(8)	68	388	712	899
		5120						1309	2102	3935	5516
BsiHKA I	(8)	133	576	1910	2100	Dde I	(19)	167	294	405	575
		3948	4446	5324	5514			1056	1150	1201	1519
BsmA I	(7)	323	399	1153	2629			2460	2605	2726	2820
		2763	3772	5044				2855	2970	3398	3938
BsmB I	(2)	400	3771					4403	4812	4978	
BsmF I	(10)	315	638	678	709	Dpn I	(25)	175	646	1284	1364
		767	798	1948	2480			1659	1970	2048	2129
		3401	5362					2138	2216	2757	2894
BsoF I	(60)	148	493	634	764			3324	4696	4771	4782
		767	770	988	1047			4790	4868	4880	4985
		1062	1093	1706	1758			5384	5462	5543	5552
		1769	1859	1864	1901			5630			
		1942	2029	2032	2035	DpnII	(25)	173	644	1282	1362
		2271	2367	2408	2422			1657	1968	2046	2127
		2523	2860	2871	2903			2136	2214	2755	2892
		2906	3160	3341	3422			3322	4694	4769	4780
		3719	3722	3768	3865			4788	4866	4878	4983
		3918	4034	4052	4055			5382	5460	5541	5550
		4173	4328	4471	4536			5628			
		4539	4745	5120	5172	Dra I	(5)	105	1145	3211	4887
		5183	5273	5278	5315			4906			
		5356	5443	5446	5449	Dra III	(1)	156			
		5685	5781	5822	5836	Drd I	(5)	1824	2873	3823	4236
Bsp120 I	(1)	601						5238			
Bsp1286 I	(3)	133	2100	5514		Dsa I	(3)	87	2229	5643	
BspH I	(2)	4848	5045			Eae I	(13)	764	1703	1877	2268
BspM I	(6)	1684	2065	2515	2817			2295	2520	2825	3157
		5098	5479					3305	5117	5291	5682
BspM II	(1)	125						5709			
Bsr I	(15)	884	905	1740	1941	Eag I	(3)	764	1703	5117	
		3055	3307	3437	3461	Ear I	(7)	538	2141	2351	2993
		3876	3907	4535	4548			4012	5555	5765	
		4662	5154	5355		Eco47 III	(1)	3384			
BsrB I	(7)	171	772	2410	2464	Eco57 I	(8)	601	1022	1344	1942
		4061	5043	5824				2374	4675	5356	5788
BsrD I	(2)	2030	5444			Eco72 I	(1)	156			
BssH II	(1)	2194				EcoN I	(2)	860	1055		
BssS I	(3)	2389	4301	5803		EcoO109 I	(3)	191	272	602	
Bst1107 I	(1)	3901				EcoR I	(1)	116			

pHDR-AAVS1 Vector

EcoR II	(16)	399	436	559	639	2194	2196	2424	2835		
		680	1457	2182	2694	3383	3729	3832	3862		
		2758	2895	3070	3148	4003	4036	4306	4373		
		4154	4275	4288	5596	4473	4647	4756	5203		
Ehe I	(3)	1301	1798	5212		5211	5275	5312	5578		
Esp I	(2)	405	575			5838					
Fnu4H I	(60)	148	493	634	764	Hpa II	(36)	126	199	599	687
		767	770	988	1047			775	850	1074	1162
		1062	1093	1706	1758			1174	1206	1297	1702
		1769	1859	1864	1901			1779	1801	1829	1960
		1942	2029	2032	2035			2050	2117	2298	2814
		2271	2367	2408	2422			3320	3467	3774	3808
		2523	2860	2871	2903			4335	4482	4508	4698
		2906	3160	3341	3422			5116	5193	5215	5243
		3719	3722	3768	3865			5374	5464	5531	5712
		3918	4034	4052	4055	Hph I	(14)	106	210	355	461
		4173	4328	4471	4536			1976	2595	2688	2984
		4539	4745	5120	5172			3096	3139	3749	3758
		5183	5273	5278	5315			4865	5390		
		5356	5443	5446	5449	Kas I	(3)	1299	1796	5210	
		5685	5781	5822	5836	Kpn I	(1)	1312			
Fok I	(20)	311	328	404	772	Mae I	(16)	518	528	580	750
		1052	1618	2121	2146			857	1008	1134	1196
		2587	2812	3172	3176			1342	1409	1637	2622
		3349	3411	3489	3675			2999	3138	4623	4876
		3816	4987	5535	5560	Mae II	(10)	155	964	1247	1913
Fsp I	(2)	1899	5313					2100	3455	3881	4831
Gdi II	(13)	763	765	1702	1704			5327	5514		
		2267	2294	2519	3156	Mae III	(20)	95	466	1276	1292
		3304	5116	5118	5681			1917	2223	2584	2677
		5708						2804	3462	3485	3569
Gsu I	(4)	101	624	2716	3656			3782	3877	4484	4547
Hae I	(12)	112	303	352	1879			4663	4946	5331	5637
		2610	2827	3053	3218	Mbo I	(25)	173	644	1282	1362
		4143	4154	4606	5293			1657	1968	2046	2127
Hae II	(8)	148	1180	1303	1800			2136	2214	2755	2892
		3386	4006	4376	5214			3322	4694	4769	4780
Hae III	(30)	112	274	303	352			4788	4866	4878	4983
		603	686	746	766			5382	5460	5541	5550
		1061	1166	1705	1879			5628			
		2270	2297	2522	2610	Mbo II	(16)	526	549	577	580
		2827	3053	3159	3218			1593	2157	2367	2449
		3307	3603	4143	4154			2981	4000	4789	4862
		4172	4606	5119	5293			5571	5781	5863	5878
		5684	5711			Mlu I	(1)	2577			
Hga I	(10)	318	1113	2506	2875	Mme I	(4)	333	617	4342	4526
		3018	3123	3665	3824	Mnl I	(57)	53	65	173	186
		4238	4816					203	220	224	345
HgiA I	(8)	133	576	1910	2100			421	430	480	522
		3948	4446	5324	5514			600	646	737	825
HgiE II	(3)	1454	3946	4707				914	1009	1051	1105
Hha I	(33)	147	799	871	1042			1121	1403	1445	1491
		1179	1274	1302	1791			1566	1712	1848	2205
		1799	1863	1900	2166			2397	2620	2623	2660
		2196	2198	2426	2837			2732	2746	2757	2780
		3385	3731	3834	3864			2851	2920	3030	3081
		4005	4038	4308	4375			3084	3172	3228	3457
		4475	4649	4758	5205			3515	3554	3734	3764
		5213	5277	5314	5580			4026	4236	4309	4560
		5840						4960	5126	5262	5619
Hinc II	(1)	1378						5811			
Hind II	(1)	1378				Msc I	(3)	1879	2827	5293	
Hind III	(1)	1382				Mse I	(17)	39	104	691	1144
Hinf I	(15)	460	1080	1199	2282			1368	1372	3210	3223
		2416	2468	2665	3286			3375	3595	3627	3909
		3684	4028	4103	4499			4834	4886	4891	4905
		5016	5696	5830				4958			
HinI I	(4)	1300	1797	2499	5211	Msl I	(4)	2234	2516	2555	5648
HinP I	(33)	145	797	869	1040	Msp I	(36)	126	199	599	687
		1177	1272	1300	1789			775	850	1074	1162
		1797	1861	1898	2164			1174	1206	1297	1702

pHDR-AAVS1 Vector

		1779	1801	1829	1960	Sau96 I	(14)	191	272	565	601
		2050	2117	2298	2814			602	665	684	744
		3320	3467	3774	3808			1164	2313	2966	3415
		4335	4482	4508	4698			3602	5727		
		5116	5193	5215	5243	ScrF I	(30)	200	401	438	561
		5374	5464	5531	5712			599	600	641	682
MspA1 I	(7)	1001	1903	3721	3840			1163	1459	1801	1961
		4470	4715	5317				2184	2696	2760	2814
Mun I	(1)	842						2897	3072	3150	3320
Nae I	(3)	1207	2299	5713				3468	3774	3809	4156
Nar I	(3)	1300	1797	5211				4277	4290	4508	5215
Nci I	(14)	200	599	600	1163			5375	5598		
		1801	1961	2814	3320	Sec I	(17)	87	399	560	598
		3468	3774	3809	4508			640	680	681	919
		5215	5375					1183	1457	1960	2229
Nco I	(3)	87	2229	5643				2759	3137	4288	5374
Nde I	(1)	3951						5643			
NgoM I	(3)	1205	2297	5711		SfaN I	(29)	211	364	561	751
Nhe I	(2)	527	1007					1033	1515	1756	2011
Nla III	(24)	20	91	231	552			2095	2159	2227	2434
		629	1600	1671	2016			2791	3328	3336	3432
		2202	2233	2259	3255			3510	3572	3795	3928
		3475	3539	3602	3767			3966	4004	4224	5170
		3872	4132	4852	5049			5425	5509	5573	5641
		5430	5616	5647	5673			5848			
Nla IV	(30)	85	175	192	250	Sfc I	(5)	1846	2903	3279	4393
		273	566	603	646			4584			
		666	745	779	854	Sma I	(1)	600			
		906	1110	1189	1301	Sph I	(3)	1600	2202	5616	
		1310	1467	1659	1798	Stu I	(4)	112	352	2610	3218
		1833	2700	2746	2757	Sty I	(5)	87	1183	2229	3137
		3417	4160	4199	4971			5643			
		5212	5247			Taq I	(19)	33	1014	1156	1377
Not I	(1)	764						1389	1396	1910	2066
Nsp7524 I	(7)	625	1596	2198	3471			2090	2126	2288	2479
		3763	4128	5612				3203	4228	5324	5480
NspB II	(7)	1001	1903	3721	3840			5504	5540	5702	
		4470	4715	5317		Tfi I	(8)	460	2282	2416	2665
NspH I	(7)	629	1600	2202	3475			3684	4103	5696	5830
		3767	4132	5616		Tsp45 I	(13)	95	466	1292	1917
Pal I	(30)	112	274	303	352			2223	2584	2677	2804
		603	686	746	766			3569	3782	3877	5331
		1061	1166	1705	1879			5637			
		2270	2297	2522	2610	Tth111 I	(3)	1915	3875	5329	
		2827	3053	3159	3218	Tth111 II	(9)	619	1223	1419	2233
		3307	3603	4143	4154			3590	4717	4726	4756
		4172	4606	5119	5293			5647			
		5684	5711			Xba I	(3)	1341	1636	2998	
PflM I	(2)	2695	3155			Xca I	(1)	3901			
Ple I	(3)	1088	3294	4507		Xcm I	(1)	3068			
Pme I	(2)	105	3211			Xho II	(15)	173	644	1282	1362
Pml I	(1)	156						1657	1968	2214	2755
PpuM I	(1)	191						3322	4769	4780	4866
Psp1406 I	(2)	964	3455					4878	5382	5628	
PspA I	(1)	598				Xma I	(1)	598			
Pst I	(2)	1850	2907			Xma III	(3)	764	1703	5117	
Pvu II	(4)	1001	1903	3721	5317	Xmn I	(1)	3688			
Rsa I	(8)	69	389	713	900						
		1310	2103	3936	5517						
Rsr II	(2)	2313	5727								
Sac I	(1)	576									
Sal I	(1)	1376									
Sap I	(7)	538	2141	2351	2993						
		4012	5555	5765							
Sau3A I	(25)	173	644	1282	1362						
		1657	1968	2046	2127						
		2136	2214	2755	2892						
		3322	4694	4769	4780						
		4788	4866	4878	4983						
		5382	5460	5541	5550						
		5628									

Site usage in pAAVS1:

Aat II	G,ACGT`C	-	Acc I	GT`MK,AC	2
Acc65 I	G`GTAC,C	1	Acc I	C`CG,C	71
Afl II	C`TTAA,G	1	Afl III	A`CRYG,T	2
Age I	A`CCGG,T	1	Aha II	GR`CG,YC	4
Ahd I	GACNN,N`NNGTC	2	Alu I	AG CT	31
Alw I	GGATC 8/9	22	AlwN I	CAG,NNN`CTG	2
Apa I	G,GGCC`C	1	ApaL I	G`TGCA,C	2
Apo I	R`AATT,Y	1	Asc I	GG`CGCG,CC	-
Ase I	AT`TA,AT	-	Asp718	G`GTAC,C	1
Ava I	C`YCGR,G	4	Ava II	G`GWC,C	7
Avr II	C`CTAG,G	1	BamH I	G`GATC,C	4

pHDR-AAVS1 Vector

Ban I	G`GYRC,C	11	Ban II	G,RCY`C	5	Sal I	G`TCGA,C	1	Sap I	GCTCTC 8/11	7
Bbe I	G,GCGC`C	3	Bbs I	GAAGAC 8/12	3	Sau3A I	`GATC,	25	Sau96 I	G`GNC,C	14
Bbv I	GCAGC 13/17	14	Bbv II	GAAGAC 7/11	3	Sca I	AGT ACT	-	ScrF I	CC`N,GG	30
Bcl I	T`GATC,A	-	Bcn I	CC,S`GG	14	Sec I	C`CNNG,G	17	SfaN I	GCATC 9/13	29
Bfa I	C`TA,G	16	Bgl I	GCCN,NNN`NGGC	-	Sfc I	C`TRYA,G	5	Sfi I	GGCCN,NNN`NGGCC	-
Bgl II	A`GATC,T	1	Blp I	GC`TNA,GC	2	Sma I	CCC GGG	1	SnaB I	TAC GTA	-
Bpm I	CTGGAG 22/20	4	Bsa I	GGTCTC 7/11	1	Spe I	A`CTAG,T	-	Sph I	G,CATG`C	3
BsaA I	YAC GTR	4	BsaB I	GATNN NNATC	1	Spl I	C`GTAC,G	-	Srf I	GCCC GGGC	-
BsaH I	GR`CG,YC	4	BsaJ I	C`CNNG,G	17	Ssp I	AAT ATT	-	Stu I	AGG CCT	4
BsaW I	W`CCGG,W	7	BseR I	GAGGAG 16/14	4	Sty I	C`CWWG,G	5	Taq I	T`CG,A	19
Bsg I	GTGCAG 22/20	2	BsiC I	TT`CG,AA	2	Tfi I	G`AWT,C	8	Tsp45 I	`GTSAC,	13
BsiE I	CG,RY`CG	5	BsiHKA I	G,WGCW`C	8	Tth111 I	GACN`N,NGTC	3	Tth111 II	CAARCA 16/14	9
BsiW I	C`GTAC,G	-	Bsm I	GAATG,C 7	-	Vsp I	AT`TA,AT	-	Xba I	T`CTAG,A	3
BsmA I	GTCTC`/9	7	BsmB I	CGTCTC 7/11	2	Xca I	GTA TAC	1	Xcm I	CCANNNN,N`NNNNTGG1	
BsmF I	GGGAC 15/19	10	BsoF I	GC`N,GC	60	Xho I	C`TCGA,G	-	Xho II	R`GATC,Y	15
Bsp120 I	G`GGCC,C	1	Bsp1286 I	G,DGCH`C	3	Xma I	C`CCGG,G	1	Xma III	C`GGCC,G	3
BspH I	T`CATG,A	2	BspM I	ACCTGC 10/14	6						
BspM II	T`CCGG,A	1	Bsr I	ACT,GG`	15						
BsrB I	GAG CGG	7	BsrD I	GCAATG, 8	2						
BsrG I	T`GTAC,A	-	BssH II	G`CGCG,C	1						
BssS I	C`TCGT,G	3	Bst1107 I	GTA TAC	1						
BstB I	TT`CG,AA	2	BstE II	G`GTNAC,C	2						
BstN I	CC`W,GG	16	BstU I	CG CG	16						
BstX I	CCAN,NNNN`NTGG	1	BstY I	R`GATC,Y	15						
Bsu36 I	CC`TNA,GG	2	Cac8 I	GCN NGC	37						
Cfr10 I	R`CCGG,Y	9	Cla I	AT`CG,AT	1						
Csp6 I	G`TA,C	8	Dde I	C`TNA,G	19						
Dpn I	GA TC	25	DpnII	`GATC,	25						
Dra I	TTT AAA	5	Dra III	CAC,NNN`GTG	1						
Drd I	GACNN,NN`NNGTC	5	Dsa I	C`CRYG,G	3						
Eae I	Y`GGCC,R	13	Eag I	C`GGCC,G	3						
Ear I	CTCTTC 7/10	7	Eco47 III	AGC GCT	1						
Eco57 I	CTGAAG 21/19	8	Eco72 I	CAC GTG	1						
EcoN I	CCTNN`N,NNAGG	2	Eco0109 I	RG`GNC,CY	3						
EcoR I	G`AATT,C	1	EcoR II	`CCWGG,	16						
EcoR V	GAT ATC	-	Ehe I	GGC GCC	3						
Esp I	GC`TNA,GC	2	Fnu4H I	GC`N,GC	60						
Fok I	GGATG 14/18	20	Fse I	GG,CCGG`CC	-						
Fsp I	TGC GCA	2	Gdi II	`YGGC,CG	13						
Gsu I	CTGGAG 21/19	4	Hae I	WGG CCW	12						
Hae II	R,GCGC`Y	8	Hae III	GG CC	30						
Hga I	GACGC 9/14	10	HgiA I	G,WGCW`C	8						
HgiE II	ACCNNNNNNGGT -1/133		Hha I	G,CG`C	33						
HinC II	GTY RAC	1	Hind II	GTY RAC	1						
HinD III	A`AGCT,T	1	Hinf I	G`ANT,C	15						
HinI I	GR`CG,YC	4	HinP I	G`CG,C	33						
Hpa I	GTT AAC	-	Hpa II	C`CG,G	36						
Hph I	GGTGA 12/11	14	Kas I	G`GCGC,C	3						
Kpn I	G,GTAC`C	1	Mae I	C`TA,G	16						
Mae II	A`CG,T	10	Mae III	`GTNAC,	20						
Mbo I	`GATC,	25	Mbo II	GAAGA 12/11	16						
Mlu I	A`CGCG,T	1	Mme I	TCCRAC 25/23	4						
Mnl I	CCTC 10/10	57	Msc I	TGG CCA	3						
Mse I	T`TA,A	17	Msl I	CAYNN NNRTG	4						
Msp I	C`CG,G	36	MspA1 I	CMG CKG	7						
Mun I	C`AATT,G	1	Nae I	GCC GGC	3						
Nar I	GG`CG,CC	3	Nci I	CC`s,GG	14						
Nco I	C`CATG,G	3	Nde I	CA`TA,TG	1						
Ngom I	G`CCGG,C	3	Nhe I	G`CTAG,C	2						
Nla III	,CATG`	24	Nla IV	GGN NCC	30						
Not I	GC`GGCC,GC	1	Nru I	TCG CGA	-						
Nsi I	A,TGCA`T	-	Nsp7524 I	R`CATG,Y	7						
NspB II	CMG CKG	7	NspH I	R,CATG`Y	7						
PaeR7 I	C`TCGA,G	-	Pal I	GG CC	30						
PflM I	CCAN,NNN`NTGG	2	Ple I	GAGTC 9/10	3						
Pme I	CTTT AAAC	2	Pml I	CAC GTG	1						
PpuM I	RG`GWC,CY	1	Psp1406 I	AA`CG,TT	2						
PspA I	C`CCGG,G	1	Pst I	C,TGCA`G	2						
Pvu I	CG,AT`CG	-	Pvu II	CAG CTG	4						
Rsa I	GT AC	8	Rsr II	CG`GWC,CG	2						
Sac I	G,AGCT`C	1	Sac II	CC,GC`GG	-						