

pSCV-His Full-Length Sequence

TGAAAGACCC CACCTGTAGG TTTGGCAAGC TAGCTTAAGT AACGCCATTT TGCAAGGCATGGAAAATACATAACTGAGAA
TAGAGAAGTT CAGATCAAGG TTAGGAACAG AGAGACAGCAGAATATGGGC CAAACAGGAT ATCTGTGGTAAGCAGTTCCCT
GCCCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGATGCGGTCCCGCCCTCAGCAGTTTCTAGAGAACCATCAGATGTTTTCCAGG
GTGCCCCAAGGACCTGAAATGACCCTGTGCCTTATTTGAACTAACCAATCAGTTTCGCTTCTCGCTTCTGTTCGCGCGCTTCTGCT
CCCCGAGCTC AATAAAAAGAG CCCACAACCCCTCACTCGGC GCGCCAGTCC TCCGATAGAC TCGCTCGCCCGGGTACCCGT
ATTCCCAATAAAAGCCTCTTG CTGTTTGCAT CCGAATCGTG GACTCGCTGA TCCTTGGGAG GGTCTCCTCAGATTGATTGA
CTGCCACCT CGGGGTCTT TCATTTGGAG GTTCCACCGA GATTTGGAGACCCCTGCCA GGGACCACCGACCCCCCGC
CGGGAGGTAA GCTGGCCAGC GGTCGTTTCGTGTCTGTCTC TGTCTTTGTG CGTGTTTGTG CCGGCATCTAATGTTTGC
CTGCGTCTGTACTAGTTAGC TAACTAGCTC TGTATCTGGC GGACCCGTGG TGAAGTGA GAGTCTGAACACCCGGCCG
CAACCTGGG AGACGTCCA GGGACTTTGG GGGCCGTTTT TGTGGCCGACCTGAGGAAG GGATCGATGTGAATCCGA
CCCCGTGAG ATATGTGGTT CTGGTAGGAGACGAGAACCT AAAACAGTTC CCGCTCCGT CTGAATTTTGTCTTTCGGTT
TGAACCGAAGCCGCGCTC TTGTCTGCTG CAGCGCTGCA GCATCGTTCT GTGTTGTCTC TGTCTGACTGTGTTTCTGTA
TTTGTCTGAA AATTAGGGCC AGACTGTTAC CACTCCCTTA AGTTTGACCTTAGGTCCTG GAAAGATGTCGAGCGGATCG
CTCACAACCA GTCGGTAGAT GTCAGAAGAGACGTTGGGT TACCTTCTGC TCTGCAGAAT GGCCAACCTTTAACGTCGGA
TGGCCGCGAGACGGCACCTT TAACCGAGAC CTCATCACC AGGTTAAGAT CAAGGTCTTT TCACCTGGCCCGCATGGACA
CCAGACCAG GTCCTTACA TCGTGACCTG GGAAGCCTTG GCTTTTGACCCCCCTCCCTG GGTCAAGCCCTTTGTACACC
CTAAGCCTCC GCCTCCTCTT CCTCCATCCGCCCGTCTCT CCCCCTTGAA CCTCCTCGTT CGACCCCGCTCGATCCTCC
CTTTATCCAGCCCTCACTCCTTCTTAGGCGCCGGAATTCACGTCGCCAAGCCTTTGTCTCAAGAAGAATCCACCCTCATTGAA
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ATGTGTGGGAGGGCTaa**gtttaaac**ATTGATTATTGACTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTTCATAGCCCAT
ATATGGAGTTCCGCTTACATAACTTACGGTAAATGGCCCCGCTGGCTGACCCGCCAACGACCCCCGCCATTGACGTCAATAAT
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AATCAACGGGACTTTCCAAAATGTCGTAACAACCTCCGCCCATTTGACGCAAAATGGGCGGTAGGCGGTGACGGTGGGAGGTCTATA
TAAGCAGAGCTCTCCCTATCAGTATAGATAGATCTCCCTATCAGTATAGATATCTCCCTATCAGTATAGATATCTCCCTATCAG
TGATAGAGATCGAGCTGTTTTAGTGAACCGTFCAGATCGCTGGAGACGCCATCCACGCTGTTTTGACCTCCATAGA**AGAtctaagc**
tt gcgg ccg cgt cga cgg atc cA CGC GT GGGCCC gga ggc ggc cat cat cac cat cac cat TGA
attc **ttaattaa** CGATAA AATAAAAAGAT TTTATTTAGT CTCCAGAAAAAGGGGGGAAT GAAAAGACCC ACCTGTAGGT
TTGGCAAGCTAGCTTAAAGTAACGCCATTTTGAAGGCATGGAAAATACATAACTGAGAATAGAGAAGTTTCAAGGTTAGGA
ACAGAGAGACAGCAGAATATGGCCAAAACAGGATATCTGTGGTAAGCAGTTTCTGCCCGGCTCAGGGCCAAGAACAGATGGTCC
CCAGATGCGGTCCCGCCCTCAGCAGTTTCTAGAGAACCATCAGATGTTTCCAGGGTGCCTCAAGGACCTGAAATGACCCTGTGCC
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TCACTCGGCGCGCAGTCTCCGATAGACTGCGTCCCGGGTACCCGTGATCCAATAAACCTCTTGAGTTGCATCCGACTT
GTGGTCTCGTGTTCCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCGTCAGCGGGGTCTTTCATGGGTAACAGTTTCTTGA
AGTTGGAGAA CAACATCTGAGGGTAGGAG TCGAATATTA AGTAATCCTG ACTCAATTAGCCACTGTTTT
GAATCCACATACTCCAATAC TCCTGAAATA GTTCATTATG GACAGCGCAGAAGAGCTGGG GAGAATTAAT TCGTAATCAT
GGTCATAGCTGTTTTCTGTG TGAAATTGTTATCCGCTCAC AATTCCACAC AACATACGAG CCGGAAGCAT AAAGTGTA
GCCTGGGGTGCTAATGAGT GAGCTAACTCACATTAATTG CGTTGCGCTC ACTGCCCGCT TTCCAGTCGGGAAAACCTGTC
GTGCCAGCTGCATTAATGAA TCGGCCAACG CGCGGGGAGA GGCGGTTTTGCGTATTGGGCG CTCTTCCGCT TCCTCGCTCA
CTGACTCGCTGCGCTCGGTG GTTCGGCTGCGGCGAGCGGT ATCAGCTCAC TCAAAGGCGG TAATACGGTT ATCCACAGAA
TCAGGGGATAACGCAGGAAA GAACATGTGAGCAAAAGGCC AGCAAAAGC CAGGAACCGT AAAAAGGCCGCTTGTGTC
GTTTTTCCATAGGCTCCGCC CCCCAGCA GCATCAAAA AATCAGAGCTCAAGTCAGAG GTGGCGAAAC CCGACAGGAC
TATAAAGATAACAGCGTTTT CCCCAGCAAGCTCCCTCGT GCGCTCTCTT GTTCCGACCC TTCCGCTTAC CGGATACCTG
TCCGCCTTTCTCCCTTCGGG AAGCGTGGCGTTTTCTCATA GCTCACGCTG TAGGTATCTC AGTTCCGGTGTAGGTCTGTCG
CTCCAAGCTGGGCTGTGTGC ACGAACCCCT CGTTCAGCCC GACCGCTGCGCCTTATCCGG TAACTATCGT CTTGAGTCCA
ACCCGGTAAGACACGACTTA TCGCCACTGGCAGCAGCCAC TGGTAACAGG ATTAGCAGAG CGAGGTATGT AGGCGGTGCT
ACAGAGTTCTTGAAGTGGTG GCCTAACTACGGCTACACTA GAAGGACAGT ATTTGGTATC TCGCTCTGCTGAAGCCAGT
TACCTTCGAAAAAGAGTTG GTAGTCTTTG ATCCGGCAAA CAAACCACCGCTGGTAGCGG TGGTTTTTTTT GTTTGCAAGC
AGCAGATTACGCGCAGAAAA AAAGGATCTCAAGAAGATCC TTTGATCTTT TCTACGGGGT CTGACGCTCA GTGGAACGAA
AACTCACGTTAAGGGATTTT GGTATGAGATTATCAAAA GGATCTTAC CTAGATCCTT TTAATTAATAAATGAAGTTT
TAAATCAATCTAAAGTATAT ATGAGTAAAC TTGGTCTGAC AGTTACCAATGCTTAATCAG TGAGGCACCT ATCTCAGCGA
TCTGTCTAATTCGTTTCATCC ATAGTTGCTGACTCCCCGT CGTGTAGATA ACTACGATAC GGGAGGGCTT ACCATCTGGC
CCCAGTGTGCAATGATACC GCGAGACCCA CGCTCACCAG CTCCAGATTT ATCAGCAATA AACCAGCCAGCCGGAAGGGC
CGAGCGCAGAAGTGGTCTCTG CAACTTTATC CGCTCCATC CAGTCTATTAATTTGTTGCCG GGAAGCTAGA GTAAGTAGTT

		5066	5254	5642	5933	Sap I	(2)	3328	3590				
		5953				Sau3A I	(31)	93	459	1046	1178		
Mbo I	(31)	93	459	1046	1178			1363	1647	1708	1722		
		1363	1647	1708	1722			2420	2441	2462	2483		
		2420	2441	2462	2483			2508	2552	2578	2774		
		2508	2552	2578	2774			4272	4272	4347	4358		
		4272	4347	4358	4366			4444	4456	4561	4902		
		4444	4456	4561	4902			4920	4966	5224	5241		
		4920	4966	5224	5241			5277	5862	6086			
		5277	5862	6086		Sau96 I	(30)	128	173	188	201		
Mbo II	(15)	1088	1301	1447	1504			256	553	692	762		
		1532	2561	3344	3578			775	987	1198	1221		
		4367	4440	5195	5273			1574	1917	2110	2590		
		5382	5870	6082				2591	2809	2854	2869		
Mlu I	(1)	2584						2882	2937	4641	4720		
Mme I	(6)	831	1108	3145	3197			4737	4959	5575	5872		
		3920	4104					6029	6214				
Mnl I	(48)	218	370	389	434	Sca I	(1)	5079					
		462	486	508	512	ScrF I	(35)	165	243	400	401		
		568	778	874	1170			550	572	725	737		
		1273	1306	1312	1315			750	1171	1196	1219		
		1321	1351	1354	1369			1239	1269	1719	1924		
		1376	1392	1456	1797			2117	2515	2594	2846		
		1798	2375	2551	2590			2924	3081	3082	3446		
		2899	3051	3070	3115			3734	3855	3868	4086		
		3142	3166	3226	3555			4782	5133	5634	5669		
		3604	3814	3887	4138			5941	6020	6218			
		4538	4619	4765	4971	Sec I	(31)	163	242	252	399		
Msc I	(3)	586	1113	1418				463	499	548	549		
Mse I	(26)	36	1009	1121	1151			696	735	736	748		
		1175	1816	1841	2630			749	1169	1238	1247		
		2634	2717	3251	3349			1267	1268	1413	1718		
		3477	3536	4412	4464			2194	2844	2923	2933		
		4469	4483	4536	4771			3080	3143	3445	3866		
		4810	5175	5547	5728	SfaN I	(21)	5940	6018	6024			
		5925	6195					187	446	643	940		
Msl I	(3)	2199	4851	5010				1487	1544	1676	1722		
Msp I	(25)	165	400	571	632			2192	2868	3126	3802		
		725	1403	2594	2846			4854	5047	5294	5655		
		3081	3424	3913	4060			5747	5785	5823	6139		
		4086	4276	4680	4714			6151					
		4781	4891	5133	5634	Sfc I	(10)	15	919	927	1103		
		5668	6020	6143	6152			1498	2696	3971	4162		
		6167						4840	6258				
MspAl I	(10)	590	1622	3182	3530	Sma I	(2)	401	3082				
		4048	4293	5234	5700	SnaB I	(1)	2174					
		5894	6250			Spe I	(2)	662	1833				
Nae I	(2)	633	6153			Sph I	(1)	5994					
Nar I	(5)	1400	5822	6005	6119	Ssp I	(2)	3249	5403				
		6140				Sty I	(7)	252	463	1247	1413		
Nci I	(15)	165	400	401	572			2194	2933	3143			
		725	2594	2846	3081	Taq I	(10)	796	1040	1351	1362		
		3082	4086	4782	5133			1707	2486	2573	3244		
		5634	5669	6020				3806	5250				
Nco I	(2)	1413	2194			Tfi I	(7)	444	804	1439	1771		
Nde I	(2)	2068	5770					3284	3541	3681			
NgoM I	(2)	631	6151			Tsp45 I	(6)	1024	1233	4855	5066		
Nhe I	(2)	30	2711					5642	5953				
Nla III	(19)	62	1207	1417	2138	Tth111 I	(4)	392	813	1219	3073		
		2198	2743	3197	3364	Tth111 II	(8)	147	424	615	634		
		3710	4430	4921	4931			2828	4295	4304	4334		
		5009	5045	5438	5543	Vsp I	(5)	1841	3349	3477	3536		
		5627	5994	6067				4771					
Nla IV	(34)	190	203	248	405	Xba I	(2)	220	2901				
		523	554	694	763	Xho II	(11)	2420	2441	2462	2552		
		895	1146	1223	1401			2578	4347	4358	4444		
		1575	1691	2301	2580			4456	5224	5241			
		2592	2871	2884	2929	Xma I	(2)	399	3080				
		3086	3452	3738	3777	Xma III	(3)	726	1531	2565			
		4549	4643	4684	4895	Xmn I	(3)	3312	3350	5198			
		5485	5823	6006	6030								
		6120	6141										
Not I	(1)	2565											
Nru I	(1)	1646											
Nsp7524 I	(3)	3706	5623	5990		Aat II	G,ACGT`C	6	Acc I	GT`MK,AC	1		
NspB II	(10)	590	1622	3182	3530	Acc65 I	G`GTAC,C	2	Aci I	C`CG,C	67		
		4048	4293	5234	5700	Afl II	C`TTAA,G	3	Afl III	A`CRYG,T	2		
		5894	6250			Age I	A`CCGG,T	-	Aha II	GR`CG,YC	13		
		3710	5627	5994		Ahd I	GACNN,N`NNGTC	4	Alu I	AG CT	30		
NspH I	(3)	3710	5627	5994		Alw I	GGATC 8/9	14	AlwN I	CAG,NNN`CTG	3		
Pac I	(1)	2634				Apa I	G,GGCC`C	1	ApaL I	G`TGCA,C	3		
Pal I	(32)	130	175	586	728	Apo I	R`AATT,Y	3	Asc I	GG`CGCG,CC	2		
		764	776	989	1113	Ase I	AT`TA,AT	5	Asp718	G`GTAC,C	2		
		1134	1199	1418	1533	Ava I	C`YCGR,G	5	Ava II	G`GWC,C	13		
		1918	2111	2567	2592	Avr II	C`CTAG,G	-	BamH I	G`GATC,C	1		
		2603	2811	2856	3547	Ban I	G`GYRC,C	13	Ban II	G,RCGY`C	9		
		3721	3732	3750	4184	Bbe I	G,CGCC`C	5	Bbs I	GAAGAC 8/12	1		
		4642	4722	4989	5576	Bbv I	GCAGC 13/17	9	Bbv II	GAAGAC 7/11	1		
		5874	6023	6031	6155	Bcl I	T`GATC,A	-	Bcn I	CC,S`GG	15		
		801	3249	4085		Bfa I	C`TA,G	13	Bgl I	GCCN,NNN`NGGC	5		
Ple I	(3)	801	3249	4085		Bgl II	A`GATC,T	4	Blp I	GC`TNA,GC	-		
Pme I	(1)	1817				Bpm I	CTGGAG 22/20	4	Bsa I	GGTCTC 7/11	6		
PpuM I	(4)	256	1221	1574	2937	BsaA I	YAC GTR	1	BsaB I	GATNN NNATC	5		
Psp1406 I	(2)	4825	5198			BsaH I	GR`CG,YC	13	BsaJ I	C`CNNG,G	31		
PspA I	(2)	399	3080			BsaW I	W`CCGG,W	3	BseR I	GAGGAG 16/14	4		
Pst I	(3)	923	931	1107		Bsg I	GTGCAG 22/20	1	BsiC I	TT`CG,AA	-		
Pvu I	(3)	1650	4969	5865		BsiE I	CG,RY`CG	10	BsiHKA I	G,WGWC`C	7		
Pvu II	(4)	1622	3530	5894	6250	BsiW I	C`GTAC,G	-	Bsm I	GAATG,C 7	-		
Rsa I	(13)	405	661	1286	2053	BsmA I	GTCTC`/9	23	BsmB I	CGTCTC 7/11	8		
		2078	2133	2166	2217	BsmF I	GGGAC 15/19	13	BsoF I	GC`N,GC	37		
		2374	3086	5079	5755	Bsp120 I	G`GGCC,C	1	Bsp1286 I	G,DGCH`C	-		
		6266				BspH I	T`CATG,A	4	BspM I	ACCTGC 10/14	-		
Sac I	(3)	340	2402	3021		BspM II	T`CCGG,A	-	Bsr I	ACT,GG`	17		
Sal I	(1)	2572											

Site usage in PSCV-HIS.TXT:

Aat II	G,ACGT`C	6	Acc I	GT`MK,AC	1
Acc65 I	G`GTAC,C	2	Aci I	C`CG,C	67
Afl II	C`TTAA,G	3	Afl III	A`CRYG,T	2
Age I	A`CCGG,T	-	Aha II	GR`CG,YC	13
Ahd I	GACNN,N`NNGTC	4	Alu I	AG CT	30
Alw I	GGATC 8/9	14	AlwN I	CAG,NNN`CTG	3
Apa I	G,GGCC`C	1	ApaL I	G`TGCA,C	3
Apo I	R`AATT,Y	3	Asc I	GG`CGCG,CC	2
Ase I	AT`TA,AT	5	Asp718	G`GTAC,C	2
Ava I	C`YCGR,G	5	Ava II	G`GWC,C	13
Avr II	C`CTAG,G	-	BamH I	G`GATC,C	1
Ban I	G`GYRC,C	13	Ban II	G,RCGY`C	9
Bbe I	G,CGCC`C	5	Bbs I	GAAGAC 8/12	1
Bbv I	GCAGC 13/17	9	Bbv II	GAAGAC 7/11	1
Bcl I	T`GATC,A	-	Bcn I	CC,S`GG	15
Bfa I	C`TA,G	13	Bgl I	GCCN,NNN`NGGC	5
Bgl II	A`GATC,T	4	Blp I	GC`TNA,GC	-
Bpm I	CTGGAG 22/20	4	Bsa I	GGTCTC 7/11	6
BsaA I	YAC GTR	1	BsaB I	GATNN NNATC	5
BsaH I	GR`CG,YC	13	BsaJ I	C`CNNG,G	31
BsaW I	W`CCGG,W	3	BseR I	GAGGAG 16/14	4
Bsg I	GTGCAG 22/20	1	BsiC I	TT`CG,AA	-
BsiE I	CG,RY`CG	10	BsiHKA I	G,WGWC`C	7
BsiW I	C`GTAC,G	-	Bsm I	GAATG,C 7	-
BsmA I	GTCTC`/9	23	BsmB I	CGTCTC 7/11	8
BsmF I	GGGAC 15/19	13	BsoF I	GC`N,GC	37
Bsp120 I	G`GGCC,C	1	Bsp1286 I	G,DGCH`C	-
BspH I	T`CATG,A	4	BspM I	ACCTGC 10/14	-
BspM II	T`CCGG,A	-	Bsr I	ACT,GG`	17

BsrB I	GAG CGG	4	BsrD I	GCAATG, 8	2	Mse I	T`TA,A	26	Msl I	CAYNN NNRTG	3
BsrG I	T`GTAC,A	1	BssH II	G`CGCG,C	4	Msp I	C`CG,G	25	MspA1 I	CMG CKG	10
BssS I	C`TCGT,G	4	Bst1107 I	GTA TAC	-	Mun I	C`AATT,G	-	Nae I	GCC GGC	2
BstB I	TT`CG,AA	-	BstE II	G`GTNAC,C	1	Nar I	GG`CG,CC	5	Nci I	CC`S,GG	15
BstN I	CC`W,GG	20	BstU I	CG CG	23	Nco I	C`CATG,G	2	Nde I	CA`TA,TG	2
BstX I	CCAN,NNNN`NTGG	-	BstY I	R`GATC,Y	11	NgoM I	G`CCGG,C	2	Nhe I	G`CTAG,C	2
Bsu36 I	CC`TNA,GG	2	Cac8 I	GCN NGC	34	Nla III	,CATG`	19	Nla IV	GGN NCC	34
Cfr10 I	R`CCGG,Y	4	Cla I	AT`CG,AT	-	Not I	GC`GGCC,GC	1	Nru I	TCG CGA	1
Csp6 I	G`TA,C	13	Dde I	C`TNA,G	20	Nsi I	A,TGCA`T	-	Nsp7524 I	R`CATG,Y	3
Dpn I	GA TC	31	DpnII	`GATC,	31	NspB II	CMG CKG	10	NspH I	R,CATG`Y	3
Dra I	TTT AAA	4	Dra III	CAC,NNN`GTG	-	Pac I	TTA,AT`TAA	1	Paer7 I	C`TCGA,G	-
Drd I	GACNN,NN`NNGTC	3	Dsa I	C`CRYG,G	4	Pal I	GG CC	32	Pf1M I	CCAN,NNN`NTGG	-
Eae I	Y`GGCC,R	12	Eag I	C`GGCC,G	3	Ple I	GAGTC 9/10	3	Pme I	CTTT AAAC	1
Ear I	CTCTTC 7/10	6	Eco47 III	AGC GCT	2	Pml I	CAC GTG	-	PpuM I	RG`GWC,CY	4
Eco57 I	CTGAAG 21/19	4	Eco72 I	CAC GTG	-	Psp1406 I	AA`CG,TT	2	PspA I	C`CCGG,G	2
EcoN I	CCTNN`N,NNAGG	2	Eco109 I	RG`GNC,CY	6	Pst I	C,TGCA`G	3	Pvu I	CG,AT`CG	3
EcoR I	G`AATT,C	2	EcoR II	`CCWGG,	20	Pvu II	CAG CTG	4	Rsa I	GT AC	13
EcoR V	GAT ATC	3	Ehe I	GGC GCC	5	Rsr II	CG`GWC,CG	-	Sac I	G,AGCT`C	3
Esp I	GC`TNA,GC	-	Fnu4H I	GC`N,GC	37	Sac II	CC,GC`GG	-	Sal I	G`TCGA,C	1
Fok I	GGATG 14/18	12	Fse I	GG,CCGG`CC	-	Sap I	GCTCTTC 8/11	2	Sau3A I	`GATC,	31
Fsp I	TGC GCA	2	Gdi II	`YGGC,CG	12	Sau96 I	G`GNC,C	30	Sca I	AGT ACT	1
Gsu I	CTGGAG 21/19	4	Hae I	WGG CCW	6	ScrF I	CC`N,GG	35	Sec I	C`CNNG,G	31
Hae II	R,GGC`Y	9	Hae III	GG CC	32	SfaN I	GCATC 9/13	21	Sfc I	C`TRYA,G	10
Hga I	GACGC 9/14	13	HgiA I	G,WGCW`C	7	Sfi I	GGCCN,NNN`NGGCC	-	Sma I	CCC GGG	2
HgiE II	ACCNNNNNNGGT -1/132	-	Hha I	G,CG`C	36	SnaB I	TAC GTA	1	Spe I	A`CTAG,T	2
Hinc II	GTY RAC	1	Hind II	GTY RAC	1	Sph I	G,CATG`C	1	Spl I	C`GTAC,G	-
Hind III	A`AGCT,T	1	Hinf I	G`ANT,C	16	Srf I	GCCC GGGC	-	Ssp I	AAT ATT	2
HinI I	GR`CG,YC	13	HinP I	G`CG,C	36	Stu I	AGG CCT	-	Sty I	C`CWVG,G	7
Hpa I	GTT AAC	-	Hpa II	C`CG,G	25	Taq I	T`CG,A	10	Tfi I	G`AWT,C	7
Hph I	GGTGA 12/11	16	Kas I	G`GCGC,C	5	Tsp45 I	`GTSAC,	6	Tth111 I	GACN`N,NGTC	4
Kpn I	G,GTAC`C	2	Mae I	C`TA,G	13	Tth111 II	CAARCA 16/14	8	Vsp I	AT`TA,AT	5
Mae II	A`CG,T	14	Mae III	`GTNAC,	21	Xba I	T`CTAG,A	2	Xca I	GTA TAC	-
Mbo I	`GATC,	31	Mbo II	GAAGA 12/11	15	Xcm I	CCANNNN,N`NNNNTGG-	-	Xho I	C`TCGA,G	-
Mlu I	A`CGCG,T	1	Mme I	TCCRAC 25/23	6	Xho II	R`GATC,Y	11	Xma I	C`CCGG,G	2
Mnl I	CCTC 10/10	48	Msc I	TGG CCA	3	Xma III	C`GGCC,G	3	Xmn I	GAANN NNTTC	3