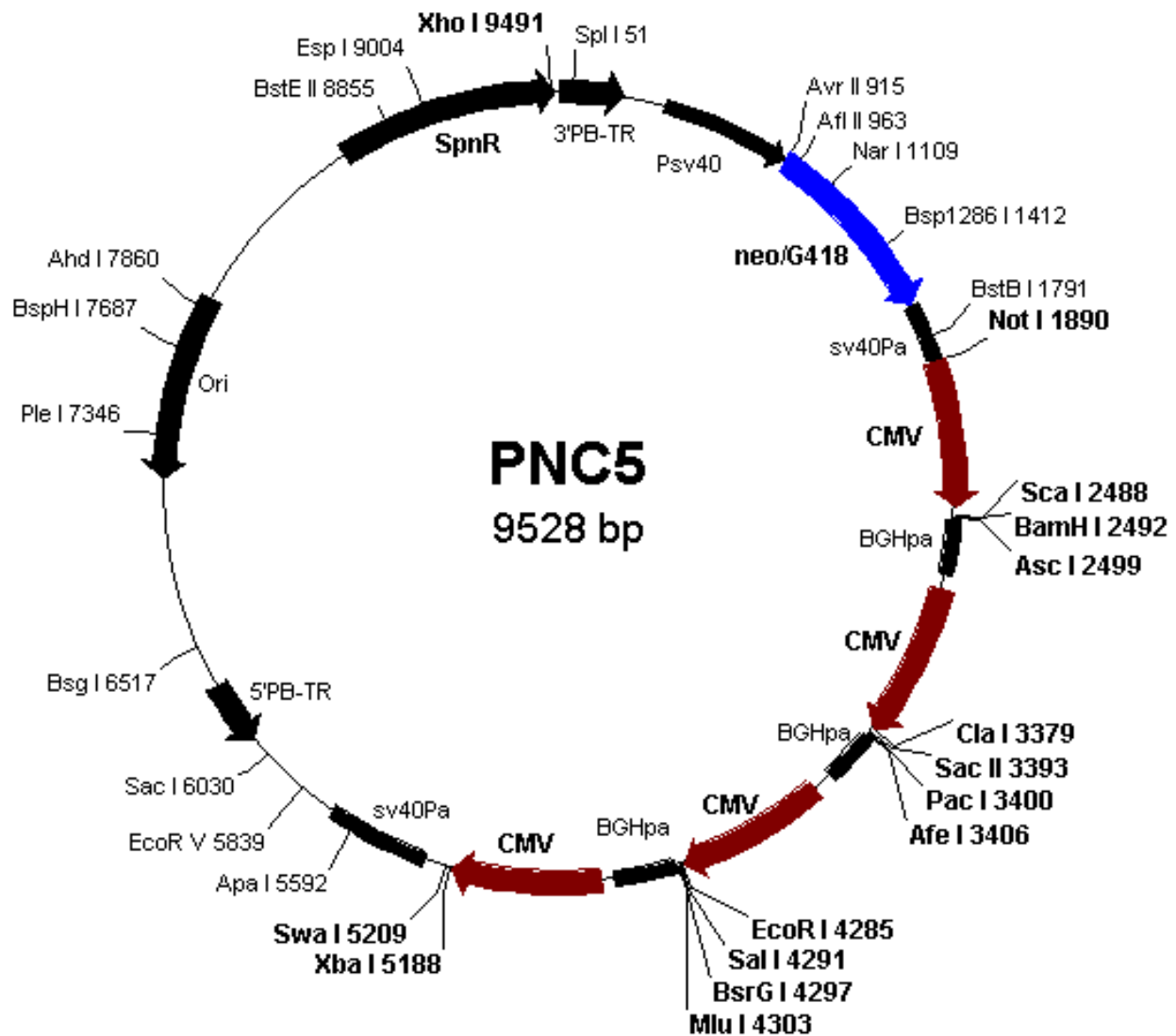


Vector: PNC5 (MOLab modified piggyBac vector with CMV promoter)

Antibiotic Selection: Spectinomycin-resistant

Creator(s): Xian Chen & Palak Shah, Molecular Oncology Lab of The University of Chicago

Date of Construction: January, 2013



PNC5 Vector Sequence

(Spectinomycin-resistant)

CTGCAGAACACGCAGCTAGATTAACTCTAGAAAAGATAATCATATTGTGACGTACGTTAAAGATAAATCATGCGTAAAATTGACGCATG
TGTTTTATCGGTCTGTATATCGAGGTTTATTTATTAATTTGAATAGATATTAAGTTTTATTATATTTACTTACATACTAATAATA
AATTCAACAAACAATTTATTTATGTTTTATTTATTTATTTAAAAAACAACAACTCAAAATTTCTTCTATAAAGTAACAAAACTTTT
ATGAGGGACAGCCCCCCCCAAAGCCCCCAGGGATGTAATTACGTCCCTCCCCCGCTAGGGGGCAGCAGCGAGCCCGCCGGGGCTCC
GCTCCGGTCCGGCGCTCCCCCGCATCCCCGAGCCGGCAGCGTGCGGGGACAGCCCCGGGCACGGGGAAGGTGGCACGGGATCGCTTT
CCTCTGAACGCTTCTCGCTGCTTTGAGCCCTGCAGACACCTGGGGGATACGGGGAAAAGGCCTCCACGGCCAGACTAGAgcgcag
caccatggcctgaaataacctctgaaagaggaacttggtaggttagtacctctgaggcggaagaaccagctgtggaatgtgtgtcagt
taggggtgaggaaagtcccaggctcccagcaggcagaagtagcaaacgcatgcatctcaattagtcagcaaccatagtcocgcccctaactcgc
cgcocctaactcgcocagttcgcocattctcgcoccatggctgactaattttttttatttatgacagaggccgaggccgcctcgg
cctctgagctattccagaagtagtgaggaggctttttggaggcctaggctttgcaaaaagcttgattctctgacacaacagctct
cgaacttaaggctagagccaccATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTTCGGCTA
TGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCCGGTGTTCCGGCTGTGAGCGCAGGGGCGCCGGTTCTTTTTGTCAAGAC
CGACCTGTCCGGTGCCTGAATGAACTGCAGGACGAGGCAGCGCGCTATCGTGGCTGGCCACGACGGGCGTTCTTGGCAGCTGT
GCTCGACGTTGTACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCAGGGCAGGATCTCTGTCTACCTTGCTCC
TGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCATTTCGACCACCAAGCGAA
ACATCGCATCGAGCGAGCAGTACTCGGATGGAAGCCGGTCTTGTGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCC
AGCCGAAGTGTTCGCCAGGCTCAAGGCGCGCATGCCCGACGGCGAGGATCTCGTCTGACCCATGGCGATGCCTGCTTGCCGAATAT
CATGGTGGAAAATGGCCGCTTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTAC
CCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCTCGTGTCTTACGGTATCGCCGCTCCCGATTTCGACGCGCAT
CGCCTTCTATCGCCTTCTTGCAGAGTTCTTCTGAgcgggactctggggttcgaaatgaccgaccaagcgacgcccacactgccatca
cgatggccgcaataaaatatctttatctttcattacatctgtgtgttgggtttttgtgtgaGCGGCCGCTAATAGTAATCAATTACGG
GGTCATTAGTTTCATAGCCCATATATGGAGTTCGCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGACCGCCCAACGACCCCC
GCCATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGT
AAACTGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACGTCAATGACGGTAAATGGCCCGCCTGGC
ATTATGCCCAGTACATGACCTTATGGGACTTTTCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGT
TTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTACTCACGGGATTTCCAAGTCTCCACCCATTGACGTCAATGGGAGTTTGT
TTTTGGCACCAAAATCAACGGGACTTTTCCAAAATGTCGTAACAACCTCCGCCATTGACGCAAAATGGGCGGTAGGCGGTGACGGTGGG
AGGTCTATATAAGCAGAGCTGGTTTGTAGTGAACCGTCAGATCCGGTACCAGTACTGGATCCGGCGCGCCGTGGCCGCTAAACCCGCT
GATCAGCCTCGACTGTGCCTTCTAGTTTGCAGCCATCTGTTTGGCCCTCCCCCGTGCCTTCTTGGCCTTGAAGGTTGCCACTC
CCTACTGCTTTTCTAATAAAAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCAATTCTATTCTGGGGGTTGGGGTGGGGCAGG
ACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCTATGGCTTCTGAGGCGGAAAGAACCAGGA
TCTGCTAGNTAATAGTAATCAATTACGGGGTTCATTAGTTTCATAGCCCATATATGGAGTTCGCGTTACATAACTTACGGTAAATGGC
CCGCTGGCTGACCGCCCAACGACCCCGCCATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAGGGACTTTCCAT
TGACGTCAATGGGTGGAGTATTTACGGTAAACTGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGAC
GTCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCAGTACATGACCTTATGGGACTTTTCTACTTGGCAGTACATCTACGTATTA
GTCATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTACTCACGGGATTTCCAAGTCTC
CACCCATTGACGTCAATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTTCCAAAATGTCGTAACAACCTCCGCCATTGACG
CAAATGGGCGGTAGGCGGTGACGGTGGGAGGTCTATATAAGCAGAGCTGGTTTGTAGTGAACCGTCAGATCCATCGATTAAGCTTCCGCG
GTTAATTAAGCGCTagatcGGCCGCTAAACCCGCTGATCAGCCTCGACTGTGCCTTCTAGTTTGCAGCCATCTGTTGTTTGGCCC
TCCCCCGTGCCTTCTTGGACCTGGAAGGTGCCACTCCACTGTCTTTTCTAATAAAAATGAGGAAATTGCATCGCATTGTCTGAGT
AGGTGTCAATTCTATTCTGGGGGTTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGCTGGGGATGCG
GTGGGCTCTATGGCTTCTGAGGCGGAAAGAACCAGGATCTGCTAGNTAATAGTAATCAATTACGGGGTTCATTAGTTTCATAGCCCAT
TATGGAGTTCGCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGACCGCCCAACGACCCCGCCATTGACGTCAATAATGAC
GTATGTTCCCATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTAAACTGCCCACTTGGCAGTACA
TCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCAGTACATGACCTT
ATGGGACTTTTCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGGCG
TGGATAGCGGTTTACTCACGGGATTTTCCAAGTCTCCACCCATTGACGTCAATGGGAGTTTGTTTTGGCACCAAAATCAACGGGA
CTTTCCAAAATGTCGTAACAACCTCCGCCATTGACGCAAAATGGGCGGTAGGCGGTGACGGTGGGAGGTCTATATAAGCAGAGCTGG
TTTGTAGTGAACCGTCAGATCCGAATTCGTGACTGTACAACCGCTGTTGGCCGCTAAACCCGCTGATCAGCCTCGACTGTGCCTTCT
AGTTGCCAGCCATCTGTTGTTTGGCCCTCCCCCGTGCCTTCTTGGACCTGGAAGGTGCCACTCCACTGTCTTTTCTAATAAAAAT
GAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCAATTCTGGGGGTTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGA
GACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCTATGGCTTCTGAGGCGGAAAGAACCAGGATCTGCTAGNTAATAGTAATCAAT
TACGGGGTTCATTAGTTCATAGCCCATATATGGAGTTCGCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGACCGCCCAACG
CCCCCGCCATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTT
ACGGTAAACTGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACGTCAATGACGGTAAATGGCCCGC
CTGGCATTATGCCCAGTACATGACCTTATGGGACTTTTCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGAT
GCGGTTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTTGACTCACGGGATTTCCAAGTCTCCACCCATTGACGTCAATGGGAG

TTTGT TTTGGCACCAAATCAACGGGACTTTCCAAAATGTCGTAACTCCGCCCATTTGACGCAAATGGGCGGTAGGCGTGTACG
 GTGGGAGGTCTATATAAGCAGAGCTGGTTTGTGAAACCGTCAGATCCATCGAATCTAGATACGTACATATGATTTAAATGATCTAAC
 TAACTAAACTTGTATTATTGCANCTTATAATGGTTACAAAATAAAGCAATAGCATCACAAATTTACAAAATAAAGCATTTTTTTCACTG
 CATTCTAGTGTGGTGTGTCAAAACCTCATCAATGTATCTTATCATGTCTGGAATGACTCAAATGATGTCAATTAGTCTATCAGAAGC
 TCATCTGGTCTCCCTTCCGGGGGACAAGACATCCCTGTTAATATTTAAACAGCAGTGTCCCAAACCTGGGTTCTTATATCCCTTGC
 TCTGGTCAACCAGGTTGCAGGGTTTCTGTCTCACAGGAACGAAGTCCCTAAAGAAACAGTGGCAGCCAGGTTTAGCCCCGGAATT
 GACTGGATTCTTTTTTAGGGCCATTGGTATGGCTTTTTCCCCGTATCCCCCAGGTGTCTGCGAGCTCAAAGAGCAGCGAGAAGC
 GTTCAGAGGAAAGCGATCCCGTGCCACCTTCCCCGTGCCCGGGCTGTCCCCGCACGCTGCCGGCTCGGGGATGCGGGGGAGCGCCG
 GACCGGAGCGGAGCCCCGGGGCTCGCTGCTGCCCCCTAGCGGGGAGGGACGTAATTACATCCCTGGGGGCTTTGGGGGGGGGCT
 GTCCCTGATATCTATAACAAGAAAATATATATAATAAGTTATCACGTAAGTAGAACATGAAATAACAATATAATTATCGTATGAG
 TTAATACTTAAAAGTCACGTAAGAAAGATAATCATGCGCTCATTTTTGACTCACGCGGTTCGTTATAGTTCAAATCAGTGACACTTACCGC
 ATTGACAAGCACGCTCACGGGAGCTCCAAGCGCGACTGAGATGTCTAAATGCACAGCGACGGATTTCGCGCTATTTAGAAAAGAGA
 GAGCAATATTTCAAGAATGCTAGCGTCAATTTACGCGAGATCTTTCTAGGGTTAATCTAGCTGCATCAGGATCATATATCGTCGGG
 TCTTTTTTTCATCGCCCAAGCTGGCGCTATCTGGGCATCGGGGAGGAAGAAGCCCGTGCCTTTTTCCCGCGAGGTTGAAGCGGCATGGA
 AAGAGTTTGCCGAGGATGACTGCTGCTGCATTGACGTTGAGCGAAAACGCACGTTTACCATGATGATTTCGGGAAGGTGTGGCCATGC
 ACGCTTTAACGGTGAACGTGTTTCGTTTCAGGCCACCTGGGATAACCAGTTTCGTGCGGGCTTTTTCCGGACACAGTTCCGGATGGTCAGCC
 CGAAGCGCATCAGCAACCCGAACAATACCGGCGACAGCCGAACTGCCGTGCCGGTGTGCAGATTAATGACAGCGGTGCGGCGCTGG
 GATATTACGTGACGAGGACGGGTATCCTGGCTGGATGCCGAGAAATGGACATGGATAACCCGTGAGTTACCCGGCGGGCGCGCTT
 GCGTAATCATGGTCATAGCTGTTTCTGTGTGAAATTGTTATCCGCTCACAAATTCACACAACATACGAGCCGGAAGCATAAAGTG
 TAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTGCTG
 CCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCATTTGGGCGCTCTTCCGCTTCTCGCTCACTGACTCGCT
 GCGCTCGGTCGTTCCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGG
 AAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCC
 TGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAAACCCGACAGGACTATAAAGATAACCAGGCGTTTTCCCTTGGAAAG
 CTCCCTCGTGCCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCA
 TAGCTCACGCTGTAGGTATCTCAGTTCCGGTGTAGGTGCTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTTCCAGCCGACCG
 CTGCGCTTATCCGGTAACTATCGTCTTTCGAGTCCAACCCGGTAAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGAT
 TAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGGACAGTATTTGGTAT
 CTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTTCGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTT
 TTTTGTTTGCAAGCAGCAGATACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTTCTACGGGCTCTGACGCTCAGTG
 GAAAGAAAACCTCAGCTTAAGGATTTTGGTCTGAGATTATCAAAAAGGATCTTCCACTAGATCCTTTTTAAATTAATAAATGAAGTTT
 TAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAAATCAGTGAGGACACTTCTCAGCGATCTGTCT
 ATTTTCGTTTCATCCATAGTTGCCTGACTCCCCGTGCTGTAGATAACTACGATACGGGAGGCTTACCATCTGCCCCAGTGTGCAAT
 GATACCGGAGACCCACGCTCACCGGCTCCAGATTTATCAGCAATAAACCAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGGTCTCTGC
 AACTTTATCCGCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAGTAGTTTCGCCAGTTAATAGTTTTCGCAACGTTGT
 TGCCATTGCTACAGGCATCGTGGTGTACGCTCGTCTGTTGGTATGGCTTCAATTCAGCTCCGGTTCCCAACGATCAAGGCGAGTTAC
 ATGATCCCCATGTTGTGCAAAAAGCGGTTAGCTCCTTCGGTCTCCGATCGTTGTGAGAAGTAAGTTGGCCGAGTGTATCACT
 CATGGTTATGGCAGCACTGCATAATTCTCTTACTGTATGCCATCCGTAAGATGCTTTTTCTGTGACTGGTGTAGTGTACAGCCAGGA
 CAGAAATGCCTCGACTTCGCTGCTACCCAAGTTGCCGGGTGACGCACACCGTGGAAACGGATGAAGGCACGAACCCAGTGGACATA
 AGCCTGTTCCGGTTCGTAAGCTGTAATGCAAGTAGCGTATGCGCTCACGCAACTGGTCCAGAACCCTTGACCGAACGCAGCGGTGGTAA
 CGGCGCAGTGGCGGTTTTTCATGGCTTGTATGACTGTTTTTTTTGGGGTACAGTCTATGCCTCGGGCATCCAAGCAGCAAGCGCGTTA
 CGCCGTGGGTGATGTTTGTATGTTATGGAGCAGCAACGATGTTACGCAGCAGGGCAGTCCGCCATAAACAAGTTAAACATTATGAG
 GGAAGCGGTGATCGCCGAAGTATCGACTCAACTATCAGAGGTAGTTGGCGTCATCGAGCGCCATCTCGAACCAGGTTGCTGGCCGT
 ACATTTGTACGGCTCCGCAAGTGGATGGCGGCCTGAAGCCACACAGTGAATTTGATTTGCTGGTTACGGTGACCGTAAGGCTTGATGA
 AACACCGCGGCGAGCTTTGATCAACGACCTTTTGGAAACTTCGGCTTCCCTTGGAGAGAGCGAGATTCTCCGCGCTGTAGAAGTAC
 CATTGTTGTGCACGACGACATCATTCCGTGGCGTTATCCAGCTAAGCGCGAACTGCAATTTGGAGAATGGCAGCGCAATGACATTCT
 TGCAGGTATCTTCGAGCCAGCCACGATCGACATTGATCTGGCTATCTTGTGACAAAAGCAAGAGAACATAGCGTTGCCTTGGTAGG
 TCCAGCGGCGGAGGAACTCTTTGATCCGGTTCCTGAACAGGATCTATTTGAGGGCGCTAAATGAAACCTTAAACGCTATGGAACCTGCC
 GCCGACTGGGCTGGCGATGAGCGAAATGTAGTGCTTACGTTGTCCCGCATTTGGTACAGCGCAGTAACCGGCAAAATCGCGCCGAA
 GGATGTCGCTGCCACTGGGCAATGGAGCGCCTGCCGGCCAGTATCAGCCCGTCACTTGAAGCTAGACAGGCTTATCTTGGACA
 AGAAGAAGATCGCTTGGCTTCGCGCGCAGATCAGTTGGAAGAATTTGTCCACTACGTGAAAGGCGAGATCACCAAGGTAGTCGGCAA
 ATAACCCTCGAGCCACCCAATGACCAAAAATCCCTTAAACGTGAGTTA

Unique enzymes in PNC5:

BsiW I	C`GTAC,G	51	BstB I	TT`CG,AA	1791
Spl I	C`GTAC,G	51	Not I	GC`GGCC,GC	1890
BseR I	GAGGAG 16/14	911	Sca I	AGT ACT	2488
Avr II	C`CTAG,G	915	BamH I	G`GATC,C	2492
Afl II	C`TTAA,G	963	Asc I	GG`CGCG,CC	2499
Kas I	G`GCGC,C	1108	Clal I	AT`CG,AT	3379
Nar I	GG`CG,CC	1109	Sac II	CC,GC`GG	3393
Ehe I	GGC GCC	1110	Pac I	TTA,AT`TAA	3400
Bbe I	G,GCGC`C	1112	Afe I	AGC GCT	3406
Tth111 I	GACN`N,NGTC	1227	Eco47 III	AGC GCT	3406
Bsp1286 I	G,DGCH`C	1412	EcoR I	G`AATT,C	4285
BsiC I	TT`CG,AA	1791	Sal I	G`TCGA,C	4291
			Acc I	GT`MK,AC	4292
			BsrG I	T`GTAC,A	4297

Mlu I	A`CGCG,T	4303				7713	8177	9154	9183
Xba I	T`CTAG,A	5188		AlwN I	(4)	2786	3693	4590	7383
Swa I	ATTT AAAT	5209		Apa I	(1)	5592			
EcoN I	CCTNN`N,NNAGG	5583		ApaL I	(2)	7281	8970		
EcoO109 I	RG`GNC,CY	5588		Apo I	(5)	175	233	4285	5278
Bsp120 I	G`GGCC,C	5588				9438			
Apa I	G,GGCC`C	5592		Asc I	(1)	2499			
EcoR V	GAT ATC	5839		Ase I	(5)	122	6503	6738	6797
Sac I	G,AGCT`C	6030				8032			
Bsg I	GTGCAG 22/20	6517		Asp718	(2)	565	2480		
Ple I	GAGTC 9/10	7346		Ava I	(8)	339	377	403	5694
BspH I	T`CATG,A	7687				5720	5758	8587	9491
Ahd I	GACNN,N`NNGTC	7860		Ava II	(7)	355	1625	5743	7998
Psp1406 I	AA`CG,TT	8086				8220	8494	9135	
BstE II	G`GTNAC,C	8855		Avr II	(1)	915			
Blp I	GC`TNA,GC	9004		BamH I	(1)	2492			
Esp I	GC`TNA,GC	9004		Ban I	(13)	565	1108	1143	2354
PaeR7 I	C`TCGA,G	9491				2480	2602	3252	3509
Xho I	C`TCGA,G	9491				4159	4406	5056	6711
Number of enzymes = 45									
				Ban II	(8)	347	1474	2755	3662
						4559	5592	5758	6030
				Bbe I	(1)	1112			
				Bbs I	(3)	2726	3633	4530	
				Bbv I	(19)	25	337	340	398
						532	1182	1224	1745
						5558	5657	7386	7389
						7595	8289	8527	8612
						8656	8672	9044	
				Bbv II	(3)	2725	3632	4529	
				Bcl I	(4)	2524	3431	4328	8893
				Bcn I	(16)	341	342	405	406
						1114	1274	5414	5563
						5696	5697	5760	5761
						6600	7348	8044	8391
				Bfa I	(22)	17	28	318	513
						916	970	2546	2790
						3408	3453	3697	4350
						4594	5189	5313	5781
						6140	6151	7462	7715
						8050	9376		
				Bgl I	(16)	504	868	1979	2101
						2172	2877	2999	3070
						3784	3906	3977	4681
						4803	4874	7980	9327
				Blp I	(1)	9004			
				Bpm I	(2)	7930	8947		
				Bsa I	(2)	5408	7921		
				BsaA I	(9)	1413	2229	3127	4034
						4931	5196	5877	5935
						9452			
				BsaH I	(19)	1109	1811	2011	2064
						2147	2333	2909	2962
						3045	3231	3816	3869
						3952	4138	4713	4766
						4849	5035	8749	
				BsaJ I	(44)	289	290	339	340
						403	476	502	526
						627	699	822	857
						866	915	1272	1541
						2249	2594	3147	3390
						3501	4054	4398	4951
						5412	5560	5621	5694
						5757	5758	5807	5808
						6275	6386	6706	7127
						8380	8403	8586	8617
						8924	8988	9127	9469
				BsaW I	(10)	352	1140	2477	5745
						6413	6425	7173	7320
						8151	9161		
				BseR I	(1)	911			
				Bsg I	(1)	6517			
				BsiC I	(1)	1791			
				BsiE I	(8)	1018	1893	3418	5972
						6883	7307	8230	9076
				BsiHKA I	(5)	1222	1412	6030	7285
						8974			
				BsiW I	(1)	51			
				Bsm I	(2)	5308	6112		
				BsmA I	(7)	959	2322	3220	4127
						5024	5407	7922	
				BsmF I	(26)	281	291	410	609
						681	745	1260	1792
						2064	2215	2383	2962
						3113	3281	3869	4020
						4188	4766	4917	5085
						5430	5513	5687	5806
						5816	9251		
				BsoF I	(66)	14	326	329	336
						387	454	521	863

The following enzymes do not cut in PNC5:

Age I	Bgl II	BsaB I	BsmB I	Bst1107 I
Bsu36 I	Eco72 I	Fse I	Hpa I	Mun I
Nhe I	Nru I	PflM I	Pme I	Pml I
PpuM I	Spe I	Xca I	Xcm I	Xmn I

PNC5: sites sorted by name:

Aat II	(16)	2014	2067	2150	2336				
		2912	2965	3048	3234				
		3819	3872	3955	4141				
		4716	4769	4852	5038				
Acc I	(1)	4292							
Acc65 I	(2)	565	2480						
Aci I	(125)	315	336	348	370				
		393	578	763	775				
		784	796	806	817				
		863	1018	1081	1175				
		1239	1340	1343	1583				
		1623	1628	1678	1694				
		1720	1776	1835	1889				
		1893	1947	1975	1987				
		2001	2168	2259	2292				
		2396	2417	2511	2520				
		2746	2770	2845	2873				
		2885	2899	3066	3157				
		3190	3294	3315	3390				
		3392	3418	3427	3653				
		3677	3752	3780	3792				
		3806	3973	4064	4097				
		4201	4222	4315	4324				
		4550	4574	4649	4677				
		4689	4703	4870	4961				
		4994	5098	5119	5706				
		5729	5751	5763	5784				
		5968	6001	6035	6243				
		6256	6405	6512	6517				
		6565	6602	6657	6760				
		6816	6826	6850	6893				
		6900	6921	7012	7040				
		7167	7186	7307	7417				
		7552	7561	7923	8014				
		8205	8251	8518	8538				
		8706	8803	8815	8882				
		8945	9141	9144	9222				
		9269							
Afe I	(1)	3406							
Afl II	(1)	963							
Afl III	(2)	4303	6967						
Aha II	(19)	1109	1811	2011	2064				
		2147	2333	2909	2962				
		3045	3231	3816	3869				
		3952	4138	4713	4766				
		4849	5035	8749					
Ahd I	(1)	7860							
Alu I	(30)	16	591	879	933				
		1215	1673	2455	3353				
		3386	4260	5157	5394				
		6028	6154	6197	6632				
		6727	6791	6909	7135				
		7225	7271	7528	8049				
		8149	8212	8459	8889				
		9003	9375						
Alw I	(24)	434	1287	1354	1533				
		2470	2488	2499	2790				
		3368	3406	3697	4275				
		4594	5172	5666	6170				
		7529	7615	7615	7712				

		1018	1070	1081	1171		1450	1528	2476	2494
		1176	1213	1254	1341		2526	2785	3374	3412
		1344	1347	1583	1679		3433	3692	4281	4330
		1720	1734	1835	1890		4589	5178	5215	5672
		1893	2511	3418	4315		6165	7535	7610	7621
		5547	5646	5713	5764		7629	7707	7719	7824
		5771	5774	6036	6155		8165	8183	8229	8712
		6257	6288	6291	6406		8895	9075	9085	9160
		6518	6565	6792	6873		9178	9406	9427	9465
		6891	6894	7012	7167	DpnII (40)	427	1280	1358	1439
		7310	7375	7378	7584		1448	1526	2474	2492
		7912	8251	8278	8373		2524	2783	3372	3410
		8516	8601	8645	8661		3431	3690	4279	4328
		8816	8883	9033	9142		4587	5176	5213	5670
		9222	9319				6163	7533	7608	7619
Bsp120 I (1)		5588					7627	7705	7717	7822
Bsp1286 I (1)		1412					8163	8181	8227	8710
BspH I (1)		7687					8893	9073	9083	9158
BspM I (4)		996	1377	1827	9042		9176	9404	9425	9463
BspM II (2)		6413	6425			Dra I (4)	5209	5442	7726	7745
Bsr I (25)		801	1052	1253	2185	Dra III (3)	8404	8832	9452	
		2485	2493	3083	3990	Drd I (4)	952	1136	6046	7075
		4887	5465	5575	6396	Dsa I (12)	502	526	822	1541
		6768	7374	7387	7501		2249	3147	3390	4054
		7907	8025	8068	8335		4951	8403	8617	8988
		8430	8495	9233	9329	Eae I (14)	505	1015	1189	1580
		9351					1607	1832	1890	2508
BsrB I (7)		350	1722	1776	1889		3415	4312	6344	6806
		5751	6659	6900			8248	8782		
BsrD I (5)		1342	7921	8095	9044	Eag I (3)	1015	1890	3415	
		9337				Ear I (3)	1453	1663	6851	
BsrG I (1)		4297				Eco47 III (1)	3406			
BssH II (4)		1506	2499	6606	9419	Eco57 I (4)	1254	1686	7514	8840
BssS I (2)		1701	7140			EcoN I (1)	5583			
BstB I (1)		1791				EcoO109 I (1)	5588			
BstE II (1)		8855				EcoR I (1)	4285			
BstN I (32)		291	477	629	684	EcoR II (32)	289	475	627	682
		701	1496	1979	2172		699	1494	1977	2170
		2596	2781	2877	3070		2594	2779	2875	3068
		3503	3688	3784	3977		3501	3686	3782	3975
		4400	4585	4681	4874		4398	4583	4679	4872
		5493	5551	5623	5809		5491	5549	5621	5807
		6387	6554	6707	6995		6385	6552	6705	6993
		7116	7129	8349	8926		7114	7127	8347	8924
BstU I (27)		1175	1476	1508	1949	EcoR V (1)	5839			
		2501	2847	3392	3754	Ehe I (1)	1110			
		4305	4651	5968	6074	Esp I (1)	9004			
		6245	6405	6608	6814	Fnu4H I (66)	14	326	329	336
		6816	7014	7595	7925		387	454	521	863
		8609	8882	8947	9010		1018	1070	1081	1171
		9303	9419	9421			1176	1213	1254	1341
BstX I (2)		1830	5599				1344	1347	1583	1679
BstY I (16)		1280	1526	2474	2492		1720	1734	1835	1890
		2783	3372	3410	3690		1893	2511	3418	4315
		4279	4587	5176	7608		5547	5646	5713	5764
		7619	7705	7717	9176		5771	5774	6036	6155
Cac8 I (61)		333	384	391	467		6257	6288	6291	6406
		642	661	714	733		6518	6565	6792	6873
		1003	1189	1408	1474		6891	6894	7012	7167
		1480	1508	1512	1553		7310	7375	7378	7584
		1557	1611	1975	2168		7912	8251	8278	8373
		2501	2554	2731	2735		8516	8601	8645	8661
		2873	3066	3461	3638		8816	8883	9033	9142
		3642	3780	3973	4358		9222	9319		
		4535	4539	4677	4870	Fok I (21)	307	359	766	1433
		5634	5710	5717	5768		1458	2755	3662	4559
		6015	6112	6199	6353		5411	5738	5790	6292
		6604	6608	6760	6789		6441	6573	7826	8007
		6898	6984	7021	7581		8294	8426	8579	8823
		7972	8605	8782	8887		9324			
		9067	9236	9342	9346	Fsp I (2)	1211	8082		
		9421				Gdi II (15)	506	1014	1016	1579
Cfr10 I (9)		382	1428	1609	5715		1606	1831	1889	1891
		6466	6490	7940	9291		2507	3414	3416	4311
		9344					6807	8247	8781	
Cla I (1)		3379				Gsu I (2)	7931	8946		
Csp6 I (36)		52	566	1414	2107	Hae I (10)	498	531	914	1191
		2132	2187	2220	2271		6346	6382	6982	6993
		2428	2481	2487	3005		7445	9414		
		3030	3085	3118	3169	Hae II (11)	364	1112	3408	5741
		3326	3912	3937	3992		6204	6523	6845	7215
		4025	4076	4233	4298		8762	9192	9341	
		4809	4834	4889	4922	Hae III (39)	498	507	531	856
		4973	5130	5197	8341		862	871	914	1017
		8574	8787	8795	9278		1191	1582	1609	1834
Dde I (14)		573	875	1772	2656		1892	1973	2166	2510
		2765	3563	3672	4460		2871	3064	3417	3778
		4569	6042	7242	7651		3971	4314	4675	4868
		7817	9004				5590	6346	6382	6808
Dpn I (40)		429	1282	1360	1441		6982	6993	7011	7445

NspH I	(9)	88	663	735	1514
		2737	3644	4541	6114
		6971			
Pac I	(1)	3400			
PaeR7 I	(1)	9491			
Pal I	(39)	498	507	531	856
		862	871	914	1017
		1191	1582	1609	1834
		1892	1973	2166	2510
		2871	3064	3417	3778
		3971	4314	4675	4868
		5590	6346	6382	6808
		6982	6993	7011	7445
		7903	7983	8250	8784
		8818	9348	9414	
Ple I	(1)	7346			
Psp1406 I	(1)	8086			
PspA I	(4)	339	403	5694	5758
Pst I	(4)	6	471	1162	5634
Pvu I	(2)	8230	9076		
Pvu II	(3)	591	1215	6791	
Rsa I	(36)	53	567	1415	2108
		2133	2188	2221	2272
		2429	2482	2488	3006
		3031	3086	3119	3170
		3327	3913	3938	3993
		4026	4077	4234	4299
		4810	4835	4890	4923
		4974	5131	5198	8342
		8575	8788	8796	9279
Rsr II	(3)	355	1625	5743	
Sac I	(1)	6030			
Sac II	(1)	3393			
Sal I	(1)	4291			
Sap I	(3)	1453	1663	6851	
Sau3A I	(40)	427	1280	1358	1439
		1448	1526	2474	2492
		2524	2783	3372	3410
		3431	3690	4279	4328
		4587	5176	5213	5670
		6163	7533	7608	7619
		7627	7705	7717	7822
		8163	8181	8227	8710
		8893	9073	9083	9158
		9176	9404	9425	9463
Sau96 I	(20)	355	1625	1972	2165
		2870	3063	3777	3970
		4674	4867	5588	5589
		5743	7902	7981	7998
		8220	8494	9135	9347
Sca I	(1)	2488			
ScrF I	(48)	291	340	341	404
		405	477	629	684
		701	1113	1273	1496
		1979	2172	2596	2781
		2877	3070	3503	3688
		3784	3977	4400	4585
		4681	4874	5413	5493
		5551	5562	5623	5695
		5696	5759	5760	5809
		6387	6554	6599	6707
		6995	7116	7129	7347
		8043	8349	8390	8926
Sec I	(44)	289	290	339	340
		403	476	502	526
		627	699	822	857
		866	915	1272	1541
		2249	2594	3147	3390
		3501	4054	4398	4951
		5412	5560	5621	5694
		5757	5758	5807	5808
		6275	6386	6706	7127
		8380	8403	8586	8617
		8924	8988	9127	9469
SfaN I	(29)	380	671	743	1068
		1323	1407	1471	1539
		1746	2247	2652	2734
		3145	3559	3641	4052
		4456	4538	4949	5279
		5717	6165	6220	6454
		6552	7063	8115	8308
		8600			
Sfc I	(8)	2	467	1158	5630
		7232	7423	8101	8950
Sfi I	(2)	504	868		
Sma I	(4)	341	405	5696	5760
SnaB I	(5)	2229	3127	4034	4931
		5196			
Sph I	(7)	663	735	1514	2737
		3644	4541	6114	

Spl I	(1)	51			
Srf I	(2)	405	5696		
Ssp I	(2)	5438	6098		
Stu I	(2)	498	914		
Sty I	(11)	526	822	915	1541
		2249	3147	4054	4951
		8380	9127	9469	
Swa I	(1)	5209			
Taq I	(23)	108	958	1222	1378
		1402	1438	1600	1791
		2533	3379	3440	4292
		4337	5183	7067	8364
		8624	8724	8755	8767
		9061	9076	9492	
Tfi I	(10)	937	1594	1728	5185
		5575	6069	6330	6802
		6942	8939		
Tsp45 I	(10)	46	1229	1535	5930
		5990	8116	8327	8392
		8855	8957		
Tth111 I	(1)	1227			
Tth111 II	(12)	198	1545	2556	3463
		4299	4360	6025	7556
		7565	7595	8612	8619
Vsp I	(5)	122	6503	6738	6797
		8032			
Xba I	(1)	5188			
Xho I	(1)	9491			
Xho II	(16)	1280	1526	2474	2492
		2783	3372	3410	3690
		4279	4587	5176	7608
		7619	7705	7717	9176
Xma I	(4)	339	403	5694	5758
Xma III	(3)	1015	1890	3415	

Site usage in PNC5:

Aat II	G,ACGT`C	16	Acc I	GT`MK,AC	1
Acc65 I	G`GTAC,C	2	Acc II	C`CG,C	125
Afe I	AGC GCT	1	Afl II	C`TTAA,G	1
Afl III	A`CRYG,T	2	Age I	A`CCGG,T	-
Aha II	GR`CG,YC	19	Ahd I	GACNN,N`NNGTC	1
Alu I	AG CT	30	Alw I	GGATC 8/9	24
AlwN I	CAG,NNN`CTG	4	Apa I	G,GGCC`C	1
ApaL I	G`TGCA,C	2	Apo I	R`AATT,Y	5
Asc I	GG`CGCG,CC	1	Ase I	AT`TA,AT	5
Asp718	G`GTAC,C	2	Ava I	C`YGR,G	8
Ava II	G`GWC,C	7	Avr II	C`CTAG,G	1
BamH I	G`GATC,C	1	Ban I	G`GYRC,C	13
Ban II	G,RCYC`C	8	Bbe I	G,GGCC`C	1
Bbs I	GAAGAC 8/12	3	Bbv I	GCAGC 13/17	19
Bbv II	GAAGAC 7/11	3	Bcl I	T`GATC,A	4
Bcn I	CC,S`GG	16	Bfa I	C`TA,G	22
Bgl I	GCCN,NNN`NGGC	16	Bgl II	A`GATC,T	-
Blp I	GC`TNA,GC	1	Bpm I	CTGGAG 22/20	2
Bsa I	GGTCTC 7/11	2	BsaA I	YAC GTR	9
BsaB I	GATNN NNATC	-	BsaH I	GR`CG,YC	19
BsaJ I	C`CNNG,G	44	BsaW I	W`CCGG,W	10
BseR I	GAGGAG 16/14	1	Bsg I	GTGGAG 22/20	1
BsiC I	TT`CG,AA	1	BsiE I	CG,RY`CG	8
BsiHKA I	G,WGCW`C	5	BsiW I	C`GTAC,G	1
Bsm I	GAATG,C 7	2	BsmA I	GTCTC`/9	7
BsmB I	CGTCTC 7/11	-	BsmF I	GGGAC 15/19	26
BsoF I	GC`N,GC	66	Bsp120 I	G`GGCC,C	1
Bsp1286 I	G,DCGC`C	1	BspH I	T`CATG,A	1
BspM I	ACCTGC 10/14	4	BspM II	T`CCGG,A	2
Bsr I	ACT,GG`	25	BsrB I	GAG CGG	7
BsrD I	GCAATG, 8	5	BsrG I	T`GTAC,A	1
BssH II	G`CGCG,C	4	BssS I	C`TGT,G	2
Bst1107 I	GTA TAC	-	BstB I	TT`CG,AA	1
BstE II	G`GTNAC,C	1	BstN I	CC`W,GG	32
BstU I	CG CG	27	BstX I	CCAN,NNNN`NTGG	2
BstY I	R`GATC,Y	16	Bsu36 I	CC`TNA,GG	-
Cac8 I	GCN NGC	61	Cfr10 I	R`CCGG,Y	9
Cla I	AT`CG,AT	1	Csp6 I	G`TA,C	36
Dde I	C`TNA,G	14	Dpn I	GA TC	40
DpnII	`GATC,	40	Dra I	TTT AAA	4
Dra III	CAC,NNN`GTG	3	Drd I	GACNN,NN`NNGTC	4
Dsa I	C`CRYG,G	12	Eae I	Y`GGCC,R	14
Eag I	C`GGCC,G	3	Ear I	CTCTTC 7/10	3
Eco47 III	AGC GCT	-	Eco57 I	CTGAAG 21/19	4
Eco72 I	CAC GTG	1	EcoN I	CCTNN`N,NNAGG	1
EcoO109 I	RG`GNC,CY	1	EcoR I	G`AATT,C	1
EcoR II	`CCWGG,	32	EcoR V	GAT ATC	1
Ehe I	GGC GCC	1	Esp I	GC`TNA,GC	1
Fnu4H I	GC`N,GC	66	Fok I	GGATG 14/18	21
Fse I	GG,CCGG`CC	-	Fsp I	TGC GCA	2
Gdi II	`YGGC,CG	15	Gsu I	CTGGAG 21/19	2
Hae I	WGG CCW	10	Hae II	R,GGC`Y	11
Hae III	GG CC	39	Hga I	GACGC 9/14	12
HgiA I	G,WGCW`C	5	HgiE II	ACCNNNNNGGT -1/134	2
Hha I	G,CG`C	44	Hinc II	GTY RAC	2
Hind II	GTY RAC	2	Hind III	A`AGCT,T	2
Hinf I	G`ANT,C	21	HinI I	GR`CG,YC	19
HinP I	G`CG,C	44	Hpa I	GTT AAC	-
Hpa II	C`CG,G	42	Hph I	GGTGA 12/11	14
Kas I	G`CGCC,C	1	Kpn I	G,GTAC`C	2
Mae I	C`TA,G	22	Mae II	A`CG,T	42
Mae III	`GTNAC,	36	Mbo I	`GATC,	40

Mbo II	GAAGA 12/11	16	Mlu I	A`CGCG,T	1
Mme I	TCCRAC 25/23	3	Mnl I	CCTC 10/10	63
Msc I	TGG CCA	2	Mse I	T`TA,A	28
Msl I	CAYNN NNRTG	11	Msp I	C`CG,G	42
MspA1 I	CMG CKG	12	Mun I	C`AATT,G	-
Nae I	GCC GGC	4	Nar I	GG`CG,CC	1
Nci I	CC`S,GG	16	Nco I	C`CATG,G	7
Nde I	CA`TA,TG	5	NgoM I	G`CCGG,C	4
Nhe I	G`CTAG,C	-	Nla III	,CATG`	39
Nla IV	GGN NCC	26	Not I	GC`GGCC,GC	1
Nru I	TCG CGA	-	Nsi I	A,TGCA`T	3
Nsp7524 I	R`CATG,Y	9	NspB II	CMG CKG	12
NspH I	R,CATG`Y	9	Pac I	TTA,AT`TAA	1
Paer7 I	C`TCGA,G	1	Pal I	GG CC	39
Pf1M I	CCAN,NNN`NTGG	-	Ple I	GAGTC 9/10	1
Pme I	CTTT AAAC	-	Pml I	CAC GTG	-
PpuM I	RG`GWC,CY	-	Psp1406 I	AA`CG,TT	1
PspA I	C`CCGG,G	4	Pst I	C,TGCA`G	4
Pvu I	CG,AT`CG	2	Pvu II	CAG CTG	3
Rsa I	GT AC	36	Rsr II	CG`GWC,CG	3
Sac I	G,AGCT`C	1	Sac II	CC,GC`GG	1
Sal I	G`TCGA,C	1	Sap I	GCTCTC 8/11	3
Sau3A I	`GATC,	40	Sau96 I	G`GNC,C	20
Sca I	AGT ACT	1	ScrF I	CC`N,GG	48
Sec I	C`CNNG,G	44	SfaN I	GCATC 9/13	29
Sfc I	C`TRYA,G	8	Sfi I	GGCCN,NNN`NGGCC	2
Sma I	CCC GGG	4	SnaB I	TAC GTA	5
Spe I	A`CTAG,T	-	Sph I	G,CATG`C	7
Sp1 I	C`GTAC,G	1	Srf I	GCCC GGGC	2
Ssp I	AAT ATT	2	Stu I	AGG CCT	2
Sty I	C`CWWG,G	11	Swa I	ATTT AAAT	1
Taq I	T`CG,A	23	Tfi I	G`AWT,C	10
Tsp45 I	`GTSAC,	10	Tth111 I	GACN`N,NGTTC	1
Tth111 II	CAARCA 16/14	12	Vsp I	AT`TA,AT	5
Xba I	T`CTAG,A	1	Xca I	GTA TAC	-
Xcm I	CCANNNN,N`NNNNTGG-	-	Xho I	C`TCGA,G	1
Xho II	R`GATC,Y	16	Xma I	C`CCGG,G	4
Xma III	C`GGCC,G	3	Xmn I	GAANN NNTTC	-